

Ecohydrologic Indicators of Low-Flow Habitat Availability in Eleven Virginia Rivers

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Abstract

Increasing demand and competition for freshwater is threatening instream uses including ecosystem services and aquatic habitat. A standard method of evaluating impacts of alternative water management scenarios on instream habitat is Instream Flow Incremental Methodology (IFIM). The primary outputs of IFIM studies are: 1) habitat rating curves that relate habitat availability to streamflow for every species, lifestage, or recreational use modelled; and 2) habitat time series under alternative water management scenarios. We compiled 428 habitat rating curves from previous IFIM studies across 11 rivers in Virginia and tested the ability to reduce this number based on similarities in flow preferences and responses to flow alteration. Individual site-species combinations were reduced from 428 objects to four groups with similar seasonal habitat availability patterns using a hierarchical, agglomerative cluster analysis. A seasonal habitat availability (SHA) ratio was proposed as a future indicator of seasonal flow preferences. Four parameters calculated from the magnitude and shape of habitat rating curves were proposed as response metrics that indicate how a lifestage responds to flow alteration. Univariate and multivariate analyses of variance and post-hoc tests identified significantly different means for the SHAR, QP ($F=63.2$, $p<2e-16$) and SK ($F=65.6$, $p<2e-16$). A reduced number of instream flow users can simplify the incorporation of aquatic habitat assessment in statewide water resources management.

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List of Terms and Abbreviations

A. Terms

Average Monthly Habitat Availability (AMHA): Mean value of long-term daily WUA values in each month, calculated from WUA values determined using PHABSIM.

Flow Percentile at Peak of Standardized Habitat Rating Curve (QP): Flow percentile at which the peak in the standardized habitat rating curve occurs. Flow percentiles are calculated from the flow duration curve produced by the long-term mean daily streamflow record. Selected to indicate a characteristic flow with suitable conditions.

Habitat Suitability Criteria (HSC): Relationship showing a specific instream flow user's preference for a hydraulic parameter. Commonly illustrated as a two-dimensional curve and developed for water depth, velocity, and substrate.

Instream Flow Incremental Methodology (IFIM): A water management tool for evaluating aquatic habitat availability under alternative water management scenarios. Developed by the U.S. Fish and Wildlife Service, Office of Biological Services (Bovee, 1982).

Physical Habitat Simulation (PHABSIM): A coupled hydraulic-habitat model to simulate physical habitat in relation to streamflow, water quality, and physical structure of streams (Milhous *et al.*, 1984). Habitat availability is reported as Weighted Usable Area (WUA).

Seasonal Habitat Availability Ratio (SHAR): Natural log of ratio of long-term average habitat availability in March to long-term average habitat availability in September, where habitat availability is calculated from the habitat time series of daily WUA values.

Skewness in Standardized Habitat Rating Curve (SK): Skewness of the discretized, univariate relationship between standardized versions of streamflow and WUA. A common measure of asymmetry of a distribution about its mean. Selected to indicate if greater habitat availability exists for low, average, or high flow conditions.

Slope in Standardized Habitat Rating Curve (SL): Slope of the rising limb of the standardized habitat rating curve. Selected to indicate how much habitat availability is lost for a unit change in flow percentile.

Standard Deviation in Standardized Habitat Rating Curve (SD): Standard deviation of the discretized, univariate relationship between standardized versions of streamflow

and WUA. A common measure of variation in a distribution. Selected to represent the width of the peak in the standardized discharge-WUA curve.

Weighted Usable Area (WUA): a composite index of overall physical habitat in a river reach that is suitable for a particular instream flow user. Determined using PHABSIM and commonly reported in units of ft²/1000 ft.

B. Abbreviations

ANOVA	Analysis of Variance
ELOHA	Ecological Limits of Hydrologic Alteration
IHA	Indicators of Hydrologic Alteration
MAF	Mean Annual Flow
MANOVA	Multivariate Analysis of Variance
MIF	Minimum Instream Flow
NHD	National Hydrography Dataset
PCA	Principal Components Analysis
POF	Percent-of-Flow
RBP	Rapid Bioassessment Protocols
SARP	Southeast Aquatic Resource Partnership
USGS	U.S. Geological Survey
VDEQ	Virginia Department of Environmental Quality
VDGIF	Virginia Department of Game and Inland Fisheries
WWAP	World Water Assessment Programme (United Nations)

Chapter 1: Introduction

1.1. Problem Statement

Freshwater systems are some of the most threatened ecosystems in the world (WWAP, 2009). These systems provide valuable ecosystem goods and services (Postel and Richter, 2003) and are home to approximately 40% of global fish diversity (Dudgeon *et al.*, 2006). As competition for water resources increases with human population growth (Jiménez Cisneros *et al.*, 2014), preserving adequate water in river channels for the needs of both humans and ecosystems is one of the most important challenges in water resources management (Richter *et al.*, 2012).

A key driver in the formation and maintenance of aquatic and riparian habitat is streamflow (Bovee *et al.*, 1998; Mathews and Richter, 2007; Petts, 2009; Poff and Zimmerman, 2010; Maddock *et al.*, 2013). Species and communities adapt to the range of habitat present over time, driven by change in streamflow (Petts, 2009). The representative pattern of inter- and intra-annual variability in streamflow over decades is considered the “natural flow regime” (Poff *et al.*, 1997) and is driven by watershed characteristics including climate, topography, bedrock/parent material, and land cover. A natural flow regime can be broken into five main components: magnitude, duration, frequency, timing, and rate of change.

Humans have managed rivers and manipulated streamflow for centuries and have significantly altered the natural variation of all flow regime components (Poff *et al.*, 1997). An estimated 86% of all rivers and streams in the U.S. are considered to have altered streamflow magnitudes (Carlisle *et al.*, 2011). In general, these flow alterations cause negative impacts on ecological conditions (Poff and Zimmerman, 2010; McManamay *et al.*, 2013).

In an effort to understand the flow components driving positive or negative responses in riverine biotic communities, the field of environmental flows has emerged (Arthington, 2015). Environmental flows are defined as the “quantity, timing and quality of water flows required to sustain freshwater and estuarine ecosystems and the human livelihoods and well-being that depend on these ecosystems” (Brisbane Declaration, 2007). The diversity of aquatic and riparian species and the complex interactions following flow events make flow needs of an aquatic ecosystem much more difficult to define than human needs.

Historically, environmental flows were established as “minimum instream flows” (MIF) based on annual statistics of streamflow (Petts, 2009; Richter *et al.*, 2012). The assumption

behind MIF was that at certain lifestages, aquatic species need some minimum amount of flow in the channel; flow below this amount would cause a decline in population or ecosystem health. The idea of a single minimum flow, however, does not encapsulate all elements of a flow regime that are important to ecosystem health (Poff *et al.*, 1997; Acreman and Dunbar, 2004).

A popular method to quantify environmental flows from the past four decades that now incorporates natural flow variability is the Instream Flow Incremental Methodology (IFIM) (Bovee *et al.*, 1998). IFIM compares physical habitat availability over a range of streamflow for proposed and baseline water management scenarios. Within IFIM, a coupled hydraulic-habitat model computes an index of habitat availability called Weighted Usable Area (WUA) at incremental values of river discharge. A river reach is split into cells along river width and length, and the WUA index is a composite of habitat suitability in each cell. Suitability within each cell is determined using depth, velocity, and substrate suitability criteria. These criteria can be developed for different lifestages of fish species, habitat use guilds, macroinvertebrates, riparian vegetation, and recreational uses such as canoeing. The main products of the hydraulic-habitat model are habitat rating curves that relate WUA to discharge for each lifestage and recreational use at each modelled location. Habitat rating curves can also be translated across river reaches when standardized and tested for validity on reaches that haven't been modelled (Lamouroux and Jowett, 2005; Wilding *et al.*, 2013).

Habitat rating curves are then used to evaluate changes to habitat availability given alternative water management scenarios. Extensive documentation on interpretation of results and computations of habitat metrics within IFIM exist (Stalnaker *et al.*, 1995; Bovee *et al.*, 1998). Common analysis approaches that are a part of IFIM include optimization and comparisons of habitat time series and habitat duration curves (Bovee *et al.*, 1998; USGS, 2001). These analyses must be completed for every lifestage and recreational activity of interest, and impacts are balanced across species, lifestages, recreational activities, and socio-economic uses of water. IFIM studies have been completed in over 20 countries (Petts, 2009), providing abundant applications of instream habitat analyses and exemplifying the method's popularity.

In Virginia, competition for water resources is largely driven by population growth, so management of water resources that balances both instream and off-stream uses is critical to protecting freshwater ecosystem functions. This research examined the utility of existing data from eight IFIM studies across Virginia in supporting environmental flow recommendations.

Specifically, this research tested if the total number of habitat uses evaluated in IFIM studies could be reduced based on similarities in the relationship between streamflow and habitat availability. The habitat rating curves and metrics derived from habitat time series were used as indicators of flow preferences and responses to flow alteration. A particular focus was placed on low-flows because of increasing occurrences of low-flow and drought conditions in Virginia, driven by increasing water demand and competition among water users (Cox, 1999).

1.2. Research Objectives

The goal of this research was to compile flow and habitat data from existing IFIM studies in Virginia and analyze the utility of these data in statewide applications. Traditional and novel metrics of flow and habitat were explored. Trends across all species and reaches were explored to find similarities that could reduce the large numbers of individual species that were studied.

Specific goals of this study were to:

- 1) Compile a general repository for flow-habitat data from existing IFIM studies in Virginia;
- 2) Model long-term habitat availability using flow time series and habitat rating curves;
- 3) Identify common patterns in the seasonal habitat availability of all site-species combinations; and
- 4) Identify habitat response metrics that capture characteristic features of habitat rating curves.

Chapter 2: Literature Review

2.1. Natural Flow Regime and Flow Alterations

Freshwaters are some of the most threatened ecosystems in the world (WWAP, 2009). Ecosystem services provided by freshwater systems include flood control, waste assimilation, water-based tourism and recreation, hydropower, protection of biodiversity, and spiritual and cultural values (Postel and Richter, 2003; WWAP, 2009). Freshwaters are also home to approximately 40% of global fish diversity (Dudgeon *et al.*, 2006). As competition for water resources increases with population growth (Jiménez Cisneros *et al.*, 2014), preserving adequate water in river channels for the needs of both humans and ecosystems is one of the most important challenges in water resources management (Poff and Richter, 2012).

Biotic community composition evolves to the range of habitat present over time (Petts, 2009). A key driver in the formation and maintenance of aquatic and riparian habitat is streamflow (Bovee *et al.*, 1998; Mathews and Richter, 2007; Petts, 2009; Poff and Zimmerman, 2010; Maddock *et al.*, 2013). The representative pattern of inter- and intra-annual variability in streamflow over decades is coined the “natural flow regime” (Poff *et al.*, 1997) and is driven by watershed characteristics including climate, topography, bedrock/parent material, and land cover. A natural flow regime can be broken into five main components: magnitude, duration, frequency, timing, and rate of change. Certain components of a flow regime can be broken down further by high, average, and low flow conditions, into a total of nine subcomponents: magnitude of low, average and high flows; duration of low and high flows; frequency of low and high flows; timing; and rate of change (Olden and Poff, 2003).

Humans have been managing rivers and manipulating streamflow for centuries and have significantly altered the natural variation of all flow regime components (Poff *et al.*, 1997). A flow alteration is commonly described or categorized by the component of the natural flow regime that is changed. Examples of flow alterations from anthropogenic activities include land use change, creation of impoundments, hydropower operations, and surface water withdrawals. An estimated 86% of rivers and streams in the U.S. are considered to have altered streamflow magnitudes (Carlisle *et al.*, 2011). In general, these flow alterations negatively impact ecological conditions (Poff and Zimmerman, 2010; McManamay *et al.*, 2013).

In an effort to understand the flow components driving positive or negative responses in riverine biotic communities, the field of environmental flows has emerged (Arthington, 2015). Environmental flows are defined as the “quantity, timing and quality of water flows required to sustain freshwater and estuarine ecosystems and the human livelihoods and well-being that depend on these ecosystems” (Brisbane Declaration, 2007). The diversity of aquatic and riparian species and the complex interactions following flow events make flow needs of an aquatic ecosystem much more difficult to define than human needs.

2.2. Quantifying Environmental Flows

Methods to determine environmental flows utilize hydrologic, hydraulic, physical habitat, or ecological parameters as indicators of the condition of the stream environment (Jowett, 1997). Thresholds of allowable degradation are assigned to these parameters and translated into flow guidelines that avoid reaching that threshold (Maddock *et al.*, 2013).

Historically, environmental flows were established as “minimum instream flows” (MIF) based on annual statistics of streamflow, such as mean annual flow (MAF) or 7Q10, the average 7-day low flow with a 10% chance of occurring annually (Petts, 2009; Richter *et al.*, 2012). The assumption behind minimum instream flows was that at certain lifestages, aquatic species need some minimum amount of flow in the channel; flow below this amount would cause a decline in population or ecosystem health. The idea of a single minimum flow, however, does not encapsulate all elements of a flow regime that are important to ecosystem health (Poff *et al.*, 1997; Acreman and Dunbar, 2004).

The focus on understanding specific relationships between flow components and ecological responses became a focal point in the 1970s (Petts, 2009; Richter *et al.*, 2012; Maddock *et al.*, 2013). This ideological shift concentrated on natural variability in hydrology (floods, droughts), in geomorphology (channel planform and cross-sectional dimensions), and in ecology (species richness, abundance, and individual biomass) as important characteristics of a healthy river. Various methods for defining environmental flows that incorporate natural variability have been developed, including the Tennant method (Tennant, 1976), hydraulic-habitat modelling (Milhous *et al.*, 1984), the Indicators of Hydrologic Alteration (IHA) software (Richter *et al.*, 1996), the Ecological Limits of Hydrologic Alteration (ELOHA) framework (Poff

et al., 2010), and the Percent of Flow (POF) method (Richter *et al.*, 2012). These approaches were reviewed in detail by Annear *et al.* (2004).

A universally appropriate method for environmental flow assessment does not exist (Richter *et al.*, 2012), partially because a final flow standard must be a negotiation between the desired state of the river and what the river will be used for (Kendy *et al.*, 2009). The selected method should also consider the time, cost, available resources, and expertise required for the assessment. Two approaches are reviewed in detail in this literature review – the IFIM approach and the ELOHA framework – due to their popularity and persistent use.

2.2.1. Instream Flow Incremental Methodology (IFIM)

Instream Flow Incremental Methodology (IFIM) is a widely used approach to set environmental flows by comparing physical habitat availability over a range of streamflow for different water management scenarios (Stalnaker *et al.*, 1995; Bovee *et al.*, 1998). Habitat availability is quantified using an index called Weighted Usable Area (WUA) that is computed from a coupled hydraulic and habitat model that links fisheries behavior science with open channel hydraulics.

Physical HABitat SIMulation (PHABSIM) is the most frequently used hydraulic-habitat model for IFIM (Milhous *et al.*, 1984). The hydraulic model simulates depth and velocity distributions with discharge, and the habitat model represents suitability of those hydraulic and habitat parameters for individual species and lifestages. Habitat Suitability Criteria (HSC), ranging from 0 to 1, are developed for depth, velocity, and substrate for individual species and lifestages. A river reach is broken up into grid cells, and within each grid cell, suitability values from HSC are multiplied by the hydraulic conditions (Figure 1). The individual cell values are summed to output the total area in a reach (typically presented as ft²/1000 ft) of optimal or suitable habitat, defined as Weighted Usable Area (WUA):

$$WUA = \sum_{i=1}^n S_i A_i \quad (1)$$

where n is the number of cells, S_i is the composite habitat suitability for the cell i , and A_i is the area represented by the cell. A total WUA value is calculated for every discharge modelled with the hydraulic model, resulting in a habitat rating curve (Figure 2).

Alternative water management scenarios are then typically evaluated by comparing changes in discharge to changes in WUA based on the habitat rating curve. Alternatives are

selected that minimize impacts of streamflow on habitat availability, with respect to previously defined project objectives (Bovee *et al.*, 1998). Methods of interpreting results include optimization, habitat time series, and habitat duration curves.

Major criticisms of assumptions made in IFIM studies include: 1) that HSC must be site-specific but criteria are often used from a similar region; 2) that WUA has a weak connection to fish population response (Scott and Shirvell, 1987); and 3) that total WUA cannot differentiate between quantities of low vs. high quality habitat since total WUA is an aggregate of all grid cells (USGS, 2001). The IFIM process also requires significant in-field hydraulic, physical and biological data collection that typically takes months to years to collect. Despite criticism, IFIM remains perhaps the most popular method of hydraulic-habitat modelling and assessment, with use in over 20 countries (Petts, 2009).

2.2.1.1. Optimization

A common first step in evaluating alternative water management scenarios using IFIM is to compare changes in discharge to changes in WUA based on the discharge-WUA rating curve. Assessments are done for every species-lifestage combination at every reach, using the respective habitat rating curve. The total number of rating curves can be reduced through “post-analysis guilding” by consolidating multiple curves for different species and lifestages that have the same basic magnitude and functional relationship (USGS, 2001). A community-level habitat rating curve is constructed using a weighted arithmetic average of individual curves. Species of concern can be selected before analyses and given a larger weight in minimizing WUA reductions. In these groupings, the magnitude of WUA should be scaled by the maximum WUA for that species to combine multiple curves (USGS, 2001).

The post-analysis consolidation of rating curves can also be done for a critically limiting combination of habitat rating curves in order to identify the “optimum flow” (Leonard *et al.*, 1986). A new habitat rating curve is developed by identifying the minimum standardized WUA value for every increment of discharge. The optimum flow then occurs at the peak of the curve of minimum habitat availability versus discharge (Figure 3). This value is interpreted as providing the best possible combination of habitat availability for all species considered.

2.2.1.2. Habitat Time Series

The developers of IFIM stress the use of habitat time series in evaluating alternative water management scenarios (Bovee *et al.*, 1998). The idea of a habitat time series is intuitive because current populations of fish are dependent in part on habitat availability from the past (USGS, 2001). A habitat time series is calculated from a flow time series and a habitat rating curve; every time step of the flow time series is translated to a WUA value using the habitat rating curve (Figure 4). Habitat time series are then used to observe changes in WUA during critical time periods or to identify problem areas (Bovee *et al.*, 1998), often during seasons with higher water withdrawal or demand, drought risk, or critical lifestage periods (see Krstolic and Ramey, 2012). Statistics from a habitat time series produced by PHABSIM that are recommended for use and comparison (USGS, 2001) include:

- Mean, median, minimum, and maximum habitat
- Index-A: mean of all habitats between 50 and 90% exceedance (i.e. the majority of low flow events)
- Index-B: mean of all habitats between 10 and 90% exceedance
- An exceedance statistic (e.g. 90th- or 95th-percentile habitat)
- Number of days below a habitat quantity threshold

2.2.1.3. Habitat Duration Curves

A habitat duration curve can be computed from a habitat time series. A habitat duration curve is similar to a flow duration curve (Searcy, 1959) and displays the percent of time that a certain WUA value is equaled or exceeded. Habitat duration curves and derived statistics are useful for comparing alternative water management scenarios over the entire range of discharges, instead of certain periods of interest (USGS, 2001). The total difference in habitat can be quantified by comparing habitat duration curves from baseline and alternative management conditions (Bovee *et al.*, 1998).

2.2.2. Ecological Limits of Hydrologic Alteration (ELOHA)

The Ecological Limits of Hydrologic Alteration (ELOHA) framework was developed in 2010 as a holistic regional framework for environmental flow management (Poff and Zimmerman, 2010). The four steps of the ELOHA framework are to: 1) establish baseline hydrologic conditions and predicted natural hydrology; 2) classify river type based on natural

hydrologic patterns; 3) assess flow alterations in relation to baseline conditions for each river class; and 4) determine flow-ecology relationships for each river class (Figure 5). The resulting flow-ecology relationships are univariate relationships between a change to a flow component and ensuing change in an ecological metric, displayed as percent changes in flow and percent ecological responses on x and y axes, respectively (Figure 6). A significant benefit of the ELOHA framework is the ability to develop environmental flow policies for regions based on classification, instead of developing standards for individual rivers.

The ELOHA method is gaining popularity and is generally considered the most holistic framework for establishing environmental flow requirements (Petts, 2009; McManamay *et al.*, 2013). This method was also developed and endorsed by 19 scientists who have been leading the field of environmental flows (Poff and Zimmerman, 2010). Elements of the ELOHA framework have been applied and used in six countries, including six U.S. states and four interstate river basins (Kendy *et al.*, 2012; Buchanan *et al.*, 2013; McManamay *et al.*, 2013).

The ELOHA framework was evaluated for its applicability to the Middle Potomac River basin, lying partially in Virginia (Buchanan *et al.*, 2013). Buchanan *et al.* (2013) found that ELOHA was successful in developing flow-ecology relationships for six of the 24 flow metrics and seven of the 20 macroinvertebrate metrics evaluated. One drawback to the ELOHA process was that the first step, establishing the hydrologic foundation, was described as “difficult and time-consuming” but vital to the assessment.

McManamay *et al.* (2013) used the ELOHA framework to develop flow-ecology relationships on the Upper Tennessee River basin using fish species richness and occupancy trends as response variables to dam operations. The selected hydrologic metrics were somewhat different than those used in the Middle Potomac River ELOHA assessment, as well as the ecological response metrics in fish instead of macroinvertebrates. Fish richness responses were generally negative for diversions and peaking dams, which both decrease the 1-day high flows and constancy (McManamay *et al.*, 2013). A major conclusion was that multivariate flow-ecology models that included non-flow variables were needed to develop predictive flow-ecology relationships that could sufficiently guide flow management (McManamay *et al.*, 2013).

2.3. Flow-Ecology Relationships

One of the crucial components of the ELOHA framework is the establishment of flow-ecology relationships (Kendy *et al.*, 2012). The purpose of a flow-ecology relationship is to quantify how much an ecological condition changes for a given hydrologic metric (Brewer and Davis, 2014). Changes to flow components are quantified and summarized using statistics to produce hydrologic metrics, while changes to ecological conditions are often measured as species abundance, population, and community metrics in fish, macroinvertebrate, and riparian vegetation species. The percent alteration is calculated from a reference condition before a flow alteration occurred. A quantitative flow-ecology relationship is typically displayed as percent of ecological response versus percent of flow alteration (Poff and Zimmerman, 2010; McManamay *et al.*, 2013; Brewer and Davis, 2014) or presented as correlations between hydrologic and ecological metrics (Freeman *et al.*, 2001; DeGasperi *et al.*, 2009; Pritchett and Pyron, 2012; Buchanan *et al.*, 2013).

An identified research need for advancing the science of environmental flows is to evaluate the use of existing data for the purpose of informing flow-ecology relationships (SARP, 2012). The existing literature on flow-ecology relationships is widely spread geographically, and is found in peer-reviewed papers, technical reports and grey literature. Global and regional meta-analyses of literature regarding flow alterations and ecological responses have been completed (Poff and Zimmerman, 2010; McManamay *et al.*, 2013). Hypotheses of regional flow-ecology relationships that apply to parts of Virginia have been developed and tested in the southeastern U.S. region (Brewer and Davis, 2014) and developed in the Middle Potomac River basin (Buchanan *et al.*, 2013) using existing literature and data.

The ecological metrics commonly chosen for flow-ecology relationships are biological indices of ecosystem health, such as scores from Rapid Bioassessment Protocols (RBP) for macroinvertebrates or fish (Barbour *et al.*, 1999). These biotic indices were typically designed for water quality monitoring, using organisms' intolerance to pollutants as an indication of stream condition (Barbour *et al.*, 1999; Acreman and Dunbar, 2004). By their design, such indices are sensitive to a range of ecosystem factors, only one of which is streamflow. Caution should be used when relating such ecological indicators to flow alterations, as is typically done in development of flow-ecology relationships (Acreman and Dunbar, 2004).

The introduction of confounding factors by using ecological indicators not designed specifically for flow alterations suggests that other physical metrics may be more suitable for

flow-ecology relationships. Physical parameters can also be simpler to link to changes in river flow regimes than biological parameters due to data collection procedures (Benda *et al.*, 2002). The use of physical indices reflects back to the idea that biological responses are closely linked to historic and current physical habitat conditions (Bovee *et al.*, 1998; Mathews and Richter, 2007; Petts, 2009; Poff and Zimmerman, 2010; Maddock *et al.*, 2013).

2.4. Habitat Metrics as Physical Indicators of Ecological Condition

The combination of a push to use existing data in flow-ecology relationships and a physical indicator as a surrogate for ecological response make habitat availability from IFIM studies a logical choice. Data from IFIM studies are available in over 20 countries (Petts, 2009) and extensive documentation on interpretation of results exist (Stalnaker *et al.*, 1995; Bovee *et al.*, 1998; Petts, 2009). Habitat metrics can be computed from habitat time series, habitat duration curves, and from the inherent relationship between flow and habitat via the habitat rating curve.

2.4.1. Quantifying Habitat Time Series

Documentation on interpreting PHABSIM output within IFIM highlights the summarization of habitat time series and duration curves using metrics (Bovee *et al.*, 1998; USGS, 2001). These metrics, often involving statistics, include summary statistics of the entire time series or selected critical time periods, Index A and Index B metrics that describe mean habitat during specific periods, exceedance statistics, and number of days below a specified threshold. These metrics lend themselves well to the idea of flow-ecology relationships, by providing individual values of a long- or short-term habitat time series that can be related to a measure of the flow time series.

2.4.2. Quantifying Shape of Habitat Rating Curve

The habitat rating curve has a typical shape with a rising limb, a maximum, and typically a falling limb (Jowett *et al.*, 2008). The rising limb of the habitat rating curve, which typically represents low flow conditions, is of more concern than the falling limb at high flows because there is usually some edge habitat at larger flows (Jowett *et al.*, 2008).

The shape of the habitat rating curve is more important to the assessment of alternative flow scenarios than the magnitude (Jowett *et al.*, 2008). Despite this, efforts to quantify the shape of the habitat rating curve have been limited in the literature. Two exceptions are the curve-fitting approaches of Wilding *et al.* (2013) and Lamouroux and Jowett (2005) that generated a shape coefficient in support of generalized habitat models (GHMs).

In order to compare habitat rating curves across species, the WUA axis is commonly standardized to a percent of maximum WUA (USGS, 2001). In order to compare habitat rating curves across rivers, the flow axis should also be standardized. Wilding *et al.* (2013) converted discharge to a percent of the Q95h, where Q95h is the flow providing 95% of maximum habitat. Lamouroux and Jowett (2005) divided discharge by channel width to get specific discharge. The standardized habitat rating curves produced by Lamouroux and Jowett (2005) visually show the similarity in habitat rating curve shape for the same species across multiple rivers (Figure 7).

2.5. Statistical Approaches to Flow-Ecology Relationships

Common statistical procedures used in developing flow-ecology relationships include measures of correlation, principal components analysis, clustering, and linear and quantile regression. Both parametric and non-parametric correlations have been calculated between flow metrics and ecological indicators to identify relationships to pursue with predictive models (DeGasperi *et al.*, 2009; Buchanan *et al.*, 2013; Jellyman *et al.*, 2013). Principal components analysis (PCA) and clustering techniques were used to reduce redundancy of flow statistics and habitat statistics to highlight the most promising relationships (Freeman *et al.*, 2001; DeGasperi *et al.*, 2009; Pritchett and Pyron, 2012). Once pairs are identified, linear or quantile regression is used to develop predictive models (Wilding and Poff, 2008; Buchanan *et al.*, 2013; Knight *et al.*, 2014). Quantile regression is a particularly promising method for use in flow-ecology relationships because it accounts for underlying variables that may influence the relationship but were not measured (Cade and Noon, 2003). In flow-ecology relationships, quantile regression allows for a predictive model based solely on flow, but understanding that other factors may affect ecological responses such as water quality or temperature.

2.6. Summary

The field of environmental flows is still developing (Petts, 2009; Arthington, 2015). Existing information can and should be used to inform flow-ecology hypotheses and test relationships. IFIM studies provide a valuable source of existing data and should be explored for use in flow-ecology relationships and water resources management. The output of IFIM studies, including time series of flow and habitat, habitat duration curves, and the shape of habitat rating curves, can be summarized to describe the instream flow uses at a site.

Chapter 3: Methods

3.1. Study Sites

Eight Instream Flow Incremental Methodology (IFIM) studies carried out between 1981-2012 in Virginia were reviewed (Table 1). The study reports are all public documents and can be accessed online from the respective organizations who completed each study. Flow-habitat relationships were developed in 23 unique river reaches; however, some of these reaches are contiguous, so study reaches occurred on only 11 unique rivers. The 23 reaches cover 644 river km and span the Valley and Ridge, Piedmont, and Coastal Plain physiographic regions (Figure 8). There were no IFIM studies within the Appalachian Plateau or Blue Ridge physiographic regions.

The major river basins in Virginia represented by the IFIM studies are the James River, New River, Potomac-Shenandoah River, Roanoke River, and York River basins. The James, Potomac-Shenandoah, and York Rivers drain to the Chesapeake Bay while the Roanoke River drains to the Albemarle Sound. The New River drains to the Ohio and Mississippi Rivers, ultimately to the Gulf of Mexico. Major river basins in Virginia not represented by IFIM studies are the Albemarle-Chowan, Rappahannock, Tennessee-Big Sandy, and Chesapeake Bay-Small Coastal River basins. The contributing drainage areas of the IFIM study reaches ranged from 438 km² to 30000 km². All but four of the study locations had contributing drainage areas below 4400 km².

3.2. Data Acquisition from Existing IFIM Studies

Flow-habitat data were identified in IFIM studies in either tabular or graphical form as Weighted Usable Area (WUA) values at increments of discharge. This flow-habitat relationship is the primary output of conventional instream habitat models such as PHABSIM. WUA tables displayed discharge (ft³/s) as rows and habitat use variables as columns, and were populated with WUA values. WUA is commonly reported in units of ft²/1000 ft. Most studies reported these flow-habitat tables for each study reach assessed. For these locations, flow-habitat relationships were copied from tabular source data and formatted to facilitate further analysis.

Two reports did not provide tabular data and only contained plots at each study reach of WUA versus flow (Potomac IFIM and North Fork Shenandoah IFIM). For these plots, flow-habitat curves were digitized to obtain a tabular version of data for further analysis. Coordinates

for each target species at each study location were extracted from the curves and WUA values were interpolated for a consistent set of discharge values.

A total of 122 unique flow-dependent biotic and abiotic factors were modeled across the twenty-three reaches. These flow-dependent factors fall into five different categories: fish species at various lifestages (n=98), habitat use guilds (n=9), macroinvertebrate taxa (n=6), mussel species (n=5), and recreational activities including canoeing and boat angling (n=4). Since the dominant number of factors studied were fish species at various lifestages, all factors are referred to as “species” for simplicity; however, factors other than fishes were kept in subsequent analyses to account for all instream habitat uses that each study found important.

A single factor may not respond to flow alteration the same way in a different environment. For example, the flow conditions suitable for adult smallmouth bass (*Micropterus dolomieu*) in the New River differed from the suitable conditions in the Upper James River or South Fork Shenandoah River, and even in a downstream reach of the New River (Figure 9). Therefore, the same lifestages in different reaches were treated as unique observations in all further analyses. As a result, the number of unique factors modeled across all reaches expanded from 122 to 428 site-species combinations.

3.3. Flow Time Series

To generate habitat time series from the available flow-habitat tables, an estimated flow time series at a location representative of the rating curve was necessary. Exact locations of reaches were compared with U.S. Geological Survey (USGS) long-term streamflow gage sites. All eight IFIM studies used at least one long-term USGS streamflow gage for calibration of the hydraulic model portion of PHABSIM. For 14 of the IFIM reaches, a USGS gage was within the reach's defined boundaries, so that gage was associated with that reach for further time series analyses (Table 2). For the nine remaining reaches that did not have a USGS gage within their boundaries, the closest nearby gage was used to estimate a flow time series. Flow from the closest gage was weighted by drainage area to a selected location by:

$$Q_s = Q_g \left(\frac{A_s}{A_g} \right) \quad (2)$$

where Q = flow (ft³/s), A = contributing drainage area (mi²), subscript s denotes selected study location, and subscript g denotes USGS gage. Drainage areas and geographic coordinates for USGS gages were determined from the respective USGS gage site information, and drainage

areas for study reach locations were estimated from the NHD+ stream network dataset (USGS NHD Model v2.0). Those drainage areas were then used to weight flow time series using Equation 1 (Table 2).

Flow time series were then used to calculate flow duration statistics of percentile flows within each reach. A percentile, or percent non-exceedance, flow indicates the percent of a long-term streamflow distribution that is equal to or below that value during all years that measurements have been made (Helsel and Hirsch, 2002). For example, flow is less than or equal to the 25th percentile flow for only 25% of the mean daily flows on record.

3.4. Habitat Metrics

Habitat time series were computed for all 428 unique site-species combinations from the respective flow time series and habitat rating curve (Figure 4). It is important to note that habitat availability estimates could not be made for flow values beyond the range of the respective habitat rating curve. These flow limits were dependent on the calibrated and modelled flows from the original IFIM reports, and varied by reach. Dates for which flow exceeded the upper limit were excluded from the overall habitat time series.

Habitat metrics were calculated from habitat time series. The primary metrics of interest were average monthly habitat availability (AMHA) values, calculated using the Index-B statistic outlined in the PHABSIM manual (USGS, 2001). Index-B is defined as the mean of all habitats between the 10% and 90% exceedance values for any desired time period. A monthly time period was selected in order to capture intra-annual variability and seasonal patterns. Average monthly habitat availability was calculated by aggregating all daily WUA values by month for the entire period of record and calculating the mean of the values between the 10th and 90th percentile. Values below the 10th percentile and above the 90th percentile were eliminated to remove extreme values in the time series (Bovee *et al.*, 1998). Average monthly habitat availability values were calculated for all site-species combinations (n=428).

