Hickory Shad (Alosa mediocris) Population Identification Using Geometric Morphometrics and

Otolith Shape

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Hickory Shad Alosa mediocris (Mitchill 1814) is an anadromous fish species with a poorly documented life history and stock status, and it is unknown if the species exhibits natal fidelity. I used otolith shape and body shape (geometric morphometrics) to explore the possibility of natal fidelity and, if so, whether these two methods could discriminate among spawning populations range-wide. Analyses of 757 Hickory Shad photographs from 21 watersheds determined significant differences (p<0.0001) in body shape between male and female samples, with body depth comprising most of the variability by sex. Therefore, all subsequent analyses were run on male and female samples separately. Out of 153 pairwise comparisons of females by watersheds, 99 (64.7%) resulted in significant differences (p < 0.05); 43 (28.1%) of those were highly significant (p<0.0001). The same watershed comparisons for males resulted in 102 (66.7%) significant differences (p<0.05), 44 (28.8%) of which were highly significant. The most heavily weighted landmark positions were PC1 = y13 and y14, PC2 = y6and y7, and PC3 = x13 and x14. Landmarks 6 and 7 are the origin and insertion of the dorsal fin and landmarks 13 and 14 are the insertion and origin of the pelvic fin. More than half of the body shape comparisons by watershed were significantly different suggesting that homing to natal

tributaries is plausible. However, inconsistency and varying results led to the conclusion that body shape analysis was not dependable for differentiating spawning populations of Hickory Shad; small sample sizes were likely contributing factors. Otolith shape analysis of 696 right sagittal otolith photographs from 22 watersheds determined highly significant differences by watershed ($F_{21, 674} = 3.4242$, p=0.001), and between Virginia and North Carolina watersheds (F_{6} . ₆₈₉=5.0122, p=0.001). Most variation was attributed to the antirostrum, excisura major, and dorsal side of the rostrum. Out of 231 total pairwise comparisons of watersheds (sexes combined), 148 (64.1%) were significantly different (p<0.05), 55 (23.8%) of which were highly significant (p=0.001). The fact that more than half of the otolith shape comparisons were significantly different again suggests that homing to natal tributaries is plausible but the varying results led to the conclusion that otolith shape alone was not reliable for differentiating spawning populations of Hickory Shad. Additional sample sizes from each watershed, along with comparing the same-aged fish and a standardized sample size and timing within the spawning season, may help in differentiating spawning populations of Hickoy Shad using otolith shape and body shape.

Hickory Shad (*Alosa mediocris*) Population Identification Using Geometric Morphometrics and Otolith Shape

A Thesis

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M.S. Biology

By

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TABLE OF CONTENTS

LIST OF TABLES		vii
LIST OF FIGURES		Х
CHAPTER 1: INTRO	DDUCTION, OBJECTIVES, AND LITERATURE REVIEW	1
Problem State	ement	1
Literature Re	view	3
Goals and Ob	jectives	10
Literature Cit	ed	12
CHAPTER 2: BODY SHAPE ANALYSIS USING GEOMETRIC MORPHOMETRICS .		18
Abstract		18
Introduction		21
Methods		24
Results		27
Discussion		34
Literature Cit	ed	40

CHAPTER 3: OTOL	ITH SHAPE ANALYSIS USING ShapeR	62
Abstract		62

Introduction		65
Methods		67
Results		69
Discussion		71
Literature Cit	ed	77

CHAPTER 4: CONCLUSIONS AND RECOMMENDATIONS	
Literature Cited	98
APPENDIX A: IACUC APPROVAL	100
APPENDIX B: DATA	101
APPENDIX C: R SCRIPT	228

LIST OF TABLES

2-1.	Table summarizing sample sizes from each watershed classified by specimen sex use	
	geometric morphometric study. Tributaries listed with parent river in parenthesis.	43
2-2.	Number and location of 16 landmarks used in this study.	44
2-3.	Table of watershed abbreviations used in the table summarizing results of DFA	44
2-4.	Eigenvalues, percent of variance, and cumulative percent of variance for PCA of sex	
	using geometric morphometrics	45
2-5.	Weight of each landmark for each of the first three principle components of PCA of se	Х
	using geometric morphometrics	45
2-6.	Eigenvalues, percent of variance, and cumulative percent of variance for PCA of North	1
	Carolina vs. Virginia female samples using geometric morphometrics	46
2-7.	Weight of each landmark for each of the first three principle components of PCA of	
	North Carolina vs. Virginia female samples using geometric morphometrics	46
2-8.	Eigenvalues, percent of variance, and cumulative percent of variance for PCA of North	1
	Carolina vs. Virginia male samples using geometric morphometrics	47
2-9.	Weight of each landmark for each of the first three principle components of PCA of	
	North Carolina vs. Virginia male samples using geometric morphometrics	47
2-10.	P values determined using DFA on females testing pairwise differences in body shape	by
	watershed.	48
2-11.	P values determined using DFA on males testing pairwise differences in body shape by	у
	watershed.	49
2-12.	Table summarizing results of DFA of females. The first number in each cell is the percent	ent
	of correct classification for the x axis watershed, the second number is the percent of	

- 2-14. Adjusted P-values using Benjamini and Hochberg's FDR-controlling procedure. P-values determined using DFA on females testing pairwise differences in body shape by watershed. Watershed abbreviations as in Table 2.3; watersheds listed in latitudinal order (north to south).
- 2-15. Adjusted P-values using Benjamini and Hochberg's FDR-controlling procedure. P-values determined using DFA on males testing pairwise differences in body shape by watershed. Watershed abbreviations as in Table 2.3; watersheds listed in latitudinal order (North to South).
 53
- 3-2. Table summarizing p value results of pairwise comparisons of watersheds using an
 ANOVA like permutation test. Sample size (n) is listed above and to the left of watershed
 abbreviations.
- 3-3. Table summarizing Benjamini and Hochberg method adjusted P-value results of pairwise comparisons of watersheds using an ANOVA like permutation test. Sample size (n) is listed above and to the left of watershed abbreviations.
 81

3-4.	The latitude of the mouth of each <i>watershed</i> and the proportion of postrostrum tails	
	counted.	82

LIST OF FIGURES

1-1.	. Image of an adult male Hickory shad #826. Specimen captured in Swift Creek on	
	20, 2018	16
1-2.	Image of an adult male Hickory shad #826 otolith. Specimen captured in Swift Creek	on
	March 20, 2018	16
2-1.	Map displaying relative location of rivers included in this body shape study as well as	
	collection sites of Hickory Shad. Tributaries Contentnea Creek, Pitchkettle Creek, Swi	ft
	Creek (Neuse), Swift Creek (Tar), and Herring Creek not shown. Revised after Melvin	et
	al. 1992	54
2-2.	Hickory Shad number 633 with the 16 landmarks digitized and ruler of scale	55
2-3.	Procrustes fit of all 757 Hickory Shad used in these analyses	55
2-4.	Discriminant function scores plotted for females vs. males	56
2-5.	Cross-validation scores plotted for females vs. males	56
2-6.	Principle components 1 and 2 plotted with males in blue and females in red	57
2-7.	Female discriminant function scores with North Carolina in red and Virginia in blue.	58
2-8.	Female cross-validation scores with North Carolina in red and Virginia in blue	58
2-9.	Male discriminant function scores with North Carolina in red and Virginia in blue.	59
2-10.	Male cross-validation scores with North Carolina in red and Virginia in blue	59
2-11.	Principle components 1 and 2 of female Hickory Shad plotted by state with 90%	
	confidence ellipses	60
2-12.	Principle components 1 and 2 of male Hickory Shad plotted by state with 90%	
	confidence ellipses.	60

3-1.	Map displaying relative location of rivers included in this otolith shape study as well as	3
	collection sites of Hickory Shad. Neuse tributaries Contentnea Creek, Pitchkettle Creek	ζ,
	and Swift Creek not shown. Revised after Melvin et al. 1992.	83
3-2.	Photograph of the right sagittal otolith of an adult Hickory Shad, fish number 879	
	captured in Contentnea Creek	84
3-3.	Photograph of the right sagittal otolith of an adult Hickory Shad, fish number 879	
	captured in Contentnea Creek with outline generated in R Studio using the ShapeR	
	package	84
3-4.	Labeled diagram of the distal surface anatomy of adult Hickory Shad otoliths without	
	(top) and with (bottom) a postrostrum tail.	85
3-5.	Average shape of otolith Wavelet coefficients from each state sampled	86
3-6.	Average shape of otolith Wavelet coefficients from each watershed sampled	86
3-7.	Average shape of otolith Wavelet coefficients from each watershed sampled in North	
	Carolina	87
3-8.	Average shape of otolith Wavelet coefficients from the Neuse River and its tributaries	
	Contentnea Creek, Pitchkettle Creek, and Swift Creek.	87
3-9.	Mean plus and minus standard deviation (sd) of the Wavelet coefficients for all combin	ied
	otoliths plotted with dot and error bars. The proportion of variance among groups or the	e
	intraclass correlation (ICC) plotted with a solid black line. The horizontal axis shows	
	angle in degrees (°) based on polar coordinates where the centroid of the otolith is the	
	center point of the polar coordinates	88
3-10.	Otolith shape of samples plotted from 22 watersheds using Canonical analysis of	
	Principal Coordinates with the Wavelet coefficients. Canonical scores on the first two	

discriminating axes CAP1 and CAP2 are shown. Black letters represent the mean	
canonical value for each watershed and smaller letters represent individual fish showing	ng
the first letter of each population. Interval surrounding the mean canonical values pres	ent
95% confidence intervals	89

CHAPTER 1: INTRODUCTION, OBJECTIVES, AND LITERATURE REVIEW

Problem Statement

The clear definition and identification of fish stocks as management units is a significant problem that has plagued fisheries biologists around the world. A particularly vexing aspect of this problem is the identification of stocks among fish species for which detailed life history traits are difficult to know, either because their ranges are broad or their migratory behavior is complex, or both. The Hickory Shad *Alosa mediocris* represents a species with both a broad range and a complex migratory behavior.

Stocks are defined as arbitrary groups of a fish species large enough to be essentially selfreproducing, with members of each group having similar life history characteristics (Hilborn and Walters 1992). The stock concept is the intersection of biological organization and human activities (Secor 1999); i.e., a management unit in fisheries management. The management unit might incorporate all the individual populations of a species within a large waterbody, such as those stocks designated for the anadromous Striped Bass *Morone saxatilis* (Walbaum, 1792) in Chesapeake Bay, Hudson River, and Albemarle/Roanoke River; all Striped Bass in oceans waters are designated the Atlantic coastal stock (Essig et al., in press). Alternately, a stock management unit might represent only one tributary of a larger waterbody if the management unit is by individual populations (e.g., the Nanticoke River or the Potomac River population of Striped Bass). Species that exhibit fidelity to a natal watershed, such as species of the Salmonidae family in the Pacific Northwest, may develop and maintain population spatial structure via genetic isolation, which leads to unique populations throughout the range (Smedbol and Wroblewski 2002). It is important to understand the population structure of a species because different populations may be exploited in different ways and experience different environmental conditions (Begg and Waldman 1999).

The Hickory Shad *Alosa mediocris* (Mitchill, 1814) is an anadromous member of the Clupeidae family with a freshwater range from the Schuylkill River in Pennsylvania (Perillo and Butler 2009) to the St. Johns River in Florida (Harris et al. 2007). This extensive range makes the Hickory Shad a multi-jurisdictional species for management purposes. Hickory Shad are currently managed under Amendment 3 of the Atlantic States Marine Fisheries Commission (ASMFC) Interstate Fishery Management Plan (IFMP) for Shad and River Herring. However, this management plan only incorporates biological information for the American Shad *Alosa sapidissima* (Wilson, 1811) and river herring (Alewife *Alosa pseudoharengus* (Wilson, 1811) and Blueback Herring *A. aestivalis* (Mitchill, 1814) (ASMFC 2010). The American Shad has been applied as a model species to Hickory Shad management (Harris et al. 2007) but many aspects of American Shad life history applied to Hickory Shad are more closely related to other species in the genus *Alosa* -- the Blueback Herring and Alewife -- than to the American Shad (Bloom and Lovejoy 2014).

The ASMFC Fishery Management Plan requires information more specific to Hickory Shad life history to better manage the species; both the Commission and the Mid-Atlantic Council have requested life history studies as high priority for years (ASMFC 2010). The Hickory Shad is considered a "largely understudied species" and more research is needed on its fundamental biology and life history (Rulifson 1994; Waldman and Limburg 2003; ASMFC 2010).

2

Understanding the migration habits and population dynamics would greatly aid the management of the species and help set specific limits for commercial and recreational harvest. State agencies believe that Hickory Shad exhibit philopatry or natal homing, though this assumption has not been confirmed (Batsavage and Rulifson 1998). Tagging studies of American Shad have found a high degree of fidelity to natal streams (Melvin et al. 1986). If Hickory Shad also exhibit fidelity to natal watersheds, then it would be helpful in calculating stock size and harvest mortality of populations.

Literature Review

Professor Samuel L. Mitchill first described the Hickory Shad Alosa mediocris in 1814 (Mitchill 1814). This description is presumed to be based on a specimen captured in New York (Jenkins and Burkhead 1993), likely from the Hudson River due to its proximity to Columbia University where Mitchill was on the faculty. The Hickory Shad is an anadromous species described in the early literature as having an Atlantic Ocean range from the Bay of Fundy, Canada, south to Florida's eastern coast (Mansueti 1962). Ocean dwelling adults enter into tidal freshwater to spawn between February and June, with later entry correlating with higher latitudes (Murauskas and Rulifson 2011). Spawning rivers range from Schuylkill River, a tributary of the Delaware River (Perillo and Butler 2009) to the St. Johns River in Florida (Harris et al. 2007). However, there is some uncertainty regarding the northern range limit of Hickory Shad spawning populations. Hildebrand and Schroeder (1928) hypothesized spawning as far north as Maine. U.S. Fish and Wildlife Service (USFWS) biologists suspect that a spawning population may exist in Wethersfield Cove of the Connecticut River near Wethersfield, Connecticut where adult Hickory Shad have been collected during spring sampling (Ken Sprankle, USFWS, personal communication). Rulifson (1994) reported that Connecticut is the northern extent of states with

³

Hickory Shad present based on state fisheries biologists' responses to questionnaires. Some of these northern accounts of Hickory Shad may be misidentifications with morphologically similar species, such as the American Shad. These accounts may also be a result of Hickory Shad wandering into bays where they were captured, but not actively spawning. It is hypothesized that water temperature cues the timing of annual migration and spawning of Hickory Shad (Mansueti 1962). Other proposed cues to initiate spawning include photoperiod, current velocity, and turbidity (Leggett and Whitney 1972).

Natal homing has not been researched for Hickory Shad, but it is hypothesized they home to natal watersheds based on results of an American Shad mark and recapture study in the Annapolis River, Nova Scotia, in which tag returns yielded a rate of 97% fidelity to the watershed (Melvin et al. 1986). The more extensively studied and closely related American Shad is often applied as a model species to Hickory Shad management (Harris et al. 2007). However, many aspects of American Shad life history that have been applied to Hickory Shad have not been supported by literature. Natal homing or philopatry is observed in many anadromous species, but the fidelity of natal homing varies between species and within species by watershed (McDowall 2001). Also, a recent genetic study found that Hickory Shad are more closely related to other species in the genus *Alosa* than they are to American Shad (Bloom and Lovejoy 2014). Our study aims to provide additional information range-wide about the Hickory shad to reduce the need for reliance on American Shad life history information for fishery management purposes.

Hickory Shad is a "largely understudied species" and more research should be focused on its fundamental biology and life history (Rulifson et al. 1982; Rulifson 1994; Waldman and Limburg 2003; ASMFC 2010). However, past research has provided us with some knowledge of

4

Hickory Shad life history. They spawn in the freshwater main channels and tributaries of rivers throughout the range (Burdick and Hightower 2006). A study in the Roanoke River found that Hickory Shad spawning took place at current velocities of at least 0.1 m/s and on all substrates except those dominated by silt (Harris and Hightower 2011). Once spawning begins, females produce transparent, spherical, relatively non-adhesive eggs that are 1.49 mm in diameter (Mansueti 1962); however, USFWS staff at the Harrison Lake National Fishery (HLNFH) treat fertilized Hickory Shad eggs with a mild solution to minimize initial adhesive qualities to allow development in McDonald hatching jars (M. Odum, HLNFH, personal communication). Fertilized eggs are semi-demersal in slow-moving water but become buoyant in fast current (Mansueti 1962). Individual fecundity in the Rappahannock and James rivers ranged from 46,600 to 847,300 oocytes (Watkinson 1999). Hatching occurs approximately 48-76 hours post fertilization, and duration of the embryonic stage may be controlled by temperature (Mansueti 1962). Larvae are transferred by water currents downstream to estuaries, which provide important nursery habitat for larval and juvenile Hickory Shad and other commercially and recreationally important fishes (Rozas and Hackney 1983). After leaving estuaries, they travel out into the Atlantic Ocean, although the timing and oceanic movements of this migration are largely unknown (Rulifson et al. 1982; Rulifson 1994).

Adult Hickory Shad mature between 2-4 years of age and most fish live a maximum of 7 years (Jenkins and Burkhead 1993), although some fish in Maryland have been aged up to 9 years (MDDNR 2016). A study in the Rappahannock and James rivers found that most males were mature by age 2, and most females were mature by age 3 (Watkinson 1999). No validated aging method exists for Hickory Shad, but researchers have used scales and otoliths to estimate specimen age (Street and Adams 1969; Pate 1972; Harris et al. 2007; Murauskas and Rulifson

2011). Hickory Shad can reach a maximum standard length of 600 mm (Jenkins and Burkhead 1993).

Hickory Shad, like the other anadromous alosines, are important to the food webs of estuarine and riverine systems. Hickory Shad are primarily piscivorous, but also consume invertebrates (Harris et al. 2007). Some investigators claim that Hickory Shad do not feed during the upstream spawning migration; however Harris et al. (2007) reported that adults in the St. Johns River, Florida fed mainly on fish from genera *Dorosoma*, *Anchoa*, and *Notropis*. Hickory Shad in the Tar/Pamlico River, North Carolina, fed on anchovies *Anchoa* spp., amphipods, and sciaenids during the upstream migration, and Atlantic menhaden *Brevoortia tyrannus* (Latrobe 1802) during the post-spawn emigration period (Murauskas and Rulifson 2011). Hickory Shad also serve as important prey species in freshwater systems. Gut analyses of Striped Bass and invasive Flathead Catfish *Pylodictis olivaris* (Rafinesque, 1818) indicate that they are predators of Hickory Shad (Pine et al. 2005; Overton et al. 2008).

The Hickory Shad is a valued sportfish for recreational anglers during the spring migration into freshwater. However, recreational and commercial landings are not well documented, leaving a knowledge gap surrounding stock status listed as "Unknown" by the ASMFC. Currently in North Carolina, there is no size limit for Hickory Shad. In 1995, the North Carolina Marine Fisheries Commission established a commercial harvest season from January 1 - April 14; after that date it is illegal to take Hickory Shad and American Shad in coastal waters by any method except hook and line through December 31. In 1999, it became illegal to possess more than 10 American Shad and Hickory Shad in aggregate in both coastal and inland waters. Beginning in 2013, a 1-fish American Shad limit within the 10-fish aggregate creel limit was implemented in joint and coastal waters of both the Albemarle Sound/Roanoke River and the

Neuse River in conjunction with the existing 1-fish limits implemented by the NC Wildlife Resources Commission (NCWRC) in the inland waters of those systems. In the Cape Fear River system, both the NCWRC and the NC Division of Marine Fisheries (NCDMF) implemented a 5fish American Shad limit within the aggregate 10-fish creel limit in their respective jurisdictional waters. All these recreational fishing limits have remained unchanged since 2013 (NCDMF and NCWRC 2017).

American Shad are considered to exhibit fidelity to natal streams through mark/recapture studies (Melvin et al. 1986) and genetics (Hasselman et al. 2010) but it is unknown whether Hickory Shad home to natal streams. To my knowledge no external tagging studies have been reported in the literature, and no genetics studies have been conducted to determine relatedness and wandering among watersheds. If Hickory Shad exhibit fidelity, then there are several methods to test the hypothesis, all of which hinge on prevailing environmental conditions and genetics of relatively isolated spawning populations (i.e., little or no wandering) for a spawning population to differentiate from other spawning populations. These methods include, but are not limited to, differences in genetics, meristics, morphology and body shape, otolith shape, and otolith chemistry.

My thesis addresses two components of these discriminatory methods: body shape, and otolith shape (Figure 1-1 and Figure 1-2). Previously, Smith (2018) reported that meristic and morphometric analyses can be used successfully to discriminate among spawning populations. My study, and that of Smith (2018), are two components of a larger research effort funded by the Sport Fish Restoration Act funds through the NCWRC to ascertain the feasibility of discriminating among spawning populations using the five methods mentioned previously. If any, some, or all these methods result in successful discrimination among spawning populations,

⁷

then we will conclude that Hickory shad do exhibit natal fidelity, and any wandering among watersheds during the spawning run is negligible. It also implies that this species is adapted to the environmental conditions of its natal watershed, which should cause fisheries managers to reconsider the current management plans associated with this species and related alosines.

Genetic and environmental factors are well known contributors to the phenotypic expression of body shape in fish (Melvin et al. 1992). Geometric morphometrics may provide a way of differentiating stocks of Hickory Shad due to differences in their genetic and environmental backgrounds. Geometric morphometric analysis of juvenile Blueback Herring and Alewife body shape determined significant differences among capture locations (Rogers 2015). Sub-populations of Banggai Cardinalfish *Pterapogon kauderni* (F.P. Koumans, 1933) were differentiated using a geometric morphometric approach to body shape analysis (Ndobe and Moore 2013). A Pontic Shad *Alosa immaculate* (Bennett, 1835) study reported significant geometric morphometric differences between years of sampling and sexes (Višnjić-Jeftić et al. 2013). Differences between years were head shape and fin position, while differences in sexes was dorsolateral expansion of the midsection. This information was instrumental in developing the methodology for my study of geometric morphometrics of Hickory Shad.

Otolith shape may help differentiate spawning populations of Hickory Shad. Previous studies of Atlantic Herring *Clupea harengus* Linnaeus, 1758 have determined that otolith shape has a significant genetic component and can be useful for studying population dynamics and connectivity (Berg et al. 2018). Another study of Atlantic Herring in Norway found that otolith shape was more similar among neighboring populations, and can be used to determine relative location of origin in semi-closed populations (Libungan et al. 2015). A study of Pacific Herring *Clupea pallasii* Valenciennes 1847 in Mexico concluded that otolith shape is useful in

8

identifying local and regional stocks of the species and could be used to differentiate populations of other species as well (Javor et al. 2011). Rogers (2015) determined that there was no difference in otolith shape of adult Blueback Herring among sampling locations in North Carolina, but that there was a significant difference in otolith shape when comparing Blueback Herring otoliths collected in North Carolina to those collected in New Jersey.

Other anadromous members of the genus *Alosa* native to the U.S. East Coast include American Shad, Blueback Herring, and Alewife. Anadromous fishes provide an important ecosystem service as they transfer marine derived nutrients into freshwater systems (Garman and Macko 1998). The anadromous life history involves energetic tradeoffs. Fish that migrate to sea may grow larger/faster due to more favorable temperatures and access to rich food resources (Gross et al. 1988). Migrations of anadromous fishes can cross long distances and salinity gradients requiring a great deal of energy, potentially limiting migration distance (Leonard and McCormick 1999). It is believed that Hickory Shad build up mesentery fat while feeding in the ocean in order to fuel their migration (Rulifson and Batsavage 2014).

One perceived threat to anadromous fishes such as Hickory Shad is loss of historic spawning habitat due to dams (Rulifson et al. 1982; Rulifson 1994; Limburg and Waldman 2009). Construction of dams on United States rivers began as early as the industrial revolution (Hall et al. 2011). Fish passage efforts were ramped up in the late 1970s through early 1990s as power companies were mandated by the Federal Energy Regulatory Commission (FERC) to provide passage for migratory fishes (Gephard and McMenemy 2004). However, recent studies looking into the effectiveness of current fish passage-ways indicate that there is still plenty of room for improvement of these structures (Moser et al. 2000; Cooke and Leach 2004; Brown et al. 2013; Smith and Rulifson 2015). Investigation of American Shad passage in the Susquehanna, Connecticut, and Merrimack rivers found that mean passage efficiencies from the first dam to historic spawning grounds were < 3% (Brown et al. 2013). The upstream extent of spawning migration of American Shad in the Pee Dee River, NC, occurs below the lowermost dam, limiting available spawning habitat (Harris and Hightower 2011).

Goals and Objectives

The goal of this study was to determine if Hickory Shad spawning populations in different watersheds can be identified for use in fishery management plans. Five different methods were selected for use on the Hickory Shad specimens collected: genetics, otolith shape, otolith chemistry, body shape (geometric morphometrics), and meristic and morphometric analyses. If one or more of these methods can separate spawning populations, then the results imply some degree of natal homing. Thus, the unique genetic and environmental conditions present in each watershed should result in statistically significant differences in body shapes and otolith shapes by each spawning population.

My portion of the study examined differences in the otolith shape using the R package named ShapeR (Libungan and Pálsson 2015), and body shape using geometric morphometrics (Klingenberg 2011).

Two hypotheses were proposed for this study:

- 1. The body shape of individuals from a specific watershed will be similar and can be used to differentiate fish from respective watersheds.
- 2. The otolith shape of individuals from a specific watershed will be similar and can be used to differentiate fish from respective watersheds.

The current chapter (Chapter 1) is devoted to a general literature review and an explanation of the problem. Chapter 2 addresses the possibility of using body shape analysis, also called body geometric morphometric analysis, as a population identifier. Chapter 3 examines the potential use of otolith shape analysis to separate populations. Chapter 4 brings together these aspects and offers recommendations for future studies and management actions.

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Figures



Figure 1-1. Image of an adult male Hickory shad #826. Specimen captured in Swift Creek on March 20, 2018.



Figure 1-2. Image of an adult male Hickory shad #826 otolith. Specimen captured in Swift Creek on March 20, 2018.

CHAPTER 2: BODY SHAPE ANALYSIS USING GEOMETRIC MORPHOMETRICS Abstract

The Hickory Shad is an economically important anadromous species in North Carolina, although little is known about its fundamental biology and life history. The overarching goal of this study was to determine if Hickory Shad spawning populations in different watersheds can be identified for use in fishery management plans. This part of the study focuses on the viability of using geometric morphometric analysis of body shape to differentiate spawning populations. Photographs were taken of 757 Hickory Shad samples from 21 watersheds. Landmarks were digitized using the software TPSDig2 and differences in body shape were determined by landmark anaylsis using the software MorphoJ. Results of Analysis of Variance (ANOVA) and Discriminant Function Analysis (DFA) determined highly significant differences (p<0.0001) in body shape between male and female samples. Principle Components Analysis (PCA) determined that body depth comprised the majority of the variation between sexes. Therefore, all analyses were run on male and female samples separately. DFA and ANOVA detected varying levels of difference from highly significant difference (p<0.0001) to no significant difference (p>0.05) between males and females of different states, watersheds, and tributaries within watersheds. Out of 153 pairwise comparisons of females by watersheds, 43 (28.1%) resulted in highly significant differences (p<0.0001) out of the 99 (64.7%) resulting in significant differences (p<0.05). Out of 153 pairwise comparisons of males by watersheds, 102 (66.7%) resulted in significant differences (p<0.05), 44 (28.8%) of which were highly significant differences (p<0.0001). DFA on females correctly classified watershed of capture by pairwise discriminant function ranging from 88.2% to 100% and correctly classified watershed of capture by cross validation ranging from 12.5% to 100%. DFA on males correctly classified watershed

of capture by pairwise discriminant funtion ranging from 83.3% to 100% and correctly classified watershed of capture by pairwise cross validation ranging from 33.3% to 100%. Type I error in watershed pairwise comparisons of body shape using DFA was controlled using Benjamini and Hochberg's false discovery rate (FDR)-controlling procedure. All 153 watershed pairwise comparison results were adjusted for both males and females. In female specimen, adjusted Pvalues resulted in 95 or 62.1% significant differences (p<0.05) as compared to 99 or 64.7% significant differences before adjusting. In male specimen, adjusted P-values resulted in 97 or 63.4% significant differences (p<0.05) as compared to 102 or 66.7% significant differences before adjusting. PCA determined that body depth was the majority of variation in body shape. The most heavily weighted landmark positions were PC1 = y13 and y14, PC2 = y6 and y7, and PC3 = x13 and x14. Landmarks 6 and 7 are the origin and insertion of the dorsal fin and landmarks 13 and 14 are the insertion and origin of the pelvic fin. Differences in body shape are thought to be affected by a combination of environmental and genetic factors. Inconsistency and varying results in both male and female samples to discriminate watersheds using body shape led to the conclusion that the methods used here were not dependable for differentiating spawning populations of Hickory Shad. However, more than half of the watershed pairwise comparisons of body shape were significantly different. This suggests that homing to natal tributaries is plausible. Increased sample size in some watersheds along with standardization of sample size, timing, and year class may help in differentiating spawning populations of Hickoy Shad using geometric morphometric analysis of body shape.

Introduction

The clear definition and identification of fish stocks as management units is a significant problem that has plagued fisheries biologists around the world. Stocks are defined as arbitrary groups of fish large enough to be essentially self-reproducing, with members of each group having similar life history characteristics (Hilborn and Walters 1992). The stock concept is the intersection of biological organization and human activities (Secor 1999); i.e., a management unit in fisheries management. A particularly vexing aspect of this problem is the identification of stocks among fish species for which detailed life history traits are difficult to know, either because their ranges are broad or their migratory behavior is complex, or both. Hickory Shad represent a species with both a broad range and a complex migratory behavior.

The Hickory Shad *Alosa mediocris* (Mitchill, 1814), is an anadromous member of the Clupeidae family that ranges from the Bay of Fundy, Canada, down to Florida's eastern coast (Mansueti 1962). Ocean dwelling adults enter coastal watersheds to spawn between February and June, with later entry correlating with higher latitudes (Murauskas and Rulifson 2011). Spawning rivers range from Schuylkill River, a tributary of the Delaware River (Perillo and Butler 2009) to the St. Johns River in Florida (Harris et al. 2007). However, there is some uncertainty regarding the northern range limit of Hickory Shad spawning populations. Hildebrand and Schroeder (1928) hypothesized spawning as far north as Maine. U.S. Fish and Wildlife Service (USFWS) biologists suspect that a spawning population exists in Wethersfield Cove in the Connecticut River near Wethersfield, Connecticut where adult Hickory Shad have been collected during spring sampling (Ken Sprankle, USFWS, personal communication). Rulifson (1994) reported that Connecticut is the northern extent of states with Hickory Shad present based on state fisheries biologists' responses to questionnaires. Some of these northern accounts of Hickory Shad may be misidentifications with morphologically similar species, such as the American Shad. These accounts may also be a result of Hickory Shad wandering into bays where they were captured, but not actively spawning. It is hypothesized that water temperature cues the timing of annual migration and spawning of Hickory Shad (Mansueti 1962). Other proposed cues to initiate spawning include photoperiod, current velocity, and turbidity (Leggett and Whitney 1972).

The extensive species range makes the Hickory Shad a multi-jurisdictional species for management purposes. Hickory Shad are currently managed under Amendment 3 of the Atlantic States Marine Fisheries Commission (ASMFC) Interstate Fishery Management Plan (IFMP) for Shad and River Herring. However, this management plan only incorporates biological information for the American Shad *Alosa sapidissima* (Wilson, 1811) and river herring (Alewife *Alosa pseudoharengus* (Wilson, 1811) and Blueback Herring *A. aestivalis* (Mitchill, 1814) (ASMFC 2010). The American Shad has been applied as a model species for Hickory Shad management (Harris et al. 2007) but many aspects of American Shad life history applied to Hickory Shad have not been supported by literature. Also, a genetic study found that Hickory Shad are more closely related to other species in the genus *Alosa* -- the Blueback Herring and Alewife -- than to the American Shad (Bloom and Lovejoy 2014).

The ASMFC Fishery Management Plan requires information more specific to Hickory Shad life history to better manage the species; both the Commission and the Mid-Atlantic Fisheries Management Council (MAFMC) have requested life history studies as high priority for years (ASMFC 2010). The Hickory Shad is considered a "largely understudied species"; more research needs to be focused on its fundamental biology and life history (Rulifson 1994; Waldman and Limburg 2003; ASMFC 2010). Our study aims to provide additional information range-wide about the Hickory Shad to reduce the need for reliance on American Shad life history information for fishery management purposes.

Understanding the migration habits and population dynamics would greatly aid the management of the species and help set specific limits for commercial and recreational harvest. State agencies believe that Hickory Shad exhibit philopatry or natal homing, though this assumption has not been explicitly determined to be true (Batsavage and Rulifson 1997). It is hypothesized that Hickory Shad home to natal watersheds based on results of American Shad mark/recapture (Melvin et al. 1986) and genetics studies (Hasselman et al. 2010). If Hickory Shad also exhibit fidelity to natal watersheds, then it would be helpful in calculating stock size and harvest mortality of populations.

The goal of this study was to determine if Hickory Shad spawning populations in different watersheds can be identified using geometric morphometric analysis of body shape for use in fishery management plans. If body shape can separate spawning populations, then the results imply some degree of natal homing. Thus, the unique genetic and environmental conditions present in each watershed should result in statistically significant differences in body shapes in each spawning population.

Genetic and environmental factors are well known contributors to the phenotypic expression of body shape in fish (Melvin et al. 1992). Geometric morphometrics may provide a way of differentiating spawning populations of Hickory Shad due to differences in their genetic and environmental backgrounds. Geometric morphometric analysis of juvenile Blueback Herring and Alewife body shapes determined significant differences among capture locations (Rogers 2015). Sub-populations of Banggai Cardinalfish *Pterapogon kauderni* (F.P. Koumans, 1933) were differentiated using a geometric morphometric approach to body shape analysis (Ndobe and Moore 2013). A Pontic Shad *Alosa immaculate* Bennett, 1835 study reported significant geometric morphometric differences between years of sampling and sexes (Višnjić-Jeftić et al. 2013). Differences between years were head shape and fin position, while differences in sexes was dorsolateral expansion of the midsection. This information was instrumental in developing the methodology for my study of geometric morphometrics of Hickory Shad.

A study conducted in concert with my study --Smith (2018) -- reported that meristic and morphometric analyses can be used successfully to discriminate among sexes and spawning populations of Hickory Shad; this result seems plausible since sexual dimorphism has been reported for American Shad (Leggett 1973). If body shape analysis results in successful discrimination among spawning populations, then we will conclude that Hickory Shad do exhibit natal fidelity as exhibited by Smith (2018) and my results presented herein; wandering among watersheds during the spawning run will be considered negligible. Successful discrimination among spawning populations also implies that this species is adapted to the environmental conditions of its natal watershed, which should cause fisheries managers to reconsider the current management plans associated with this species and related alosines.

Methods

Sample Collection and Processing

A total of 1079 Hickory Shad individuals were collected from watersheds in Florida, Georgia, South Carolina, North Carolina, Virginia, Maryland, Delaware, and the District of Columbia. These fish were collected from the different watersheds by hook and line, gill net, and electrofishing. The samples captured in rivers outside of North Carolina were collected and donated to this study by state fisheries agencies. North Carolina samples were collected by the North Carolina Wildlife Resources Commission (NCWRC) and the North Carolina Division of Marine Fisheries (NCDMF). Additional sampling was conducted by the Rulifson Lab using electrofishing and rod and reel (Scientific Collection Permit Number 17-SFC00133; AUP #D330).

All specimens were frozen in water to minimize freezer burn and transferred to the Rulifson Lab at ECU for examination. Fish were then bagged individually without water, assigned a unique fish identification number, and kept frozen (-20° C) until examination. Information such as date and location of capture were stored in a database along with the fish identification number. Each fish was weighed (g) and measured (SL, FL, and TL, mm), and then processed by collecting a fin clip, gonads, scales, otoliths, gill rakers, morphological measurements, and meristic counts; these samples were for examination by other members of the research team.

Body Shape Analysis

Fish were brought to the imaging lab on the first floor of ECU's Flanagan Building for photographs. Each fish was placed on a board with fins spread and pinned; within the photograph was a label with the fish identification number and a ruler used for scale. A total of 757 Hickory Shad from 21 watersheds were usable for photographic analysis (Table 2-1, Figure 2-1). Photos were taken by suspending a Nikon D3500 digital camera above the fish and obtaining an overhead image. Photos were converted from TIFF files to TPS files and loaded into TPS Dig2, a landmark digitizing software (https://life.bio.sunysb.edu/morph/). The scale of the picture was set by counting the number of pixels equal to 10 mm on the ruler. Next 16 landmarks along the body were marked using the same landmark and numbering sequence and the digitized image was saved (Table 2-2, Figure 2-2). Digitized images were identified using a naming system where the first two characters represent the state where the sample was collected, the 3rd-5th characters represent the name of the watershed where the sample was collected, the 6th-9th characters represent the fish identification number, and the 10th character represents the sex of the sample. For example, the specimen named "MDSus0090F" was a female, ID number 90, from the Susquehanna River in Maryland. This naming system allowed grouping of samples by state, watershed, and sex within the software. All digitized images were imported into MorphoJ for geometric morphometric analyses (Klingenberg 2011). All specimens were shrunk or stretched proportionally using procrustes fit to minimize the effect of length in shape comparison (Figure 2-3). Differences in body shape were determined between samples of different sex, states, watersheds, and tributaries of the same watershed using pairwise Discriminate Function Analysis (DFA), Principle Component Analysis (PCA), and Analysis of Variance (ANOVA). Significant differences (p < 0.05) between groups were determined using DFA and ANOVA, and the three most heavily weighted components of PCA were used for comparisons. Percent of correct classification was determined using discriminate function, and the reliability of the discrimination was assessed by leave-one-out cross-validation. Type I error in watershed pairwise comparisons of body shape using DFA was controlled using Benjamini and Hochberg's false discovery rate (FDR)-controlling procedure (Benjamini and Hochberg 1995) and adjusted P-values were reported separately from unadjusted P-values.

