

# MCMC Posterior Probability Methods

William Stockhausen  
Alaska Fisheries Science Center  
NOAA/NMFS

## Why bother with the “posterior probability distribution”(PPD)?

- better characterizes parameter uncertainty
  - yields full marginal posterior distribution
  - .std file uses multivariate normal assumption and “delta” method
- captures uncertainty for any model output
  - not just parameters and sd\_report variables
- want distribution of OFL for  $p^*$  ABC
  - using the PPD captures full model uncertainty
  - projection model only captures some uncertainty (e.g., starting biomass)

# What does MCMC (Markov Chain Monte Carlo) do?

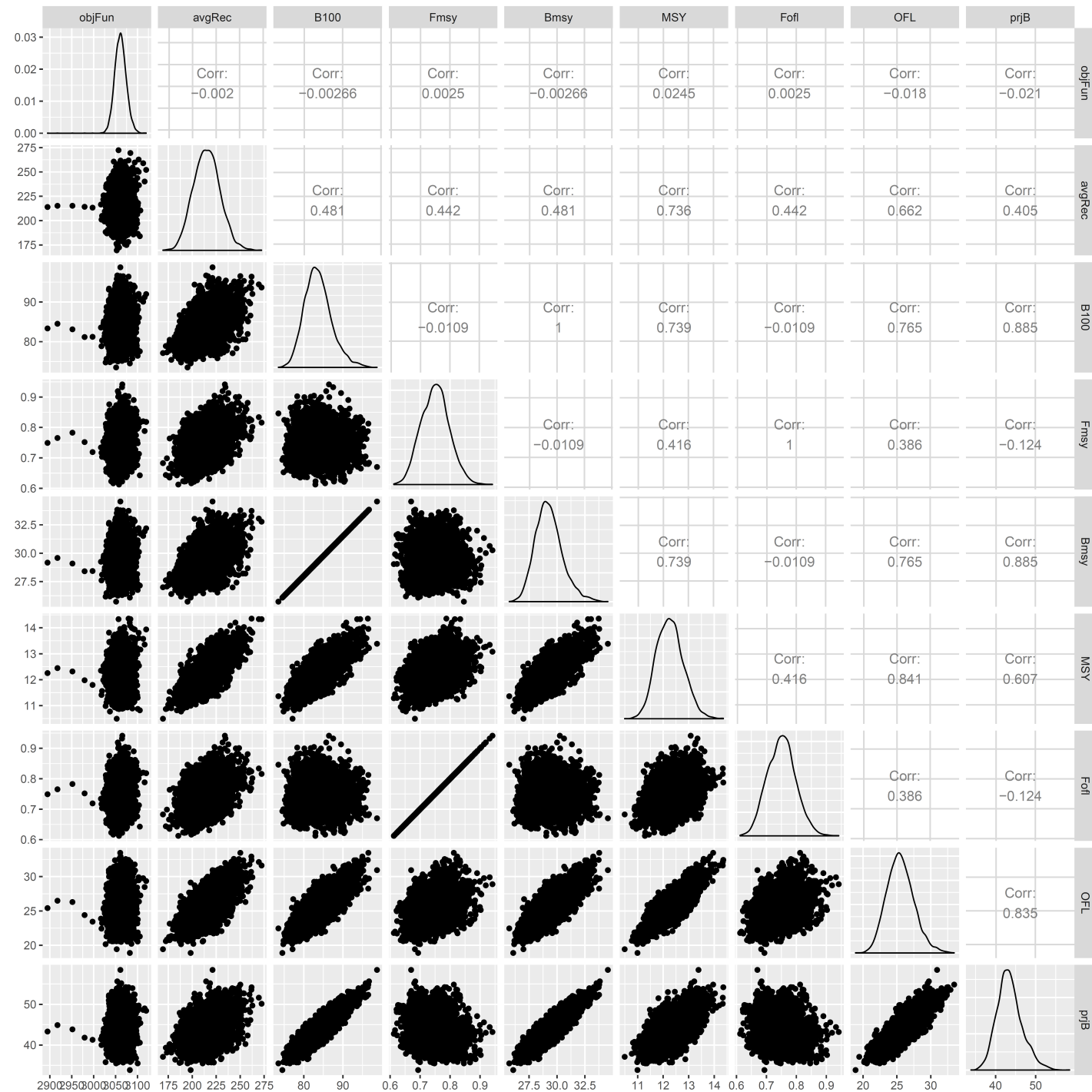
- ideally, want to integrate over the model's PPD to get the marginal posterior distribution for any desired quantity
- generally, too many parameters to do this using standard integration techniques
- MCMC randomly samples desired quantities using the model's PPD to determine relative sampling rates
  - areas with “high” PPD should have many samples taken
  - areas with “low” PPD should have few samples taken
  - sampling should cover the “entire” PPD
  - for ADMB models, the PPD is based on the objective function = likelihood + priors + constraints

