

Ecology and Conservation in River Networks

Tectonic Controls over Ecological Transitions and Linkages Through River Drainage Networks, **MARY E. POWER^{1*}, WILLIAM E. DIETRICH², and JACQUES C. FINLAY³** (¹Department of Integrative Biology, University of California, Berkeley, CA 94720; ²Department of Earth and Planetary Science, University of California, Berkeley, CA 94720; ³Department of Ecology, Evolution, and Behavior, University of Minnesota, Minneapolis, MN 55455; mepower@berkeley.edu).

Like branching trees and circulatory systems, river drainages are hierarchical networks, with concentrative fluxes downstream and dispersive upstream-directed backflows. Unlike trees and circulatory plumbing, river networks are also shaped by the long profile of the hillslopes on which they evolve. The 9546 km² basin of the Eel River of northwestern California is steepened, and tipped out of geomorphic equilibrium, by tectonic uplift along the Mendocino Triple Junction near its mouth. As in most rivers, channel slopes are steep in headwaters and generally decline downstream, but in the Eel, mainstem reaches draining large areas remain surprisingly steep, with important consequences for bed texture, solar radiation and hydraulic disturbance regimes; food web interactions; and ecosystem exchanges among channel, upland, and coastal marine habitats. Nick points (steps) along the river long profile also exert ecological controls on longitudinal distributions of riparian and channel biota. The degree of network branching along the long profile, potentially responding to lithology, vegetation, land use, and hydrology of the region, will in turn determine the frequency and areal extent of sub-basins with different drainage area and slopes that differentiate local ecological regimes. These sub-basins will cumulatively influence basin-wide production of watershed currencies like runoff, dissolved nitrogen, diatoms, cyanotoxins, insect emergence, or salmon, although probably not in a simple additive fashion. Considering sub-basin slopes as well as drainage areas partitioned by network branching should help us predict landscape transitions of basins from sinks to sources for atmospheric carbon and other biogeochemical fluxes.

Mainstem-Tributary Food Web Interactions in River Networks Mediated by Migratory Mayflies and Anadromous Fish, **HIROMI UNO* and MARY E. POWER** (Department of Integrative Biology, University of California, Berkeley, CA 94720; hiromiuno1@berkeley.edu).

Many organisms living in river networks are migratory. It is important to take into account the migratory life cycles of key species when we consider the ecology in river networks. Over their life cycles, salmonids, lampreys, shrimp, snails, and Anguillid eels migrate between rivers and oceans. Within river network, other organisms (frogs, aquatic invertebrates) migrate between mainstems and tributaries to exploit habitats and resources that are seasonally favorable for particular life stages. We will describe a hidden but important interaction of one mayfly *Ephemerella maculata* (Ephemerellidae), that has been discovered to migrate between mainstems and tributaries, and steelhead trout (*Oncorhynchus mykiss*) that migrate between the river and the ocean. *E. maculata* nymphs rear and emerge from productive mainstem rivers in summer. Female adults mate, then fly up adjacent small tributaries to oviposit. Subsequently, spent females drift and collect in pools, where they feed aquatic and riparian predators that

would otherwise find little to eat in dark, unproductive tributary habitats. In field manipulations of mayfly subsidies, the migratory mayfly subsidy, but not terrestrial allochthonous inputs, significantly increased growth of juvenile steelhead trout rearing in tributaries. The habitat of juvenile steelhead trout in river networks in California is increasingly restricted to cool tributaries due to mainstem warming. The biological backflow mediated by this mayfly migration may deliver critical trophic support to Pacific salmonids near the southern limits of their ranges.

A Strategy for Aquatic Biodiversity Conservation in California, **REBECCA M. QUIÑONES*, TED E. GRANTHAM, RYAN PEEK, ERIC HOMES, NICK SANTOS, ANDY BELL, PETER B. MOYLE, and JOSHUA H. VIERS** (Center for Watershed Sciences, University of California, Davis, CA 95616; rmquinones@ucdavis.edu).

Freshwater biodiversity in the Mediterranean biome is among the most threatened worldwide. In areas where fishes are the best studied aquatic organisms, such as in California, USA, fishes can serve as surrogates for aquatic biodiversity as a whole. We evaluate patterns of fish distribution, identify factors likely driving changes in biodiversity, and evaluate reserve designs that optimize aquatic biodiversity conservation in California. We used a newly developed geospatial database (PISCES) to calculate extent of historical and current distributional range of all freshwater fishes (n = 181) in California. All records are spatially referenced to watersheds (Hydrologic Unit Code 12; HUC 12). Current species assemblages are being shaped by factors different from those that shaped historical assemblages. Assemblages in novel ecosystems appear to be driven by climatic factors (maximum temperature, mean precipitation), indicating ecosystems increasingly dominated by alien species. Because novel ecosystems differ in form and function from their historical counterparts, new strategies are needed to preserve biodiversity. We use the program Zonation to prioritize reserve selection that incorporates habitat connectivity and heterogeneity. Algorithms within the program are used to preserve watershed units with the highest conservation value while considering species richness and rarity. Two reserve designs are compared, one within the historical context (what would have been the best reserve design?) with one set in the current landscape (what is now the best reserve design?). Our methodology provides a roadmap for protecting endemic aquatic biodiversity in California, which will likely suffer high rates of extinction without systematic protection of watersheds.