I also analyzed whether body shape analysis could discriminate between tributaries within one watershed using DFA. Four sets of parent rivers and tributaries were analyzed for this study. One watershed was the main stem Neuse River and its tributaries Contentnea, Pitchkettle, and Swift creeks, all in North Carolina. The second was Tar River and its tributary, a different Swift Creek, also within North Carolina. The third watershed was Chowan River in North Carolina; all the large headwater tributaries are in Virginia. Two tributaries, the Nottoway River and Blackwater River, were tested but the Meherrin River lacked an adequate number of specimens and so was eliminated from the analysis. The fourth watershed was the James River in Virginia, and two of its tributaries, the Appomattox River and Herring Creek, were tested.

Results

Sex

ANOVA on the output from the Procrustes scaling technique determined highly significant difference in body shape between males and females ($F_{28, 21140}$ =270.3, p<0.0001) as did DFA (T^2 =1089.6, p<0.0001), which correctly classified females at a rate of 85.2% and males at a rate of 92.8% (Figure 2-4). Cross-validation correctly classified females at a rate of 83.2% and males at a rate of 90.9% (Figure 2-5). PCA found 79.8% of variance in the samples within the first three principle components (Table 2-4). The most heavily weighted landmark positions were PC1 = y13 and y14, PC2 = y6 and y7, and PC3 = x13 and x14 (Table 2-5). Landmarks 6 and 7 are the origin and insertion of the dorsal fin and landmarks 13 and 14 are the insertion and origin of the pelvic fin. Y indicates y axis variation while x indicates x axis variation. These results indicate that body depth is the main source of variation in shape between male and female specimens (Figure 2-6). Thereafter, all analyses to determine state and watershed differences were conducted by sex.

State

ANOVA on the output from the Procrustes scaling technique determined highly significant differences in body shape among states for both females ($F_{9688,140}=10.7$, p<0.0001) and males (F_{11172.140=}5.0, p<0.0001). Only Virginia and North Carolina were used in the state analysis due to lack of watershed replication in other states, ANOVA found highly significant difference in body shape between Virgina and North Carolina in females ($F_{6272, 28}=7.2, <0.0001$) but not in males (F_{73292, 28}=1.2, p<0.2382). DFA found highly significant difference in body shape between Virgina and North Carolina for males ($T^2=101.7$, p<0.0001) and significant difference for females (T²=75.4, p=0.0003). Discriminant function analysis correctly classified North Carolina females at a rate of 71.1% and Virgina females at a rate of 68.7% (Figure 2-7). Cross-validation correctly classified North Carolina females at a rate of 62.1% and Virgina females at a rate of 59.1% (Figure 2-8). For males, DFA correctly classified North Carolina fish at 75% and Virgina fish at 72% (Figure 2-9). Cross-validation correctly classified 66.9% of the North Carolina males and Virgina males at a rate of 65.3% (Figure 2-10). PCA found that 75.8% of the variance in North Carolina and Virginia males, and 81% variance in females, was in the first three principle components (Table 2-6 and Table 2-8). In both males and females, the first three principle component's most heavily weighted landmark positions were PC1 = y13 and y14, PC2 = y6 and y7, and PC3 = x13 and x14 (Table 2-7, Table 2-9, Figure 2-13 and Figure 2-14).

North Carolina

This section focuses on differentiation of all watersheds sampled within North Carolina. Some North Carolina watersheds were found to differ in body shape from other watersheds in both males and females based on DFA. P-values ranged from <0.0001 to 0.9343 in females, and from <0.0001 to 0.7018 in males and are summarized in Table 2-10 and Table 2-11. North Carolina males and females had different watersheds with samples available to test. Female samples had slightly less discrimination rates; out of 15 watershed pairwise comparisons, 60% or 9 comparisons resulted in significant differences (p<0.05), 2 of the 15 comparisons (13.3%) showed highly significant differences (p<0.0001). For males: 21 pairwise watershed comparisons resulted in 15 or 71.4% of the comparisons significant differences (p<0.05), and 3 or 14.3% of the significant results were highly significant differences (p<0.001). Pairwise DFA on females correctly classified watershed of capture at rates ranging from 94.1% to 100% and correctly classified watershed of capture by cross validation ranging from 25% to 94.1% (Table 2-12). Pairwise DFA on males correctly classified watershed of capture by pairwise cross validation ranging from 50% to 96% (Table 2-13).

Watershed

ANOVA on the output from the Procrustes scaling technique determined resulted in highly significant differences in body shape among watersheds in both females ($F_{9352,476}$ =8.4, p<0.0001) and males ($F_{10836,476}$ =3.4, p<0.0001). Some watersheds were found to differ in body shape from other watersheds in both males and females based on DFA. P-values ranged from <0.0001 to 0.9343 in females, and from <0.0001 to 0.9807 in males and are summarized in Table 2-10 and Table 2-11. For female Hickory Shad, 153 pairwise watershed comparisons resulted in 64.7% (n=99) with significant differences (p<0.05); 28.1% (n=43) of the total showed highly significant differences (p<0.0001). Similar results were obtained for males: 153 pairwise watershed comparisons resulted in 102 (66.7%) with significant differences (p<0.05); 44 (28.8%) of the total were highly significant differences (p<0.0001). Pairwise DFA on females correctly classified watershed of capture at rates ranging from 88.2% to 100% and correctly classified watershed of capture by cross validation ranging from 12.5% to 100% (Table 2-12). Pairwise DFA on males correctly classified watershed of capture by ranging from 83.3% to 100% and correctly classified watershed of capture by pairwise cross validation ranging from 33.3% to 100% (Table 2-13).

Tributaries

Neuse River and tributaries Contentnea Creek, Pitchkettle Creek, and Swift Creek:

Specimens from the Neuse River watershed were collected from the main stem of the Neuse River, and from the tributaries known to support Hickory Shad spawning. Swift Creek was the most downstream tributary sampled and Contentnea Creek was the most upstream; Pitchkettle Creek was between the others. We assumed that specimens collected from the Neuse main stem represented individuals from all the tributaries above the collection site as they migrated upstream; i.e., a mixture of adult fish migrating to individual tributaries. Therefore, I hypothesized that main stem samples collected upstream of the target tributaries should not contain fish from target tributaries downstream of the collection point. Unfortunately, no female Hickory Shad were collected from the mainstem Neuse River and so no comparisons between tributary and mainstem females could be conducted.

Females: No female samples were collected from the main stem Neuse River, so analysis was run on the three tributaries. DFA found highly significant differences in body shapes of females between pairwise comparisons of Contentnea Creek and Pitchkettle Creek ($T^2=412.3$, p<0.0001), and Pitchkettle Creek and Swift Creek ($T^2=432.8$, p<0.0001), but not between Swift Creek and Contentnea Creek ($T^2=510.3$, p=0.5388) (Table 2-10). Discriminant function correctly classified females in pairwise comparisons of the three watersheds at a rate of 100%. Cross validation correctly classified females in pairwise comparisons of Pitchkettle-Swift and

Pitchkettle-Contentnea between 71.4% and 87.9%. Cross validation correctly classified females in pairwise comparisons of Swift-Contentnea at a rate of 41.2% for Contentnea Creek and 50% for Swift Creek (Table 2-12).

Males: DFA found significant differences in body shapes of males between pairwise comparisons of the Neuse River with Pitchkettle Creek ($T^2=189.4$, p=0.0011) and Swift Creek ($T^2=405.5$, p=0.0045), but not between the Neuse River and Contentnea Creek ($T^2=3971.9$, p=0.3397). However, there were significant differences (p<0.05) in body shapes of males in all pairwise comparisons of the three tributaries (Table 2-11). Discriminant function correctly classified males in pairwise comparisons of the four watersheds between 93.4% and 100%. Cross validation correctly classified males in pairwise comparisons of the four watersheds between 57.1% and 87.5% (Table 2-13).

Tar River and tributary Swift Creek:

Females: DFA found no significant difference ($T^2=105.5$, p=0.9343) in body shapes of females between pairwise comparison of Tar River and Swift Creek of the Tar watershed (Table 2-10). Discriminant function correctly classified females in pairwise comparisons of the two watersheds at a rate of 100%. Cross validation correctly classified females in pairwise comparisons of Tar River and Swift Creek at a rate of 25% for Tar River and 50% for Swift Creek (Table 2-12).

Males: No male samples were collected from Swift Creek (Tar River tributary). Chowan River and tributaries Nottoway River and Blackwater River: Females: DFA found highly significant differences in body shapes of females between pairwise comparisons of the Chowan and Nottoway Rivers (T^2 =399.7, p<0.0001), and significant differences in body shapes of females between pairwise comparisons of Chowan-Blackwater (T^2 =933.5, p=0.0160) and Blackwater-Nottoway (T^2 =330.9, p=0.0068) (Table 2-10). Discriminant function correctly classified females in pairwise comparisons of the three watersheds at a rate of 100%. Cross validation correctly classified females in pairwise comparisons of Chowan and Nottoway Rivers at a rate of 86.4% for Chowan River and 79.3% for Nottoway River. Cross validation correctly classified females in pairwise comparisons of Chowan-Blackwater and Blackwater-Nottoway between 53.8% and 86.4% (Table 2-12).

Males: DFA found highly significant differences in body shapes of males between pairwise comparisons of the Chowan River and Blackwater River ($T^2=1266.6$, p<0.0001), and the Chowan River and Nottoway River ($T^2=398.1$, p<0.0001), but no significant difference between the Nottoway River and Blackwater River ($T^2=913.6$, p=0.0852) (Table 2-11). Discriminant function correctly classified males in pairwise comparisons of the three watersheds at a rate of 100%. Cross validation correctly classified males in pairwise comparisons of Chowan-Blackwater and Chowan-Nottoway ranging between 68.2% and 96.7%. Cross validation correctly classified males in pairwise comparisons of the Blackwater and Nottoway Rivers at a rate of 63.6% for Blackwater River and 68.2% for Nottoway River (Table 2-13).

James River and tributaries Appomattox River and Herring Creek:

Females: DFA found significant differences in body shapes of females between pairwise comparisons of the James and Appomattox Rivers ($T^2=631.4$, p=0.0212), but no significant differences in body shapes of females between pairwise comparisons of James-Herring Creek

(T²=462.2, p=0.7042) and Appomattox-Herring Creek (T²=332.9, p=0.0713) (Table 2-10). Discriminant function correctly classified females in pairwise comparisons of the three watersheds at a rate of 100%. Cross validation correctly classified females in pairwise comparisons of the James and Appomattox Rivers at a rate of 83.3% for James River and 79.2% for Appomattox River. Cross validation correctly classified females in pairwise comparisons of James-Herring Creek and Appomattox-Herring Creek between 50% and 100% (Table 2-12).

Males: DFA found no significant differences in body shapes of males between pairwise comparisons of the James River and Appomattox River ($T^2=82.2$, p=0.1769), James River and Herring Creek ($T^2=161.4$, p=0.2341), and Appomattox River and Herring Creek ($T^2=578.5$, p=0.0971) (Table 2-11). Discriminant function correctly classified males in pairwise comparisons of the three watersheds ranging between 86.7% and 100%. Cross validation correctly classified males in pairwise comparisons of the three watersheds ranging between 86.7% and 100%. Cross validation 55.6% and 73.3% (Table 2-13).

Benjamini and Hochberg's FDR-controlling procedure

Watershed pairwise comparisons of body shape using DFA P-values were adjusted using Benjamini and Hochberg's method to control for false discovery rate. All 153 watershed pairwise comparison results were adjusted for both males and females. Analyses were run in RStudio using the p.adjust command. Adjusted P-values ranged from 0.0004 to 0.9343 for females and from 0.0003 to 0.9807 for males. In female specimens, adjusted P-values resulted in 95 (62.1%) significant differences (p<0.05) as compared to 99 (64.7%) significant differences before adjusting (Table 2-14). In male specimen, adjusted P-values resulted in 97 (63.4%) significant differences (p<0.05) as compared to 102 (66.7%) significant differences before adjusting (Table 2-15).

Discussion

The goal of this study was to investigate the feasibility of using geometric morphometric analysis of body shape to differentiate spawning populations of Hickory Shad. Photographs were taken of fish that had previously been frozen and then thawed the day of photographing. This practice is common because it does not require samples to be processed immediately, making this methodology practical to fishery managers and biologists. Difference in body shape between sexes of Hickory Shad is consistent with findings of those for Blueback Herring, Alewife, American Shad, Pontic Shad, and a co-occurring study of Hickory Shad (Melvin et al. 1992; Višnjić-Jeftić et al. 2013; Rogers 2015; Smith 2018). Results of my study indicate that there is a significant difference between body shapes of male and female Hickory Shad and between some, but not all, of the spawning populations sampled in this study.

Significant differences between watersheds may be dependent upon sample size. Watersheds with many samples have the most significant differences when compared to other watersheds using DFA. For example, the males from Potomac River (n=48) and Pitchkettle Creek (n=40) were found to have significantly different body shapes compared to the specimens for the remaining watersheds. A number of post-hoc tests can be utilized for data sets with unequal sample sizes, but these post-hoc tests have all been found to be conservative (Shingala et al. 2015). Post-hoc tests are especially conservative in cases with a high number of pairwise comparisons as used in my study. Benjamini and Hochberg's method to control for false discovery rate was used in this report because it is not overly conservative in cases with a high number of comparisons like other post-hoc tests; e.g., Bonferroni correction. Results of the Benjamini and Hochberg method adjusted P-values were somewhat different from results of unadjusted P-values. The adjusted P-values resulted in four watershed pairwise comparisons of female specimens changing from significantly different to insignificantly different, and five watershed pairwise comparisons of male specimens changing from significantly different to insignificantly different.

The differences, or lack thereof, in Hickory Shad body shape between watersheds are likely due to a combination of environmental and genetic factors. Since researchers believe Hickory Shad juveniles migrate to the Atlantic Ocean relatively soon after hatching, diet is likely similar for all adult fish (Rulifson et al. 1982). This would mean that difference in body shape due to diet would have to be determined within the first few weeks or months of life. The different distances migrated upstream may affect body shape, as Hickory Shad burn a large amount of mesentery fat during upstream migration (Rulifson and Batsavage 2014). Hickory Shad populations that travel farther to reach spawning grounds would expend more energy, perhaps affecting body shape due to reduction in abdominal fat storage. Body shape has been shown to differ between fish occupying different flow regimes (Meyers and Belk 2014). Varied flow conditions among watersheds sampled could be contributing to differences in body shape. In addition, natal spawning at distant geographic locations may lead to differences in genetics and result in differences in body shape (Rodgers 2015). Under this assumption, populations that are farther from each other geographically would display significant differences in body shape. This result was not always true in this study (i.e., the DFA comparison of male body shape between the Ogeechee River and the Susquehanna River (Table 2-11)). The closely-related Alewife and American Shad are suspected of some degree of wandering from natal tributaries to

spawn in nearby watersheds during spawning migrations (Messieh 1977; Melvin 1986). This wandering could result in mixing between different local populations of spawning adults thereby homogenizing populations or misidentifying some fish to their watersheds of origin. Mark-recapture studies can assist with providing information on the frequency of wandering; however, one caveat to these types of studies is that a fish tagged on the spawning grounds may, or may not, belong to that spawning population. Only alternative types of analyses, such as body shape analysis or meristic and morphometric analysis (Smith 2018) can provide additional insight into whether a tagged specimen appears to be related to others in the spawning population. The genetic component of this study remains on-going. Results of genetic analysis are unlikely to be dynamic enough to differentiate between tributaries. If Hickory Shad genetics analyses provide similar results as those found in American Shad, Blueback Herring, and Alewife studies, we would expect differentiation to be on the watershed and regional level (Hasselman et al. 2010; Palkovacs et al. 2014).

Artificially dividing spawning groups along state lines is likely not biologially meaningful but could be helpful to different states trying to manage Hickory Shad spawning populations within a particular state. Grouping samples by state resulted in significant differences in body shape between Virginia and North Carolina in both males and females. These two states had the most samples and replication of watersheds. Analyses were run on 136 males and 116 females from North Carolina, and 118 males and 127 females from Virginia. There were eight total North Carolina watersheds, six watersheds for females and seven watersheds for males, and six Virginia watersheds for both males and females. No other states had more than two watersheds sampled. To find out more about differences among body shape by state, more replication of watersheds is necessary. Analysis of body shape between tributaries and the parent river gave varying results from insignificant differences (p>0.05) to highly significant differences (p<0.0001). These differences were inconsistent between males and females in the same pairwise comparison of watersheds. Comparisons of parent rivers with their tributaries that resulted in no significant difference may be a result of mainstem fish being captured on their way to or from the tributary spawning grounds. Absence of significant difference in body shape bewteen some triburies may be in part influenced by regular flooding during spring spawning, which results in conectivity between tributaries like the Nottoway and Blackwater Rivers of the Chowan watershed. Results may vary depending on whether sampling took place before or after flooding that connected geographically neighboring tributaries or their parent rivers.

Lack of consistency in separating tributaries from each other and from their parent river coupled with varying results by sex and river systems could be the result of small samples sizes. We asked specimen providers to acquire at least 20 specimens of each sex for each tributary or watershed. Some state agency staff were more successful than others due to seasonal timing and watershed flooding. In some cases some watersheds or tributaries had to be left out of analyses due to small sample size. However, many watershed or tributary comparisons did show that Hickory Shad had significantly different body shapes suggesting that body shape analysis may be a viable technique for population identification. Other comparisons of watersheds separated by large geographic distances in which we would expect population differentiation did not yield significant differnces in body shape. Additional sampling to boost sample size for those watersheds that could not be included in analyses, or for those having inconsistent results between males and females, should be encouraged to determine the consistency of the body shape method in population discrimination. It also may be beneficial to use equal sample sizes in each watershed when making comparisons.

Along with adding more samples per watershed, specifying the timing and duration of sample collection will be important for future studies trying to separate spawning populations of Hickory Shad using body shape. Hickory Shad migrate into freshwater earlier than many other anadromous species, so state agencies going about their regular spring sampling for anadromous fishes may only be capturing Hickory Shad from the end of the run. Anecdotally, we observed Hickory Shad in February and March of 2019 in the Neuse River and its tributaries, when at the same time anglers reported catching Hickory Shad on Avalon Pier on the Outer Banks of North Carolina. This indicates there may be multiple waves of Hickory Shad during the ocean migratory phase and the estuarine and riverine prespawning periods. If this is the case, when sampling occurs may be just as important as where samples are collected. Respective state agencies go about their spring sampling in their own unique ways. Some of the sample sets of Hickory Shad we received were captured within a watershed over a period of weeks or months, while others were captured in a single day.

Our study used samples captured from three different years: 2016, 2017, and 2018, and specimens of all ages were analyzed together. This resulted in multiple year classes being mixed together and compared to other mixtures of year classes. While this may be the most practical way for researchers and fishery managers to analyze large data sets, it may not be the best way to objectively discriminate among spawning populations. We would encourage future researchers to standardize their sampling techniques including when, where, and how many samples are collected. Under the methods used in this study, average body shape of a watershed may be dependent on the amount of younger or older fish present in each sample size. It may be worth

38

trying to compare using body shapes of a single year class to others of the same year class. This would help reduce the effect of allometric growth on body shape.

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Tables

Table 2-1. Table summarizing sample sizes from each watershed classified by specimen sex used	
in geometric morphometric study. Tributaries listed with parent river in parenthesis.	

Watershed	State	F	Μ	Total
Altamaha River	GA	26	0	26
Appomattox River	VA	24	25	49
Blackwater River	VA	13	11	24
Cape Fear River	NC	0	24	24
Cashie River	NC	17	17	34
Chowan River	MD	22	30	52
Contentnea Creek (Neuse)	NC	17	14	31
Herring Creek (James)	VA	13	9	22
James River	VA	12	30	42
Nanticoke River	DE	16	0	16
Neuse River	NC	0	16	16
Nottoway River	VA	29	22	51
Ogeechee River	GA	23	19	42
Pitchkettle Creek (Neuse)	NC	33	40	73
Potomac River	DC	26	48	74
Rappahannock River	VA	24	21	45
St. Johns River	FL	0	33	33
Susquehanna River	MD	13	9	22
Swift Creek (Neuse)	NC	14	25	39
Swift Creek (Tar)	NC	22	0	22
Tar River	NC	8	12	20
Grand Total		352	405	757

Landmark	Location
1	Snout
2	Mouth
3	Orbit (anterior wall)
4	Orbit (posterior wall)
5	Operculum
6	Dorsal fin (origin)
7	Dorsal fin (insertion)
8	Caudal Peduncle (dorsal)
9	Caudal Peduncle (mid-line)
10	Caudal Peduncle (ventral)
11	Anal fin (insertion)
12	Anal fin (origin)
13	Pelvic fin (insertion)
14	Pelvic fin (origin)
15	Pectoral fin (insertion)
16	Pectoral fin (origin)

Table 2-2. Number and location of 16 landmarks used in this study.

Table 2-3. Table of watershed abbreviations used in the table summarizing n	results of DFA
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Abbreviation	Watershed
Alt	Altamaha River
App	Appomattox River
Bla	Blackwater River
Cas	Cashie River
Cap	Cape Fear River
Cho	Chowan River
Con	Contentnea Creek
Her	Herring Creek
Jam	James River
Nan	Nanticoke River
Neu	Neuse River
Not	Nottoway River
Oge	Ogeechee River
Pit	Pitchkettle Creek
Pot	Potomac River
Rap	Rappahannock River
StJ	St. John's River
Sus	Susquehanna River
SwN	Swift Creek (Neuse)
SwT	Swift Creek (Tar)
Tar	Tar River

PC	Eigenvalues	% Variance	Cumulative %
1	0.00071728	61.449	61.449
2	0.00014745	12.632	74.081
3	0.00006628	5.678	79.759

Table 2-4. Eigenvalues, percent of variance, and cumulative percent of variance for PCA of sex using geometric morphometrics.

Table 2-5. Weight of each landmark for each of the first three principle components of PCA of sex using geometric morphometrics.

Landmark	PC1	PC2	PC3
x1	-0.12205	0.137177	0.095506
y1	-0.27040	-0.24154	-0.13788
x2	-0.13945	0.129934	0.080758
y2	-0.26007	-0.22177	-0.12707
x3	-0.09674	0.082205	0.077495
y3	-0.13723	-0.03154	-0.01898
x4	-0.07213	0.03608	0.074695
y4	-0.13893	-0.01992	-0.01233
x5	0.077118	0.012249	0.072862
y5	0.088413	0.200846	0.172149
xб	-0.03775	0.023055	0.015264
уб	0.222015	0.51184	-0.09921
x7	0.025351	0.00955	0.019909
у7	0.129967	0.485846	-0.23314
x8	0.095838	-0.03318	0.121182
y8	-0.15087	-0.09958	0.194091
x9	0.074129	-0.00311	0.113702
y9	-0.19312	-0.09737	0.215457
x10	0.056018	-0.07014	0.23752
y10	-0.21721	-0.054	0.097139
x11	-0.03197	-0.03047	0.06449
y11	-0.15788	-0.02913	-0.04802
x12	-0.18607	0.012741	-0.08454
y12	0.006386	0.040775	-0.23327
x13	-0.02665	-0.04229	-0.51834
y13	0.442087	-0.3311	-0.08098
x14	-0.02471	-0.04815	-0.49536
y14	0.45064	-0.33613	-0.03883
x15	0.227514	-0.11895	0.05863
y15	0.12945	0.086716	0.186683
x16	0.181539	-0.0967	0.066222
y16	0.056743	0.136045	0.164183

PC	Eigenvalues	% Variance	Cumulative %
1	0.0007453	63.428	63.428
2	0.00014175	12.063	75.492
3	0.00006415	5.460	80.951

Table 2-6. Eigenvalues, percent of variance, and cumulative percent of variance for PCA of North Carolina vs. Virginia female samples using geometric morphometrics.

Table 2-7. Weight of each landmark for each of the first three principle components of PCA of North Carolina vs. Virginia female samples using geometric morphometrics.

Landmark	PC1	PC2	PC3
x1	-0.131618	0.134616	-0.041359
y1	-0.29022	-0.242598	-0.169411
x2	-0.142812	0.11877	-0.034972
y2	-0.273205	-0.230045	-0.138353
x3	-0.099426	0.096724	-0.000054
y3	-0.134900	-0.021711	-0.000099
x4	-0.07906	0.0741	0.021512
y4	-0.135373	-0.008724	0.002250
x5	0.085737	0.047763	0.143817
y5	0.109133	0.215757	0.204019
x6	-0.025946	0.007265	0.20315
уб	0.239592	0.486517	-0.127834
x7	0.023425	-0.01538	0.164075
у7	0.136757	0.461386	-0.346166
x8	0.080534	-0.012516	-0.00905
y8	-0.167495	-0.039441	0.194761
x9	0.078384	-0.014306	0.017139
y9	-0.19680	-0.05634	0.244175
x10	0.044247	-0.04493	0.142010
y10	-0.210015	-0.046541	0.165827
x11	-0.021129	-0.03724	0.065750
y11	-0.158925	-0.043207	-0.056043
x12	-0.158639	0.007733	-0.007205
y12	0.012061	-0.026673	-0.300478
x13	-0.018486	-0.078842	-0.411489
y13	0.432683	-0.362841	-0.066269
x14	-0.02858	-0.074322	-0.405987
y14	0.434105	-0.354175	-0.024564
x15	0.216718	-0.120758	0.070661
y15	0.134117	0.109359	0.223037
x16	0.176651	-0.088676	0.082004
y16	0.068484	0.159274	0.195148

PC	Eigenvalues	% Variance	Cumulative %
1	0.00051315	58.144	58.144
2	0.00008104	9.183	67.327
3	0.00007466	8.460	75.786

Table 2-8. Eigenvalues, percent of variance, and cumulative percent of variance for PCA of North Carolina vs. Virginia male samples using geometric morphometrics.

Table 2-9. Weight of each landmark for each of the first three principle components of PCA of North Carolina vs. Virginia male samples using geometric morphometrics.

Landmark	PC1	PC2	PC3
x1	-0.079214	0.168989	0.089628
y1	-0.329328	-0.164729	-0.084878
x2	-0.096130	0.147703	0.052357
y2	-0.309597	-0.152384	-0.092743
x3	-0.077385	0.110433	0.042609
у3	-0.138659	-0.005822	-0.038327
x4	-0.057374	0.093732	0.019930
y4	-0.139045	0.015226	-0.024145
x5	0.07946	0.101802	-0.012377
y5	0.138746	0.195706	0.076876
x6	-0.040944	0.025208	-0.071959
уб	0.357556	0.374949	-0.327753
x7	0.03476	0.066767	-0.053904
у7	0.276936	0.254299	-0.405567
x8	0.074405	0.02469	0.163293
y8	-0.19842	0.09155	0.115778
x9	0.055144	0.010868	0.168623
y9	-0.232975	0.09374	0.157432
x10	0.015312	0.065809	0.265437
y10	-0.225512	0.046188	0.056056
x11	-0.040271	0.003351	0.073195
y11	-0.144583	-0.029453	-0.064502
x12	-0.170366	-0.063065	-0.0505
y12	0.048885	-0.127339	-0.117543
x13	-0.005674	-0.311607	-0.421299
y13	0.320600	-0.419285	0.208270
x14	-0.001892	-0.303863	-0.395407
y14	0.330066	-0.411474	0.245724
x15	0.174111	-0.068912	0.051450
y15	0.149209	0.102119	0.158830
x16	0.136058	-0.071905	0.078925
y16	0.096122	0.136709	0.136492

	Sus	Nan	Pot	Rap	Jam	Her	App	Cho	Not	Bla	Cas	Tar	SwT	Pit	SwN	Con	Oge	Alt
Sus	-	0.5885	<.0001	0.1378	0.8058	0.5266	0.0038	0.0402	0.0009	0.4912	0.2583	0.893	0.0012	<.0001	0.7499	0.1104	0.0007	<.0001
Nan	0.5885	-	<.0001	0.0028	0.4412	0.2418	0.0252	<.0001	<.0001	0.1031	0.005	0.8294	0.0048	<.0001	0.2209	0.1016	0.0006	<.0001
Pot	<.0001	<.0001	-	0.0049	0.0209	<.0001	<.0001	<.0001	<.0001	<.0001	0.0017	0.0149	0.0008	0.0003	<.0001	0.0005	<.0001	<.0001
Rap	0.1378	0.0028	0.0049	-	0.097	0.0245	0.0016	0.0003	<.0001	0.0469	0.1545	0.1788	0.2409	0.0705	0.026	0.0203	<.0001	<.0001
Jam	0.8058	0.4412	0.0209	0.097	-	0.7042	0.0212	0.0006	0.072	0.8536	0.592	0.8791	0.4438	0.0014	0.5374	0.777	0.009	0.0002
Her	0.5266	0.2418	<.0001	0.0245	0.7042	-	0.0713	<.0001	0.0047	0.4929	0.3094	0.9331	0.7592	0.0024	0.7823	0.2715	0.1375	0.0036
App	0.0038	0.0252	<.0001	0.0016	0.0212	0.0713	-	<.0001	<.0001	0.0257	0.004	0.4927	<.0001	<.0001	0.0108	0.0003	0.0004	<.0001
Cho	0.0402	<.0001	<.0001	0.0003	0.0006	<.0001	<.0001	-	<.0001	0.016	0.0042	0.1059	0.0014	<.0001	<.0001	<.0001	<.0001	<.0001
Not	0.0009	<.0001	<.0001	<.0001	0.072	0.0047	<.0001	<.0001	-	0.0068	0.0051	0.0354	<.0001	<.0001	0.1787	0.3014	<.0001	<.0001
Bla	0.4912	0.1031	<.0001	0.0469	0.8536	0.4929	0.0257	0.016	0.0068	-	0.0662	0.9091	0.0044	0.0039	0.889	0.8629	0.0076	0.0015
Cas	0.2583	0.005	0.0017	0.1545	0.592	0.3094	0.004	0.0042	0.0051	0.0662	-	0.8863	0.0024	0.0094	0.0101	0.2682	<.0001	<.0001
Tar	0.893	0.8294	0.0149	0.1788	0.8791	0.9331	0.4927	0.1059	0.0354	0.9091	0.8863	-	0.8099	0.0076	0.9343	0.8812	0.1406	0.052
SwT	0.0012	0.0048	0.0008	0.2409	0.4438	0.7592	<.0001	0.0014	<.0001	0.0044	0.0024	0.8099	-	0.0012	0.0367	0.0074	0.0002	<.0001
Pit	<.0001	<.0001	0.0003	0.0705	0.0014	0.0024	<.0001	<.0001	<.0001	0.0039	0.0094	0.0076	0.0012	-	<.0001	<.0001	<.0001	<.0001
SwN	0.7499	0.2209	<.0001	0.026	0.5374	0.7823	0.0108	<.0001	0.1787	0.889	0.0101	0.9343	0.0367	<.0001	-	0.5388	0.2048	0.0083
Con	0.1104	0.1016	0.0005	0.0203	0.777	0.2715	0.0003	<.0001	0.3014	0.8629	0.2682	0.8812	0.0074	<.0001	0.5388	-	0.0991	0.0063
Oge	0.0007	0.0006	<.0001	<.0001	0.009	0.1375	0.0004	<.0001	<.0001	0.0076	<.0001	0.1406	0.0002	<.0001	0.2048	0.0991	-	<.0001
Alt	<.0001	<.0001	<.0001	<.0001	0.0002	0.0036	<.0001	<.0001	<.0001	0.0015	<.0001	0.052	<.0001	<.0001	0.0083	0.0063	<.0001	-

Table 2-10. P-values determined using DFA on females testing pairwise differences in body shape by watershed. Watershed abbreviations as in Table 2.3; watersheds listed in latitudinal order (north to south).

Table 2-11. P-values determined using DFA on males testing pairwise differences in body shape by watershed. Watershed abbreviations as in Table 2-3; watersheds listed north to south.

	Sus	Pot	Rap	Jam	Her	App	Cho	Not	Bla	Cas	Tar	Neu	Pit	Con	SwN	Cap	Oge	StJ
Sus	-	0.0002	0.5463	0.6814	0.8809	0.0602	0.0415	0.843	0.9732	0.7854	0.8321	0.6803	<.0001	0.8752	0.0997	0.0863	0.3961	0.0058
Pot	0.0002	-	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Rap	0.5463	<.0001	-	0.0329	0.4005	0.1308	<.0001	0.0026	0.4638	0.0417	0.0004	0.4171	0.0036	0.2135	0.0005	0.0002	0.0022	<.0001
Jam	0.6814	<.0001	0.0329	-	0.2341	0.1769	0.0019	0.0031	0.1273	<.0001	0.1347	0.0854	0.0096	0.0103	0.0019	0.0002	0.0163	<.0001
Her	0.8809	<.0001	0.4005	0.2341	-	0.0971	<.0001	0.3076	0.8036	0.693	0.9807	0.8953	0.0007	0.6879	0.3926	0.0202	0.8232	0.0013
App	0.0602	<.0001	0.1308	0.1769	0.0971	-	<.0001	0.0108	0.483	0.0044	0.0017	0.0514	0.0005	0.0311	0.0004	0.0001	0.0003	<.0001
Cho	0.0415	<.0001	<.0001	0.0019	<.0001	<.0001	-	<.0001	<.0001	<.0001	0.0068	<.0001	<.0001	<.0001	0.0021	<.0001	<.0001	<.0001
Not	0.843	<.0001	0.0026	0.0031	0.3076	0.0108	<.0001	-	0.0852	0.0038	0.0134	0.0517	0.0004	0.0187	0.0146	0.0002	0.0013	<.0001
Bla	0.9732	<.0001	0.4638	0.1273	0.8036	0.483	<.0001	0.0852	-	0.5827	0.837	0.418	0.0029	0.7081	0.1801	0.143	0.2091	0.0004
Cas	0.7854	<.0001	0.0417	<.0001	0.693	0.0044	<.0001	0.0038	0.5827	-	0.1884	0.0403	<.0001	0.3563	0.0019	0.0003	0.0027	<.0001
Tar	0.8321	<.0001	0.0004	0.1347	0.9807	0.0017	0.0068	0.0134	0.837	0.1884	-	0.7018	0.0028	0.491	0.1611	0.0017	0.0125	<.0001
Neu	0.6803	<.0001	0.4171	0.0854	0.8953	0.0514	<.0001	0.0517	0.418	0.0403	0.7018	-	0.0011	0.3397	0.0045	0.007	0.0644	0.0001
Pit	<.0001	<.0001	0.0036	0.0096	0.0007	0.0005	<.0001	0.0004	0.0029	<.0001	0.0028	0.0011	-	0.0027	0.0006	<.0001	<.0001	<.0001
Con	0.8752	<.0001	0.2135	0.0103	0.6879	0.0311	<.0001	0.0187	0.7081	0.3563	0.491	0.3397	0.0027	-	0.002	0.0382	0.1384	0.0004
SwN	0.0997	<.0001	0.0005	0.0019	0.3926	0.0004	0.0021	0.0146	0.1801	0.0019	0.1611	0.0045	0.0006	0.002	-	<.0001	0.0018	<.0001
Cap	0.0863	<.0001	0.0002	0.0002	0.0202	0.0001	<.0001	0.0002	0.143	0.0003	0.0017	0.007	<.0001	0.0382	<.0001	-	0.0221	<.0001
Oge	0.3961	<.0001	0.0022	0.0163	0.8232	0.0003	<.0001	0.0013	0.2091	0.0027	0.0125	0.0644	<.0001	0.1384	0.0018	0.0221	-	<.0001
StJ	0.0058	<.0001	<.0001	<.0001	0.0013	<.0001	<.0001	<.0001	0.0004	<.0001	<.0001	0.0001	<.0001	0.0004	<.0001	<.0001	<.0001	-

Table 2-12. Table summarizing results of DFA of females. The first number in each cell is the percent of correct classification for the x axis watershed, the second number is the percent of correct classification for the y axis watershed. Cells above the diagonal dashes are results of discriminant function classification, cells bellow the diagonal dashes are results of cross validation classification. Values are reported in percentages. Watersheds listed in alphabetical order.

	Alt	Арр	Bla	Cas	Cho	Con	Her	Jam	Nan	Not	Oge	Pit	Pot	Rap	Sus	SwN	SwT	Tar
Alt	-	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)
App	96.2(87.5)	-	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(95.7)	100(100)	100(100)	100(95.8)	100(100)	100(100)	100(100)	100(100)
Bla	88.5(76.9)	66.7(84.6)	-	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)
Cas	84.6(88.2)	79.2(58.8)	30.8(5.9)	-	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	94.1(97)	100(100)	94.1(100)	100(100)	100(100)	100(100)	100(100)
Cho	88.5(90.9)	91.7(100)	53.8(86.4)	58.8(77.3)	-	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)
Con	76.9(70.6)	83.3(82.4)	69.2(52.9)	52.9(52.9)	95.5(94.1)	-	100(100)	100(100)	100(100)	88.2(96.6)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)
Her	76.9(76.9)	50(61.5)	76.9(76.9)	76.5(84.6)	95.5(84.6)	47.1(46.2)	-	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	92.3(100)	100(100)
Jam	96.2(83.3)	79.2(83.3)	61.5(66.7)	70.6(41.7)	100(83.3)	58.8(50)	84.6(100)	-	100(100)	100(100)	100(100)	100(97)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)
Nan	92.3(93.8)	75(56.3)	61.5(56.3)	88.2(87.5)	100(100)	70.6(50)	84.6(87.5)	83.3(62.5)	-	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)
Not	84.6(82.8)	79.2(82.8)	61.5(72.4)	70.6(69)	86.4(79.3)	41.2(55.2)	69.2(82.8)	41.7(58.6)	100(93.1)	-	100(100)	100(100)	100(100)	100(100)	100(100)	100(92.9)	100(100)	100(100)
Oge	80.8(82.6)	79.2(73.9)	76.9(73.9)	94.1(91.3)	95.5(87)	64.7(47.8)	46.2(65.2)	75(87)	93.8(91.3)	79.3(73.9)	-	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)
Pit	84.6(97)	91.7(100)	53.8(81.8)	58.8(78.8)	68.2(84.8)	82.4(87.9)	61.5(81.8)	75(81.8)	87.5(97)	75.9(87.9)	82.6(90.9)	-	97(84.6)	93.9(95.8)	100(100)	100(100)	100(100)	100(100)
Pot	84.6(100)	87.5(100)	76.9(96.2)	58.8(96.2)	95.5(100)	64.7(80.8)	84.6(96.2)	41.7(76.9)	87.5(100)	79.3(92.3)	78.3(100)	81.8(84.6)	-	100(100)	100(100)	100(100)	96.2(100)	100(100)
Rap	92.3(95.8)	66.7(79.2)	76.9(70.8)	47.1(62.5)	86.4(70.8)	70.6(75)	76.9(66.7)	41.7(70.8)	81.3(83.3)	82.8(79.2)	78.2(83.3)	57.6(45.8)	76.9(50)	-	95.8(100)	100(100)	95.8(90.9)	100(100)
Sus	92.3(84.6)	66.7(92.3)	76.9(76.9)	47.1(46.2)	77.3(61.5)	82.4(61.5)	92.3(76.9)	58.3(76.9)	50(53.8)	93.1(76.9)	91.3(92.3)	87.9(76.9)	100(76.9)	66.7(61.5)	-	100(100)	100(100)	100(100)
SwN	84(71.4)	83.3(78.6)	53.8(64.3)	94.1(85.7)	100(100)	41.2(50)	53.8(42.9)	66.7(71.4)	56.3(64.3)	62.1(57.1)	65.2(50)	84.8(71.4)	96.2(92.9)	62.5(71.4)	61.5(64.3)	-	100(100)	100(100)
SwT	96.2(81.8)	95.8(81.8)	76.9(81.8)	82.4(72.7)	77.3(68.2)	82.4(59.1)	38.5(45.5)	33.3(45.5)	75(81.8)	86.2(72.7)	87(77.3)	84.8(59.1)	88.5(68.2)	50(63.6)	100(90.9)	71.4(59.1)	-	100(100)
Tar	73.1(62.5)	54.2(25)	53.8(75)	52.9(50)	86.4(25)	76.5(50)	69.2(12.5)	75(50)	56.3(50)	72.4(62.5)	56.5(62.5)	87.9(50)	88.5(50)	58.3(37.5)	76.9(75)	57.1(62.5)	50(25)	-

Table 2-13. Table summarizing results of DFA of males. The first number in each cell is the percent of correct classification for the x axis watershed, the second number is the percent of correct classification for the y axis watershed. Cells above the diagonal dashes are results of discriminant function classification, cells bellow the diagonal dashes are results of cross validation classification. Values are reported in percentages. Watersheds listed in alphabetical order.

