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CSE 490 Class Project - Homework 15

**Introduction**

The purpose of our program is to analyze the population variations that occur from changes in the food chain progression. A **food chain** is a linear sequence of links in a foodweb starting from "producer" species and ending at apex predator species, detritivores, or decomposer species [1]. In using our program, scientists will be able to analyze and predict variations of population size for a wide array of species, from events directly. These events vary from weather influenced population boom/bust(s), and political policies of species conservation, which lead to compounding effects on the food chain progression (The effect influenced on one species, will have an exponential effect on species below/above the food chain).

**Functional Specification**

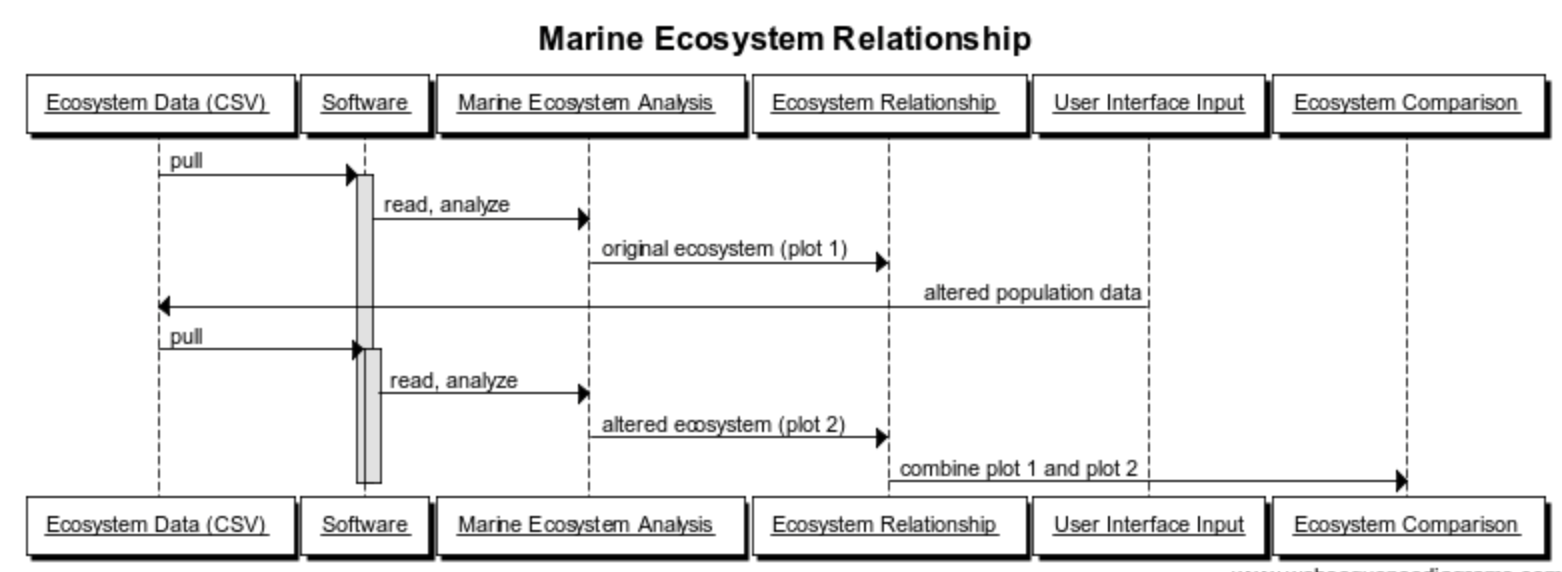
User profile:

The targeted users that will use the marine ecosystem models are marine enthusiasts, biologists, and for the one high school student that knows how to use terminal. The user should know how to run the .py files in terminal, enter in the filename, species name, and call the functions.

Use cases:

The user should have a CSV file that lists the parameters estimates for the five species. There will be a Read method where the CSV file will be read after the user inputs the file name. After the CSV file is read, the data will be organized and each parameter will be sorted respectively. The original CSV data will be solved and plotted as bar graphs. The bar graph will show the population difference for each species displayed with different color bars for easy comparison. The user can then enter in another CSV file with altered parameters which would be read, analyzed and plotted against the original ecosystem data. This will display ecosystem comparisons before and after the parameter changes. Any unknowns that are not specified will be solved using systems of linear equations before any plot is generated. The bar graph will plot the solved biomass of each species for two specified parameters.