# MCMC Methods: Metropolis-Hastings Random Walk Method (MHRWM)

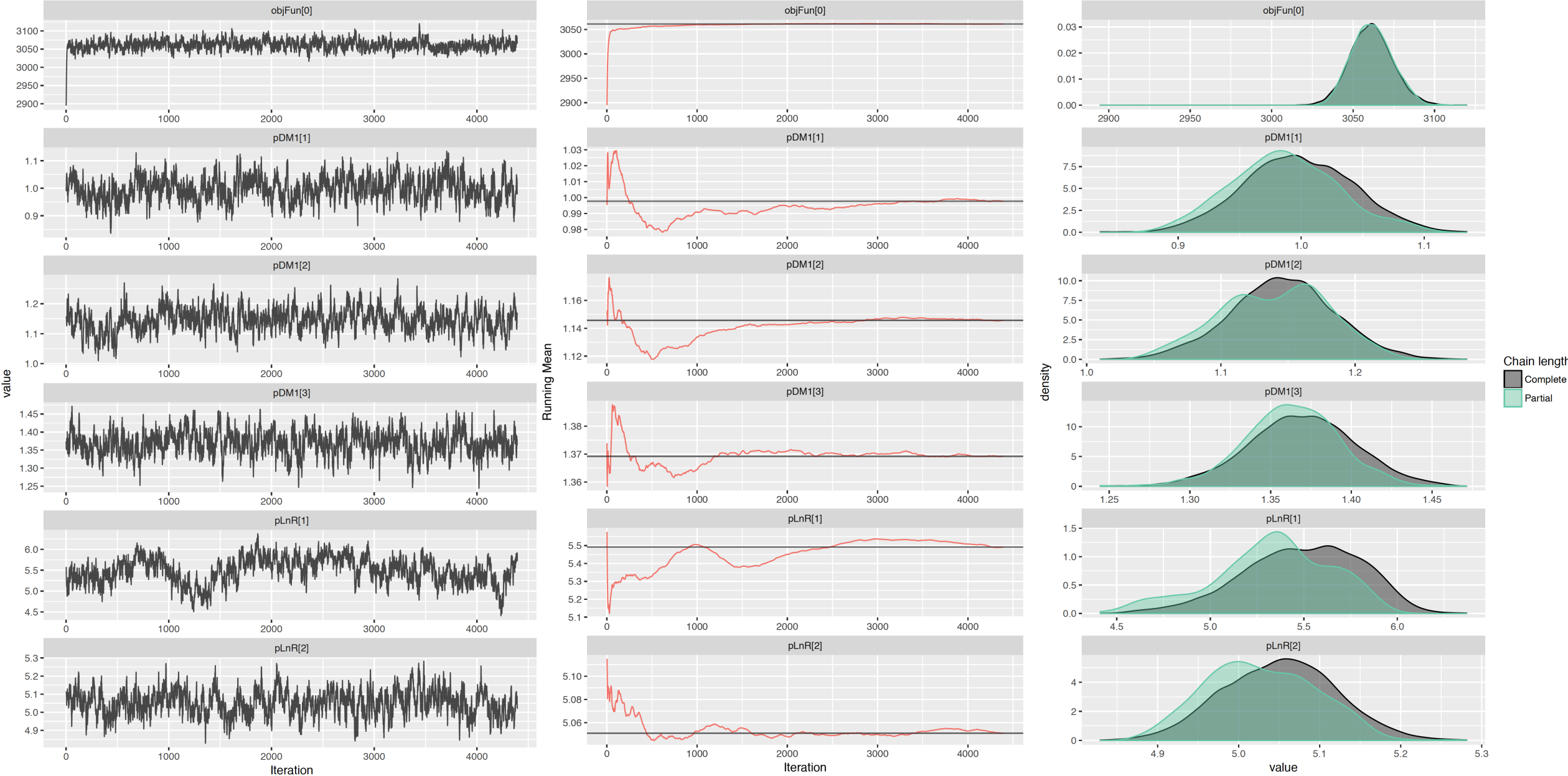
- standard method in ADMB
- runs single chain from MLE solution
- requires multiple runs for multiple chains
  - all start at MLE solution
- can require substantial time for complex models
  - long “burn in”
  - substantial thinning of samples for independence
  - can get trapped near local maxima for long times