	Арр	Bla	Cap	Cas	Cho	Con	Her	Jam	Neu	Not	Oge	Pit	Pot	Rap	StJ	Sus	SwN	Tar
App	-	96(100)	100(100)	100(100)	100(100)	100(100)	100(100)	96(86.7)	100(100)	100(95.5)	100(100)	96(97.5)	100(100)	92(90.5)	100(100)	100(100)	100(100)	100(100)
Bla	52(45.5)	-	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(88.9)	100(100)	100(100)
Cap	80(70.8)	45.5(62.5)	-	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(95.5)	100(100)	95.8(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)
Cas	76(82.4)	54.5(52.9)	95.8(88.2)	-	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(97.5)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)
Cho	84(93.3)	90.9(96.7)	62.5(90)	94.1(100)	-	100(100)	100(100)	96.7(86.7)	100(100)	100(100)	100(100)	100(97.5)	96.7(100)	100(100)	100(100)	100(100)	96.7(100)	100(100)
Con	72(71.4)	90.9(78.6)	66.7(50)	52.9(57.1)	96.7(92.9)	-	100(100)	100(100)	100(100)	100(100)	100(100)	100(97.5)	100(97.9)	100(100)	100(100)	100(100)	100(100)	100(100)
Her	72(55.6)	81.8(100)	87.5(66.7)	64.7(44.4)	93.3(77.8)	100(88.9)	-	100(96.7)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)
Jam	56(60)	63.6(76.7)	83.3(80)	76.5(86.7)	73.3(66.7)	57.1(76.7)	66.7(73.3)	-	93.3(93.8)	96.7(95.5)	96.7(100)	83.3(90)	93.3(100)	93.3(95.2)	100(100)	100(100)	100(92)	96.7(100)
Neu	64(62.5)	54.5(43.8)	70.8(75)	58.8(81.3)	86.7(68.8)	78.6(68.8)	44.4(75)	66.7(56.3)	-	100(100)	100(100)	93.4(97.5)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)
Not	64(63.6)	63.6(68.2)	79.2(86.4)	82.4(68.2)	90(68.2)	64.3(68.2)	44.4(50)	80(63.6)	62.5(63.6)	-	100(100)	95.5(97.5)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)
Oge	84(84.2)	36.4(57.9)	66.7(73.7)	76.5(84.2)	93.3(89.5)	50(73.7)	44.4(63.2)	63.3(68.4)	56.3(73.7)	81.8(78.9)	-	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)	100(100)
Pit	68(80)	54.5(70)	75(82.5)	70.6(85)	86.7(72.5)	57.1(87.5)	66.7(90)	60(70)	68.8(80)	63.6(77.5)	78.9(87.5)	-	100(100)	95(95.2)	100(100)	100(100)	95(100)	100(100)
Pot	80(95.8)	72.7(97.9)	79.2(95.8)	88.2(95.8)	83.3(87.5)	71.4(95.8)	88.9(93.8)	80(87.5)	87.5(93.8)	90.9(91.7)	89.5(93.8)	75(91.7)	-	97.9(95.2)	100(100)	97.9(100)	95.8(100)	100(100)
Rap	64(52.4)	45.5(47.6)	79.2(81)	64.7(71.4)	96.7(90.5)	57.1(47.6)	44.4(52.4)	63.3(71.4)	50(57.1)	81.8(71.4)	84.2(66.7)	75(61.9)	87.5(61.9)	-	100(100)	100(100)	100(100)	100(100)
StJ	84(93.9)	72.7(87.9)	79.2(81.8)	88.2(93.9)	93.3(90.9)	85.7(81.8)	88.9(84.8)	83.3(90.9)	68.8(78.8)	90.9(97)	94.7(87.9)	95(93.9)	100(87.9)	85.7(90.9)	-	100(100)	100(100)	100(100)
Sus	68(66.7)	63.6(44.4)	70.8(66.7)	58.8(44.4)	73.3(33.3)	64.3(55.6)	88.9(88.9)	60(44.4)	68.8(55.6)	50(33.3)	78.9(55.6)	95(55.6)	91.7(66.7)	38.1(55.6)	75.8(66.7)	-	100(100)	100(100)
SwN	80(72)	54.5(60)	75(96)	76.5(84)	80(60)	78.6(84)	44.4(56)	76.7(76)	68.8(72)	59.1(60)	68.4(76)	77.5(60)	85.4(72)	81(80)	97(100)	66.7(60)	-	100(100)
Tar	88(91.7)	72.7(75)	91.7(66.7)	58.8(66.7)	86.7(58.3)	57.1(83.3)	44.4(58.3)	63.3(66.7)	68.8(58.3)	81.8(75)	89.5(83.3)	85(58.3)	93.8(66.7)	95.2(100)	90.9(83.3)	55.6(50)	64(50)	-

Table 2-14. Adjusted P-values using Benjamini and Hochberg's FDR-controlling procedure. P-values determined using DFA on females testing pairwise differences in body shape by watershed. Watershed abbreviations as in Table 2.3; watersheds listed in latitudinal order (north to south).

	Sus	Nan	Pot	Rap	Jam	Her	Арр	Cho	Not	Bla	Cas	Tar	SwT	Pit	SwN	Con	Oge	Alt
Sus	/	0.6709	0.0004	0.1882	0.8726	0.6150	0.0087	0.0628	0.0025	0.5801	0.3266	0.9109	0.0032	0.0004	0.8375	0.1536	0.0020	0.0004
Nan	0.6709	/	0.0004	0.0066	0.5347	0.3083	0.0415	0.0004	0.0004	0.1461	0.0102	0.8874	0.0101	0.0004	0.2864	0.1453	0.0018	0.0004
Pot	0.0004	0.0004	/	0.0101	0.0355	0.0004	0.0004	0.0004	0.0004	0.0004	0.0042	0.0262	0.0023	0.0010	0.0004	0.0015	0.0004	0.0004
Rap	0.1882	0.0066	0.0101	/	0.1413	0.0407	0.0040	0.0010	0.0004	0.0725	0.2074	0.2358	0.3083	0.1058	0.0419	0.0349	0.0004	0.0004
Jam	0.8726	0.5347	0.0355	0.1413	/	0.7922	0.0356	0.0018	0.1059	0.9070	0.6709	0.9109	0.5347	0.0036	0.6198	0.8549	0.0166	0.0007
Her	0.6150	0.3083	0.0004	0.0407	0.7922	/	0.1059	0.0004	0.0100	0.5801	0.3787	0.9343	0.8417	0.0057	0.8549	0.3377	0.1882	0.0083
App	0.0087	0.0415	0.0004	0.0040	0.0356	0.1059	/	0.0004	0.0004	0.0418	0.0089	0.5801	0.0004	0.0004	0.0192	0.0010	0.0012	0.0004
Cho	0.0628	0.0004	0.0004	0.0010	0.0018	0.0004	0.0004	/	0.0004	0.0278	0.0092	0.1486	0.0036	0.0004	0.0004	0.0004	0.0004	0.0004
Not	0.0025	0.0004	0.0004	0.0004	0.1059	0.0100	0.0004	0.0004	/	0.0133	0.0103	0.0564	0.0004	0.0004	0.2358	0.3719	0.0004	0.0004
Bla	0.5801	0.1461	0.0004	0.0725	0.9070	0.5801	0.0418	0.0278	0.0133	/	0.1003	0.9211	0.0095	0.0088	0.9109	0.9105	0.0144	0.0038
Cas	0.3266	0.0102	0.0042	0.2074	0.6709	0.3787	0.0089	0.0092	0.0103	0.1003	/	0.9109	0.0057	0.0171	0.0182	0.3363	0.0004	0.0004
Tar	0.9109	0.8874	0.0262	0.2358	0.9109	0.9343	0.5801	0.1486	0.0564	0.9211	0.9109	/	0.8726	0.0144	0.9343	0.9109	0.1904	0.0796
SwT	0.0032	0.0101	0.0023	0.3083	0.5347	0.8417	0.0004	0.0036	0.0004	0.0095	0.0057	0.8726	/	0.0032	0.0579	0.0143	0.0007	0.0004
Pit	0.0004	0.0004	0.0010	0.1058	0.0036	0.0057	0.0004	0.0004	0.0004	0.0088	0.0171	0.0144	0.0032	/	0.0004	0.0004	0.0004	0.0004
SwN	0.8375	0.2864	0.0004	0.0419	0.6198	0.8549	0.0192	0.0004	0.2358	0.9109	0.0182	0.9343	0.0579	0.0004	/	0.6198	0.2678	0.0155
Con	0.1536	0.1453	0.0015	0.0349	0.8549	0.3377	0.0010	0.0004	0.3719	0.9105	0.3363	0.9109	0.0143	0.0004	0.6198	/	0.1430	0.0125
Oge	0.0020	0.0018	0.0004	0.0004	0.0166	0.1882	0.0012	0.0004	0.0004	0.0144	0.0004	0.1904	0.0007	0.0004	0.2678	0.1430	/	0.0004
Alt	0.0004	0.0004	0.0004	0.0004	0.0007	0.0083	0.0004	0.0004	0.0004	0.0038	0.0004	0.0796	0.0004	0.0004	0.0155	0.0125	0.0004	/

Table 2-15. Adjusted P-values using Benjamini and Hochberg's FDR-controlling procedure. P-values determined using DFA on males testing pairwise differences in body shape by watershed. Watershed abbreviations as in Table 2.3; watersheds listed in latitudinal order (North to South).

	Sus	Pot	Rap	Jam	Her	App	Cho	Not	Bla	Cas	Tar	Neu	Pit	Con	SwN	Cap	Oge	StJ
Sus	/	0.0006	0.6191	0.7555	0.8985	0.0877	0.0626	0.8715	0.9796	0.8403	0.8712	0.7555	0.0003	0.8985	0.1374	0.1211	0.4735	0.0106
Pot	0.0006	/	0.0003	0.0003	0.0003	0.0003	0.0003	0.0003	0.0003	0.0003	0.0003	0.0003	0.0003	0.0003	0.0003	0.0003	0.0003	0.0003
Rap	0.6191	0.0003	/	0.0514	0.475	0.1771	0.0003	0.0054	0.5376	0.0626	0.0011	0.4882	0.0069	0.2678	0.0013	0.0006	0.0046	0.0003
Jam	0.7555	0.0003	0.0514	/	0.2912	0.2294	0.0042	0.006	0.1739	0.0003	0.1808	0.121	0.0169	0.0179	0.0042	0.0006	0.0268	0.0003
Her	0.8985	0.0003	0.475	0.2912	/	0.1351	0.0003	0.3795	0.8538	0.7574	0.9807	0.9072	0.0018	0.7572	0.473	0.0325	0.8686	0.0031
App	0.0877	0.0003	0.1771	0.2294	0.1351	/	0.0003	0.0186	0.5556	0.0082	0.0039	0.0761	0.0013	0.0491	0.0011	0.0003	0.0009	0.0003
Cho	0.0626	0.0003	0.0003	0.0042	0.0003	0.0003	/	0.0003	0.0003	0.0003	0.0122	0.0003	0.0003	0.0003	0.0045	0.0003	0.0003	0.0003
Not	0.8715	0.0003	0.0054	0.006	0.3795	0.0186	0.0003	/	0.121	0.0072	0.0225	0.0761	0.0011	0.0304	0.0243	0.0006	0.0031	0.0003
Bla	0.9796	0.0003	0.5376	0.1739	0.8538	0.5556	0.0003	0.121	/	0.6555	0.8712	0.4882	0.0057	0.763	0.2316	0.1886	0.2644	0.0011
Cas	0.8403	0.0003	0.0626	0.0003	0.7574	0.0082	0.0003	0.0072	0.6555	/	0.2402	0.0617	0.0003	0.4327	0.0042	0.0009	0.0054	0.0003
Tar	0.8712	0.0003	0.0011	0.1808	0.9807	0.0039	0.0122	0.0225	0.8712	0.2402	/	0.7615	0.0056	0.5606	0.2107	0.0039	0.0213	0.0003
Neu	0.7555	0.0003	0.4882	0.121	0.9072	0.0761	0.0003	0.0761	0.4882	0.0617	0.7615	/	0.0027	0.4158	0.0083	0.0125	0.093	0.0003
Pit	0.0003	0.0003	0.0069	0.0169	0.0018	0.0013	0.0003	0.0011	0.0057	0.0003	0.0056	0.0027	/	0.0054	0.0015	0.0003	0.0003	0.0003
Con	0.8985	0.0003	0.2678	0.0179	0.7572	0.0491	0.0003	0.0304	0.763	0.4327	0.5606	0.4158	0.0054	/	0.0043	0.059	0.1841	0.0011
SwN	0.1374	0.0003	0.0013	0.0042	0.473	0.0011	0.0045	0.0243	0.2316	0.0042	0.2107	0.0083	0.0015	0.0043	/	0.0003	0.0041	0.0003
Cap	0.1211	0.0003	0.0006	0.0006	0.0325	0.0003	0.0003	0.0006	0.1886	0.0009	0.0039	0.0125	0.0003	0.059	0.0003	/	0.0352	0.0003
Oge	0.4735	0.0003	0.0046	0.0268	0.8686	0.0009	0.0003	0.0031	0.2644	0.0054	0.0213	0.093	0.0003	0.1841	0.0041	0.0352	/	0.0003
StJ	0.0106	0.0003	0.0003	0.0003	0.0031	0.0003	0.0003	0.0003	0.0011	0.0003	0.0003	0.0003	0.0003	0.0011	0.0003	0.0003	0.0003	/

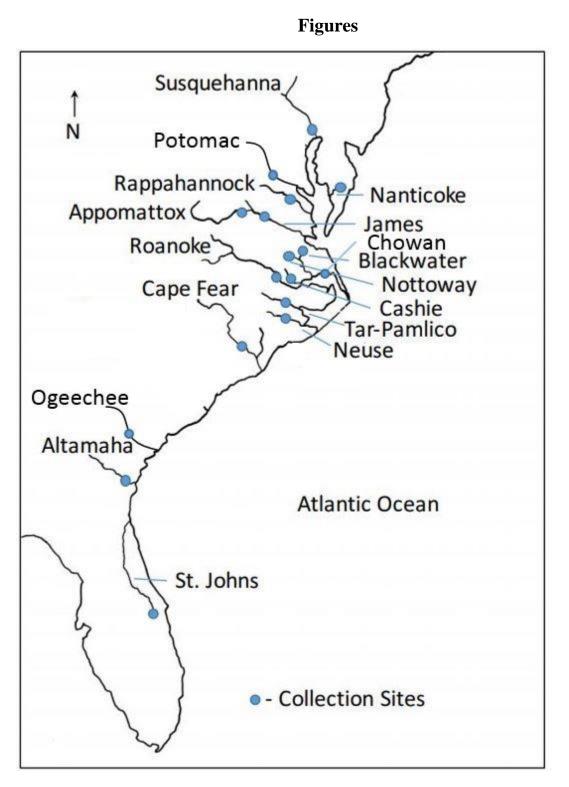


Figure 2-1. Map displaying relative location of rivers included in this body shape study as well as collection sites of Hickory Shad. Tributaries Contentnea Creek, Pitchkettle Creek, Swift Creek (Neuse), Swift Creek (Tar), and Herring Creek not shown. Revised after Melvin et al. (1992).



Figure 2-2. Hickory Shad number 633 with the 16 landmarks digitized and ruler of scale.

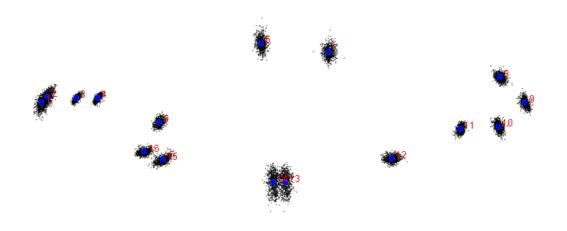


Figure 2-3. Procrustes fit of all 757 Hickory Shad used in these analyses.

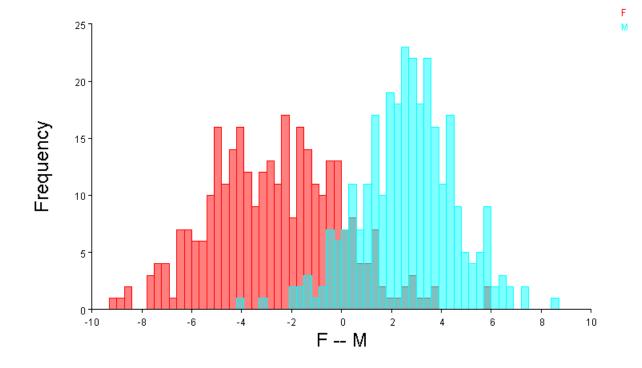


Figure 2-4. Discriminant function scores plotted for Hickory Shad females vs. males.

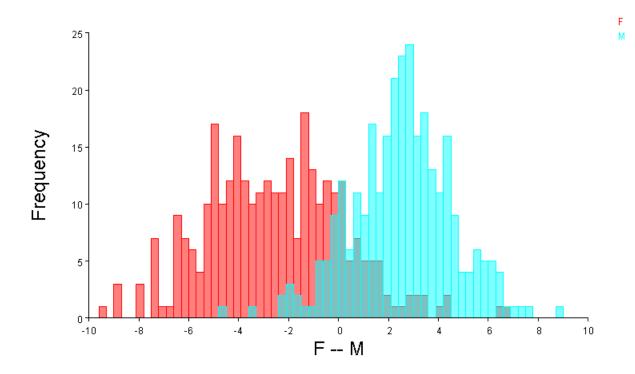


Figure 2-5. Cross-validation scores plotted for Hickory Shad females vs. males.

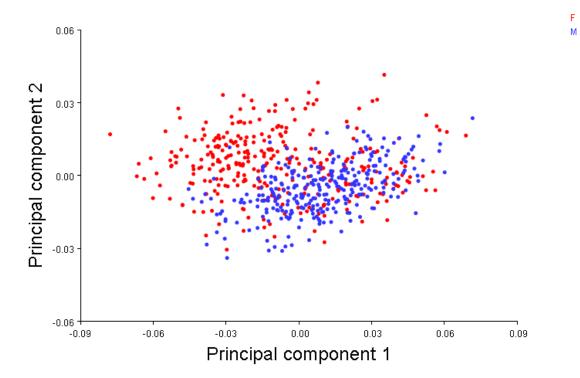


Figure 2-6. Principle components 1 and 2 plotted with Hickory Shad males in blue and females in red.

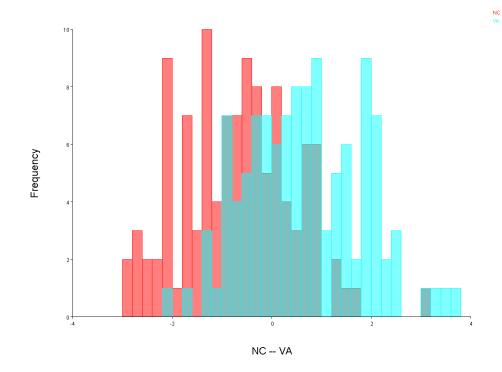


Figure 2-7. Female Hickory Shad discriminant function scores with North Carolina in red and Virginia in blue.

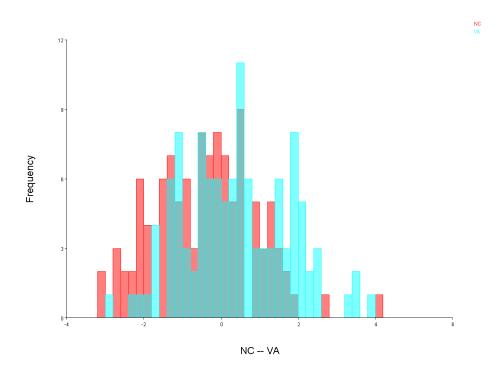


Figure 2-8. Female Hickory Shad cross-validation scores with North Carolina in red and Virginia in blue.

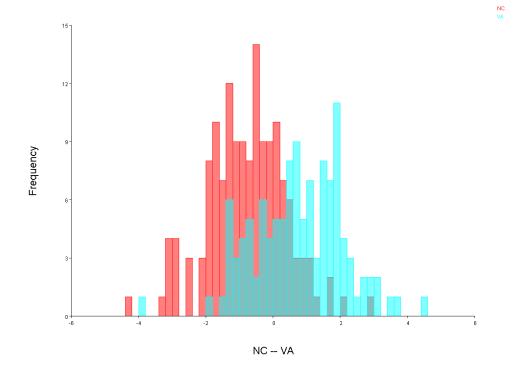


Figure 2-9. Male Hickory Shad discriminant function scores with North Carolina in red and Virginia in blue.

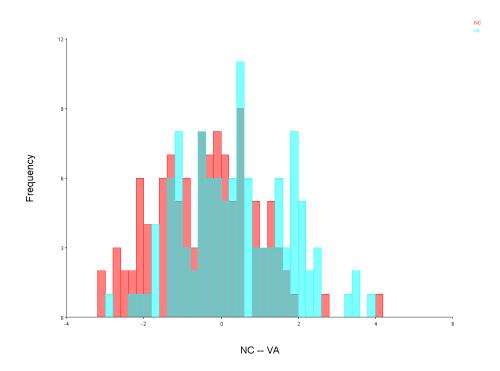


Figure 2-10. Male Hickory Shad cross-validation scores with North Carolina in red and Virginia in blue.

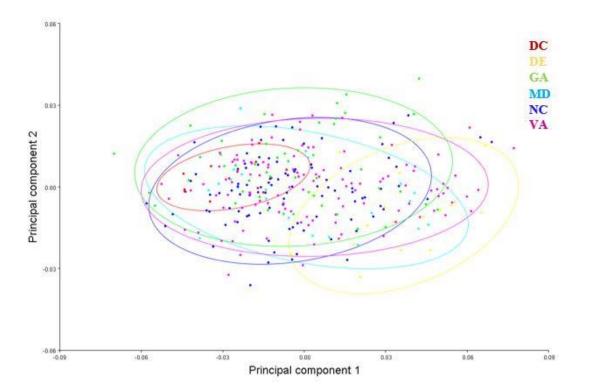


Figure 2-11. Principle components 1 and 2 of female Hickory Shad plotted by state with 90% confidence ellipses.

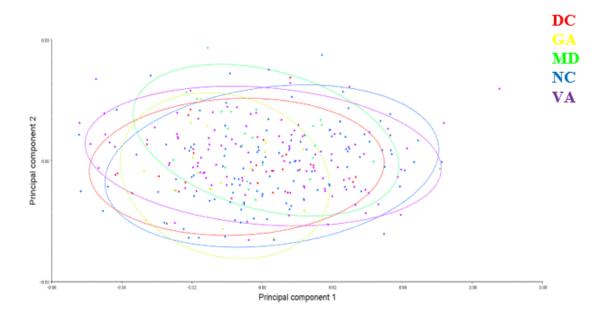


Figure 2-12. Principle components 1 and 2 of male Hickory Shad plotted by state with 90% confidence ellipses.

CHAPTER 3: OTOLITH SHAPE ANALYSIS

Abstract

Hickory Shad are economically important anadromous species in North Carolina, although little is known about their fundamental biology and life history. The overarching goal of this study was to determine if Hickory Shad spawning populations in different watersheds can be identified for use in fishery management plans. This part of the study focuses on the viability of using otolith shape analysis to differentiate spawning populations. Photographs were taken of 696 right sagittal otoliths from 22 watersheds. Shapes of the otolith outlines were generated and analyzed using the ShapeR package in RStudio. This package generated an outline of each otolith, smoothed each outline to eliminate pixel noise, adjusted the otolith shape with respect to allometric relationships with the fish lengths, conducted Wavelet transform to the outlines, and visualized the mean shape of each watershed. Overall determination of differences in shape coefficients by watershed were determined using an ANOVA test. Differences in otolith shape between watersheds were visualized using Canonical Analysis of Principal Coordinates (CAP) and pairwise comparisons of watersheds using an ANOVA-like permutation test. ANOVA determined there were highly significant differences in otolith shape by watershed ($F_{21, 674}$ =3.4242, p=0.001) and by state ($F_{6, 689}$ =5.0122, p=0.001). Most of the otolith shape variation can be attributed to the otolith regions of the antirostrum, excisura major, and dorsal side of the rostrum. Pairwise comparisons of otolith shape for every watershed using an ANOVA-like permutation test resulted in P-values ranging from highly significant (p=0.001) in 55 pairwise comparisons of watersheds, to (p=0.902) in the comparison of the Rappahannock River and the Potomac River. Out of 231 total pairwise comparisons of watersheds, 148 or 64.1% resulted in significant differences (p<0.05), 55 or 23.8% of which were highly significant differences

(p=0.001). Type I error in watershed pairwise comparisons of otolith shape using ANOVA was controlled using Benjamini and Hochberg's false discovery rate (FDR)-controlling procedure. Benjamini and Hochberg adjusted P-values resulted in 131 or 56.7% significant differences (p<0.05) as compared to 148 or 64.1% significant differences before adjusting. Differences in otolith shape were hypothesized to be influenced by a combination of environmental and genetic factors. Varying results of this study attempting to discriminate sample sets captured in 22 watersheds by otolith shape led to the conclusion that the methods used here were not reliable for differentiating spawning populations of Hickory Shad; however, the fact that more than half of the otolith shape comparisons were significantly different suggests that homing to natal tributaries is plausible. More sampling and standardization of sample size, timing, and age may help in differentiating spawning populations of Hickory Shad using otolith shape.

Introduction

Fisheries agencies manage fish species in management units, often referred to as "stocks". Stocks as management units are defined as arbitrary groups of a fish species large enough to be essentially self-reproducing, with members of each group having similar life history characteristics (Hilborn and Walters 1992). Good fisheries management requires adequate knowledge of the life history traits of the species in question, but for some species this detailed knowledge is difficult to acquire either because the species range is broad or the migratory behavior is complex, or both. The Hickory Shad *Alosa mediocris* (Mitchill 1814) represents a species with both a broad range and a complex migratory behavior.

Little information has been published about the species since Mitchill's first description published in 1814. It is an anadromous member of the Clupeidae family that ranges from the Bay of Fundy, Canada, down to Florida's eastern coast (Mansueti 1962). Ocean dwelling adults enter coastal watersheds to spawn between February and June, with later entry correlating with higher latitudes (Murauskas and Rulifson 2011). Spawning rivers range from Schuylkill River, a tributary of the Delaware River (Perillo and Butler 2009) to the St. Johns River in Florida (Harris et al. 2007). However, there is some uncertainty regarding the northern range limit of Hickory Shad spawning populations. Hildebrand and Schroeder (1928) hypothesized spawning as far north as Maine. U.S. Fish and Wildlife Service (USFWS) biologists suspect that a spawning population exists in Wethersfield Cove in the Connecticut River near Wethersfield, Connecticut where adult Hickory Shad have been collected during spring sampling (Ken Sprankle, USFWS, personal communication). Rulifson (1994) reported that Connecticut is the northern extent of states with Hickory Shad present based on state fisheries biologist responses to questionnaires. It is hypothesized that water temperature cues the timing of annual migration and spawning of Hickory Shad (Mansueti 1962). Other proposed cues to initiate spawning include photoperiod, current velocity, and turbidity (Leggett and Whitney 1972).

The extensive range makes the Hickory Shad a multi-jurisdictional species for management purposes. Hickory Shad are currently managed under Amendment 3 of the Atlantic States Marine Fisheries Commission (ASMFC) Interstate Fishery Management Plan (IFMP) for Shad and River Herring. However, this management plan is missing even basic life history information for the Hickory Shad, so it is managed like the American Shad *Alosa sapidissima* (Wilson, 1811), for which there is considerably more information coastwide (ASMFC 2010). The ASMFC Fishery Management Plan requires information more specific to Hickory Shad life history to better manage the species; both the Commission and the Mid-Atlantic Council have requested life history studies as high priority for years (ASMFC 2010).

State agencies believe that Hickory Shad exhibit philopatry or natal homing, though this assumption has not been explicitly determined to be true (Batsavage and Rulifson 1997). It is hypothesized Hickory Shad home to natal watersheds based on results of American Shad mark/recapture (Melvin et al. 1986) and genetics studies (Hasselman et al. 2010). If Hickory Shad also exhibit fidelity to natal watersheds, then it would be helpful in calculating stock size and harvest mortality of populations.

Otolith shape may provide a way of differentiating spawning populations of Hickory Shad due to differences in their genetic and environmental backgrounds. A previous study of Atlantic Herring *Clupea harengus* Linnaeus, 1758 by Berg et al. (2018) determined that otolith shape has a significant genetic component and can be useful for studying population dynamics and connectivity. Another study of Atlantic Herring in Norway found that otolith shape was more similar among neighboring populations, and can be used to determine relative location of origin in semi-closed populations (Libungan et al. 2015). A study of Pacific Herring *Clupea pallasii* Valenciennes, 1847 in Mexico concluded that otolith shape is useful in identifying local and regional stocks of the species and could be used to differentiate populations of other species as well (Javor et al. 2011). Rogers (2015) determined that there was no difference in otolith shape of adult Blueback Herring *Alosa aestivalis* (Mitchill 1814) among sampling locations in North Carolina, but that there was a significant difference in otolith shape when comparing Blueback Herring otoliths collected in North Carolina to those collected in New Jersey.

The goal of my study was to determine if Hickory Shad spawning populations in different watersheds can be identified using otolith shape analyzed in the RStudio package ShapeR for use in fishery management plans. If otolith shape can separate spawning populations, then the results imply some degree of natal homing. Thus, the unique genetic and environmental conditions present in each watershed should result in statistically significant differences in otolith shape for each spawning population. A study conducted in concert with my study --Smith (2018) -- reported that meristic and morphometric analyses can be used successfully to discriminate among spawning populations of Hickory Shad. If otolith shape analysis results in successful discrimination among spawning populations, then we will conclude that Hickory shad do exhibit natal fidelity, as exhibited by Smith (2018) and results presented herein; wandering among watersheds during the spawning run will be considered negligible.

Methods

Sample Collection and Processing

A total of 1079 Hickory Shad samples were collected from watersheds in Florida, Georgia, South Carolina, North Carolina, Virginia, Maryland, Delaware, and the District of Columbia. These samples were collected from the different watersheds by hook and line, gill net, and electrofishing. The samples captured in rivers outside of North Carolina were collected and donated to this study by state fisheries agencies. North Carolina samples were collected by the NC Wildlife Resources Commission (NCWRC) and the NC Division of Marine Fisheries (NCDMF). Additional sampling was conducted by the Rulifson Lab using electrofishing and rod and reel (Scientific Collection Permit Number 17-SFC00133; AUP #D330). All specimens were initially frozen in water to minimize freezer burn and transferred to the Rulifson Lab at ECU for examination. Fish were bagged individually without water, assigned a unique fish identification number, and retained frozen at -20°C until each could be examined.

Otolith Shape Analysis

Right and left sagittal otoliths were extracted, cleaned, and stored dry in microcentrifuge tubes. Photographs were captured of 696 right sagittal otoliths from 22 watersheds (Figure 3-1). Otolith pictures were taken on a black background while immersed in mineral oil using an Olympus SZX16 microscope with a 0.5X lens and 5X magnification. All otoliths were oriented sulcus side down with the anterior side of the otolith on the left side of the image (Figure 3-2). Image scale was calibrated by determining the number of pixels spanning 1 millimeter on a stage micrometer. Outlines of the otoliths were generated and analyzed using the ShapeR package in RStudio; methods were described in detail by Libungan and Pálsson (2015) (Figure 3-3). Briefly, the ShapeR package generated an outline of each otolith, smoothed each outline to eliminate pixel noise, adjusted the otolith shape with respect to allometric relationships with the fish lengths, conducted Wavelet transform to the outlines, and visualized the mean shape of each

watershed. Overall determination of differences in shape coefficients by watershed were determined using an ANOVA test. The mean and standard deviation of the coefficients were plotted against the position around the outline to determine how the variation in the Wavelet coefficients is dependent on the position. Differences in otolith shape between watersheds were visualized using Canonical Analysis of Principal Coordinates (CAP) and discriminated with pairwise comparisons of watersheds using an ANOVA-like permutation test. Significant differences (p<0.05) and highly significant differences (p=0.001) were determined between paired groups. Type I error in watershed pairwise comparisons of otolith shape using ANOVA was controlled using Benjamini and Hochberg's false discovery rate (FDR)-controlling procedure (Benjamini and Hochberg 1995). Adjusted P-values were reported separately from unadjusted P-values. The variability in presence of postrostrum tails was noted while photographing otoliths (Figure 3-4). After all analyses were completed, postrostrum tails were counted for presence or absence. Proportion of otoliths with postrostrum tails were plotted vs. the latitude of the coastal watershed mouth opening.

Results

The average shape of Wavelet coefficients from each state and each watershed were plotted (Figure 3-5 and Figure 3-6). Average shape of Wavelet coefficients from watershed in North Carolina were plotted (Figure 3-7). Average shape of Wavelet coefficients from the Neuse River and its tributaries were plotted (Figure 3-8). ANOVA determined there was highly significant differences in otolith shape by watershed ($F_{21, 674}$ =3.4242, p=0.001) and by state ($F_{6, 689}$ =5.0122, p=0.001). Most of the variation among otolith shape can be attributed to angles 120-170° (Figure 3-9), which corresponds to the antirostrum, exciscura major, and dorsal side of the rostrum (Figure 3-4). Results of CAP were visualized (Figure 3-10). Pairwise comparisons of otolith shape in every watershed which were executed using an ANOVA-like permutation test resulted in P-values ranging from highly significant p=0.001 (55 pairwise comparisons of watersheds) to p=0.902 (Rappahannock River vs. Potomac River) and are summarized in Table 3-2 with associated watershed abbreviations in Table 3-1. Out of 231 total pairwise comparisons of watersheds, 148 or 64.1% resulted in significant differences (p<0.05), and 55 or 23.8% of those were highly significant differences (p=0.001).

All 231 watershed pairwise comparisons of otolith shape P-values were adjusted using Benjamini and Hochberg's method to control for false discovery rate. Analyses were run in RStudio using the p.adjust command. Adjusted P-values ranged from 0.004 to 0.902. Adjusted Pvalues resulted in 131 or 56.7% significant differences (p<0.05) as compared to 148 or 64.1% significant differences before adjusting (Table 3-3).

North Carolina

This section focuses more closely on North Carolina watersheds. Pairwise comparisons of otolith shape for every North Carolina watershed were executed using an ANOVA-like permutation test. 28 Pairwise comparisons resulted in P-values ranging from highly significant p=0.001 (11 pairwise comparisons of watersheds) to p=0.427 (Tar River vs. Contentnea Creek) and are summarized in Table 3-2 with associated watershed abbreviations in Table 3-1. Fourteen (14) or 50% of North Carolina watershed comparisons resulted in significant differences (p<0.05), and 11 or 39.3% of those significant differences were highly significant (p=0.001).

Postrostrum Tails

Out of all 696 otoliths used in this study, 283 (40%) had a postrostrum tail present. Postrostrum tails were observed in each of the 22 watersheds sampled in this study. Proportion of otoliths with a postrostrum tail by watershed ranged from 13% in main stem Neuse River samples to 75% in Altamaha River samples (Table 3-4). There was a negative relationship between latitude of watershed mouth and proportion of otolith postrostrum tail presence:

Y = -0.0428x + 1.9409 with $R^2 = 0.4641$ (Figure 3-11).

Discussion

The goal of this study was to investigate the feasibility of using otolith shape analysis to differentiate spawning populations of Hickory Shad. Right and left sagittal otoliths were extracted, and right sagittal otoliths were used in this study while left otoliths were used in a co-occurring study of otolith micro-chemical make-up. Results of ANOVA indicated that there was highly significant (p=0.001) differences in Hickory Shad otolith shape by watersheds, but pairwise comparisons of sampling locations indicated that there is a significant (p<0.05) difference between some, but not all, of the spawning populations sampled in this study.

A study of Atlantic Herring in Norway found that otolith shape was more similar among neighboring populations (Libungan et al. 2015). These results do not always hold true in this study of Hickory Shad otolith shape. For example, some neighboring populations such as the Susquehanna River and Patapsco River show highly significant differences in otolith shape (p=0.001). The Susquehanna River's average otolith shape extends farther upward toward the 90° mark in the region between the rostrum and anti-rostrum than the Patapsco River's average otolith shape. In contrast, some Hickory Shad populations on opposite ends of its range such as the Susquehanna River and St. Johns River do not show significantly different otolith shapes (p=0.122). Other examples of this inconsistency in differentiating geographically distant rivers can be seen in throughout Table 3-2.