Seasonal variability in WUA was quantified by the ratio of March monthly average (m3) to September monthly average (m9). When seasonal maximum habitat availability occurred in spring ($m3 > m9$), this ratio was greater than one; when seasonal maximum habitat availability occurred in summer ($m3 < m9$), this ratio was less than one. The natural logarithm of the ratio of m3 to m9 was computed in order to separate ratio values into positive and negative: a positive

ratio occurs when seasonal maximum habitat availability occurred in spring ($m3 > m9$), and a negative ratio occurs when seasonal maximum habitat availability occurred in summer ($m3 < m9$). The seasonal habitat availability ratio, SHAR, is of the form:

$$SHAR = \ln\left(\frac{m3}{m9}\right) \quad (3)$$

where *SHA* is the seasonal habitat variability ratio, *m3* is the average of all WUA values in March, and *m9* is the average of all WUA values in September.

3.5. Habitat Rating Curve Parameters

Both axes of the habitat rating curves were standardized to facilitate comparison across species and reaches (Figure 10). Magnitude of WUA was standardized to a percent of the maximum WUA (Bovee *et al.*, 1998). Discharge was standardized by expressing values in terms of percentile flow, based on the flow duration curve (Searcy, 1959). A total of 428 standardized rating curves were developed for all unique combinations of reaches and species.

The rating curves were described using four parameters of the magnitude and functional relationship between WUA and discharge: flow percentile associated with the maximum habitat availability (QP), slope preceding peak (SL), skewness (SK), and standard deviation (SD) (Table 3). These parameters were selected because they are well-known metrics of curves or distributions, do not involve equation-fitting, and were hypothesized to reveal important characteristics about the way that habitat availability responds to flow.

Flow at peak habitat availability, QP, was selected to represent the flow preferences of the lifestage for which the habitat rating curve was developed. This flow is not the only suitable flow condition but was selected as the characteristic flow. The flow value at the peak of the habitat rating curve was converted to a percentile based on the flow duration curve to facilitate comparison across rivers. The slope parameter, SL, describes how sensitive the lifestage is to flow alteration below the flow at peak habitat availability by calculating the change in WUA divided by the change in discharge on the rising limb of the curve. A larger slope value means a larger decrease in habitat availability occurs for an equivalent change in flow, indicating an increased sensitivity to flow alteration. Skewness, SK, is a measure of asymmetry of a distribution about its mean (Pearson, 1895). A positive SK value means the distribution is right-skewed and the mass of the distribution is concentrated on the right of the figure; a negative SK value means the distribution is left-skewed and the mass is concentrated on the left. In the

application to a habitat rating curve, SK was hypothesized to mimic QP by indicating how far off center the peak of the curve was. Standard deviation, SD, is a common measure of variation (Pearson, 1895), and was selected to represent the width of the habitat rating curve. A larger width of the habitat rating curve was hypothesized to indicate a wider range of suitable flow conditions and less sensitivity to flow alteration.

QP and SL were calculated from the standardized habitat rating curve. SK and SD were calculated by discretizing the standardized rating curve into a univariate distribution of percentile flow weighted by percent of maximum WUA. In the discretized distribution, each percentile flow value was repeated n times, where n is the percent of WUA value associated with that flow value. This weighting enabled a histogram to be created from the new univariate distribution that mimics the shape of the habitat rating curve. SK and SD were then calculated with standard equations for skewness and standard deviation (Helsel and Hirsch, 2002).

3.6. Statistical Analyses

Site-species combinations with similar patterns in average monthly habitat availability (AMHA) were organized into seasonal habitat regimes. Groups were identified using a hierarchical, agglomerative cluster analysis (Ward's algorithm, Borcard *et al.*, 2011). The objects were clustered on the 12 AMHA variables. The optimal number of clusters to retain was determined using the maximum silhouette width and the maximum Mantel correlation (Borcard *et al.*, 2011; Legendre and Legendre, 2012).

The first approach to determine an optimal number of clusters was the maximum silhouette width. The silhouette width measures how well an object belongs to its cluster using the average distance between the object and all other objects in its cluster; this distance measure is then compared to the same measure for the next closest cluster (Borcard *et al.*, 2011). These distances are averaged over all objects in a cluster and the partition with the largest average silhouette width is selected as the optimal number of groups. The second approach to determining an optimal number of clusters is a comparison between the original distance matrix and binary matrices representing partitions of the dendrogram at various cut levels (Borcard *et al.*, 2011). The correlation between these two matrices (Mantel correlation) is the equivalent of a Spearman's ρ correlation (Siegel and Castellan, 1988) between values in the distance matrices.

The level at which the dendrogram is cut (or the number of clusters) that results in the highest Mantel correlation is the optimal number of clusters.

Curve parameters were compared between seasonal habitat regimes and tested for statistical significance using a multivariate analysis of variance (MANOVA) and the Wilk's lambda multivariate F-statistic. If the multivariate test was significant at the 95% confidence level ($\alpha = 0.05$), then univariate F-tests were examined for each variable to interpret the respective effects. Post-hoc tests for all possible pairs of groups were performed using Tukey's Honest Significant Difference. Since F-tests are generally robust to deviations from normality and to unequal variances, no transformations were made on the variables (Lindman, 1974). The four curve parameters were also compared to each other using Spearman's ρ correlation coefficient (Siegel and Castellan, 1988). An ANOVA and post-hoc tests were performed for SHAR between seasonal habitat regimes.

3.7. Key Assumptions

The methodology and results presented in this study depend on the following assumptions:

- a) Mean daily streamflow values are appropriate for developing flow duration statistics used to calculate percentile flows (versus using 15-min or monthly data).
- b) Data from the entire period of record from long-term streamflow gages for flow duration statistics are appropriate, regardless of periods with regulated streamflow as determined by the USGS.
- c) IFIM studies used in analyses were carried out following the original and updated manuals (Bovee, 1982; Stalnaker *et al.*, 1995; Bovee *et al.*, 1998) and were consistent in their methods.
- d) Inputs to the IFIM studies used in analyses were correct and appropriate.
- e) Summer season occurs in July, August, and September, consistent with the months that historically have the lowest streamflow in Virginia.

Chapter 4: Results

4.1. Habitat Metrics

Inspection of individual ranges of Index B values within a year across all reaches and species appeared to fall into one of three categories: 1) relative constancy in average monthly habitat availability; 2) less habitat availability in spring than in summer; and 3) greater habitat availability in spring than in summer. Some flow time series contained months in which the observed discharge was never within the habitat rating curve range, resulting in no estimate of average WUA for that month. This scenario occurred mostly for the month of April, when streamflow is typically greatest in Virginia rivers (VDEQ, 2014). This scenario also occurred for additional spring months at reaches with the largest contributing drainage area (reaches T8&9 and T11&12 on the Potomac River). These observations were removed from subsequent analyses, reducing the total sample size from 428 to 382.

Seasonal habitat availability ranges were divided into four regimes (Figure 11): constant high, seasonal summer, seasonal spring, and constant low habitat availability (Figure 12). The choice of four clusters was determined as the optimal number of clusters from both the maximum silhouette width and the maximum Mantel correlation between the original distance matrix and binary matrices computed from the dendrogram at various cut levels. The groups were named based on the magnitudes of the median monthly habitat availability values within each group; the constant high and low groups have all average monthly habitat availability values greater than or less than 0.5, respectively, while the seasonal groups are above and below 0.5 depending on the month (Table 4).

The seasonal habitat availability (SHA) ratios ranged from -4.75 to 2.62 (mean: -0.38 ± 0.89). More species observed a decrease in seasonal habitat availability in the summer ($n=284$) than in the spring ($n=139$), suggesting that more species experience critical time periods during the summer. The three site-species combinations that showed the most sensitivity to summer decreases (the most negative ratios) in habitat availability all occurred in the Pamunkey Coastal Plain reach: benthic macroinvertebrates, spawning Northern hogsucker, and the shallow-fast habitat guild with seasonal habitat variability ratios equal to -4.75, -3.85, and -3.44, respectively. The four site-species combinations that showed the most sensitivity to spring decreases in habitat availability (the largest positive ratios) were spawning American shad in both the North Anna Piedmont and Above Harvell Dam reaches (2.62 and 2.10, respectively) and the Eastern

lampmussel in both the North Anna Piedmont and Fall Zone reaches (2.15 and 2.25, respectively).

Within each seasonal habitat regime, the mean SHAR values were -0.10 ± 0.38 , -0.96 ± 0.37 , 1.22 ± 0.52 , and -1.27 ± 0.75 for the constant high, seasonal summer, seasonal spring, and constant low habitat availability groups, respectively (Figure 13). Mean values of SHAR differed between groups. All groups were significantly different than each other at a significance level of less than 0.0001. The constant high group contained both positive and negative ratios within one standard deviation of the mean, confirming that the group does not have a tendency toward spring or summer habitat availability that is greater than the other season. Both the seasonal summer and seasonal spring group had only negative and only positive ratios, respectively, within one standard deviation of the mean. The constant low group had a more negative mean than the seasonal summer group and had only negative ratios within one standard deviation of the mean.

4.2. Shape Parameters of Standardized Habitat Rating Curves

All slope values were less than one except for a single outlier – the algae-midge guild at the Spring Hollow reach. This species was removed and summary statistics were computed for each curve parameter (Table 5). 31% of the species had slope values equal to zero ($n=133$). Location of peak (QP) ranged from 0-94th percentile. Standard deviation (SD) ranged from 4.89 to 30.95, and skewness (SK) ranged from -1.63 to 3.33. Several pairs of curve parameters were highly correlated (Figure 14), with the largest correlation between QP and SK (Spearman's $\rho=0.82$).

Curve parameters were also compared among seasonal habitat regimes (Figure 15). The mean values for QP for each habitat availability regime were the 31st, 16th, 79th and 13th flow percentiles, respectively. All groups except the seasonal spring regime contained at least one habitat rating curve with a slope of zero, and contained one habitat rating curve with a very large slope close to the maximum slope (0.1541). The standard deviations of the habitat rating curves appeared to be very similar across all groups, all within one unit (flow percentile) of each other. Only the seasonal spring group had a negative median skewness value; all other groups had positive median skewness.

Seasonal habitat regime had a statistically significant effect on the curve parameters (Wilk's lambda = 0.60, $F=17.4$, $p < 2e-16$). QP and SK were significantly different between groups (QP: $F=63.2$, $p < 2e-16$; SK: $F=65.6$, $p < 2e-16$) but SL and SD were not (SL: $F=2.2$, $p = 0.09$; SD: $F=2.3$, $p = 0.07$). For QP and SK, all pairs of groups had significantly different mean values except for groups 2 and 4, the seasonal summer and constant low habitat availability regimes, respectively. Contrastingly, for SL, none of the pairs of groups had significantly different mean values, but groups 2 and 4 came the closest ($p = 0.09$). For SD, no pairs of groups were significantly different.

Chapter 5: Discussion

5.1. Seasonal Habitat Regimes

The identification of only four seasonal habitat regimes for grouping objects of instream flow users can help water resource managers since it reduces the number of “users” or “lifestages” that need to be evaluated and accounted for when making decisions. Seasonal habitat regimes developed from historic habitat availability showed common preferences that appeared to follow seasonal flow patterns. General characteristics can be gleaned from these groups and comparisons can be drawn across seasonal habitat regimes.

The constant high habitat availability group (Figure 12a) observed greater than 50% of the maximum habitat availability for all months of the year. This group contained most of the canoeing observations from 11 different river reaches. In addition, common aquatic species found within this group included channel catfish, the deep-slow habitat guild, Northern hogsucker, and smallmouth bass. The high habitat availability throughout all months shows that the objects within this group are not as sensitive to seasonal flow patterns; they tend to be generalists for which a majority of habitat is available with most low flows as well as high flows.

The seasonal spring group (Figure 12b) has increased habitat availability during spring peak flows, and smaller average habitat availability during summer low flows. The most common species within this group was the Northern hogsucker (both adult and spawning lifestages). This group also contained approximately half of the canoeing observations, eight of the mussel observations, and two of the deep-fast habitat guild observations, which all prefer fast-flowing, deeper water. The separation of these objects from the constant high habitat availability group indicates that the summer low flows, where average monthly habitat availability dropped for the seasonal spring group, are not as suitable for these objects as spring peak flows.

The seasonal summer group (Figure 12c) has the opposite preference from the seasonal spring group. Species within this group included sub-adult and spawning smallmouth bass, riffle and shallow-fast habitat use guilds, rock bass, and redbreast sunfish. Higher habitat availability in summer months indicate preferences toward lower flows that occur in summer months in Virginia. The riffle dwellers that assembled in this group have also been identified as sensitive to flow alterations in other studies (Knight *et al.*, 2014).

The constant low habitat availability group (Figure 12d) has less than 50% of maximum habitat availability for all months of the year. Objects within this group included algae-midge, shallow-fast, and shallow-slow habitat use guilds, and the group is comprised of over 50% juvenile, fry and spawning lifestages. Before fish species reach the adult lifestage, high velocities associated with high flows can exceed the swimming capacity (Leopold, 1953; Nelson *et al.*, 2003).

The objects that fell into each seasonal habitat regime seemed to be most similar in their water velocity preferences. Similarities in depth preferences were also apparent, but velocity appeared to be the more dominant hydraulic condition in separating the objects into groups. This observation is consistent with other studies where velocity was found to be the critical variable in determining habitat suitability (Leonard and Orth, 1988; Aarts *et al.*, 2004).

While not performed in this study, an additional cluster analysis could be used to classify instream flow users into groups based on the HSC curves for depth, velocity, or substrate. The HSC curves are the original input variables into PHABSIM, and therefore drive most of the observations seen in this study. A cluster analysis based on quantifiable shape parameters of the HSC curves could eliminate the intermediate procedures of a PHABSIM or IFIM study and generate groups of instream flow users based strictly on their hydraulic preferences.

By generating these seasonal habitat regimes or other clusters, the total number of unique instream flow users that should be evaluated in a water management decision was drastically reduced. These groups can simplify the amount of assessment that must be done when evaluating a proposed change in water consumption from an individual river. For example, one or two species from each group could be selected as a representative species for a detailed evaluation and assessment. One possible method for selecting this representative species would be to calculate the minimum sum of squared error from the median Index B values for the group. These representative species then preserve the characteristic seasonal patterns of all species within the group. By balancing impacts of alternative water management scenarios for one or two representative species from each group, all possible seasonal patterns, and potentially critical time periods, are protected.

Ideally, the seasonal habitat regimes developed in this study could be used as a representative “species.” However, only 10 of the 23 reaches had an individual from all four clusters present (Table 6). Only six unique, non-contiguous reaches were present among those

10. The inadequate sample size limits the applicability of any findings because of the limited spatial extent. This problem also occurred at the species and lifestage level; the maximum number of reaches for which a single species or lifestage was studied was 14.

The tools developed for these analyses also assimilated existing habitat rating curves with an existing network of streamflow gaging stations. This structure enables future examination of long-term habitat availability and the ecological communities that have adapted to physical conditions over time. Detailed inspection of individual lifestages that were studied across multiple rivers may identify specific commonalities; these trends could lend themselves to generalized models that can predict habitat availability in rivers that have not experienced IFIM studies (Lamouroux and Jowett, 2005). The seasonal habitat regimes developed in this study should also be tested using IFIM studies and habitat rating curves from other states and physiographic regions.

5.2. Shape Parameters of Standardized Habitat Rating Curves

Metrics that described the overall shape and magnitude of the standardized habitat rating curves were significantly different among groups and are promising metrics for future instream flow regime evaluations/studies. The seasonal habitat availability ratios (SHAR) were different between all groups, highlighting March and September as the two months with the most extreme differences in average monthly habitat availability. September has previously been included in low-flow analyses of habitat availability (Krstolic and Ramey, 2012), but spring months (e.g. March) are not commonly included. Future studies should investigate the importance of these months for environmental flow recommendations.

The flow percentile at peak (QP) values were also significantly different between seasonal habitat regime groups. The average QP values for each group reflected the seasonality of habitat availability. The average QP value for the constant high habitat availability regime was the 31st percentile flow, which was the only group average within a normal flow range (25th to 75th percentile). The seasonal spring regime's average QP value was above normal at a 79th flow percentile, and the seasonal summer regime's average QP value was below normal at a 13th flow percentile. These observations are in line with the seasonal flow patterns; in Virginia, peak flows above normal flow conditions typically occur in the spring and low flows below normal conditions typically occur in the summer. Species with higher suitability during low flows

clustered into the seasonal summer regime and contributed to the group's low average QP value. Alternatively, species with higher suitability during higher flows clustered into the seasonal spring regime and contributed to the group's high average QP value.

The observations of average QP values by group were mimicked by the average SK values by group. The group with a median SK value closest to 0 was the constant high habitat availability group (SK=0.17), which was the only group with an average QP value in the normal flow range. Seasonal summer and constant low groups had positive median SK values and average QP values below normal flow conditions. The seasonal spring group had a negative median SK value (SK=-0.56) and an average QP value greater than normal flow conditions. The close relationship between QP and SK was also evident by the high correlation coefficient. Due to this correlation, only one flow response metric may need to be retained. Since SK is more difficult to calculate from a habitat rating curve, it is recommended that QP is the flow response metric to retain and SK can be ignored. The value of the QP metric is also more directly relatable to flow recommendations.

The median slope values between all groups were similar, except for the constant low group (SL=0). The ranges between all groups were also similar in that each group contained habitat rating curves with very small or zero slopes and with slopes close to the maximum overall value. The lack of difference in slope values between groups indicate that patterns in response to low-flow alteration may not be accounted for in average monthly habitat availability, since the clusters were based on average conditions instead of extreme conditions.

The ability of the shape parameters to quantify the functional relationship between discharge and WUA is a powerful tool for water resource managers. All four parameters (QP, SL, SK, and SD) are common, quantitative metrics of a curve or distribution that are simple to explain and visualize. In a management decision such as approving a water withdrawal permit, these parameters can provide bounds or thresholds for which instream users need to be evaluated for impacts, based on what flow range would be altered by the permit. Screening tools such as applicable ranges of shape parameters are useful for water resources management at the state-level when selection of instream uses to evaluate must be efficient and complete. The shape parameters also benefit water resources management at the state-level because the metrics are standardized to be applicable across river systems and across types of instream flow users.

5.3. Evaluation of Study Methodology for Future Research

The methods used in this study illustrated a repeatable process to calculate and analyze habitat time series from flow time series and habitat rating curves. Results were comparable across all instream flow users, including specific lifestages of fish species, macroinvertebrates, habitat use guilds, mussels, and recreational activities. Results were also comparable across rivers of different size, ranging from drainage areas of 420 to 30,000 km².

These analyses should be repeated for other PHABSIM and IFIM studies that have produced habitat rating curves. Repeated analyses could help reinforce the identification of seasonal habitat regimes, as well as the identification of shape parameters that describe a standardized habitat rating curve. Relevant contexts such as physiographic province or stream classification should be explored to identify if there is a regional effect.

Another context that should be explored for its effect on seasonal habitat availability and the standardized habitat rating curves is regulation of streamflow by dams. A key assumption made in this study was that the entire period of record of available streamflow data would be the most representative time period to calculate flow percentiles. Eleven of the reaches in this study experience regulated streamflow from an upstream impoundment. Only six of these reaches had adequate periods of streamflow data before regulation began.

Regulated streamflow, especially by dam operations, typically lowers peak flows and elevates low-flows (Poff *et al.*, 1997; McManamay *et al.*, 2012). Over a long period of time, this altered hydrology can change the flow duration curve at the high and low ends. Since flow duration statistics were used to calculate flow percentiles in this study, an effect will likely be seen in the standardized habitat rating curves as a result of streamflow regulation.

Initial assessments of this effect indicated that regulated flows in Virginia rivers did not have a large impact on flow duration curves or standardized habitat rating curves. Flow duration curves and one standardized habitat rating curve were plotted from pre- and post-regulation time periods for the six reaches that had adequate pre-regulation discharge record (Figure 16, Figure 17). Flow duration curves from unregulated and regulated periods indicated only small changes. These small changes were then reflected by small shifts in magnitude of the standardized habitat rating curves.

Future evaluations of the standardized habitat rating curves should explore the differences between pre- and post-regulation discharge records further. The shifts in standardized

habitat rating curves can be quantified by the shape parameters. The cluster analysis to identify groups of instream flow users with unregulated flow regimes may reveal different group memberships than those with regulated flow regimes.

A second assumption related to the flow duration curves was the use of mean daily discharge. Historically, flow duration curves have also been developed from mean weekly or monthly discharge (Searcy, 1959). More recently, sub-daily discharge values are being used to characterize flow regimes, especially in the context of regulated flows from dam operations (Bevelhimer *et al.*, 2014). Sub-daily discharge values were not used in this study because of the long periods of record and the interest in seasonal patterns of habitat availability; however, analyses of sub-daily fluctuations in streamflow and therefore habitat availability should be explored over shorter time periods. For example, effects of hydropeaking on availability of spawning habitat could be observed within a window of a few weeks or months, instead of multiple years, during which spawning for a certain species occurs.

5.4. Hydrology as Driving Force

Hydrology is the foundation of riverine functions and processes (Harman *et al.*, 2012). Without maintaining or restoring the correct hydrology, a healthy stream ecosystem will not be sustainable. The results of this study reinforced the critical link between hydrology, hydraulics, and biology. The historic flow regime dictates the current physical conditions of a river, and aquatic communities adapt to these conditions over time. Maintaining the variability and seasonality of habitat that has historically been available will help maintain the biological functions of a stream ecosystem. Water resources management can benefit from the reduction of instream flow users that must be managed for, while still maintaining natural variability and accommodating for other beneficial uses.

Chapter 6: Conclusions and Future Research

6.1. Conclusions

A seasonal habitat availability ratio and shape metrics of habitat rating curves were shown to be effective grouping parameters for aquatic species with similar flow preferences across 11 rivers in Virginia. These metrics were successfully calculated using existing habitat rating curves and long-term streamflow gaging stations. Individual species-site combinations were reduced from 428 objects to four groups with similar seasonal habitat availability patterns using cluster analysis.

A repeatable method to calculate habitat time series from flow time series and habitat rating curves was developed. These new metrics and patterns can be incorporated into assessments of future water usages. Habitat rating curves are a product of PHABSIM and IFIM, popular methods of instream habitat assessment from the past thirty years in Virginia. By compiling habitat rating curves across Virginia into a single repository, habitat time series analysis can be included in statewide water withdrawal permitting and management scenarios. IFIM studies alone have been completed in over 20 countries, providing abundant existing data sources for validation of the results presented here.

6.2. Future Research

- Validate seasonal habitat availability clusters for prediction of new observations into the correct group.
- Conduct a sensitivity analysis of changes in shape parameters of the standardized habitat rating curves due to changes in flow time series, such as regulation by dam operations.
- Repeat analyses presented here with PHABSIM and IFIM studies in other regions to check for consistency or irregularity in clusters or shape parameters.
- Generate and test predictive models from species and site combinations that can be used to evaluate seasonal habitat availability in river reaches that have not been studied.
- Compare annual or seasonal habitat metrics to species abundance data from different years.

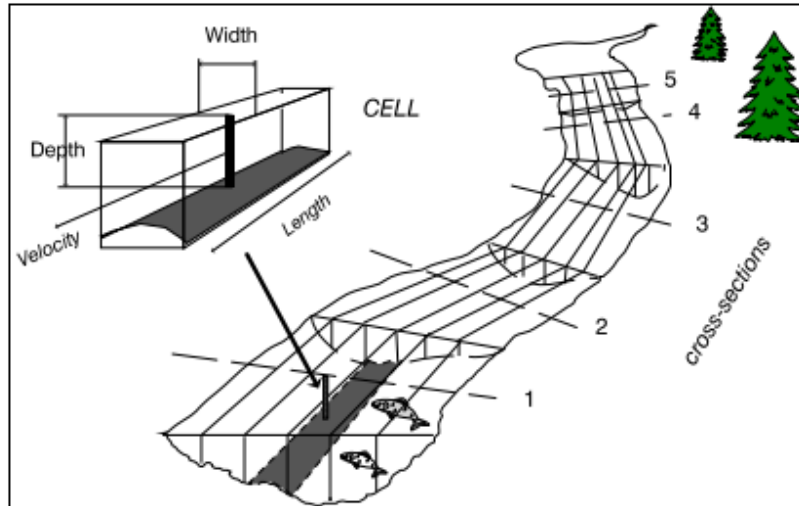


Figure 1. Conceptual diagram of a habitat survey of a representative stream reach using point measurements in order to calculate total Weighted Usable Area (WUA), Jowett IG. 1997. Instream flow methods: a comparison of approaches. *Regulated Rivers: Research & Management*, 13, 115–127. Used under fair use, 2015.

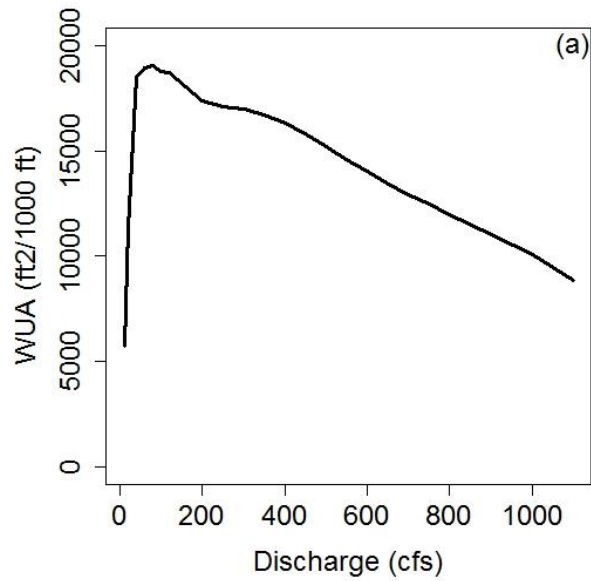


Figure 2. Example of a habitat rating curve generated from the Physical HABitat SIMulation (PHABSIM) program and used in Instream Flow Incremental Methodology (IFIM). Total Weighted Usable Area (WUA) is plotted versus increments of discharge. WUA is an index of habitat availability for an individual species based on depth, velocity, and substrate preferences.

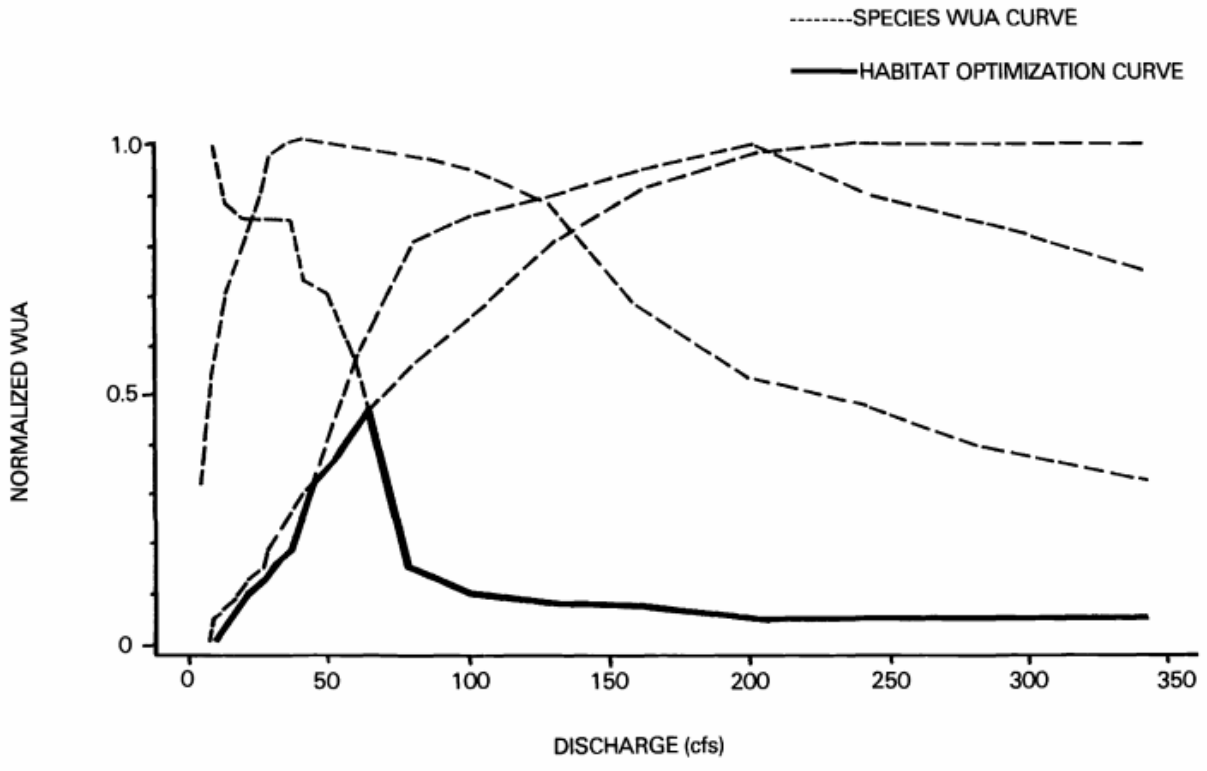


Figure 3. Schematic of the derivation of an "optimum flow" using habitat rating curves for all species at a site, Leonard PM, Orth DJ and Goudreau CJ. 1986. Development of a Method for Recommending Instream Flows for Fishes in the Upper James River, Virginia. Used under fair use, 2015.

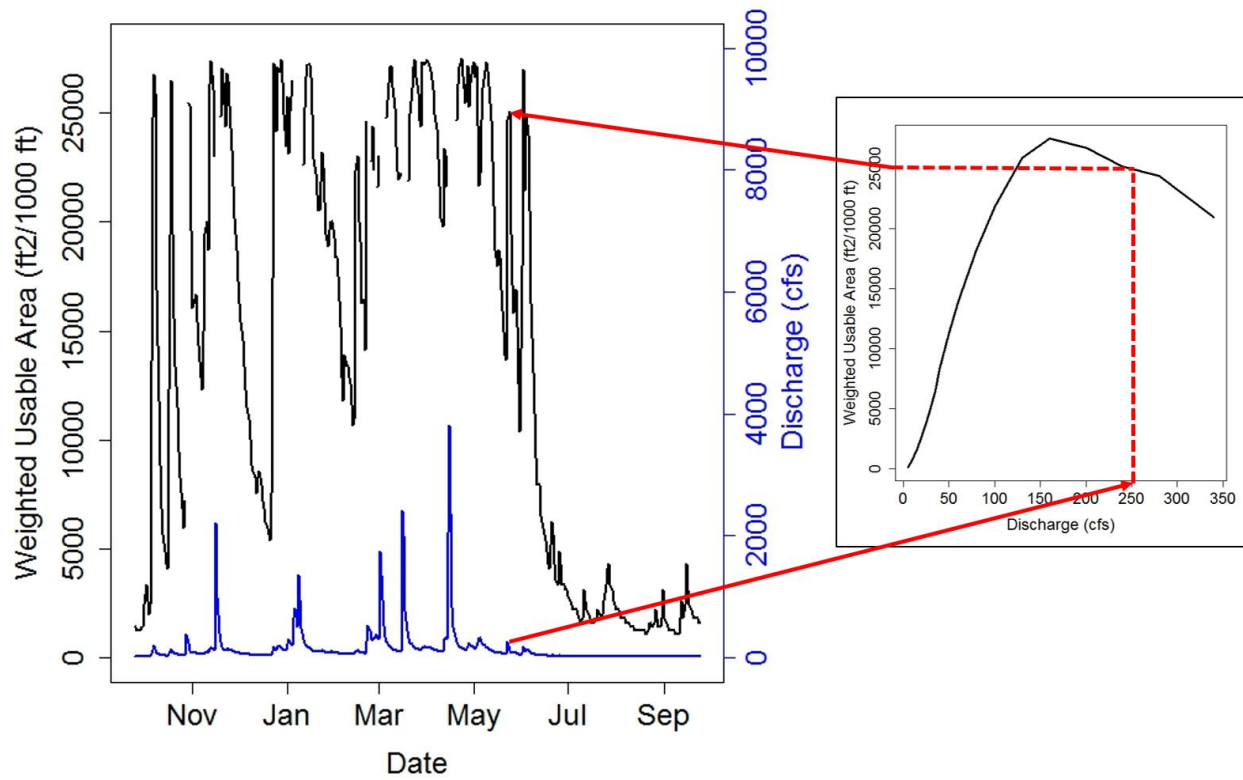


Figure 4. Schematic of calculating habitat time series from a flow time series and a habitat rating curve. Example flow and habitat time series shown are for Black Jumprock (*Moxostoma cervinum*) adult lifestage at the Dunlap reach for water year 2007.

