

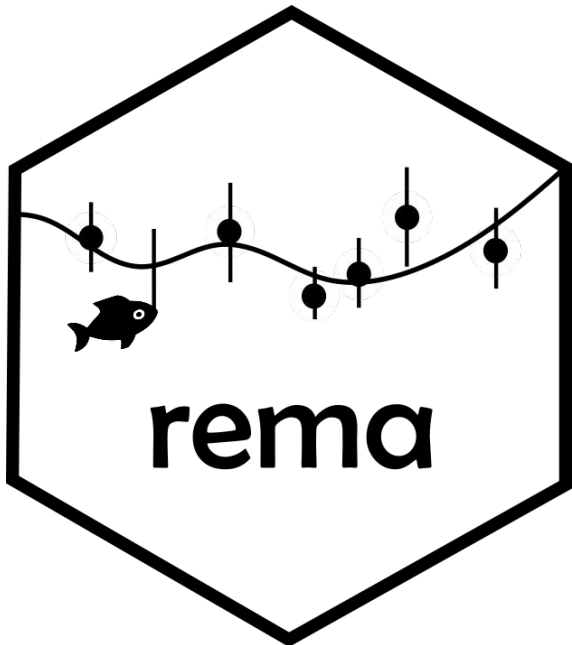


NOAA
FISHERIES

Model Validation in REMA

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Why do we need model validation for REMA?

State-space models increasing in popularity in fisheries due to flexibility and ability to estimate process & observation error (Aeberhard et al., 2018)

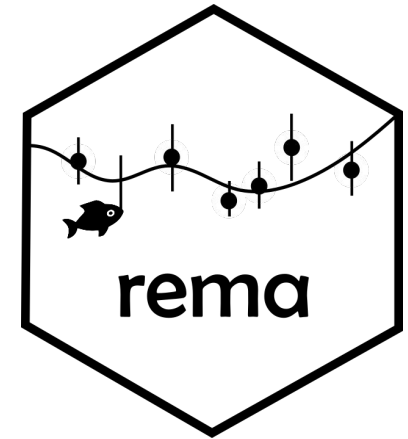
State-space models can suffer from estimation issues that are not always easy to diagnose (Auger-Méthé et al., 2016)

The random effects model (REMA) is by far our most common state-space model, yet we have no standard diagnostics in place

Our goal: Create a plain language model validation guide for users and reviewers that builds on best practices for validation of state-space models

New release!

New features include simulation and one-step ahead residuals



[New code-enhanced model validation guide](#)

- Two test cases (AI Pcod and GOA Thornyhead) that book-end the range of complexity we see for operational REMA models

Plan for today:

- 1) Model validation overview
- 2) Diagnostic tools
- 3) Highlight key results
- 4) Preliminary recommendations

Model validation is...

Checking that the model is operating correctly:

- Assumptions are valid
- Code is error-free
- Check that the data could have reasonably come from the model