Differences in otolith shape are likely due to a combination of environmental and genetic factors. A study of Atlantic Herring determined that otolith shape has a significant genetic component and can be useful for studying population dynamics and connectivity (Berg et al. 2018). Vergara-Solana et al. (2013) used otolith shape for stock discrimination of Pacific sardine *Sardinops sagax* (Jenyns, 1842) with results similar to body shape analysis of the same samples. Javor et al. (2011) concluded that otolith shape was a useful tool for identifying local and regional stocks of Pacific Herring in Mexico, and could be used to differentiate populations of other species as well (Javor et al. 2011). Results of otolith shape analysis of Hickory Shad otoliths in this study showed variation in the ability to separate spawning populations, finding significant differences in 64.1% of all pairwise comparisons of sampling locations.

Rogers (2015) determined no differences in otolith shape of adult Blueback Herring among sampling locations in North Carolina, but there was a significant difference in otolith shape comparing adult Blueback Herring otoliths collected in North Carolina to those collected in New Jersey. These results comparing otolith shape between states are similar to the findings of this study comparing Hickory Shad otolith shape from North Carolina samples to Virginia samples.

There are number of variables that may have influenced the ability to discriminate spawning populations of Hickory Shad using otolith shape. The closely-related Alewife and American shad are suspected of some degree of wandering from natal tributaries to spawn in nearby watersheds during spawning migrations (Messieh 1977; Melvin 1986). This wandering could result in mixing between different local populations of spawning adults thereby homogenizing populations or misidentifying some fish to their watersheds of origin. Markrecapture studies can assist with providing information on the frequency of wandering; however, one caveat to these types of studies is that a fish tagged on the spawning grounds may, or may not, belong to that spawning population. Only alternative types of analyses, such as otolith shape analysis or meristic and morphometric analysis (Smith 2018) can provide additional insight into whether a tagged specimen appears to be related to others in the spawning population. The genetic component of this study remains on-going. Results of genetic analysis are unlikely to be dynamic enough to differentiate between tributaries. If Hickory Shad genetics analyses provide similar results as those found in American Shad, Blueback Herring, and Alewife studies, we would expect differentiation to be on the watershed and regional level (Hasselman et al. 2010; Palkovacs et al. 2014).

The presence of postrostrum tails on some otoliths in each watershed was noted during photographing under the microscope. The function of these tails is unknown but has been observed in the otoliths of other species such as Swordfish. After counting presence/absence in each watershed, it was observed that the three southernmost watersheds-- the Altamaha River, Ogeechee River, and St. Johns River -- had above average presence of postrostrum tails. Regression analysis revealed a significant relationship between latitude of watershed mouth and proportion of otoliths with postrostrum tails. Despite otoliths sampled in Georgia and Florida having between 62% and 75% presence of postrostrum tails, presence of the tail was not incorporated into the average shape of the otolith outlines as defined by the software package (Figure 3-5). This may be a result of using the ShapeR package to smooth out each outline to eliminate pixel noise. The lack of postrostrum tails in the average shape of those southern watersheds could also be due to the variation in placement of those tails making it difficult for them to show up in one location in the average shape.

In addition to postrostrum tails, other properties of the otolith such as color, holes, spacing of annuli, and three-dimensional shape are overlooked using this outline shape type of analysis. It was observed while photographing that otoliths varied in shade of white and transparency. Differences in color may affect how the ShapeR program is able to accurately detect outlines. Some otoliths displayed holes through the entirety of the otolith in varied regions, but these holes would not influence the outline. Differences in length of annuli were noted but were not analyzed further in this study. Three-dimensional shape variation was a factor we pondered; however, the technology to analyze it was not available.

Timing of sample collection should be considered for future studies attempting to differentiate spawning populations of Hickory Shad using otolith shape. Hickory Shad migrate into coastal rivers earlier than other anadromous species. This may affect state agencies going about their spring sampling for anadromous fishes, causing them to capture Hickory Shad mainly from the end of the downstream post-spawn migration. Anecdotally, we observed Hickory Shad in February and March of 2019 in the Neuse River and its tributaries, while at the same time anglers were reporting Hickory Shad being caught off Avalon Pier on the Outer Banks of North Carolina. This indicates that there may be multiple waves in the Hickory Shad migration. For these reasons, when samples are collected could be as important as where samples are collected. Respective state agencies go about their spring sampling in their own unique ways. Some of the sample sets of Hickory Shad used in this study were collected in a single day, while others were collected over a period of weeks or months.

This study used samples captured over three springs between 2016-2018 and included fish of all ages. This allowed for multiple year classes to be mixed together and compared to other combinations of year classes. While this could be the most practical way for researchers and fishery managers to analyze many watersheds, it may not be the optimal method for discriminating spawning populations. We encourage future researchers to standardize their sampling techniques including when, where, and how many samples are collected. Under the methods used in this study, average otolith shape of a watershed may be dependent on the ages and year classes of fish present in each sample set. It may be worth trying to compare otolith shapes of a single year class to others of the same year class.

Sample size varied between watersheds. We asked specimen providers to acquire at least 20 specimens of each sex for each tributary or watershed. Some state agency staff were more successful than others due to seasonal timing and watershed flooding. In some cases some watersheds or tributaries had to be left out of analyses due to small sample size. Standardization of sample size in each watershed is something we would recommend to future studies of Hickory Shad otolith shape. A number of post-hoc tests can be utilized for data sets with unequal sample sizes, but these post-hoc tests have all been found to be conservative (Shingala et al. 2015). Many post-hoc tests are especially conservative in cases with a high number of pairwise comparison such as this study. Benjamini and Hochberg's procedure for controlling for false discovery rate was used in this study in part because it is not overly conservative in cases with a high number of comparisons like other post-hoc tests e.g. Bonferroni correction. Results of the Benjamini and Hochberg method adjusted P-values were different from results of unadjusted P-values. The adjusted P-values resulted in 17 or 7.4% of watershed pairwise comparisons changing from significantly different to insignificantly different.

Despite potential issues with the sampling methods of this research, otoltith shape still found significant differences in 64.1% (56.7% after Benjamini and Hochberg FDR procedure) of pairwise comparisons of watersheds. Varying results of this study attempting to discriminate

sample sets captured in 22 watersheds by otolith shape led to the conclusion that the methods used here were not reliable for differentiating spawning populations of Hickory Shad; however, the fact that more than half of the otolith shape comparisons were significantly different suggests that homing to natal tributaries is plausible More sampling and standardization of sample size, timing, and age may help in differentiating spawning populations of Hickory Shad using otolith shape.

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Tables

Abbreviation	Watershed							
SU	Susquehanna River							
PA	Patapsco River							
PO	Potomac River							
PX	Patuxent River							
JA	James River							
AP	Appomattox River							
RA	Rappahannock River							
NT	Nanticoke River							
СН	Choptank River							
NO	Nottoway River							
BL	Blackwater River							
RO	Roanoke River							
CA	Cashie River							
ТА	Tar River							
NE	Neuse River							
CO	Contentnea Creek							
SW	Swift Creek (Neuse)							
PI	Pitchkettle Creek							
CF	Cape Fear River							
OG	Ogeechee River							
AL	Altamaha River							
SJ	St. Johns River							

Table 3-1. Table of watershed abbreviations used in the otolith shape study.

Table 3-2. Table summarizing P-value results of pairwise comparisons of watersheds using an ANOVA like permutation test. Sample size (n) is listed above and to the left of watershed abbreviations.

PA PO F	PX JA																30
	ΓΛ JΑ	AP I	RA N	T Cł	I NO	BL	RO	CA	TA	NE	CO	SW	PI	CF	OG	AL	SJ
.001 0.517 0.3	0.398 0.359	0.166 0.	.456 0.	0.4	8 0.093	0.056	0.059	0.004	0.012	0.007	0.004	0.001	0.03	0.006	0.086	0.025	0.122
/ 0.001 0.	0.086 0.001	0.002 0.	.002 0.	0.00	0.001	0.002	0.019	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001
.001 / 0.4	0.491 0.139	0.146 0.	.902 0.	027 0.6	6 0.026	0.018	0.004	0.009	0.008	0.002	0.006	0.001	0.024	0.001	0.016	0.016	0.022
.086 0.491	/ 0.846	0.488 0.	.837 0.	537 0.52	4 0.268	0.349	0.648	0.006	0.048	0.092	0.007	0.001	0.024	0.007	0.153	0.093	0.575
.001 0.139 0.1).846 /	0.087 0.	.293 0.1	321 0.2	0.31	0.634	0.053	0.005	0.046	0.042	0.005	0.002	0.003	0.001	0.156	0.081	0.411
.002 0.146 0.4	0.488 0.087	/ 0.	.189 0.	181 0.0	3 0.005	0.029	0.033	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.011	0.003	0.005
.002 0.902 0.3	0.837 0.293	0.189	/ 0.0	058 0.3	0.019	0.041	0.014	0.002	0.007	0.014	0.003	0.001	0.007	0.001	0.024	0.011	0.047
.027 0.027 0.	0.637 0.321	0.181 0.	.058	/ 0.0	5 0.023	0.14	0.657	0.001	0.001	0.002	0.001	0.001	0.002	0.001	0.025	0.005	0.354
.001 0.666 0.	0.524 0.269	0.03 0.	.387 0.0)35 /	0.188	0.052	0.013	0.106	0.129	0.008	0.062	0.01	0.286	0.03	0.075	0.134	0.068
.001 0.026 0.1	0.268 0.31	0.005 0.	.019 0.0	023 0.1	8 /	0.408	0.002	0.003	0.005	0.002	0.003	0.001	0.001	0.001	0.668	0.321	0.086
.002 0.018 0.1	0.349 0.634	0.029 0.	.041 0.	14 0.03	0.408	/	0.136	0.001	0.03	0.037	0.008	0.001	0.001	0.003	0.466	0.152	0.635
.019 0.004 0.	0.648 0.053	0.033 0.	.014 0.6	557 0.0	3 0.002	0.136	/	0.001	0.001	0.062	0.001	0.001	0.001	0.001	0.004	0.002	0.241
.001 0.009 0.0	0.006 0.005	0.001 0.	.002 0.0	001 0.1	6 0.003	0.001	0.001	/	0.093	0.001	0.179	0.27	0.309	0.147	0.001	0.005	0.002
.001 0.008 0.0	0.048 0.046	0.001 0.	.007 0.0	001 0.12	9 0.005	0.03	0.001	0.093	/	0.006	0.427	0.005	0.062	0.067	0.011	0.036	0.019
.001 0.002 0.0	0.092 0.042	0.001 0.	.014 0.0	0.00	0.002	0.037	0.062	0.001	0.006	/	0.001	0.001	0.001	0.001	0.006	0.005	0.192
.001 0.006 0.0	0.007 0.005	0.001 0.	.003 0.0	001 0.0	0.003	0.008	0.001	0.179	0.427	0.001	/	0.077	0.094	0.381	0.012	0.033	0.006
.001 0.001 0.0	0.001 0.002	0.001 0.	.001 0.0	0.0 0.0	0.001	0.001	0.001	0.27	0.005	0.001	0.077	/	0.263	0.036	0.001	0.001	0.001
.001 0.024 0.0	0.024 0.003	0.001 0.	.007 0.0	002 0.2	6 0.001	0.001	0.001	0.309	0.062	0.001	0.094	0.263	/	0.061	0.002	0.016	0.002
.001 0.001 0.	0.007 0.001	0.001 0.	.001 0.0	0.0 0.0	3 0.001	0.003	0.001	0.147	0.067	0.001	0.381	0.036	0.061	/	0.003	0.043	0.006
.001 0.016 0.	0.153 0.156	0.011 0.	.024 0.0	025 0.0	5 0.668	0.466	0.004	0.001	0.011	0.006	0.012	0.001	0.002	0.003	/	0.416	0.1
.001 0.016 0.0	0.093 0.081	0.003 0.	.011 0.0	005 0.13	4 0.321	0.152	0.002	0.005	0.036	0.005	0.033	0.001	0.016	0.043	0.416	/	0.127
.001 0.022 0	0.575 0.411	0.005 0.	.047 0.1	354 0.0	8 0.086	0.635	0.241	0.002	0.019	0.192	0.006	0.001	0.002	0.006	0.1	0.127	/
/ .001 .086 .001 .002 .002 .002 .001 .001 .001 .001	0.001 (, , (, 0.491 0.139 (0.139 (0.0902 (0.0027 (0.026 (0.026 (0.026 (0.004 (0.009 (0.0008 (0.0001 (0.0001 (0.001 (0.001 (0.001 (0.016 (0.001 (0.0016 (0.001 (0.001 0.086 0.001 / 0.491 0.139 5 0.491 / 0.846 0.139 0.846 / 2 0.146 0.488 0.087 2 0.146 0.488 0.087 2 0.146 0.488 0.087 2 0.146 0.488 0.087 2 0.146 0.488 0.087 2 0.146 0.488 0.087 2 0.146 0.488 0.293 0.027 0.637 0.321 0.666 0.524 0.269 0.026 0.268 0.31 2 0.018 0.349 0.634 0 0.004 0.648 0.053 0.009 0.006 0.005 0.0042 0.008 0.048 0.046 0.002 0.092 0.042 0.006 0.007 0.005 0.001 0.001 0.002 0.024 0.024 0.003 0.016 0.153	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	0.001 0.086 0.001 0.002 0.002 0.027 0.001 $/$ 0.491 0.139 0.146 0.902 0.027 0.666 5 0.491 $/$ 0.846 0.488 0.837 0.637 0.52 0.139 0.846 $/$ 0.087 0.293 0.321 0.266 2 0.146 0.488 0.087 $/$ 0.189 0.181 0.07 2 0.146 0.488 0.087 $/$ 0.189 0.181 0.07 2 0.146 0.488 0.087 $/$ 0.189 0.181 0.07 2 0.902 0.837 0.293 0.181 0.058 0.387 0.027 0.637 0.321 0.181 0.058 0.387 0.035 $/$ 0.026 0.268 0.31 0.005 0.019 0.023 0.18 2 0.018 0.349 0.634 0.029 0.041 0.14 <	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	0.001 0.086 0.001 0.002 0.002 0.027 0.001 0.002 0.019 0.001 0.001 / 0.491 0.139 0.146 0.902 0.027 0.666 0.026 0.018 0.004 0.009 0.008 5 0.491 / 0.846 0.488 0.837 0.637 0.524 0.268 0.349 0.648 0.006 0.048 0.139 0.846 / 0.087 0.293 0.321 0.269 0.31 0.634 0.053 0.005 0.001 2 0.146 0.488 0.087 / 0.189 0.181 0.03 0.005 0.029 0.033 0.001 0.001 2 0.902 0.837 0.293 0.189 / 0.035 0.023 0.144 0.657 0.001 0.001 2 0.902 0.837 0.293 0.189 / 0.035 0.023 0.148 0.657 0.001 0.001 0.001 0.026 0.637 0.31 0.005 0.019 0.023	0.001 0.086 0.001 0.002 0.002 0.027 0.001 0.002 0.019 0.001 <th< th=""><th>0.001 0.086 0.001 0.002 0.002 0.027 0.001 0.002 0.019 0.001 <th< th=""><th>$\begin{array}{cccccccccccccccccccccccccccccccccccc$</th><th>0.001 0.086 0.001 0.002 0.027 0.001 <t< th=""><th>0.001 0.086 0.001 0.002 0.002 0.001 <t< th=""><th>0.001 0.086 0.001 0.002 0.002 0.027 0.001 <th< th=""><th>0.001 0.086 0.001 0.002 0.027 0.001 <th< th=""></th<></th></th<></th></t<></th></t<></th></th<></th></th<>	0.001 0.086 0.001 0.002 0.002 0.027 0.001 0.002 0.019 0.001 <th< th=""><th>$\begin{array}{cccccccccccccccccccccccccccccccccccc$</th><th>0.001 0.086 0.001 0.002 0.027 0.001 <t< th=""><th>0.001 0.086 0.001 0.002 0.002 0.001 <t< th=""><th>0.001 0.086 0.001 0.002 0.002 0.027 0.001 <th< th=""><th>0.001 0.086 0.001 0.002 0.027 0.001 <th< th=""></th<></th></th<></th></t<></th></t<></th></th<>	$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	0.001 0.086 0.001 0.002 0.027 0.001 <t< th=""><th>0.001 0.086 0.001 0.002 0.002 0.001 <t< th=""><th>0.001 0.086 0.001 0.002 0.002 0.027 0.001 <th< th=""><th>0.001 0.086 0.001 0.002 0.027 0.001 <th< th=""></th<></th></th<></th></t<></th></t<>	0.001 0.086 0.001 0.002 0.002 0.001 <t< th=""><th>0.001 0.086 0.001 0.002 0.002 0.027 0.001 <th< th=""><th>0.001 0.086 0.001 0.002 0.027 0.001 <th< th=""></th<></th></th<></th></t<>	0.001 0.086 0.001 0.002 0.002 0.027 0.001 <th< th=""><th>0.001 0.086 0.001 0.002 0.027 0.001 <th< th=""></th<></th></th<>	0.001 0.086 0.001 0.002 0.027 0.001 <th< th=""></th<>

Table 3-3. Table summarizing Benjamini and Hochberg method adjusted P-value results of pairwise comparisons of watersheds using an ANOVA like permutation test. Sample size (n) is listed above and to the left of watershed abbreviations.

n		18	45	30	12	54	40	41	17	18	58	23	32	31	43	15	29	33	34	32	37	24	30
		SU	PA	РО	РХ	JA	AP	RA	NT	СН	NO	BL	RO	CA	TA	NE	СО	SW	PI	CF	OG	AL	SJ
18	SU	/	0.004	0.545	0.440	0.403	0.205	0.490	0.196	0.453	0.126	0.086	0.089	0.012	0.025	0.016	0.012	0.004	0.051	0.014	0.120	0.045	0.162
45	PA	0.004	/	0.004	0.120	0.004	0.007	0.007	0.048	0.004	0.004	0.007	0.036	0.004	0.004	0.004	0.004	0.004	0.004	0.004	0.004	0.004	0.004
30	РО	0.545	0.004	/	0.520	0.179	0.186	0.902	0.048	0.677	0.047	0.035	0.012	0.020	0.018	0.007	0.014	0.004	0.044	0.004	0.032	0.032	0.042
12	РХ	0.440	0.120	0.520	/	0.850	0.519	0.844	0.657	0.550	0.317	0.395	0.665	0.014	0.075	0.126	0.016	0.004	0.044	0.016	0.192	0.126	0.601
54	JA	0.403	0.004	0.179	0.850	/	0.121	0.340	0.365	0.317	0.356	0.657	0.082	0.013	0.073	0.067	0.013	0.007	0.009	0.004	0.195	0.116	0.450
40	AP	0.205	0.007	0.186	0.519	0.121	/	0.229	0.221	0.051	0.013	0.051	0.055	0.004	0.004	0.004	0.004	0.004	0.004	0.004	0.023	0.009	0.013
41	RA	0.490	0.007	0.902	0.844	0.340	0.229	/	0.088	0.430	0.036	0.066	0.028	0.007	0.016	0.028	0.009	0.004	0.016	0.004	0.044	0.023	0.074
17	NT	0.196	0.048	0.048	0.657	0.365	0.221	0.088	/	0.058	0.043	0.180	0.672	0.004	0.004	0.007	0.004	0.004	0.007	0.004	0.045	0.013	0.399
18	CH	0.453	0.004	0.677	0.550	0.317	0.051	0.430	0.058	/	0.229	0.081	0.027	0.142	0.169	0.018	0.091	0.022	0.334	0.051	0.108	0.175	0.099
∞ 58	NO	0.126	0.004	0.047	0.317	0.356	0.013	0.036	0.043	0.229	/	0.449	0.007	0.009	0.013	0.007	0.009	0.004	0.004	0.004	0.677	0.365	0.120
► 23	BL	0.086	0.007	0.035	0.395	0.657	0.051	0.066	0.180	0.081	0.449	/	0.176	0.004	0.051	0.060	0.018	0.004	0.004	0.009	0.498	0.192	0.657
32	RO	0.089	0.036	0.012	0.665	0.082	0.055	0.028	0.672	0.027	0.007	0.176	/	0.004	0.004	0.091	0.004	0.004	0.004	0.004	0.012	0.007	0.288
31	CA	0.012	0.004	0.020	0.014	0.013	0.004	0.007	0.004	0.142	0.009	0.004	0.004	/	0.126	0.004	0.220	0.317	0.356	0.187	0.004	0.013	0.007
43	TA	0.025	0.004	0.018	0.075	0.073	0.004	0.016	0.004	0.169	0.013	0.051	0.004	0.126	/	0.014	0.461	0.013	0.091	0.098	0.023	0.059	0.036
15	NE	0.016	0.004	0.007	0.126	0.067	0.004	0.028	0.007	0.018	0.007	0.060	0.091	0.004	0.014	/	0.004	0.004	0.004	0.004	0.014	0.013	0.231
29	СО	0.012	0.004	0.014	0.016	0.013	0.004	0.009	0.004	0.091	0.009	0.018	0.004	0.220	0.461	0.004	/	0.110	0.127	0.425	0.025	0.055	0.014
33	SW	0.004	0.004	0.004	0.004	0.007	0.004	0.004	0.004	0.022	0.004	0.004	0.004	0.317	0.013	0.004	0.110	/	0.313	0.059	0.004	0.004	0.004
34	PI	0.051	0.004	0.044	0.044	0.009	0.004	0.016	0.007	0.334	0.004	0.004	0.004	0.356	0.091	0.004	0.127	0.313	/	0.091	0.007	0.032	0.007
32	CF	0.014	0.004	0.004	0.016	0.004	0.004	0.004	0.004	0.051	0.004	0.009	0.004	0.187	0.098	0.004	0.425	0.059	0.091	/	0.009	0.069	0.014
37	OG	0.120	0.004	0.032	0.192	0.195	0.023	0.044	0.045	0.108	0.677	0.498	0.012	0.004	0.023	0.014	0.025	0.004	0.007	0.009	/	0.453	0.134
24	AL	0.045	0.004	0.032	0.126	0.116	0.009	0.023	0.013	0.175	0.365	0.192	0.007	0.013	0.059	0.013	0.055	0.004	0.032	0.069	0.453	/	0.168
30	SJ	0.162	0.004	0.042	0.601	0.450	0.013	0.074	0.399	0.099	0.120	0.657	0.288	0.007	0.036	0.231	0.014	0.004	0.007	0.014	0.134	0.168	/

Watershed	Latitude of Mouth	Proportion with Tail					
Susquehanna River	39.535471	0.28					
Patapsco River	39.184458	0.27					
Choptank River	38.645058	0.28					
Patuxent River	38.316452	0.33					
Nanticoke River	38.222745	0.35					
Potomac River	37.983646	0.40					
Rappahannock River	37.591594	0.32					
James River	36.991086	0.37					
Appomattox River	36.991086	0.48					
Nottoway River	36.024193	0.43					
Blackwater River	36.024193	0.57					
Roanoke River	35.942867	0.38					
Cashie River	35.94015	0.48					
Tar River	35.327228	0.33					
Neuse River	35.113611	0.13					
Contentnea Creek	35.113611	0.28					
Swift Creek	35.113611	0.30					
Pitchkettle Creek	35.113611	0.26					
Cape Fear River	33.884715	0.53					
Ogeechee River	31.835503	0.62					
Altamaha River	31.315629	0.75					
St Johns River	30.402105	0.70					
	Average proportion	0.40					

Table 3-4. The latitude of the mouth of each watershed and the proportion of postrostrum tails counted.

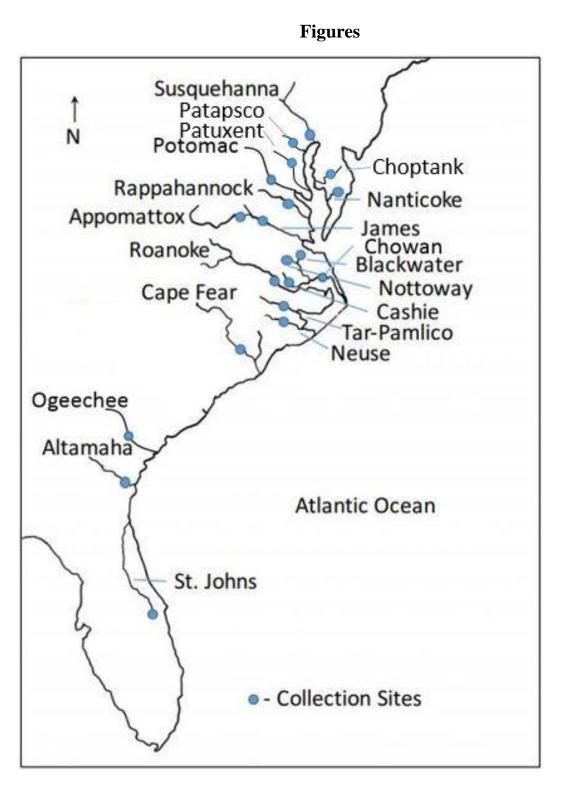


Figure 3-1. Map displaying relative location of rivers included in this otolith shape study as well as collection sites of Hickory Shad. Neuse tributaries Contentnea Creek, Pitchkettle Creek, Swift Creek, not shown. Revised after Melvin et al. 1992.

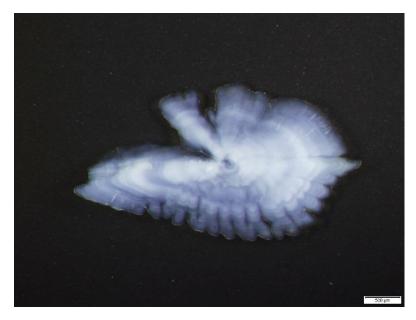


Figure 3-2. Photograph of the right sagittal otolith of an adult Hickory Shad, fish number 879 captured in Contentnea Creek.

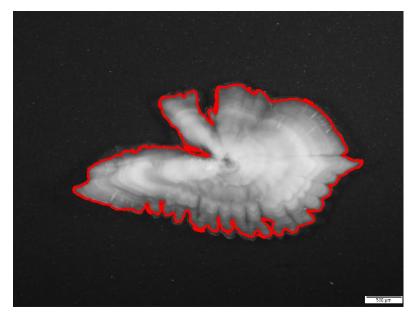


Figure 3-3. Photograph of the right sagittal otolith of an adult Hickory Shad, fish number 879 captured in Contentnea Creek with outline generated in R Studio using the ShapeR package.

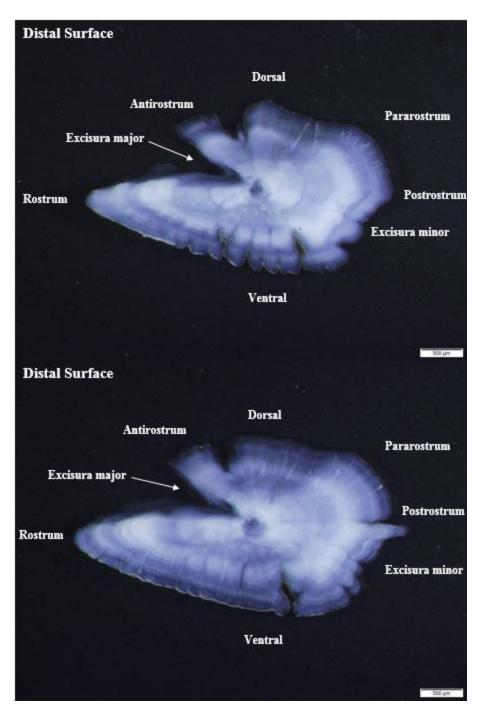


Figure 3-4. Labeled diagram of the distal surface anatomy of adult Hickory Shad otoliths without (top) and with (bottom) a postrostrum tail.

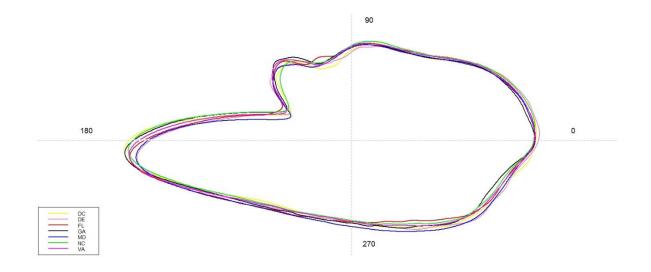


Figure 3-5. Average shape of otolith Wavelet coefficients from each state sampled.



Figure 3-6. Average shape of otolith Wavelet coefficients from each watershed sampled.

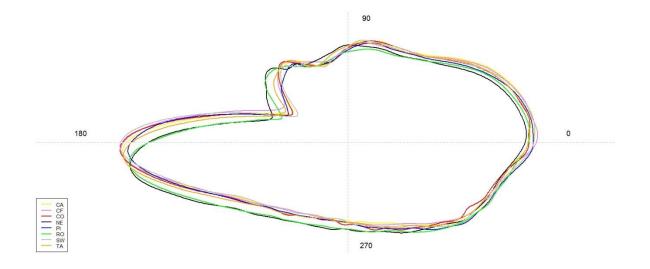


Figure 3-7. Average shape of otolith Wavelet coefficients from each watershed sampled in North Carolina.

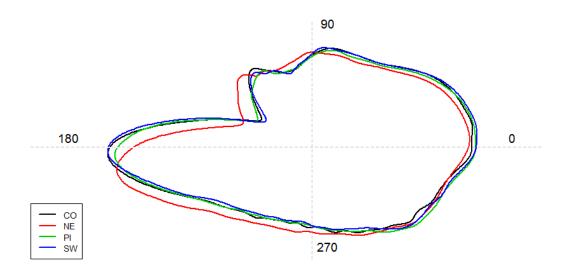


Figure 3-8. Average shape of otolith Wavelet coefficients from the Neuse River and its tributaries Contentnea Creek, Pitchkettle Creek, and Swift Creek.

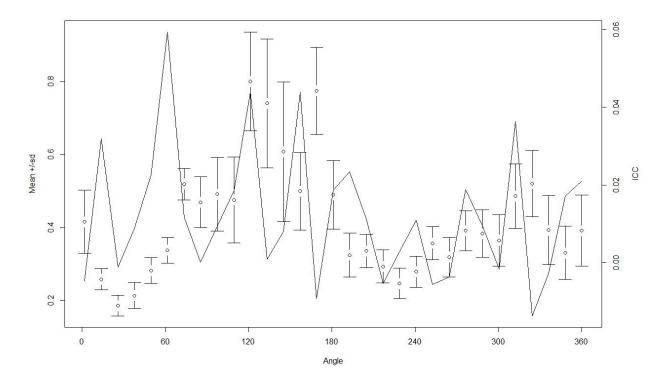


Figure 3-9. Mean plus and minus standard deviation (sd) of the Wavelet coefficients for all combined otoliths plotted with dot and error bars. The proportion of variance among groups or the intraclass correlation (ICC) plotted with a solid black line. The horizontal axis shows angle in degrees (°) based on polar coordinates (see also Figure 3-4, Figure 3-5, Figure 3-6, and Figure 3-7) where the centroid of the otolith is the center point of the polar coordinates.

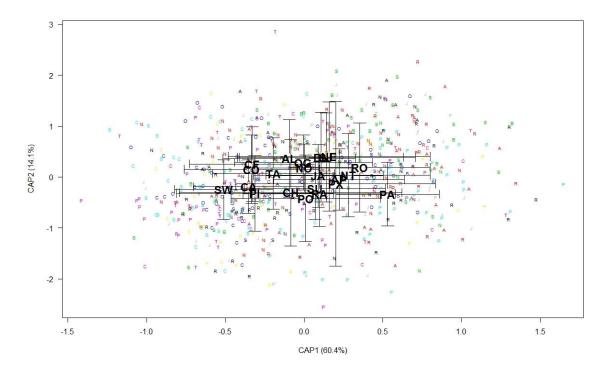


Figure 3-10. Otolith shape of samples plotted from 22 watersheds using Canonical analysis of Principal Coordinates with the Wavelet coefficients. Canonical scores on the first two discriminating axes CAP1 and CAP2 are shown. Black letters represent the mean canonical value for each watershed and smaller letters represent individual fish showing the first letter of each population. Interval surrounding the mean canonical values present 95% confidence intervals.

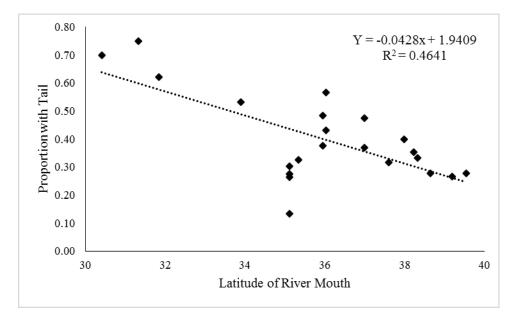


Figure 3-11. Graph showing linear regression of proportion of otoliths with a postrostrum tail vs. the latitude of the mouth of the watershed in which the sample was captured.

CHAPTER 4: CONCLUSIONS AND RECOMMENDATIONS

Stocks are defined as arbitrary groups of a fish species large enough to be essentially selfreproducing, with members of each group possessing similar life history characteristics (Hilborn and Walters 1992). The stock concept is the intersection of biological organization and human activities (Secor 1999); i.e., a management unit in fisheries management. The management unit might incorporate all the individual populations of a species within a large waterbody, such as those stocks designated for the anadromous Striped Bass Morone saxatilis (Walbaum, 1792) in Chesapeake Bay, Hudson River, and Albemarle/Roanoke River; all Striped Bass in oceans waters are designated the Atlantic coastal stock (Essig et al., in press). Alternately, a stock management unit might represent only one tributary of a larger waterbody if the management unit is by individual populations (e.g., the Nanticoke River or the Potomac River population of Striped Bass). Species that exhibit fidelity to a natal watershed, such as species of the Salmonidae family in the Pacific Northwest, may develop and maintain population spatial structure via genetic isolation, which leads to unique populations throughout the range (Smedbol and Wroblewski 2002). It is important to understand the population structure of a species because different populations may be exploited in different ways and experience different environmental conditions (Begg and Waldman 1999).

Begg and Waldman (1999) suggested that stock identification take on a 'holistic' approach, and that multiple techniques should be utilized to separate management units of fish. Combining multiple techniques allows for reliable inferences on stock structure by involving multiple aspects of the biology of a species. Utilizing different methods allows for comparative studies based upon the same sample sets, allowing regulatory bodies to develop stronger management strategies (Begg et al. 1999). The Hickory Shad *Alosa mediocris* (Mitchill, 1814) is an anadromous member of the Clupeidae family with a freshwater range from the Schuylkill River in Pennsylvania (Perillo and Butler 2009) to the St. Johns River in Florida (Harris et al. 2007). This extensive range makes the Hickory Shad a multi-jurisdictional species for management purposes. Hickory Shad are currently managed under Amendment 3 of the Atlantic States Marine Fisheries Commission (ASMFC) Interstate Fishery Management Plan (IFMP) for Shad and River Herring. However, this management plan only incorporates biological information for the American Shad *Alosa sapidissima* (Wilson, 1811) and river herring (Alewife *Alosa pseudoharengus* (Wilson, 1811) and Blueback Herring *A. aestivalis* (Mitchill, 1814) (ASMFC 2010). The American Shad has been applied as a model species for Hickory Shad management (Harris et al. 2007) but many aspects of American Shad life history applied to Hickory Shad have not been supported by literature.

The goal of this study was to determine if Hickory Shad spawning populations in different watersheds can be identified for use in fishery management plans. Five methods were selected for use on the Hickory Shad specimens collected: genetics, otolith shape, otolith chemistry, body shape (geometric morphometrics), and meristic and morphometric analyses. If one or more of these methods can separate spawning populations, then the results imply some degree of natal homing. Thus, the unique genetic and environmental conditions present in each watershed should result in statistically significant differences in body shapes and otolith shapes by each spawning population. My portion of the study examined differences in the otolith shape using the R package named ShapeR (Libungan and Pálsson 2015), and body shape using geometric morphometrics (Klingenberg 2011). The otolith shape analysis portion of this study was able differentiate among watershed 64.1% of pairwise comparisons, while body shape analysis was able to differentiate between watershed in 64.7% of pairwise comparisons of female samples, and 66.7% of male samples. This study gave results similar to those described by Vergara-Solana et al. (2013), which compared body shape and otolith shape as methods for stock delineation of Pacific sardine *Sardinops sagax* (Jenyns, 1842); their study claimed body shape was more discriminatory than otolith shape between groups of Pacific Sardine but considered that the population structure interpretations resulting from the two methods were relatively similar.

Results of geometric morphometric analysis of body shape in my study were similar to those of the concurrent Smith (2018) study of Hickory Shad stock identification using meristics and morphometrics. Both studies support the hypothesis of sexual dimorphism in Hickory Shad, and both were able to differentiate spawning populations to the tributary level in some cases. Meristics and morphometric analyses were able to determine significant difference between the James River spawning population and its tributary the Appomattox River population in both male and female specimens, but body shape analyses only determined significant difference between these populations in female specimens. Another parent river and tributary, the Roanoke and Cashie Rivers, were found to be significantly different in meristics and morphometric analyses, but lack of photographs of Roanoke specimens prevented testing differences in these watersheds using body shape analysis.

The results of the otolith shape analysis of Hickory Shad are similar with those of Rogers (2015) which determined no differences in otolith shape of adult Blueback Herring among sampling locations in North Carolina, but a significant difference in otolith shape comparing adult Blueback Herring otoliths collected in North Carolina to those collected in New Jersey.

Otolith shape was able to discriminate between some but not all Hickory Shad watersheds within North Carolina. Rogers (2015) results which revealed differences in otolith shape of Blueback Herring between North Carolina and New Jersey samples are similar to the findings of my study, which discovered differences in Hickory Shad otolith shape comparing North Carolina samples and Virginia samples.

Future studies should carefully consider sampling technique before attempting to identify spawning populations of an anadromous species such as Hickory Shad. Sample size varied between watersheds for various reasons. We asked specimen providers to acquire at least 20 specimens of each sex for each tributary or watershed. Some state agency staff were more successful than others due to seasonal timing and watershed flooding. In some cases some watersheds or tributaries had to be left out of analyses due to small sample size. Standardization of sample size in each watershed is something we would recommend to future studies looking to differentiate spawning populations of Hickory Shad.