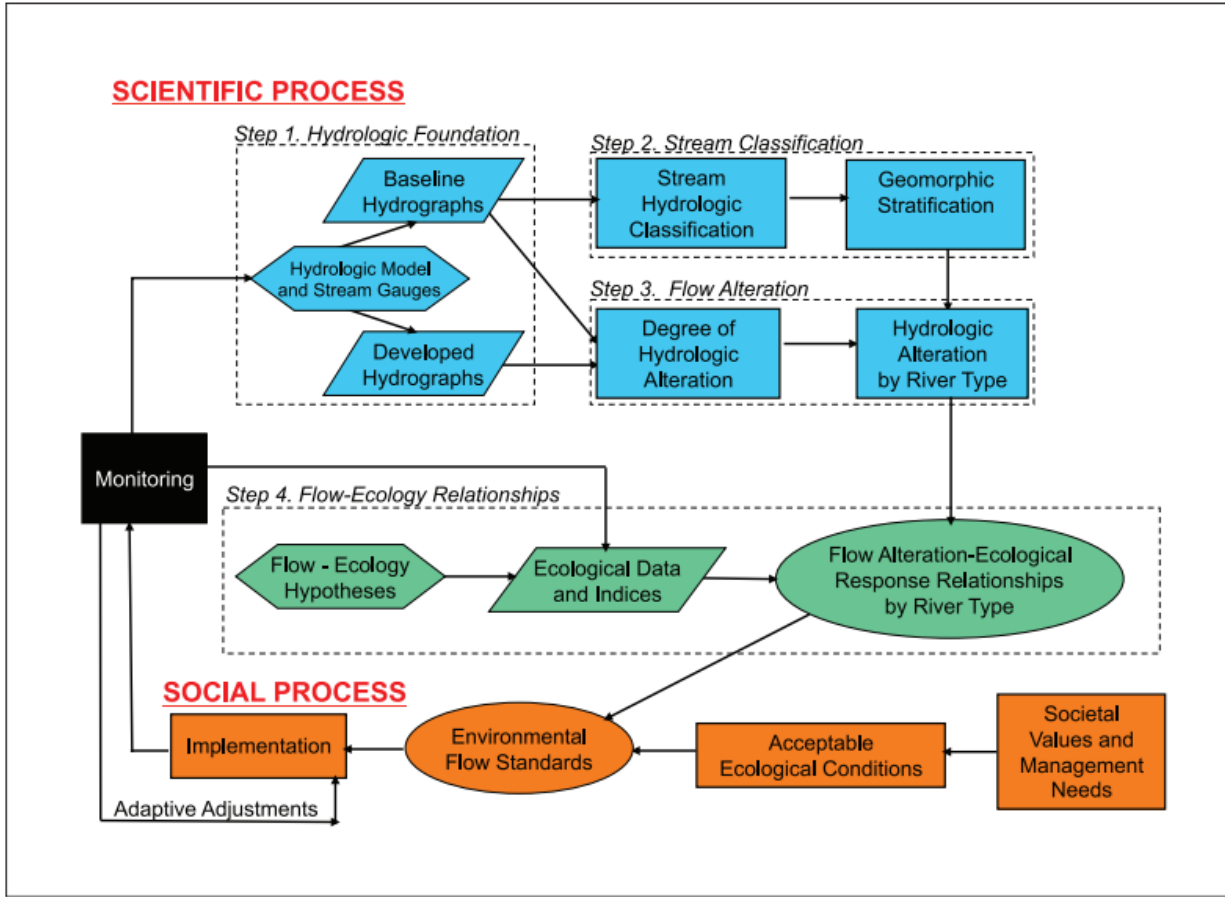


Figure 5. Conceptual model of the Ecological Limits of Hydrologic Alteration (ELOHA) framework, Poff NL, Richter BD, Arthington AH, Bunn SE, Naiman RJ, Kendy E, Acreman M, Apse C, Bledsoe BP, Freeman MC, Henriksen J, Jacobson RB, Kennen JG, Merritt DM, O’Keeffe JH, Olden JD, Rogers K, Tharme RE and Warner A. 2010. The ecological limits of hydrologic alteration (ELOHA): a new framework for developing regional environmental flow standards. *Freshwater Biology*, 55(1), 147–170. <http://doi.org/10.1111/j.1365-2427.2009.02204.x>. Used under fair use, 2015.

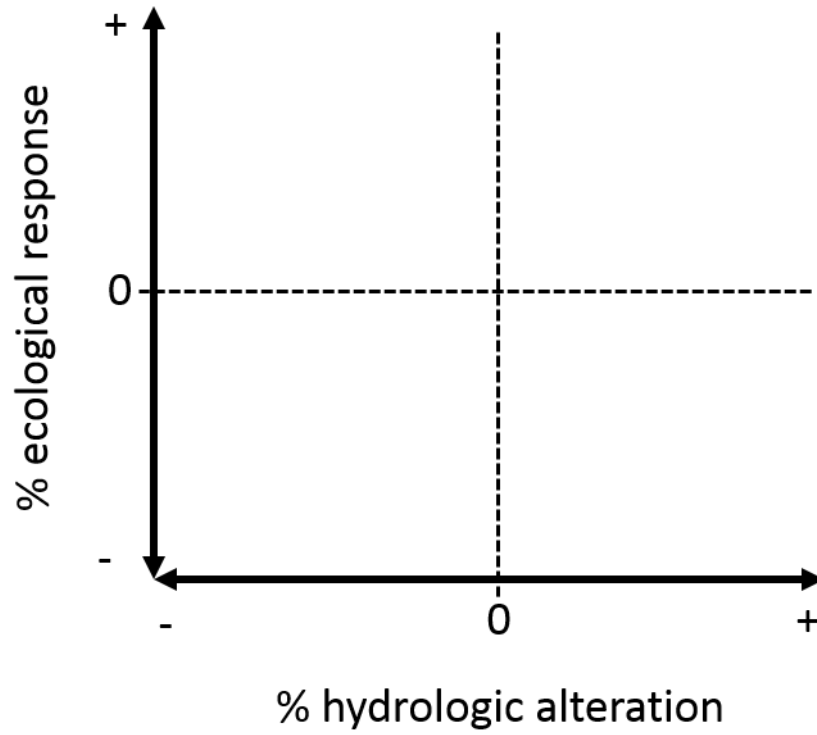


Figure 6. Schematic of a flow-ecology relationship, showing ecological response (%) versus hydrologic alteration (%).

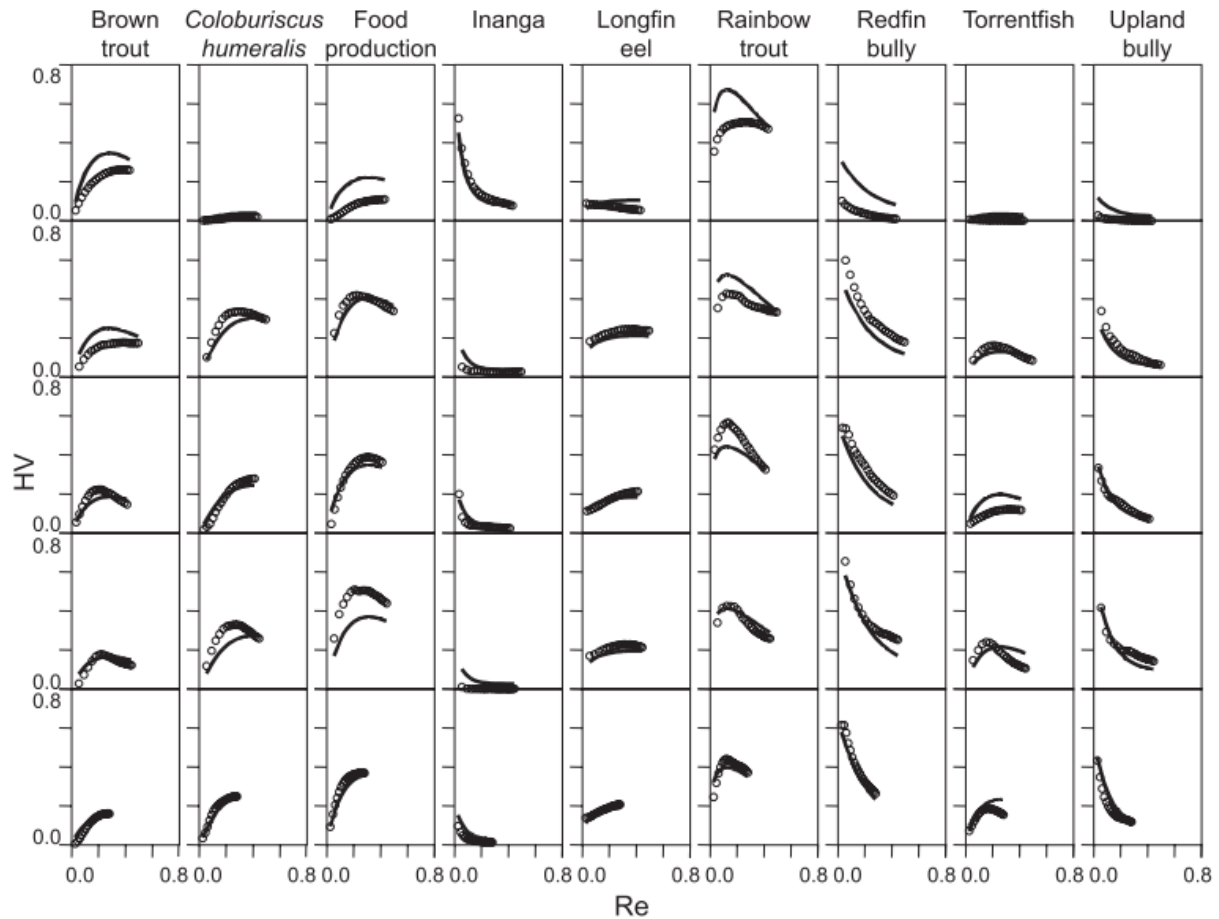


Figure 7. Standardized habitat rating curves that show the similarity in shape for the same species (columns) across five different rivers (rows). Plots show observed habitat values (HV) versus specific discharge (Reynolds number, Re) curves for five reaches, where circles are outputs of the river hydraulics and habitat simulation software (RHYHABSIM) and solid lines are modeled curves from average characteristics of reaches using generalized habitat models, Lamouroux N and Jowett IG. 2005. Generalized instream habitat models. Canadian Journal of Fisheries and Aquatic Sciences, 62(1), 7–14. <http://doi.org/10.1139/f04-163>. Used under fair use, 2015.

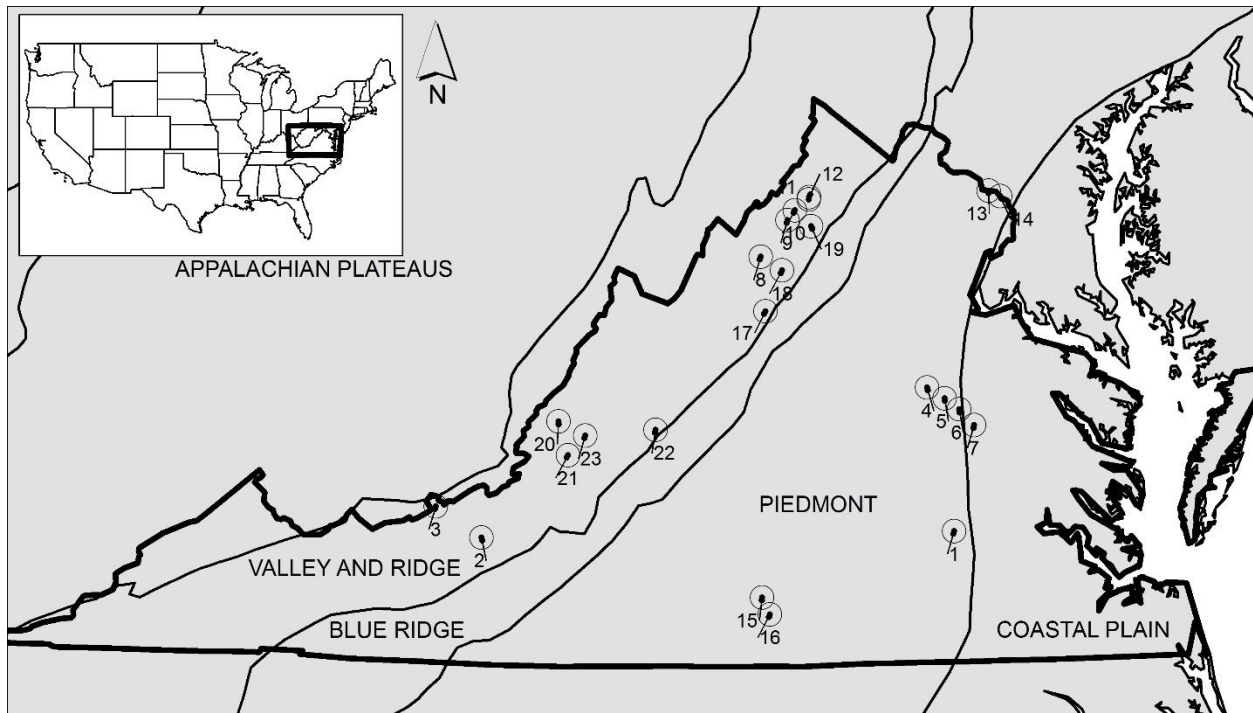


Figure 8. Locations of twenty-three Instream Flow Incremental Methodology (IFIM) study locations across Virginia, showing distribution across physiographic province (physiographic provinces from Fenneman NM and Johnson DW. 1946. Physiographic divisions of the conterminous US. Reston, VA: U.S. Geological Survey. Retrieved from <http://water.usgs.gov/lookup/getspatial?physio>. Used under fair use, 2015).

- ¹Above Harvell Dam, ²Claytor to Pembroke, ³Pembroke to Glen Lyn, ⁴North Anna Piedmont, ⁵North Anna Fall Zone, ⁶North Anna Coastal Plain, ⁷Pamunkey Coastal Plain, ⁸Plains Mill, ⁹Laurel Hill, ¹⁰Spring Hollow, ¹¹Posey Hollow, ¹²Rt 648, ¹³T8&9, ¹⁴T11&12, ¹⁵Staunton, ¹⁶Head Kerr Lake, ¹⁷Lynnwood, ¹⁸Luray, ¹⁹Front Royal, ²⁰Craig Creek, ²¹Dunlap Creek, ²²Maury River, ²³James River.

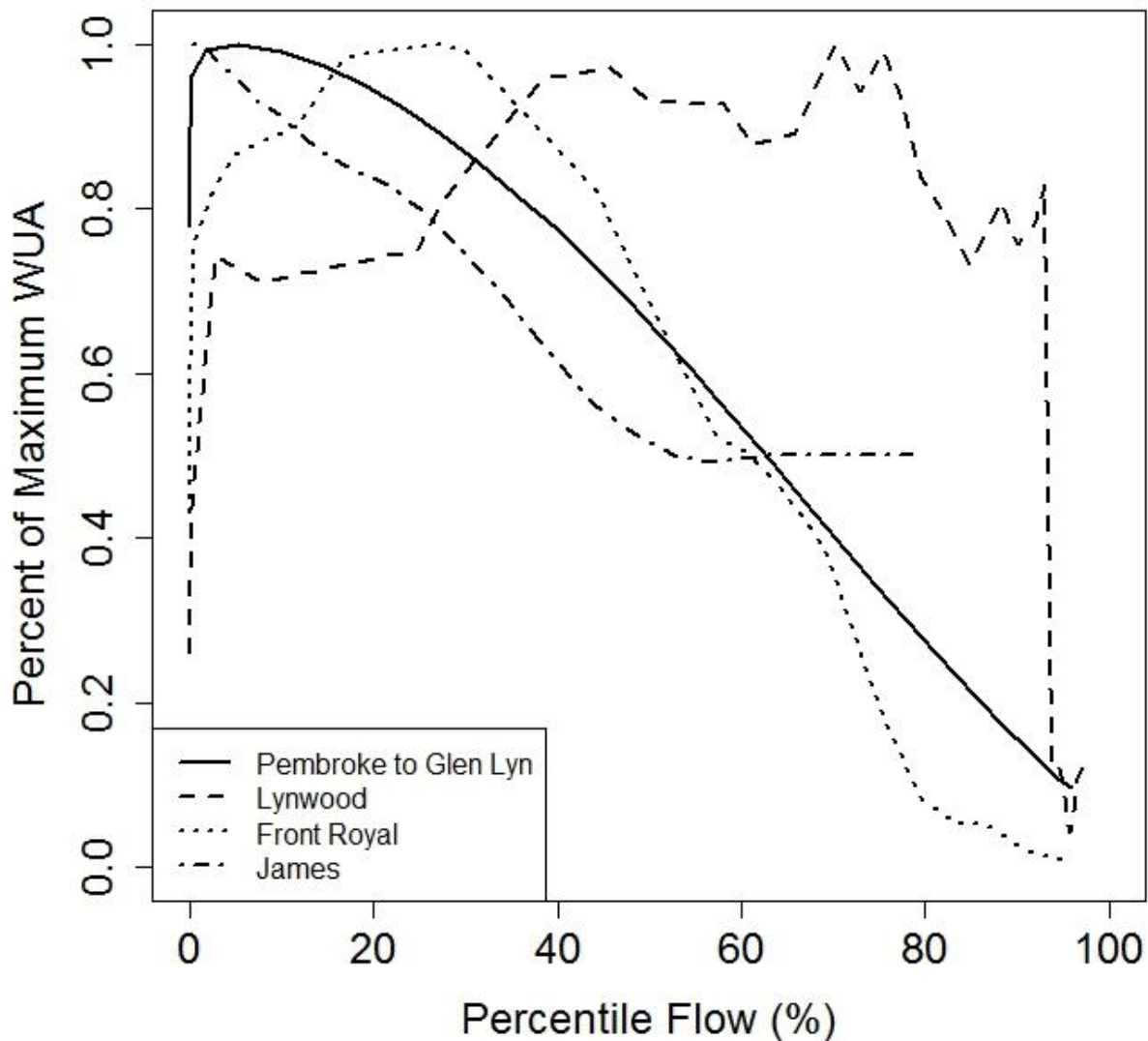


Figure 9. Flow-habitat rating curves for adult smallmouth bass at four river reaches in Virginia. Percent of maximum Weighted Usable Area (WUA) is an index of aquatic habitat availability developed from the instream habitat model PHABSIM. Curves were adapted from habitat studies in the Pembroke to Glen Lyn reach on the New River (Thomas R. Payne and Associates. 2008. Appalachian Power Company Claytor Hydroelectric Project No. 793-018: Instream Flow Needs Study Final Report. Arcata, CA, and Needham, MA, used under fair use, 2015), the Lynwood and Front Royal reaches on the South Fork Shenandoah River (Krstolic JL and Ramey RC. 2012. South Fork Shenandoah River Habitat-Flow Modeling to Determine Ecological and Recreational Characteristics during Low-Flow Periods, used under fair use, 2015), and the James reach on the Upper James River (Leonard PM, Orth DJ and Goudreau CJ. 1986. Development of a Method for Recommending Instream Flows for Fishes in the Upper James River, Virginia, used under fair use, 2015).

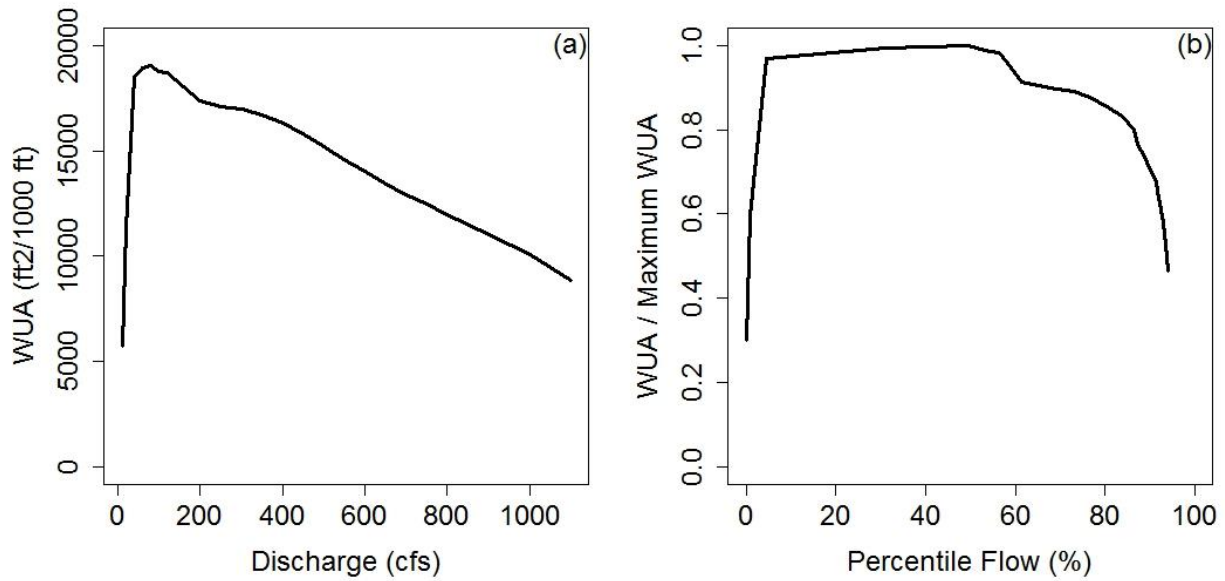


Figure 10. Original (a) and standardized (b) habitat rating curve. Example shown is for adult smallmouth bass in the North Anna Piedmont reach. Weighted Usable Area (WUA) is an index of habitat availability commonly expressed in units of ft²/1000 ft. Flow percentiles calculated from long-term mean daily streamflow record.

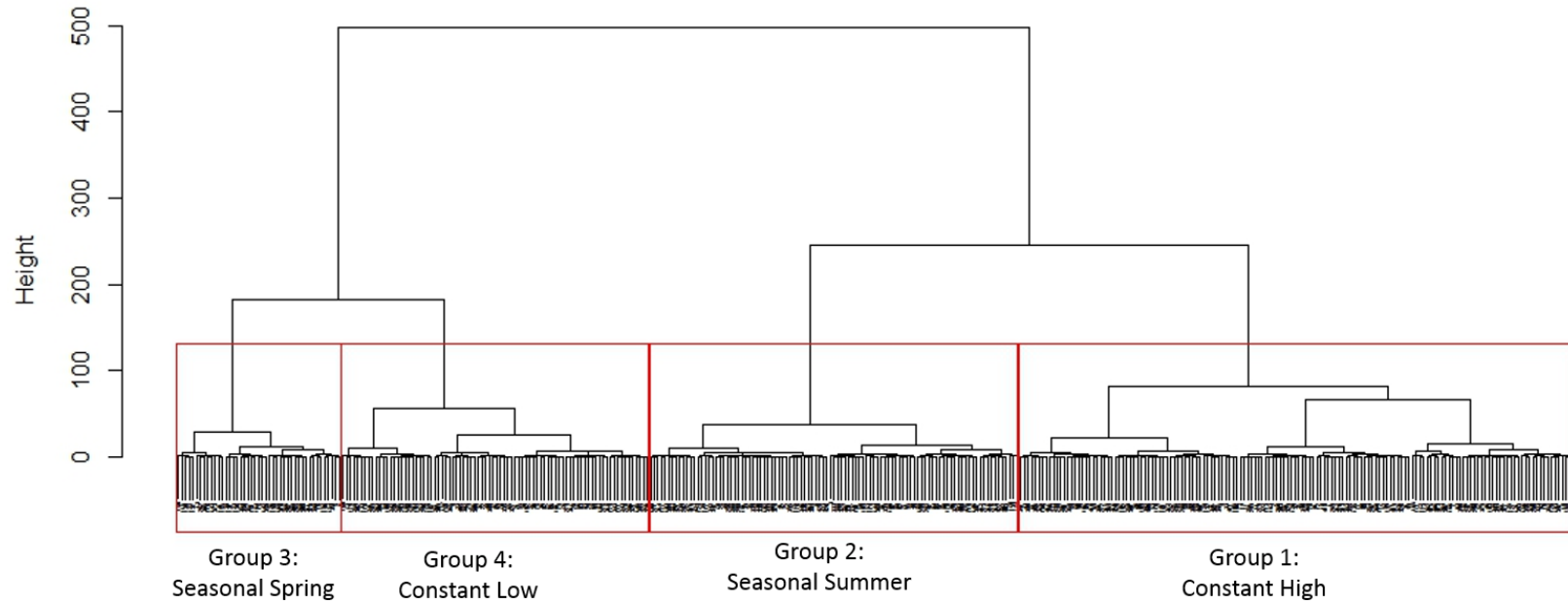


Figure 11. Dendrogram of site-species combinations (n=428) based on average monthly habitat availability. A hierarchical, agglomerative clustering method (Ward's) was used to identify four partitions. The optimal number of partitions was determined using maximum silhouette width and a Mantel correlation.

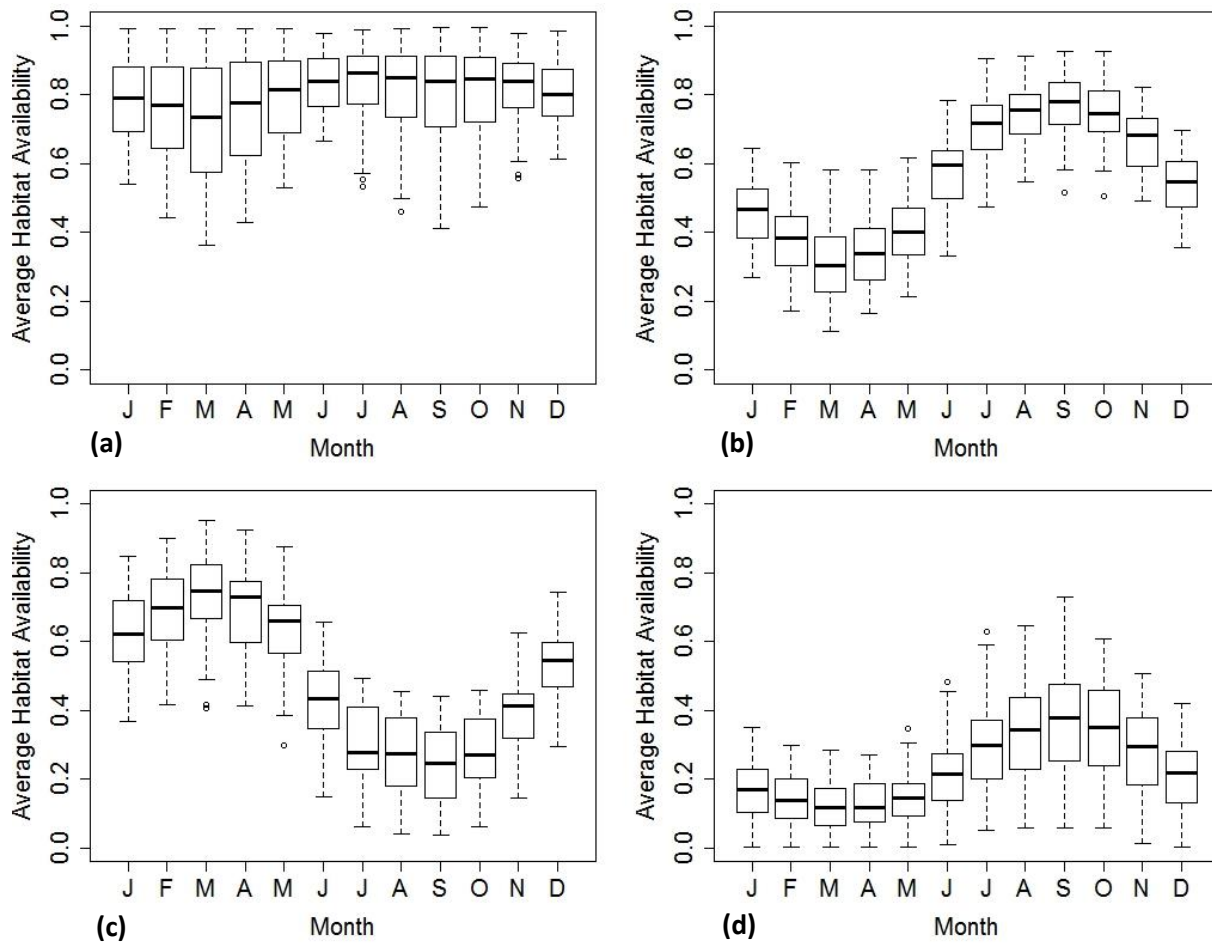


Figure 12. Ranges of average monthly habitat availability for four seasonal habitat regimes: (a) constant high, (b) seasonal summer, (c) seasonal spring, and (d) constant low habitat availability. Average monthly habitat availability is calculated from all daily Weighted Usable Area (WUA) values within the long-term habitat time series, aggregated by respective month. The bottom and top whisker show the minimum and maximum value, excluding outliers that are 1.5 times the lower or upper quartile. The boundaries of the box indicate, from bottom to top, the lower quartile, median, and upper quartile values.

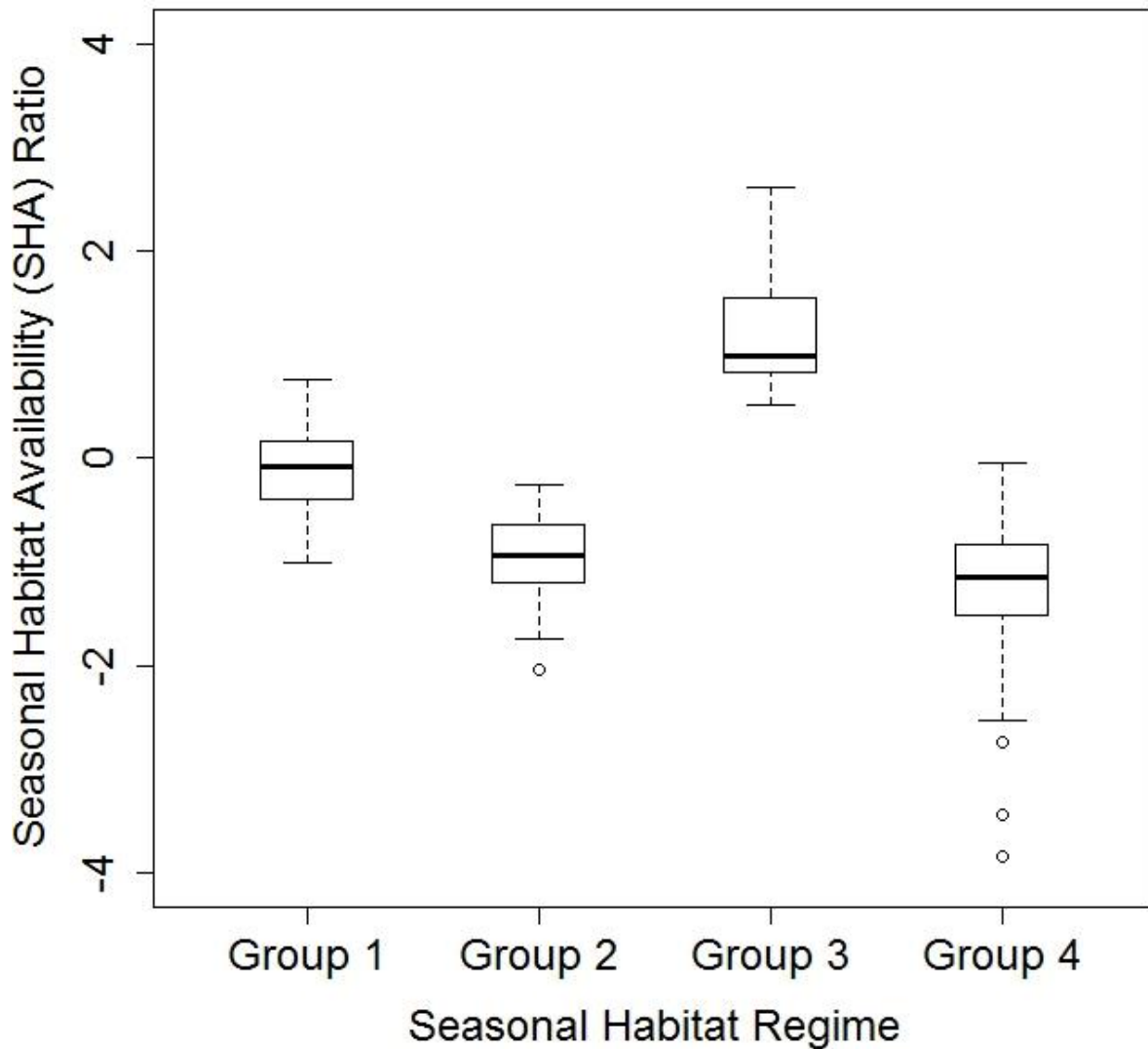


Figure 13. Boxplots of seasonal habitat availability (SHA) ratios for each seasonal habitat regime. Regimes were determined from a cluster analysis of average monthly habitat availability for 382 site-species combinations. SHA ratio is calculated as the log of March average habitat availability divided by September average habitat availability. The bottom and top whisker show the minimum and maximum value, excluding outliers that are 1.5 times the lower or upper quartile. The boundaries of the box indicate, from bottom to top, the lower quartile, median, and upper quartile values.

