Archipelago Migration Simulation

**Function Definitions**

***CvNs***

* Returns
  + A 3D matrix of communities with varying connectomes and population sizes integrated through time using the specified model type (cascade or niche).
  + A 3D matrix of the species survival count per community
  + A 2D matrix of the mean survival rate for each connectome and species pairing
  + A 2D matrix of the standard deviations of the survival rate across the communities

***heatMap***

* Returns
  + A 2D matrix as a heatmap

***subsetPath***

* Returns
  + A list of 100 (arbitrary number) samplings of the mainland transferred to an island; each sampling contains 4 lists: Before, Between, After, and Living
    - Before lists the starting persistence of each species on the island
    - Between lists the persistence through time for each species on the island (for each step of the integration function)
    - After lists the persistence of each species on the island after the integration period
    - Living lists all of the species and their corresponding persistence values in After that survived the integration through time

***nStarGraph***

* Prints
  + A 2D matrix of the mean survival rate for each community on the C vs N grid
* Selects
  + A community from the matrix with the specified mean survival rate (or close to it)
* Calls
  + ***subsetPath*** a variable number of times and stores the returned data
* Returns
  + A line plot showing each path generated, along with the mean path through time
  + Each generated path for the community, along with a mean path

***meanMatrix***

* Returns
  + A matrix with the mean path of each community in the C vs N grid, along with the mean path for the entire matrix (Essentially executes ***nStarGraph*** for multiple communities and returns the data)

***massMatrix***

* Calls
  + ***meanMatrix*** for every possible combination of the specified immigrant sample sizes and integration time intervals
* Returns
  + A list with each matrix generated

***matrixGraph***

* Graphs
  + The desired paths in the matrix passed
  + An optional mean path of the specified paths

**Function Details**

***CvNs***

* Parameters
  + S – The max number of species for the C vs N grid, or simply N
  + C – The max connectivity for the C vs N grid, or simply C
  + step - The size of the step to take between each community
  + intTime – The length of the initial integration for each community
    - Defaults to 100 steps
  + replicates – The number of replicate C vs N grids to generate
    - Defautls to 10
  + modelType – The type of food web model for each community to be based on, currently allows for the Cascade and Niche models
    - Defaults to “Cascade”
  + CvNs(200, 0.5, 0.05) would generate a matrix of communities of size 10 x 10 x 10, with S steps (20, 40 … 200), C steps (0.05, 0.1 … 0.5), and where each community is integrated through 100 steps
* Generate the x and y dimensions of the matrix
* For every replicate, for every C step, for every S step
  + Generate the designated model