Timing of sample collection should be considered for future studies attempting to differentiate spawning populations of Hickory Shad. Hickory Shad migrate into coastal rivers earlier than other anadromous species. This may affect state agencies going about their spring sampling for anadromous fishes, causing them to capture Hickory Shad mainly from the end of the spawning period. Some of the sample sets of Hickory Shad used in this study were collected in a single day, while others were collected over a period of weeks or months. Sample sizes within watersheds were not large enough to test differences in samples acquired throughout the spawning season; whether Hickory Shad migrate in watershed or tributary cohorts during the pre-spawning period could not be determined. My study used samples captured over three springs between 2016-2018 and included fish of all ages. This allowed for multiple year classes to be mixed together and compared to other combinations of year classes. While this method could be the most practical way for researchers and fishery managers to analyze many watersheds, it may not be the optimal method for discriminating spawning populations. We encourage future researchers to standardize their sampling techniques including when, where, and how many samples are collected. Under the methods used in this study, difference among watersheds may be dependent on the ages and year classes of fish present in each sample set. It may be worth trying to compare a single year class to others of the same year class among the watersheds, or tributaries within a watershed.

One perceived threat to Hickory Shad is loss of spawning habitat due to dams (Rulifson et al. 1982; Rulifson 1994; Limburg and Waldman 2009). Dam construction on U.S. rivers began as early as the industrial revolution (Hall et al. 2011). Fish passage efforts increased in the late 1970s through early 1990s as mandated by the Federal Energy Regulatory Commission (FERC) to provide passage for migratory fishes (Gephard and McMenemy 2004). Nevertheless, studies inspecting the effectiveness of current fish passage-ways point out that there is still room for improvement of passage-ways (Moser et al. 2000; Cooke and Leach 2004; Brown et al. 2013; Smith and Rulifson 2015). Fortunately for diadromous fish, dam removal has become a priority on many rivers, and the ASMFC (2010) lists this as one of their strategies to restore "shad" and river herring populations. Perillo (2006) studied the ability of Hickory Shad to use a fish ladder in a Schuylkill River tributary and determined that they were successful. Additional studies testing Hickory Shad success to navigate various fishway designs would be beneficial.

Another possible threat to Hickory Shad is overfishing. The ASMFC's American Shad stock assessment reported that American Shad stocks had reached "all-time lows" (ASMFC

2010). Stock declines were attributed to high mortality, habitat decrease/degradation, and barriers to migration; i.e., dams (ASMFC 2010). Since Hickory Shad are believed to share a similar life history to American Shad, these anthropogenic factors could have a comparable effect on Hickory Shad populations (Rulifson 1994). In addition, declining stocks of American Shad could negatively impact Hickory Shad if recreational fishing effort is shifted to focus on the more abundant Hickory Shad.

With Hickory Shad populations vulnerable to factors like habitat degradation and overfishing, it is increasingly important that more research be focused on the species. More information on their fundamental biology, life history, and population structure would make for better decision making by fishery managers. While this study was a first attempt at stock delineation of Hickory Shad, it should not be the last. Future studies should consider the results of this study and the lessons learned in further attempts to discover the population structure of Hickory Shad. Only through better understanding of the species can we hope to protect it throughout the entirety of its range.

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APPENDIX A: IACUC APROVAL East Carolina University.

Animal Care and Use Committee 212 Ed Warren Life Sciences Building East Carolina University Greenville, NC 27834

August 11, 2015

252-744-2436 office 252-744-2355 (ax Roger Rulifson, Ph.D. Department of ICSP/Biology Flanagan Building East Carolina University

Dear Dr. Rulifson:

Your Animal Use Protocol entitled, "Hickory Shad 2015" (AUP #D330) was reviewed by this institution's Animal Care and Use Committee on August 10, 2015. The following action was taken by the Committee:

"Approved as submitted"

Note: IACUC administratively changed the word mutilate to euthanize in the nontechnical summary, changed Fintrol to Finquel, and deleted the extraneous MS 222 information under V.C since it is contained in the Appendix 1.

A copy is enclosed for your laboratory files. Please be reminded that all animal procedures must be conducted as described in the approved Animal Use Protocol. Modifications of these procedures cannot be performed without prior approval of the ACUC. The Animal Welfare Act and Public Health Service Guidelines require the ACUC to suspend activities not in accordance with approved procedures and report such activities to the responsible University Official (Vice Chancellor for Health Sciences or Vice Chancellor for Academic Affairs) and appropriate federal Agencies. Please ensure that all personnel associated with this protocol have access to this approved copy of the AUP and are familiar with its contents.

Sincerely yours,

Bhckar

Susan McRae, Ph.D. Chair, Animal Care and Use Committee

SM/jd

enclosure

Eut Carolina University is a construction networken of the University of Narob Carolina, Auroped opperations intervents.

APPENDIX B: DATA

Body Shape (Geometric Morphometrics)

ANOVA

Procrustes ANOVA: Procrustes ANOVA ... Dataset: newDataset Classifiers used for the Procrustes ANOVA: Individuals: Sex Centroid size: SS F P (param.) Effect MS df Individual 391955.201444 391955.201444 1 270.26 <.0001 Residual 1094966.092910 1450.286216 755 Shape, Procrustes ANOVA: MS df F P (param.) Pillai tr. P (param.) Effect SS Individual 0.10893698 0.0038906065 28 106.33 <.0001 0.59 <.0001 Residual 0.77352720 0.0000365907 21140 Procrustes ANOVA: Procrustes ANOVA ... Females by State Dataset: F Classifiers used for the Procrustes ANOVA: Individuals: State Centroid size: SS MS df F P (param.) Effect Individual 66023.771875 13204.754375 9.54 5 <.0001 Residual 478999.205386 1384.390767 346 Shape, Procrustes ANOVA: MS F P (param.) Pillai tr. P (param.) Effect SS df Individual 0.05919803 0.0004228430 140 10.69 <.0001 1.57 <.0001 Residual 0.38329707 0.0000395641 9688 Procrustes ANOVA: Procrustes ANOVA ... Males by state Dataset: M Classifiers used for the Procrustes ANOVA: Individuals: State Centroid size: Effect SS MS df F P (param.) Individual 27554.753532 5510.950706 5 4.21 0.0010 Residual 522388.362116 1309.244015 399 Shape, Procrustes ANOVA: df F P (param.) Pillai tr. P (param.) Effect SS MS Individual 0.01956958 0.0001397827 140 5.01 <.0001 1.44 <.0001 Residual 0.31152484 0.0000278844 11172 Procrustes ANOVA: Procrustes ANOVA ... Females by watershed Dataset: F Classifiers used for the Procrustes ANOVA: Individuals: Watershed Centroid size: Effect SS MS df F P (param.) Individual 177512.603573 10441.917857 17 9.49 <.0001 Residual 367510.373688 1100.330460 334 Shape, Procrustes ANOVA: Effect SS MS df F P (param.) Pillai tr. P (param.) Individual 0.13245137 0.0002782592 476 8.39 <.0001 3.84 <.0001 Residual 0.31004373 0.0000331527 9352 Procrustes ANOVA: Procrustes ANOVA ... Males by Watershed Dataset: M Classifiers used for the Procrustes ANOVA: Individuals: Watershed

Centroid siz	ze:						
Effect	SS	MS	df	F	P (param.)		
Individual	153073.44158	7 9004.320093	17	8.78	<.0001		
Residual	396869.674062	2 1025.503034	387				
Shape, Proc	rustes ANOVA	A:					
Effect	SS	MS	df	F	P (param.)	Pillai tr.	P (param.)
Individual	0.04286498	0.0000900525	476	3.39	<.0001	3.52	<.0001
Residual	0.28822944	0.0000265992	10836				

PCA

16 landmarks in 1 dimensions. The dataset contains 757 observations, of which 757 are included for analyses.

Data matrices in this dataset: - PC scores, CovMatrix, newDataset, Procrustes coordinates

Principal Component Analysis: PCA: CovMatrix, newDataset, Procrustes coordinates

	Eigenvalues	% Variance	Cumulative %
1.	0.00071728	61.449	61.449
2.	0.00014745	12.632	74.081
3.	0.00006628	5.678	79.759
4.	0.00004424	3.790	83.549
5.	0.00004232	3.625	87.174
6.	0.00002792	2.392	89.566
7.	0.00002143	1.836	91.402
8.	0.00001727	1.479	92.881
9.	0.00001422	1.219	94.100
10.	0.00001254	1.075	95.175
11.	0.00000992	0.849	96.024
12.	0.00000841	0.720	96.744
13.	0.00000793	0.679	97.423
14.	0.00000629	0.539	97.962
15.	0.00000374	0.320	98.282
16.	0.00000331	0.283	98.565
17.	0.00000281	0.241	98.806
18.	0.00000253	0.217	99.023
19.	0.00000235	0.202	99.224
20.	0.00000223	0.191	99.416
21.	0.00000160	0.137	99.553
22.	0.00000131	0.113	99.665
23.	0.00000104	0.089	99.754
24.	0.00000093	0.079	99.834
25.	0.00000071	0.061	99.895
26.	0.00000057	0.049	99.944
27.	0.00000039	0.034	99.978
28.	0.00000026	0.022	100.000

Total variance: 0.00116728

Variance of the eigenvalues: 0.0000000177836 Eigenvalue variance scaled by total variance: 0.01305 Eigenvalue variance scaled by total variance and number of variables: 0.37898 Note: throughout all calculations of eigenvalue variances, the dimensionality used was 28. Please double-check because this dimensionality may not be appropriate for all situations.

Principal Component Analysis: PCA: CovMatrix, F, Procrustes coordinates

	Eigenvalues 9	% Variance	Cumulative %
1.	0.00081026	64.273	64.273
2.	0.00015270	12.112	76.385
3.	0.00006379	5.060	81.445
4.	0.00004297	3.408	84.853
5.	0.00003845	3.050	87.904
6.	0.00003241	2.571	90.475
7.	0.00001961	1.556	92.030
8.	0.00001845	1.463	93.494
9.	0.00001419	1.125	94.619
10.	0.00001274	1.011	95.630
11.	0.00000944	0.749	96.378
12.	0.00000862	0.684	97.062
13.	0.00000748	0.594	97.656
14.	0.00000700	0.555	98.211

15.	0.00000371	0.294	98.505
16.	0.00000283	0.224	98.730
17.	0.00000262	0.208	98.938
18.	0.00000260	0.206	99.144
19.	0.00000216	0.171	99.315
20.	0.00000212	0.168	99.483
21.	0.00000155	0.123	99.606
22.	0.00000128	0.102	99.708
23.	0.00000105	0.083	99.791
24.	0.00000092	0.073	99.864
25.	0.00000058	0.046	99.910
26.	0.00000053	0.042	99.952
27.	0.0000038	0.030	99.982
28.	0.00000022	0.018	100.000

Total variance: 0.00126067

Variance of the eigenvalues: 0.000000226050 Eigenvalue variance scaled by total variance: 0.01422 Eigenvalue variance scaled by total variance and number of variables: 0.41300 Note: throughout all calculations of eigenvalue variances, the dimensionality used was 28. Please double-check because this dimensionality may not be appropriate for all situations.

Principal Component Analysis: PCA: CovMatrix, M, Procrustes coordinates

			G 1.1 M
			Cumulative %
1.	0.00046237		56.418
2.	0.00007640	9.322	65.741
3.	0.00006880		74.136
4.	0.00004455		79.572
5.	0.00002901	3.540	83.112
6.	0.00002313	2.823	85.934
7.	0.00002169	2.647	88.581
8.	0.00001692	2.065	90.646
9.	0.00001371	1.673	92.320
10.	0.00001180	1.440	93.760
11.	0.00000855	1.044	94.804
12.	0.00000786	0.960	95.763
13.	0.00000708	0.864	96.627
14.	0.00000487	0.595	97.221
15.	0.00000360	0.439	97.660
16.	0.00000345	0.421	98.081
17.	0.00000257	0.314	98.395
18.	0.00000244	0.298	98.693
19.	0.00000233	0.285	98.977
20.	0.00000206	0.252	99.229
21.	0.00000147	0.179	99.408
22.	0.00000119	0.146	99.554
23.	0.00000094	0.115	99.669
24.	0.00000089	0.109	99.777
25.	0.00000067	0.081	99.859
26.	0.00000054	0.066	99.924
27.	0.00000034	0.042	99.966
28.	0.0000028	0.034	100.000

Total variance: 0.00081954

Variance of the eigenvalues: 0.000000073242 Eigenvalue variance scaled by total variance: 0.01090 Eigenvalue variance scaled by total variance and number of variables: 0.31664 Note: throughout all calculations of eigenvalue variances, the dimensionality used was 28. Please double-check because this dimensionality may not be appropriate for all situations.

Principal Component Analysis: PCA: Procrustes ANOVA ... Female NC vs VA: Residual

	Eigenvalues	% Variance	Cumulative %
1.	0.00074530	63.428	63.428
2.	0.00014175	12.063	75.492
3.	0.00006415	5.460	80.951
4.	0.00004233	3.602	84.553
5.	0.00003590	3.055	87.608
6.	0.00002853	2.428	90.036
7.	0.00002037	1.734	91.770
8.	0.00001816	1.546	93.315
9.	0.00001461	1.243	94.558
10.	0.00001108	0.943	95.501
11.	0.00000885	0.753	96.254

12.	0.00000811	0.690	96.944
13.	0.00000716	0.609	97.553
14.	0.00000630	0.536	98.089
15.	0.00000374	0.318	98.407
16.	0.00000293	0.250	98.657
17.	0.00000277	0.236	98.893
18.	0.00000251	0.214	99.106
19.	0.00000235	0.200	99.306
20.	0.00000198	0.168	99.475
21.	0.00000159	0.135	99.610
22.	0.00000125	0.106	99.717
23.	0.00000096	0.082	99.798
24.	0.00000072	0.061	99.859
25.	0.00000058	0.049	99.908
26.	0.00000054	0.046	99.954
27.	0.00000035	0.030	99.984
28.	0.00000019	0.016	100.000

Total variance: 0.00117503

Variance of the eigenvalues: 0.0000000191297 Eigenvalue variance scaled by total variance: 0.01386 Eigenvalue variance scaled by total variance and number of variables: 0.40231 Note: throughout all calculations of eigenvalue variances, the dimensionality used was 28. Please double-check because this dimensionality may not be appropriate for all situations.

Principal Component Analysis: PCA: CovMatrix, Combined dataset ...Male NC vs VA, Procrustes coordinates

	Eigenvalues 9	% Variance	Cumulative %
1.	0.00051315	58.144	58.144
2.	0.00008104	9.183	67.327
3.	0.00007466	8.460	75.786
4.	0.00004634	5.251	81.037
5.	0.00002685	3.043	84.080
6.	0.00002682	3.039	87.119
7.	0.00002238	2.536	89.654
8.	0.00001473	1.669	91.323
9.	0.00001326	1.502	92.825
10.	0.00001142	1.294	94.119
11.	0.00000913	1.035	95.154
12.	0.00000773	0.876	96.030
13.	0.00000724	0.821	96.850
14.	0.00000506	0.574	97.424
15.	0.00000413	0.468	97.892
16.	0.00000334	0.379	98.271
17.	0.00000274	0.310	98.581
18.	0.00000222	0.252	98.833
19.	0.00000214	0.242	99.075
20.	0.00000189	0.214	99.289
21.	0.00000141	0.160	99.449
22.	0.00000121	0.138	99.586
23.	0.00000093	0.105	99.692
24.	0.00000080	0.091	99.782
25.	0.00000067	0.076	99.858
26.	0.00000059	0.067	99.926
27.	0.00000035	0.040	99.965
28.	0.00000031	0.035	100.000

DFA Males vs Females

Discriminant Function Analysis 'Discriminant function ...' Comparison: F -- M

Difference between means: Procrustes distance: 0.02405120 Mahalanobis distance: 2.4054 T-square: 1089.6442, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: F Group 2: M From discriminant function: True Allocated to Group Group 2 Total Group 1 300 Group 1 52 352 Group 2 29 376 405 From cross-validation: True Allocated to Group Group 2 Group 1 Total Group 1 293 59 352 Group 2 37 368 405

DFA Females NC vs Virginia

Discriminant Function Analysis 'Discriminant function ...Females by State' Comparison: NC -- VA

Difference between means: Procrustes distance: 0.01219826 Mahalanobis distance: 1.1556 T-square: 75.4302, P-value (parametric): 0.0003 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0020 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: NC Group 2: VA From discriminant function: True Allocated to Group 2 Group Group 1 Total Group 1 79 32 111 Group 2 36 79 115 From cross-validation: Allocated to True Group Group 1 Group 2 Total Group 1 42 69 111 Group 2 47 68 115

DFA Males NC vs Virginia

Discriminant Function Analysis 'Discriminant function ...Males by State' Comparison: NC -- VA

Difference between means: Procrustes distance: 0.00397576 Mahalanobis distance: 1.2447 T-square: 101.7174, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2650 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: NC Group 2: VA From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 111 37 148 Group 2 85 118 33 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 99 49 148 Group 2 41 77 118

DFA Females by watershed

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Alt -- App

Difference between means: Procrustes distance: 0.04427030 Mahalanobis distance: 7.7315 T-square: 746.0135, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Alt Group 2: App From discriminant function: True Allocated to Group Group 1 Total Group 2 Group 1 0 26 26 Group 2 0 24 24 From cross-validation: Allocated to True Group Group 1 Group 2 Total Group 1 25 1 26 3 Group 2 21 24

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Alt -- Bla

Difference between means: Procrustes distance: 0.02585036 Mahalanobis distance: 9.0050 T-square: 702.7844, P-value (parametric): 0.0015 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0190 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Alt Group 2: Bla From discriminant function: True Allocated to Group Group 1 Group 2 Total 26 Group 1 26 0 13 Group 2 0 13 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 23 3 26 Group 2 3 10 13

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Alt -- Cas

Difference between means: Procrustes distance: 0.02562791 Mahalanobis distance: 8.0190 T-square: 660.9878, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0030 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.) Classification/misclassification tables Group 1: Alt Group 2: Cas From discriminant function: True Allocated to Group 1 Total Group Group 2 Group 1 0 26 26 Group 2 0 17 17 From cross-validation: True Allocated to Group Group 1 Group 2 Total 26 Group 1 22 4 Group 2 2 15 17

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Alt -- Cho

Difference between means: Procrustes distance: 0.02768086 Mahalanobis distance: 9.6071 T-square: 1099.8752, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Alt Group 2: Cho From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 26 0 26 22 Group 2 0 22 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 23 3 26 2 20 22 Group 2

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Alt -- Con

Difference between means: Procrustes distance: 0.01788764 Mahalanobis distance: 5.4414 T-square: 304.3531, P-value (parametric): 0.0063 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0890 T-square: 0.0060 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Alt Group 2: Con From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 26 0 26 Group 2 0 17 17 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 20 6 26 Group 2 5 12 17

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Alt -- Her

Difference between means: Procrustes distance: 0.03774151 Mahalanobis distance: 8.1277 T-square: 572.5148, P-value (parametric): 0.0036 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0010 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Alt Group 2: Her From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 26 0 26 Group 2 0 13 13 From cross-validation: Allocated to True Group Group 1 Group 2 Total 26 Group 1 20 6 Group 2 3 10 13

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Alt -- Jam

Difference between means: Procrustes distance: 0.01609779 Mahalanobis distance: 13.5217 T-square: 1501.1779, P-value (parametric): 0.0002 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1780 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Alt Group 2: Jam From discriminant function: True Allocated to Group 1 Group Group 2 Total Group 1 0 26 26 Group 2 0 12 12 From cross-validation: Allocated to True Group Group 1 Group 2 Total 25 26 Group 1 1 2 Group 2 10 12

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Alt -- Nan

Difference between means: Procrustes distance: 0.05356470 Mahalanobis distance: 12.1275 T-square: 1456.7501, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Alt Group 2: Nan From discriminant function: True Allocated to Group Group 1 Group 2 Total 26 Group 1 26 0 Group 2 0 16 16 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 2 26 24 15 Group 2 1 16

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Alt -- Not

Difference between means: Procrustes distance: 0.01728303 Mahalanobis distance: 5.6226 T-square: 433.3897, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0200 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Alt Group 2: Not From discriminant function: True Allocated to Group 1 Group Group 2 Total 26 Group 1 26 0 Group 2 0 29 29 From cross-validation: True Allocated to Total Group Group 1 Group 2 Group 1 22 4 26 5 24 29 Group 2

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Alt -- Oge

Difference between means: Procrustes distance: 0.02323101 Mahalanobis distance: 6.3903 T-square: 498.3644, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0040 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

```
Classification/misclassification tables
Group 1: Alt
Group 2: Oge
From discriminant function:
True
             Allocated to
Group
           Group 1
                        Group 2
                                     Total
Group 1
             26
                        0
                                 26
Group 2
             0
                       23
                                  23
From cross-validation:
True
             Allocated to
Group
           Group 1
                        Group 2
                                     Total
Group 1
             21
                        5
                                 26
Group 2
              4
                       19
                                 23
```

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Alt -- Pit

Difference between means: Procrustes distance: 0.02397688 Mahalanobis distance: 6.6289 T-square: 639.0201, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classificat	Classification/misclassification tables					
Group 1: A	Alt					
Group 2: I	Pit					
From disc	riminant fur	nction:				
True	Allocat	ed to				
Group	Group 1	Group 2		Total		
Group 1	26	0	26			
Group 2	0	33	33			
From cros	s-validation	:				
True	Allocat	ed to				
Group	Group 1	Group 2		Total		
Group 1	22	4	26			
Group 2	1	32	33			

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Alt -- Pot

Difference between means: Procrustes distance: 0.02406428 Mahalanobis distance: 7.7079 T-square: 772.3556, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0010 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Alt Group 2: Pot From discriminant function: Allocated to True Group Group 1 Group 2 Total 26 Group 1 26 0 Group 2 0 26 26 From cross-validation: True Allocated to Group 1 Group Group 2 Total Group 1 22 4 26 0 26 Group 2 26

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Alt -- Rap

Difference between means: Procrustes distance: 0.01830805 Mahalanobis distance: 6.9069 T-square: 595.3641, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0330 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Alt Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total

Group 1	26	0	26	
Group 2	0	24	24	
From cros	s-validation	:		
True	Allocated to			
Group	Group 1	Group 2		Total
Group 1	24	2	26	
Group 2	1	23	24	

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Alt -- Sus

Difference between means: Procrustes distance: 0.03709720 Mahalanobis distance: 12.5776 T-square: 1371.0332, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Alt Group 2: Sus From discriminant function: True Allocated to Group Group 1 Group 2 Total 26 Group 1 26 0 13 Group 2 0 13 From cross-validation: True Allocated to Group Group 1 Group 2 Total 26 Group 1 24 2 2 11 Group 2 13

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Alt -- SwN

Difference between means: Procrustes distance: 0.01990071 Mahalanobis distance: 6.6380 T-square: 400.9739, P-value (parametric): 0.0083 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0610 T-square: 0.0060 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Alt Group 2: SwN From discriminant function: Allocated to True Group Group 1 Group 2 Total Group 1 26 0 26 Group 2 0 14 14 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 21 5 26 10 14 Group 2 4

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Alt -- SwT

Difference between means: Procrustes distance: 0.02342798 Mahalanobis distance: 6.0430 T-square: 435.1739, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0040 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Alt Group 2: SwT From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 26 26 0 0 22 22 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total 26 25 Group 1 1 Group 2 4 18 22

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Alt -- Tar

Difference between means: Procrustes distance: 0.02442672 Mahalanobis distance: 11.3776 T-square: 791.9345, P-value (parametric): 0.0520 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0730 T-square: 0.0530 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Alt Group 2: Tar From discriminant function: True Allocated to Group Group 1 Group 2 Total 26 Group 1 26 0 0 8 Group 2 8 From cross-validation: Allocated to True Group Group 1 Group 2 Total Group 1 19 7 26 Group 2 3 5 8

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: App -- Bla

Difference between means: Procrustes distance: 0.03880705 Mahalanobis distance: 7.5026 T-square: 474.6506, P-value (parametric): 0.0257 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: 0.0200 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Bla From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 24 0 24 0 13 Group 2 13 From cross-validation:

True	Allocat			
Group	Group 1	Group 2		Total
Group 1	16	8	24	
Group 2	2	11	13	

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: App -- Cas

Difference between means: Procrustes distance: 0.03450836 Mahalanobis distance: 6.4752 T-square: 417.2382, P-value (parametric): 0.0040 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: 0.0040 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Cas From discriminant function: True Allocated to Group 1 Group 2 Total Group Group 1 24 0 24 Group 2 0 17 17 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 19 5 24 7 17 Group 2 10

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: App -- Cho

Difference between means: Procrustes distance: 0.05363580 Mahalanobis distance: 11.6026 T-square: 1545.1982, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Cho From discriminant function: True Allocated to Group 1 Group Group 2 Total Group 1 24 0 24 0 22 22 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 22 2 24 Group 2 0 22 22

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: App -- Con

Difference between means: Procrustes distance: 0.03145512 Mahalanobis distance: 8.5663 T-square: 730.2437, P-value (parametric): 0.0003 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Con From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 24 0 24 Group 2 0 17 17 From cross-validation: True Allocated to Group 1 Group 2 Total Group Group 1 20 4 24 3 17 Group 2 14

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: App -- Her

Difference between means: Procrustes distance: 0.01016327 Mahalanobis distance: 6.2834 T-square: 332.9251, P-value (parametric): 0.0713 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.4650 T-square: 0.0620 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Her From discriminant function: True Allocated to Group 1 Group Group 2 Total 24 Group 1 24 0 0 13 Group 2 13 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 12 12 24 13 Group 2 5 8

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: App -- Jam

Difference between means: Procrustes distance: 0.03574386 Mahalanobis distance: 8.8838 T-square: 631.3718, P-value (parametric): 0.0212 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0040 T-square: 0.0210 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Jam From discriminant function: True Allocated to Group 1 Group 2 Total Group Group 1 24 0 24 0 12 Group 2 12 From cross-validation: True Allocated to Group 1 Group Group 2 Total Group 1 19 5 24

Group 2 2 10 12

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: App -- Nan

Difference between means: Procrustes distance: 0.01599526 Mahalanobis distance: 5.6128 T-square: 302.4323, P-value (parametric): 0.0252 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1090 T-square: 0.0220 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Nan From discriminant function: True Allocated to Group Group 1 Group 2 Total 0 24 Group 1 24 Group 2 0 16 16 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 18 6 24 Group 2 7 9 16

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: App -- Not

Difference between means: Procrustes distance: 0.03953821 Mahalanobis distance: 5.6412 T-square: 417.8976, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Not From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 24 24 0 Group 2 0 29 29 From cross-validation: True Allocated to Group 1 Group 2 Group Total Group 1 19 5 24 5 29 Group 2 24

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: App -- Oge

Difference between means: Procrustes distance: 0.02820891 Mahalanobis distance: 5.5009 T-square: 355.3992, P-value (parametric): 0.0004 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0010 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.) Classification/misclassification tables Group 1: App Group 2: Oge From discriminant function: True Allocated to Group 1 Total Group Group 2 Group 1 0 24 24 Group 2 1 22 23 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 24 19 5 Group 2 17 23 6

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: App -- Pit

Difference between means: Procrustes distance: 0.05180895 Mahalanobis distance: 5.8205 T-square: 470.7332, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Pit From discriminant function: True Allocated to Group 1 Group Group 2 Total Group 1 24 0 24 0 33 Group 2 33 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 22 2 24 0 33 33 Group 2

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: App -- Pot

Difference between means: Procrustes distance: 0.05550589 Mahalanobis distance: 7.9454 T-square: 787.8468, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Pot From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 24 0 24 Group 2 0 26 26 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 21 3 24 Group 2 0 26 26

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: App -- Rap

Difference between means: Procrustes distance: 0.03429697 Mahalanobis distance: 4.7010 T-square: 265.1911, P-value (parametric): 0.0016 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: 0.0010 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 24 0 24 Group 2 1 23 24 From cross-validation: Allocated to True Group Group 1 Group 2 Total 24 Group 1 16 8 Group 2 5 19 24

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: App -- Sus

Difference between means: Procrustes distance: 0.01652315 Mahalanobis distance: 10.0702 T-square: 855.1208, P-value (parametric): 0.0038 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1230 T-square: 0.0060 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Sus From discriminant function: True Allocated to Group 1 Group 2 Group Total Group 1 0 24 24 0 Group 2 13 13 From cross-validation: Allocated to True Group Group 1 Group 2 Total Group 1 16 8 24 Group 2 1 12 13

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: App -- SwN

Difference between means: Procrustes distance: 0.03946133 Mahalanobis distance: 7.6063 T-square: 511.5707, P-value (parametric): 0.0108 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: 0.0080 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: SwN From discriminant function: True Allocated to Group Group 1 Group 2 Total 24 Group 1 24 0 Group 2 0 14 14 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 20 4 24 3 14 Group 2 11

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: App -- SwT

Difference between means: Procrustes distance: 0.02791984 Mahalanobis distance: 6.4156 T-square: 472.4477, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0010 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: SwT From discriminant function: True Allocated to Group 1 Group Group 2 Total 24 Group 1 24 0 Group 2 0 22 22 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 23 1 24 4 18 22 Group 2

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: App -- Tar

Difference between means: Procrustes distance: 0.02243728 Mahalanobis distance: 7.6644 T-square: 352.4571, P-value (parametric): 0.4927 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0870 T-square: 0.4970 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

```
Classification/misclassification tables
Group 1: App
Group 2: Tar
From discriminant function:
True
             Allocated to
Group
           Group 1
                        Group 2
                                      Total
Group 1
             24
                        0
                                  24
Group 2
             0
                        8
                                  8
From cross-validation:
True
             Allocated to
Group
           Group 1
                        Group 2
                                      Total
Group 1
             13
                        11
                                  24
Group 2
              6
                        2
                                  8
```

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Bla -- Cas

Difference between means: Procrustes distance: 0.00860120 Mahalanobis distance: 122.9920 T-square: 111435.7878, P-value (parametric): 0.0662 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.6970 T-square: 0.0530 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables					
Group 1: 1	Bla				
Group 2: 0	Cas				
From disc	riminant fui	nction:			
True	Allocat	ed to			
Group	Group 1	Group 2		Total	
Group 1	13	0	13		
Group 2	0	17	17		
From cros	s-validation	:			
True	Allocat	ed to			
Group	Group 1	Group 2		Total	
Group 1	4	9	13		
Group 2	16	1	17		

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Bla -- Cho

Difference between means: Procrustes distance: 0.01929979 Mahalanobis distance: 10.6883 T-square: 933.4987, P-value (parametric): 0.0160 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0210 T-square: 0.0070 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Cho From discriminant function: True Allocated to Group Group 1 Group 2 Total 13 Group 1 13 0 Group 2 0 22 22 From cross-validation: True Allocated to Group 1 Total Group Group 2 Group 1 7 6 13 19 3 22 Group 2

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Bla -- Con

Difference between means: Procrustes distance: 0.01342606 Mahalanobis distance: 6.7398 T-square: 334.6310, P-value (parametric): 0.8629 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.3080 T-square: 0.8150 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Con From discriminant function: True Allocated to Group Group 1 Group 2 Total

Group 1	13	0	13				
Group 2	0	17	17				
From cross-validation:							
True	Allocated to						
Group	Group 1	Group 2		Total			
Group 1	9	4	13				
Group 2	8	9	17				

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Bla -- Her

Difference between means: Procrustes distance: 0.03368814 Mahalanobis distance: 13.9773 T-square: 1269.8773, P-value (parametric): 0.4929 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0050 T-square: 0.0030 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Her From discriminant function: True Allocated to Group Group 1 Group 2 Total 13 Group 1 13 0 13 Group 2 0 13 From cross-validation: True Allocated to Group Group 1 Group 2 Total 13 Group 1 10 3 3 10 13 Group 2

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Bla -- Jam

Difference between means: Procrustes distance: 0.01549791 Mahalanobis distance: 6.1259 T-square: 234.1638, P-value (parametric): 0.8536 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2960 T-square: 0.0430 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Jam From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 13 0 13 Group 2 0 12 12 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 8 5 13 8 Group 2 4 12

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Bla -- Nan

Difference between means: Procrustes distance: 0.04536023 Mahalanobis distance: 77.0824 T-square: 42616.2841, P-value (parametric): 0.1031 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Nan From discriminant function: True Allocated to Total Group Group 1 Group 2 Group 1 13 13 0 Group 2 0 16 16 From cross-validation: True Allocated to Group Group 1 Group 2 Total 13 5 Group 1 8 Group 2 7 9 16

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Bla -- Not

Difference between means: Procrustes distance: 0.01463939 Mahalanobis distance: 6.0712 T-square: 330.8546, P-value (parametric): 0.0068 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1180 T-square: 0.0130 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Not From discriminant function: True Allocated to Group Group 1 Group 2 Total 13 Group 1 13 0 0 29 Group 2 29 From cross-validation: Allocated to True Group Group 1 Group 2 Total Group 1 8 5 13 Group 2 8 21 29

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Bla -- Oge

Difference between means: Procrustes distance: 0.01654856 Mahalanobis distance: 10.3931 T-square: 897.1447, P-value (parametric): 0.0076 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0850 T-square: 0.0080 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Oge From discriminant function: True Allocated to Group Group 1 Group 2 Total 13 Group 1 13 0 23 Group 2 0 23 From cross-validation:

True	Allocated to			
Group	Group 1	Group 2		Total
Group 1	10	3	13	
Group 2	6	17	23	

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Bla -- Pit

Difference between means: Procrustes distance: 0.01835395 Mahalanobis distance: 5.2868 T-square: 260.6691, P-value (parametric): 0.0039 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0250 T-square: 0.0050 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Pit From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 13 0 13 Group 2 0 33 33 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 7 6 13 Group 2 6 27 33

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Bla -- Pot

Difference between means: Procrustes distance: 0.02366781 Mahalanobis distance: 13.0453 T-square: 1474.8921, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Pot From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 13 0 13 0 26 26 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 10 3 13 Group 2 1 25 26

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Bla -- Rap

Difference between means: Procrustes distance: 0.01253822 Mahalanobis distance: 6.7755 T-square: 387.1074, P-value (parametric): 0.0469 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2870 T-square: 0.0460 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 13 0 13 Group 2 0 24 24 From cross-validation: True Allocated to Group 1 Group 2 Total Group Group 1 10 3 13 17 7 24 Group 2

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Bla -- Sus

Difference between means: Procrustes distance: 0.02901286 Mahalanobis distance: 14.0353 T-square: 1280.4249, P-value (parametric): 0.4912 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0210 T-square: 0.0070 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Sus From discriminant function: True Allocated to Group 1 Group Group 2 Total 13 Group 1 13 0 13 Group 2 0 13 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 10 3 13 10 13 Group 2 3

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Bla -- SwN

Difference between means: Procrustes distance: 0.00978818 Mahalanobis distance: 5.8288 T-square: 229.0193, P-value (parametric): 0.8890 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.6810 T-square: 0.0770 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: SwN From discriminant function: True Allocated to Group 1 Group 2 Group Total Group 1 13 0 13 0 14 Group 2 14 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 7 6 13

Group 2 5 9 14

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Bla -- SwT

Difference between means: Procrustes distance: 0.01614250 Mahalanobis distance: 13.6013 T-square: 1511.6840, P-value (parametric): 0.0044 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1150 T-square: 0.0060 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: SwT From discriminant function: True Allocated to Group Group 1 Group 2 Total 0 13 Group 1 13 Group 2 0 22 22 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 10 3 13 Group 2 4 18 22

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Bla -- Tar

Difference between means: Procrustes distance: 0.02048474 Mahalanobis distance: 4.7937 T-square: 113.8015, P-value (parametric): 0.9091 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2110 T-square: 0.1310 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Tar From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 13 0 13 Group 2 0 8 8 From cross-validation: True Allocated to Group 1 Group 2 Group Total Group 1 7 6 13 2 Group 2 8 6

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cas -- Cho

Difference between means: Procrustes distance: 0.02345676 Mahalanobis distance: 7.5840 T-square: 551.5766, P-value (parametric): 0.0042 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: 0.0010 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.) Classification/misclassification tables Group 1: Cas Group 2: Cho From discriminant function: True Allocated to Group 1 Group Group 2 Total Group 1 0 17 17 Group 2 0 22 22 From cross-validation: True Allocated to Group Group 1 Group 2 Total 17 Group 1 10 7 Group 2 17 22 5

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cas -- Con

Difference between means: Procrustes distance: 0.01212591 Mahalanobis distance: 6.1523 T-square: 321.7298, P-value (parametric): 0.2682 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2270 T-square: 0.2490 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: Con From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 17 0 17 17 Group 2 0 17 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 9 8 17 8 9 17 Group 2

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cas -- Her

Difference between means: Procrustes distance: 0.02940857 Mahalanobis distance: 25.6540 T-square: 4848.2212, P-value (parametric): 0.3094 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0020 T-square: 0.3130 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: Her From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 17 0 17 Group 2 0 13 13 From cross-validation: True Allocated to Group Group 1 Group 2 Total 17 Group 1 13 4 13 Group 2 2 11

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cas -- Jam

Difference between means: Procrustes distance: 0.01337397 Mahalanobis distance: 12.1118 T-square: 1031.9210, P-value (parametric): 0.5920 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2560 T-square: 0.4060 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: Jam From discriminant function: True Allocated to Group 1 Group Group 2 Total Group 1 17 0 17 Group 2 0 12 12 From cross-validation: True Allocated to Group Group 1 Group 2 Total 17 Group 1 12 5 7 5 Group 2 12

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cas -- Nan

Difference between means: Procrustes distance: 0.04135592 Mahalanobis distance: 22.8721 T-square: 4311.8913, P-value (parametric): 0.0050 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: 0.0060 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: Nan From discriminant function: Allocated to True Group 1 Group 2 Group Total Group 1 0 17 17 Group 2 0 16 16 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 15 2 17 Group 2 2 14 16

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cas -- Not

Difference between means: Procrustes distance: 0.01622886 Mahalanobis distance: 4.8150 T-square: 248.4723, P-value (parametric): 0.0051 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0130 T-square: 0.0030 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: Not From discriminant function: True Allocated to Group Group 1 Group 2 Total 17 Group 1 17 0 Group 2 0 29 29 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 17 12 5 9 20 29 Group 2

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cas -- Oge

Difference between means: Procrustes distance: 0.01582909 Mahalanobis distance: 11.3354 T-square: 1255.9942, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0350 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: Oge From discriminant function: True Allocated to Group 1 Group Group 2 Total 17 Group 1 17 0 Group 2 0 23 23 From cross-validation: True Allocated to Group Group 1 Group 2 Total 17 Group 1 16 1 21 Group 2 2 23