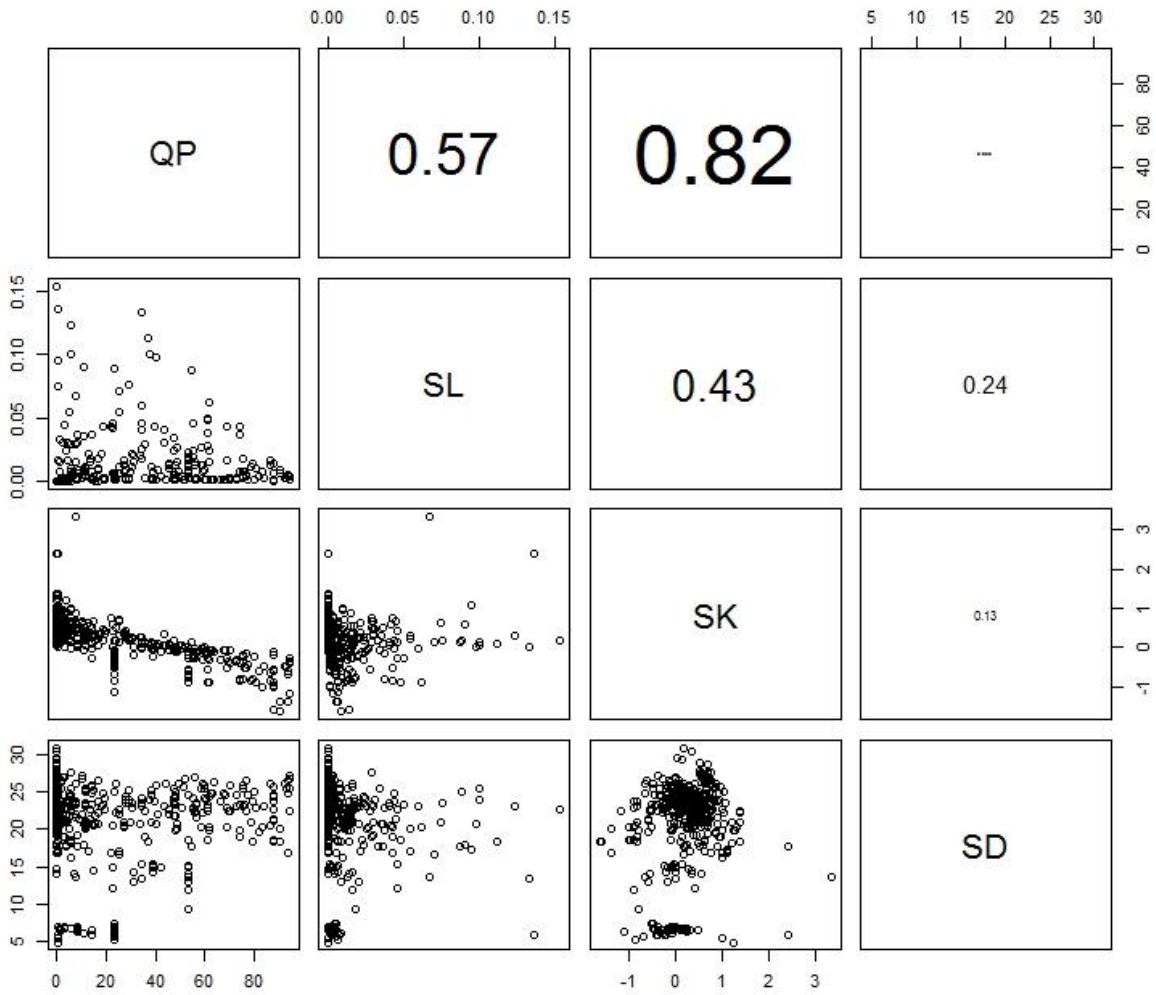


Figure 14. Pairwise scatterplots of habitat rating curve parameters. Curve parameters are defined in Table 3. Upper panel shows correlation coefficient (Spearman's ρ) between pairs, where text size of coefficient is proportional to the correlation.

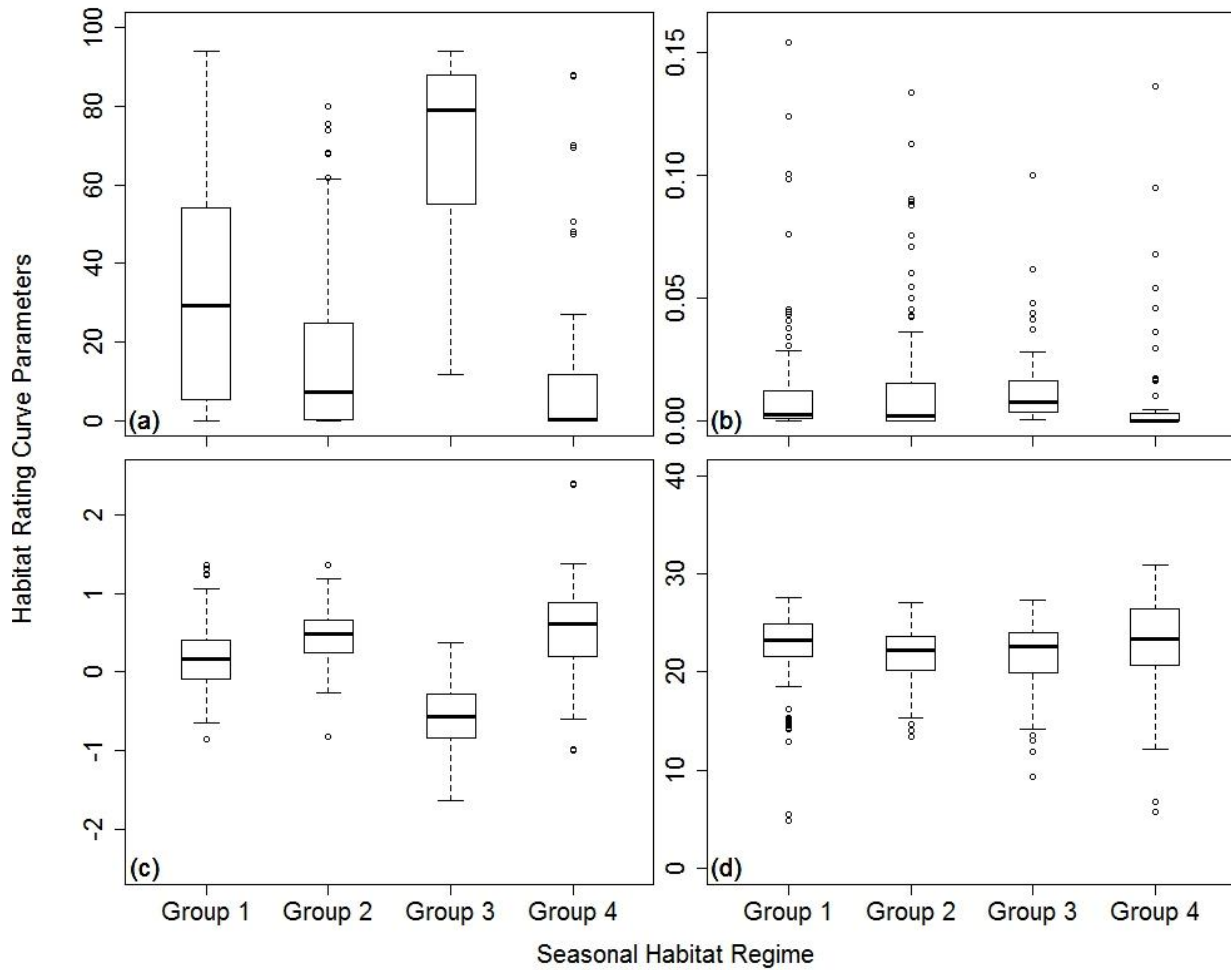


Figure 15. Boxplots of (a) QP, (b) SL, (c) SK, and (d) SD for each seasonal habitat regime. Regimes were determined from a cluster analysis of average monthly habitat availability for 382 site-species combinations. Curve parameters were calculated from the magnitude and fundamental shape of the habitat rating curve and are described in Table 3. The bottom and top whisker show the minimum and maximum value, excluding outliers that are 1.5 times the lower or upper quartile. The boundaries of the box indicate, from bottom to top, the lower quartile, median, and upper quartile values.

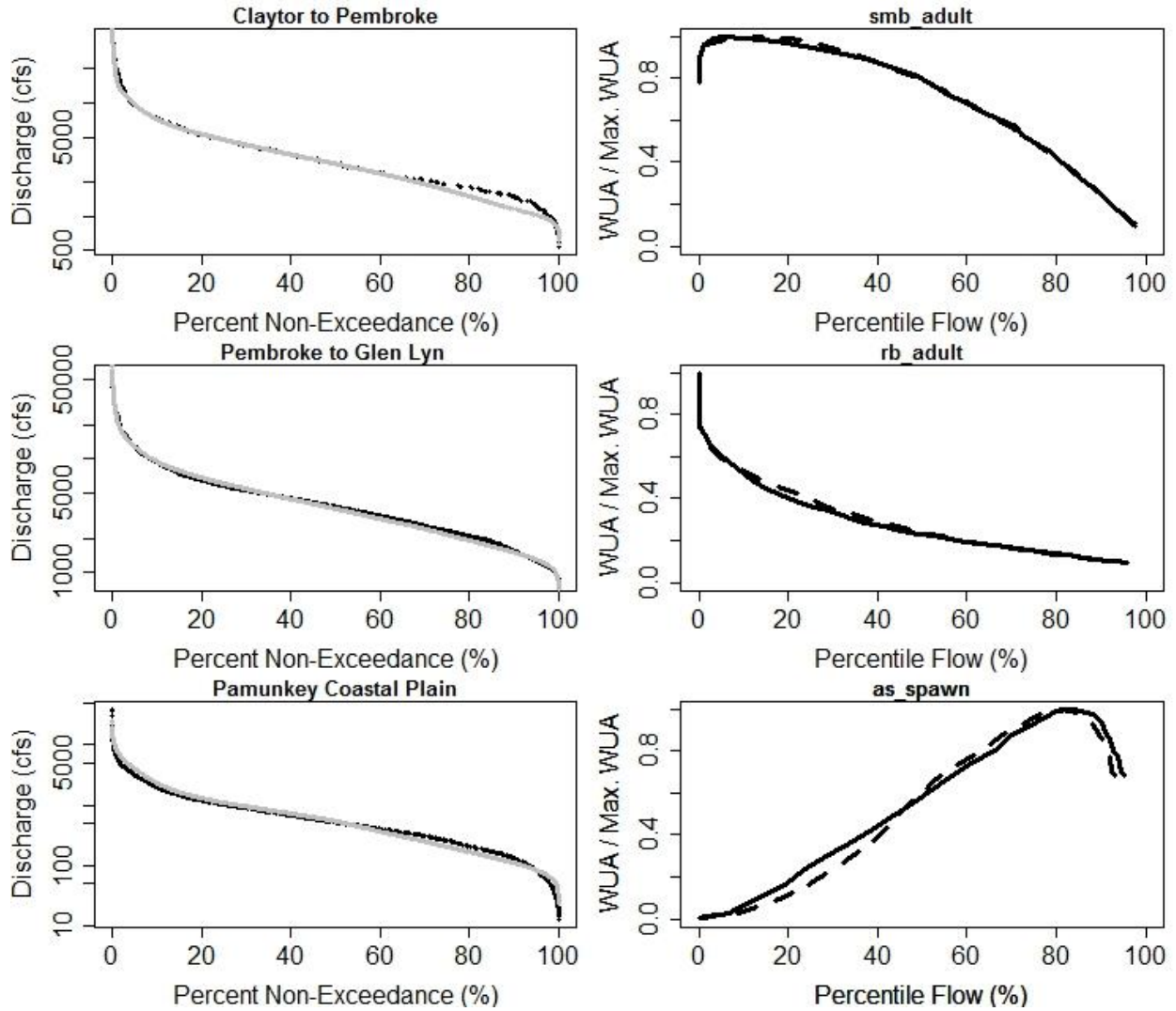


Figure 16. Flow duration curves (left) and example standardized habitat rating curves (right) for first three reaches with adequate periods of flow record both before and after flow regulation by dam operations. Flow duration curves show pre-regulated (black) and post-regulated (gray) periods of record. Standardized habitat rating curves show flow percentiles calculated from pre-regulated flow duration curve (solid) and from post-regulated flow duration curve (dashed). The standardized habitat rating curve shows one example instream flow user from the river reach for which the flow duration curve is depicted to the left of it.

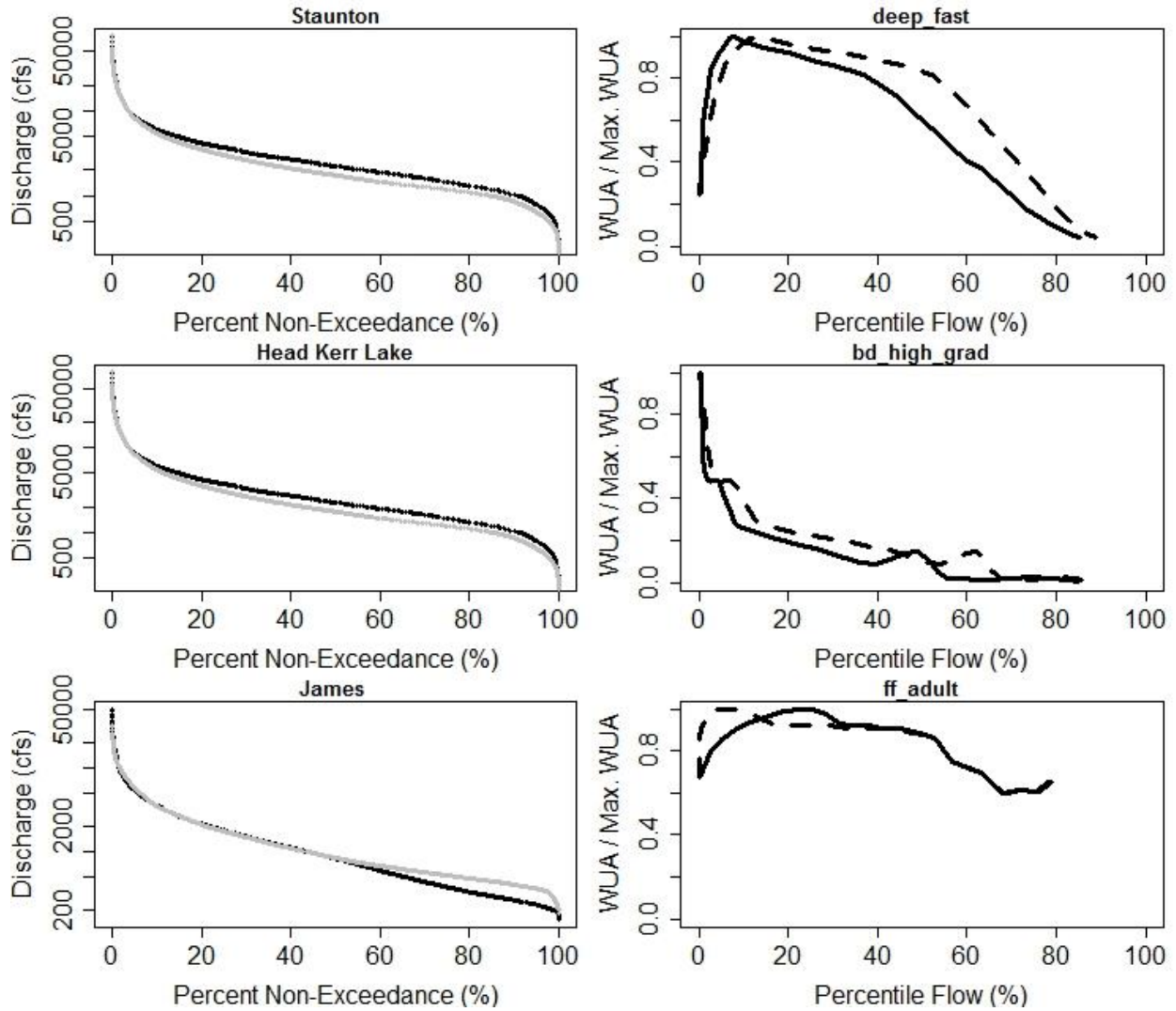


Figure 17. Flow duration curves (left) and example standardized habitat rating curves (right) for second three reaches with adequate periods of flow record both before and after flow regulation by dam operations. Flow duration curves show pre-regulated (black) and post-regulated (gray) periods of record. Standardized habitat rating curves show flow percentiles calculated from pre-regulated flow duration curve (solid) and from post-regulated flow duration curve (dashed). The standardized habitat rating curve shows one example instream flow user from the river reach for which the flow duration curve is depicted to the left of it.

Table 1. Summary of Instream Flow Incremental Methodology (IFIM) studies completed in Virginia.

Study	Major River Basin	Year Completed	Number of Reaches	Number of Species Evaluated	Source
Appomattox River	James River	2012	1	19	(EA, 2012)
New River	New River	2008	2	43	(Thomas R. Payne and Associates, 2008)
North Anna/Pamunkey River	York River	2009	4	15	(EA, 2009)
North Fork Shenandoah River	Potomac River	2004	5	5	(Averett <i>et al.</i> , 2004)
Potomac River	Potomac River	1981	2	23	(MD DNR, 1981)
Roanoke River	Roanoke River	2006	2	43	(Gore, 2006)
South Fork Shenandoah River	Potomac River	2012	3	8	(Krstolic and Ramey, 2012)
Upper James River	James River	1986	4	20	(Leonard <i>et al.</i> , 1986)

Table 2. Summary of U.S. Geological Survey (USGS) long-term streamflow gages used to calculate flow time series for 23 reaches in Virginia that have been a part of an Instream Flow Incremental Methodology (IFIM) study.

Reach Name	IFIM Report	USGS Gage ID	Lat/Long of USGS Gage Location	Lat/Long of Representative Reach Location	Drainage Area (mi²) at USGS Gage Location	Drainage Area (mi²) at Representative Reach Location
Above Harvell Dam	Appomattox	02041650				
Claytor to Pembroke	New River	03171000				
Pembroke to Glen Lyn	New River	03176500				
North Anna Piedmont	North Anna	01670400*	38.012778,-77.701389	37.964547,-77.627623	344	411.9
North Anna Fall Zone	North Anna	01670400*	38.012778,-77.701389	37.919196,-77.528059	344	435.8
North Anna Coastal Plain	North Anna	01671020				
Pamunkey Coastal Plain	North Anna	01673000				
Plains Mill	NF Shenandoah	01632000*		+	210	321
Laurel Hill	NF Shenandoah	01633000*		+	508	653
Spring Hollow	NF Shenandoah	01634000*		+	770	694
Posey Hollow	NF Shenandoah	01634000*		+	770	738
Rt 648	NF Shenandoah	01634000*		+	770	743
T8&9	Potomac	01646500*	38.949722,-77.127778	38.969416,-77.201618	11587	11549
T11&12	Potomac	01646500				
Staunton	Roanoke	02066000				
Head Kerr Lake	Roanoke	02066000*	36.915,-78.741111	36.881731,-78.699533	2966	2997.5
Lynnwood	SF Shenandoah	01628500				
Luray	SF Shenandoah	01629500				
Front Royal	SF Shenandoah	01631000				
Craig Creek	Upper James	02018000				
Dunlap Creek	Upper James	02013000				
Maury River	Upper James	02024000				
James River	Upper James	02016500				

* denotes a reach where USGS gage flow time series were weighted by drainage area to the reach location.

+ denotes a reach where drainage areas were explicitly stated in the IFIM report so lat-long coordinates were not needed.

Table 3. Parameters used to describe the magnitude, shape, and functional relationship of discharge-WUA rating curves.

Parameter	Definition	Calculation
QP	Percentile flow associated with maximum habitat availability	Locate peak WUA value of standardized rating curve and identify the percentile flow at which this peak occurs.
SL	Slope of discharge-WUA rating curve preceding the peak	Slope from peak WUA to half the “distance” or discharge to the peak WUA.
SK	Skewness of the discharge-WUA rating curve	A measure of how far the mean of a distribution is from the median (Helsel and Hirsch, 2002). Positive skewness indicates a right-skewed distribution.
SD	Standard deviation of the discharge-WUA rating curve	A measure of spread of a distribution (Helsel and Hirsch, 2002).

Table 4. Average monthly habitat availability values for four clusters of site-species combinations (n=382) from twenty-three river reaches in Virginia.

	Group 1: Constant High (n=152)		Group 2: Seasonal Summer (n=101)		Group 3: Seasonal Spring (n=45)		Group 4: Constant Low (n=84)	
	Mean	Standard Deviation	Mean	Standard Deviation	Mean	Standard Deviation	Mean	Standard Deviation
J	0.79	± 0.11	0.46	± 0.09	0.62	± 0.13	0.17	± 0.08
F	0.76	± 0.14	0.38	± 0.10	0.69	± 0.12	0.14	± 0.07
M	0.72	± 0.18	0.32	± 0.11	0.74	± 0.12	0.12	± 0.07
A	0.75	± 0.16	0.34	± 0.10	0.71	± 0.13	0.12	± 0.07
M	0.79	± 0.13	0.40	± 0.09	0.63	± 0.13	0.14	± 0.08
J	0.83	± 0.08	0.57	± 0.09	0.43	± 0.13	0.21	± 0.11
J	0.83	± 0.11	0.70	± 0.09	0.31	± 0.11	0.29	± 0.14
A	0.81	± 0.13	0.74	± 0.08	0.27	± 0.11	0.33	± 0.15
S	0.79	± 0.15	0.78	± 0.08	0.24	± 0.11	0.37	± 0.16
O	0.80	± 0.13	0.75	± 0.08	0.28	± 0.11	0.34	± 0.15
N	0.82	± 0.10	0.67	± 0.08	0.39	± 0.12	0.28	± 0.13
D	0.81	± 0.09	0.54	± 0.08	0.54	± 0.12	0.21	± 0.10

Table 5. Summary statistics of habitat rating curve parameters calculated from habitat rating curves for each seasonal habitat regime and for all site-species combinations. Regimes were determined from a cluster analysis of average monthly habitat availability. Curve parameters are described in Table 3.

	Group 1: Constant High (n=152)		Group 2: Seasonal Summer (n=101)		Group 3: Seasonal Spring (n=45)		Group 4: Constant Low (n=84)		All Observations (n=427)	
	Median	Range	Median	Range	Median	Range	Median	Range	Median	Range
QP	29	(0 - 94)	7	(0 - 80)	79	(12 - 94)	0	(0 - 88)	14	(0 - 94)
SL	0.003	(0 - 0.154)	0.015	(0 - 0.134)	0.008	(0 - 0.099)	0	(0 - 0.136)	0.002	(0 - 0.154)
SK	0.17	(-0.86 - 1.37)	0.48	(-0.83 - 1.37)	-0.56	(-1.63 - 0.38)	0.61	(-1.00 - 3.33)	0.24	(-1.63 - 3.33)
SD	23.3	(4.9 - 27.6)	22.2	(13.4 - 27.1)	22.6	(9.3 - 27.3)	23.4	(5.8 - 31.0)	22.5	(4.9 - 31.0)

Table 6. Number of species at each site that fall in each seasonal habitat availability regime. Regimes were determined from a cluster analysis of 382 site-species combinations across all reaches.

Reach	Group 1: Constant High (n=152)	Group 2: Seasonal Summer (n=101)	Group 3: Seasonal Spring (n=45)	Group 4: Constant Low (n=84)
Above Harvell Dam	11	2	5	1
Claytor to Pembroke	18	11	0	17
Pembroke to Glen Lyn	15	14	0	17
North Anna Piedmont	5	4	5	1
North Anna Fall Zone	5	2	7	1
North Anna Coastal Plain	2	3	8	1
Pamunkey Coastal Plain	6	1	2	5
Plains Mill	3	1	0	1
Laurel Hill	0	4	0	1
Spring Hollow	0	4	0	1
Posey Hollow	2	1	0	1
Rt 648	2	1	0	1
T8&9	0	0	0	0
T11&12	0	0	0	0
Staunton	17	7	5	14
Head Kerr Lake	17	7	5	14
Lynwood	3	4	0	1
Luray	1	6	0	1
Front Royal	2	5	0	1
Dunlap	12	2	5	1
Craig	11	4	2	3
Maury	11	7	1	1
James	9	11	0	0

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Appendices: Supplemental Data

A. Species Codes

Table A.1. Flow-dependent biotic and abiotic factors for which habitat rating curves were developed. Scientific names from VDGIF (2012).

Code	Description	Scientific Name
alg_mid	Algae and Midge Guild	
as_fry	American shad, fry	<i>Alosa sapidissima</i>
as_juv	American Shad, juvenile lifestage	
as_spawn	American Shad, spawning lifestage	
bd_high_grad	Benthos Diversity, high gradient	
bd_low_grad	Benthos Diversity, low gradient	
benth_mac	Benthic Macroinvertebrates	
bg_adult	Bluegill, adult lifestage	<i>Lepomis macrochirus</i>
bg_fry	Bluegill, fry lifestage	
bg_juv	Bluegill, juvenile lifestage	
bg_spawn	Bluegill, spawning lifestage	
bj_adult	Black Jumprock, adult lifestage	<i>Moxostoma cervinum</i>
bj_juv	Black Jumprock, juvenile lifestage	
bmc_adult	Bigmouth Chub, adult lifestage	<i>Nocomis platyrhynchus</i>
bmc_spawn	Bigmouth Chub, spawning lifestage	
boat	Boat angling	
canoe	Canoe, non experience level specific	
canoe_mid	Canoe, middle experience level	
canoe_nov	Canoe, novice experience level	
cc_adult	Channel Catfish, adult lifestage	<i>Ictalurus punctatus</i>
cc_fry	Channel Catfish, fry lifestage	
cc_juv	Channel Catfish, juvenile lifestage	
cc_juv_fall	Channel catfish, fall juvenile	
cc_juv_summ	Channel catfish, summer juvenile	
cc_spawn	Channel Catfish, spawning lifestage	
cd_adult	composite Darter species, adult	<i>Percina</i>
cf	Crayfish	<i>Cambarus upenus</i>
chub_adult	Composite chub species, adult	
chub_spawn	Composite chub species, spawn	
chub_spp._spawn	Chub species (Bluehead and Bull), spawning	<i>Nocomis leptocephalus, raneyi</i>
cs_adult	Common Shiner, adult lifestage	<i>Luxilus cornutus</i>
cs_fry	Common Shiner, fry lifestage	
cs_juv	Common Shiner, juvenile lifestage	
cs_spawn	Common Shiner, spawning lifestage	
csr_adult	Central Stoneroller, adult lifestage	<i>Campostoma anomalum</i>
cyp	Cyprinella (several species of shiner)	<i>Cyprinella analostana, spiloptera</i>
deep_fast	Deep Guild fast	

deep_slow	Deep Guild slow	
e_comp	Eastern Elliptio mussel, Elliptio complanata	<i>Elliptio complanata</i>
eph_mac	Mayfly	<i>Ephemeroptera</i>
fast_gen	Fast Generalist guild	
ff_adult	Fallfish, adult lifestage	<i>Semotilus corporalis</i>
ff_juv	Fallfish, juvenile lifestage	
fhc_adult_summer	Flathead Catfish, adult lifestage in the Summer	<i>Pylodictis olivaris</i>
fhc_adult_winter	Flathead Catfish, adult lifestage in the Winter	
fhc_spawn	Flathead Catfish, spawning lifestage	
gd_adult	Greenside Darter, adult lifestage	<i>Etheostoma blennioides</i>
gd_juv	Greenside Darter, juvenile lifestage	
gd_spawn	Greenside Darter, spawning lifestage	
gs_adult	Gizzard Shad, adult lifestage	<i>Dorosoma cepedianum</i>
gs_fry	Gizzard Shad, fry lifestage	
gs_juv	Gizzard Shad, juvenile lifestage	
gs_spawn	Gizzard Shad, spawning lifestage	
l_rad	Eastern lampmussel	<i>Lampsilis radiata</i>
lmb_adult	Largemouth bass, adult	<i>Micropterus salmoides</i>
lmb_fry	Largemouth bass, fry	
lmb_juv	Largemouth bass, juvenile	
lmb_spawn	Largemouth bass, spawn	
lp_adult	Logperch, adult lifestage	<i>Percina caprodes</i>
lp_spawn	Logperch, spawning lifestage	
ml_adult_summer	Muskellunge, adult lifestage in the Summer	<i>Esox masquinongy</i>
ml_adult_winter	Muskellunge, adult lifestage in the Winter	
ml_spawn	Muskellunge, spawning lifestage	
mm	Margined madtom, all lifestages	<i>Noturus insignis</i>
nh_adult	Northern Hogsucker, adult lifestage	<i>Hypentelium nigricans</i>
nh_spawn	Northern Hogsucker, spawning lifestage	
nh_yoy	Northern Hogsucker, YoY lifestage	
plec_mac	Stonefly	<i>Plecoptera</i>
pool_cov	Pool-cover guild	
pool_run	Pool-run guild	
pwb	Purple Wartyback mussel	<i>Cyclonaias tuberculata</i>
rb_adult	Rock Bass, adult lifestage	<i>Ambloplites rupestris</i>
rb_fry	Rock Bass, fry lifestage	
rb_juv	Rock Bass, juvenile lifestage	
rb_spawn	Rock Bass, spawning lifestage	
rb_yoy	Rock Bass, YoY lifestage	
rbs_adult	Redbreast Sunfish, adult lifestage	<i>Lepomis auritus</i>
rbs_fry	Redbreast Sunfish, fry lifestage	
rbs_juv	Redbreast Sunfish, juvenile lifestage	
rbs_sub_adult	Redbreast Sunfish, sub	

rbs_spawn	Redbreast Sunfish, spawning lifestage	
rc	River Chub, all lifestages	<i>Nocomis micropogon</i>
rfs_adult	Rosefin Shiner, adult lifestage	<i>Lythrurus ardens</i>
rfs_yoy	Rosefin Shiner, YoY lifestage	
rh_spawn	River Herring, spawning lifestage	
rhg_adult	Golden Redhorse, adult	<i>Moxostoma erythrurum</i>
rhg_juv	Golden Redhorse, juvenile	
rhg_yoy	Golden Redhorse, year of young	
rhsh_adult	Shorthead Redhorse, adult	<i>Moxostoma macrolepidotum</i>
rhsh_juv	Shorthead Redhorse, juvenile	
rhsh_spawn	Shorthead redhorse, spawn	
rhsh_yoy	Shorthead redhorse, year of young	
rhsi_adult	Silver redhorse, adult	<i>Moxostoma anisurum</i>
rhsi_yoy	Silver redhorse, year of young	
riffle	Riffle Guild	
shallow_fast	Shallow Guild fast	
shallow_slow	Shallow Guild slow	
sm_shal_slow	Spike Mussel, Shallow	<i>Elliptio dilatata</i>
sm_int	Spike Mussel, Intermediate	
smb_adult	Smallmouth Bass, adult lifestage	<i>Micropterus dolomieu</i>
smb_fry	Smallmouth Bass, fry lifestage	
smb_inc	Smallmouth Bass, incubation lifestage	
smb_juv	Smallmouth Bass, juvenile lifestage	
smb_sub_adult	Smallmouth Bass, sub	
smb_spawn	Smallmouth Bass, spawning lifestage	
smb_yoy	Smallmouth Bass, YoY lifestage	
spb_adult	Spotted bass, adult	<i>Micropterus punctulatus</i>
spb_fry	Spotted bass, fry	
spb_juv	Spotted bass, juvenile	
spb_spawn	Spotted bass, spawn	
stb_adult	Striped bass, adult	<i>Morone saxatilis</i>
stb_fry	Striped bass, fry	
stb_juv	Striped bass, juvenile	
stb_spawn	Striped bass, spawn	
tric_mac	Caddisfly	<i>Trichoptera</i>
we_adult	Walleye, adult lifestage	<i>Sander vitreus vitreus</i>
we_fry	Walleye, fry lifestage	
we_juv	Walleye, juvenile lifestage	
we_spawn	Walleye, spawning lifestage	
ws_adult	White Sucker, adult lifestage	<i>Catostomus commersoni</i>
ws_fry	White Sucker, fry lifestage	
ws_juv	White Sucker, juvenile lifestage	
ws_spawn	White Sucker, spawning lifestage	

B. Habitat Metrics for All Site-Species Combinations

Table B.1. Habitat metrics calculated for all site-species combinations (n=428). Flow response metrics are calculated from habitat rating curves and are described in Table 3. Average monthly habitat availability is calculated from modelled habitat time series.

