***List and description of all the files***

***Adapted by Stephanie Bland from Tonin (2011)***

**Simulations**

- START\_RunCluster Runs the model with appropriate parameters and saves results. **Launch this one first with command:**START\_RunCluster(0,x,x)
where x is a positive integer.
A note about input parameters: str2num converts shell script parameters to parameters MATLAB can use. It is necessary for running the model in the cluster. However, it breaks when you run the model from MATLAB, so I commented out all the str2num lines. TAKE AWAY POINT: Not all input parameters will be used – they will default to those in “Parameter.m” instead. seed\_0, simnum\_0, and simnum\_f are used. seed\_0 makes the simulation reproducible. simnum\_0 and simnum\_f are the simulation numbers to run, so the model will run all simulations simnum\_0 through simnum\_f. **So to call the model all you need is the first three parameters**, ex: START\_RunCluster(0,2,2).
I suggest setting simnum\_0=simnum\_f. The simulation is reproducible, meaning the output will be identical for any given simnum (simulation number).

- DateVersion Labels output with version number

- Parameters Sets the parameters for the model.

- simulations Solves the ODEs, runs the simulations, and plots graphs. Saves all simulation relevant results. This is the computationally expensive part of the model.

**Initializing**

- setup creates the food web, sets all the web-dependent parameter values and the initial conditions for biomasses and efforts.

- NicheModel Calls “CreateWeb.m” and then tests whether it satisfies the conditions we want our original web to meet.

- CreateWeb Function called by “NicheModel.m” that takes the number of species and the connectance as inputs and calculates a “nicheweb” matrix of feeding links (rows eat columns). This function is called twice, so it has the restrictions that we want any web to meet (ex: all new life stages have some prey).

- TrophicLevels function called by “setup.m” that calculates the trophic levels of every species. Called a second time for the new life stages.

- MassCalc Called by “setup.m” to calculate their body-size

- LifeHistories Called by “setup.m” to declare new life stages. Finds the body size for new species using von-Bertalanffy. Keeps track of which nodes belong to which species, how many nodes each species has… And extends the food web to include the new lifestages (Various methods – some of them are deterministic, others call “CreateWeb.m” to fill in empty rows/columns while preserving original nodes). Also calls “LeslieMatrix.m”

- LeslieMatrix Called by “LifeHistories.m” and makes a leslie growth matrix.

- metabolic\_scaling Called by “setup.m” to calculate their metabolic rates.

- func\_resp\_scaling function called by “setup.m” that calculates the parameters values for the functional response: half saturation density and predator interference.

- attach Function from:
https://www.mathworks.com/matlabcentral/fileexchange/35436-attach/content/attach.m
that allows parameters to be packaged as fields to get pushed through functions cleanly, without long function calls.

**Dynamics**

- Dietary\_evolution Called by “simulations.m” and shifts the food web to represent diet food shifts that occur when fish species get smaller. This only has an effect if evolv\_diet is non zero – that tells you how much the web is shifted by, and in which direction. It’s a test for later (evolv\_diet is currently set at 0).

- prob\_of\_maturity Called by “simulations.m” and finds the probability of each life stage maturing.

**Dynamics**

- dynamic\_fn function that takes all the web parameters as inputs and solves the differential equations using the “ode45” function. It takes into account the extinction threshold.

- biomass function called by the “ode45” function that calculates the derivatives of the biomasses and the efforts as a unique array dx/dt.

- gr\_func function called by “biomass.m” to calculate the growth vector for the biomasses, using the ATN equations.

**Analysis**

- isConnected function that takes the food web matrix as input and determines whether the graph is connected (no isolated species, no partitioning into several isolated sub-webs).

- web\_properties function that takes the food web matrix as input and calculates the 17 structural properties of a web.