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cas -- Pit

Difference between means: Procrustes distance: 0.02130751 Mahalanobis distance: 3.9765 T-square: 177.4152, P-value (parametric): 0.0094 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0020 T-square: 0.0050 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: Pit From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 16 17 1 Group 2 32 33 1 From cross-validation: True Allocated to Group Group 1 Group 2 Total 17 Group 1 10 7 7 Group 2 26 33

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cas -- Pot

Difference between means: Procrustes distance: 0.02670308 Mahalanobis distance: 6.1957 T-square: 394.5822, P-value (parametric): 0.0017 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: 0.0020 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables				
Group 1: 0	Cas			
Group 2: H	Pot			
From disc	riminant fur	action:		
True	Allocat	ed to		
Group	Group 1	Group 2		Total
Group 1	17	0	17	
Group 2	0	26	26	
From cros	s-validation	:		
True	Allocat	ed to		
Group	Group 1	Group 2		Total
Group 1	10	7	17	
Group 2	1	25	26	

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cas -- Rap

Difference between means: Procrustes distance: 0.01181433 Mahalanobis distance: 3.9973 T-square: 159.0064, P-value (parametric): 0.1545 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1710 T-square: 0.1740 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total 17 Group 1 16 1 Group 2 0 24 24 From cross-validation: True Allocated to Group 1 Total Group Group 2 Group 1 8 9 17 9 15 24 Group 2

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cas -- Sus

Difference between means: Procrustes distance: 0.02454788 Mahalanobis distance: 30.9926 T-square: 7075.9839, P-value (parametric): 0.2583 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0050 T-square: 0.2400 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: Sus From discriminant function: True Allocated to Group Group 1 Group 2 Total

Group 1	17	0	17	
Group 2	0	13	13	
From cross	-validation	1:		
True	Allocat	ted to		
Group	Group 1	Group 2		Total
Group 1	8	9	17	
Group 2	7	6	13	

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cas -- SwN

Difference between means: Procrustes distance: 0.01009360 Mahalanobis distance: 72.1996 T-square: 40020.6790, P-value (parametric): 0.0101 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.5450 T-square: 0.0090 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: SwN From discriminant function: True Allocated to Group Group 1 Group 2 Total 17 Group 1 17 0 14 Group 2 0 14 From cross-validation: True Allocated to Group Group 1 Total Group 2 17 Group 1 16 1 2 14 Group 2 12

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cas -- SwT

Difference between means: Procrustes distance: 0.01384388 Mahalanobis distance: 8.1303 T-square: 633.9046, P-value (parametric): 0.0024 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0870 T-square: 0.0030 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: SwT From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 17 0 17 Group 2 0 22 22 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 14 3 17 22 Group 2 6 16

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cas -- Tar

Difference between means: Procrustes distance: 0.01701479 Mahalanobis distance: 5.9972 T-square: 195.6566, P-value (parametric): 0.8863 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1490 T-square: 0.1230 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: Tar From discriminant function: True Allocated to Group Group 1 Group 2 Total 17 Group 1 17 0 0 8 8 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total 8 17 9 Group 1 Group 2 4 4 8

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cho -- Con

Difference between means: Procrustes distance: 0.02537028 Mahalanobis distance: 15.6963 T-square: 2362.6589, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0010 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cho Group 2: Con From discriminant function: True Allocated to Group Group 1 Group 2 Total 22 Group 1 22 0 0 17 Group 2 17 From cross-validation: Allocated to True Group Group 1 Group 2 Total Group 1 21 1 22 Group 2 1 16 17

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cho -- Her

Difference between means: Procrustes distance: 0.04864314 Mahalanobis distance: 30.4209 T-square: 7562.0977, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cho Group 2: Her From discriminant function: True Allocated to Group Group 1 Group 2 Total 22 Group 1 22 0 0 13 Group 2 13 From cross-validation:

True	Allocat	ed to		
Group	Group 1	Group 2		Total
Group 1	21	1	22	
Group 2	2	11	13	

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cho -- Jam

Difference between means: Procrustes distance: 0.02254219 Mahalanobis distance: 26.6419 T-square: 5511.3374, P-value (parametric): 0.0006 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0060 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cho Group 2: Jam From discriminant function: True Allocated to Group 1 Group 2 Total Group Group 1 22 0 22 Group 2 0 12 12 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 22 0 22 12 Group 2 2 10

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cho -- Nan

Difference between means: Procrustes distance: 0.06200441 Mahalanobis distance: 26.8592 T-square: 6682.6110, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cho Group 2: Nan From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 22 0 22 0 16 16 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 22 0 22 Group 2 0 16 16

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cho -- Not

Difference between means: Procrustes distance: 0.01737782 Mahalanobis distance: 5.6528 T-square: 399.7395, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0010 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cho Group 2: Not From discriminant function: True Allocated to Group Group 1 Group 2 Total 22 Group 1 22 0 Group 2 0 29 29 From cross-validation: True Allocated to Group 1 Group 2 Total Group Group 1 19 3 22 29 6 23 Group 2

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cho -- Oge

Difference between means: Procrustes distance: 0.02927387 Mahalanobis distance: 7.8017 T-square: 684.4159, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cho Group 2: Oge From discriminant function: True Allocated to Group 1 Group Group 2 Total 22 Group 1 22 0 0 23 Group 2 23 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 21 1 22 23 Group 2 3 20

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cho -- Pit

Difference between means: Procrustes distance: 0.00974739 Mahalanobis distance: 4.6077 T-square: 280.2529, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0550 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cho Group 2: Pit From discriminant function: True Allocated to Group 1 Group 2 Group Total Group 1 22 0 22 0 33 Group 2 33 From cross-validation: True Allocated to Group 1 Group Group 2 Total Group 1 15 7 22

Group 2 5 28 33

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cho -- Pot

Difference between means: Procrustes distance: 0.01185940 Mahalanobis distance: 8.6871 T-square: 899.2899, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0050 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cho Group 2: Pot From discriminant function: True Allocated to Group Group 1 Group 2 Total 0 22 Group 1 22 Group 2 0 26 26 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 21 1 22 Group 2 0 26 26

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cho -- Rap

Difference between means: Procrustes distance: 0.02200920 Mahalanobis distance: 5.8356 T-square: 390.8787, P-value (parametric): 0.0003 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0010 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cho Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total 22 Group 1 22 0 Group 2 0 24 24 From cross-validation: True Allocated to Group 1 Group 2 Group Total Group 1 19 3 22 7 17 24 Group 2

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cho -- Sus

Difference between means: Procrustes distance: 0.04464361 Mahalanobis distance: 8.8833 T-square: 644.8283, P-value (parametric): 0.0402 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: 0.0280 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.) Classification/misclassification tables Group 1: Cho Group 2: Sus From discriminant function: True Allocated to Group 1 Total Group Group 2 Group 1 0 22 22 Group 2 0 13 13 From cross-validation: True Allocated to Group Group 1 Group 2 Total 22 Group 1 17 5 Group 2 8 13 5

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cho -- SwN

Difference between means: Procrustes distance: 0.01837117 Mahalanobis distance: 26.8596 T-square: 6172.3250, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0150 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cho Group 2: SwN From discriminant function: True Allocated to Group Group 1 Group 2 Total 22 Group 1 22 0 0 14 Group 2 14 From cross-validation: True Allocated to Total Group Group 1 Group 2 Group 1 22 0 22 0 14 Group 2 14

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cho -- SwT

Difference between means: Procrustes distance: 0.02702968 Mahalanobis distance: 5.7998 T-square: 370.0095, P-value (parametric): 0.0014 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cho Group 2: SwT From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 22 0 22 Group 2 0 22 22 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 17 5 22 22 Group 2 7 15

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Cho -- Tar

Difference between means: Procrustes distance: 0.03351463 Mahalanobis distance: 86.0790 T-square: 43469.6046, P-value (parametric): 0.1059 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: 0.0950 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cho Group 2: Tar From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 22 0 22 Group 2 0 8 8 From cross-validation: True Allocated to Group Group 1 Group 2 Total 22 Group 1 19 3 2 Group 2 6 8

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Con -- Her

Difference between means: Procrustes distance: 0.02555887 Mahalanobis distance: 29.4245 T-square: 6378.0764, P-value (parametric): 0.2715 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0180 T-square: 0.2540 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Con Group 2: Her From discriminant function: True Allocated to Group 1 Group 2 Group Total Group 1 0 17 17 Group 2 0 13 13 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 8 9 17 7 Group 2 6 13

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Con -- Jam

Difference between means: Procrustes distance: 0.00901634 Mahalanobis distance: 8.1614 T-square: 468.5527, P-value (parametric): 0.7770 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.6550 T-square: 0.5640 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Con Group 2: Jam From discriminant function: True Allocated to Group Group 1 Group 2 Total 17 Group 1 17 0 Group 2 0 12 12 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 7 17 10 12 Group 2 6 6

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Con -- Nan

Difference between means: Procrustes distance: 0.03983005 Mahalanobis distance: 9.9821 T-square: 821.2937, P-value (parametric): 0.1016 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: 0.1010 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Con Group 2: Nan From discriminant function: True Allocated to Group 1 Group Group 2 Total 17 Group 1 17 0 Group 2 0 16 16 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 12 5 17 8 16 Group 2 8

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Con -- Not

Difference between means: Procrustes distance: 0.01111666 Mahalanobis distance: 2.9427 T-square: 92.8055, P-value (parametric): 0.3014 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1990 T-square: 0.2970 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Con Group 2: Not From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 15 2 17 Group 2 28 29 1 From cross-validation: True Allocated to Group Group 1 Group 2 Total 17 Group 1 7 10 13 Group 2 16 29

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Con -- Oge

Difference between means: Procrustes distance: 0.00938453 Mahalanobis distance: 4.5468 T-square: 202.0840, P-value (parametric): 0.0991 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.3780 T-square: 0.0840 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classifica	Classification/misclassification tables				
Group 1: 0	Con				
Group 2: 0	Oge				
From disc	riminant fun	action:			
True	Allocat	ed to			
Group	Group 1	Group 2		Total	
Group 1	17	0	17		
Group 2	0	23	23		
From cros	s-validation	:			
True	Allocat	ed to			
Group	Group 1	Group 2		Total	
Group 1	11	6	17		
Group 2	12	11	23		

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Con -- Pit

Difference between means: Procrustes distance: 0.02319628 Mahalanobis distance: 6.0616 T-square: 412.2622, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Con Group 2: Pit From discriminant function: Allocated to True Group Group 1 Group 2 Total 17 Group 1 17 0 Group 2 0 33 33 From cross-validation: True Allocated to Group 1 Group Group 2 Total Group 1 14 3 17 4 29 33 Group 2

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Con -- Pot

Difference between means: Procrustes distance: 0.02663929 Mahalanobis distance: 6.8974 T-square: 489.0183, P-value (parametric): 0.0005 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Con Group 2: Pot From discriminant function: True Allocated to Group Group 1 Group 2 Total

Group 1	17	0	17	
Group 2	0	26	26	
From cross-validation:				
True	Allocat	ted to		
Group	Group 1	Group 2		Total
Group 1	11	6	17	
Group 2	5	21	26	

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Con -- Rap

Difference between means: Procrustes distance: 0.00770658 Mahalanobis distance: 5.3593 T-square: 285.8235, P-value (parametric): 0.0203 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.6170 T-square: 0.0170 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Con Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total 17 Group 1 17 0 24 Group 2 0 24 From cross-validation: True Allocated to Group Group 1 Group 2 Total 17 Group 1 12 5 24 Group 2 6 18

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Con -- Sus

Difference between means: Procrustes distance: 0.02388411 Mahalanobis distance: 73.6508 T-square: 39960.0452, P-value (parametric): 0.1104 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0220 T-square: 0.0830 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Con Group 2: Sus From discriminant function: Allocated to True Group Group 1 Group 2 Total Group 1 17 0 17 Group 2 0 13 13 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 14 3 17 8 Group 2 5 13

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Con -- SwN

Difference between means: Procrustes distance: 0.01116494 Mahalanobis distance: 8.1524 T-square: 510.2561, P-value (parametric): 0.5388 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.4340 T-square: 0.5450 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Con Group 2: SwN From discriminant function: True Allocated to Total Group Group 1 Group 2 Group 1 17 17 0 0 14 Group 2 14 From cross-validation: True Allocated to Group Group 1 Group 2 Total 17 10 Group 1 7 Group 2 7 7 14

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Con -- SwT

Difference between means: Procrustes distance: 0.00961439 Mahalanobis distance: 7.0601 T-square: 478.0019, P-value (parametric): 0.0074 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.4010 T-square: 0.0060 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Con Group 2: SwT From discriminant function: True Allocated to Group Group 1 Group 2 Total 17 Group 1 17 0 0 22 22 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 14 3 17 Group 2 9 13 22

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Con -- Tar

Difference between means: Procrustes distance: 0.01105684 Mahalanobis distance: 6.0864 T-square: 201.5219, P-value (parametric): 0.8812 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.6030 T-square: 0.1120 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Con Group 2: Tar From discriminant function: True Allocated to Group Group 1 Group 2 Total 17 Group 1 17 0 0 8 8 Group 2 From cross-validation:

True	Allocate	ed to		
Group	Group 1	Group 2		Total
Group 1	13	4	17	
Group 2	4	4	8	

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Her -- Jam

Difference between means: Procrustes distance: 0.03016702 Mahalanobis distance: 8.6067 T-square: 462.2306, P-value (parametric): 0.7042 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0240 T-square: 0.0230 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Her Group 2: Jam From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 13 0 13 Group 2 0 12 12 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 11 2 13 Group 2 6 6 12

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Her -- Nan

Difference between means: Procrustes distance: 0.01885490 Mahalanobis distance: 32.4155 T-square: 7536.5022, P-value (parametric): 0.2418 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0510 T-square: 0.2270 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Her Group 2: Nan From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 13 0 13 0 16 16 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 11 2 13 Group 2 2 14 16

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Her -- Not

Difference between means: Procrustes distance: 0.03434043 Mahalanobis distance: 6.3176 T-square: 358.2632, P-value (parametric): 0.0047 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: 0.0080 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Her Group 2: Not From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 13 0 13 Group 2 0 29 29 From cross-validation: True Allocated to Group 1 Group 2 Total Group Group 1 9 4 13 5 29 Group 2 24

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Her -- Oge

Difference between means: Procrustes distance: 0.02370424 Mahalanobis distance: 6.0406 T-square: 303.0571, P-value (parametric): 0.1375 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0110 T-square: 0.1230 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Her Group 2: Oge From discriminant function: True Allocated to Group 1 Group Group 2 Total 13 Group 1 13 0 0 23 Group 2 23 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 7 13 6 15 23 Group 2 8

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Her -- Pit

Difference between means: Procrustes distance: 0.04681174 Mahalanobis distance: 5.5163 T-square: 283.7930, P-value (parametric): 0.0024 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: 0.0030 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Her Group 2: Pit From discriminant function: True Allocated to Group 1 Group 2 Group Total Group 1 13 0 13 0 Group 2 33 33 From cross-validation: True Allocated to Group 1 Group Group 2 Total Group 1 8 5 13

Group 2 6 27 33

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Her -- Pot

Difference between means: Procrustes distance: 0.05026828 Mahalanobis distance: 12.8158 T-square: 1423.4558, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Her Group 2: Pot From discriminant function: True Allocated to Group Group 1 Group 2 Total 0 13 Group 1 13 Group 2 0 26 26 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 11 2 13 Group 2 1 25 26

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Her -- Rap

Difference between means: Procrustes distance: 0.02898235 Mahalanobis distance: 7.5587 T-square: 481.7747, P-value (parametric): 0.0245 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0020 T-square: 0.0270 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Her Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 13 0 13 Group 2 0 24 24 From cross-validation: True Allocated to Group 1 Group 2 Group Total Group 1 10 3 13 24 Group 2 8 16

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Her -- Sus

Difference between means: Procrustes distance: 0.01333050 Mahalanobis distance: 12.9224 T-square: 1085.4324, P-value (parametric): 0.5266 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2950 T-square: 0.0020 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.) Classification/misclassification tables Group 1: Her Group 2: Sus From discriminant function: True Allocated to Group 1 Total Group Group 2 Group 1 0 13 13 Group 2 0 13 13 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 12 1 13 Group 2 3 10 13

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Her -- SwN

Difference between means: Procrustes distance: 0.03325818 Mahalanobis distance: 7.6153 T-square: 390.9187, P-value (parametric): 0.7823 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0040 T-square: 0.3420 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Her Group 2: SwN From discriminant function: True Allocated to Group 1 Group Group 2 Total 13 Group 1 13 0 14 Group 2 0 14 From cross-validation: True Allocated to Total Group Group 1 Group 2 Group 1 7 6 13 8 14 Group 2 6

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Her -- SwT

Difference between means: Procrustes distance: 0.02263874 Mahalanobis distance: 3.6385 T-square: 108.1773, P-value (parametric): 0.7592 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0220 T-square: 0.7600 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Her Group 2: SwT From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 12 1 13 Group 2 0 22 22 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 5 8 13 12 10 22 Group 2

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Her -- Tar

Difference between means: Procrustes distance: 0.01718536 Mahalanobis distance: 4.3932 T-square: 95.5813, P-value (parametric): 0.9331 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2410 T-square: 0.3290 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Her Group 2: Tar From discriminant function: True Allocated to Group 1 Group Group 2 Total Group 1 13 0 13 Group 2 0 8 8 From cross-validation: True Allocated to Group Group 1 Group 2 Total 9 4 13 Group 1 7 Group 2 1 8

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Jam -- Nan

Difference between means: Procrustes distance: 0.04505599 Mahalanobis distance: 16.7653 T-square: 1927.3674, P-value (parametric): 0.4412 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: 0.0920 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Jam Group 2: Nan From discriminant function: Allocated to True Group 1 Group 2 Group Total Group 1 0 12 12 Group 2 0 16 16 From cross-validation: Allocated to True Group Group 1 Group 2 Total Group 1 10 2 12 Group 2 6 10 16

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Jam -- Not

Difference between means: Procrustes distance: 0.00883677 Mahalanobis distance: 4.8908 T-square: 203.0262, P-value (parametric): 0.0720 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.5190 T-square: 0.0640 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Jam Group 2: Not From discriminant function: True Allocated to Group Group 1 Group 2 Total 12 Group 1 12 0 Group 2 0 29 29 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 7 12 5 12 17 29 Group 2

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Jam -- Oge

Difference between means: Procrustes distance: 0.01527801 Mahalanobis distance: 12.1394 T-square: 1162.0828, P-value (parametric): 0.0090 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1460 T-square: 0.0080 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Jam Group 2: Oge From discriminant function: True Allocated to Group 1 Group Group 2 Total 12 Group 1 12 0 Group 2 0 23 23 From cross-validation: True Allocated to Total Group Group 1 Group 2 Group 1 9 3 12 3 20 23 Group 2

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Jam -- Pit

Difference between means: Procrustes distance: 0.01920671 Mahalanobis distance: 6.1686 T-square: 334.8512, P-value (parametric): 0.0014 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0190 T-square: 0.0020 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

```
Classification/misclassification tables
Group 1: Jam
Group 2: Pit
From discriminant function:
True
             Allocated to
Group
           Group 1
                        Group 2
                                      Total
Group 1
             12
                        0
                                  12
Group 2
                       32
                                  33
              1
From cross-validation:
True
             Allocated to
Group
           Group 1
                        Group 2
                                      Total
                                 12
Group 1
              9
                        3
Group 2
              6
                       27
                                  33
```

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Jam -- Pot

Difference between means: Procrustes distance: 0.02207928 Mahalanobis distance: 7.1771 T-square: 422.9269, P-value (parametric): 0.0209 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0010 T-square: 0.0210 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables				
Group 1:	Jam			
Group 2:	Pot			
From disc	criminant fur	nction:		
True	Allocat	ed to		
Group	Group 1	Group	2	Total
Group 1	12	0	12	
Group 2	0	26	26	
From cross	ss-validation	:		
True	Allocat	ed to		
Group	Group 1	Group	2	Total
Group 1	5	7	12	
Group 2	6	20	26	

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Jam -- Rap

Difference between means: Procrustes distance: 0.00840695 Mahalanobis distance: 6.6412 T-square: 352.8471, P-value (parametric): 0.0970 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.6620 T-square: 0.1050 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Jam Group 2: Rap From discriminant function: True Allocated to Group 2 Group Group 1 Total 12 Group 1 12 0 Group 2 0 24 24 From cross-validation: True Allocated to Group 1 Group Group 2 Total Group 1 5 7 12 7 17 24 Group 2

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Jam -- Sus

Difference between means: Procrustes distance: 0.02759182 Mahalanobis distance: 6.8856 T-square: 295.8464, P-value (parametric): 0.8058 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0190 T-square: 0.0050 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Jam Group 2: Sus From discriminant function: True Allocated to Group Group 1 Group 2 Total

Group 1	12	0	12	
Group 2	0	13	13	
From cros	s-validation	:		
True	Allocat	ed to		
Group	Group 1	Group 2		Total
Group 1	7	5	12	
Group 2	3	10	13	

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Jam -- SwN

Difference between means: Procrustes distance: 0.01130944 Mahalanobis distance: 12.6484 T-square: 1033.7316, P-value (parametric): 0.5374 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.5850 T-square: 0.0130 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Jam Group 2: SwN From discriminant function: True Allocated to Group Group 1 Group 2 Total 12 Group 1 12 0 14 14 Group 2 0 From cross-validation: True Allocated to Group Group 1 Group 2 Total 12 Group 1 8 4 10 14 Group 2 4

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Jam -- SwT

Difference between means: Procrustes distance: 0.01164985 Mahalanobis distance: 5.3566 T-square: 222.7917, P-value (parametric): 0.4438 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.3570 T-square: 0.4080 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Jam Group 2: SwT From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 12 0 12 Group 2 0 22 22 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 4 8 12 12 10 22 Group 2

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Jam -- Tar

Difference between means: Procrustes distance: 0.01560828 Mahalanobis distance: 5.0471 T-square: 122.2738, P-value (parametric): 0.8791 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.3730 T-square: 0.0640 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Jam Group 2: Tar From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 12 12 0 0 8 Group 2 8 From cross-validation: True Allocated to Group Group 1 Group 2 Total 9 12 3 Group 1 Group 2 4 4 8

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Nan -- Not

Difference between means: Procrustes distance: 0.04872185 Mahalanobis distance: 12.5893 T-square: 1634.2243, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Nan Group 2: Not From discriminant function: True Allocated to Group Group 1 Group 2 Total 16 Group 1 16 0 0 29 29 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 16 0 16 Group 2 2 27 29

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Nan -- Oge

Difference between means: Procrustes distance: 0.03755951 Mahalanobis distance: 9.6372 T-square: 876.3603, P-value (parametric): 0.0006 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: 0.0010 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Nan Group 2: Oge From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 0 16 16 23 Group 2 0 23 From cross-validation:

True	Allocat	ed to		
Group	Group 1	Group 2		Total
Group 1	15	1	16	
Group 2	2	21	23	

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Nan -- Pit

Difference between means: Procrustes distance: 0.06069572 Mahalanobis distance: 9.9943 T-square: 1076.3275, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Nan Group 2: Pit From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 16 0 16 Group 2 0 33 33 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 14 2 16 Group 2 1 32 33

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Nan -- Pot

Difference between means: Procrustes distance: 0.06500897 Mahalanobis distance: 17.6402 T-square: 3082.1438, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Nan Group 2: Pot From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 16 0 16 0 26 26 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 14 2 16 Group 2 0 26 26

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Nan -- Rap

Difference between means: Procrustes distance: 0.04340767 Mahalanobis distance: 7.3474 T-square: 518.2445, P-value (parametric): 0.0028 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: 0.0040 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Nan Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 16 0 16 Group 2 0 24 24 From cross-validation: True Allocated to Group 1 Group 2 Total Group Group 1 13 3 16 Group 2 4 20 24

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Nan -- Sus

Difference between means: Procrustes distance: 0.02172588 Mahalanobis distance: 12.0849 T-square: 1047.4993, P-value (parametric): 0.5885 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0140 T-square: 0.1400 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Nan Group 2: Sus From discriminant function: True Allocated to Group 1 Group Group 2 Total 16 Group 1 16 0 13 Group 2 0 13 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 8 8 16 7 Group 2 6 13

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Nan -- SwN

Difference between means: Procrustes distance: 0.04707454 Mahalanobis distance: 36.1768 T-square: 9772.0660, P-value (parametric): 0.2209 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: 0.1820 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Nan Group 2: SwN From discriminant function: True Allocated to Group 1 Group 2 Total Group Group 1 16 0 16 0 14 Group 2 14 From cross-validation: True Allocated to Group 1 Group Group 2 Total Group 1 9 7 16

Group 2 5 9 14

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Nan -- SwT

Difference between means: Procrustes distance: 0.03780834 Mahalanobis distance: 8.3102 T-square: 639.7042, P-value (parametric): 0.0048 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: 0.0040 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Nan Group 2: SwT From discriminant function: True Allocated to Group Group 1 Group 2 Total 0 16 Group 1 16 Group 2 0 22 22 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 12 4 16 Group 2 4 18 22

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Nan -- Tar

Difference between means: Procrustes distance: 0.03237544 Mahalanobis distance: 6.7246 T-square: 241.1726, P-value (parametric): 0.8294 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0060 T-square: 0.1350 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Nan Group 2: Tar From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 16 0 16 Group 2 0 8 8 From cross-validation: True Allocated to Group 1 Group Group 2 Total Group 1 9 7 16 4 4 8 Group 2

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Not -- Oge

Difference between means: Procrustes distance: 0.01683275 Mahalanobis distance: 4.9811 T-square: 318.2519, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0060 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.) Classification/misclassification tables Group 1: Not Group 2: Oge From discriminant function: True Allocated to Group 1 Total Group Group 2 29 0 29 Group 1 Group 2 0 23 23 From cross-validation: True Allocated to Group Group 1 Group 2 Total 29 Group 1 23 6 Group 2 23 6 17

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Not -- Pit

Difference between means: Procrustes distance: 0.01667382 Mahalanobis distance: 4.4627 T-square: 307.4094, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0020 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Not Group 2: Pit From discriminant function: True Allocated to Group 1 Group Group 2 Total 29 29 Group 1 0 0 33 Group 2 33 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 22 7 29 4 29 33 Group 2

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Not -- Pot

Difference between means: Procrustes distance: 0.01924312 Mahalanobis distance: 5.6159 T-square: 432.3604, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Not Group 2: Pot From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 29 29 0 Group 2 0 26 26 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 23 6 29 2 26 Group 2 24

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Not -- Rap

Difference between means: Procrustes distance: 0.01021341 Mahalanobis distance: 4.8996 T-square: 315.2456, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1330 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Not Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 29 0 29 Group 2 0 24 24 From cross-validation: Allocated to True Group Group 1 Group 2 Total 29 Group 1 24 5 5 Group 2 19 24

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Not -- Sus

Difference between means: Procrustes distance: 0.03209426 Mahalanobis distance: 7.4786 T-square: 502.0384, P-value (parametric): 0.0009 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Not Group 2: Sus From discriminant function: True Allocated to Group 1 Group Group 2 Total Group 1 29 0 29 0 13 Group 2 13 From cross-validation: Allocated to True Group Group 1 Group 2 Total Group 1 27 2 29 Group 2 3 10 13

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Not -- SwN

Difference between means: Procrustes distance: 0.01203673 Mahalanobis distance: 3.7263 T-square: 131.1061, P-value (parametric): 0.1787 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1940 T-square: 0.1770 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Not Group 2: SwN

From discriminant function:				
True	Allocat	ted to		
Group	Group 1	Group 2		Total
Group 1	29	0	29	
Group 2	1	13	14	
From cross	s-validation	:		
True	Allocat	ted to		
Group	Group 1	Group 2		Total
Group 1	18	11	29	
Group 2	6	8	14	

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Not -- SwT

Difference between means: Procrustes distance: 0.01446402 Mahalanobis distance: 5.1155 T-square: 327.3662, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0260 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Not Group 2: SwT From discriminant function: True Allocated to Group Group 1 Group 2 Total 29 Group 1 29 0 22 Group 2 0 22 From cross-validation: True Allocated to Total Group Group 1 Group 2 29 Group 1 25 4 Group 2 16 22 6

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Not -- Tar

Difference between means: Procrustes distance: 0.01924539 Mahalanobis distance: 8.2487 T-square: 426.6382, P-value (parametric): 0.0354 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0530 T-square: 0.0320 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

```
Classification/misclassification tables
Group 1: Not
Group 2: Tar
From discriminant function:
True
             Allocated to
Group
           Group 1
                       Group 2
                                     Total
Group 1
             29
                        0
                                 29
Group 2
             0
                       8
                                 8
From cross-validation:
True
             Allocated to
Group
           Group 1
                       Group 2
                                     Total
                                 29
Group 1
             21
                        8
             3
                       5
Group 2
                                 8
```

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Oge -- Pit

Difference between means: Procrustes distance: 0.02652010 Mahalanobis distance: 6.0632 T-square: 498.2645, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classificat	Classification/misclassification tables			
Group 1: 0	Oge			
Group 2: I	Pit			
From disc	riminant fui	nction:		
True	Allocat	ted to		
Group	Group 1	Group 2		Total
Group 1	23	0	23	
Group 2	0	33	33	
From cros	s-validation	:		
True	Allocat	ted to		
Group	Group 1	Group 2		Total
Group 1	19	4	23	
Group 2	3	30	33	

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Oge -- Pot

Difference between means: Procrustes distance: 0.03042026 Mahalanobis distance: 6.4765 T-square: 511.9009, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Oge Group 2: Pot From discriminant function: True Allocated to Group Group 1 Group 2 Total 23 Group 1 23 0 Group 2 0 26 26 From cross-validation: True Allocated to Group 1 Group Group 2 Total Group 1 18 5 23 0 26 Group 2 26

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Oge -- Rap

Difference between means: Procrustes distance: 0.01172873 Mahalanobis distance: 6.8887 T-square: 557.3289, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1380 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Oge Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total

Group 1	23	0	23	
Group 2	0	24	24	
From cross	s-validation	:		
True	Allocat	ed to		
Group	Group 1	Group 2		Total
Group 1	18	5	23	
Group 2	4	20	24	

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Oge -- Sus

Difference between means: Procrustes distance: 0.02268552 Mahalanobis distance: 15.2888 T-square: 1941.4020, P-value (parametric): 0.0007 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0100 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Oge Group 2: Sus From discriminant function: True Allocated to Group Group 1 Group 2 Total 23 Group 1 23 0 13 Group 2 0 13 From cross-validation: True Allocated to Group Group 1 Group 2 Total 23 Group 1 21 2 12 13 Group 2 1

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Oge -- SwN

Difference between means: Procrustes distance: 0.01585665 Mahalanobis distance: 4.9802 T-square: 215.8466, P-value (parametric): 0.2048 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0930 T-square: 0.1890 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Oge Group 2: SwN From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 23 0 23 0 Group 2 14 14 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 15 8 23 7 14 Group 2 7

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Oge -- SwT

Difference between means: Procrustes distance: 0.01034584 Mahalanobis distance: 6.4203 T-square: 463.5018, P-value (parametric): 0.0002 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1990 T-square: 0.0010 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Oge Group 2: SwT From discriminant function: True Allocated to Group 2 Total Group Group 1 Group 1 23 23 0 0 22 22 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total 23 20 3 Group 1 Group 2 5 17 22

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Oge -- Tar

Difference between means: Procrustes distance: 0.00985034 Mahalanobis distance: 21.1925 T-square: 2665.7562, P-value (parametric): 0.1406 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.5580 T-square: 0.1550 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Oge Group 2: Tar From discriminant function: True Allocated to Group Group 1 Group 2 Total 23 Group 1 23 0 0 8 8 Group 2 From cross-validation: True Allocated to Group Group 2 Group 1 Total Group 1 13 10 23 Group 2 3 5 8

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Pit -- Pot

Difference between means: Procrustes distance: 0.00827628 Mahalanobis distance: 3.7165 T-square: 200.8607, P-value (parametric): 0.0003 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1150 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Pit Group 2: Pot From discriminant function: True Allocated to Group Group 1 Group 2 Total 33 Group 1 32 1 22 Group 2 4 26 From cross-validation:

True	Allocated to			
Group	Group 1	Group 2		Total
Group 1	27	6	33	
Group 2	4	22	26	

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Pit -- Rap

Difference between means: Procrustes distance: 0.01938991 Mahalanobis distance: 2.6392 T-square: 96.7853, P-value (parametric): 0.0705 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0030 T-square: 0.0610 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Pit Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 31 2 33 Group 2 1 23 24 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 19 14 33 Group 2 13 11 24

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Pit -- Sus

Difference between means: Procrustes distance: 0.04248121 Mahalanobis distance: 7.2186 T-square: 485.9648, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Pit Group 2: Sus From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 33 0 33 0 13 13 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 29 4 33 Group 2 3 10 13

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Pit -- SwN

Difference between means: Procrustes distance: 0.01575087 Mahalanobis distance: 6.6357 T-square: 432.8354, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0380 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Pit Group 2: SwN From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 33 0 33 Group 2 0 14 14 From cross-validation: True Allocated to Group 1 Group 2 Total Group Group 1 28 5 33 4 10 14 Group 2

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Pit -- SwT

Difference between means: Procrustes distance: 0.02530384 Mahalanobis distance: 3.8307 T-square: 193.7039, P-value (parametric): 0.0012 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: 0.0010 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Pit Group 2: SwT From discriminant function: True Allocated to Group 1 Group Group 2 Total 33 Group 1 33 0 0 22 22 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 28 5 33 22 9 Group 2 13

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Pit -- Tar

Difference between means: Procrustes distance: 0.03086722 Mahalanobis distance: 7.4828 T-square: 360.5340, P-value (parametric): 0.0076 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0030 T-square: 0.0040 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Pit Group 2: Tar From discriminant function: True Allocated to Group 1 Group 2 Group Total Group 1 33 0 33 0 Group 2 8 8 From cross-validation: True Allocated to Group 1 Group Group 2 Total Group 1 29 4 33

Group 2 4 4 8

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Pot -- Rap

Difference between means: Procrustes distance: 0.02270813 Mahalanobis distance: 3.9806 T-square: 197.7461, P-value (parametric): 0.0049 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: 0.0010 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Pot Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total 0 26 Group 1 26 Group 2 0 24 24 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 20 6 26 Group 2 12 12 24

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Pot -- Sus

Difference between means: Procrustes distance: 0.04710842 Mahalanobis distance: 13.8880 T-square: 1671.6003, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Pot Group 2: Sus From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 26 26 0 Group 2 0 13 13 From cross-validation: True Allocated to Group 1 Group 2 Group Total Group 1 26 0 26 3 Group 2 10 13

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Pot -- SwN

Difference between means: Procrustes distance: 0.02016671 Mahalanobis distance: 14.8467 T-square: 2005.8567, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0020 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.) Classification/misclassification tables Group 1: Pot Group 2: SwN From discriminant function: True Allocated to Group 1 Total Group Group 2 Group 1 0 26 26 Group 2 0 14 14 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 25 1 26 Group 2 14 1 13

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Pot -- SwT

Difference between means: Procrustes distance: 0.02856500 Mahalanobis distance: 4.9454 T-square: 291.4400, P-value (parametric): 0.0008 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Pot Group 2: SwT From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 25 1 26 0 22 22 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 23 3 26 7 22 Group 2 15

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Pot -- Tar

Difference between means: Procrustes distance: 0.03464390 Mahalanobis distance: 15.2065 T-square: 1414.6258, P-value (parametric): 0.0149 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: 0.0260 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Pot Group 2: Tar From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 26 0 26 Group 2 0 8 8 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 23 3 26 4 Group 2 4 8

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Rap -- Sus

Difference between means: Procrustes distance: 0.02712996 Mahalanobis distance: 5.5207 T-square: 257.0051, P-value (parametric): 0.1378 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0010 T-square: 0.1440 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Rap Group 2: Sus From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 23 1 24 Group 2 0 13 13 From cross-validation: True Allocated to Group Group 1 Group 2 Total 24 Group 1 16 8 Group 2 5 8 13

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Rap -- SwN

Difference between means: Procrustes distance: 0.01008711 Mahalanobis distance: 6.6886 T-square: 395.5741, P-value (parametric): 0.0260 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.4410 T-square: 0.0290 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Rap Group 2: SwN From discriminant function: Allocated to True Group 1 Group 2 Group Total Group 1 0 24 24 0 14 Group 2 14 From cross-validation: Allocated to True Group Group 1 Group 2 Total Group 1 15 9 24 Group 2 4 10 14

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Rap -- SwT

Difference between means: Procrustes distance: 0.00978208 Mahalanobis distance: 2.9637 T-square: 100.8173, P-value (parametric): 0.2409 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2900 T-square: 0.2270 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Rap Group 2: SwT From discriminant function: True Allocated to Group Group 1 Group 2 Total 24 Group 1 23 1 Group 2 2 20 22 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 24 12 12 8 22 Group 2 14

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Rap -- Tar

Difference between means: Procrustes distance: 0.01432637 Mahalanobis distance: 12.3607 T-square: 916.7254, P-value (parametric): 0.1788 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2650 T-square: 0.1700 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Rap Group 2: Tar From discriminant function: True Allocated to Group 1 Group Group 2 Total 24 Group 1 24 0 Group 2 0 8 8 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 14 10 24 5 3 8 Group 2

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Sus -- SwN

Difference between means: Procrustes distance: 0.02947210 Mahalanobis distance: 8.1780 T-square: 450.8232, P-value (parametric): 0.7499 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0070 T-square: 0.0280 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

```
Classification/misclassification tables
Group 1: Sus
Group 2: SwN
From discriminant function:
True
             Allocated to
Group
           Group 1
                        Group 2
                                     Total
Group 1
             13
                        0
                                  13
Group 2
             0
                       14
                                  14
From cross-validation:
True
             Allocated to
Group
           Group 1
                        Group 2
                                     Total
                                 13
Group 1
              8
                       5
              5
                       9
Group 2
                                 14
```

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Sus -- SwT

Difference between means: Procrustes distance: 0.02157654 Mahalanobis distance: 17.1019 T-square: 2389.9268, P-value (parametric): 0.0012 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0150 T-square: 0.0010 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

		sification tab	oles	
Group 1: S	Sus			
Group 2: S	SwT			
From disc	riminant fur	nction:		
True	Allocat	ed to		
Group	Group 1	Group 2		Total
Group 1	13	0	13	
Group 2	0	22	22	
From cros	s-validation	:		
True	Allocat	ed to		
Group	Group 1	Group 2		Total
Group 1	13	0	13	
Group 2	2	20	22	