Assessing the Performance of Geometric and Habitat-Based Indices of Population Persistence Using Continuous Space Models of River Networks, **KURT E. ANDERSON*, JONATHAN SARHAD, and SCOTT MANIFOLD** (Department of Biology, University of California, Riverside, CA 92521; kurt.anderson@ucr.edu).

Freshwater scientists are increasingly demonstrating that the branching structure of river networks has substantial ecological consequences. This is especially true when considering metapopulation and metacommunity dynamics in river watersheds, where natural and anthropogenic disruptions to connectivity can dramatically reduce long term persistence potential. We explore population persistence by expanding a framework for modeling branching river networks as continuous systems using dynamic, spatially-explicit models linked to metric graphs. Unlike traditional graphs,

metric graphs encode a continuous branching system where edges represent actual domain rather than simple connections among discrete nodes. Graph edges are connected by junction conditions that represent branch confluences. Using the metric graph framework, we model the effects of movement, network geometry, and the distribution of habitat within the network on population persistence in both radial and stochastic model networks. Via numerical simulations, we show that movement rates, habitat length, and the distribution of habitable area all play large roles in determining persistence potential. In particular, movement behaviors and habitat distributions that reduce the encounter rate between individuals and lethal habitat boundaries increase population persistence across all model types. We identify an index related to the distribution of habitable volume in the network as a promising indicator of population persistence potential. This index outperforms other metrics such as the maximum and minimum distance from the river outflow to an upstream boundary and the total habitable volume of a tree. We conclude by describing extensions and other potential applications of our framework.

Spatial Sampling on Streams: Principles for Inference on Aquatic Networks, **NICHOLAS A. SOM**^{1*}, **PASCAL MONESTIEZ**², **JAY M. VER HOEF**³, **DALE L. ZIMMERMAN**⁴, and **ERIN E. PETERSON**⁵ (¹Arcata Fish and Wildlife Office, US Fish and Wildlife Service, Arcata, CA 95521; ²Biostatistique et Processus Spatiaux, INRA, Avignon, France; ³National Marine Mammal Laboratory, Alaska Fisheries Science Center, National Oceanographic and Atmospheric Administration, Seattle, WA 98115; ⁴Department of Statistics and Actuarial Science, University of Iowa, Iowa City, IA 52242; ⁵CSIRO Computational Informatics, Dutton Park, QLD, Australia; nicholas_som@fws.gov).

For ecological and environmental data, prior inquiries into spatial sampling designs have considered 2-dimensional (2-D) domains, and have shown that design optimality depends on the characteristics of the target spatial domain and intended inference. The structure and water-driven continuity of streams prompted the development of spatial autocovariance models for stream networks. The unique properties of stream networks, and their spatial processes, warrant evaluation of sampling design characteristics in comparison to their 2-D counterparts. Common inference scenarios in stream networks include spatial prediction, estimation of fixed effects parameters, and estimation of autocovariance parameters, with prediction and fixed effects estimation most commonly coupled with autocovariance parameter estimation. We consider these inference scenarios under a suite of network characteristics and stream-network spatial processes. Our results demonstrate, for parameter estimation and prediction, the importance of collecting samples from specific network locations. Additionally, our results mirror aspects from the prior 2-D sampling design inquiries; namely, the importance of collecting some samples within clusters when autocovariance parameter estimation is required. These results can be applied to help refine sample site selection for future studies, and further showcase that understanding the characteristics of the targeted spatial domain is essential for sampling design planning.

Stream Temperature Variability over Time and Space: Metrics and Models, **E. ASHLEY STEEL** (Pacific Northwest Research Station, USDA Forest Service, Seattle WA, 98103; asteel@fs.fed.us).

Variability in stream temperature within a stream network and

over time matters for aquatic biota; yet, it is impossible to measure completely and challenging to model. A great deal of research has focused on human-induced increases in water temperature; however, human activities, e.g., dams, land-use, and climate change, impact the variability and complexity of water temperature regimes as well. We apply network models to map variability at multiple time scales; explore spatial pattern across metrics and over time; and conceptualize which aspects of temporal variance are driven by within network versus out-of-network processes. Using data collected every 30-min across the Snoqualmie River, WA, we demonstrate, for example, that while the spatial distribution of mean temperature over the stream network varies little between summer and winter, the spatial distribution of variance varies tremendously between summer and winter. Changes in variance have the potential for dramatic sub-lethal effects on food web dynamics, species phenology, and community composition. As evidence, we summarize results from a series of laboratory experiments measuring the impact of altered thermal regimes on the egg to fry lifestages of Chinook salmon. Understanding the drivers and patterns of thermal complexity as well as their impacts on biota are essential for effective management of aquatic systems.