Species/Lifestage/ Recreational Use*	Reach	Average Monthly Habitat Availability (Percent of Maximum WUA)												Flow Response Metrics			
		J	F	M	A	M	J	J	A	S	O	N	D	QP	SL	SK	SD
smb_juv	Above Harvell Dam	0.987	0.989	0.991	0.992	0.983	0.939	0.887	0.856	0.832	0.873	0.941	0.964	42	0.003	-0.12	15.0
smb_adult	Above Harvell Dam	0.956	0.951	0.944	0.941	0.962	0.967	0.964	0.944	0.939	0.955	0.968	0.961	23	0.006	0.00	15.0
smb_spawn	Above Harvell Dam	0.385	0.364	0.340	0.328	0.413	0.596	0.753	0.791	0.855	0.775	0.588	0.491	7	0.004	0.54	14.0
rbs_spawn	Above Harvell Dam	0.557	0.536	0.510	0.498	0.586	0.744	0.862	0.883	0.924	0.874	0.737	0.653	15	0.004	0.35	14.5
nh_adult	Above Harvell Dam	0.730	0.758	0.791	0.806	0.697	0.513	0.373	0.333	0.284	0.350	0.520	0.617	53	0.013	-0.66	13.6
nh_spawn	Above Harvell Dam	0.693	0.720	0.753	0.771	0.661	0.505	0.389	0.355	0.314	0.371	0.513	0.596	53	0.014	-0.56	14.2
bd_high_grad	Above Harvell Dam	0.696	0.674	0.636	0.612	0.731	0.781	0.781	0.758	0.770	0.773	0.770	0.748	31	0.016	0.01	14.3
bd_low_grad	Above Harvell Dam	0.476	0.458	0.434	0.421	0.501	0.608	0.685	0.706	0.729	0.698	0.603	0.546	0	0.000	0.28	14.7
shallow_slow	Above Harvell Dam	0.317	0.296	0.269	0.254	0.346	0.455	0.533	0.549	0.579	0.546	0.448	0.391	0	0.000	0.34	14.0
shallow_fast	Above Harvell Dam	0.794	0.776	0.750	0.741	0.811	0.764	0.671	0.609	0.544	0.640	0.771	0.772	31	0.020	-0.19	12.9
deep_slow	Above Harvell Dam	0.980	0.980	0.980	0.980	0.980	0.957	0.926	0.907	0.891	0.916	0.959	0.969	39	0.003	-0.07	15.2
deep_fast	Above Harvell Dam	0.973	0.973	0.975	0.976	0.970	0.894	0.796	0.741	0.693	0.771	0.899	0.938	39	0.007	-0.22	14.2
as_spawn	Above Harvell Dam	0.616	0.655	0.701	0.722	0.568	0.339	0.174	0.139	0.086	0.152	0.346	0.470	53	0.018	-0.78	9.3
as_juv	Above Harvell Dam	0.993	0.993	0.993	0.994	0.992	0.975	0.949	0.922	0.909	0.938	0.977	0.986	39	0.001	-0.06	15.0
l_rad	Above Harvell Dam	0.674	0.708	0.748	0.767	0.631	0.417	0.260	0.221	0.168	0.237	0.425	0.540	53	0.016	-0.88	11.9
e_comp	Above Harvell Dam	0.839	0.862	0.887	0.898	0.809	0.618	0.450	0.398	0.333	0.422	0.624	0.727	53	0.009	-0.60	13.1
rh_spawn	Above Harvell Dam	0.993	0.993	0.994	0.994	0.993	0.979	0.960	0.948	0.939	0.955	0.979	0.987	39	0.001	-0.04	15.3
canoe_nov	Above Harvell Dam	0.954	0.961	0.968	0.971	0.945	0.870	0.793	0.758	0.723	0.776	0.874	0.914	53	0.003	-0.19	15.0
canoe_mid	Above Harvell Dam	0.867	0.881	0.897	0.905	0.850	0.752	0.672	0.644	0.614	0.657	0.756	0.809	53	0.006	-0.26	15.2
rb_fry	Claytor to Pembroke	0.199	0.170	0.156	0.159	0.169	0.206	0.252	0.304	0.337	0.324	0.282	0.234	0	0.000	0.67	28.6
rb_juv	Claytor to Pembroke	0.191	0.158	0.141	0.147	0.164	0.204	0.250	0.299	0.328	0.316	0.275	0.227	0	0.000	0.69	27.3
rb_adult	Claytor to Pembroke	0.282	0.230	0.200	0.214	0.246	0.309	0.378	0.437	0.472	0.456	0.404	0.335	0	0.000	0.63	26.1
rb_spawn	Claytor to Pembroke	0.351	0.283	0.239	0.258	0.305	0.391	0.486	0.552	0.587	0.570	0.506	0.419	0	0.000	0.65	25.2
smb_fry	Claytor to Pembroke	0.296	0.224	0.179	0.198	0.243	0.334	0.436	0.513	0.556	0.535	0.464	0.369	0	0.000	0.80	24.0
smb_juv	Claytor to Pembroke	0.547	0.453	0.391	0.424	0.496	0.612	0.728	0.796	0.830	0.811	0.740	0.634	0	0.000	0.49	25.0
smb_adult	Claytor to Pembroke	0.668	0.571	0.506	0.547	0.631	0.747	0.852	0.894	0.914	0.902	0.846	0.749	14	0.002	0.35	24.9
smb_spawn	Claytor to Pembroke	0.172	0.127	0.104	0.112	0.131	0.186	0.252	0.322	0.365	0.347	0.290	0.222	0	0.000	1.02	25.1
fhc_adult_summer	Claytor to Pembroke	0.219	0.179	0.156	0.165	0.188	0.238	0.295	0.348	0.380	0.366	0.320	0.262	0	0.000	0.70	26.6
fhc_adult_winter	Claytor to Pembroke	0.244	0.201	0.177	0.187	0.211	0.264	0.324	0.382	0.415	0.401	0.352	0.291	0	0.000	0.67	26.9
fhc_spawn	Claytor to Pembroke	0.201	0.162	0.141	0.149	0.170	0.218	0.274	0.329	0.361	0.347	0.301	0.244	0	0.000	0.76	26.6

cc_juv	Claytor to Pembroke	0.848	0.848	0.855	0.873	0.899	0.885	0.858	0.801	0.758	0.772	0.804	0.834	60	0.001	-0.10	25.8
cc_adult	Claytor to Pembroke	0.917	0.907	0.903	0.917	0.941	0.943	0.940	0.913	0.894	0.900	0.912	0.917	56	0.001	-0.01	27.1
cc_spawn	Claytor to Pembroke	0.632	0.546	0.487	0.518	0.588	0.697	0.805	0.859	0.886	0.870	0.808	0.711	7	0.001	0.41	26.0
ml_adult_summer	Claytor to Pembroke	0.482	0.375	0.303	0.338	0.417	0.554	0.695	0.775	0.818	0.793	0.712	0.583	7	0.003	0.63	23.6
ml_adult_winter	Claytor to Pembroke	0.510	0.401	0.329	0.365	0.446	0.584	0.726	0.800	0.840	0.819	0.737	0.610	7	0.003	0.59	23.7
ml_spawn	Claytor to Pembroke	0.218	0.205	0.204	0.203	0.203	0.215	0.231	0.272	0.298	0.289	0.262	0.236	0	0.000	0.34	30.5
rbs_fry	Claytor to Pembroke	0.277	0.238	0.216	0.225	0.247	0.295	0.350	0.402	0.433	0.420	0.375	0.319	0	0.000	0.55	27.6
rbs_juv	Claytor to Pembroke	0.418	0.331	0.276	0.301	0.361	0.471	0.589	0.668	0.712	0.690	0.613	0.504	0	0.000	0.66	24.7
rbs_adult	Claytor to Pembroke	0.434	0.344	0.285	0.314	0.379	0.492	0.611	0.688	0.730	0.709	0.631	0.522	0	0.000	0.62	24.3
bmc_adult	Claytor to Pembroke	0.763	0.685	0.631	0.671	0.751	0.840	0.915	0.922	0.922	0.919	0.888	0.823	29	0.002	0.22	25.2
bmc_spawn	Claytor to Pembroke	0.530	0.415	0.330	0.375	0.476	0.625	0.775	0.833	0.861	0.842	0.764	0.635	24	0.001	0.49	22.2
gd_juv	Claytor to Pembroke	0.547	0.436	0.357	0.398	0.490	0.633	0.772	0.838	0.871	0.851	0.774	0.648	14	0.002	0.51	23.3
gd_adult	Claytor to Pembroke	0.818	0.753	0.711	0.751	0.826	0.890	0.934	0.919	0.908	0.910	0.899	0.860	38	0.001	0.12	25.3
gd_spawn	Claytor to Pembroke	0.837	0.828	0.831	0.854	0.890	0.881	0.857	0.799	0.758	0.772	0.803	0.828	60	0.001	-0.10	25.4
lp_adult	Claytor to Pembroke	0.903	0.889	0.883	0.900	0.928	0.935	0.936	0.907	0.886	0.892	0.903	0.906	52	0.001	0.00	26.8
lp_spawn	Claytor to Pembroke	0.765	0.798	0.839	0.841	0.836	0.771	0.680	0.599	0.544	0.564	0.631	0.712	73	0.001	-0.34	24.7
cs_fry	Claytor to Pembroke	0.268	0.207	0.173	0.184	0.215	0.293	0.385	0.467	0.517	0.496	0.425	0.335	0	0.000	0.87	25.6
cs_juv	Claytor to Pembroke	0.274	0.223	0.194	0.205	0.233	0.297	0.370	0.437	0.477	0.460	0.402	0.329	0	0.000	0.70	26.4
cs_adult	Claytor to Pembroke	0.542	0.445	0.381	0.416	0.492	0.610	0.729	0.795	0.829	0.810	0.738	0.631	0	0.000	0.48	24.6
cs_spawn	Claytor to Pembroke	0.453	0.337	0.257	0.294	0.381	0.532	0.694	0.780	0.824	0.799	0.706	0.563	7	0.001	0.67	22.1
nh_yoy	Claytor to Pembroke	0.380	0.289	0.228	0.251	0.310	0.430	0.565	0.656	0.707	0.681	0.593	0.472	0	0.000	0.81	24.0
nh_adult	Claytor to Pembroke	0.890	0.897	0.909	0.918	0.932	0.911	0.879	0.827	0.787	0.801	0.835	0.870	63	0.001	-0.11	26.4
nh_spawn	Claytor to Pembroke	0.694	0.607	0.545	0.591	0.686	0.788	0.878	0.878	0.873	0.871	0.838	0.762	29	0.003	0.25	24.1
we_fry	Claytor to Pembroke	0.120	0.118	0.118	0.118	0.118	0.119	0.121	0.133	0.140	0.138	0.129	0.124	0	0.000	0.16	31.0
we_juv	Claytor to Pembroke	0.199	0.171	0.156	0.162	0.176	0.210	0.250	0.295	0.321	0.311	0.276	0.231	0	0.000	0.59	28.0
we_adult	Claytor to Pembroke	0.237	0.200	0.180	0.188	0.207	0.252	0.305	0.361	0.394	0.380	0.334	0.279	0	0.000	0.63	27.4
we_spawn	Claytor to Pembroke	0.722	0.771	0.820	0.813	0.791	0.708	0.596	0.514	0.459	0.484	0.559	0.655	78	0.001	-0.44	24.5
shallow_fast	Claytor to Pembroke	0.580	0.471	0.395	0.438	0.531	0.668	0.802	0.851	0.876	0.861	0.793	0.675	19	0.002	0.45	23.4
eph_mac	Claytor to Pembroke	0.736	0.655	0.600	0.636	0.708	0.803	0.889	0.920	0.936	0.926	0.882	0.804	14	0.001	0.28	25.9
plec_mac	Claytor to Pembroke	0.731	0.645	0.586	0.625	0.702	0.803	0.892	0.925	0.939	0.930	0.884	0.802	14	0.001	0.29	25.6
tric_mac	Claytor to Pembroke	0.832	0.769	0.727	0.760	0.823	0.890	0.944	0.949	0.952	0.948	0.927	0.878	24	0.001	0.17	26.2
pwb	Claytor to Pembroke	0.441	0.341	0.274	0.307	0.383	0.508	0.642	0.716	0.756	0.735	0.654	0.536	0	0.000	0.59	23.1
sm_shal_slow	Claytor to Pembroke	0.750	0.706	0.682	0.727	0.804	0.831	0.843	0.780	0.733	0.748	0.764	0.765	47	0.003	-0.04	23.8
sm_int	Claytor to Pembroke	0.767	0.701	0.659	0.699	0.781	0.847	0.899	0.876	0.860	0.862	0.851	0.811	38	0.002	0.14	24.7
cf	Claytor to Pembroke	0.242	0.170	0.132	0.148	0.185	0.271	0.371	0.471	0.531	0.506	0.422	0.319	0	0.000	0.98	22.7
rb_fry	Pembroke to Glen Lyn	0.167	0.154	0.150	0.150	0.153	0.174	0.212	0.246	0.285	0.273	0.232	0.191	0	0.000	0.52	28.9
rb_juv	Pembroke to Glen Lyn	0.153	0.134	0.123	0.127	0.137	0.170	0.213	0.245	0.281	0.268	0.227	0.182	0	0.000	0.62	27.4

rb_adult	Pembroke to Glen Lyn	0.219	0.183	0.159	0.170	0.194	0.257	0.327	0.370	0.418	0.398	0.340	0.270	0	0.000	0.65	25.7
rb_spawn	Pembroke to Glen Lyn	0.266	0.216	0.181	0.195	0.228	0.321	0.422	0.476	0.535	0.506	0.431	0.338	0	0.000	0.73	24.8
smb_fry	Pembroke to Glen Lyn	0.208	0.159	0.126	0.138	0.168	0.260	0.365	0.425	0.492	0.461	0.380	0.282	0	0.000	0.90	23.7
smb_juv	Pembroke to Glen Lyn	0.426	0.347	0.286	0.316	0.378	0.520	0.657	0.716	0.780	0.745	0.653	0.530	0	0.000	0.60	24.1
smb_adult	Pembroke to Glen Lyn	0.539	0.446	0.369	0.411	0.493	0.657	0.797	0.841	0.889	0.856	0.775	0.652	5	0.002	0.48	23.7
smb_spawn	Pembroke to Glen Lyn	0.120	0.097	0.086	0.090	0.100	0.139	0.196	0.244	0.298	0.280	0.222	0.160	0	0.000	0.95	25.7
fhc_adult_summer	Pembroke to Glen Lyn	0.170	0.145	0.129	0.135	0.150	0.196	0.252	0.288	0.329	0.313	0.264	0.209	0	0.000	0.68	26.6
fhc_adult_winter	Pembroke to Glen Lyn	0.192	0.166	0.149	0.156	0.171	0.219	0.277	0.317	0.361	0.344	0.292	0.233	0	0.000	0.64	26.8
fhc_spawn	Pembroke to Glen Lyn	0.155	0.132	0.119	0.123	0.136	0.177	0.230	0.267	0.308	0.293	0.245	0.191	0	0.000	0.72	26.8
cc_juv	Pembroke to Glen Lyn	0.844	0.818	0.787	0.827	0.874	0.903	0.900	0.854	0.812	0.818	0.843	0.855	48	0.001	0.02	25.0
cc_adult	Pembroke to Glen Lyn	0.901	0.873	0.847	0.873	0.911	0.946	0.957	0.937	0.920	0.920	0.926	0.921	44	0.001	0.05	26.2
cc_spawn	Pembroke to Glen Lyn	0.520	0.445	0.388	0.415	0.474	0.610	0.741	0.792	0.848	0.813	0.731	0.617	2	0.001	0.50	25.4
ml_adult_summer	Pembroke to Glen Lyn	0.347	0.262	0.201	0.227	0.287	0.443	0.606	0.681	0.762	0.717	0.607	0.463	2	0.003	0.79	22.7
ml_adult_winter	Pembroke to Glen Lyn	0.372	0.284	0.220	0.248	0.312	0.474	0.640	0.712	0.790	0.746	0.638	0.492	2	0.003	0.75	22.7
ml_spawn	Pembroke to Glen Lyn	0.205	0.202	0.201	0.202	0.203	0.204	0.209	0.228	0.251	0.248	0.228	0.211	0	0.000	0.15	29.5
rbs_fry	Pembroke to Glen Lyn	0.230	0.206	0.191	0.197	0.211	0.255	0.307	0.343	0.383	0.368	0.321	0.268	0	0.000	0.50	27.4
rbs_juv	Pembroke to Glen Lyn	0.310	0.245	0.201	0.219	0.263	0.382	0.511	0.577	0.650	0.614	0.520	0.402	0	0.000	0.76	24.2
rbs_adult	Pembroke to Glen Lyn	0.320	0.250	0.199	0.221	0.272	0.400	0.534	0.599	0.671	0.633	0.538	0.417	0	0.000	0.75	23.6
bmc_adult	Pembroke to Glen Lyn	0.658	0.567	0.488	0.535	0.623	0.776	0.892	0.908	0.932	0.909	0.853	0.756	19	0.002	0.35	24.1
bmc_spawn	Pembroke to Glen Lyn	0.382	0.274	0.192	0.229	0.310	0.509	0.698	0.760	0.833	0.783	0.672	0.516	15	0.001	0.68	20.5
gd_juv	Pembroke to Glen Lyn	0.401	0.303	0.227	0.262	0.339	0.519	0.694	0.757	0.829	0.786	0.677	0.528	5	0.002	0.68	21.9
gd_adult	Pembroke to Glen Lyn	0.729	0.643	0.563	0.618	0.711	0.848	0.934	0.930	0.934	0.920	0.887	0.814	28	0.001	0.25	24.1
gd_spawn	Pembroke to Glen Lyn	0.820	0.777	0.737	0.785	0.850	0.896	0.897	0.851	0.810	0.816	0.838	0.843	48	0.001	0.02	24.4
lp_adult	Pembroke to Glen Lyn	0.883	0.849	0.818	0.847	0.891	0.936	0.953	0.933	0.915	0.914	0.918	0.908	40	0.001	0.07	26.0
lp_spawn	Pembroke to Glen Lyn	0.800	0.805	0.811	0.841	0.864	0.831	0.753	0.682	0.609	0.634	0.705	0.770	61	0.001	-0.19	24.0
cs_fry	Pembroke to Glen Lyn	0.197	0.162	0.144	0.149	0.164	0.228	0.313	0.374	0.446	0.417	0.340	0.255	0	0.000	0.84	26.1
cs_juv	Pembroke to Glen Lyn	0.213	0.182	0.163	0.170	0.188	0.244	0.314	0.362	0.416	0.395	0.333	0.262	0	0.000	0.68	26.5
cs_adult	Pembroke to Glen Lyn	0.416	0.333	0.269	0.300	0.367	0.516	0.658	0.717	0.780	0.744	0.651	0.525	0	0.000	0.60	23.4
cs_spawn	Pembroke to Glen Lyn	0.306	0.215	0.149	0.175	0.238	0.411	0.594	0.676	0.766	0.716	0.593	0.435	2	0.001	0.89	20.8
nh_yoy	Pembroke to Glen Lyn	0.270	0.205	0.167	0.180	0.213	0.333	0.473	0.551	0.641	0.595	0.491	0.364	0	0.000	0.93	23.9
nh_adult	Pembroke to Glen Lyn	0.895	0.884	0.871	0.896	0.924	0.933	0.917	0.878	0.837	0.845	0.875	0.895	51	0.001	-0.02	25.7
nh_spawn	Pembroke to Glen Lyn	0.578	0.476	0.389	0.437	0.535	0.716	0.856	0.869	0.897	0.867	0.803	0.690	19	0.003	0.42	22.8
we_fry	Pembroke to Glen Lyn	0.118	0.118	0.118	0.118	0.118	0.117	0.117	0.120	0.123	0.124	0.120	0.118	0	0.000	0.04	29.5
we_juv	Pembroke to Glen Lyn	0.166	0.149	0.139	0.143	0.153	0.182	0.217	0.245	0.276	0.265	0.230	0.191	0	0.000	0.50	27.8
we_adult	Pembroke to Glen Lyn	0.192	0.170	0.156	0.162	0.176	0.215	0.262	0.298	0.339	0.325	0.279	0.227	0	0.000	0.56	27.2
we_spawn	Pembroke to Glen Lyn	0.777	0.798	0.818	0.839	0.845	0.780	0.674	0.600	0.523	0.555	0.640	0.727	66	0.001	-0.29	23.8
shallow_fast	Pembroke to Glen Lyn	0.440	0.337	0.257	0.296	0.378	0.562	0.734	0.788	0.853	0.813	0.712	0.567	10	0.002	0.62	22.1

eph_mac	Pembroke to Glen Lyn	0.628	0.545	0.477	0.516	0.590	0.730	0.846	0.880	0.918	0.891	0.825	0.723	5	0.001	0.38	24.9
plec_mac	Pembroke to Glen Lyn	0.615	0.526	0.453	0.495	0.575	0.726	0.848	0.882	0.920	0.894	0.824	0.717	5	0.001	0.39	24.5
tric_mac	Pembroke to Glen Lyn	0.746	0.671	0.606	0.647	0.722	0.842	0.927	0.938	0.956	0.940	0.899	0.824	15	0.001	0.26	25.2
pwb	Pembroke to Glen Lyn	0.313	0.232	0.170	0.198	0.258	0.408	0.558	0.626	0.699	0.659	0.557	0.423	0	0.000	0.75	21.7
sm_shal_slow	Pembroke to Glen Lyn	0.686	0.607	0.531	0.595	0.698	0.824	0.879	0.835	0.795	0.789	0.792	0.754	36	0.003	0.15	22.5
sm_int	Pembroke to Glen Lyn	0.680	0.593	0.513	0.565	0.659	0.805	0.902	0.894	0.897	0.880	0.846	0.769	28	0.002	0.29	23.6
cf	Pembroke to Glen Lyn	0.157	0.114	0.088	0.099	0.124	0.199	0.292	0.359	0.435	0.408	0.321	0.223	0	0.000	1.02	22.3
smb_juv	North Anna Piedmont	0.889	0.923	0.929	0.921	0.897	0.844	0.812	0.806	0.801	0.799	0.821	0.878	77	0.004	-0.13	26.6
smb_adult	North Anna Piedmont	0.896	0.890	0.873	0.905	0.922	0.970	0.982	0.982	0.986	0.982	0.961	0.927	49	0.008	0.06	26.1
smb_spawn	North Anna Piedmont	0.355	0.241	0.182	0.268	0.370	0.627	0.760	0.774	0.793	0.796	0.683	0.450	0	0.000	0.37	19.3
nh_adult	North Anna Piedmont	0.423	0.503	0.560	0.469	0.387	0.206	0.132	0.126	0.119	0.118	0.184	0.337	94	0.003	-1.16	22.5
nh_spawn	North Anna Piedmont	0.367	0.458	0.418	0.493	0.444	0.316	0.243	0.232	0.221	0.221	0.249	0.409	61	0.062	-0.90	20.3
rbs_spawn	North Anna Piedmont	0.488	0.372	0.303	0.413	0.522	0.785	0.906	0.912	0.926	0.928	0.822	0.593	1	0.007	0.34	20.9
shallow_slow	North Anna Piedmont	0.088	0.048	0.031	0.041	0.075	0.157	0.218	0.240	0.254	0.259	0.209	0.123	0	0.000	1.00	16.8
shallow_fast	North Anna Piedmont	0.325	0.239	0.198	0.325	0.391	0.646	0.704	0.691	0.683	0.677	0.562	0.383	54	0.088	0.16	17.7
deep_slow	North Anna Piedmont	0.893	0.896	0.876	0.912	0.918	0.923	0.917	0.912	0.910	0.910	0.909	0.913	59	0.007	-0.01	26.1
deep_fast	North Anna Piedmont	0.710	0.768	0.757	0.798	0.768	0.679	0.611	0.591	0.575	0.577	0.607	0.726	61	0.023	-0.32	24.4
l_rad	North Anna Piedmont	0.465	0.571	0.649	0.529	0.420	0.182	0.089	0.084	0.076	0.074	0.158	0.361	87	0.014	-1.58	18.3
e_comp	North Anna Piedmont	0.645	0.755	0.811	0.736	0.640	0.399	0.275	0.263	0.246	0.243	0.344	0.569	81	0.011	-0.90	22.8
benth_mac	North Anna Piedmont	0.379	0.227	0.161	0.266	0.399	0.729	0.893	0.907	0.924	0.925	0.783	0.486	1	0.033	0.19	17.7
canoe_nov	North Anna Piedmont	0.787	0.835	0.863	0.824	0.778	0.671	0.616	0.606	0.597	0.595	0.642	0.740	94	0.001	-0.28	26.8
canoe_mid	North Anna Piedmont	0.585	0.634	0.669	0.614	0.565	0.454	0.406	0.402	0.396	0.395	0.438	0.528	94	0.003	-0.39	27.3
smb_juv	North Anna Fall Zone	0.779	0.845	0.862	0.847	0.800	0.667	0.590	0.578	0.567	0.563	0.619	0.751	75	0.007	-0.36	25.4
smb_adult	North Anna Fall Zone	0.847	0.895	0.894	0.898	0.872	0.797	0.748	0.736	0.729	0.724	0.753	0.840	75	0.004	-0.20	25.6
smb_spawn	North Anna Fall Zone	0.557	0.443	0.363	0.480	0.595	0.859	0.976	0.979	0.989	0.990	0.885	0.664	1	0.015	0.35	21.6
nh_adult	North Anna Fall Zone	0.499	0.600	0.679	0.563	0.457	0.217	0.120	0.113	0.103	0.102	0.189	0.393	91	0.006	-1.39	20.2
nh_spawn	North Anna Fall Zone	0.604	0.718	0.745	0.696	0.616	0.403	0.297	0.289	0.278	0.275	0.349	0.557	79	0.013	-0.81	23.7
rbs_spawn	North Anna Fall Zone	0.640	0.547	0.469	0.587	0.687	0.906	0.990	0.991	0.995	0.995	0.917	0.734	4	0.000	0.27	22.7
shallow_slow	North Anna Fall Zone	0.120	0.096	0.082	0.102	0.124	0.177	0.205	0.211	0.209	0.213	0.188	0.141	0	0.000	0.55	23.7
shallow_fast	North Anna Fall Zone	0.396	0.355	0.312	0.428	0.482	0.611	0.619	0.600	0.584	0.579	0.531	0.448	59	0.027	-0.04	20.2
deep_slow	North Anna Fall Zone	0.822	0.831	0.803	0.858	0.863	0.871	0.855	0.844	0.841	0.841	0.837	0.849	59	0.013	-0.04	25.4
deep_fast	North Anna Fall Zone	0.634	0.742	0.781	0.730	0.645	0.419	0.302	0.291	0.276	0.272	0.361	0.580	75	0.017	-0.82	23.1
l_rad	North Anna Fall Zone	0.443	0.541	0.626	0.499	0.395	0.163	0.077	0.072	0.066	0.065	0.144	0.337	91	0.008	-1.63	18.4
e_comp	North Anna Fall Zone	0.620	0.718	0.784	0.693	0.599	0.372	0.262	0.252	0.240	0.237	0.331	0.533	88	0.006	-0.88	23.7
benth_mac	North Anna Fall Zone	0.384	0.249	0.171	0.272	0.399	0.712	0.879	0.890	0.915	0.915	0.771	0.486	4	0.024	0.25	18.1
canoe_nov	North Anna Fall Zone	0.718	0.789	0.836	0.775	0.705	0.545	0.464	0.454	0.442	0.440	0.508	0.653	92	0.002	-0.48	26.2
canoe_mid	North Anna Fall Zone	0.496	0.551	0.604	0.532	0.470	0.336	0.279	0.273	0.266	0.265	0.315	0.431	94	0.004	-0.61	26.5

nh_adult	North Anna Coastal Plain	0.667	0.772	0.824	0.754	0.616	0.376	0.210	0.161	0.144	0.205	0.376	0.590	83	0.007	-1.00	20.3
nh_spawn	North Anna Coastal Plain	0.391	0.416	0.407	0.473	0.478	0.347	0.240	0.197	0.178	0.218	0.271	0.412	61	0.048	-0.90	18.6
rbs_spawn	North Anna Coastal Plain	0.327	0.246	0.203	0.254	0.364	0.560	0.725	0.780	0.807	0.737	0.578	0.397	0	0.075	0.65	20.9
shallow_slow	North Anna Coastal Plain	0.106	0.076	0.069	0.076	0.105	0.192	0.324	0.401	0.451	0.360	0.229	0.130	0	0.000	1.38	21.0
shallow_fast	North Anna Coastal Plain	0.348	0.220	0.138	0.203	0.329	0.565	0.716	0.729	0.712	0.686	0.581	0.357	34	0.133	0.00	13.4
deep_slow	North Anna Coastal Plain	0.661	0.599	0.562	0.636	0.728	0.844	0.860	0.853	0.840	0.845	0.793	0.710	48	0.024	0.20	23.6
deep_fast	North Anna Coastal Plain	0.626	0.666	0.677	0.710	0.679	0.544	0.412	0.367	0.342	0.393	0.469	0.621	61	0.028	-0.54	22.4
as_juv	North Anna Coastal Plain	0.872	0.871	0.870	0.892	0.897	0.886	0.837	0.808	0.784	0.816	0.846	0.871	48	0.034	-0.05	25.5
as_spawn	North Anna Coastal Plain	0.367	0.442	0.490	0.415	0.298	0.147	0.063	0.042	0.036	0.062	0.166	0.294	93	0.005	-1.36	16.8
l_rad	North Anna Coastal Plain	0.688	0.782	0.824	0.774	0.659	0.444	0.269	0.217	0.192	0.261	0.420	0.627	79	0.011	-0.84	20.9
e_comp	North Anna Coastal Plain	0.769	0.828	0.854	0.840	0.773	0.619	0.461	0.406	0.375	0.443	0.571	0.734	76	0.008	-0.51	23.3
benth_mac	North Anna Coastal Plain	0.301	0.172	0.112	0.178	0.335	0.638	0.822	0.861	0.862	0.806	0.636	0.369	34	0.045	0.14	15.4
canoe_nov	North Anna Coastal Plain	0.726	0.785	0.817	0.776	0.694	0.557	0.450	0.414	0.398	0.443	0.550	0.675	93	0.002	-0.48	25.5
canoe_mid	North Anna Coastal Plain	0.542	0.606	0.641	0.591	0.503	0.370	0.276	0.247	0.236	0.272	0.371	0.489	93	0.004	-0.67	24.9
nh_adult	Pamunkey Coastal Plain	0.911	0.931	0.941	0.937	0.886	0.748	0.573	0.500	0.443	0.536	0.733	0.859	73	0.003	-0.30	23.2
nh_spawn	Pamunkey Coastal Plain	0.104	0.035	0.012	0.036	0.178	0.484	0.628	0.578	0.568	0.554	0.467	0.236	22	0.046	0.42	12.2
rbs_spawn	Pamunkey Coastal Plain	0.112	0.073	0.056	0.079	0.160	0.381	0.590	0.646	0.694	0.608	0.389	0.199	1	0.095	1.10	17.4
shallow_slow	Pamunkey Coastal Plain	0.012	0.012	0.011	0.012	0.013	0.028	0.071	0.116	0.168	0.108	0.034	0.015	0	0.000	2.40	17.8
shallow_fast	Pamunkey Coastal Plain	0.015	0.014	0.014	0.013	0.014	0.075	0.302	0.409	0.447	0.334	0.108	0.023	8	0.068	3.33	13.7
deep_slow	Pamunkey Coastal Plain	0.652	0.589	0.540	0.621	0.733	0.856	0.906	0.892	0.881	0.879	0.844	0.736	17	0.017	0.24	23.8
deep_fast	Pamunkey Coastal Plain	0.370	0.295	0.250	0.316	0.471	0.687	0.743	0.680	0.651	0.670	0.662	0.491	22	0.042	0.61	20.6
as_juv	Pamunkey Coastal Plain	0.907	0.896	0.886	0.901	0.923	0.950	0.969	0.968	0.964	0.962	0.950	0.925	17	0.000	0.06	26.6
as_spawn	Pamunkey Coastal Plain	0.760	0.825	0.861	0.807	0.667	0.433	0.253	0.206	0.163	0.237	0.440	0.642	82	0.004	-0.60	19.8
l_rad	Pamunkey Coastal Plain	0.685	0.643	0.594	0.701	0.779	0.726	0.553	0.461	0.412	0.502	0.673	0.713	48	0.013	-0.10	20.0
e_comp	Pamunkey Coastal Plain	0.688	0.623	0.567	0.670	0.792	0.844	0.774	0.710	0.675	0.729	0.802	0.760	41	0.009	0.08	22.1
benth_mac	Pamunkey Coastal Plain	0.003	0.002	0.002	0.002	0.003	0.009	0.068	0.147	0.226	0.137	0.013	0.004	1	0.136	2.39	5.8
canoe_nov	Pamunkey Coastal Plain	0.916	0.935	0.945	0.927	0.891	0.819	0.729	0.686	0.651	0.705	0.815	0.883	87	0.001	-0.18	25.8
canoe_mid	Pamunkey Coastal Plain	0.652	0.686	0.710	0.671	0.606	0.510	0.425	0.392	0.364	0.408	0.512	0.599	94	0.001	-0.35	25.5
riffle	Plains Mill	0.557	0.499	0.363	0.437	0.555	0.742	0.656	0.546	0.517	0.505	0.580	0.560	37	0.112	0.10	18.3
fast_gen	Plains Mill	0.633	0.604	0.489	0.576	0.663	0.733	0.589	0.499	0.477	0.476	0.567	0.615	53	0.023	-0.10	18.6
pool_run	Plains Mill	0.693	0.661	0.545	0.622	0.710	0.795	0.681	0.598	0.574	0.576	0.652	0.682	49	0.026	-0.06	20.2
pool_cov	Plains Mill	0.661	0.637	0.540	0.599	0.685	0.772	0.656	0.571	0.537	0.536	0.624	0.653	40	0.098	0.03	20.7
alg_mid	Plains Mill	0.149	0.117	0.090	0.096	0.114	0.212	0.387	0.443	0.482	0.465	0.328	0.197	4	0.000	1.21	21.1
riffle	Laurel Hill	0.496	0.406	0.273	0.317	0.410	0.645	0.787	0.733	0.715	0.723	0.731	0.590	25	0.054	0.29	17.0
fast_gen	Laurel Hill	0.529	0.442	0.305	0.355	0.458	0.705	0.801	0.729	0.711	0.728	0.743	0.618	25	0.071	0.16	16.7
pool_run	Laurel Hill	0.643	0.588	0.482	0.534	0.616	0.784	0.815	0.737	0.710	0.731	0.765	0.698	36	0.029	0.15	19.1
pool_cov	Laurel Hill	0.355	0.256	0.154	0.174	0.231	0.431	0.659	0.703	0.739	0.714	0.635	0.473	22	0.043	0.74	16.9