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: Sus -- Tar

Difference between means: Procrustes distance: 0.01691951 Mahalanobis distance: 5.0467 T-square: 126.1317, P-value (parametric): 0.8930 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2720 T-square: 0.0290 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Sus Group 2: Tar From discriminant function: True Allocated to Group Group 1 Group 2 Total 13 Group 1 13 0 Group 2 0 8 8 From cross-validation: True Allocated to Group 1 Group Group 2 Total Group 1 10 3 13 2 6 8 Group 2

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: SwN -- SwT

Difference between means: Procrustes distance: 0.01449552 Mahalanobis distance: 7.7789 T-square: 517.7056, P-value (parametric): 0.0367 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1620 T-square: 0.0440 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: SwN Group 2: SwT From discriminant function: True Allocated to Group Group 1 Group 2 Total

14	0	14	
0	22	22	
s-validation	:		
Allocat	ed to		
Group 1	Group 2		Total
10	4	14	
9	13	22	
	0 s-validation Allocat Group 1 10	0 22 s-validation: Allocated to Group 1 Group 2 10 4	0 22 22 s-validation: Allocated to Group 1 Group 2 10 4 14

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: SwN -- Tar

Difference between means: Procrustes distance: 0.01910903 Mahalanobis distance: 4.5518 T-square: 105.4800, P-value (parametric): 0.9343 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2180 T-square: 0.3330 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: SwN Group 2: Tar From discriminant function: True Allocated to Group Group 1 Group 2 Total 14 Group 1 14 0 0 8 Group 2 8 From cross-validation: True Allocated to Group Group 1 Group 2 Total 14 Group 1 8 6 Group 2 3 5 8

Discriminant Function Analysis 'Discriminant function ...Female by watershed' Comparison: SwT -- Tar

Difference between means: Procrustes distance: 0.00917942 Mahalanobis distance: 8.6086 T-square: 434.7674, P-value (parametric): 0.8099 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.7230 T-square: 0.7990 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: SwT Group 2: Tar From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 22 0 22 0 Group 2 8 8 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 11 11 22 Group 2 2 6 8

DFA Males by watershed

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: App -- Bla

Difference between means: Procrustes distance: 0.01292477 Mahalanobis distance: 4.4365 T-square: 150.3539, P-value (parametric): 0.4830 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1400 T-square: 0.4790 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Bla From discriminant function: True Allocated to Group Group 1 Total Group 2 Group 1 24 25 1 Group 2 0 11 11 From cross-validation: Allocated to True Group Group 1 Group 2 Total Group 1 13 12 25 Group 2 6 5 11

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: App -- Cap

Difference between means: Procrustes distance: 0.01565489 Mahalanobis distance: 5.4240 T-square: 360.2404, P-value (parametric): 0.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0160 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Cap From discriminant function: True Allocated to Group Group 1 Group 2 Total 25 Group 1 25 0 0 24 Group 2 24 From cross-validation: True Allocated to Group Group 1 Total Group 2 Group 1 20 5 25 Group 2 7 17 24

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: App -- Cas

Difference between means: Procrustes distance: 0.01766308 Mahalanobis distance: 5.9911 T-square: 363.2045, P-value (parametric): 0.0044 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0230 T-square: 0.0050 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.) Classification/misclassification tables Group 1: App Group 2: Cas From discriminant function: True Allocated to Group 1 Total Group Group 2 Group 1 25 0 25 17 Group 2 0 17 From cross-validation: True Allocated to Group Group 1 Group 2 Total 25 Group 1 19 6 Group 2 3 17 14

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: App -- Cho

Difference between means: Procrustes distance: 0.01416481 Mahalanobis distance: 6.3837 T-square: 555.7077, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Cho From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 25 0 25 0 30 Group 2 30 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 21 4 25 2 28 30 Group 2

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: App -- Con

Difference between means: Procrustes distance: 0.01021911 Mahalanobis distance: 6.0047 T-square: 323.5868, P-value (parametric): 0.0311 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2650 T-square: 0.0330 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Con From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 25 0 25 Group 2 0 14 14 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 18 7 25 14 Group 2 4 10

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: App -- Her

Difference between means: Procrustes distance: 0.01208537 Mahalanobis distance: 9.3497 T-square: 578.4987, P-value (parametric): 0.0971 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1760 T-square: 0.1020 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Her From discriminant function: True Allocated to Group 1 Group Group 2 Total Group 1 25 0 25 Group 2 0 9 9 From cross-validation: Allocated to True Group Group 1 Group 2 Total 7 25 Group 1 18 5 9 Group 2 4

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: App -- Jam

Difference between means: Procrustes distance: 0.01763258 Mahalanobis distance: 2.4545 T-square: 82.1502, P-value (parametric): 0.1769 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0060 T-square: 0.1870 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Jam From discriminant function: Allocated to True Group 1 Group Group 2 Total Group 1 1 25 24 30 Group 2 4 26 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 14 11 25 30 Group 2 12 18

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: App -- Neu

Difference between means: Procrustes distance: 0.00635003 Mahalanobis distance: 4.7893 T-square: 223.7748, P-value (parametric): 0.0514 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.6920 T-square: 0.0600 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Neu From discriminant function: True Allocated to Group Group 1 Group 2 Total 25 Group 1 25 0 Group 2 0 16 16 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 9 25 16 10 Group 2 6 16

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: App -- Not

Difference between means: Procrustes distance: 0.01803267 Mahalanobis distance: 4.1640 T-square: 202.9044, P-value (parametric): 0.0108 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0090 T-square: 0.0110 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Not From discriminant function: True Allocated to Group 1 Group Group 2 Total 25 Group 1 25 0 22 Group 2 1 21 From cross-validation: True Allocated to Total Group Group 1 Group 2 25 Group 1 16 9 14 22 Group 2 8

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: App -- Oge

Difference between means: Procrustes distance: 0.02404310 Mahalanobis distance: 6.6569 T-square: 478.3963, P-value (parametric): 0.0003 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Oge From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 25 0 25 Group 2 0 19 19 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 25 21 4 Group 2 3 16 19

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: App -- Pit

Difference between means: Procrustes distance: 0.01380096 Mahalanobis distance: 3.2071 T-square: 158.2407, P-value (parametric): 0.0005 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0100 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

		sification tab	oles	
Group 1: .	Арр			
Group 2: 1	Pit			
From disc	riminant fui	nction:		
True	Allocat	ed to		
Group	Group 1	Group 2		Total
Group 1	24	1	25	
Group 2	1	39	40	
From cross	ss-validation	:		
True	Allocat	ed to		
Group	Group 1	Group 2		Total
Group 1	17	8	25	
Group 2	8	32	40	

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: App -- Pot

Difference between means: Procrustes distance: 0.02024092 Mahalanobis distance: 5.5505 T-square: 506.4388, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Pot From discriminant function: Allocated to True Group Group 1 Total Group 2 25 Group 1 25 0 Group 2 0 48 48 From cross-validation: True Allocated to Group 1 Group Group 2 Total Group 1 20 5 25 2 48 46 Group 2

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: App -- Rap

Difference between means: Procrustes distance: 0.01087385 Mahalanobis distance: 3.2726 T-square: 122.2319, P-value (parametric): 0.1308 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1370 T-square: 0.1260 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total

Group 1	23	2	25	
Group 2	2	19	21	
From cros	s-validation	:		
True	Allocat	ed to		
Group	Group 1	Group	2	Total
Group 1	16	9	25	
Group 2	10	11	21	

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: App -- Stj

Difference between means: Procrustes distance: 0.01062118 Mahalanobis distance: 5.6548 T-square: 454.8402, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0590 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Stj From discriminant function: True Allocated to Group Group 1 Group 2 Total 25 Group 1 25 0 0 33 33 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total 25 Group 1 21 4 2 31 33 Group 2

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: App -- Sus

Difference between means: Procrustes distance: 0.01525217 Mahalanobis distance: 10.5534 T-square: 737.0402, P-value (parametric): 0.0602 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0970 T-square: 0.0620 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Sus From discriminant function: Allocated to True Group Group 1 Group 2 Total Group 1 25 0 25 0 9 Group 2 9 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 17 8 25 6 9 Group 2 3

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: App -- SwN

Difference between means: Procrustes distance: 0.01471897 Mahalanobis distance: 4.7542 T-square: 282.5338, P-value (parametric): 0.0004 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0180 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: SwN From discriminant function: True Allocated to Total Group Group 1 Group 2 Group 1 25 25 0 0 25 25 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total 25 20 5 Group 1 Group 2 7 18 25

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: App -- Tar

Difference between means: Procrustes distance: 0.01955858 Mahalanobis distance: 11.5148 T-square: 1075.0502, P-value (parametric): 0.0017 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0080 T-square: 0.0010 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: App Group 2: Tar From discriminant function: True Allocated to Group Group 1 Group 2 Total 25 Group 1 25 0 0 12 Group 2 12 From cross-validation: Allocated to True Group 2 Group Group 1 Total Group 1 22 3 25 Group 2 1 11 12

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Bla -- Cap

Difference between means: Procrustes distance: 0.00715318 Mahalanobis distance: 6.9437 T-square: 363.6743, P-value (parametric): 0.1430 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.6790 T-square: 0.1410 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Cap From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 0 11 11 0 24 Group 2 24 From cross-validation:

True	Allocated to			
Group	Group 1	Group 2		Total
Group 1	5	6	11	
Group 2	9	15	24	

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Bla -- Cas

Difference between means: Procrustes distance: 0.01213263 Mahalanobis distance: 12.2048 T-square: 994.8259, P-value (parametric): 0.5827 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.3540 T-square: 0.2030 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Cas From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 11 0 11 Group 2 0 17 17 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 6 5 11 9 Group 2 8 17

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Bla -- Cho

Difference between means: Procrustes distance: 0.00933975 Mahalanobis distance: 12.5446 T-square: 1266.6080, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2290 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Cho From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 11 0 11 30 30 0 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 10 1 11 Group 2 1 29 30

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Bla -- Con

Difference between means: Procrustes distance: 0.01468227 Mahalanobis distance: 8.5903 T-square: 454.5716, P-value (parametric): 0.7081 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2270 T-square: 0.0010 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Con From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 11 0 11 Group 2 0 14 14 From cross-validation: True Allocated to Group 1 Group 2 Total Group Group 1 10 1 11 Group 2 3 14 11

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Bla -- Her

Difference between means: Procrustes distance: 0.01591533 Mahalanobis distance: 6.0306 T-square: 180.0220, P-value (parametric): 0.8036 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1970 T-square: 0.1840 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Her From discriminant function: True Allocated to Group 1 Group Group 2 Total Group 1 11 0 11 9 9 Group 2 0 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 9 2 11 0 9 9 Group 2

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Bla -- Jam

Difference between means: Procrustes distance: 0.00927813 Mahalanobis distance: 4.5938 T-square: 169.8540, P-value (parametric): 0.1273 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.5050 T-square: 0.1330 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Jam From discriminant function: True Allocated to Group 1 Group 2 Total Group Group 1 11 0 11 0 30 Group 2 30 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 7 4 11

Group 2 7 23 30

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Bla -- Neu

Difference between means: Procrustes distance: 0.01443200 Mahalanobis distance: 17.5578 T-square: 2009.5053, P-value (parametric): 0.4180 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1830 T-square: 0.4170 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Neu From discriminant function: True Allocated to Group Group 1 Group 2 Total 0 11 Group 1 11 Group 2 0 16 16 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 6 5 11 7 Group 2 9 16

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Bla -- Not

Difference between means: Procrustes distance: 0.01186005 Mahalanobis distance: 11.1618 T-square: 913.6211, P-value (parametric): 0.0852 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2930 T-square: 0.0890 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Not From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 0 11 11 Group 2 0 22 22 From cross-validation: True Allocated to Group 1 Group 2 Group Total Group 1 7 4 11 Group 2 7 15 22

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Bla -- Oge

Difference between means: Procrustes distance: 0.01940899 Mahalanobis distance: 39.6357 T-square: 10944.5740, P-value (parametric): 0.2091 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0130 T-square: 0.1910 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.) Classification/misclassification tables Group 1: Bla Group 2: Oge From discriminant function: True Allocated to Group 1 Group Group 2 Total 0 11 Group 1 11 Group 2 0 19 19 From cross-validation: True Allocated to Group 1 Group Group 2 Total 7 11 Group 1 4 Group 2 8 11 19

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Bla -- Pit

Difference between means: Procrustes distance: 0.01078149 Mahalanobis distance: 4.8683 T-square: 204.4736, P-value (parametric): 0.0029 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2190 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Pit From discriminant function: True Allocated to Group 1 Group Group 2 Total Group 1 11 0 11 40 Group 2 0 40 From cross-validation: True Allocated to Total Group Group 1 Group 2 Group 1 6 5 11 12 28 40 Group 2

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Bla -- Pot

Difference between means: Procrustes distance: 0.01524323 Mahalanobis distance: 7.4268 T-square: 493.6166, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0560 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Pot From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 11 0 11 Group 2 0 48 48 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 8 3 11 47 Group 2 48 1

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Bla -- Rap

Difference between means: Procrustes distance: 0.00854579 Mahalanobis distance: 7.2319 T-square: 377.5420, P-value (parametric): 0.4638 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.6040 T-square: 0.4850 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 110 11 Group 2 0 21 21 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 11 5 6 Group 2 11 10 21

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Bla -- Stj

Difference between means: Procrustes distance: 0.01848767 Mahalanobis distance: 7.5196 T-square: 466.4886, P-value (parametric): 0.0004 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0160 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Stj From discriminant function: True Allocated to Group 1 Group 2 Group Total Group 1 0 11 11 Group 2 0 33 33 From cross-validation: True Allocated to Group Group 1 Group 2 Total 11 Group 1 8 3 Group 2 4 29 33

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Bla -- Sus

Difference between means: Procrustes distance: 0.01241307 Mahalanobis distance: 3.3556 T-square: 55.7371, P-value (parametric): 0.9732 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.4390 T-square: 0.6600 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: Sus From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 11 0 11 Group 2 1 8 9 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 4 11 7 4 5 9 Group 2

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Bla -- SwN

Difference between means: Procrustes distance: 0.01765160 Mahalanobis distance: 5.9142 T-square: 267.1948, P-value (parametric): 0.1801 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0510 T-square: 0.2040 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Bla Group 2: SwN From discriminant function: True Allocated to Group 1 Group Group 2 Total Group 1 11 0 11 Group 2 0 25 25 From cross-validation: True Allocated to Total Group Group 1 Group 2 Group 1 6 5 11 15 10 25 Group 2

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Bla -- Tar

Difference between means: Procrustes distance: 0.01468576 Mahalanobis distance: 6.0637 T-square: 211.0187, P-value (parametric): 0.8370 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1730 T-square: 0.0070 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

```
Classification/misclassification tables
Group 1: Bla
Group 2: Tar
From discriminant function:
True
             Allocated to
Group
           Group 1
                        Group 2
                                     Total
Group 1
             11
                        0
                                  11
Group 2
             0
                       12
                                  12
From cross-validation:
True
             Allocated to
Group
           Group 1
                        Group 2
                                     Total
Group 1
              8
                        3
                                 11
              3
                        9
Group 2
                                 12
```

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cap -- Cas

Difference between means: Procrustes distance: 0.01461795 Mahalanobis distance: 8.4701 T-square: 713.9332, P-value (parametric): 0.0003 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0650 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables					
Group 1:	Сар				
Group 2:	Cas				
From disc	riminant fun	ction:			
True	Allocat	ed to			
Group	Group 1	Group 2		Total	
Group 1	24	0	24		
Group 2	0	17	17		
From cross	ss-validation	:			
True	Allocat	ed to			
Group	Group 1	Group 2		Total	
Group 1	23	1	24		
Group 2	2	15	17		

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cap -- Cho

Difference between means: Procrustes distance: 0.01076350 Mahalanobis distance: 5.0887 T-square: 345.2698, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0330 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cap Group 2: Cho From discriminant function: True Allocated to Group Total Group 1 Group 2 24 Group 1 24 0 Group 2 0 30 30 From cross-validation: True Allocated to Group 1 Group Group 2 Total Group 1 15 9 24 27 30 3 Group 2

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cap -- Con

Difference between means: Procrustes distance: 0.01465556 Mahalanobis distance: 6.3028 T-square: 351.2502, P-value (parametric): 0.0382 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1000 T-square: 0.0430 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cap Group 2: Con From discriminant function: True Allocated to Group Group 1 Group 2 Total

Group 1	24	0	24	
Group 2	0	14	14	
From cros	s-validation	1:		
True	Allocat	ted to		
Group	Group 1	Group 2		Total
Group 1	16	8	24	
Group 2	7	7	14	

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Cap -- Her

Difference between means: Procrustes distance: 0.01612025 Mahalanobis distance: 17.7715 T-square: 2067.2342, P-value (parametric): 0.0202 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0780 T-square: 0.0250 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cap Group 2: Her From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 24 0 24 0 9 9 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total 24 Group 1 21 3 3 6 9 Group 2

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cap -- Jam

Difference between means: Procrustes distance: 0.00966659 Mahalanobis distance: 4.4146 T-square: 259.8515, P-value (parametric): 0.0002 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1860 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cap Group 2: Jam From discriminant function: Allocated to True Group Group 1 Group 2 Total Group 1 24 0 24 0 Group 2 30 30 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 20 4 24 24 30 Group 2 6

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cap -- Neu

Difference between means: Procrustes distance: 0.01679210 Mahalanobis distance: 6.6005 T-square: 418.2432, P-value (parametric): 0.0070 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0200 T-square: 0.0060 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cap Group 2: Neu From discriminant function: True Allocated to Total Group Group 1 Group 2 24 Group 1 24 0 0 16 Group 2 16 From cross-validation: True Allocated to Group Group 1 Group 2 Total 7 24 Group 1 17 Group 2 4 12 16

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cap -- Not

Difference between means: Procrustes distance: 0.01181254 Mahalanobis distance: 5.9774 T-square: 410.1064, P-value (parametric): 0.0002 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1320 T-square: 0.0010 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cap Group 2: Not From discriminant function: True Allocated to Group Group 1 Group 2 Total 24 Group 1 24 0 22 21 Group 2 1 From cross-validation: Allocated to True Group Group 1 Group 2 Total Group 1 19 5 24 Group 2 3 19 22

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Cap -- Oge

Difference between means: Procrustes distance: 0.01846135 Mahalanobis distance: 4.6772 T-square: 231.9935, P-value (parametric): 0.0221 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: 0.0210 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cap Group 2: Oge From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 24 0 24 0 19 19 Group 2 From cross-validation:

True	Allocated to			
Group	Group 1	Group 2		Total
Group 1	16	8	24	
Group 2	5	14	19	

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cap -- Pit

Difference between means: Procrustes distance: 0.01273903 Mahalanobis distance: 3.6663 T-square: 201.6276, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0200 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cap Group 2: Pit From discriminant function: True Allocated to Group 1 Group 2 Total Group Group 1 23 1 24 Group 2 0 40 40 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 18 6 24 7 40 Group 2 33

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Cap -- Pot

Difference between means: Procrustes distance: 0.01509483 Mahalanobis distance: 4.8327 T-square: 373.6848, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0050 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cap Group 2: Pot From discriminant function: True Allocated to Group 1 Group Group 2 Total Group 1 24 0 24 0 48 48 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 19 5 24 Group 2 2 46 48

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cap -- Rap

Difference between means: Procrustes distance: 0.00855140 Mahalanobis distance: 6.3423 T-square: 450.5234, P-value (parametric): 0.0002 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.3690 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cap Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total 24 Group 1 24 0 Group 2 0 21 21 From cross-validation: True Allocated to Group 1 Group 2 Total Group Group 1 19 5 24 4 17 21 Group 2

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cap -- Stj

Difference between means: Procrustes distance: 0.01786990 Mahalanobis distance: 4.7266 T-square: 310.4205, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0010 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cap Group 2: Stj From discriminant function: True Allocated to Group Group 1 Group 2 Total 24 Group 1 24 0 0 33 Group 2 33 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 19 5 24 27 33 Group 2 6

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Cap -- Sus

Difference between means: Procrustes distance: 0.01194160 Mahalanobis distance: 11.7697 T-square: 906.7123, P-value (parametric): 0.0863 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2910 T-square: 0.0950 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cap Group 2: Sus From discriminant function: True Allocated to Group 1 Group 2 Group Total Group 1 24 0 24 0 9 9 Group 2 From cross-validation: True Allocated to Group 1 Group Group 2 Total Group 1 17 7 24

Group 2 3 6 9

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Cap -- SwN

Difference between means: Procrustes distance: 0.01752350 Mahalanobis distance: 5.7207 T-square: 400.7280, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0060 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cap Group 2: SwN From discriminant function: True Allocated to Group Group 1 Group 2 Total 0 24 Group 1 24 Group 2 0 25 25 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 18 6 24 25 Group 2 1 24

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cap -- Tar

Difference between means: Procrustes distance: 0.01400110 Mahalanobis distance: 13.4268 T-square: 1442.2277, P-value (parametric): 0.0017 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0850 T-square: 0.0030 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cap Group 2: Tar From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 24 0 24 Group 2 0 12 12 From cross-validation: True Allocated to Group 2 Group Group 1 Total Group 1 22 2 24 4 8 12 Group 2

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cas -- Cho

Difference between means: Procrustes distance: 0.01413144 Mahalanobis distance: 13.6776 T-square: 2029.9962, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0190 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.) Classification/misclassification tables Group 1: Cas Group 2: Cho From discriminant function: True Allocated to Group 1 Group Group 2 Total Group 1 0 17 17 Group 2 0 30 30 From cross-validation: True Allocated to Group Group 1 Group 2 Total 17 Group 1 16 1 Group 2 30 30 0

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Cas -- Con

Difference between means: Procrustes distance: 0.01818088 Mahalanobis distance: 10.8701 T-square: 907.1611, P-value (parametric): 0.3563 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0900 T-square: 0.3650 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: Con From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 17 0 17 14 Group 2 0 14 From cross-validation: True Allocated to Total Group Group 1 Group 2 Group 1 9 8 17 8 14 Group 2 6

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cas -- Her

Difference between means: Procrustes distance: 0.01936228 Mahalanobis distance: 9.4788 T-square: 528.7144, P-value (parametric): 0.6930 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0720 T-square: 0.1050 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: Her From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 17 0 17 Group 2 0 9 9 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 11 6 17 9 Group 2 5 4

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cas -- Jam

Difference between means: Procrustes distance: 0.01037633 Mahalanobis distance: 6.4976 T-square: 458.1177, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2780 T-square: 0.0010 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: Jam From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 17 0 17 Group 2 0 30 30 From cross-validation: True Allocated to Group Group 1 Group 2 Total 17 Group 1 4 13 Group 2 4 26 30

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cas -- Neu

Difference between means: Procrustes distance: 0.01743208 Mahalanobis distance: 13.0863 T-square: 1411.5294, P-value (parametric): 0.0403 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0590 T-square: 0.0500 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: Neu From discriminant function: Allocated to True Group 1 Group 2 Group Total Group 1 0 17 17 Group 2 0 16 16 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 10 7 17 Group 2 3 13 16

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Cas -- Not

Difference between means: Procrustes distance: 0.01256603 Mahalanobis distance: 7.6888 T-square: 566.9208, P-value (parametric): 0.0038 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2020 T-square: 0.0050 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: Not From discriminant function: True Allocated to Group Group 1 Group 2 Total 17 Group 1 17 0 Group 2 0 22 22 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 17 14 3 7 15 22 Group 2

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cas -- Oge

Difference between means: Procrustes distance: 0.01569429 Mahalanobis distance: 11.8413 T-square: 1258.0622, P-value (parametric): 0.0027 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0400 T-square: 0.0040 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: Oge From discriminant function: True Allocated to Group 1 Group Group 2 Total 17 Group 1 17 0 Group 2 0 19 19 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 13 4 17 16 19 Group 2 3

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Cas -- Pit

Difference between means: Procrustes distance: 0.01068787 Mahalanobis distance: 4.6204 T-square: 254.6830, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1400 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: Pit From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 17 0 17 Group 2 39 40 1 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 17 12 5 Group 2 6 34 40

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cas -- Pot

Difference between means: Procrustes distance: 0.01363463 Mahalanobis distance: 5.5295 T-square: 383.8383, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0320 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: Pot From discriminant function: Allocated to True Group Group 1 Group 2 Total 17 Group 1 17 0 Group 2 0 48 48 From cross-validation: True Allocated to Group Group 1 Total Group 2 Group 1 15 2 17 Group 2 2 46 48

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cas -- Rap

Difference between means: Procrustes distance: 0.01456121 Mahalanobis distance: 6.0278 T-square: 341.3509, P-value (parametric): 0.0417 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1050 T-square: 0.0300 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total 17 Group 1 17 0 Group 2 0 21 21 From cross-validation: True Allocated to Group Group 1 Total Group 2 Group 1 11 6 17 6 21 Group 2 15

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cas -- Stj

Difference between means: Procrustes distance: 0.02174368 Mahalanobis distance: 7.4508 T-square: 622.8796, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: Stj From discriminant function: True Allocated to Group Group 1 Group 2 Total

Group 1	17	0	17	
Group 2	0	33	33	
From cross	-validation	1:		
True	Alloca	ted to		
Group	Group 1	Group 2		Total
Group 1	15	2	17	
Group 2	2	31	33	

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Cas -- Sus

Difference between means: Procrustes distance: 0.01862984 Mahalanobis distance: 7.7611 T-square: 354.4566, P-value (parametric): 0.7854 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1270 T-square: 0.2300 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: Sus From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 17 0 17 9 9 Group 2 0 From cross-validation: True Allocated to Group Group 1 Group 2 Total 17 Group 1 10 7 5 4 9 Group 2

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cas -- SwN

Difference between means: Procrustes distance: 0.02140828 Mahalanobis distance: 6.5145 T-square: 429.4336, P-value (parametric): 0.0019 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0030 T-square: 0.0010 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: SwN From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 17 0 17 25 Group 2 0 25 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 13 4 17 21 Group 2 4 25

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cas -- Tar

Difference between means: Procrustes distance: 0.01586209 Mahalanobis distance: 42.2922 T-square: 12582.1110, P-value (parametric): 0.1884 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0930 T-square: 0.0520 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cas Group 2: Tar From discriminant function: True Allocated to Total Group Group 1 Group 2 Group 1 17 17 0 0 12 Group 2 12 From cross-validation: True Allocated to Group Group 1 Group 2 Total 17 10 Group 1 7 Group 2 4 8 12

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cho -- Con

Difference between means: Procrustes distance: 0.01405240 Mahalanobis distance: 10.2070 T-square: 994.4811, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0250 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cho Group 2: Con From discriminant function: True Allocated to Group Group 1 Group 2 Total 30 Group 1 30 0 0 14 Group 2 14 From cross-validation: Allocated to True Group Group 1 Group 2 Total Group 1 29 1 30 Group 2 1 13 14

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cho -- Her

Difference between means: Procrustes distance: 0.01655690 Mahalanobis distance: 15.4405 T-square: 1650.5201, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0050 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cho Group 2: Her From discriminant function: True Allocated to Group Group 1 Group 2 Total 30 Group 1 30 0 0 9 9 Group 2 From cross-validation:

True	Allocat	ed to		
Group	Group 1	Group 2		Total
Group 1	28	2	30	
Group 2	2	7	9	

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cho -- Jam

Difference between means: Procrustes distance: 0.01027155 Mahalanobis distance: 3.2173 T-square: 155.2701, P-value (parametric): 0.0019 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0670 T-square: 0.0020 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cho Group 2: Jam From discriminant function: True Allocated to Group 1 Group 2 Total Group Group 1 29 1 30 Group 2 4 26 30 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 22 8 30 Group 2 10 20 30

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Cho -- Neu

Difference between means: Procrustes distance: 0.01407036 Mahalanobis distance: 6.8690 T-square: 492.3401, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0070 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cho Group 2: Neu From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 30 0 30 0 16 16 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 26 4 30 Group 2 5 11 16

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cho -- Not

Difference between means: Procrustes distance: 0.01076789 Mahalanobis distance: 5.6006 T-square: 398.1226, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0780 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cho Group 2: Not From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 30 0 30 Group 2 0 22 22 From cross-validation: True Allocated to Group 1 Group 2 Total Group Group 1 27 3 30 7 22 Group 2 15

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Cho -- Oge

Difference between means: Procrustes distance: 0.01818301 Mahalanobis distance: 7.4943 T-square: 653.3369, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cho Group 2: Oge From discriminant function: True Allocated to Group Group 1 Group 2 Total 30 Group 1 30 0 0 19 Group 2 19 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 28 2 30 2 17 19 Group 2

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Cho -- Pit

Difference between means: Procrustes distance: 0.00955349 Mahalanobis distance: 3.8718 T-square: 256.9834, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0300 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cho Group 2: Pit From discriminant function: True Allocated to Group 1 Group 2 Group Total Group 1 30 0 30 40 Group 2 1 39 From cross-validation: True Allocated to Group 1 Group Group 2 Total Group 1 26 4 30

Group 2 11 29 40

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Cho -- Pot

Difference between means: Procrustes distance: 0.01243693 Mahalanobis distance: 4.0752 T-square: 306.5947, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0040 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cho Group 2: Pot From discriminant function: True Allocated to Group Group 1 Group 2 Total 30 Group 1 29 1 Group 2 0 48 48 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 25 5 30 Group 2 6 42 48

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cho -- Rap

Difference between means: Procrustes distance: 0.01026731 Mahalanobis distance: 7.7485 T-square: 741.6595, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0980 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cho Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 30 30 0 Group 2 0 21 21 From cross-validation: True Allocated to Group 1 Group Group 2 Total Group 1 29 1 30 2 21 Group 2 19

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cho -- Stj

Difference between means: Procrustes distance: 0.01791592 Mahalanobis distance: 6.6625 T-square: 697.5423, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.) Classification/misclassification tables Group 1: Cho Group 2: Stj From discriminant function: True Allocated to Group 1 Total Group Group 2 Group 1 30 0 30 Group 2 0 33 33 From cross-validation: True Allocated to Group Group 1 Group 2 Total 30 Group 1 28 2 Group 2 3 30 33

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Cho -- Sus

Difference between means: Procrustes distance: 0.01358028 Mahalanobis distance: 6.5514 T-square: 297.1468, P-value (parametric): 0.0415 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0490 T-square: 0.0470 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cho Group 2: Sus From discriminant function: True Allocated to Group 1 Group Group 2 Total Group 1 30 0 30 0 9 9 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 22 8 30 3 9 Group 2 6

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cho -- SwN

Difference between means: Procrustes distance: 0.01342198 Mahalanobis distance: 3.6380 T-square: 180.4741, P-value (parametric): 0.0021 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0070 T-square: 0.0020 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cho Group 2: SwN From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 29 1 30 25 Group 2 0 25 From cross-validation: True Allocated to Group 1 Group Group 2 Total Group 1 24 6 30 15 25 Group 2 10

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Cho -- Tar

Difference between means: Procrustes distance: 0.01177468 Mahalanobis distance: 6.2120 T-square: 330.7617, P-value (parametric): 0.0068 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0370 T-square: 0.0110 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Cho Group 2: Tar From discriminant function: True Allocated to Group 1 Group Group 2 Total Group 1 30 0 30 Group 2 0 12 12 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 30 26 4 7 Group 2 5 12

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Con -- Her

Difference between means: Procrustes distance: 0.00942593 Mahalanobis distance: 8.6623 T-square: 411.0620, P-value (parametric): 0.6879 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.6190 T-square: 0.0050 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Con Group 2: Her From discriminant function: True Allocated to Group 1 Group 2 Group Total Group 1 0 14 14 9 9 Group 2 0 From cross-validation: Allocated to True Group Group 1 Group 2 Total Group 1 14 0 14 Group 2 1 8 9

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Con -- Jam

Difference between means: Procrustes distance: 0.01643187 Mahalanobis distance: 5.1419 T-square: 252.3723, P-value (parametric): 0.0103 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0660 T-square: 0.0090 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Con Group 2: Jam From discriminant function: True Allocated to Group Group 1 Group 2 Total 14 Group 1 14 0 Group 2 0 30 30 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 14 8 6 7 23 30 Group 2

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Con -- Neu

Difference between means: Procrustes distance: 0.01171889 Mahalanobis distance: 23.0639 T-square: 3971.8576, P-value (parametric): 0.3397 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.3040 T-square: 0.3370 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Con Group 2: Neu From discriminant function: True Allocated to Group 1 Group Group 2 Total 14 Group 1 14 0 Group 2 0 16 16 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 11 3 14 11 16 Group 2 5

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Con -- Not

Difference between means: Procrustes distance: 0.01471366 Mahalanobis distance: 8.7864 T-square: 660.4984, P-value (parametric): 0.0187 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1530 T-square: 0.0210 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Con Group 2: Not From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 14 0 14 Group 2 0 22 22 From cross-validation: True Allocated to Group Group 1 Group 2 Total 14 Group 1 9 5 7 Group 2 15 22

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Con -- Oge

Difference between means: Procrustes distance: 0.01855278 Mahalanobis distance: 9.1594 T-square: 676.2459, P-value (parametric): 0.1384 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0220 T-square: 0.1510 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables					
Group 1: 0	Con				
Group 2: 0	Oge				
From disc	riminant fur	action:			
True	Allocat	ed to			
Group	Group 1	Group 2		Total	
Group 1	14	0	14		
Group 2	0	19	19		
From cros	From cross-validation:				
True	Allocat	ed to			
Group	Group 1	Group 2		Total	
Group 1	7	7	14		
Group 2	5	14	19		

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Con -- Pit

Difference between means: Procrustes distance: 0.01160752 Mahalanobis distance: 4.1793 T-square: 181.1328, P-value (parametric): 0.0027 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1520 T-square: 0.0040 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Con Group 2: Pit From discriminant function: Allocated to True Group Group 1 Group 2 Total 14 Group 1 14 0 Group 2 39 40 1 From cross-validation: True Allocated to Group 1 Total Group Group 2 Group 1 8 6 14 5 35 40 Group 2

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Con -- Pot

Difference between means: Procrustes distance: 0.01633513 Mahalanobis distance: 5.6250 T-square: 342.9424, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0270 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Con Group 2: Pot From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 14 14 0 Group 2 1 47 48 From cross-validation: True Allocated to Group Group 1 Group 2 Total 10 4 14 Group 1 Group 2 2 46 48

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Con -- Rap

Difference between means: Procrustes distance: 0.01231366 Mahalanobis distance: 5.9250 T-square: 294.8824, P-value (parametric): 0.2135 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2730 T-square: 0.1880 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Con Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 14 0 14 21 Group 2 0 21 From cross-validation: True Allocated to Group Group 1 Total Group 2 14 Group 1 8 6 Group 2 11 10 21

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Con -- Stj

Difference between means: Procrustes distance: 0.01091608 Mahalanobis distance: 5.9128 T-square: 343.6615, P-value (parametric): 0.0004 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1750 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Con Group 2: Stj From discriminant function: True Allocated to Group 2 Group Group 1 Total 14 0 Group 1 14 Group 2 0 33 33 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 12 2 14 27 Group 2 6 33

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Con -- Sus

Difference between means: Procrustes distance: 0.01679380 Mahalanobis distance: 5.6120 T-square: 172.5357, P-value (parametric): 0.8752 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2200 T-square: 0.1050 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Con Group 2: Sus From discriminant function: True Allocated to Group Group 1 Group 2 Total 14 Group 1 14 0 0 9 9 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total 14 9 5 Group 1 Group 2 4 5 9

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Con -- SwN

Difference between means: Procrustes distance: 0.00987721 Mahalanobis distance: 8.5681 T-square: 658.8348, P-value (parametric): 0.0020 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.3420 T-square: 0.0010 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Con Group 2: SwN From discriminant function: True Allocated to Group Group 1 Group 2 Total 14 Group 1 14 0 0 25 25 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 11 3 14 Group 2 4 21 25

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Con -- Tar

Difference between means: Procrustes distance: 0.01559101 Mahalanobis distance: 14.0846 T-square: 1281.8126, P-value (parametric): 0.4910 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1550 T-square: 0.0400 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Con Group 2: Tar From discriminant function: True Allocated to Group Group 1 Group 2 Total 14 Group 1 14 0 0 12 Group 2 12 From cross-validation:

True	Allocat			
Group	Group 1	Group 2		Total
Group 1	8	6	14	
Group 2	2	10	12	

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Her -- Jam

Difference between means: Procrustes distance: 0.01867288 Mahalanobis distance: 4.8288 T-square: 161.4299, P-value (parametric): 0.2341 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0550 T-square: 0.2260 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Her Group 2: Jam From discriminant function: True Allocated to Group 1 Group 2 Total Group 9 Group 1 9 0 Group 2 1 29 30 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 9 6 3 30 Group 2 8 22

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Her -- Neu

Difference between means: Procrustes distance: 0.01168565 Mahalanobis distance: 5.6740 T-square: 185.4406, P-value (parametric): 0.8953 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.3240 T-square: 0.1590 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Her Group 2: Neu From discriminant function: True Allocated to Group Group 1 Group 2 Total 9 Group 1 9 0 0 16 16 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 4 5 9 Group 2 4 12 16

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Her -- Not

Difference between means: Procrustes distance: 0.01663043 Mahalanobis distance: 13.0641 T-square: 1090.0831, P-value (parametric): 0.3076 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1340 T-square: 0.3250 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Her Group 2: Not From discriminant function: True Allocated to Group Group 1 Group 2 Total 9 0 Group 1 9 Group 2 0 22 22 From cross-validation: True Allocated to Group 1 Group 2 Total Group Group 1 4 5 9 22 11 Group 2 11

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Her -- Oge

Difference between means: Procrustes distance: 0.02250428 Mahalanobis distance: 7.5777 T-square: 350.6801, P-value (parametric): 0.8232 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0040 T-square: 0.0820 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Her Group 2: Oge From discriminant function: True Allocated to Group 1 Group Group 2 Total 9 0 Group 1 9 0 19 Group 2 19 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 4 5 9 19 7 12 Group 2

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Her -- Pit

Difference between means: Procrustes distance: 0.01466202 Mahalanobis distance: 6.1543 T-square: 278.2718, P-value (parametric): 0.0007 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0600 T-square: 0.0020 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Her Group 2: Pit From discriminant function: True Allocated to Group 1 Group 2 Total Group 9 Group 1 9 0 0 40 Group 2 40 From cross-validation: True Allocated to Group 1 Group Group 2 Total Group 1 6 3 9

