Pella-Tomlinson in AD Model Builder

Arni Magnusson

6 January 2011

1 Background

Recently, I needed a Pella-Tomlinson model for a project and wrote an ADMB model called ‘pella’. The main reasons I’d like to distribute this model are the following:

(a) Provide a simple model that is useful for learning ADMB, demonstrating the use of a control file and MCMC

(b) Discuss possible ways to make this model less sensitive to initial parameter values

(c) Discuss the possibility of developing a ‘pella-re’ counterpart in ADMB-RE, e.g. where the intrinsic growth rate *r* varies between years, resulting in more stable convergence

(d) Discuss the differences between the simple ‘pella’ model and the more complex ‘pella-t’ that comes with ADMB as an example model

2 Datasets

The study by Polacheck et al. (1993, Table 1) includes three datasets of catch and biomass index: New Zealand rock lobster, Namibian hake, and South Atlantic albacore.

3 Model

Dynamics and likelihood

The Pella-Tomlinson model generalizes the Schaefer model,

$$B_{t+1} = B_t + rB_t\left(1-\frac{B_t}{k}\right) - C_t \quad (1)$$

by adding a shape parameter p:

$$B_{t+1} = B_t + \frac{r}{p}B_t\left[1-\left(\frac{B_t}{k}\right)^p\right] - C_t \quad (2)$$

The Pella-Tomlinson model is equivalent to the Schaefer model when $p = 1$.

A scaling parameter a sets the initial biomass as a proportion of k:

$$B_{\text{init}} = ak \quad (3)$$

The biomass in the first year is k when $a = 1$.

The model is fitted by minimizing the negative log-likelihood,

$$-\log L = \left[0.5n\log(2\pi)\right] + n\log\sigma + \frac{\sum(\log I_t - \log \hat{I}_t)^2}{2\sigma^2} \quad (4)$$

where $\hat{I}_t = qB_t$ is the fitted biomass index.

Thus, the model consists of four estimated parameters, r, k, q, and σ, as well as two optionally estimated parameters, a and p. Both q and σ are estimated as free parameters, as opposed to derived parameters using concentrated likelihood. This leads to the same point estimates, but makes a difference in the uncertainty evaluation, where q and σ in MCMC analysis are not forcibly set to the MLE.

Features

In each model run, the user sets estimation phases, bounds, and initial values in a control file, separate from the data file.

Biomass index values are not required in all years.

The objective function is the full negative log-likelihood, including the constant terms (square brackets in Eq. 4).

MCMC capability is provided, so there are two built-in methods to evaluate uncertainty: the delta method (Hessian) and MCMC.

All parameters are estimated in log space. For the MCMC, the lower and upper bounds on each parameter serve as a uniform prior for that log-transformed parameter.

Besides standard ADMB output files, there are two kinds of output files that are convenient for the user: (1) 'pella.rep' showing parameter estimates, objective function value, predicted biomass, and fitted biomass index, and (2) 'mcmc_bio.csv' and 'mcmc_par.csv' containing MCMC draws of year-specific biomass, parameters, and objective function value.

Running the model

The control file uses a four-number PLUI (phase, lower, upper, init) format to set parameter specifications for each model run. Negative estimation phase means that the parameter should be fixed.

The Pella-Tomlinson model is highly sensitive to bounds and initial values, so the user needs to modify the control file between model runs, until it converges properly. Lack of convergence is indicated with a warning: "Hessian does not appear to be positive definite".

To fit the model to data in 'run.dat' with parameter specifications from 'run.ctl' type:

```
pella -ind run.dat
```

After a model run has finished, the user may want to rename the files 'pella.cor' (point estimates, standard errors, and covariance), 'pella.par' (full precision point estimates), and 'pella.rep' to 'run.cor', 'run.par', and 'run.rep'. This way, an archived model run consists of two input files (ctl, dat) and three output files (cor, par, rep).

The 'pella.cor' file is only generated when a model run converges successfully. Likewise, convergence is required before MCMC analysis.

To invoke MCMC analysis, first type

```
pella -ind run.dat -mcmc 1e6 -mcsave 1e3
```

to run 1 000 000 iterations, saving every 1 000th, and then

```
pella -ind run.dat -mceval
```

to write the MCMC draws from 'pella.psv' to the 'mcmc_bio.csv' and 'mcmc_par.csv' files. Longer chains may be necessary for MCMC convergence, for example:

```
pella -ind run.dat -mcmc 1e7 -mcsave 1e4
```

Here we run 10 000 000 MCMC iterations and save every 10 000th, so the number of saved MCMC draws will be 1000, as in the previous example.

4 Results

The following tables show estimated quantities from five model runs: 1993 (From Table 2 in Polacheck et al. 1993), Schaefer (fixing a=1 and p=1), Schaefer-init (a free, p=1), Pella (a=1, p free), and Pella-init (a free, p free). Depletion level is B_{current} / B_{init}.

Albacore

	1993	Schaefer	Schaefer-init	Pella	Pella-init
r	0.328	0.320	0.308	0.246	0.247
k	240	243	252	232	233
a	1	1	1.15	1	1.02
p	1	1	1	0.000	0.000
q	0.267	0.264	0.240	0.293	0.289
σ	0.111	0.110	0.108	0.106	0.106
–log L	ca. –18.0	–18.1	–18.6	–18.9	–18.9
B_{init}	240	243	290	232	237
B_{current}	75	75	86	71	72
Depletion	0.315	0.308	0.296	0.304	0.303

Hake

	1993	Schaefer	Schaefer-init	Pella	Pella-init
r	0.379	0.370	0.364	0.234	0.375
k	2770	2820	2900	3020	2910
a	1	1	1.72	1	1.72
p	1	1	1	0.000	1.111
q	4.36e-4	4.27e-4	3.54e-4	4.12e-4	3.56e-4
σ	0.124	0.125	0.087	0.116	0.087
$-\log L$	ca. –15.9	–15.9	–24.6	–17.7	–24.6
B_{init}	2770	2820	5000	3020	4990
B_{current}	1650	1660	1920	1660	1920
Depletion	0.594	0.589	0.384	0.551	0.384

Rock lobster

	1993	Schaefer	Schaefer-init	Pella	Pella-init
r	0.066	0.048	0.004*	0.059	0.012
k	129 000	145 000	344 000	115 000	57 400
a	1	1	7.39*	1	6.93
p	1	1	1	0.000	0.000
q	2.46e–5	2.17e–5	1.07e–5	2.95e–5	0.93e–5
σ	0.207	0.212	0.201	0.201	0.198
$-\log L$	ca. –5.9	–6.0	–8.6	–8.6	–9.3
B_{init}	129 000	145 000	344 000	115 000	398 000
B_{current}	21 200	24 400	54 400	19 100	64 200
Depletion	0.164	0.168	0.158	0166	0.161

*: The Schaefer-init model runs into bounds for the r and a parameters.

5 Discussion

The high sensitivity of the model to parameter bounds and starting values is an issue. This is a well known feature of the Schaefer and Pella-Tomlinson models, but it is worthwhile to consider ways to improve the robustness.

Concentrated likelihood could be used, treating q and σ as derived parameters, instead of free estimated parameters. This is often done in practice, but in my experience forcing q and σ to be exactly at the MLE will lead to underestimation of the overall uncertainty in MCMC analysis.

► See discussion points (b), (c), and (d) on the front page.

6 References

Polacheck, T., R. Hilborn, and A.E. Punt. 1993. Fitting surplus production models: Comparing methods and measuring uncertainty. Can. J. Fish. Aquat. Sci. 50:2597–2607.