**Instructions for using “runLinkedPRM.R’” package to calculate B/Bmsy**

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**Summary:**

“runLinkedPRM.R” produces estimates of B/Bmsy for any group of fisheries (from 1 to world), along with supporting statistics, using catch history data and where available improved life history information. All methods are identical to those reported in Costello et al. 2012, except for the estimation of B/Bmsy for invertebrates. All invertebrate estimates should be considered experimental at this point, and have been turned off in this code.

**Key features:**

You can use runLinkedPRM.R to calculate estimates of B/Bmsy using the methods in Costello et al. 2012. The primary purpose of this package is for providing new estimates of B/Bmsy using additional catch or life history data obtained. A few key features

* runLinkedPRM.R will calculate aggregated estimates of B/Bmsy for whatever is fed to it. So, if you have catch histories for several species categories in the same country and want individual estimates for each country, you will need to create your own loop to feed the catch histories for each species category to runLinkedPRM.R
* For any individual fishery to be included, it can’t be missing more than 10% of its data, and after accounting for that, must have at least 7 years of data. If less than 10% of data is missing, runLinkedPRM.R will fill in the blanks by interpolation
  + If only some fisheries out of the whole group fed to runLinkedPRM.R can’t be used, runLinkedPRM.R will still work, but will drop the fisheries that can’t be run, and display a warning message letting you know which fisheries weren’t included
* You can pass improved life history information to runLinkedPRM.R. The package will mine fishbase for data for each fishery first. If you provide additional data, it will then replace any fishbase data with your data, or fill in any blanks that aren’t in fishbase but that you were able to find
  + Every fishery at least needs its ISSCAAP species category. If only some fisheries out of the whole group fed to runLinkedPRM.R don’t have species categories, runLinkedPRM.R will still work, but will drop the fisheries that can’t be run, and display a warning message letting you know which fisheries weren’t included since they are missing species categories
* RunLinkedPRM spits out a lot of results. The most useful is the $summary table, which has the years, median B/Bmsy, confidence intervals, yield changes, biomass changes, and landings

**Instructions:**

1. Download and expand the “runLinkedPRM.zip” file
2. Place contents in folder (called ‘FOLDER’ here for the hell of it ) of your choice
3. Open FOLDER>YOURDATA
4. Inside this folder are two files, catchhistory.csv and lifehistory.csv. These are example files, but represent the format that new catch history or life history data MUST be formatted to input into runLinkedPRM.R
   1. Catchhistory.csv
      1. This file contains the catch history that will be used to calculate B/Bmsy. You need data in here or you can’t do anything. The first column, ‘id’, is an arbitrary identifier to mark different fisheries in the dataset. You can have as many of these as you want, and they can be any numeric code you want. The second column ‘sname’, is the scientific name of the species. Capitalization doesn’t matter, but watch out for trailing spaces. The third column, ‘year’, is the year of that catch data. The fourth column, catch, is the total catch for that fishery in that year in tons
   2. Lifehistory.csv
      1. This file can be used to add in supplementary life history data. If you don’t have any new life history data, the easiest option is to leave all entries under the column names blank. The first column, ‘id’, corresponds to the ‘id’ column in catchhistory.csv, and is how the catches are linked to the life history. The following columns, for each fishery *f*, are in order maximum length (cm), Von Bertalanffy K, range, age at maturity (years), preferred temperature range (centigrade), and the numeric ISSCAAP species category. Anything that you don’t know, leave blank. If though through research a location specific estimate of max length is obtained for fishery *f* , then place the max length in cm in the appropriate row for fishery *f*
5. Open the ‘example script for runLinkedPRM.R’ script
   1. This script provides an idea of how to use ‘runLinkedPRM.R’, you can tweak this as suits your needs (e.g. looping over countries, species categories, etc.), but there are a few steps below that you will need to do any time you want to use runLinkedPRM.R
   2. Change the working directory (‘setwd(XX)’) to wherever the folder you put the contents of runLinkedPRM.zip in to
   3. source(‘runLinkedPRM.R’)
   4. set testvariance to 0 (long story why this needs to be, but it does)
   5. load your catch and life history parameters. You can call these whatever you want
   6. Pass files to runLinkedPRM.R
      1. The first feed to the function is the catch history file
      2. The second is the life history file. You can also input 999 here if you don’t have a custom life history file
      3. The third are the years that you want to spit summary statistics out for. You can set a specific year(e.g. 2009), a range (2000:2009), or set it to ‘FINAL’, which will calculate whatever the most recent year of data is in the dataset and spit that out
      4. The 4th is theta. If you set theta to 0, this assumes that the fishery is in steady state, and current and future yield changes will be the same. If you set theta to any other value between >0 and 1, current percent yield change will show the percent yield change from B/Bmsy and U/Umsy calculated using theta. Future percent yield change will show the percent yield change from U/Umsy calculated using theta, and the B/Bmsy that will restul in steady state from U/Umsy (always complicated I know).
6. The object you create (in this case example) to store the results of the function has a lot of data. The most useful is example$summary. This has
   1. Year
   2. Number of fisheries
   3. Total landings (tons)
   4. Median B/Bmsy
   5. Lower CI
   6. Upper CI
   7. Current percent yield change
   8. Future percent yield change
   9. Percent biomass change (this is always current to MSY)

**Caveats**

It is challenging to interpret the results for any individual fishery. Individual B/Bmsy values run through the retransformation bias tend to be biased in an upwards direction (hence if you manually take the mean/median of the individual values you get a much higher estimate than the aggregate median calculated by the retransformation bias). Alternatively, you can use the raw B/Bmsy values predicted by the regression for individual fisheries (which are included in the example$result$ind$rawbvb