Group 2 4 36 40

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Her -- Pot

Difference between means: Procrustes distance: 0.01921379 Mahalanobis distance: 7.5992 T-square: 437.6692, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0140 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Her Group 2: Pot From discriminant function: True Allocated to Group Group 1 Group 2 Total 0 9 Group 1 9 Group 2 0 48 48 From cross-validation: True Allocated to Group Group 1 Group 2 Total 9 Group 1 8 1 Group 2 3 45 48

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Her -- Rap

Difference between means: Procrustes distance: 0.01216524 Mahalanobis distance: 21.0034 T-square: 2779.2117, P-value (parametric): 0.4005 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.3530 T-square: 0.3820 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Her Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total 9 Group 1 0 9 Group 2 0 21 21 From cross-validation: True Allocated to Group 1 Group Group 2 Total Group 1 4 5 9 10 11 21 Group 2

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Her -- Stj

Difference between means: Procrustes distance: 0.01279672 Mahalanobis distance: 8.1078 T-square: 464.8524, P-value (parametric): 0.0013 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1170 T-square: 0.0010 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.) Classification/misclassification tables Group 1: Her Group 2: Stj From discriminant function: True Allocated to Group 1 Total Group Group 2 9 0 9 Group 1 Group 2 0 33 33 From cross-validation: True Allocated to Group 1 Group 2 Group Total 9 Group 1 8 1 Group 2 28 33 5

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Her -- Sus

Difference between means: Procrustes distance: 0.01628323 Mahalanobis distance: 4.5796 T-square: 94.3758, P-value (parametric): 0.8809 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2350 T-square: 0.0050 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Her Group 2: Sus From discriminant function: True Allocated to Group Group 1 Group 2 Total 9 9 Group 1 0 0 9 9 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 8 1 9 8 9 Group 2 1

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Her -- SwN

Difference between means: Procrustes distance: 0.01100566 Mahalanobis distance: 6.0937 T-square: 245.7306, P-value (parametric): 0.3926 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2910 T-square: 0.3950 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Her Group 2: SwN From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 9 9 0 0 Group 2 25 25 From cross-validation: True Allocated to Group Group 1 Group 2 Total 9 Group 1 4 5 25 Group 2 11 14

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Her -- Tar

Difference between means: Procrustes distance: 0.01580569 Mahalanobis distance: 3.2783 T-square: 55.2713, P-value (parametric): 0.9807 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1140 T-square: 0.6220 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Her Group 2: Tar From discriminant function: True Allocated to Group Group 1 Total Group 2 Group 1 8 1 9 Group 2 12 1 11 From cross-validation: Allocated to True Group Group 1 Group 2 Total 9 Group 1 4 5 5 7 Group 2 12

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Jam -- Neu

Difference between means: Procrustes distance: 0.01833016 Mahalanobis distance: 3.6269 T-square: 137.2611, P-value (parametric): 0.0854 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0190 T-square: 0.0700 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Jam Group 2: Neu From discriminant function: True Allocated to Group 1 Group 2 Group Total Group 1 2 30 28 Group 2 15 16 1 From cross-validation: Allocated to True Group Group 1 Group 2 Total Group 1 20 10 30 Group 2 7 9 16

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Jam -- Not

Difference between means: Procrustes distance: 0.00896015 Mahalanobis distance: 3.8952 T-square: 192.5780, P-value (parametric): 0.0031 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.3230 T-square: 0.0040 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Jam Group 2: Not

From discu	iminant fui	nction:		
True	Allocat			
Group	Group 1	Group 2		Total
Group 1	29	1	30	
Group 2	1	21	22	
From cross	s-validation	:		
True	Allocat	ed to		
Group	Group 1	Group 2		Total
Group 1	24	6	30	
Group 2	8	14	22	

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Jam -- Oge

Difference between means: Procrustes distance: 0.01333207 Mahalanobis distance: 3.8097 T-square: 168.8306, P-value (parametric): 0.0163 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0510 T-square: 0.0120 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Jam Group 2: Oge From discriminant function: True Allocated to Group Group 1 Group 2 Total 30 Group 1 29 1 Group 2 0 19 19 From cross-validation: True Allocated to Group 2 Total Group Group 1 30 Group 1 19 11 Group 2 13 19 6

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Jam -- Pit

Difference between means: Procrustes distance: 0.00934172 Mahalanobis distance: 2.4563 T-square: 103.4271, P-value (parametric): 0.0096 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1010 T-square: 0.0100 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Jam Group 2: Pit From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 25 5 30 Group 2 4 36 40 From cross-validation: True Allocated to Group Group 1 Group 2 Total 30 Group 1 18 12 40 Group 2 12 28

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Jam -- Pot

Difference between means: Procrustes distance: 0.01000048 Mahalanobis distance: 3.8626 T-square: 275.4446, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0670 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Jam Group 2: Pot From discriminant function: Allocated to True Group Group 1 Total Group 2 30 Group 1 28 2 Group 2 0 48 48 From cross-validation: True Allocated to Group Group 1 Total Group 2 Group 1 24 6 30 Group 2 6 42 48

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Jam -- Rap

Difference between means: Procrustes distance: 0.01163807 Mahalanobis distance: 3.3119 T-square: 135.4993, P-value (parametric): 0.0329 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1390 T-square: 0.0270 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Jam Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total 30 Group 1 28 2 Group 2 20 21 1 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 19 11 30 21 6 Group 2 15

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Jam -- Stj

Difference between means: Procrustes distance: 0.02202426 Mahalanobis distance: 5.3217 T-square: 445.0322, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Jam Group 2: Stj From discriminant function: True Allocated to Group Group 1 Group 2 Total

Group 1	30	0	30			
Group 2	0	33	33			
From cross-validation:						
True	Allocat	ed to				
Group	Group 1	Group 2		Total		
Group 1	25	5	30			
Group 2	3	30	33			

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Jam -- Sus

Difference between means: Procrustes distance: 0.01536023 Mahalanobis distance: 3.4961 T-square: 84.6185, P-value (parametric): 0.6814 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1420 T-square: 0.6820 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Jam Group 2: Sus From discriminant function: True Allocated to Group Group 1 Group 2 Total 30 Group 1 30 0 9 9 Group 2 0 From cross-validation: True Allocated to Group Group 1 Group 2 Total 30 Group 1 18 12 5 9 Group 2 4

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Jam -- SwN

Difference between means: Procrustes distance: 0.01897131 Mahalanobis distance: 3.6611 T-square: 182.7785, P-value (parametric): 0.0019 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0030 T-square: 0.0010 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Jam Group 2: SwN From discriminant function: True Allocated to Group Group 1 Group 2 Total 30 0 Group 1 30 2 Group 2 23 25 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 23 7 30 19 25 Group 2 6

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Jam -- Tar

Difference between means: Procrustes distance: 0.01029517 Mahalanobis distance: 4.2410 T-square: 154.1688, P-value (parametric): 0.1347 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.3190 T-square: 0.1380 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Jam Group 2: Tar From discriminant function: True Allocated to Group Group 1 Group 2 Total 29 30 Group 1 1 0 12 Group 2 12 From cross-validation: True Allocated to Group Group 1 Group 2 Total 30 19 Group 1 11 Group 2 4 8 12

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Neu -- Not

Difference between means: Procrustes distance: 0.01842290 Mahalanobis distance: 5.8627 T-square: 318.3840, P-value (parametric): 0.0517 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0200 T-square: 0.0400 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Neu Group 2: Not From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 16 0 16 0 22 Group 2 22 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 10 6 16 Group 2 8 14 22

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Neu -- Oge

Difference between means: Procrustes distance: 0.02471954 Mahalanobis distance: 7.7904 T-square: 527.1355, P-value (parametric): 0.0644 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: 0.0540 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Neu Group 2: Oge From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 0 16 16 19 Group 2 0 19 From cross-validation:

True	Allocat			
Group	Group 1	Group 2		Total
Group 1	9	7	16	
Group 2	5	14	19	

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Neu -- Pit

Difference between means: Procrustes distance: 0.01470064 Mahalanobis distance: 4.0710 T-square: 189.4050, P-value (parametric): 0.0011 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0190 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Neu Group 2: Pit From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 15 1 16 Group 2 1 39 40 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 11 5 16 Group 2 8 32 40

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Neu -- Pot

Difference between means: Procrustes distance: 0.02083954 Mahalanobis distance: 6.5910 T-square: 521.2909, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Neu Group 2: Pot From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 16 0 16 48 48 0 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 14 2 16 Group 2 3 45 48

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Neu -- Rap

Difference between means: Procrustes distance: 0.01149706 Mahalanobis distance: 4.0287 T-square: 147.3903, P-value (parametric): 0.4171 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2540 T-square: 0.4220 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Neu Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 16 0 16 Group 2 0 21 21 From cross-validation: True Allocated to Group 1 Group 2 Total Group Group 1 8 8 16 9 12 Group 2 21

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Neu -- Stj

Difference between means: Procrustes distance: 0.01082197 Mahalanobis distance: 5.7501 T-square: 356.2771, P-value (parametric): 0.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0920 T-square: 0.0020 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Neu Group 2: Stj From discriminant function: True Allocated to Group Group 1 Group 2 Total 16 Group 1 16 0 33 Group 2 0 33 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 11 5 16 Group 2 7 26 33

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Neu -- Sus

Difference between means: Procrustes distance: 0.01684707 Mahalanobis distance: 9.4215 T-square: 511.2836, P-value (parametric): 0.6803 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1220 T-square: 0.2270 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Neu Group 2: Sus From discriminant function: True Allocated to Group 1 Group 2 Group Total Group 1 16 0 16 0 9 Group 2 9 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 11 5 16

Group 2 4 5 9

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Neu -- SwN

Difference between means: Procrustes distance: 0.01480379 Mahalanobis distance: 6.4472 T-square: 405.5268, P-value (parametric): 0.0045 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0580 T-square: 0.0070 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Neu Group 2: SwN From discriminant function: True Allocated to Group Group 1 Group 2 Total 0 16 Group 1 16 Group 2 0 25 25 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 11 5 16 Group 2 7 18 25

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Neu -- Tar

Difference between means: Procrustes distance: 0.01921682 Mahalanobis distance: 9.3527 T-square: 599.8186, P-value (parametric): 0.7018 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0180 T-square: 0.0850 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Neu Group 2: Tar From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 16 0 16 Group 2 0 12 12 From cross-validation: True Allocated to Group 1 Group 2 Group Total Group 1 11 5 16 Group 2 7 5 12

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Not -- Oge

Difference between means: Procrustes distance: 0.01098656 Mahalanobis distance: 7.1884 T-square: 526.8133, P-value (parametric): 0.0013 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1510 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.) Classification/misclassification tables Group 1: Not Group 2: Oge From discriminant function: True Allocated to Group 1 Total Group Group 2 0 22 Group 1 22 Group 2 0 19 19 From cross-validation: True Allocated to Group Group 1 Group 2 Total 22 Group 1 18 4 Group 2 4 15 19

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Not -- Pit

Difference between means: Procrustes distance: 0.00711778 Mahalanobis distance: 3.5378 T-square: 177.6501, P-value (parametric): 0.0004 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.4150 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Not Group 2: Pit From discriminant function: True Allocated to Group Group 1 Group 2 Total 22 Group 1 21 1 39 40 Group 2 1 From cross-validation: True Allocated to Total Group Group 1 Group 2 Group 1 14 8 22 9 31 40 Group 2

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Not -- Pot

Difference between means: Procrustes distance: 0.00776923 Mahalanobis distance: 5.1390 T-square: 398.4073, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2590 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Not Group 2: Pot From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 22 22 0 Group 2 0 48 48 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 20 2 22 48 Group 2 4 44

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Not -- Rap

Difference between means: Procrustes distance: 0.01321483 Mahalanobis distance: 5.8139 T-square: 363.1673, P-value (parametric): 0.0026 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1270 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Not Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 22 0 22 Group 2 0 21 21 From cross-validation: Allocated to True Group Group 1 Group 2 Total 22 Group 1 18 4 Group 2 6 15 21

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Not -- Stj

Difference between means: Procrustes distance: 0.02059366 Mahalanobis distance: 5.9018 T-square: 459.7753, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Not Group 2: Stj From discriminant function: True Allocated to Group 1 Group 2 Group Total Group 1 0 22 22 0 33 Group 2 33 From cross-validation: Allocated to True Group Group 1 Group 2 Total Group 1 20 2 22 32 Group 2 1 33

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Not -- Sus

Difference between means: Procrustes distance: 0.01516559 Mahalanobis distance: 5.6668 T-square: 205.1086, P-value (parametric): 0.8430 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2070 T-square: 0.8430 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Not Group 2: Sus From discriminant function: True Allocated to Group Group 1 Group 2 Total 22 Group 1 22 0 Group 2 0 9 9 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 22 11 11 9 6 3 Group 2

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Not -- SwN

Difference between means: Procrustes distance: 0.01571115 Mahalanobis distance: 4.0475 T-square: 191.7049, P-value (parametric): 0.0146 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0530 T-square: 0.0150 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Not Group 2: SwN From discriminant function: True Allocated to Group 1 Group Group 2 Total 22 Group 1 22 0 25 Group 2 0 25 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 13 9 22 15 25 Group 2 10

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Not -- Tar

Difference between means: Procrustes distance: 0.00865122 Mahalanobis distance: 13.8208 T-square: 1483.1701, P-value (parametric): 0.0134 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.5140 T-square: 0.0110 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

```
Classification/misclassification tables
Group 1: Not
Group 2: Tar
From discriminant function:
True
             Allocated to
Group
           Group 1
                        Group 2
                                     Total
Group 1
             22
                        0
                                 22
Group 2
             0
                       12
                                  12
From cross-validation:
True
             Allocated to
Group
           Group 1
                        Group 2
                                     Total
Group 1
                                 22
             18
                        4
                        9
Group 2
              3
                                 12
```

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Oge -- Pit

Difference between means: Procrustes distance: 0.01203492 Mahalanobis distance: 4.2301 T-square: 230.4977, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0330 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Oge Group 2: Pit From discriminant function: Allocated to True Group Group 1 Total Group 2 19 Group 1 19 0 Group 2 0 40 40 From cross-validation: True Allocated to Group Group 1 Total Group 2 Group 1 15 4 19 Group 2 5 35 40

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Oge -- Pot

Difference between means: Procrustes distance: 0.01001734 Mahalanobis distance: 5.5624 T-square: 421.1514, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0720 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Oge Group 2: Pot From discriminant function: True Allocated to Group Group 1 Group 2 Total 19 Group 1 19 0 Group 2 0 48 48 From cross-validation: True Allocated to Group Group 1 Total Group 2 Group 1 17 2 19 48 3 45 Group 2

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Oge -- Rap

Difference between means: Procrustes distance: 0.02046895 Mahalanobis distance: 7.4020 T-square: 546.5224, P-value (parametric): 0.0022 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0020 T-square: 0.0020 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Oge Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total

Group 1	19	0	19			
Group 2	0	21	21			
From cross-validation:						
True	Alloca	ted to				
Group	Group 1	Group 2		Total		
Group 1	16	3	19			
Group 2	7	14	21			

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Oge -- Stj

Difference between means: Procrustes distance: 0.02562561 Mahalanobis distance: 6.1998 T-square: 463.4646, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Oge Group 2: Stj From discriminant function: True Allocated to Group Group 1 Group 2 Total 19 Group 1 19 0 33 Group 2 0 33 From cross-validation: True Allocated to Group Group 1 Group 2 Total 19 Group 1 18 1 4 29 33 Group 2

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Oge -- Sus

Difference between means: Procrustes distance: 0.02372616 Mahalanobis distance: 20.0307 T-square: 2450.3678, P-value (parametric): 0.3961 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: 0.0580 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Oge Group 2: Sus From discriminant function: Allocated to True Group Group 1 Group 2 Total Group 1 19 0 19 Group 2 0 9 9 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 15 4 19 5 Group 2 4 9

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Oge -- SwN

Difference between means: Procrustes distance: 0.02106786 Mahalanobis distance: 5.7049 T-square: 351.3451, P-value (parametric): 0.0018 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0020 T-square: 0.0020 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Oge Group 2: SwN From discriminant function: True Allocated to Group Group 1 Group 2 Total 19 Group 1 19 0 0 25 25 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total 19 Group 1 13 6 Group 2 6 19 25

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Oge -- Tar

Difference between means: Procrustes distance: 0.01344884 Mahalanobis distance: 66.2421 T-square: 32273.1598, P-value (parametric): 0.0125 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0360 T-square: 0.0110 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Oge Group 2: Tar From discriminant function: True Allocated to Group Group 1 Group 2 Total 19 Group 1 19 0 0 12 Group 2 12 From cross-validation: Allocated to True Group Group 1 Group 2 Total Group 1 19 17 2 Group 2 2 10 12

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Pit -- Pot

Difference between means: Procrustes distance: 0.00856125 Mahalanobis distance: 4.2297 T-square: 390.3298, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0820 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Pit Group 2: Pot From discriminant function: True Allocated to Group Group 1 Group 2 Total 40 Group 1 40 0 0 48 Group 2 48 From cross-validation:

True	Allocat		
Group	Group 1	Group 2	Total
Group 1	30	10	40
Group 2	4	44	48

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Pit -- Rap

Difference between means: Procrustes distance: 0.01219308 Mahalanobis distance: 3.1882 T-square: 139.9689, P-value (parametric): 0.0036 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0510 T-square: 0.0030 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Pit Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 38 2 40 Group 2 1 20 21 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 30 10 40 Group 2 8 13 21

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Pit -- Stj

Difference between means: Procrustes distance: 0.01802286 Mahalanobis distance: 4.7717 T-square: 411.7154, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Pit Group 2: Stj From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 40 0 40 0 33 33 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 38 2 40 Group 2 2 31 33

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Pit -- Sus

Difference between means: Procrustes distance: 0.01643683 Mahalanobis distance: 7.3686 T-square: 398.9113, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0410 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Pit Group 2: Sus From discriminant function: True Allocated to Group Group 1 Group 2 Total 40 40 Group 1 0 Group 2 0 9 9 From cross-validation: True Allocated to Group 1 Group 2 Total Group Group 1 38 2 40 5 4 9 Group 2

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Pit -- SwN

Difference between means: Procrustes distance: 0.01401053 Mahalanobis distance: 3.1876 T-square: 156.3181, P-value (parametric): 0.0006 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0170 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Pit Group 2: SwN From discriminant function: True Allocated to Group 1 Group Group 2 Total 2 40 Group 1 38 0 25 25 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 31 9 40 15 Group 2 10 25

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Pit -- Tar

Difference between means: Procrustes distance: 0.01018067 Mahalanobis distance: 4.6039 T-square: 195.6557, P-value (parametric): 0.0028 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2130 T-square: 0.0040 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Pit Group 2: Tar From discriminant function: True Allocated to Group 1 Group 2 Group Total Group 1 40 0 40 0 12 Group 2 12 From cross-validation: True Allocated to Group 1 Group Group 2 Total Group 1 34 6 40

Group 2 5 7 12

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Pot -- Rap

Difference between means: Procrustes distance: 0.01692329 Mahalanobis distance: 3.9961 T-square: 233.2844, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0070 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Pot Group 2: Rap From discriminant function: True Allocated to Group Group 1 Group 2 Total 48 Group 1 47 1 Group 2 1 20 21 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 42 6 48 Group 2 8 13 21

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Pot -- Stj

Difference between means: Procrustes distance: 0.02323201 Mahalanobis distance: 6.3958 T-square: 799.9411, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: <.0001 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Pot Group 2: Stj From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 48 48 0 Group 2 0 33 33 From cross-validation: True Allocated to Group 1 Group 2 Group Total Group 1 48 0 48 Group 2 4 29 33

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Pot -- Sus

Difference between means: Procrustes distance: 0.01856829 Mahalanobis distance: 5.3911 T-square: 220.2751, P-value (parametric): 0.0002 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0160 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.) Classification/misclassification tables Group 1: Pot Group 2: Sus From discriminant function: True Allocated to Group 1 Group Group 2 Total 47 48 Group 1 1 Group 2 0 9 9 From cross-validation: True Allocated to Group Group 1 Group 2 Total 48 Group 1 44 4 Group 2 3 6 9

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Pot -- SwN

Difference between means: Procrustes distance: 0.01728536 Mahalanobis distance: 3.6826 T-square: 222.9331, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0020 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Pot Group 2: SwN From discriminant function: True Allocated to Group 1 Group Group 2 Total Group 1 46 2 48 25 25 Group 2 0 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 41 7 48 7 25 Group 2 18

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Pot -- Tar

Difference between means: Procrustes distance: 0.00931138 Mahalanobis distance: 5.8888 T-square: 332.9092, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.2240 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Pot Group 2: Tar From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 48 0 48 Group 2 0 12 12 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 45 3 48 12 Group 2 4 8

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Rap -- Stj

Difference between means: Procrustes distance: 0.01429414 Mahalanobis distance: 6.2541 T-square: 501.9586, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0220 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Rap Group 2: Stj From discriminant function: True Allocated to Group 1 Group Group 2 Total Group 1 21 0 21 Group 2 0 33 33 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 21 18 3 Group 2 3 30 33

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Rap -- Sus

Difference between means: Procrustes distance: 0.01103548 Mahalanobis distance: 14.6803 T-square: 1357.7296, P-value (parametric): 0.5463 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.4670 T-square: 0.5170 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Rap Group 2: Sus From discriminant function: Allocated to True Group 1 Group Group 2 Total Group 1 0 21 21 0 9 9 Group 2 From cross-validation: Allocated to True Group Group 1 Group 2 Total Group 1 8 13 21 Group 2 4 5 9

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Rap -- SwN

Difference between means: Procrustes distance: 0.01453414 Mahalanobis distance: 5.6331 T-square: 362.1578, P-value (parametric): 0.0005 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0520 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Rap Group 2: SwN From discriminant function: True Allocated to Group Group 1 Group 2 Total 21 Group 1 21 0 Group 2 0 25 25 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 4 21 17 25 5 20 Group 2

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Rap -- Tar

Difference between means: Procrustes distance: 0.01421145 Mahalanobis distance: 45.0681 T-square: 15510.4875, P-value (parametric): 0.0004 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.1440 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Rap Group 2: Tar From discriminant function: True Allocated to Group 1 Group Group 2 Total 21 Group 1 21 0 Group 2 0 12 12 From cross-validation: True Allocated to Total Group Group 1 Group 2 Group 1 20 1 21 0 12 12 Group 2

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Stj -- Sus

Difference between means: Procrustes distance: 0.01738481 Mahalanobis distance: 6.9560 T-square: 342.1567, P-value (parametric): 0.0058 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0360 T-square: 0.0040 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Stj Group 2: Sus From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 33 0 33 Group 2 0 9 9 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 25 8 33 3 Group 2 6 9

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Stj -- SwN

Difference between means: Procrustes distance: 0.01514488 Mahalanobis distance: 8.4402 T-square: 1013.2775, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0030 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

	sification ta	bles	
Stj			
SwN			
riminant fur	nction:		
Allocat	ed to		
Group 1	Group 2	!	Total
33	0	33	
0	25	25	
s-validation	:		
Allocat	ed to		
Group 1	Group 2	2	Total
32	1	33	
0	25	25	
	Stj SwN riminant fur Allocat Group 1 33 0 s-validation Allocat Group 1	Stj SwN riminant function: Allocated to Group 1 Group 2 33 0 0 25 s-validation: Allocated to Group 1 Group 2 32 1	SwN riminant function: Allocated to Group 1 Group 2 33 0 33 0 25 25 s-validation: Allocated to Group 1 Group 2 32 1 33

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Stj -- Tar

Difference between means: Procrustes distance: 0.02227495 Mahalanobis distance: 8.6896 T-square: 664.4838, P-value (parametric): <.0001 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0010 T-square: <.0001 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Stj Group 2: Tar From discriminant function: True Allocated to Group Group 1 Group 2 Total 33 Group 1 33 0 Group 2 0 12 12 From cross-validation: True Allocated to Group 1 Group Group 2 Total Group 1 30 3 33 2 10 12 Group 2

Discriminant Function Analysis 'Discriminant function ...Males by Watershed' Comparison: Sus -- SwN

Difference between means: Procrustes distance: 0.01747514 Mahalanobis distance: 9.2842 T-square: 570.4198, P-value (parametric): 0.0997 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0810 T-square: 0.1030 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Sus Group 2: SwN From discriminant function: True Allocated to Group Group 1 Group 2 Total

9	0	9	
0	25	25	
s-validation:			
Allocate	ed to		
Group 1	Group 2		Total
6	3	9	
7	18	25	
	Allocate Group 1	s-validation: Allocated to Group 1 Group 2 6 3	s-validation: Allocated to Group 1 Group 2 6 3 9

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: Sus -- Tar

Difference between means: Procrustes distance: 0.01776350 Mahalanobis distance: 5.8443 T-square: 175.6578, P-value (parametric): 0.8321 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0850 T-square: 0.2190 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: Sus Group 2: Tar From discriminant function: True Allocated to Group Group 1 Group 2 Total 9 Group 1 9 0 0 12 12 Group 2 From cross-validation: True Allocated to Group Group 1 Group 2 Total 9 Group 1 5 4 6 12 Group 2 6

Discriminant Function Analysis 'Discriminant function ... Males by Watershed' Comparison: SwN -- Tar

Difference between means: Procrustes distance: 0.01466049 Mahalanobis distance: 5.4459 T-square: 240.4652, P-value (parametric): 0.1611 P-values for permutation tests (1000 permutation runs): Procrustes distance: 0.0750 T-square: 0.1680 (Note: The permutation test using the T-square statistic is equivalent to a test using Mahalanobis distance.)

Classification/misclassification tables Group 1: SwN Group 2: Tar From discriminant function: True Allocated to Group Group 1 Group 2 Total Group 1 25 0 25 0 Group 2 12 12 From cross-validation: True Allocated to Group Group 1 Group 2 Total Group 1 16 9 25 6 12 Group 2 6

Otolith Shape:

<u>Mean</u>	<u>area per</u>	<u>river</u>							
AL	AP	BL	CA	CF	CH	CO	JA	NE	NO

1.331570 1.110079 1.120034 1.109761 1.061413 1.221533 1.146316 1.136499 1.062638 1.119914 NT OG PA PI PO PX RA RO SJ SU 1.273321 1.048857 1.209769 1.108089 1.165717 1.143252 1.243269 1.096643 1.130640 1.156393 SW TA 1.099734 1.086134 <u>Mean area per State</u> DC DE FL GΑ MD NC VA 1.165717 1.273321 1.130640 1.160088 1.193132 1.097643 1.145666 All Rivers Permutation test for capscale under reduced model Terms added sequentially (first to last) Permutation: free Number of permutations: 999 Model: capscale(formula = getStdwavelet(shape) ~ getMasterlist(shape)\$pop) Df Variance F Pr(>F) getMasterlist(shape)\$pop 21 0.28077 3.4242 0.001 *** 674 2.63167 Residual All States

Permutation test for capscale under reduced model Terms added sequentially (first to last) Permutation: free Number of permutations: 999 Model: capscale(formula = getStdWavelet(shape) ~ getMasterlist(shape)\$State) Df Variance F Pr(>F)

getMasterlist(shape)\$State 6 0.1218 5.0122 0.001 *** Residual 689 2.7906

shape = stdCoefs(shape, classes = "pop", "length_cm", bonferroni = FALSE)
Wavelet standardization. Removed coefficients: 2,4,7,61
Fourier standardization. Removed coefficients: 2,9
Measurement standardization. No coefficients removed

APPENDIX C: R SCRIPT

- #This will implement the code in the paper
- #set working directory
- setwd("C:/Users/meyerst18/Desktop/ShapeAnalysis")
- #open these libraries in current session
- library("vegan", lib.loc="C:/Program Files/R/R-3.5.0/library")
- library("ipred", lib.loc="C:/Program Files/R/R-3.5.0/library")
- library("gplots", lib.loc="C:/Program Files/R/R-3.5.0/library")
- library("jpeg", lib.loc="C:/Program Files/R/R-3.5.0/library")
- library("pixmap", lib.loc="C:/Program Files/R/R-3.5.0/library")
- library("shapeR", lib.loc="C:/Program Files/R/R-3.5.0/library")
- library("wavethresh", lib.loc="C:/Program Files/R/R-3.5.0/library")
- #import Data.csv and perform shape R Analysis
- shape = shapeR("C:/Users/meyerst18/Desktop/ShapeAnalysis", "DATA.csv")
- shape = detect.outline(shape, threshold = 0.25, write.outline.w.org = TRUE)
- shape = remove.outline(shape,"AL","GA-ALTA-0793")
- shape = remove.outline(shape,"JA","VA-JAME-0174")
- shape = remove.outline(shape,"JA","VA-JAME-0183")
- shape = remove.outline(shape,"JA","VA-JAME-0443")
- shape = remove.outline(shape,"JA","VA-JAME-0445")
- shape = remove.outline(shape,"JA","VA-JAME-0538")
- shape = remove.outline(shape,"NO","VA-NOTO-0562")
- shape = remove.outline(shape,"NO","VA-NOTO-0904")
- shape = remove.outline(shape,"NO","VA-NOTO-0936")
- shape = remove.outline(shape,"OG","GA-OGEE-0967")
- shape = remove.outline(shape,"PA","MD-PATA-0740")
- shape = remove.outline(shape,"PA","MD-PATA-0783")
- shape = remove.outline(shape,"PI","NC-PITC-0290")

- shape = remove.outline(shape,"PI","NC-PITC-0294")
- shape = remove.outline(shape,"PI","NC-PITC-0298")
- shape = remove.outline(shape,"PI","NC-PITC-0530")
- shape = remove.outline(shape,"PX","MD-PATU-1075")
- shape = remove.outline(shape,"RA","VA-RAPP-0229")
- shape = remove.outline(shape,"RO","NC-ROAN-0375")
- shape = remove.outline(shape,"RO","NC-ROAN-0378")
- shape = detect.outline(shape, threshold = 0.25, mouse.click = TRUE)
- shape = remove.outline(shape,"AP","VA-APPO-0210")
- shape = remove.outline(shape,"BL","VA-BLAC-0580")
- shape = remove.outline(shape,"NT","DE-NANT-0148")
- shape = remove.outline(shape,"PA","MD-PATA-0779")
- shape = remove.outline(shape,"PI","NC-PITC-0297")
- shape = remove.outline(shape,"PX","MD-PATU-1076")
- shape = remove.outline(shape,"RA","VA-RAPP-0229")
- shape = remove.outline(shape,"RO","NC-ROAN-0369")
- shape = remove.outline(shape,"RO","NC-ROAN-0378")
- shape = remove.outline(shape,"SJ","FL-STJO-1137")
- shape = detect.outline(shape, threshold = 0.3, mouse.click = TRUE)
- shape = remove.outline(shape,"AP","VA-APPO-0210")
- shape = remove.outline(shape,"PA","MD-PATA-0779")
- shape = detect.outline(shape, threshold = 0.3, mouse.click = TRUE)
- shape = remove.outline(shape,"PA","MD-PATA-0779")
- shape = detect.outline(shape, threshold = 0.35, mouse.click = TRUE)
- #show.original.with.outline(shape,"PI","NC-PITC-0297")
- shape = smoothout(shape, n = 100)
- shape = generateShapeCoefficients(shape)
- shape = enrich.master.list(shape)

save(shape,file = "test.RData")

getMeasurements(shape)

tapply(getMeasurements(shape)\$otolith.area, getMasterlist(shape)\$pop, mean)

plotWaveletShape(shape, "pop", show.angle = TRUE, lwd = 2,lty = 1)

shape = stdCoefs(shape, classes = "pop", "length_cm", bonferroni = FALSE)

est.list = estimate.outline.reconstruction(shape)

outline.reconstruction.plot(est.list, max.num.harmonics = 15)

plotWavelet(shape, level = 5, class.name = "pop", useStdcoef= TRUE)

cap.res = capscale(getStdWavelet(shape) ~ getMasterlist(shape)\$pop)

anova(cap.res, by = "terms", step = 1000)

eig = eigenvals(cap.res, model = "constrained")

eig.ratio = eig/sum(eig)

cluster.plot(scores(cap.res)\$sites[,1:2],getMasterlist(shape)\$pop, xlim =
range(scores(cap.res)\$sites[,1]), ylim = range(scores(cap.res)\$sites[,2]), xlab = paste("CAP1
(",round(eig.ratio[1]*100,1),"%)",sep = ""),

ylab = paste("CAP2 (",round(eig.ratio[2*100,1),"%)",sep = ""), plotCI = TRUE,conf.level = 0.95,las = 1)

#Pairwise Comparisons

pop.uniq=unique(pop)

i=1;j=2;adonis(ws.dist[popxx==pop.uniq[i]|popxx==pop.uniq[j],popxx==pop.uniq[i]|popxx==pop.uniq[j]]~popxx[popxx==pop.uniq[i]|popxx==pop.uniq[j]])

i=1;j=3;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=1;j=4;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=1;j=5;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=1;j=6;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=1;j=7;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=1;j=8;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=1;j=9;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=1;j=10;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=1;j=11;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=1;j=12;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=1;j=13;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=1;j=14;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=1;j=15;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=1;j=16;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=1;j=17;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=1;j=18;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=1;j=19;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=1;j=20;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=1;j=21;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=1;j=22;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=2;j=3;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=2;j=4;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]]) i=2;j=5;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=2;j=6;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=2;j=7;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=2;j=8;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=2;j=9;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=2;j=10;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=2;j=11;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=2;j=12;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=2;j=13;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=2;j=14;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=2;j=15;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=2;j=16;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=2;j=17;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=2;j=18;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=2;j=19;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=2;j=20;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=2;j=21;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]]) i=2;j=22;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=3;j=4;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=3;j=5;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=3;j=6;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=3;j=7;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=3;j=8;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=3;j=9;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=3;j=10;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=3;j=11;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=3;j=12;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=3;j=13;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=3;j=14;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=3;j=15;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=3;j=16;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=3;j=17;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=3;j=18;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=3;j=19;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]]) i=3;j=20;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=3;j=21;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=3;j=22;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=4;j=5;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=4;j=6;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=4;j=7;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=4;j=8;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=4;j=9;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=4;j=10;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=4;j=11;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=4;j=12;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=4;j=13;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=4;j=14;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=4;j=15;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=4;j=16;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=4;j=17;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=4;j=18;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]]) i=4;j=19;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=4;j=20;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=4;j=21;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=4;j=22;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=5;j=6;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=5;j=7;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=5;j=8;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=5;j=9;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=5;j=10;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=5;j=11;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=5;j=12;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=5;j=13;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=5;j=14;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=5;j=15;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=5;j=16;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=5;j=17;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=5;j=18;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]]) i=5;j=19;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=5;j=20;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=5;j=21;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=5;j=22;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=6;j=7;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=6;j=8;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=6;j=9;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=6;j=10;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=6;j=11;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=6;j=12;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=6;j=13;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=6;j=14;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=6;j=15;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=6;j=16;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=6; j=17; adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j], pop==pop.uniq[i]|pop==pop.uniq[j]], pop=pop.uniq[i]|pop==pop.uniq[j]])

i=6;j=18;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=6;j=19;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]]) i=6;j=20;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=6;j=21;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=6;j=22;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=7;j=8;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=7;j=9;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=7;j=10;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=7;j=11;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=7;j=12;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=7;j=13;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=7;j=14;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=7;j=15;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=7;j=16;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=7;j=17;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=7;j=18;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=7;j=19;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=7;j=20;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=7;j=21;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]]) i=7;j=22;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=8;j=9;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]] ~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=8;j=10;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=8;j=11;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=8;j=12;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=8;j=13;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=8;j=14;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=8;j=15;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=8;j=16;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=8;j=17;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=8;j=18;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=8;j=19;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=8;j=20;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=8;j=21;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=8;j=22;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=9;j=10;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=9;j=11;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]]) i=9;j=12;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=9;j=13;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=9;j=14;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=9;j=15;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=9;j=16;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=9;j=17;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=9;j=18;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=9;j=19;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=9;j=20;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=9;j=21;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=9;j=22;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=10;j=11;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=10;j=12;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=10;j=13;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=10;j=14;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=10;j=15;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=10;j=16;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]]) i=10;j=17;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=10;j=18;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=10;j=19;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=10;j=20;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=10;j=21;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=10;j=22;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=11;j=12;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=11;j=13;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=11;j=14;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=11;j=15;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=11;j=16;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=11;j=17;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=11;j=18;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=11;j=19;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=11;j=20;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=11;j=21;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=11;j=22;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]]) i=12;j=13;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=12;j=14;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=12;j=15;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=12;j=16;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=12;j=17;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=12;j=18;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=12;j=19;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=12;j=20;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=12;j=21;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=12;j=22;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=13;j=14;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=13;j=15;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=13;j=16;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=13;j=17;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=13;j=18;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=13;j=19;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=13;j=20;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]]) i=13;j=21;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=13;j=22;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=14;j=15;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=14;j=16;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=14;j=17;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=14;j=18;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=14;j=19;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=14;j=20;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=14;j=21;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=14;j=22;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=15;j=16;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=15;j=17;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=15;j=18;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=15;j=19;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=15;j=20;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=15;j=21;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=15;j=22;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]]) i=16;j=17;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=16;j=18;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=16;j=19;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=16;j=20;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=16;j=21;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=16;j=22;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=17;j=18;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=17;j=19;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=17;j=20;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=17;j=21;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=17;j=22;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=18;j=19;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=18;j=20;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=18;j=21;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=18;j=22;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=19;j=20;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=19;j=21;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]]) i=19;j=22;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=20;j=21;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=20;j=22;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

i=21;j=22;adonis(ws.dist[pop==pop.uniq[i]|pop==pop.uniq[j],pop==pop.uniq[i]|pop==pop.uniq[j]]~pop[pop==pop.uniq[i]|pop==pop.uniq[j]])

#Plotting NC Rivers

shape = setFilter (shape, getMasterlist(shape, useFilter = FALSE)\$State %in% c("NC"))

plotWaveletShape(shape, "pop", show.angle = TRUE, lwd = 2,lty = 1)

#Plotting Neuse and Tributaries

shape = setFilter (shape, getMasterlist(shape, useFilter = FALSE)\$pop %in%
c("NE","CO","PI","SW"))

plotWaveletShape(shape, "pop", show.angle = TRUE, lwd = 2,lty = 1)