**Update\_function\_JAGS.r**

**Purpose**  This is the workhouse function for running the update model for Georges A and Browns north. This function loads necessary data, runs the update, produces the projections and decision tables, and makes the figures for the update document. The default setting will a: process all the data, b: run the models, c: make the diagnostics, d: do the prediction evaluations, e: and make all figures, but any of these steps can be skipped if you have already have the data needed.

**Version Control**  This is a DK original, this combines a number of scripts that do similar things but none as nicely as this.

**Required packages** R2jags (the locally derived functions have their own package needs as well)

**Locally Derived Functions**

1. logs\_and\_fishery\_data.r
2. fishery.dat.r
3. projections.r
4. decision.r
5. post.plt.R
6. exploit.plt.r
7. fit.plt.R
8. diag.plt.R
9. peR\_jags.r
10. biomass.plt.r
11. ScallopMap.r
12. contour.gen.r

**Section 1**

After the functions are loaded Section one is the pre-processing step to load in all the necessary data. This probably only needs to occur once so once you have it you can skip this step (see the argument options). It uses the output from survey summary (Survey\_all\_results.Rdata must exist) but by default updates the fishery data to the latest information available. For GBa and BBn the fishery CPUE data is calculated and added to the model data. The von Bertalanffy parameters are used to get the actual and projected growth of the scallop.

**Section 2**

In section 2 we run the model. Note that we are now using a JAGS parallel model for these, doesn’t speed up the model runs much, but really helps speed up running the projections!! You have several options in this section, the big ones include: a: not run the model (if you already have results), b: run the models in parallel or just on one processor, c: save the model results as final or testing. The decision table is also produced automatically whenever the model is run.

**Section 3**

This section processes the model results and returns information we need to summarize. It also runs the model diagnostics (not the model diagnostic figures, they are in Section 4) and saves these results as an R data file.

**Section 4**

This section makes all the figures you might be interested in, you have options to plot a: model diagnostic figures, b: prediction evaluation plot,. and c: figures for the update document. This is also the section in which the prediction evaluation models can be run (these are slow so only run them as necessary!). The figures can be printed to screen or saved as pdf’s and the figures will be saved in the directory specified by “plotsGo” argument.

***Argument(s)***

1. direct The root directory to work from Default = "Y:/Offshore

scallop/Assessment"

1. yr The year of the survey used to generate update. Default =

as.numeric(format(Sys.time(), "%Y"))-1. Since the updates occur the year after the survey this gets confusing, for example the 2015 survey was used to create the 2016 update, in this case you specifiy yr = 2015 even though the update is the 2016 update and all the files related to the update are found in Update/2016/...

1. strt.mod.yr Start year for the models. Set to 1986 but note that BBn doesn't

have data back that far so starts in 1991 if set to anything less than 1991

1. bank The bank to run. Default is both banks c("GBa","BBn"), but

specifying either works as well.

1. use.final If run.mod = F do you want to use the "final results" for figures or

use the temporary results. (T/F) default = F which loads

Model\_testing\_results.RData. If set to T it will load

Final\_model\_results.RData

1. fig Print to 'pdf' or to screen. default="screen"

*Output options. These options are specified to determine which bit of the function you run*

(The default processes all data, runs models, makes diagnostics, does prediction evaluation,and makes all figures)

1. preprocessed If you have already run Section 1 of this script you can skip

runing that section each time. (T/F) default = F

1. run.mod Run the model? If a 'final model' has been saved you can skip re-

running the model. T/F, default = T

1. make.diag Create diagnostic summary, model results, and model

convergence pdf found in Section 3. T/F default = T

1. make.figs T/F, default = T. Do you want to make figures? This is a high level

call that will stop any figures from being made and will also stop the prediction evaluations being run when set to F

1. make.update.figs Make the figures used in the Update? T/F, default = T. If set to T

make sure make.figs =T

1. make.diag.figs Do you want to make the diagnositic figures. T/F, default = T.

If set to T make sure make.figs=T

1. run.pred.eval.model For the prediction evalutions do you need to (re)run the

models. (T/F) Default = T (these take a while if you've run them once the results are saved so only set to T if needed a fresh run. If set to T make make sure make.figs=T

1. make.pred.eval.figs Do you want to make the prediction evaluation figures. T/F,

default = T. If set to T make sure make.figs=T

*Model options. By and large these options will only be used if run.mod=T*

1. nchains Number of chains to run. Default = 8. When running in parallel

each chain gets it's own thread. The best way to get more saved replicates if the model has converged is to increase the number of chains run (depending on the number of processors on you CPU)

1. niter Number of iterations to run. Default = 175000
2. nburn Number of initial iterations to ignore. Default = 50000
3. nthin Thinning rate of iterations. Default = 20
4. final.run If you are happy with testing results run the model as a final

model. T/F, default = F. If true this saves an R workspace called Final\_model\_results.RData, if False it saves to Model\_testing\_results.RData

1. para Run in parallel using jags.parallel? T/F, default =T. Number of

processors = nchains

1. jags.model Get the model to use (same model used in prediction

evaluations). By deFault it looks the the folder "direct"/Assessment\_fns/Model/DDwSE3\_jags.bug where direct was specified above.

1. parallel Do you want to run JAGS in parallel. (T/F), F will run JAGS but just

using one core.

1. seed If running JAGS in parallel you can set a "seed" so that your model results

are reproducible. Default = 123

1. parameters Model parameters to output. Default = NULL which will produce all of

the priors + the following parameters 'K','P','B','R','mu', 'Imed', 'Ipred', 'Irep', 'IRmed','IRpred', 'IRrep','sIresid','sIRresid', 'sPresid', 'Iresid', 'IRresid', 'Presid'

1. export.tables Export the Decision tables, should only be done when satisified with

results. T/F, default = F

*Prediction Evaluation options***.**

(To run the prediction evaluation model or make the figures make sure that make.figs=T)

1. pred.eval.fig.type If making the prediction evalulation figures which figure do you

want. Default ="box" (options "ts" or "ts\_all")

1. pe.years The years to run the prediction evaluation plots. Default = NULL which

selects the current year back to 2000.

1. pe.iter The number of iterations to run the prediction evaluation runs. Default =

NULL which uses the nchains for the model

1. pe.burn The number of iterations to drop from prediction evaluation runs. Default

= NULL which uses the model nchains

1. pe.thin The thinning rate for the prediction evaluation runs. Default = NULL

which uses the nchains use for the model

1. pe.chains The number of chains to run for the prediction evaluation runs. Default =

NULL which uses the model nchains

1. db.con The database to connect to. Default ="ptran",
2. un Your username to connect to SQL database. Default = un.ID
3. pw Your password to connect to SQL database. Default = pwd.ID