

AlaskaHerring Folder Organization

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Model naming conventions:

Time block parameterization = # survival time blocks, # maturity time blocks, # selectivity time blocks

E.g. HER_123 = 1 survival time block, 2 maturity blocks, 3 survival blocks

The model number for model selection is shown before the time block parameterization.

E.g. HER 10_123 = Model 10 with 1 survival time block, 2 maturity blocks, 3 survival blocks

HER_bestLS_### = HER model with best-fitting parameterization of LS model by AICc

HER_best_condCatch.#_### = HER model with best-fitting parameterization of HER by AIC when conditioned on catch

HER_best_condEffort.#_### = HER model with best-fitting parameterization of HER by AIC when conditioned on effort

HER_condEffort_fixedmat.4_3 = HER model conditioned on effort with a_{50} fixed at 3.67 (from FishLife) and $a_{95} = 4.48$ from regression provided by SD. One time block for selectivity, 3 blocks estimated for survival

HER_confEffort_1929 = HER model conditioned on effort with data file going back to 1929. Still exploratory, not running well. STARS on PDO looking pre-1980, you get different time blocks. If you rerun pdo_breaks.R for 1929-2018, there are so many breaks that I didn't kill the process for the loop code before it was finished. No figure output was generated but prelim results in results/model_selection/HER_historical_1929. One path forward with this is to choose single (instead of time-varying) parameterization pre-1980 because the model only has catch and catch comps to work with and they may not be informative enough to estimate much. May be informative to use the same natural mortality/selectivity/maturity assumption that were used in Williams and Quinn's cohort analysis. Historical data from Reid 1971 is in data/.

HER_mature_catch = NEW EXPLORATORY MODEL that estimates selectivity from mature not total population. Assumes catch comps come from mature population (catch = 100% mature). All other models (HER and LS) assume selectivity comes from total population.

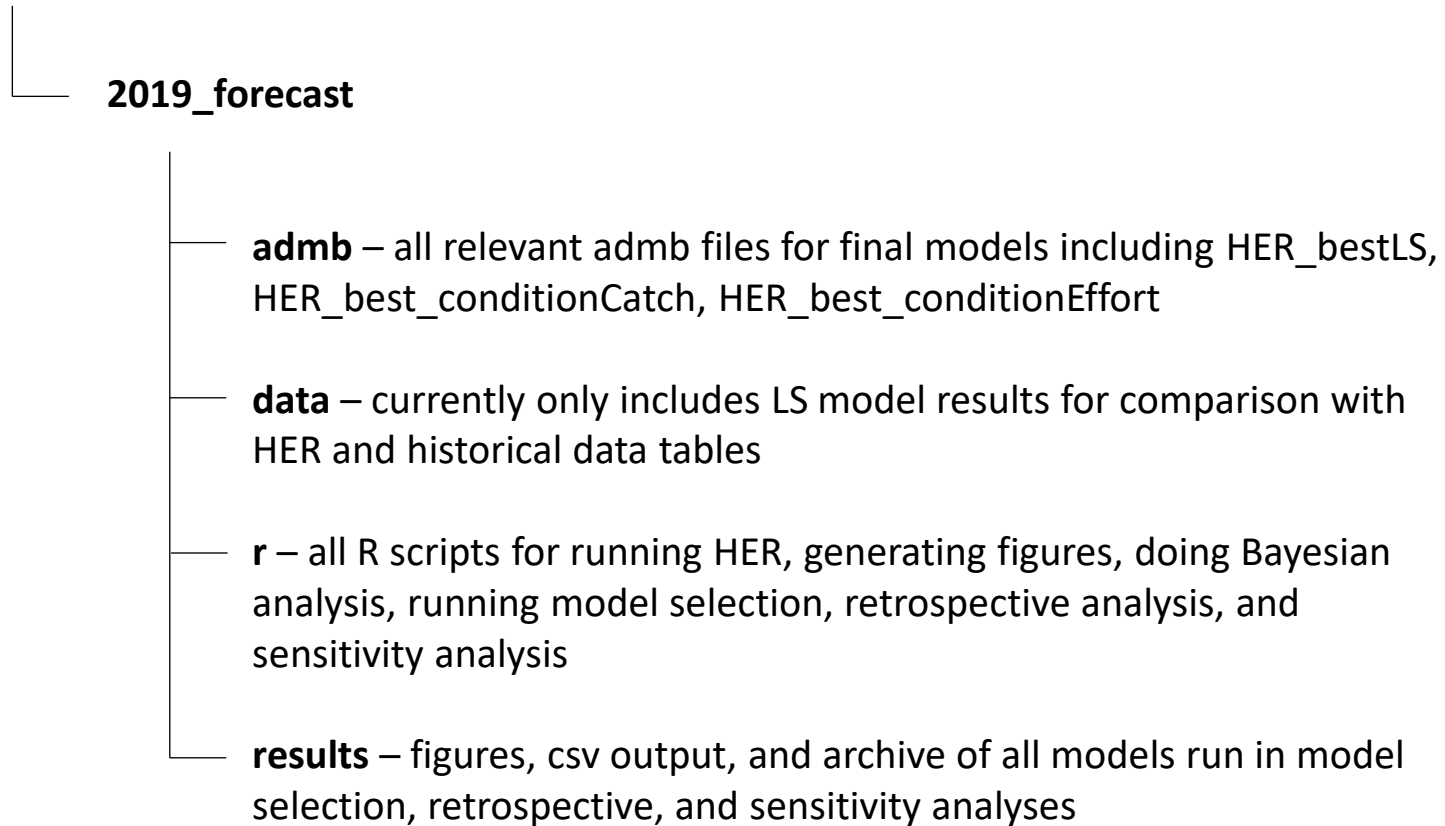
Folder directory (part 1): General overview

