Modeling fish species diversity in river networks



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Introduction

- River basins across the world are shaped by local land topography and generally have a dendritic structure formed by convergence of river streams originating in a watershed until they end up in the main river.
- They are home to a plethora of aquatic lifeforms. Movement patterns of riverine biodiversity, especially fishes, are shaped by dendritic structure of river networks (see Figure) and habitat capacity of river basins [1].

Mississippi-Missouri River System (MMRS)





- Neutral biodiversity models [2] have been able to successfully explain a suite of biodiversity indices of plant and animal species across various ecological systems, but have been poorly studies for systems characterized by dendritic geormetry [1].
- The river networks project at CASUS is aimed at developing models to study the effects of dendritic network topology on fish biodiversity.

Neutral Model of Biodiversity

Under `neutral' assumption, species are assumed to be equivalent on a *per capita* basis [2]. Species abundances are evolved via Markovian process until the system reaches a steady state.

A death at a randomly chosen site p or \mathcal{V} diversification dispersal End Equilibrium?

$$HC_i = C_H * N * -$$

v is diversification probability

Habitat capacity:

$$N * \frac{AARP_i * WA_i}{\sum_{i=1}^{N} (AARP_i * WA_i)}$$

$$L_{ij} = C \Big[a^{L_{ij}} + \frac{b^2}{L_{ii}^2 + b^2} \Big]$$

Dispersal Kernel:

Dispersal probability:
$$P_{ij} = (1$$

WA is the watershed area, AARP is average annual runoff production

$$= (1 - v) \frac{K_{ij}H_j}{\sum_{k=1}^N K_{ik}H_k}$$

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Impact of dendritic geoemtry: Square Lattice vs. Optimal Channel Network (OCN)





N is the number of sites in the system

L_{ii} is the topological distance between nodes i & j

a, b set local and global dispersal over the network

Steps:

- →Obtain a river network, watershed area, runoff from hydrological data.
- Obtain local species richness (LSR), species occurrences for finding empirical biodiversity patterns.
- Set neutral model parameters, and probabilities of dispersion.
- →Run the neutral model, until the steady-state is reached. Obtain the model biodiversity patterns.
- Re-calibrate the model by optimizing the parameters.



Results (on MMRS network)

Model LSR (alpha diversity) and Jaccard Similarity Index (for beta diversity) trend matched with that of empirical. Model results do not perfectly reproduce the empirical bi-modal distribution of LSR and straight line nature of the rank-occupancy curve.







Challenges and Outlook

There are different possible network representations of the same river system. Our goal is to reproduce the empirical patterns for all geometries and compare them. The sequential implementation of the model is a computationally heavy task. We are exploring parallel implemetation on GPU. Our initial results are promising.

Biodiversity modeling enables understanding the factors shaping present biodiversity and allows us to simulate how climate change might affect future riverine biodiversity.

References:

[1] Hubbell, S. P. (2011). The unified neutral theory of biodiversity and biogeography(MPB-32). In The Unified Neutral Theory of Biodiversity and Biogeography(MPB-32). Princeton University Press.

[2] Muneepeerakul, R., Bertuzzo, E., Lynch, H. J., Fagan, W. F., Rinaldo, A., & Rodriguez-Iturbe, I. (2008). Neutral metacommunity models predict fish diversity patterns in Mississippi-Missouri basin. Nature, 453(7192), 220-222.





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