

Introduction to PBSsynth

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1 What is PBSsynth?

PBSsynth provides tools for running population models using Stock Synthesis 3 (SS), which is maintained by the NOAA's [Virtual Lab for Stock Synthesis](#). This package is not intended for public distribution – lots of code has been taken and modified from other packages and R code, including ‘r4ss’ by Ian Taylor et al. and ‘adnuts’ by Cole Monnahan and Kelli Kristensen. We have not fully credited the original sources of functions that we have modified.

In this package, we use the Sweave approach, which, via \LaTeX , produces a single .pdf file that contains multiple figures and tables of output. This enables easy comparison of stock assessment model runs, as well as direct insertion of the results and tables (with automated captions) into the final stock assessment document.

2 What is PBS?

The initials **PBS** refer to the [Pacific Biological Station](#), a major fisheries laboratory operated by Fisheries and Oceans Canada on the Pacific coast in Nanaimo, British Columbia, Canada.

3 Where is the User's Guide?

Users of Stock Synthesis are encouraged to go to NOAA's website and download the latest [SS Manual and support documentation](#).

4 Running the PBSsynth code – not updated (still PBSawatea)

4.1 Load the package

```
require("PBSsynth")
```

The current version of **PBSsynth** includes the namespace functions from the following packages: **methods**, **PBSmodelling**, **scape**, **plotMCMC**, **xtable**, and **lattice**.

Additionally, select functions from the following namespaces have been imported: mcmc from **coda**, plotCI from **gplots**, Cbind and panel.xyplot from **Hmisc**.

Note that the namespace support functions are only accessible by the **PBSsynth** code; users will not have command line access to these functions unless they explicitly load the packages (e.g., `require(PBSmodelling)`).

4.2 Running the model

See the `PBSsynth-commands-SPP-AREA.rwh` file in each folder for the actual functions (and options) to run for species (SPP) and assessment area (AREA). Basically there are five stages to running the model, illustrated below using Queen Charlotte Sound (5ABC) Pacific Ocean Perch (POP). The input file is called `POP-5ABC-04.txt`.

4.2.1 runADMB – Mode of Posterior Distribution (MPD)

The binary executable `awatea.exe` (built by ADMB) is called from a user-selected base directory (e.g. `C:/Stock Synthesis/POP/5ABC`); therefore, (i) the executable needs to be on the path or its directory must be specified by the argument `awateaPath`, and (ii) R's working directory must be set to the base directory (check using `getwd()`). All Stock Synthesis calculations occur in the base directory. The function `runADMB` runs through the number of reweights specified (if any) and automatically puts the original and modified input files, along with various output files, into a new subdirectory. Assuming that the input file is `POP-5ABC-04.txt`, the new subdirectory will be `C:/Stock Synthesis/POP/5ABC/POPrun04`:

```
out = runADMB("POP-5ABC-04.txt", strSpp="POP", runNo=4, doMPD=TRUE,
  N.reweight=3, mean.age=TRUE, cvpro=0.2, clean=TRUE)}
```

4.2.2 runSweave – Run Sweave on MPD Results

To see the MPD results, run Sweave on the results to generate figures and tables and to create postscript and pdf files containing all the results:

```
runSweave(strSpp="POP", filename="POP-5ABC-04.txt", runNo=4, rwtNo=3,
  Nsex=2, Ncpue=0, Nsurvey=3, SApos=c(TRUE,TRUE,FALSE),
  Snames=c("GIG.historical","QCS.synoptic","QCS.shrimp"))
```

Or you can run a wrapper function `runMPD` that calls `runSweave` using multiple runs and/or multiple reweights:

```
runMPD(strSpp="POP", prefix=c("POP","5ABC"), runs=4, rwts=0:3,
  Nsex=2, Ncpue=0, Nsurvey=3, SApos=c(TRUE,TRUE,FALSE), delim="-",
  Snames=c("GIG.historical","QCS.synoptic","QCS.shrimp"))
```

This creates one or more subdirectories (in this case, `C:/Stock Synthesis/POP/5ABC/POPrun04/MPD.run.rwt`, where `run=04` and `rwt=c(00,01,02,03)`), each of which contains a customized Sweave file (e.g., `POPrun04-3.Snw`), the compiled latex file (`POPrun04-3.tex`), and a postscript document file (`POPrun04-3.pdf`), along with the numerous .eps image files used in making the .pdf file.

4.2.3 Run MCMC Sampling for Posterior Distribution

It's best to run the MCMC calculations on a stand-alone power desktop. Use the reweight input file that best suits the data (e.g., getting SDNRs close to 1), transfer this to the desktop where the same version of `awatea.exe` is available, and issue the commands:

```
awatea -ind POP-5ABC.04.03.txt -mcmc 10000000 -mcsave 10000
awatea -ind pop-5ABC.04.03.txt -mceval
```

The first command will take many hours to complete; therefore, the second command is issued after the first is completed. Next, copy the resulting output files (e.g., `.pst`, `.out`, `Stock Synthesis.psv`, etc.) files *twice* into two new subdirectories on your workstation:

```
C:/Stock Synthesis/POP/5ABC/POPrun04/MCMC.04.03
C:/Stock Synthesis/POP/5ABC/POPrun04/MCMC.04.03/PRJ.04.03
```

4.2.4 Maximum Sustainable Yield (MSY)

Next, calculate maximum sustainable yield for each of your posterior samples.

```
out = runADMB("POP-5ABC-04.txt", strSpp="POP", runNo=4, rwtNo=3,
  doMSY=TRUE, msyMaxIter=15000, msyTolConv=0.01, endStrat=0.301,
  stepStrat=0.001)
```

4.2.5 runSweaveMCMC – Run Sweave on MCMC Results

As with the MPD output, run Sweave on the MCMC output to generate figures and tables and to create postscript and pdf files containing all the MCMC results:

```
runSweaveMCMC(strSpp="POP", filename="POP-5ABC-04.txt", runNo=4,
  rwtNo=3, skip.last.year=FALSE)
```

The final argument in the above call defaults to `skip.last.year=TRUE` for all assessments to remove the last year of projections. The POP 5ABC assessment in 2010 requires that the last year of projections be kept.

There is also a wrapper function called `runMCMC` for `runSweaveMCMC` that loops through runs and reweights:

```
runMCMC(prefix=c("POP", "5ABC"), runs=4, rwts=3)
```

Note: For details of all **PBSsynth** functions, see the package documentation help files.