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- **YEAR_forecast** – all data, code, and results for a given forecast year
- **smartell_archive** – deprecated code from Steve Martell's contract
- **technical_docs** – documentation for project-level organization and model details
- **.gitignore** – all file types and folders not tracked by git
- **ReadMe.md** – Summary of repository

Folder directory (part 2): Forecast folders

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Folder directory (part 3):
2019 R scripts

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2019_forecast

r – all R code

helper.R– libraries, ggplot2 themes, and user-defined functions (sourced by all other script files)

her.R– Run any version/tpl of HER (MLE and Bayesian/MCMC) and compare with LS. Saves output to subdirectory in results/ named after the HER version/tpl

model_selection.R– recreates model selection “loop code”. Examines all permutations of time-varying parameters given user-defined time blocks. Saves output to subdirectory of results/model_selection/ named after the HER version/tpl

model_selection_natmat.R – same as model_selection.R, except only examines survival/natural mortality. Also saves output to subdirectory of results/model_selection/ named after the HER version/tpl.

retrospective.R – run retrospective analysis (peel years of data from assessment to compare current results with past results assuming the same model structure. Results in retrospective/ for given HER tpl versions.

pdo_breaks.R – get PDO breaks using STARS algorithm, which is sourced in **stars.R**. Results stored in results/stars_pdo

sensitivity_sigmaM.R – sensitivity analysis for sigmaM, parameter controlling variability in natural mortality deviations by block. Uses **create_ctl.R**. Results in results/sensitivity_sigmaM. sigmaM = 0.09 had best convergence diagnostics.

sensitivity_maturity.R – compare a range of fixed to estimated maturities. Results in results/sensitivity_maturity

presentation_figs.R – creates presentation-quality figs in presentation/ subdirectory of results/ under various model versions

Folder directory (part 3):
2019 results folder

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2019_forecast

results –
figures, csv
output, and
archive of all
models run in
model
selection,
retrospective,
and sensitivity
analyses

HER_bestLS_321 – includes comparison figures of this model's results with LS best, HER-specific figures, diagnostics for the Bayesian analysis, and csv files of all the posterior sample summaries

HER_best_condCatch.12_322 – same as above

HER_best_condEffort.12_322 – same as above

model_selection – includes model selection results for HER conditioned on catch and effort

retrospective – results for the retrospective analysis for HER_bestLS_321, HER_best_condCatch.12_322, and HER_best_condCatch.12_322

sensitivity_sigmaM – results for sensitivity analysis examining convergence diagnostics and model output for sigmaM from 0.05-0.10. sigmaM = 0.09 had best convergence diagnostics

reference_points – currently only includes saved biological reference point output from posterior samples. This is still under development. Some reference pt results also in results/sensitivity_maturity/figures that show how maturity assumptions affect reference point assumptions

sensitivity_maturity – results from sensitivity analysis on maturity comparing a range of a50 and rate of maturation

Steps to run a new assessment

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1. Create new 2020_forecast or 2021_forecast folder
2. Create folders for data, r, results, text in forecast folder
3. Copy appropriate tpl, updated ctl, and updated dat files into correctly named subdirectory of admb/ (need to update dat file with the new data but also update the terminal years for the time blocks in the ctl file)
4. Copy correctly formatted LS results into data/ subdirectory
5. Use her.R to run base model (the tpl copied into admb/ subdirectory – see step 3). Be sure to update relevant user inputs in her.R.
6. If you want to run the traditional loop code, first run pdo_breaks.R then model_selection.R or if you just wanted to look at time-varying natural mortality (single blocks for maturity and selectivity), use model_selection_natmat.R
7. If you want to examine a range of maturity values, use sensitivity_maturity.R – this code (as well as sensitivity_sigmaM) could be adapted to evaluate other model parameters and assumptions. For example, a sensitivity on recruitment compensation ratio (recK), which is related to steepness (h)
8. Any time you want to run her.R on a model (e.g. the results of a maturity analysis or model selection), you'll need to copy the resultant tpl, ctl, and dat files over to a subdirectory of admb/. The her.R is the script file that runs the full MCMC model.
9. Take best model and run it through her.R again to get final results.
10. Run a retrospective analysis on final model using retrospective.R
11. Use presentation_figs.R to get presentation quality figures.

Next steps

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1. Continuing to explore the alternative population dynamics model ($t_{pl} = HER_mature_catch$) – and the impacts on the estimation and interpretation of selectivity
2. Sensitivity analysis on $recK$ (recruitment compensation ratio) – $\theta[7]$. This is related to steepness value seen in other stock assessments (h). Changes to parameters happens in ctl .
 1. Fixed maturity, fixed natural mortality, estimated selectivity over a range of steepness values (0.7-1.0)
3. Fleshing out the HER model document
4. If you keep with LS and want to get rid of the spawner-recruit relationship but still want to estimate biological reference point internally, potentially moving towards spawning potential ratio (SPR) based reference points

Notes on convergence

1. Baseline convergence: Hessian to be positive definite and Maximum gradient component - <0.001 , preferably <0.00001
2. Parameters are not converging on the bounds and that they are reasonable
3. Parameter correlation could lead to variable results with seemingly small changes to parameterization (example: sensitivity analysis on a range of fixed maturity estimates resulted in large spread in natural mortality and recruitment)
4. Potential fixes to parameter correlation could include fixing parameters when possible or reparametrizing the model. E.g. logistic the a_{50}/a_{95} parameterization suffers from extreme parameter correlation compared with a_{50}/k
5. In Bayesian model, you can see the parameter correlation in the pairwise scatterplot, also caterpillar plots that show trends (want a bushy caterpillar!)