Interactions details:



**Ecosystem**

The selected ecosystem is in a marine environment. The five species selected are harbor seals, pacific cod, shrimp, microzooplankton, and gelatinous zooplankton. These species are interrelated by a food chain where seal eats the cod, cod eats the shrimp, and so on. The ecosystem model was selected where there are no cross consumption of multiple species in the same chain, allowing easier analysis of steady state relationships between species over a sufficiently long period of time.

**Parameter Estimates**

Steady State Biomass of Species (i: Bi)

--> Sum of the mass (in kilograms) of all members of the species in the ecosystem

Production Ration per Year: (P/B)i

-->Ratio of mass produced each year to steady-state biomass

Consumption ratio per year: (*Q*/*B*)*i*

-->Ratio of mass consumed to steady-state biomass

Diet percentage: *DCji*

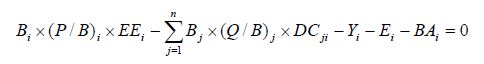
-->Fraction (by mass) of *i*'s diet that is members of species *j*, equal to one for all species

Ecotrophic efficiency: *EEi*

Fishery yield: *Yi* - assumed to be zero

All *Ei* assumed to equal zero.

**System of Linear Equations used to model the ecosystem:**



Another method to estimate parameters if not given for the animal:

where , where *T* is in degrees K of mean annual temperature of the ecosystem; is the maximum weight of an individual, is for a predator (and 0 otherwise); and is 1 for a herbivore (and 0 otherwise).

where is the lifespan of species *i*.

The parameter values should be reasonable and taken from published literature and peer reviewed sources. Source for equations used is indicated in references [2].

**Parameter Values:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Species | TL | B (mt km-2) | P/B (yr-1) | Q/B (yr-1) | EE | BA (yr-1) | P/Q |
| Harbor Seals | 4.44 | 0.0240 | 0.126 | 24.594 | 0.397 | 0 | 0.005 |
| Pacific Cod | 4.07 | 0.2000 | 0.260 | 3.784 | 0.520 | 0 | 0.069 |
| Shrimp | 2.94 | 8.134 | 2.250 | 12.000 | 0.900 | 0 | 0.344 |
| Microzooplankton | 2.05 | 5.343 | 100.000 | 285.714 | 0.800 | 0 | 0.200 |
| Gelatinous Zooplankton | 2.59 | 6.388 | 7.00 | 35.000 | 0.500 | 0 | 0.200 |

**User Details/Design Specifcations:**

The CSV file should contain a maximum of five species of animal. Three parameters should be specified in the CSV file in order for the biomass to be solved. When user input is needed, the filename and species name must be entered in quotations. This code only works for marine ecosystems, as the equation and parameters are specific to marine animals. An example of how the CSV file should be like is given below:

|  |  |  |  |
| --- | --- | --- | --- |
| marine data (P/B)\*(EE) | | -(Q/B) | -(B/A) |
| harbor seals | 0.050022 | -24.594 | 0.03 |
| pacific cod | 0.1352 | -3.784 | 0.04 |
| shrimp | 2.025 | -12 | 0.02 |
| microzooplankton | 80 | -285.714 | 0.5 |
| small gelatinous zooplankton | 7.2 | -30 | 0 |

There are three python files the user must have in the same directory as their two CSV files:

1. csv\_raw\_file\_reader\_withUnitTest.py or .ipynb extension
2. csv\_new\_file\_reader\_withUnitTest.py or .ipynb extension
3. BarGraphPlot\_withUnitTest.py or .ipynb extension

The user must enter the filename and species name in quotations, failure to do so means that the user must restart the kernel and re-enter in the specified requirements.

**References**

1. Wikipedia,. 'Food Chain'. N.p., 2015. Web. 27 May 2015.
2. Harvey C. J., Bartz K. K., Davies J., Francis T. B., Good T. P., Guerry A. D., Hanson B., et al. A mass-balance model for evaluating food web structure and community-scale indicators in the central basin of Puget Sound. U.S. Dept. Commerce, NOAA Technical Memorandum NMFS-NWFSC-106 2010. 18