alg_mid	Laurel Hill	0.123	0.092	0.075	0.076	0.083	0.120	0.215	0.274	0.304	0.276	0.219	0.160	0	0.000	1.03	20.8
riffle	Spring Hollow	0.426	0.305	0.201	0.191	0.269	0.463	0.699	0.781	0.806	0.793	0.703	0.522	13	0.021	0.62	17.1
fast_gen	Spring Hollow	0.472	0.352	0.250	0.244	0.326	0.525	0.735	0.806	0.827	0.815	0.734	0.568	8	0.036	0.51	17.7
pool_run	Spring Hollow	0.547	0.436	0.343	0.338	0.417	0.596	0.773	0.830	0.848	0.837	0.768	0.625	8	0.030	0.46	19.1
pool_cov	Spring Hollow	0.609	0.538	0.497	0.524	0.590	0.716	0.717	0.698	0.693	0.695	0.674	0.660	62	0.015	-0.08	19.8
alg_mid	Spring Hollow	0.309	0.297	0.284	0.272	0.272	0.283	0.341	0.368	0.379	0.376	0.364	0.316	0	1.886	0.35	24.1
riffle	Posey Hollow	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0.000	NaN	NA
fast_gen	Posey Hollow	0.820	0.763	0.728	0.727	0.768	0.871	0.921	0.915	0.917	0.920	0.919	0.861	14	0.036	0.11	20.7
pool_run	Posey Hollow	0.701	0.625	0.558	0.556	0.614	0.737	0.856	0.889	0.898	0.896	0.859	0.762	11	0.035	0.30	20.7
pool_cov	Posey Hollow	0.633	0.604	0.582	0.581	0.593	0.634	0.694	0.737	0.753	0.744	0.708	0.659	0	0.154	0.20	22.7
alg_mid	Posey Hollow	0.037	0.026	0.019	0.019	0.023	0.035	0.051	0.058	0.057	0.057	0.051	0.040	0	0.000	0.70	19.5
riffle	Rt 648	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0.000	NaN	NA
fast_gen	Rt 648	0.564	0.425	0.313	0.299	0.375	0.561	0.766	0.810	0.809	0.813	0.805	0.616	11	0.090	0.58	17.9
pool_run	Rt 648	0.722	0.624	0.549	0.553	0.625	0.780	0.886	0.913	0.920	0.917	0.883	0.790	5	0.054	0.24	20.0
pool_cov	Rt 648	0.808	0.806	0.813	0.831	0.846	0.852	0.798	0.735	0.708	0.722	0.763	0.803	49	0.015	-0.10	20.8
alg_mid	Rt 648	0.053	0.039	0.028	0.027	0.032	0.051	0.088	0.120	0.137	0.125	0.095	0.067	0	0.000	1.19	18.2
bg_fry	T8&9	0.098	0.107	0.034	NA	0.020	0.090	0.144	0.199	0.245	0.214	0.151	0.170	0	0.000	1.25	4.9
bg_juv	T8&9	0.153	0.163	0.075	NA	0.050	0.145	0.206	0.261	0.309	0.279	0.210	0.232	0	0.000	0.99	5.5
bg_spawn	T8&9	0.912	0.911	0.869	NA	0.804	0.914	0.933	0.938	0.948	0.948	0.927	0.940	8	0.001	0.07	6.7
bg_adult	T8&9	0.750	0.754	0.652	NA	0.585	0.747	0.807	0.839	0.875	0.861	0.800	0.817	3	0.001	0.22	6.7
cc_fry	T8&9	0.702	0.700	0.815	NA	0.904	0.710	0.638	0.599	0.552	0.574	0.642	0.617	23	0.004	-0.38	6.6
cc_adult	T8&9	0.953	0.950	0.980	NA	0.991	0.955	0.935	0.920	0.905	0.913	0.935	0.928	23	0.001	-0.08	6.9
cc_spawn	T8&9	0.984	0.981	0.980	NA	0.974	0.984	0.985	0.984	0.984	0.985	0.983	0.985	8	0.001	0.00	6.9
gd_spawn	T8&9	0.826	0.821	0.907	NA	0.954	0.832	0.775	0.733	0.694	0.715	0.776	0.756	23	0.003	-0.27	6.6
gd_juv	T8&9	0.699	0.706	0.601	NA	0.539	0.696	0.757	0.792	0.830	0.815	0.751	0.771	2	0.000	0.25	6.6
gd_adult	T8&9	0.921	0.927	0.966	NA	0.985	0.925	0.891	0.861	0.835	0.851	0.889	0.876	23	0.001	-0.15	6.7
gs_fry	T8&9	0.693	0.699	0.603	NA	0.545	0.688	0.748	0.785	0.823	0.805	0.743	0.765	1	0.000	0.25	6.7
gs_juv	T8&9	0.926	0.922	0.961	NA	0.980	0.927	0.903	0.885	0.868	0.877	0.904	0.894	23	0.001	-0.10	6.9
gs_adult	T8&9	0.926	0.924	0.961	NA	0.981	0.929	0.904	0.886	0.869	0.879	0.905	0.895	23	0.001	-0.10	6.9
gs_spawn	T8&9	NA	NA	NA	NA	NA	NA	0.997	0.988	0.993	0.996	NA	3	0.003	0.00	6.9	
smb_fry	T8&9	0.963	0.962	0.945	NA	0.918	0.964	0.971	0.973	0.976	0.977	0.968	0.975	8	0.001	0.03	6.8
smb_juv	T8&9	0.970	0.966	0.974	NA	0.954	0.977	0.981	0.990	NA	0.999	0.984	0.988	0	0.000	0.01	6.9
smb_spawn	T8&9	NA	0.996	NA	NA	NA	NA	0.989	0.966	0.962	0.965	0.968	0.974	5	0.003	-0.02	6.8
smb_inc	T8&9	0.852	0.842	0.951	NA	0.983	0.862	0.790	0.735	0.683	0.713	0.791	0.764	23	0.003	-0.33	6.4
smb_adult	T8&9	0.856	0.853	0.919	NA	0.959	0.859	0.819	0.791	0.763	0.777	0.820	0.805	23	0.002	-0.18	6.8
ws_fry	T8&9	0.641	0.647	0.535	NA	0.468	0.631	0.705	0.750	0.795	0.773	0.699	0.726	1	0.000	0.31	6.6
ws_spawn	T8&9	0.876	0.873	0.810	NA	0.735	0.880	0.906	0.911	0.925	0.927	0.897	0.916	8	0.002	0.09	6.6

bg_fry	T11&12	0.918	0.904	0.974	NA	0.974	0.931	0.862	0.784	0.722	0.768	0.855	0.826	14	0.007	-0.26	5.9
bg_juv	T11&12	0.936	0.931	0.927	NA	0.926	0.941	0.928	0.879	0.849	0.881	0.904	0.905	11	0.008	-0.06	6.1
bg_adult	T11&12	0.549	0.544	0.741	NA	0.874	0.557	0.441	0.377	0.306	0.336	0.453	0.411	23	0.006	-0.85	5.2
cc_fry	T11&12	0.948	0.946	0.968	NA	0.982	0.951	0.932	0.910	0.891	0.905	0.927	0.920	23	0.001	-0.10	6.7
cc_juv	T11&12	0.868	0.863	0.922	NA	0.959	0.872	0.832	0.801	0.771	0.789	0.832	0.816	23	0.002	-0.19	6.6
cc_spawn	T11&12	0.389	0.396	0.557	NA	0.762	0.385	0.298	0.266	0.218	0.229	0.312	0.281	23	0.006	-1.11	6.4
cc_adult	T11&12	0.708	0.738	0.821	NA	0.908	0.712	0.643	0.615	0.571	0.586	0.656	0.629	23	0.004	-0.37	6.9
gd_juv	T11&12	0.519	0.533	0.402	NA	0.357	0.512	0.594	0.647	0.703	0.675	0.584	0.611	1	0.000	0.48	6.5
gd_spawn	T11&12	0.889	0.872	0.873	NA	0.832	0.898	0.895	0.875	0.867	0.881	0.886	0.885	14	0.003	-0.04	6.6
gd_adult	T11&12	0.823	0.816	0.768	NA	0.707	0.825	0.851	0.868	0.887	0.880	0.853	0.859	1	0.000	0.12	6.8
gs_fry	T11&12	0.902	0.890	0.977	NA	0.994	0.912	0.846	0.780	0.724	0.762	0.839	0.815	23	0.002	-0.27	6.0
gs_juv	T11&12	0.534	0.541	0.666	NA	0.824	0.529	0.468	0.450	0.419	0.422	0.483	0.452	23	0.005	-0.47	7.3
gs_spawn	T11&12	0.886	0.866	0.983	NA	0.996	0.901	0.811	0.729	0.659	0.705	0.809	0.774	23	0.003	-0.38	5.9
gs_adult	T11&12	0.521	0.580	0.661	NA	0.823	0.515	0.451	0.430	0.396	0.399	0.466	0.433	23	0.005	-0.53	7.3
smb_fry	T11&12	0.684	0.669	0.863	NA	0.942	0.697	0.577	0.506	0.425	0.463	0.589	0.542	23	0.005	-0.69	5.6
smb_juv	T11&12	0.933	0.928	0.966	NA	0.983	0.938	0.904	0.855	0.817	0.848	0.890	0.880	23	0.001	-0.16	6.3
smb_spawn	T11&12	0.860	0.840	0.968	NA	0.989	0.874	0.784	0.709	0.638	0.680	0.783	0.747	23	0.004	-0.40	6.0
smb_inc	T11&12	0.637	0.635	0.775	NA	0.886	0.641	0.562	0.522	0.475	0.492	0.571	0.541	23	0.004	-0.50	6.7
smb_adult	T11&12	0.708	0.703	0.833	NA	0.918	0.714	0.636	0.592	0.543	0.564	0.646	0.623	23	0.004	-0.44	6.7
ws_fry	T11&12	0.938	0.924	0.990	NA	0.996	0.949	0.888	0.812	0.754	0.800	0.875	0.853	23	0.002	-0.22	5.9
ws_juv	T11&12	0.968	0.964	0.991	NA	0.996	0.971	0.951	0.929	0.911	0.924	0.948	0.941	23	0.001	-0.10	6.6
ws_spawn	T11&12	0.699	0.707	0.599	NA	0.548	0.701	0.744	0.755	0.780	0.780	0.715	0.764	8	0.007	0.24	6.3
ws_adult	T11&12	0.935	0.932	0.968	NA	0.984	0.938	0.913	0.889	0.868	0.881	0.910	0.902	23	0.001	-0.12	6.6
cd_adult	Staunton	0.539	0.491	0.461	0.466	0.474	0.615	0.712	0.739	0.780	0.745	0.681	0.597	6	0.003	0.41	24.5
bd_low_grad	Staunton	0.032	0.024	0.020	0.021	0.021	0.044	0.062	0.076	0.085	0.077	0.057	0.041	0	0.000	1.26	19.9
bd_high_grad	Staunton	0.103	0.078	0.063	0.066	0.069	0.142	0.197	0.227	0.252	0.229	0.180	0.132	0	0.000	0.86	19.7
shallow_slow	Staunton	0.041	0.031	0.029	0.028	0.026	0.057	0.082	0.092	0.106	0.096	0.073	0.054	0	0.000	1.37	22.3
shallow_fast	Staunton	0.157	0.118	0.094	0.095	0.096	0.231	0.331	0.375	0.427	0.387	0.299	0.214	4	0.000	0.90	17.8
deep_slow	Staunton	0.740	0.675	0.635	0.655	0.692	0.791	0.846	0.848	0.873	0.856	0.831	0.782	12	0.004	0.20	23.6
deep_fast	Staunton	0.630	0.539	0.464	0.496	0.537	0.736	0.840	0.830	0.858	0.829	0.810	0.715	12	0.010	0.31	20.7
as_fry	Staunton	0.801	0.852	0.879	0.878	0.882	0.713	0.597	0.554	0.501	0.546	0.633	0.733	70	0.003	-0.38	22.4
as_juv	Staunton	0.801	0.852	0.879	0.878	0.882	0.713	0.597	0.554	0.501	0.546	0.633	0.733	70	0.003	-0.38	22.4
nh_adult	Staunton	0.740	0.675	0.635	0.655	0.692	0.791	0.846	0.848	0.873	0.856	0.831	0.782	12	0.004	0.19	23.4
nh_spawn	Staunton	0.327	0.243	0.193	0.205	0.222	0.451	0.597	0.635	0.694	0.643	0.551	0.420	6	0.007	0.60	18.6
nh_yoy	Staunton	0.041	0.031	0.029	0.028	0.026	0.057	0.082	0.092	0.106	0.096	0.073	0.054	0	0.000	1.37	22.3
rhg_adult	Staunton	0.957	0.961	0.962	0.965	0.972	0.947	0.926	0.915	0.904	0.913	0.932	0.948	63	0.001	-0.06	24.9
rhg_juv	Staunton	0.635	0.549	0.480	0.509	0.545	0.734	0.827	0.815	0.841	0.812	0.800	0.712	12	0.010	0.33	21.1

rhg_yoy	Staunton	0.045	0.031	0.024	0.025	0.026	0.067	0.100	0.124	0.141	0.127	0.089	0.062	0	0.000	1.36	18.4
rhsh_adult	Staunton	0.901	0.893	0.879	0.897	0.925	0.898	0.871	0.843	0.821	0.835	0.874	0.892	48	0.003	-0.06	23.4
rhsh_juv	Staunton	0.526	0.444	0.387	0.405	0.432	0.634	0.754	0.762	0.805	0.769	0.719	0.612	9	0.009	0.46	21.4
rhsh_spawn	Staunton	0.539	0.453	0.388	0.409	0.448	0.657	0.772	0.791	0.825	0.794	0.736	0.624	5	0.016	0.39	21.2
rhsh_yoy	Staunton	0.295	0.237	0.200	0.211	0.228	0.379	0.477	0.518	0.560	0.523	0.446	0.357	2	0.000	0.60	21.0
rhsi_adult	Staunton	0.678	0.581	0.498	0.537	0.585	0.787	0.881	0.862	0.879	0.855	0.851	0.760	12	0.011	0.25	20.2
rhsi_yoy	Staunton	0.078	0.053	0.039	0.040	0.042	0.119	0.179	0.216	0.247	0.222	0.160	0.110	0	0.000	1.10	17.0
cc_juv_summ	Staunton	0.930	0.920	0.911	0.914	0.917	0.942	0.957	0.953	0.958	0.953	0.952	0.940	12	0.003	0.05	25.1
cc_juv_fall	Staunton	0.223	0.144	0.103	0.106	0.109	0.347	0.519	0.562	0.644	0.579	0.465	0.323	6	0.010	0.98	16.3
we_adult	Staunton	0.461	0.557	0.616	0.593	0.565	0.329	0.202	0.174	0.133	0.177	0.244	0.369	88	0.001	-1.00	18.6
we_fry	Staunton	0.092	0.092	0.094	0.092	0.092	0.095	0.097	0.100	0.117	0.108	0.106	0.096	6	0.029	0.69	27.6
we_juv	Staunton	0.792	0.767	0.736	0.767	0.812	0.801	0.773	0.732	0.698	0.719	0.773	0.786	48	0.005	-0.02	21.8
stb_adult	Staunton	0.618	0.692	0.742	0.726	0.699	0.515	0.409	0.377	0.338	0.375	0.444	0.544	88	0.001	-0.54	22.6
stb_spawn	Staunton	0.611	0.692	0.746	0.730	0.704	0.496	0.372	0.336	0.288	0.332	0.413	0.528	88	0.001	-0.60	21.3
stb_fry	Staunton	0.615	0.699	0.751	0.735	0.708	0.500	0.376	0.339	0.291	0.335	0.417	0.532	88	0.001	-0.59	21.3
stb_juv	Staunton	0.618	0.692	0.742	0.726	0.699	0.515	0.409	0.377	0.338	0.375	0.444	0.544	88	0.001	-0.54	22.6
spb_adult	Staunton	0.939	0.955	0.964	0.963	0.960	0.915	0.881	0.858	0.840	0.855	0.892	0.921	88	0.000	-0.09	24.4
spb_spawn	Staunton	0.944	0.950	0.952	0.957	0.968	0.926	0.882	0.836	0.805	0.829	0.894	0.927	57	0.002	-0.09	23.4
spb_fry	Staunton	0.591	0.558	0.541	0.538	0.523	0.644	0.733	0.737	0.784	0.751	0.712	0.643	12	0.008	0.38	25.4
spb_juv	Staunton	0.775	0.712	0.657	0.680	0.718	0.848	0.909	0.905	0.920	0.905	0.892	0.831	12	0.005	0.21	23.1
lmb_adult	Staunton	0.443	0.419	0.417	0.404	0.373	0.500	0.612	0.649	0.713	0.669	0.578	0.498	3	0.000	0.54	26.9
lmb_spawn	Staunton	0.231	0.208	0.199	0.194	0.180	0.278	0.353	0.395	0.436	0.404	0.333	0.271	0	0.000	0.81	25.5
lmb_fry	Staunton	0.238	0.223	0.220	0.213	0.185	0.274	0.329	0.343	0.373	0.348	0.311	0.271	2	0.000	0.66	26.4
lmb_juv	Staunton	0.409	0.383	0.382	0.362	0.318	0.476	0.603	0.643	0.720	0.665	0.566	0.474	10	0.002	0.68	26.9
chub_adult	Staunton	0.151	0.111	0.087	0.091	0.098	0.214	0.300	0.350	0.395	0.358	0.273	0.200	3	0.000	0.94	19.1
chub_spawn	Staunton	0.157	0.118	0.094	0.095	0.096	0.231	0.331	0.375	0.427	0.387	0.299	0.214	4	0.000	0.90	17.8
canoe_nov	Staunton	0.971	0.977	0.980	0.981	0.985	0.957	0.934	0.918	0.905	0.915	0.941	0.959	68	0.000	-0.06	24.7
canoe_mid	Staunton	0.781	0.815	0.837	0.830	0.818	0.734	0.683	0.661	0.640	0.659	0.699	0.747	88	0.001	-0.19	24.7
boat	Staunton	0.941	0.922	0.902	0.915	0.934	0.953	0.958	0.945	0.942	0.941	0.954	0.949	48	0.001	0.03	24.3
cd_adult	Head Kerr Lake	0.536	0.490	0.458	0.464	0.472	0.611	0.706	0.735	0.777	0.742	0.677	0.593	5	0.003	0.41	24.6
bd_low_grad	Head Kerr Lake	0.032	0.024	0.020	0.020	0.021	0.044	0.061	0.074	0.085	0.076	0.056	0.041	0	0.000	1.24	19.8
bd_high_grad	Head Kerr Lake	0.101	0.078	0.062	0.065	0.068	0.140	0.193	0.223	0.251	0.227	0.177	0.130	0	0.000	0.87	19.5
shallow_slow	Head Kerr Lake	0.040	0.031	0.028	0.028	0.026	0.056	0.080	0.090	0.105	0.094	0.072	0.053	0	0.000	1.37	22.5
shallow_fast	Head Kerr Lake	0.154	0.118	0.092	0.093	0.094	0.226	0.325	0.369	0.422	0.382	0.295	0.210	4	0.000	0.89	17.8
deep_slow	Head Kerr Lake	0.736	0.674	0.633	0.653	0.689	0.789	0.844	0.846	0.871	0.855	0.829	0.780	12	0.004	0.20	23.5
deep_fast	Head Kerr Lake	0.624	0.534	0.465	0.491	0.532	0.733	0.836	0.828	0.856	0.828	0.811	0.709	12	0.010	0.32	20.6
as_fry	Head Kerr Lake	0.805	0.853	0.882	0.880	0.886	0.718	0.603	0.560	0.505	0.552	0.638	0.736	69	0.003	-0.37	22.4

as_juv	Head Kerr Lake	0.805	0.853	0.882	0.880	0.886	0.718	0.603	0.560	0.505	0.552	0.638	0.736	69	0.003	-0.37	22.4
nh_adult	Head Kerr Lake	0.736	0.674	0.633	0.653	0.689	0.789	0.844	0.846	0.871	0.855	0.829	0.780	12	0.004	0.20	23.4
nh_spawn	Head Kerr Lake	0.321	0.243	0.189	0.201	0.217	0.445	0.590	0.629	0.690	0.638	0.546	0.414	5	0.007	0.62	18.5
nh_yoy	Head Kerr Lake	0.040	0.031	0.028	0.028	0.026	0.056	0.080	0.090	0.105	0.094	0.072	0.053	0	0.000	1.37	22.5
rhg_adult	Head Kerr Lake	0.958	0.961	0.962	0.965	0.972	0.948	0.928	0.917	0.905	0.914	0.933	0.949	63	0.001	-0.06	24.9
rhg_juv	Head Kerr Lake	0.628	0.547	0.477	0.504	0.540	0.729	0.826	0.813	0.841	0.814	0.800	0.708	12	0.010	0.34	21.1
rhg_yoy	Head Kerr Lake	0.044	0.031	0.023	0.024	0.025	0.065	0.097	0.121	0.140	0.125	0.088	0.061	0	0.000	1.36	18.4
rhsh_adult	Head Kerr Lake	0.903	0.893	0.878	0.896	0.924	0.899	0.873	0.847	0.823	0.837	0.878	0.893	47	0.003	-0.05	23.4
rhsh_juv	Head Kerr Lake	0.520	0.443	0.383	0.400	0.429	0.628	0.748	0.759	0.801	0.766	0.716	0.607	9	0.009	0.47	21.4
rhsh_spawn	Head Kerr Lake	0.534	0.450	0.384	0.405	0.443	0.652	0.767	0.787	0.823	0.791	0.734	0.620	4	0.016	0.40	21.1
rhsh_yoy	Head Kerr Lake	0.292	0.237	0.198	0.208	0.224	0.375	0.472	0.513	0.557	0.519	0.442	0.353	2	0.000	0.60	20.9
rhsi_adult	Head Kerr Lake	0.672	0.577	0.493	0.533	0.577	0.784	0.879	0.863	0.880	0.855	0.853	0.755	12	0.011	0.26	20.2
rhsi_yoy	Head Kerr Lake	0.077	0.053	0.038	0.039	0.041	0.117	0.175	0.212	0.245	0.218	0.158	0.108	0	0.000	1.10	16.9
cc_juv_summ	Head Kerr Lake	0.930	0.919	0.910	0.913	0.917	0.941	0.956	0.952	0.958	0.954	0.952	0.940	12	0.003	0.05	25.1
cc_juv_fall	Head Kerr Lake	0.219	0.144	0.100	0.103	0.105	0.339	0.510	0.554	0.636	0.573	0.459	0.317	5	0.010	1.01	16.2
we_adult	Head Kerr Lake	0.467	0.558	0.620	0.598	0.571	0.335	0.207	0.178	0.135	0.181	0.246	0.375	88	0.001	-0.98	18.6
we_fry	Head Kerr Lake	0.092	0.091	0.092	0.091	0.091	0.095	0.097	0.101	0.116	0.107	0.105	0.095	5	0.029	0.75	27.6
we_juv	Head Kerr Lake	0.791	0.768	0.736	0.766	0.811	0.803	0.776	0.736	0.703	0.723	0.777	0.788	47	0.005	-0.01	21.9
stb_adult	Head Kerr Lake	0.623	0.692	0.745	0.730	0.703	0.520	0.414	0.382	0.341	0.378	0.446	0.549	88	0.001	-0.54	22.6
stb_spawn	Head Kerr Lake	0.617	0.693	0.749	0.734	0.709	0.502	0.378	0.342	0.292	0.336	0.416	0.533	88	0.001	-0.59	21.3
stb_fry	Head Kerr Lake	0.622	0.698	0.755	0.739	0.714	0.506	0.382	0.345	0.294	0.340	0.421	0.538	88	0.001	-0.59	21.3
stb_juv	Head Kerr Lake	0.623	0.692	0.745	0.730	0.703	0.520	0.414	0.382	0.341	0.378	0.446	0.549	88	0.001	-0.54	22.6
spb_adult	Head Kerr Lake	0.940	0.955	0.965	0.963	0.961	0.916	0.883	0.860	0.842	0.857	0.893	0.922	88	0.000	-0.09	24.5
spb_spawn	Head Kerr Lake	0.945	0.950	0.953	0.958	0.968	0.928	0.886	0.840	0.808	0.833	0.896	0.928	56	0.002	-0.09	23.5
spb_fry	Head Kerr Lake	0.587	0.557	0.539	0.535	0.520	0.639	0.729	0.734	0.780	0.746	0.708	0.640	12	0.008	0.38	25.5
spb_juv	Head Kerr Lake	0.772	0.709	0.654	0.676	0.714	0.846	0.908	0.904	0.920	0.904	0.892	0.827	12	0.005	0.22	23.1
lmb_adult	Head Kerr Lake	0.441	0.420	0.416	0.402	0.373	0.495	0.604	0.643	0.707	0.662	0.571	0.493	3	0.000	0.53	27.0
lmb_spawn	Head Kerr Lake	0.229	0.207	0.198	0.194	0.178	0.274	0.348	0.390	0.432	0.400	0.329	0.268	0	0.000	0.80	25.6
lmb_fry	Head Kerr Lake	0.238	0.222	0.220	0.210	0.184	0.271	0.328	0.340	0.371	0.344	0.308	0.268	2	0.000	0.67	26.6
lmb_juv	Head Kerr Lake	0.406	0.384	0.382	0.361	0.319	0.470	0.596	0.634	0.713	0.657	0.559	0.471	10	0.002	0.66	27.1
chub_adult	Head Kerr Lake	0.149	0.111	0.085	0.089	0.096	0.210	0.294	0.344	0.391	0.354	0.269	0.196	3	0.000	0.95	19.1
chub_spawn	Head Kerr Lake	0.154	0.118	0.092	0.093	0.094	0.226	0.325	0.369	0.422	0.382	0.295	0.210	4	0.000	0.89	17.8
canoe_nov	Head Kerr Lake	0.971	0.977	0.980	0.981	0.985	0.958	0.936	0.920	0.906	0.917	0.942	0.960	68	0.000	-0.06	24.7
canoe_mid	Head Kerr Lake	0.783	0.815	0.838	0.831	0.819	0.737	0.686	0.664	0.641	0.662	0.701	0.749	88	0.001	-0.19	24.7
boat	Head Kerr Lake	0.940	0.920	0.902	0.914	0.933	0.953	0.958	0.945	0.942	0.942	0.955	0.949	47	0.001	0.03	24.3
smb_sub_adult	Lynwood	0.440	0.354	0.251	0.283	0.360	0.595	0.782	0.802	0.820	0.791	0.696	0.537	25	0.011	0.71	22.6
smb_adult	Lynwood	0.859	0.860	0.853	0.875	0.890	0.887	0.841	0.800	0.784	0.787	0.811	0.842	70	0.001	-0.07	26.0

rbs_juv	Lynwood	0.225	0.178	0.147	0.157	0.176	0.257	0.387	0.481	0.538	0.528	0.422	0.307	0	0.000	0.94	24.8
rbs_adult	Lynwood	0.612	0.543	0.439	0.480	0.567	0.764	0.875	0.857	0.859	0.833	0.781	0.678	28	0.009	0.41	24.4
c_ssp.	Lynwood	0.313	0.230	0.150	0.173	0.230	0.416	0.606	0.683	0.733	0.714	0.586	0.424	8	0.015	0.89	21.6
mm	Lynwood	0.513	0.427	0.315	0.363	0.447	0.654	0.801	0.832	0.859	0.840	0.750	0.612	8	0.029	0.52	23.3
rc	Lynwood	0.423	0.320	0.203	0.242	0.332	0.581	0.773	0.810	0.842	0.818	0.702	0.532	3	0.044	0.69	21.4
canoe	Lynwood	0.860	0.890	0.908	0.918	0.911	0.850	0.748	0.686	0.649	0.659	0.728	0.812	76	0.002	-0.21	25.8
smb_sub_adult	Luray	0.473	0.378	0.286	0.312	0.360	0.594	0.784	0.841	0.845	0.820	0.726	0.547	25	0.007	0.67	22.0
smb_adult	Luray	0.394	0.312	0.251	0.263	0.289	0.468	0.660	0.756	0.792	0.759	0.645	0.469	1	0.000	0.82	23.8
rbs_juv	Luray	0.226	0.173	0.137	0.141	0.157	0.268	0.417	0.515	0.574	0.542	0.424	0.291	0	0.000	1.06	23.5
rbs_adult	Luray	0.505	0.425	0.340	0.372	0.420	0.618	0.754	0.774	0.776	0.761	0.685	0.557	0	0.000	0.48	23.2
c_ssp.	Luray	0.424	0.323	0.231	0.257	0.307	0.539	0.741	0.811	0.836	0.808	0.691	0.501	2	0.030	0.69	20.9
mm	Luray	0.524	0.432	0.343	0.374	0.422	0.639	0.805	0.857	0.867	0.845	0.758	0.595	14	0.017	0.56	22.6
rc	Luray	0.509	0.408	0.304	0.339	0.395	0.641	0.824	0.872	0.880	0.857	0.762	0.584	14	0.015	0.56	21.4
canoe	Luray	0.872	0.837	0.785	0.830	0.867	0.932	0.920	0.890	0.866	0.872	0.890	0.872	53	0.002	0.03	24.7
smb_sub_adult	Front Royal	0.611	0.523	0.380	0.433	0.545	0.778	0.914	0.918	0.925	0.908	0.831	0.701	17	0.009	0.35	22.3
smb_adult	Front Royal	0.507	0.410	0.264	0.311	0.429	0.700	0.869	0.864	0.868	0.844	0.760	0.606	27	0.007	0.38	20.4
rbs_juv	Front Royal	0.171	0.121	0.068	0.076	0.110	0.230	0.386	0.443	0.475	0.459	0.353	0.236	0	0.000	1.01	19.9
rbs_adult	Front Royal	0.517	0.446	0.340	0.383	0.456	0.619	0.770	0.820	0.845	0.828	0.736	0.605	7	0.006	0.43	23.5
c_ssp.	Front Royal	0.466	0.381	0.248	0.289	0.397	0.646	0.799	0.776	0.778	0.759	0.683	0.552	27	0.012	0.39	20.4
mm	Front Royal	0.508	0.436	0.306	0.352	0.464	0.698	0.813	0.767	0.756	0.733	0.690	0.584	27	0.016	0.36	21.0
rc	Front Royal	0.533	0.444	0.297	0.348	0.470	0.728	0.869	0.849	0.846	0.818	0.758	0.625	17	0.010	0.34	20.8
canoe	Front Royal	0.896	0.929	0.945	0.954	0.943	0.879	0.763	0.692	0.654	0.666	0.762	0.849	80	0.001	-0.21	25.1
bj_juv	Dunlap	0.805	0.782	0.766	0.835	0.832	0.718	0.621	0.573	0.524	0.586	0.666	0.742	61	0.050	-0.26	23.3
bj_adult	Dunlap	0.728	0.810	0.895	0.867	0.750	0.420	0.228	0.171	0.126	0.191	0.350	0.571	74	0.042	-0.83	19.1
csr_adult	Dunlap	0.807	0.835	0.869	0.888	0.827	0.597	0.399	0.312	0.233	0.338	0.502	0.692	69	0.043	-0.51	20.2
chub_spp._spawn	Dunlap	0.810	0.770	0.740	0.814	0.835	0.783	0.694	0.641	0.570	0.651	0.714	0.775	61	0.038	-0.16	22.9
ff_juv	Dunlap	0.846	0.797	0.737	0.787	0.870	0.929	0.888	0.852	0.796	0.852	0.878	0.873	37	0.100	0.04	24.0
nh_spawn	Dunlap	0.731	0.791	0.862	0.858	0.752	0.443	0.266	0.212	0.167	0.237	0.381	0.584	74	0.037	-0.80	19.9
rfs_yoy	Dunlap	0.841	0.760	0.676	0.763	0.858	0.946	0.905	0.849	0.795	0.859	0.894	0.873	43	0.040	0.04	23.1
rfs_adult	Dunlap	0.938	0.942	0.945	0.967	0.964	0.845	0.673	0.578	0.472	0.600	0.744	0.878	55	0.045	-0.28	22.6
ff_adult	Dunlap	0.756	0.834	0.897	0.885	0.791	0.434	0.222	0.157	0.122	0.198	0.362	0.589	79	0.014	-0.81	18.5
nh_adult	Dunlap	0.647	0.751	0.858	0.792	0.661	0.371	0.225	0.180	0.142	0.198	0.319	0.511	86	0.013	-0.86	20.6
smb_yoy	Dunlap	0.767	0.677	0.583	0.665	0.764	0.921	0.949	0.935	0.919	0.937	0.920	0.837	29	0.076	0.18	23.5
smb_juv	Dunlap	0.913	0.898	0.887	0.920	0.933	0.894	0.819	0.765	0.708	0.774	0.842	0.890	55	0.024	-0.12	24.2
smb_adult	Dunlap	0.851	0.839	0.838	0.885	0.880	0.770	0.635	0.562	0.491	0.579	0.690	0.796	69	0.016	-0.28	23.0
rb_yoy	Dunlap	0.657	0.627	0.604	0.640	0.649	0.678	0.750	0.800	0.850	0.791	0.725	0.671	0	0.016	0.16	25.7
rb_juv	Dunlap	0.502	0.455	0.412	0.439	0.493	0.630	0.717	0.755	0.779	0.738	0.666	0.568	0	0.000	0.33	24.8

