A Newbie Ports ADMB to TMB

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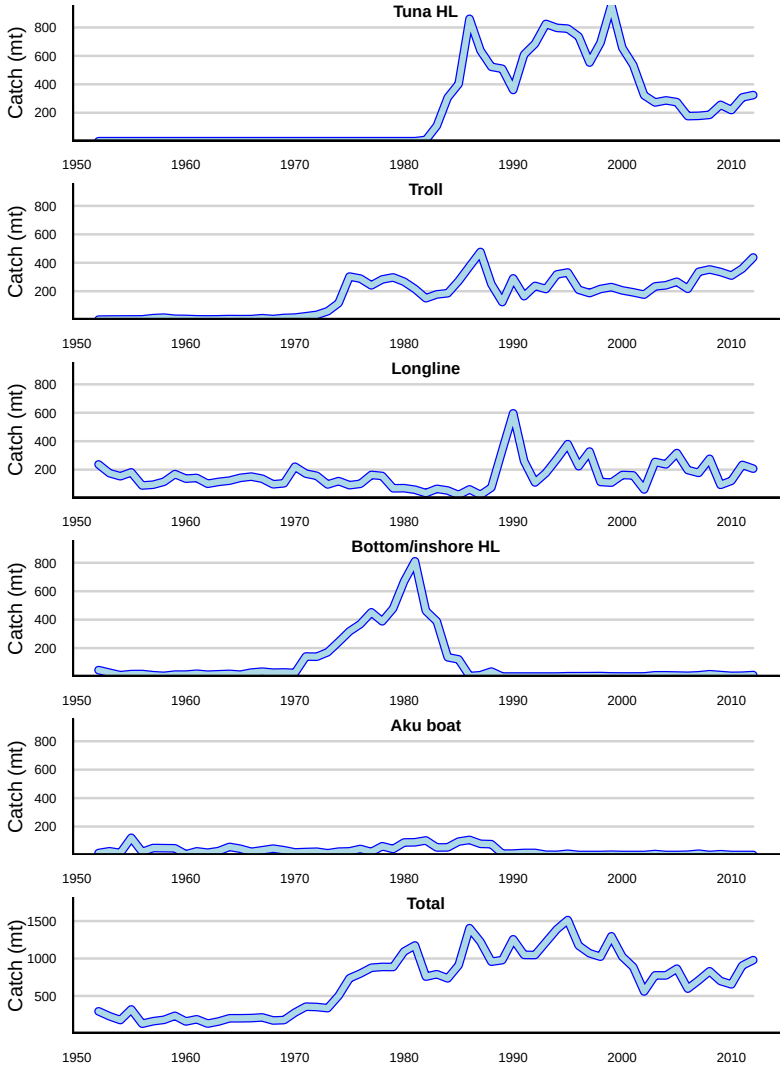
`issams` Model

- State-space Schaefer model (Nielsen and Berg, 2014)
- No effort data
- Five parameters; 366 random effects
- Process errors on biomass transition and fishing mortailty
- Zero-inflated log-normal likelihood
- Prior on r
- Optional index of abundance
- `https://github.com/johnrsibert/XSSA.git`

Combined HDAR and NOAA Catch Time Series



No Recreational Data

General Strategy

- Implement DATA_SECTION and PRELIMINARY_CALCS_SECTION in R code (issams.R)
- Include parts of the SEPARABLE_FUNCTION and the PROCEDURE_SECTION in C++ code (issams.cpp)
- Estimation phases are all set a 1 in the ADMB version and not implemented in the TMB version.
- Both implementations read the same data file (issams.dat)

Results

- Timing:
  - ADMB 17.6s
  - TMB 0.359s
- Likelihood:
  - ADMB: $-logL = 247.175; |G| = 3.51082e-05$
  - TMB: $-logL = 231.375; |G| = 3.79808e-05$
- After fixing some bugs:
  - ADMB: $-logL = 247.174699743560; |G| = 3.51082264130123e-05$
  - TMB: $-logL = 247.377482806857; |G| = 0.0002058118072727 21$
- MCMC
  - ADMB: reasonable posteriors
  - TMB: fails with non-positive definte Hessian

Conclusions

- Not too difficult
- Much faster for random effects
- Missing Dox for macros (fixed)
- Writing and testing R code time consuming. C++ I/O much easier.
- My biggest gripe with TMB is its utter dependence on R. I realize that many users may see this feature as perhaps the best feature of TMB, but I do not share that view. As a programming language, R is broken. It generally takes me at least twice as long to write code in R than the equivalent code in C++. In my opinion, TMB would be a better product if it produced stand-alone executables. I realize such a change would probably require major surgery for TMB developers, but in the long run it would be a worthwhile exercise.

Thanks for your attention