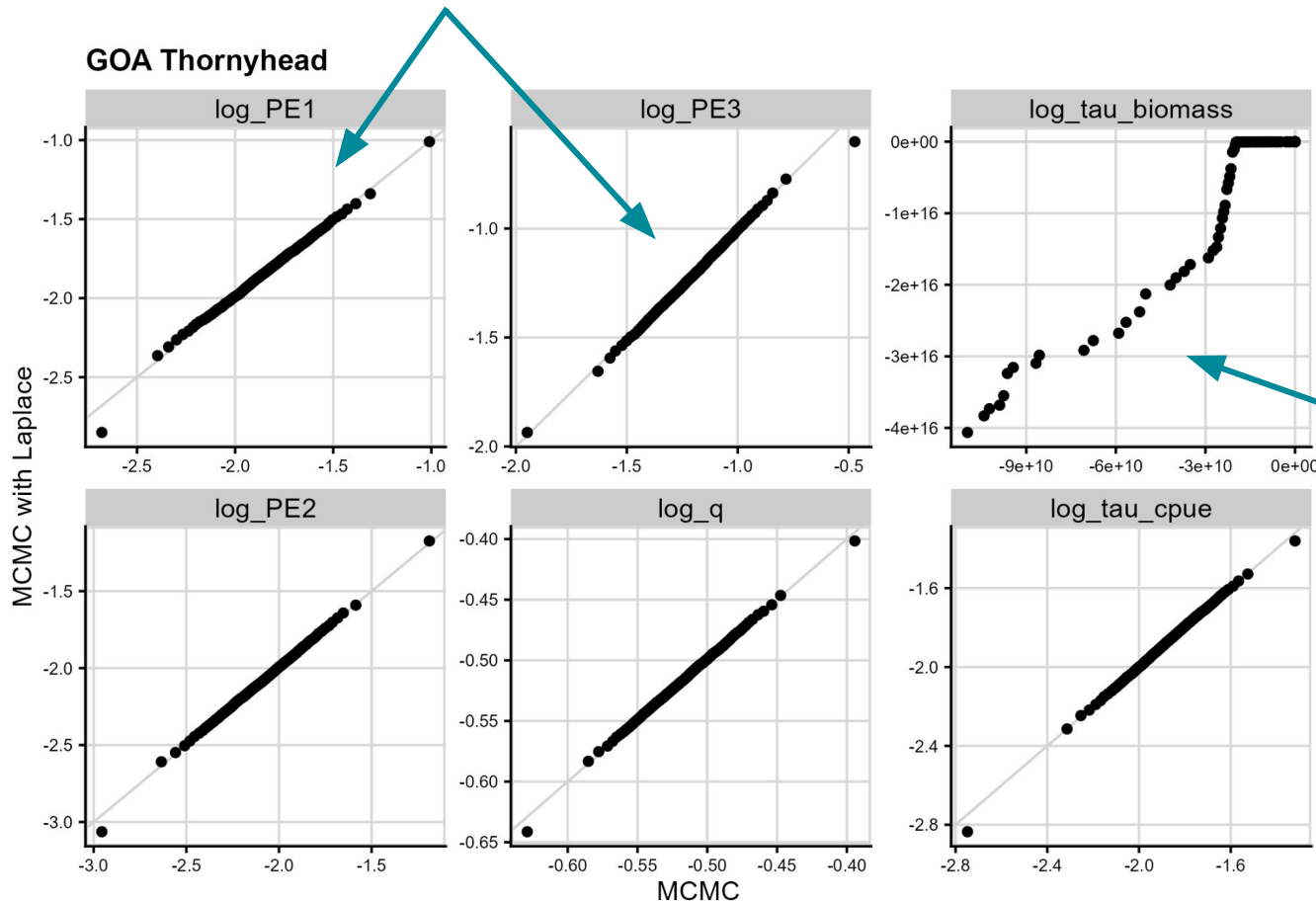
Model validation is NOT...

- Indicating models are biologically “right” or able to make “better” predictions
- A replacement for model selection

Simulation self-test	OSA residuals	Laplace approximation	Parameter correlation and convergence
Does the model perform as expected, or does it introduce bias?	Is it plausible that our data could have been generated by the model?	Are the normality assumptions made when estimating random effects via the LA accurate?	Is there evidence of overparameterization in the model? Is the model converged?
<ul style="list-style-type: none"> *Use parameters to simulate new data & re-fit model *Compare “true” parameters to “re-fit” parameters *Uses new simulation features in <i>rema</i> 	<ul style="list-style-type: none"> *Random effects induce correlations in predicted data such that traditional residuals are no longer iid (recall C. Monnahan’s presentation on why OSA) *OSA residuals will be iid with $N(0, 1)$ *SDNR should be ~ 1 *New <code>get_osa_residuals()</code> function in <i>rema</i> 	<ul style="list-style-type: none"> *REMA and other TMB models with random effects assume RE follow a normal distribution *Test assumption using <i>tmbstan</i> by comparing distributions of fixed effects from MCMC models fit with and without LA 	<ul style="list-style-type: none"> *Pairwise correlation plots using the MCMC posterior samples *Rhat is MCMC convergence diagnostic (at convergence, $R_{hat}=1$) *Trace plots visual diagnostic to evaluate mixing across MCMC chains

Example: Issue with Laplace approximation and estimation of additional observation error

MCMC with and without Laplace approximation: distributions should fall on 1:1 line



Clear divergence from 1:1 for log_tau_biomass (extra obs error for trawl survey) indicates violation of LA normality assumption

Note different scales on x- and y- axis and tendency of estimates towards zero in natural space

Preliminary recommendations

- More complex models necessitate model validation
- OSA residuals and MCMC diagnostics (Laplace approximation, parameter correlation, convergence) especially useful
- Failing diagnostics might signal need for simplification or reparameterization, especially because estimation of additional observation error impacts predicted biomass (quantity of interest for management)

Next steps: Reevaluate how additional observation error is estimated in REMA

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