# MCMC Results from the 2017 Tanner crab OFL Calculation

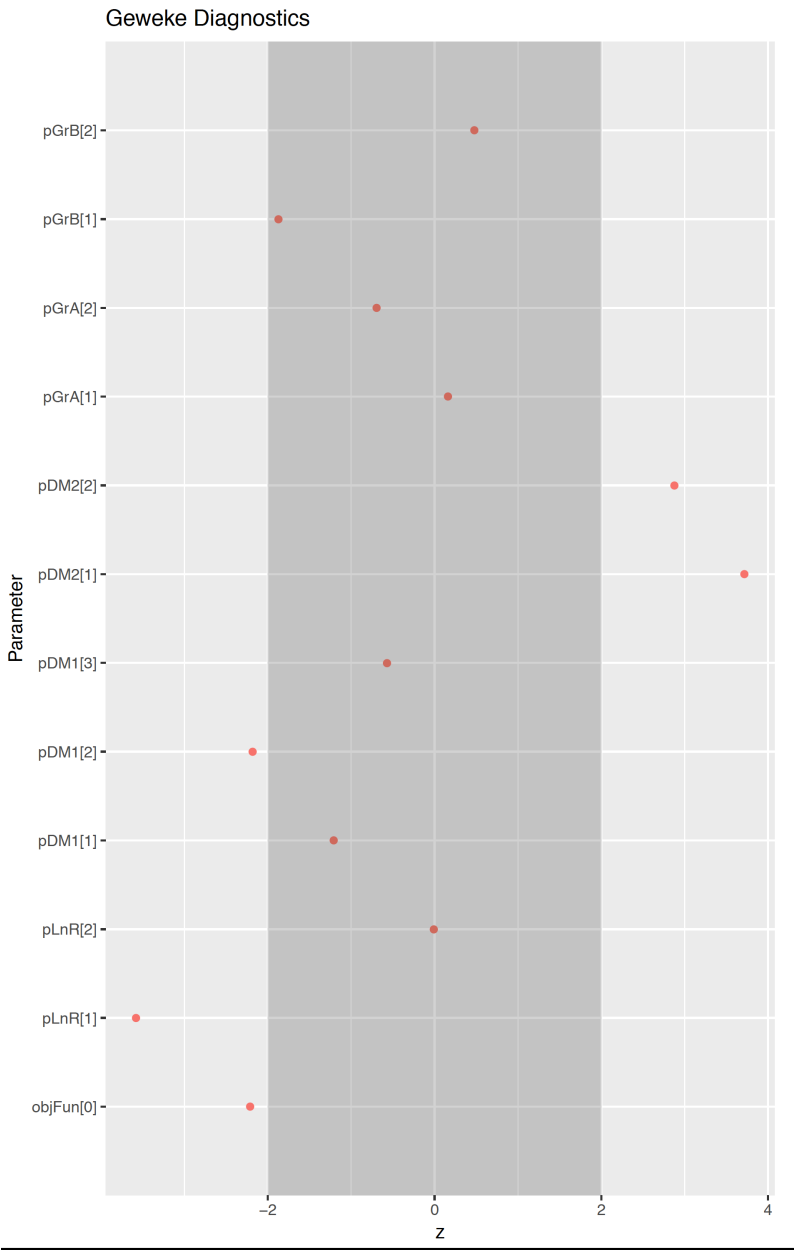
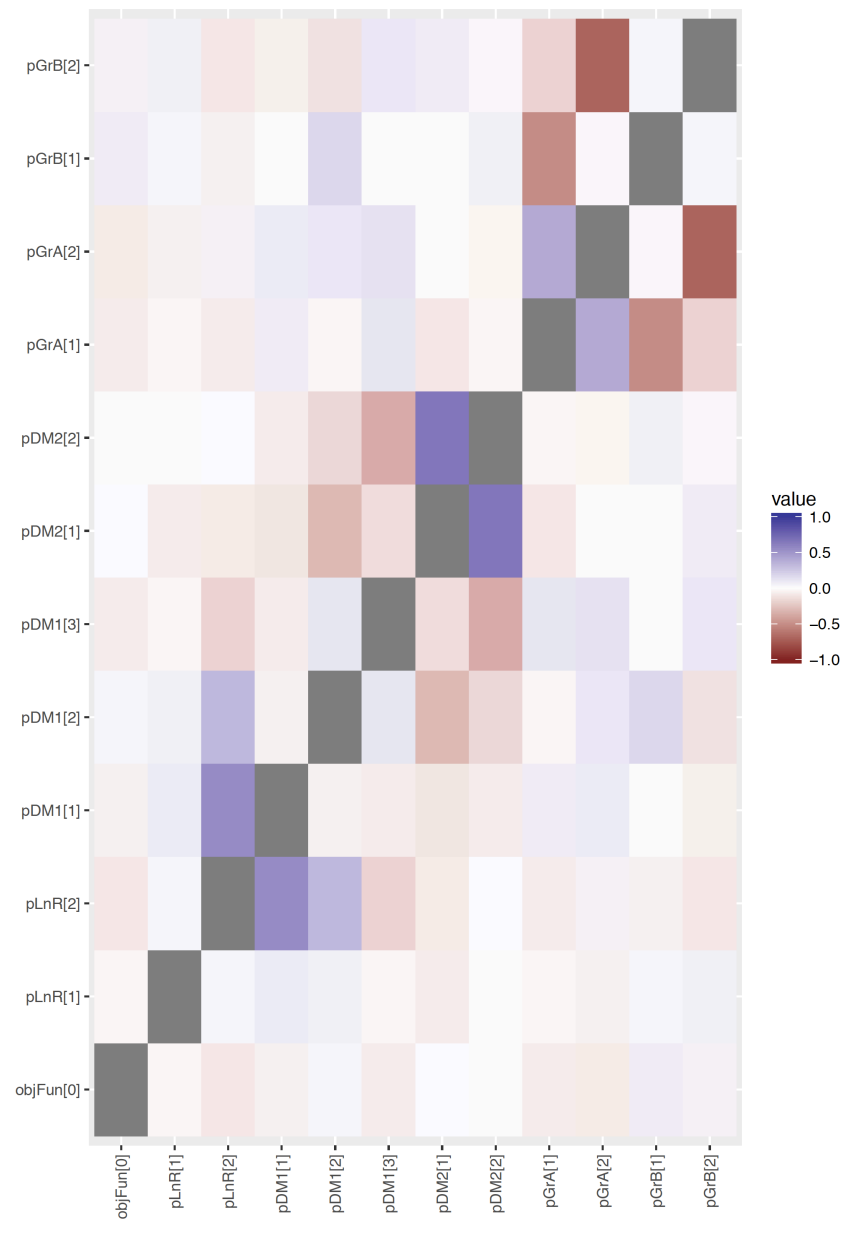
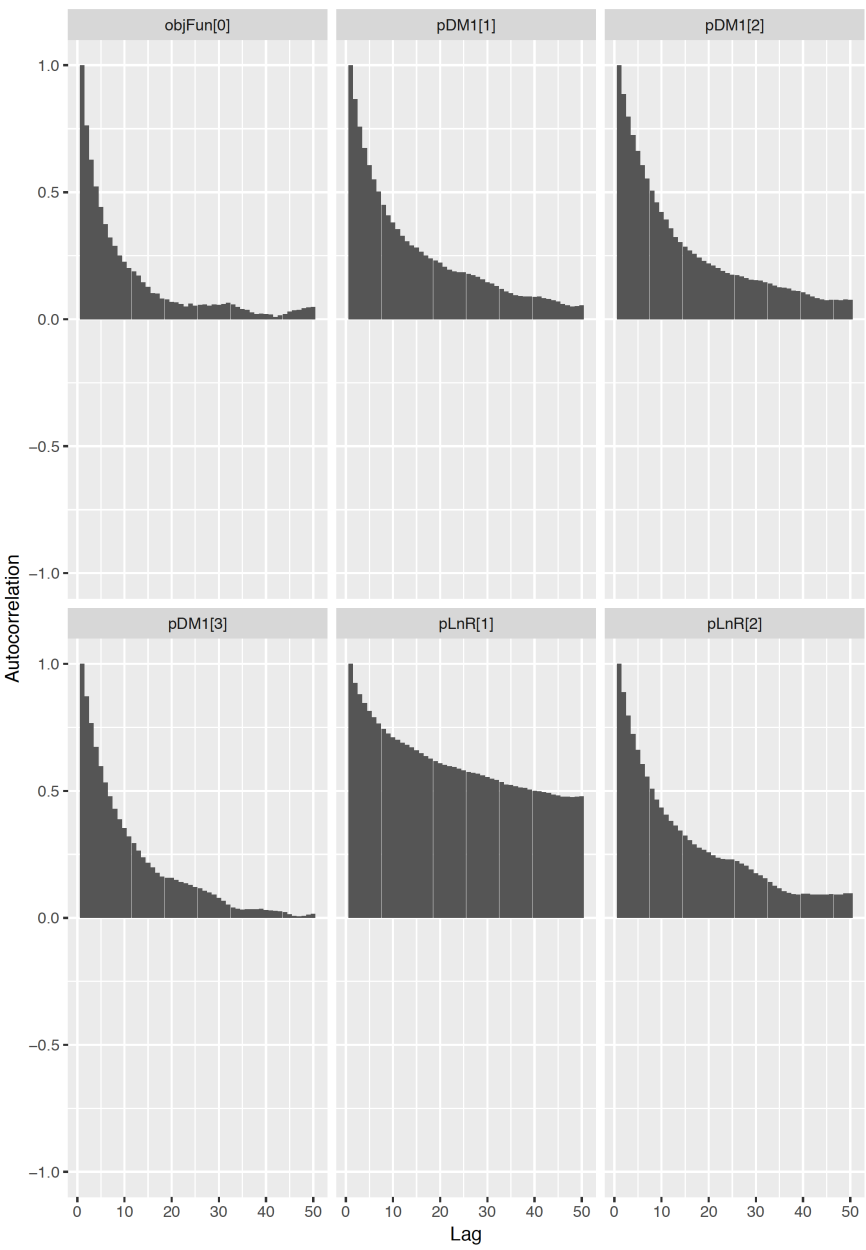
- MCMC used MHRW Method
- 1 chain
- ~3 days to run ~4.4 million iterations
- thinned by factor of 1000
  - ~4,400 samples from PPD



# MCMC Results from the 2017 Tanner crab model



# MCMC Results from the 2017 Tanner crab model



# MCMC Analysis

- Best practices (?)
  - run multiple chains from "dispersed" starting points
  - assess convergence of sampling
    - Potential Scale Reduction Factor ( $\hat{R}$ )
      - compares between-chain to within-chain variability
    - Geweke z-score statistic
      - compares first, last parts of single chain
    - trace plots
    - autocorrelation plots
    - cross correlation
- R Packages
  - coda
  - ggmmcmc
  - GGally (pairs plots)



# SAFE Reporting Practices: What statistics to report (and when)?

- Tables
  - MLE
  - posterior mean, median, and/or mode?
  - which convergence diagnostics?
- Figures
  - single model
    - MLE
    - posterior mean, median, and/or mode?
    - posterior distribution?
    - which convergence diagnostics?
  - multiple models/quantities
    - MLEs
    - posterior means, medians, and/or modes?
    - posterior distributions?

## MCMC Methods: No U-Turn Sampler (NUTS)

- new in ADMB 12 (released Dec., 2017)
- seems to have better sampling/coverage properties than MHRWM
  - better “burn in”
  - sampling more uncorrelated
  - faster
- R package “adnuts” generates multiple chains for ADMB model