rb_adult	Dunlap	0.781	0.747	0.719	0.752	0.776	0.827	0.885	0.919	0.942	0.907	0.862	0.808	6	0.100	0.13	25.4
rbs_spawn	Dunlap	0.127	0.100	0.093	0.101	0.107	0.260	0.499	0.636	0.731	0.598	0.415	0.208	0	0.000	1.31	20.3
nh_yoy	Dunlap	0.800	0.756	0.706	0.739	0.794	0.913	0.957	0.954	0.948	0.955	0.923	0.855	23	0.089	0.18	25.1
smb_spawn	Dunlap	0.614	0.520	0.429	0.506	0.605	0.803	0.904	0.937	0.959	0.929	0.846	0.709	6	0.124	0.32	23.2
rb_spawn	Dunlap	0.288	0.221	0.155	0.164	0.268	0.577	0.733	0.762	0.780	0.738	0.617	0.442	0	0.000	0.70	21.1
bj_juv	Craig	0.881	0.818	0.784	0.846	0.895	0.923	0.921	0.917	0.914	0.920	0.920	0.908	59	0.008	0.03	24.1
bj_adult	Craig	0.909	0.902	0.915	0.942	0.941	0.836	0.644	0.566	0.500	0.585	0.729	0.852	56	0.015	-0.28	22.2
csr_adult	Craig	0.875	0.837	0.817	0.856	0.905	0.932	0.867	0.801	0.752	0.813	0.879	0.885	34	0.060	-0.01	23.2
chub_spp._spawn	Craig	0.659	0.587	0.524	0.560	0.685	0.853	0.889	0.856	0.842	0.854	0.836	0.743	34	0.025	0.26	23.1
ff_juv	Craig	0.424	0.530	0.604	0.512	0.398	0.274	0.245	0.239	0.234	0.241	0.273	0.344	87	0.016	-0.64	26.2
nh_spawn	Craig	0.817	0.827	0.862	0.878	0.840	0.679	0.533	0.500	0.462	0.514	0.614	0.739	74	0.007	-0.41	23.3
rfs_yoy	Craig	0.783	0.744	0.724	0.744	0.782	0.875	0.937	0.939	0.946	0.936	0.897	0.832	18	0.043	0.17	24.9
rfs_adult	Craig	0.863	0.840	0.819	0.850	0.897	0.908	0.825	0.768	0.725	0.774	0.843	0.865	39	0.043	-0.04	23.7
ff_adult	Craig	0.824	0.803	0.787	0.827	0.862	0.805	0.632	0.560	0.498	0.572	0.697	0.792	56	0.013	-0.20	22.4
nh_adult	Craig	0.847	0.900	0.944	0.922	0.844	0.657	0.486	0.437	0.390	0.458	0.593	0.744	84	0.003	-0.46	23.2
smb_yoy	Craig	0.486	0.432	0.397	0.425	0.488	0.643	0.804	0.850	0.892	0.835	0.713	0.576	5	0.031	0.45	24.0
smb_juv	Craig	0.820	0.768	0.723	0.762	0.841	0.934	0.939	0.918	0.906	0.918	0.918	0.871	34	0.017	0.12	24.2
smb_adult	Craig	0.745	0.691	0.642	0.682	0.775	0.885	0.874	0.833	0.810	0.832	0.850	0.801	34	0.041	0.14	23.5
rb_yoy	Craig	0.271	0.220	0.184	0.206	0.274	0.427	0.529	0.554	0.581	0.538	0.453	0.349	0	0.000	0.53	22.3
rb_juv	Craig	0.316	0.258	0.213	0.242	0.323	0.488	0.602	0.630	0.657	0.614	0.521	0.404	0	0.000	0.51	22.2
rb_adult	Craig	0.493	0.432	0.386	0.419	0.500	0.656	0.750	0.770	0.792	0.757	0.679	0.574	0	0.000	0.35	23.7
rbs_spawn	Craig	0.132	0.095	0.062	0.069	0.142	0.237	0.289	0.332	0.367	0.306	0.238	0.177	0	0.000	0.71	21.4
nh_yoy	Craig	0.540	0.467	0.406	0.427	0.574	0.768	0.830	0.827	0.826	0.807	0.753	0.638	44	0.030	0.33	23.2
smb_spawn	Craig	0.349	0.278	0.217	0.254	0.364	0.539	0.658	0.694	0.724	0.674	0.570	0.444	0	0.000	0.48	21.9
rb_spawn	Craig	0.204	0.150	0.100	0.113	0.217	0.381	0.462	0.467	0.474	0.452	0.390	0.287	0	0.000	0.53	20.2
bj_juv	Maury	0.592	0.532	0.459	0.519	0.560	0.688	0.772	0.833	0.842	0.819	0.754	0.649	2	0.000	0.29	23.7
bj_adult	Maury	0.745	0.702	0.621	0.701	0.749	0.833	0.797	0.732	0.707	0.733	0.770	0.758	46	0.013	0.04	22.1
csr_adult	Maury	0.845	0.788	0.699	0.784	0.830	0.922	0.917	0.887	0.873	0.886	0.900	0.869	51	0.004	0.06	22.9
chub_spp._spawn	Maury	0.712	0.638	0.519	0.622	0.690	0.843	0.839	0.811	0.804	0.812	0.816	0.757	46	0.010	0.10	22.1
ff_juv	Maury	0.737	0.739	0.697	0.765	0.771	0.715	0.612	0.549	0.547	0.563	0.630	0.704	55	0.019	-0.24	23.0
nh_spawn	Maury	0.805	0.815	0.796	0.850	0.842	0.754	0.641	0.557	0.543	0.575	0.662	0.755	59	0.013	-0.29	22.3
rfs_yoy	Maury	0.644	0.561	0.470	0.527	0.591	0.808	0.910	0.939	0.929	0.923	0.858	0.722	18	0.022	0.37	23.1
rfs_adult	Maury	0.722	0.671	0.615	0.655	0.695	0.826	0.875	0.861	0.838	0.851	0.836	0.763	30	0.021	0.22	23.5
ff_adult	Maury	0.869	0.862	0.838	0.875	0.889	0.892	0.809	0.704	0.680	0.721	0.792	0.845	46	0.014	-0.08	22.6
nh_adult	Maury	0.818	0.893	0.952	0.924	0.876	0.656	0.495	0.406	0.400	0.436	0.555	0.727	77	0.004	-0.52	22.5
smb_yoy	Maury	0.433	0.346	0.267	0.310	0.373	0.623	0.787	0.865	0.866	0.836	0.719	0.534	4	0.000	0.63	22.1
smb_juv	Maury	0.704	0.626	0.532	0.597	0.661	0.855	0.918	0.916	0.902	0.906	0.872	0.767	30	0.011	0.28	23.0

smb_adult	Maury	0.621	0.516	0.375	0.476	0.576	0.835	0.876	0.839	0.815	0.832	0.816	0.697	34	0.021	0.28	20.7
rb_yoy	Maury	0.418	0.387	0.352	0.379	0.400	0.477	0.555	0.623	0.636	0.607	0.541	0.460	0	0.000	0.35	24.9
rb_juv	Maury	0.411	0.372	0.344	0.359	0.380	0.487	0.585	0.656	0.667	0.637	0.558	0.459	0	0.000	0.43	24.8
rb_adult	Maury	0.551	0.501	0.457	0.488	0.517	0.643	0.738	0.798	0.804	0.781	0.709	0.606	0	0.000	0.34	24.5
rbs_spawn	Maury	0.324	0.275	0.227	0.259	0.292	0.418	0.515	0.595	0.611	0.575	0.489	0.380	0	0.000	0.52	23.1
nh_yoy	Maury	0.665	0.649	0.617	0.635	0.660	0.723	0.720	0.718	0.724	0.716	0.705	0.685	0	0.000	0.09	25.0
smb_spawn	Maury	0.413	0.335	0.282	0.302	0.350	0.583	0.754	0.846	0.848	0.814	0.687	0.508	4	0.000	0.67	23.0
rb_spawn	Maury	0.357	0.315	0.288	0.300	0.323	0.452	0.586	0.680	0.692	0.655	0.551	0.421	0	0.000	0.59	24.5
bj_juv	James	0.506	0.452	0.366	0.371	0.447	0.634	0.760	0.809	0.865	0.841	0.753	0.607	3	0.000	0.46	20.9
bj_adult	James	0.739	0.692	0.597	0.625	0.705	0.866	0.916	0.911	0.898	0.898	0.877	0.805	30	0.007	0.20	21.0
csr_adult	James	0.623	0.560	0.454	0.494	0.563	0.744	0.851	0.887	0.927	0.916	0.845	0.714	16	0.000	0.35	20.8
chub_spp._spawn	James	0.481	0.465	0.441	0.438	0.463	0.523	0.588	0.631	0.685	0.665	0.610	0.530	0	0.000	0.30	22.9
ff_juv	James	0.667	0.664	0.649	0.668	0.670	0.664	0.667	0.681	0.707	0.690	0.678	0.670	0	0.000	0.01	23.3
nh_spawn	James	0.881	0.875	0.844	0.863	0.892	0.930	0.902	0.850	0.774	0.803	0.846	0.881	38	0.011	-0.03	20.9
rfs_yoy	James	0.680	0.665	0.641	0.656	0.667	0.699	0.738	0.764	0.799	0.788	0.754	0.706	0	0.000	0.13	22.9
rfs_adult	James	0.760	0.733	0.687	0.701	0.735	0.816	0.876	0.901	0.931	0.925	0.882	0.809	6	0.000	0.18	22.4
ff_adult	James	0.787	0.754	0.690	0.704	0.762	0.873	0.919	0.919	0.917	0.927	0.905	0.839	16	0.000	0.17	21.8
nh_adult	James	0.955	0.966	0.967	0.980	0.975	0.938	0.871	0.823	0.759	0.782	0.841	0.918	57	0.002	-0.15	21.7
smb_yoy	James	0.570	0.537	0.501	0.488	0.523	0.603	0.676	0.713	0.761	0.742	0.685	0.616	0	0.000	0.30	22.5
smb_juv	James	0.709	0.672	0.631	0.616	0.657	0.747	0.832	0.872	0.920	0.905	0.842	0.763	0	0.000	0.28	22.4
smb_adult	James	0.561	0.530	0.504	0.501	0.518	0.616	0.723	0.769	0.834	0.808	0.764	0.622	0	0.000	0.34	22.7
rb_yoy	James	0.437	0.409	0.383	0.374	0.398	0.461	0.540	0.592	0.661	0.634	0.566	0.485	0	0.000	0.40	22.7
rb_juv	James	0.509	0.467	0.418	0.399	0.450	0.554	0.653	0.705	0.769	0.744	0.667	0.572	0	0.000	0.45	21.8
rb_adult	James	0.580	0.553	0.522	0.509	0.542	0.608	0.676	0.716	0.767	0.747	0.691	0.623	0	0.000	0.29	22.6
rbs_spawn	James	0.412	0.352	0.267	0.226	0.329	0.486	0.586	0.628	0.672	0.635	0.560	0.480	6	0.000	0.49	18.1
nh_yoy	James	0.483	0.454	0.426	0.421	0.447	0.537	0.662	0.718	0.796	0.780	0.682	0.554	6	0.000	0.43	22.7
smb_spawn	James	0.547	0.520	0.484	0.472	0.506	0.579	0.655	0.702	0.760	0.735	0.673	0.596	0	0.000	0.34	22.6
rb_spawn	James	0.482	0.422	0.361	0.340	0.397	0.538	0.655	0.706	0.766	0.746	0.660	0.553	0	0.000	0.53	21.0

C. Seasonal Habitat Regimes

Table C.1. Site-species combinations within each seasonal habitat regime. Seasonal habitat regimes were determined using a cluster analysis of average monthly habitat availability.

Group 1: Constant High (n=152)		Group 2: Seasonal Summer (n=101)		Group 3: Seasonal Spring (n=45)		Group 4: Constant Low (n=84)	
Species	Site	Species	Site	Species	Site	Species	Site
as_fry	Staunton	bd_low_grad	Above Harvell Dam	as_spawn	Above Harvell Dam	alg_mid	Plains Mill
as_fry	Head Kerr Lake	benth_mac	North Anna Piedmont	as_spawn	North Anna Coastal Plain	alg_mid	Laurel Hill
as_juv	Above Harvell Dam	benth_mac	North Anna Fall Zone	as_spawn	Pamunkey Coastal Plain	alg_mid	Spring Hollow
as_juv	North Anna Coastal Plain	benth_mac	North Anna Coastal Plain	bj_adult	Dunlap	alg_mid	Posey Hollow
as_juv	Pamunkey Coastal Plain	bj_juv	Mauzy	canoe_mid	North Anna Piedmont	alg_mid	Rt 648
as_juv	Staunton	bj_juv	James	canoe_mid	North Anna Fall Zone	bd_high_grad	Staunton
as_juv	Head Kerr Lake	bmc_spawn	Claytor to Pembroke	canoe_mid	North Anna Coastal Plain	bd_high_grad	Head Kerr Lake
bd_high_grad	Above Harvell Dam	bmc_spawn	Pembroke to Glen Lyn	canoe_mid	Pamunkey Coastal Plain	bd_low_grad	Staunton
bj_adult	Craig	c_ssp.	Lynwood	canoe_nov	North Anna Fall Zone	bd_low_grad	Head Kerr Lake
bj_adult	Mauzy	c_ssp.	Luray	canoe_nov	North Anna Coastal Plain	benth_mac	Pamunkey Coastal Plain
bj_adult	James	c_ssp.	Front Royal	csr_adult	Dunlap	cc_juv_fall	Staunton
bj_juv	Dunlap	cc_spawn	Pembroke to Glen Lyn	deep_fast	North Anna Fall Zone	cc_juv_fall	Head Kerr Lake
bj_juv	Craig	cd_adult	Staunton	deep_fast	North Anna Coastal Plain	cf	Claytor to Pembroke
bmc_adult	Claytor to Pembroke	cd_adult	Head Kerr Lake	e_comp	Above Harvell Dam	cf	Pembroke to Glen Lyn
bmc_adult	Pembroke to Glen Lyn	chub_spp._spawn	James	e_comp	North Anna Piedmont	chub_adult	Staunton
boat	Staunton	cs_adult	Claytor to Pembroke	e_comp	North Anna Fall Zone	chub_adult	Head Kerr Lake
boat	Head Kerr Lake	cs_adult	Pembroke to Glen Lyn	e_comp	North Anna Coastal Plain	chub_spawn	Staunton
canoe	Lynwood	cs_spawn	Claytor to Pembroke	ff_adult	Dunlap	chub_spawn	Head Kerr Lake
canoe	Luray	cs_spawn	Pembroke to Glen Lyn	ff_juv	Craig	cs_fry	Claytor to Pembroke
canoe	Front Royal	deep_fast	Pamunkey Coastal Plain	l_rad	Above Harvell Dam	cs_fry	Pembroke to Glen Lyn
canoe_mid	Above Harvell Dam	fast_gen	Laurel Hill	l_rad	North Anna Piedmont	cs_juv	Claytor to Pembroke
canoe_mid	Staunton	fast_gen	Spring Hollow	l_rad	North Anna Fall Zone	cs_juv	Pembroke to Glen Lyn
canoe_mid	Head Kerr Lake	fast_gen	Rt 648	l_rad	North Anna Coastal Plain	fhc_adult_summer	Claytor to Pembroke
canoe_nov	Above Harvell Dam	gd_juv	Claytor to Pembroke	nh_adult	Above Harvell Dam	fhc_adult_summer	Pembroke to Glen Lyn
canoe_nov	North Anna Piedmont	gd_juv	Pembroke to Glen Lyn	nh_adult	North Anna Piedmont	fhc_adult_winter	Claytor to Pembroke
canoe_nov	Pamunkey Coastal Plain	lmb_adult	Staunton	nh_adult	North Anna Fall Zone	fhc_adult_winter	Pembroke to Glen Lyn
canoe_nov	Staunton	lmb_adult	Head Kerr Lake	nh_adult	North Anna Coastal Plain	fhc_spawn	Claytor to Pembroke
canoe_nov	Head Kerr Lake	lmb_juv	Staunton	nh_adult	Dunlap	fhc_spawn	Pembroke to Glen Lyn
cc_adult	Claytor to Pembroke	lmb_juv	Head Kerr Lake	nh_adult	Craig	lmb_fry	Staunton
cc_adult	Pembroke to Glen Lyn	ml_adult_summer	Claytor to Pembroke	nh_adult	Mauzy	lmb_fry	Head Kerr Lake
cc_juv	Claytor to Pembroke	ml_adult_summer	Pembroke to Glen Lyn	nh_spawn	Above Harvell Dam	lmb_spawn	Staunton

cc_juv	Pembroke to Glen Lyn	ml_adult_winter	Claytor to Pembroke	nh_spawn	North Anna Piedmont	lmb_spawn	Head Kerr Lake
cc_juv_summ	Staunton	ml_adult_winter	Pembroke to Glen Lyn	nh_spawn	North Anna Fall Zone	ml_spawn	Claytor to Pembroke
cc_juv_summ	Head Kerr Lake	mm	Lynwood	nh_spawn	North Anna Coastal Plain	ml_spawn	Pembroke to Glen Lyn
cc_spawn	Claytor to Pembroke	mm	Luray	nh_spawn	Dunlap	nh_spawn	Pamunkey Coastal Plain
chub_spp._spawn	Dunlap	mm	Front Royal	stb_adult	Staunton	nh_yoy	Staunton
chub_spp._spawn	Craig	nh_spawn	Staunton	stb_adult	Head Kerr Lake	nh_yoy	Head Kerr Lake
chub_spp._spawn	Maury	nh_spawn	Head Kerr Lake	stb_fry	Staunton	rb_adult	Claytor to Pembroke
csr_adult	Craig	nh_yoy	Claytor to Pembroke	stb_fry	Head Kerr Lake	rb_adult	Pembroke to Glen Lyn
csr_adult	Maury	nh_yoy	Pembroke to Glen Lyn	stb_juv	Staunton	rb_fry	Claytor to Pembroke
csr_adult	James	nh_yoy	James	stb_juv	Head Kerr Lake	rb_fry	Pembroke to Glen Lyn
deep_fast	Above Harvell Dam	pool_cov	Laurel Hill	stb_spawn	Staunton	rb_juv	Claytor to Pembroke
deep_fast	North Anna Piedmont	pool_cov	Spring Hollow	stb_spawn	Head Kerr Lake	rb_juv	Pembroke to Glen Lyn
deep_fast	Staunton	pool_cov	Posey Hollow	we_adult	Staunton	rb_spawn	Claytor to Pembroke
deep_fast	Head Kerr Lake	pool_run	Laurel Hill	we_adult	Head Kerr Lake	rb_spawn	Pembroke to Glen Lyn
deep_slow	Above Harvell Dam	pool_run	Spring Hollow			rb_spawn	Craig
deep_slow	North Anna Piedmont	pwb	Claytor to Pembroke			rb_yoy	Craig
deep_slow	North Anna Fall Zone	pwb	Pembroke to Glen Lyn			rbs_fry	Claytor to Pembroke
deep_slow	North Anna Coastal Plain	rb_adult	Craig			rbs_fry	Pembroke to Glen Lyn
deep_slow	Pamunkey Coastal Plain	rb_adult	Maury			rbs_juv	Lynwood
deep_slow	Staunton	rb_adult	James			rbs_juv	Luray
deep_slow	Head Kerr Lake	rb_juv	Dunlap			rbs_juv	Front Royal
e_comp	Pamunkey Coastal Plain	rb_juv	Craig			rbs_spawn	Pamunkey Coastal Plain
eph_mac	Claytor to Pembroke	rb_juv	Maury			rbs_spawn	Dunlap
eph_mac	Pembroke to Glen Lyn	rb_juv	James			rbs_spawn	Craig
fast_gen	Plains Mill	rb_spawn	Dunlap			rbs_spawn	Maury
fast_gen	Posey Hollow	rb_spawn	Maury			rhg_yoy	Staunton
ff_adult	Craig	rb_spawn	James			rhg_yoy	Head Kerr Lake
ff_adult	Maury	rb_yoy	Maury			rhsh_yoy	Staunton
ff_adult	James	rb_yoy	James			rhsh_yoy	Head Kerr Lake
ff_juv	Dunlap	rbs_adult	Claytor to Pembroke			rhsi_yoy	Staunton
ff_juv	Maury	rbs_adult	Pembroke to Glen Lyn			rhsi_yoy	Head Kerr Lake
ff_juv	James	rbs_adult	Luray			shallow_fast	Pamunkey Coastal Plain
gd_adult	Claytor to Pembroke	rbs_adult	Front Royal			shallow_fast	Staunton
gd_adult	Pembroke to Glen Lyn	rbs_juv	Claytor to Pembroke			shallow_fast	Head Kerr Lake
gd_spawn	Claytor to Pembroke	rbs_juv	Pembroke to Glen Lyn			shallow_slow	Above Harvell Dam
gd_spawn	Pembroke to Glen Lyn	rbs_spawn	North Anna Piedmont			shallow_slow	North Anna Piedmont
l_rad	Pamunkey Coastal Plain	rbs_spawn	North Anna Coastal Plain			shallow_slow	North Anna Fall Zone
lp_adult	Claytor to Pembroke	rbs_spawn	James			shallow_slow	North Anna Coastal Plain
lp_adult	Pembroke to Glen Lyn	rc	Lynwood			shallow_slow	Pamunkey Coastal Plain
lp_spawn	Claytor to Pembroke	rc	Luray			shallow_slow	Staunton
lp_spawn	Pembroke to Glen Lyn	rc	Front Royal			shallow_slow	Head Kerr Lake

nh_adult	Claytor to Pembroke	rhsh_juv	Staunton	smb_fry	Claytor to Pembroke
nh_adult	Pembroke to Glen Lyn	rhsh_juv	Head Kerr Lake	smb_fry	Pembroke to Glen Lyn
nh_adult	Pamunkey Coastal Plain	rhsh_spawn	Staunton	smb_spawn	Claytor to Pembroke
nh_adult	Staunton	rhsh_spawn	Head Kerr Lake	smb_spawn	Pembroke to Glen Lyn
nh_adult	Head Kerr Lake	riffle	Plains Mill	we_adult	Claytor to Pembroke
nh_adult	James	riffle	Laurel Hill	we_adult	Pembroke to Glen Lyn
nh_spawn	Claytor to Pembroke	riffle	Spring Hollow	we_fry	Claytor to Pembroke
nh_spawn	Pembroke to Glen Lyn	shallow_fast	Pembroke to Glen Lyn	we_fry	Pembroke to Glen Lyn
nh_spawn	Craig	shallow_fast	North Anna Piedmont	we_fry	Staunton
nh_spawn	Maury	shallow_fast	North Anna Fall Zone	we_fry	Head Kerr Lake
nh_spawn	James	shallow_fast	North Anna Coastal Plain	we_juv	Claytor to Pembroke
nh_yoy	Dunlap	smb_adult	Pembroke to Glen Lyn	we_juv	Pembroke to Glen Lyn
nh_yoy	Craig	smb_adult	Luray		
nh_yoy	Maury	smb_adult	Front Royal		
plec_mac	Claytor to Pembroke	smb_adult	James		
plec_mac	Pembroke to Glen Lyn	smb_juv	Claytor to Pembroke		
pool_cov	Plains Mill	smb_juv	Pembroke to Glen Lyn		
pool_cov	Rt 648	smb_spawn	Above Harvell Dam		
pool_run	Plains Mill	smb_spawn	North Anna Piedmont		
pool_run	Posey Hollow	smb_spawn	Craig		
pool_run	Rt 648	smb_spawn	Maury		
rb_adult	Dunlap	smb_spawn	James		
rb_yoy	Dunlap	smb_sub_adult	Lynwood		
rbs_adult	Lynwood	smb_sub_adult	Luray		
rbs_spawn	Above Harvell Dam	smb_yoy	Craig		
rbs_spawn	North Anna Fall Zone	smb_yoy	Maury		
rfs_adult	Dunlap	smb_yoy	James		
rfs_adult	Craig	spb_fry	Staunton		
rfs_adult	Maury	spb_fry	Head Kerr Lake		
rfs_adult	James				
rfs_yoy	Dunlap				
rfs_yoy	Craig				
rfs_yoy	Maury				
rfs_yoy	James				
rh_spawn	Above Harvell Dam				
rhg_adult	Staunton				
rhg_adult	Head Kerr Lake				
rhg_juv	Staunton				
rhg_juv	Head Kerr Lake				
rhsh_adult	Staunton				
rhsh_adult	Head Kerr Lake				

rhsi_adult	Staunton
rhsi_adult	Head Kerr Lake
shallow_fast	Above Harvell Dam
shallow_fast	Claytor to Pembroke
sm_int	Claytor to Pembroke
sm_int	Pembroke to Glen Lyn
sm_shal_slow	Claytor to Pembroke
sm_shal_slow	Pembroke to Glen Lyn
smb_adult	Above Harvell Dam
smb_adult	Claytor to Pembroke
smb_adult	North Anna Piedmont
smb_adult	North Anna Fall Zone
smb_adult	Lynwood
smb_adult	Dunlap
smb_adult	Craig
smb_adult	Maury
smb_juv	Above Harvell Dam
smb_juv	North Anna Piedmont
smb_juv	North Anna Fall Zone
smb_juv	Dunlap
smb_juv	Craig
smb_juv	Maury
smb_juv	James
smb_spawn	North Anna Fall Zone
smb_spawn	Dunlap
smb_sub_adult	Front Royal
smb_yoy	Dunlap
spb_adult	Staunton
spb_adult	Head Kerr Lake
spb_juv	Staunton
spb_juv	Head Kerr Lake
spb_spawn	Staunton
spb_spawn	Head Kerr Lake
tric_mac	Claytor to Pembroke
tric_mac	Pembroke to Glen Lyn
we_juv	Staunton
we_juv	Head Kerr Lake
we_spawn	Claytor to Pembroke
we_spawn	Pembroke to Glen Lyn

D. R Scripts

D-1. readUSGSflowsAll.r

```
### Read in Flow Time Series from USGS Gages

# Read in information about the study reaches
#setwd("C:/Users/Grad/Google Drive/Flow-Ecology")
setwd("C:/Users/Kinsey/Google Drive/Flow-Ecology")
raw.info <- read.csv("information.csv")
attach(raw.info)

gageid <- sprintf("%08d", gageid) #add leading zero to USGS gage IDs

# Initialize variables
flow.matrix <- vector("list", dim(raw.info)[1]) #set up list to store all flow time series
startdate <- c()
enddate <- c()

# Loop through each site
for (i in 1:dim(raw.info)[1]) {

    ## Load Streamflow Data from USGS Gage
    url_base <-
"http://waterservices.usgs.gov/nwis/dv/?variable=00060&format=rdb&startDT=1838-01-
01&site="
    url <- paste(url_base, gageid[i], "&endDT=2014-09-30", sep="") #set end of water year
2014 as end date
    raw.data <- read.table(url, skip = 25, comment.char = "#") #skip first 25 lines of header

    # Print status message
    print(paste("Reading data from gage ", gageid[i], "...", sep=""))

    # Check to make sure all header rows are removed
    if (raw.data[1,1] != "USGS") {
        raw.data <- raw.data[-1,] #remove first line
    }

    # Store start and end dates
    startdate[i] <- as.character(raw.data[1,3]) #read first date on record (column 3)
    enddate[i] <- as.character(raw.data[dim(raw.data)[1],3]) #read last date on record
(column 3)

    # Weight streamflow if a study site drainage area is provided
    if (is.na(da.wua.sqmi[i]) == "FALSE") {
```

```
        raw.data[,4] <- as.numeric(as.vector(raw.data[,4]))*(da.wua.sqmi[i] /
da.gage.sqmi[i])
    }

    # Store date & time in flow.matrix list
    flow.matrix[[i]] <- raw.data[,3:4]
}
```

D-2. readWUATablesAll.r

```
### Read in Weighted Usable Area for All Reaches from OM

# Run "readUSGSflowsAll.R" before running this script.
# Output of previous script is "flow.matrix": a list of matrices containing flow time series
# readUSGSflowsAll.R will also read in the "information.csv" file about the reaches
# and create a matrix of this information called "raw.info"

# Load Necessary Libraries
#For JSON handling:
library(reshape2)
library('RJSONIO')
library(data.table)

# Initialize results matrix
wua.matrix <- vector("list", dim(raw.info)[1]) #set up list to store all WUA tables

for (k in 1:length(flow.matrix)) {

  ## Load WUA Table from OM
  # Create URL to read WUA from OM
  WUA_url<-
paste("http://deq2.bse.vt.edu/om/remote/get_modelData.php?operation=1&variables=wua&elem
entid=",
      aqbiotaid[k], "&debug=0&view=matrix", sep="")

  # Print status message
  print(paste("Reading data from reach ", reachname[k], "...", sep=""))

  #Adapt '&variables=' in WUA_url for Spring Hollow, Posey Hollow, and Rt 648
  if (reachname[k]=="Spring Hollow"|reachname[k]=="Posey
Hollow"|reachname[k]=="Rt 648") {
    if(reachname[k]=="Spring Hollow"){
      WUA_url<-
paste("http://deq2.bse.vt.edu/om/remote/get_modelData.php?operation=1&variables=wua_SH&
elementid=",aqbiotaid[k], "&debug=0&view=matrix", sep="")
    }
    if(reachname[k]=="Posey Hollow"){
      WUA_url<-
paste("http://deq2.bse.vt.edu/om/remote/get_modelData.php?operation=1&variables=wua_PH&
elementid=",aqbiotaid[k], "&debug=0&view=matrix", sep="")
    }
    if(reachname[k]=="Rt 648"){
```

```

        WUA_url<-
paste("http://deq2.bse.vt.edu/om/remote/get_modelData.php?operation=1&variables=wua_R648
&elementid=",aqbiotaid[k],"&debug=0&view=matrix",sep="")
    }
}

# Import data in JSON format
json_data<-fromJSON(WUA_url)

# Re-form WUA table in R
WUA.by.q <- do.call(data.table, json_data) #read matrix in w/ discharge as column
headers
discharges <- as.numeric(names(json_data)) #store row names (discharge values)
targets <- sapply(json_data[1], function(x){names(x)}) #store column names (target
factors)
WUA.asvector<-c(discharges,t(WUA.by.q)) #merge discharges and WUA values into
one long vector
WUA.table<-matrix(as.numeric(WUA.asvector), nrow=length(discharges),
byrow=FALSE) #sort WUA table in proper columns
colnames(WUA.table) <- c("discharge", targets) #set column names to discharge & target
factors
#View(WUA.table)

# Delete first row if Q = 0
if (WUA.table[1,1] == 0) {
    WUA.table <- WUA.table[-1,]
}

# Store WUA.table in list of matrices
wua.matrix[[k]] <- WUA.table
}

### Save each WUA matrix as a csv file
for (w in 1:length(wua.matrix)) {
    wua <- wua.matrix[[w]]
    filename <- paste("WUA ", hydrocode[w], " ", reachname[w], ".csv", sep="")
    write.csv(wua, file=filename)
}

```

D-3. readDrainAreaAll.r

```
### Read in Drainage Area
# from study site drainage area (raw.info spreadsheet) or from USGS XML Parse

library('XML')

drain_area <- c()
review_gage <- c()
for (i in 1:dim(raw.info)[1]) {
  if (is.na(da.wua.sqmi[i]) == "FALSE") {
    drain_area[i] <- da.wua.sqmi[i]
    next
  }

  #XML extract code to pull drainage area
  xml_url2<-paste("http://nwis.waterdata.usgs.gov/nwis/inventory?search_site_no=",
    gageid[i],
    "&search_site_no_match_type=exact&site_tp_cd=ST&drain_area_va_conjunction=and
    &group_key=county_cd&format=sitefile_output&sitefile_output_format=xml&column_name=a
    gency_cd&column_name=site_no&column_name=station_nm&column_name=site_tp_cd&colu
    mn_name=huc_cd&column_name=drain_area_va&list_of_search_criteria=search_site_no%2Csi
    te_tp_cd%2Cdrain_area_va",sep="")
  data2<-htmlParse(xml_url2)
  if (class(data2)=="try-error") {
    print(paste("Error: empty file",xml_url2))
    drain_area[i]<- "NA"
    review_gage[i] <- gageid[i]
    next
  }

  drain_area[i]<-as.numeric(xpathSApply(data2, '//site/drain_area_va',xmlValue))
}
```

D-4. calcHabitatTsAll.r

```
### Calculate Habitat Time Series using flow.matrix and wua.matrix

# Run "readUSGSGageAll.r" and "readWUAtableAll.r" before this script...
# output will be "flow.matrix" and "wua.matrix" - lists of 23 matrices

# Initialize results matrix
habitat.matrix <- vector("list", dim(raw.info)[1]) #set up list to store all WUA tables

habitat.P.matrix <- vector("list", dim(raw.info)[1])

## Generate Habitat Time Series

for (m in 1:length(flow.matrix)) {

  # Print status message
  print(paste("Calculating habitat times series for reach ", reachname[m], "...", sep=""))

  # Extract flow time series from flow.matrix
  flow.ts <- flow.matrix[[m]]
  q <- as.numeric(as.vector(flow.ts[,2])) #store just the flows in vector q
  # Extract WUA table from wua.matrix
  wua.table <- wua.matrix[[m]]

  # Initialize individual habitat time series matrix
  habitat.ts <- matrix(0, nrow=length(q), ncol=ncol(wua.table))
  colnames(habitat.ts) <- colnames(wua.table)
  rownames(habitat.ts) <- as.vector(flow.ts[,1])
  habitat.ts[,1] <- as.vector(as.numeric(q))

  for (n in 1:length(q)) {
    currentq <- q[n] #keep track of what flow the loop is on

    # Check if currentq is NA
    if (is.na(currentq) == "TRUE") {
      habitat.ts[n,] <- NA
      next
    }

    # Check if currentq is beyond range of WUA table
    min.q <- min(wua.table[,1])
    max.q <- max(wua.table[,1])
  }
}
```

```

    if (currentq < min.q) {
      habitat.ts[n,2:dim(habitat.ts)[2]] <- NA
      next
    } else if (currentq > max.q) {
      habitat.ts[n,2:dim(habitat.ts)[2]] <- NA
      next
    }
  }

  rowkey <- which.min(abs(as.numeric(wua.table[,1]) - currentq)) #find flow
closest to desired q

  # Determine the given flows (and row indices) that bound the desired flow
  if ((as.numeric(wua.table[rowkey,1]) - currentq) > 0) {
    uplim.key <- which.min(abs(as.numeric(wua.table[,1]) - currentq))
#uplim.key = rowkey
    lowlim.key <- uplim.key - 1 #lowlim.key = rowkey - 1
  } else if ((as.numeric(wua.table[rowkey,1]) - currentq) < 0) {
    lowlim.key <- which.min(abs(as.numeric(wua.table[,1]) - currentq))
#lowlim.key=rowkey
    uplim.key <- lowlim.key + 1 #uplim.key = rowkey + 1
  } else if ((as.numeric(wua.table[rowkey,1]) - currentq) == 0) {
    lowlim.key <- which.min(abs(as.numeric(wua.table[,1]) - currentq))
    uplim.key <- which.min(abs(as.numeric(wua.table[,1]) - currentq))
  }

  # Interpolate (linear) btwn WUA values for bounding flows
  targets <- colnames(wua.table)[-1]
  for (p in 1:length(targets)) {
    if (lowlim.key == uplim.key) {
      habitat.ts[n,p+1] <- wua.table[lowlim.key, p+1]
    } else {
#linear interpolation:  $Y_q = Y_{low} + ((Y_{up} - Y_{low}) * (X_q - X_{low}) / (X_{up} - X_{low}))$ 
      Xup <- wua.table[uplim.key, 1]
      Yup <- wua.table[uplim.key, p+1]
      Xlow <- wua.table[lowlim.key, 1]
      Ylow <- wua.table[lowlim.key, p+1]
      habitat.ts[n,p+1] <- Ylow + ((Yup - Ylow) * (currentq - Xlow) / (Xup - Xlow))
    }
  }
}

# Store current reach's "habitat.ts" matrix in "habitat.matrix"
habitat.matrix[[m]] <- habitat.ts

