SCIE3250 – Research Project

File directory

Tasks

* **Data files**
  + *RAMCore[asmt][v4.495].rdata*
    - Data set.
  + *non\_det\_cols.csv*
    - Column numbers corresponding to the 325 species with non-deterministic data.
* **R files**
  + *SCIE3250\_task\_1.1.R*
    - Plots biomass TS for all species
    - 479 species
  + *SCIE3250\_task\_1.4.R*
    - Plots R\_{t} vs R\_{t+1} for all species with overlapping catch data
    - 476 species
  + *SCIE3250\_task\_2.0\_optim.R*
    - Fits BH and HS models to each species using optim
    - Plots each model against data
    - Counts how many times BH and HS each have a lower RSS
    - 325 species
  + *SCIE3250\_task\_2.1.0\_hs\_optim\_vs\_other.R*
    - Compares optim to other technique for HS for all species
    - 415 species (64 species removed for computing problems)
  + *SCIE3250\_task\_2.1.1\_bh\_optim\_hs\_other.R*
    - Compares BH optim to HS other
    - 415 species (64 species removed for computing problems)
* **Plots**
  + *SCIE3250\_task\_1.1\_plots.pdf*
    - Biomass TS plots for all 479 species
  + *SCIE3250\_task\_1.4\_plots.pdf*
    - Bio\_{t}-Mcatch\_{t} vs Bio\_{t+1} for all 476 species
    - 3 species removed because no correlating data points between Bio and Catch
  + *SCIE3250\_task\_1.5.pdf*
    - Deterministic (elliptic looking) graphs marked and removed from data set leaving 325 species.
  + *SCIE3250\_task\_2.0\_plots.pdf* 
    - BH vs HS v data (optim used to generate parameters)
  + *SCIE3250\_task\_2.1.0\_plots.pdf*
    - Compares optim to other technique for HS for all species
  + *SCIE3250\_task\_2.1.1\_plots.pdf*
    - Compares BH optim to HS other
* *SCIE3250\_logbook.docx*
  + Log-book keeping track of ‘scientific process’