Question is the effect of fragmentation on metapopulation persistence in directional dendritic networks (streams). Response variables are metapopulation mean life time (MMLT) and metapopulation growth rate (GR).

H1: fragmentation is cumulative and most species can tolerate some fragmentation.

Pred 1: non-linear relationship between connectivity (as measured with DCI) and the both response variables. This is a strawman hypothesis which validate the model produces expected results.

H2: Species traits associated with Dispersal and Life History affect the response to fragmentation

Pred 2: The relationship between fragmentation and MMLT and GR will vary due to species traits as outlined below.

Exploratory analyses after, which traits have the largest effect?

Analyses: GLMM modelling and effect sizes

Species traits are parameterized based on values for stream fish communities in five watersheds in the Toronto region. After running simulations, each stream network is analyzed and inferences made about species that are likely to persist in these streams based on trait combinations.

1. Create random network, 50 nodes with a defined structure
2. For each node record
   1. Strahler stream order
3. Define node characteristics
   1. Node ID: Number that identifies each node (0-n)
   2. Area: Amount of habitat (0-100)
   3. Quality: Changes for each species group, used to define headwater or trunk habitat and is based on a poisson distribution. Random number from a poission distribution is assigned to each node stratified by Strahler order
   4. Up Stream permeability: Permeability to move out of node upstream (0-1)
   5. Down Stream permeability: Permeability to move into node from upstream (0-1)
4. Define variables for each species that will be run
   1. Define quality attribute for headwater/trunk
      1. Adult survival: Percent of adults that survive in node
      2. Juvenile survival: Percent of juveniles that survive in node
      3. Fecundity: Number of eggs or offspring produce in node
      4. Vagility: Proportion of adult population that disperses from node i to node j. Used to modify permeability
         1. Correlates with rank of species based on aspect ratio of caudal fin (Correlated with dispersal ability).
         2. Pij’ = Pij \* Vagility
      5. Max density: Number of individuals per unit area used to estimate population size in node i
         1. Representative values from the literature
         2. Pop size = Roundup (Area \* Density \* Quality)
   2. Calculate
      1. Metapopulation Mean Lifetime (MMLT)
      2. Growth Rate
5. Add dams to network
   1. Record
      1. Strahler stream order of barrier
   2. Calculate
      1. DCIp and DCId to estimate connectivity for the network
   3. Define quality attribute for headwater/trunk
      1. For every combination of species as defined in 4.1 calculate
         1. MMLT
         2. Growth Rate

Step 4.2 is repeated for each combination of fish traits (4.1.x) within the headwater and trunk scenarios (Step 4.1). DCIp and DCId both are equal to 100 because there are no barriers so it does not need to be calculated and is left out to reduce processing time.

Step 6 is repeated for each level of fragmentation scenario created by adding dams to the network. Headwater or trunk (Step 6.3), is repeated for every level of fragmentation (step 6). All species trait groups (Step 6.3.1) are repeated within every level of headwater v trunk (step 6.3)

Choosing species trait values

Vagility

Range 0-0.5

Adult survival

Range 0 – 0.9

Juvenile survival

Range 0-0.9

Fecundity

Range 100-500000

Density

Range 0.05 - 1

Use a Latin hypercube design to select a reasonable number of combinations for species traits, 3 000 to 5 000. Number of combinations determined by trade-off between fully sampling and processing time.

5 000 trait combinations \* 2 (headwater v trunk) \* n barrier scenarios

Barrier scenarios (number of barriers) determine levels of fragmentation (DCI). Simulations with 5 replicates of 1:25 random barriers on a 50 node network show a negative correlation between number of barriers and DCIp and DCId (expected). However residuals are not randomly distributed. Residuals are over dispersed with low number of barriers and under dispersed with high numbers of barriers. Non-randomly distributed residuals are expected because variation in the location of barriers decreases with increasing number of barriers.

The non-randomly distributed residuals demonstrates that both the number of barriers and DCI values should be retained and kept in analyses. Additionally, multiple scenarios for each number of barriers should possibly be kept in the scenarios.

Next step is to run 100 replicates of 1:25 random barriers on a 50 node network to check preliminary results and resole the following issue (processing time, running tonight). Issue to be resolved is how many barriers to include and how many replicates of those barrier scenarios should be included. Do this by looking at non-linear relationship between number of barriers and DCI values. Interpolate lower inflection point to determine when system is completely fragmented (DCIp and DCId ~ 0). Plot residuals to make sure variation is limited at this point. The interpolation point determines the max number of barriers to run.