```

```

### Calculate Habitat Time Series as % of Maximum WUA
# Find maximum WUA for each species of current wua.table
max.wua <- c()
for (c in 1:dim(wua.table)[2]) {
  max.wua[c] <- max(wua.table[,c], na.rm=TRUE)
}

# Calculate WUA as the % of Maximum WUA (from WUA table)
# Initialize individual % habitat time series matrix
habitat.P.ts <- matrix(0, nrow=length(q), ncol=ncol(wua.table))
colnames(habitat.P.ts) <- colnames(wua.table)
rownames(habitat.P.ts) <- as.vector(flow.ts[,1])
habitat.P.ts[,1] <- as.vector(as.numeric(q))

for (c in 2:dim(wua.table)[2]) {
  max.wua.c <- max.wua[c]
  habitat.P.ts[,c] <- habitat.ts[,c]/max.wua.c
}

#Store current reach's "habitat.P.ts" matrix in "habitat.P.matrix"
habitat.P.matrix[[m]] <- habitat.P.ts
}

```


D-5. calcStandardWUAcurve.r

```
### Calculate Standard WUA Table/Curves
```

```
# Run "readWUATablesAll.r" before this script...
```

```
# output will be "wua.matrix" - list of 23 matrices
```

```
# Initialize results matrix
```

```
wua.P.matrix <- vector("list", length(wua.matrix)) #set up list to store all WUA tables
```

```
for (j in 1:length(wua.matrix)) {
```

```
  # Load WUA table
```

```
  wua <- wua.matrix[[j]]
```

```
  flow <- flow.matrix[[j]]
```

```
  colnames(flow) <- c("date", "discharge")
```

```
  # Initialize standard WUA table
```

```
  wua.P <- matrix(ncol=ncol(wua)+1, nrow=nrow(wua))
```

```
  colnames(wua.P) <- c(colnames(wua), "P")
```

```
  wua.P[, "discharge"] <- wua[, "discharge"] #fill first column (discharge)
```

```
  # Run through each species and divide by maximum WUA
```

```
  for (sp in 2:dim(wua)[2]) {
```

```
    WUApeak <- max(wua[,sp])
```

```
    wua.P[,sp] <- wua[,sp]/WUApeak
```

```
  }
```

```
  # Calculate exceedance probabilities for flow time series
```

```
  sortflow <- sort(na.omit(flow[, "discharge"]), decreasing=TRUE)
```

```
  m <- 1:length(sortflow)
```

```
  P <- 100*(m/(1+length(sortflow)))
```

```
  # Fill P column with exceedance probability
```

```
  for (q in 1:nrow(wua.P)) {
```

```
    wua.P[q, "P"] <- P[which.min(abs(sortflow-wua[q, "discharge"]))]
```

```
  }
```

```
wua.P.matrix[[j]] <- wua.P
```

```
}
```

D-6. calcIndexB.r

```
#### Calculate Index B

# Run "calcHabitatTsAll.r" before this script...
# output will be "habitat.matrix" and "habitat.P.matrix" - lists of 23 matrices

library('IHA')
library('zoo')

# Calculate number of species per WUA table
n <- c()
for (w in 1:length(habitat.P.matrix)) {
  n[w] <- ncol(habitat.P.matrix[[w]])-1
}
N <- sum(n) #sum number of species for ALL sites

# Initialize results matrix & row counter
indexB <- matrix(nrow=N, ncol=14)
colnames(indexB) <- c("species", "site", "m1", "m2", "m3", "m4", "m5", "m6", "m7", "m8",
"m9", "m10", "m11", "m12")
rowit <- 1
reachnameX <- c()
speciesCode <- c()

for (i in 1:length(habitat.P.matrix)) {
  #extract standardized habitat time series
  hab <- habitat.P.matrix[[i]]

  #print status message
  print(paste("Calculating IndexB values for ", reachname[i], sep=""))

  for (sp in 2:dim(hab)[2]) {
    species <- colnames(hab)[sp]
    # Populate species and site columns of indexB matrix
    indexB[rowit,"species"] <- species
    reachnameX[rowit] <- as.character(reachname[i])

    # Create matrix of month (from date) and current species' habitat time series
    m.sp <- cbind(month(as.Date(rownames(hab))), hab[,species])
    colnames(m.sp) <- c("month", species)
    # Calculate 10th and 90th percentile of WUA values by month
    q90.m <- tapply(hab[,species], month(as.Date(rownames(hab))), quantile, 0.90,
na.rm=TRUE)
```

```

q10.m <- tapply(hab[,species], month(as.Date(rownames(hab))), quantile, 0.10,
na.rm=TRUE)

# Only keep values within 10th and 90th percentile of each month
above <- m.sp[m.sp[,species] > q10.m[m.sp[, "month"],]
below <- above[above[,species] < q90.m[above[, "month"],]

# Calculate monthly mean of habitat values in matrix "below"
m.mean <- tapply(below[,species], below[, "month"], FUN=mean, na.rm=TRUE)
#Check if "m.mean" is missing any values
m.means <- c()
for (m in 1:12) {
  if (length(which(rownames(m.mean) == as.character(m))) != 0) {
    m.means[m] <-
m.mean[rownames(m.mean)==as.character(m)]
  } else
    m.means[m] <- NA
}

# Fill m.mean with available

# Populate indexB matrix with mean WUA values by month
indexB[rowit,3:14] <- m.means
rowit <- rowit + 1 #add 1 to row counter
}
}

indexB[, "site"] <- reachnameX

write.csv(indexB, file="indexB.csv")

#### Plot barplot of Monthly IndexB Values
par(mfrow=c(2,2))
rows <- sample(1:dim(indexB)[1], 4)

row <- rows[1]
barplot(as.numeric(as.vector(indexB[row,3:14])), names.arg=colnames(indexB)[3:14],
xlab="Month", ylab="Avg Monthly WUA / Maximum WUA",
ylim=c(0,1), cex.lab=1.5,
main=paste(indexB[row,"site"], " - ", indexB[row,"species"], sep=""))
row <- rows[2]
barplot(as.numeric(as.vector(indexB[row,3:14])), names.arg=colnames(indexB)[3:14],
xlab="Month", ylab="Avg Monthly WUA / Maximum WUA",
ylim=c(0,1), cex.lab=1.5,

```

```

    main=paste(indexB[row,"site"], " - ", indexB[row,"species"], sep="")
row <- rows[3]
barplot(as.numeric(as.vector(indexB[row,3:14])), names.arg=colnames(indexB)[3:14],
        xlab="Month", ylab="Avg Monthly WUA / Maximum WUA",
        ylim=c(0,1), cex.lab=1.5,
        main=paste(indexB[row,"site"], " - ", indexB[row,"species"], sep=""))
row <- rows[4]
barplot(as.numeric(as.vector(indexB[row,3:14])), names.arg=colnames(indexB)[3:14],
        xlab="Month", ylab="Avg Monthly WUA / Maximum WUA",
        ylim=c(0,1), cex.lab=1.5,
        main=paste(indexB[row,"site"], " - ", indexB[row,"species"], sep=""))
par(mfrow=c(1,1))

```

D-7. calcWUAcurveChars.r

```
#### Calculate Peak and Location of Peak from WUA Curves
#All Species x Sites

# Run "readUSGSflowsAll.r", "readWUAtablesAll.r", and "calcStandardWUAcurve.r"
# before this script...
# outputs will be "flow.matrix" and "wua.matrix" - lists of 23 matrices

library('IHA')
library('zoo')
library('e1071')

# Calculate number of species per WUA table
n <- c()
for (w in 1:length(wua.matrix)) {
  n[w] <- ncol(wua.matrix[[w]])-1
}
N <- sum(n) #sum number of species for ALL sites

# Initialize results matrix & row counter
curve.char <- matrix(nrow=N, ncol=8)
colnames(curve.char) <- c("species", "site", "WUApeak", "FlowPeak", "QP", "SL", "SK", "SD")
rowit <- 1
speciesCode <- c()

for (i in 1:length(wua.matrix)) {
  # Pull out WUA table from wua.matrix and flow time series from flow.matrix
  wua <- wua.matrix[[i]]
  wua.P <- wua.P.matrix[[i]]
  flow <- flow.matrix[[i]]
  colnames(flow) <- c("date", "discharge")

  # Calculate exceedance probabilities for flow time series
  sortflow <- sort(na.omit(flow[, "discharge"]), decreasing=TRUE)
  m <- 1:length(sortflow)
  P <- 100*(m/(1+length(sortflow)))

  # For each species, calculate curve characteristics
  for (sp in 2:dim(wua)[2]) {
    # Populate species & site columns
    curve.char[rowit, "species"] <- colnames(wua)[sp]
    curve.char[rowit, "site"] <- as.character(reachname[i])

    # Determine maximum WUA value and flow value where max WUA occurs
```

```

WUApeak <- max(wua[,sp])
WUApeak.ind <- which.max(wua[,sp])
FlowPeak <- wua[WUApeak.ind, "discharge"]
curve.char[rowit,"WUApeak"] <- WUApeak
curve.char[rowit,"FlowPeak"] <- FlowPeak

#### Calculate percentile of flow value where max WUA occurs
Ppeak <- P[which.min(abs(sortflow - FlowPeak))]
#curve.char[rowit,"Ppeak"] <- round(Ppeak, 1)
curve.char[rowit,"QP"] <- round(100-Ppeak, 1)

#### Calculate slope of WUA curve from 1/2-distance-to-peak to the peak WUA
# Check if 0.5*FlowPeak is less than minimum flow
min.q <- min(wua[,"discharge"])
if (0.5*FlowPeak < min.q) {
  slope <- 0
} else if (0.5*FlowPeak >= min.q) {

# Find WUA value at 1/2-distance-to-peak WUA
rowkey <- which.min(abs(as.numeric(wua[,1]) - 0.5*FlowPeak)) #find flow
closest to desired q

# Determine the given flows (and row indices) that bound the desired flow
if ((as.numeric(wua[rowkey,1]) - 0.5*FlowPeak) > 0) {
  uplim.key <- which.min(abs(as.numeric(wua[,1]) -
0.5*FlowPeak)) #uplim.key = rowkey
  lowlim.key <- uplim.key - 1 #lowlim.key = rowkey - 1
} else if ((as.numeric(wua[rowkey,1]) - 0.5*FlowPeak) < 0) {
  lowlim.key <- which.min(abs(as.numeric(wua[,1]) -
0.5*FlowPeak)) #lowlim.key=rowkey
  uplim.key <- lowlim.key + 1 #uplim.key = rowkey + 1
} else if ((as.numeric(wua[rowkey,1]) - 0.5*FlowPeak) == 0) {
  lowlim.key <- which.min(abs(as.numeric(wua[,1]) -
0.5*FlowPeak))
  uplim.key <- which.min(abs(as.numeric(wua[,1]) -
0.5*FlowPeak))
}
# Interpolate (linear) btwn WUA values for bounding flows to get Y1
for (p in 1:length(targets)) {
  if (lowlim.key == uplim.key) {
    Y1 <- wua[lowlim.key, sp]
  } else {
    #linear interpolation: Yq = Ylow + ((Yup-Ylow)*(Xq-
Xlow)/(Xup-Xlow))
    Xup <- wua[uplim.key, "discharge"]

```

```

        Yup <- wua[uplim.key, sp]
        Xlow <- wua[lowlim.key, "discharge"]
        Ylow <- wua[lowlim.key, sp]
        Y1 <- Ylow + ((Yup-Ylow)*(0.5*FlowPeak-Xlow)/(Xup-Xlow))
    }
}

Y1 <- Y1/WUApeak
Y2 <- WUApeak/WUApeak
X1 <- 0.5*FlowPeak
X2 <- FlowPeak
slope <- (Y2-Y1)/(X2-X1)

}

curve.char[rowit,"SL"] <- round(10*slope, 5)

### Calculate skewness and standard deviation of curve
# Create bins for percentile flows
nbin <- 100
bins <- seq(0,100,100/nbin)

# Calculate WUA/maxWUA associated with each bin
height <- c(); X <- c()
for (x in 2:length(bins)) {
    XL <- bins[x-1]
    XR <- bins[x]
    X[x] <- 0.5*(XL+XR)
    if (XL > max(100-wua.P[,"P"])) {
        height[x:length(bins)] <- NA
    } else if (XL <= max(100-wua.P[,"P"])) {
        XR <- bins[x]
        XL.ind <- which.min(abs((100-wua.P[,"P"])-XL))
        YL <- wua.P[XL.ind, sp]
        XR.ind <- which.min(abs((100-wua.P[,"P"])-XR))
        YR <- wua.P[XR.ind, sp]

        height[x] <- 0.5*(YL+YR)
    }
}

H <- round(height*100, 0); H[is.na(H)] <- 0; X[is.na(X)] <- 0
distr <- c()
for (h in 1:length(H)) {
    distr <- c(distr, rep(X[h], H[h]))
}

```

```
## Plot histogram of 'distr' and check that it looks like Q-WUA curve
#hist(distr, breaks=bins)
#plot(100-wua.P[, "P"], wua.P[,sp])

# Calculate skewness and standard deviation of curve
curve.char[rowit,"SK"] <- round(skewness(distr),2)
curve.char[rowit,"SD"] <- round(sd(distr), 2)

# Add counter before next loop
rowit <- rowit + 1
}
}

write.csv(curve.char, file="curvecharacters.csv")
```


D-8. cluster-mdata.r

```
# Read in Index B Values
setwd("C:/Users/grad/Google Drive/Flow-Ecology")
info <- read.csv("information.csv")
attach(info)

indexB <- read.csv("indexB.csv")
attach(indexB)
species <- indexB$species
site <- factor(indexB$site)
mdata <- indexB[,4:15]
rownames(mdata) <- indexB$X

# Dendrogram
mdata2 <- mdata[complete.cases(mdata),]
indexB2 <- indexB[complete.cases(indexB),]
d <- dist(scale(mdata2), method="euclidean")
tree <- hclust(d, method="ward")
plot(tree, xlab="Monthly Habitat Availability (WUA)", sub=NA, cex=0.25)

#Cut Tree
g <- 3
group3 <- cutree(tree, k=g)
plot(tree); rect.hclust(tree, k=g, border="red")
indexB2$group3 <- factor(group3)
#### FOUR CLUSTERS
g4 <- 4
group4 <- cutree(tree, k=g4)
plot(tree, xlab="Site-Species Combinations", main=NA, sub=NA, cex=0.25)
rect.hclust(tree, k=g4, border="red")
indexB2$group4 <- factor(group4)
####
g5 <- 5
group5 <- cutree(tree, k=g5)
plot(tree); rect.hclust(tree, k=g5, border="red")
indexB2$group5 <- factor(group5)
g6 <- 6
group6 <- cutree(tree, k=g6)
plot(tree); rect.hclust(tree, k=g6, border="red")
indexB2$group6 <- factor(group6)
```

```

#### Determine best number of clusters
# Silhouette Width
library("cluster")
asw <- numeric(nrow(mdata2))
for (k in 2:(nrow(mdata2)-1)) {
  sil <- silhouette(cutree(tree, k=k), d)
  asw[k] <- summary(sil)$avg.width
}
k.best.sil <- which.max(asw)

# Mantel statistic
grpdist <- function(X) {
  require(cluster)
  gr <- as.data.frame(as.factor(X))
  distgr <- daisy(gr, "gower")
  distgr
}
kt <- data.frame(k=1:nrow(mdata2), r=0)
for (i in 2:(nrow(mdata2)-1)) {
  gr <- cutree(tree, i)
  distgr <- grpdist(gr)
  mt <- cor(d, distgr, method="spearman")
  kt[i,2] <- mt
}
k.best.mantel <- which.max(kt$r)

# Silhouette Plot of Final Partition
library("cluster")
k <- 4
cutg <- cutree(tree, k=k)
sil <- silhouette(cutg, d)
silo <- sortSilhouette(sil)
rownames(silo) <- row.names(mdata2)[attr(silo,"iOrd")]
plot(silo, main="Silhouette Plot", cex.names=0.75, col=cutg+1, nmax.lab=100)

####Store species & site variables for each group

gr31 <- (indexB2[indexB2[, "group3"]==1,])
gr32 <- (indexB2[indexB2[, "group3"]==2,])
gr33 <- (indexB2[indexB2[, "group3"]==3,])

gr41 <- (indexB2[indexB2[, "group4"]==1,])
gr42 <- (indexB2[indexB2[, "group4"]==2,])
gr43 <- (indexB2[indexB2[, "group4"]==3,])
gr44 <- (indexB2[indexB2[, "group4"]==4,])

```

```

gr51 <- (indexB2[indexB2[,"group5"]==1,])
gr52 <- (indexB2[indexB2[,"group5"]==2,])
gr53 <- (indexB2[indexB2[,"group5"]==3,])
gr54 <- (indexB2[indexB2[,"group5"]==4,])
gr55 <- (indexB2[indexB2[,"group5"]==5,])

par(mfrow=c(1,3))
boxplot(as.matrix(gr31[,4:15]), ylim=c(0,1))
boxplot(as.matrix(gr32[,4:15]), ylim=c(0,1))
boxplot(as.matrix(gr33[,4:15]), ylim=c(0,1))
par(mfrow=c(1,1))

par(mfrow=c(1,4))
boxplot(as.matrix(gr41[,4:15]), ylim=c(0,1))
boxplot(as.matrix(gr42[,4:15]), ylim=c(0,1))
boxplot(as.matrix(gr43[,4:15]), ylim=c(0,1))
boxplot(as.matrix(gr44[,4:15]), ylim=c(0,1))
par(mfrow=c(1,1))

par(mfrow=c(1,5))
boxplot(as.matrix(gr51[,4:15]), ylim=c(0,1))
boxplot(as.matrix(gr52[,4:15]), ylim=c(0,1))
boxplot(as.matrix(gr53[,4:15]), ylim=c(0,1))
boxplot(as.matrix(gr54[,4:15]), ylim=c(0,1))
boxplot(as.matrix(gr55[,4:15]), ylim=c(0,1))
par(mfrow=c(1,1))

# Plot avg monthly values for each group (n=4)
mos <- c("J", "F", "M", "A", "M", "J", "J", "A", "S", "O", "N", "D")
par(mfrow=c(2,2), mar=c(5.1,4.1,0.5,2.1 ))
boxplot(as.matrix(gr41[,4:15]), ylim=c(0,1),
        cex.lab=1.5, cex.axis=1.5, names=mos,
        xlab="Month", ylab="Average Habitat Availability")
boxplot(as.matrix(gr42[,4:15]), ylim=c(0,1),
        cex.lab=1.5, cex.axis=1.5, names=mos,
        xlab="Month", ylab="Average Habitat Availability")
boxplot(as.matrix(gr43[,4:15]), ylim=c(0,1),
        cex.lab=1.5, cex.axis=1.5, names=mos,
        xlab="Month", ylab="Average Habitat Availability")
boxplot(as.matrix(gr44[,4:15]), ylim=c(0,1),
        cex.lab=1.5, cex.axis=1.5, names=mos,
        xlab="Month", ylab="Average Habitat Availability")
par(mfrow=c(1,1), mar=c(5.1, 4.1, 4.1, 2.1))

```

```
#Versus avg monthly values for all site-species combos
boxplot(as.matrix(mdata2), ylim=c(0,1))
```

```
### Site - Species within each cluster
```

```
gr41 <- (indexB2[indexB2[, "group4"]==1,])
gr42 <- (indexB2[indexB2[, "group4"]==2,])
gr43 <- (indexB2[indexB2[, "group4"]==3,])
gr44 <- (indexB2[indexB2[, "group4"]==4,])
names.g1 <- cbind(as.character(gr41$species), as.character(gr41$site))
names.g2 <- cbind(as.character(gr42$species), as.character(gr42$site))
names.g3 <- cbind(as.character(gr43$species), as.character(gr43$site))
names.g4 <- cbind(as.character(gr44$species), as.character(gr44$site))
write.csv(names.g1, file="namesg1.csv")
write.csv(names.g2, file="namesg2.csv")
write.csv(names.g3, file="namesg3.csv")
write.csv(names.g4, file="namesg4.csv")
write.csv(gr41, file="gr41.csv")
write.csv(gr42, file="gr42.csv")
write.csv(gr43, file="gr43.csv")
write.csv(gr44, file="gr44.csv")
```

```
### Test for Statistical Significance
```

```
Ys <- as.matrix(indexB2[,4:15])
grp <- factor(indexB2[, "group4"])
mod <- lm(Ys ~ grp)
summary(mod)
```

```
t.test(gr41[,4:15], gr42[,4:15])
t.test(gr41[,4:15], gr43[,4:15])
t.test(gr41[,4:15], gr44[,4:15])
t.test(gr42[,4:15], gr43[,4:15])
t.test(gr42[,4:15], gr44[,4:15])
t.test(gr43[,4:15], gr44[,4:15])
```

```
### Identify Representative Species for Each Group
```

```
# by calculating site-species combo with minimum SSE from median
#group 1
g1.meds <- sapply(gr41[,4:15], FUN=median)
sse1 <- c()
```

```

for (r in 1:nrow(gr41)) {
  sse1[r] <- sum((gr41[r,4:15] - g1.meds)^2)
}
g1.rep <- gr41[which.min(sse1),]

par(mfrow=c(1,2))
boxplot(g1.rep[4:15], ylim=c(0,1))
boxplot(as.matrix(gr41[4:15]), ylim=c(0,1))
par(mfrow=c(1,2))

#group 2
g2.meds <- sapply(gr42[4:15], FUN=median)
sse2 <- c()
for (r in 1:nrow(gr42)) {
  sse2[r] <- sum((gr42[r,4:15] - g2.meds)^2)
}
g2.rep <- gr42[which.min(sse2),]

#group 3
g3.meds <- sapply(gr43[4:15], FUN=median)
sse3 <- c()
for (r in 1:nrow(gr43)) {
  sse3[r] <- sum((gr43[r,4:15] - g3.meds)^2)
}
g3.rep <- gr43[which.min(sse3),]

#group 4
g4.meds <- sapply(gr44[4:15], FUN=median)
sse4 <- c()
for (r in 1:nrow(gr44)) {
  sse4[r] <- sum((gr44[r,4:15] - g4.meds)^2)
}
g4.rep <- gr44[which.min(sse4),]

par(mfrow=c(2,4))
boxplot(as.matrix(gr41[4:15]), ylim=c(0,1))
boxplot(as.matrix(gr42[4:15]), ylim=c(0,1))
boxplot(as.matrix(gr43[4:15]), ylim=c(0,1))
boxplot(as.matrix(gr44[4:15]), ylim=c(0,1))
boxplot(g1.rep[4:15], ylim=c(0,1))
boxplot(g2.rep[4:15], ylim=c(0,1))
boxplot(g3.rep[4:15], ylim=c(0,1))
boxplot(g4.rep[4:15], ylim=c(0,1))
par(mfrow=c(1,2))

g1.rep[1:3]

```

```
g2.rep[1:3]
g3.rep[1:3]
g4.rep[1:3]
```

```
### Calculate Seasonal Habitat Availability (SHA) Ratio for each group
SHA <- log(indexB[,"m3"] / indexB[,"m9"])
SHA1 <- log(gr41[,"m3"] / gr41[,"m9"])
SHA2 <- log(gr42[,"m3"] / gr42[,"m9"])
SHA3 <- log(gr43[,"m3"] / gr43[,"m9"])
SHA4 <- log(gr44[,"m3"] / gr44[,"m9"])
summary(SHA1); summary(SHA2);summary(SHA3);summary(SHA4);
sd(SHA1); sd(SHA2); sd(SHA3); sd(SHA4);
summary(SHA); sd(SHA, na.rm=TRUE)
```

```
# Test for statistical significance
Ys <- c(SHA1, SHA2, SHA3, SHA4)
inds <- factor( c( rep(1, length(SHA1)), rep(2, length(SHA2)), rep(3, length(SHA3)), rep(4,
length(SHA4))))
fit <- lm(Ys ~ inds)
summary(fit, test="Wilks")
```

```
# Boxplot of ratios by groups
#Set plot region (when set 'ylim' skip first row with headers)
boxplot( c(),
  xlim=c(0.5,4.5), ylim=c(-4,4), cex.axis=1.5, cex.lab=1.5,
  xaxt='n', xlab='Seasonal Habitat Regime', ylab='Seasonal Habitat Availability (SHA) Ratio'
)
axis(1, labels=c("Group 1", "Group 2", "Group 3", "Group 4"), at=1:4, cex.axis=1.5)
for (b in 1:4) {
  if (b == 1) {
    SHAadd <- SHA1
  } else if (b==2) {
    SHAadd <- SHA2
  } else if (b==3) {
    SHAadd <- SHA3
  } else {
    SHAadd <- SHA4
  }
}
boxplot(SHAadd, add=T, at=b, yaxt="n" )
}
```

```

#### Summarize habitat rating curve parameters within each group
# Read in curves data and store just curve parameters
curves <- read.csv("curvecharacters.csv")
cdata <- curves[,6:9]
rownames(cdata) <- curves[,"X"]
Cdata <- cdata[complete.cases(cdata),]
Cdata <- Cdata[-184,] #remove algae-midge species with slope > 1

curves.g1 <- Cdata[gr41[,"X"],]
curves.g2 <- Cdata[gr42[,"X"],]
curves.g3 <- Cdata[gr43[,"X"],]
curves.g4 <- Cdata[gr44[,"X"],]

## Test groups for stat significance
YQP <- c(curves.g1$QP, curves.g2$QP, curves.g3$QP, curves.g4$QP)
fitQP <- lm(YQP ~ inds)
summary(fitQP, test="Wilks")
anova(fitQP)

YSL <- c(curves.g1$SL, curves.g2$SL, curves.g3$SL, curves.g4$SL)
fitSL <- lm(YSL ~ inds)
summary(fitSL, test="Wilks")
anova(fitSL)

YSK <- c(curves.g1$SK, curves.g2$SK, curves.g3$SK, curves.g4$SK)
fitSK <- lm(YSK ~ inds)
summary(fitSK, test="Wilks")

YSD <- c(curves.g1$SD, curves.g2$SD, curves.g3$SD, curves.g4$SD)
fitSD <- lm(YSD ~ inds)
summary(fitSD, test="Wilks")

wilcox.test(curves.g1$QP, curves.g2$QP)
kruskal.test(curves.g1$QP, curves.g2$QP)

#### Create table of sites vs. groups with counts of species
group.by.site <- matrix(nrow=length(reachname), ncol=4)
colnames(group.by.site) <- c("g1", "g2", "g3", "g4")
rownames(group.by.site) <- reachname
SHAmeans <- matrix(nrow=length(reachname), ncol=4)
colnames(SHAmeans) <- c("g1", "g2", "g3", "g4")

```

```

rownames(SHAMEANS) <- reachname

for (n in 1:nrow(group.by.site)) {
  nsite <- rownames(group.by.site)[n]
  ng1 <- length(which(gr41[, "site"] == nsite))
  ng2 <- length(which(gr42[, "site"] == nsite))
  ng3 <- length(which(gr43[, "site"] == nsite))
  ng4 <- length(which(gr44[, "site"] == nsite))
  group.by.site[n,] <- c(ng1, ng2, ng3, ng4)

  # Calculate average SHA ratio for each group
  indG1 <- which(gr41[, "site"] == nsite)
  ratiosg1 <- log(gr41[indG1, "m3"] / gr41[indG1, "m9"])
  SHAg1 <- mean(ratiosg1, na.rm=TRUE)
  indG2 <- which(gr42[, "site"] == nsite)
  ratiosg2 <- log(gr42[indG2, "m3"] / gr42[indG2, "m9"])
  SHAg2 <- mean(ratiosg2, na.rm=TRUE)
  indG3 <- which(gr43[, "site"] == nsite)
  ratiosg3 <- log(gr43[indG3, "m3"] / gr43[indG3, "m9"])
  SHAg3 <- mean(ratiosg3, na.rm=TRUE)
  indG4 <- which(gr44[, "site"] == nsite)
  ratiosg4 <- log(gr44[indG4, "m3"] / gr44[indG4, "m9"])
  SHAg4 <- mean(ratiosg4, na.rm=TRUE)
  SHAMEANS[n,] <- c(SHAg1, SHAg2, SHAg3, SHAg4)
}
group.by.site
write.csv(group.by.site, file="n-groups-by-site.csv")

ngrps.reduce <- read.csv("n-groups-by-site-reduce.csv")
ngrpsR <- ngrps.reduce[, 2:5]
rownames(ngrpsR) <- ngrps.reduce[, 1]
flows <- read.csv("indices-full.csv")
flows.reduce <- c()
for (R in 1:nrow(ngrpsR)) {
  rname <- rownames(ngrpsR)[R]
  flowsAdd <- flows[flows[, "X"] == rname, ]
  flows.reduce <- rbind(flows.reduce, flowsAdd)
}
flowsR <- flows.reduce[, -1]
rownames(flowsR) <- as.character(flows.reduce[, 1])

cor.flows.groups <- round(cor(flowsR, ngrpsR, method="spearman"), 2)
write.csv(cor.flows.groups, file="cor-flows-groups.csv")

```


D-9. plotFlowDurCurvesandHRCs.r

```
#### Plot Unregulated and Regulated Flow Duration Curves

# Run "readUSGSflowsAll.r" and "readWUAtablesAll.r" before this script...
# output will be "flow.matrix" and "wua.matrix" - lists of 23 matrices

# Initialize unregulated and regulated flow time series matrices
unreg.matrix <- vector("list", length(flow.matrix))
reg.matrix <- vector("list", length(flow.matrix))

#### Set regulated flow start dates
# startdate, enddate generated from readUSGSflowsAll.r
unregenddate <- enddate
regstartdate <- startdate

# Set New River regulation date
regstartdate[2] <- "1939-08-01"
regstartdate[3] <- "1939-06-01"

# Set Pamunkey River regulation date
regstartdate[7] <- "1972-01-01"

# Set Roanoke River regulation date
regstartdate[15] <- "1962-10-01"
regstartdate[16] <- "1962-10-01"

# Set James River regulation date
regstartdate[23] <- "1979-12-01"

#### Set up plot window
par(mfrow=c(3,2), mar=c(4,4.2,1.5,1))

# List reach numbers that have regulated flows
regNos <- c(2,3,7,15,16,23)
specInd <- c(8, 4, 10, 11, 42, 6)
regNos <- c(2,3,7)
regNos <- c(15,16,23)

for (loop in 1:length(regNos)) {
  j <- regNos[loop]
```

```

# Load flow table
wua <- wua.matrix[[j]]
flow <- flow.matrix[[j]]
colnames(flow) <- c("date", "discharge")

# Initialize standard WUA table
wua.P <- matrix(ncol=ncol(wua)+2, nrow=nrow(wua))
colnames(wua.P) <- c(colnames(wua), "Punreg", "Preg")
wua.P[, "discharge"] <- wua[, "discharge"] #fill first column (discharge)

# Run through each species and divide by maximum WUA
for (sp in 2:dim(wua)[2]) {
  WUApeak <- max(wua[,sp])
  wua.P[,sp] <- wua[,sp]/WUApeak
}

# Set unregulated start and end date
unreg.start <- startdate[j]
unreg.end <- unregenddate[j]
# Set regulated start and end date
reg.start <- regstartdate[j]
reg.end <- enddate[j]

# Split flow matrix into pre and post-regulation matrices
flow.unreg <- flow[as.Date(flow$date) < as.Date(regstartdate[j]),]
flow.reg <- flow[as.Date(flow$date) > as.Date(regstartdate[j]),]

# Calculate exceedance probabilities for UNREGULATED flow time series
sortflow.unreg <- sort(na.omit(flow.unreg[, "discharge"]), decreasing=TRUE)
m <- 1:length(sortflow.unreg)
Pur <- 100*(m/(1+length(sortflow.unreg)))
# Fill P column with exceedance probability
for (q in 1:nrow(flow.unreg)) {
  flow.unreg[q, "P"] <- Pur[which.min(abs(sortflow.unreg -
flow.unreg[q, "discharge"]))]
}
flow.unreg[, "NP"] <- 100 - flow.unreg[, "P"]

# Calculate exceedance probabilities for REGULATED flow time series
sortflow.reg <- sort(na.omit(flow.reg[, "discharge"]), decreasing=TRUE)
m <- 1:length(sortflow.reg)
Pr <- 100*(m/(1+length(sortflow.reg)))
# Fill P column with exceedance probability
for (q in 1:nrow(flow.reg)) {
  flow.reg[q, "P"] <- Pr[which.min(abs(sortflow.reg - flow.reg[q, "discharge"]))]
}

```

```

}
flow.reg[,"NP"] <- 100 - flow.reg[,"P"]

# Fill Punreg column with exceedance probability for unregulated flows
for (q in 1:nrow(wua.P)) {
  wua.P[q,"Punreg"] <- Pur[which.min(abs(sortflow.unreg-wua[q,"discharge"]))]
  wua.P[q,"Preg"] <- Pr[which.min(abs(sortflow.reg-wua[q,"discharge"]))]
}

unreg.matrix[[j]] <- flow.unreg
reg.matrix[[j]] <- flow.reg

# Plot both flow duration curves
plot(flow.unreg[,"P"], flow.unreg[,"discharge"], log="y",
      cex.axis=1.5, cex.lab=1.5,
      main=reachname[j],
      xlab="Percent Non-Exceedance (%)", ylab="Discharge (cfs)", pch=20)
points(flow.reg[,"P"], flow.reg[,"discharge"], col="gray", pch=20)

# Plot standardized habitat rating curve
s <- specInd[loop]

plot((100-wua.P[,"Punreg"]), wua.P[,s], type="n", xlim=c(0,100), ylim=c(0,1),
      cex.axis=1.5, cex.lab=1.5,
      main=colnames(wua)[s],
      xlab="Percentile Flow (%)", ylab="WUA / Max. WUA")
lines((100-wua.P[,"Punreg"]), wua.P[,s], type="l", lty=1, lwd=3)
lines((100-wua.P[,"Preg"]), wua.P[,s], type="l", lty=2, lwd=3)

}

par(mfrow=c(1,1))

```