

Appendix B – Generalized linear mixed models (GLMMs) for Goliath grouper and mutton snapper.

For comparison with the site-structured demographic model presented in Appendix A, we also present results for the same data using a generalized linear mixed model (GLMM). Specifically, we specified the number of individuals $N_{s,t}$ at site s and year t (i.e. for all years) as a Poisson-distributed random variable:

$$N_{s,t} \sim \text{Poisson}(n_{s,t})$$

where $n_{s,t}$ is expected abundance at site s and year t . $n_{s,t}$ was affected by year-specific environmental factors and habitat-specific environmental factors:

$$\ln(n_{s,t}) = \rho_t + \sum_{h=1}^{n_h} \eta_h I(h = H_s)$$

where η_h is the effect of habitat h on expected abundance, H_s is the habitat-type for site s , and $I(x=X)$ is an indicator function that equals 1 when $x=X$ and 0 otherwise. Both habitat and temporal effects on abundance were specified as random effects:

$$\rho_t \sim \text{Normal}(\mu_\rho, \sigma_\rho^2)$$

and

$$\eta_h \sim \text{Normal}(0, \sigma_\eta^2)$$

where μ_ρ is the median abundance in each site and year and σ_ρ^2 and σ_η^2 are the variance of year and habitat-specific effects on site-specific abundance.

Finally, the observation process was again approximated using a zero-inflated binned-Poisson distribution:

$$\begin{aligned}
\Pr(c_{s,t,r} = 0) &= \varphi + (1 - \varphi) \frac{(N_{s,t})^0}{0!} e^{-N_{s,t}} \\
\Pr(c_{s,t,r} = 1) &= (1 - \varphi) \frac{(N_{s,t})^1}{1!} e^{-N_{s,t}} \\
\Pr(10 \geq c_{s,t,r} \geq 2) &= (1 - \varphi) \sum_{C=2}^{10} \frac{(N_{s,t})^C}{C!} e^{-N_{s,t}} \\
\Pr(c_{s,t,r} \geq 11) &= (1 - \varphi) \left(1 - \sum_{C=0}^{10} \frac{(N_{s,t})^C}{C!} e^{-N_{s,t}} \right)
\end{aligned}$$

where $c_{s,t,r}$ is the r -th survey at site s in year t . This GLMM has no ability to estimate detection probabilities, and hence detectability p is implicitly fixed at 1. However, it still estimates φ (the “zero-inflation” parameter).

We again fitted this model using a Bayesian statistical paradigm and Markov chain Monte Carlo. We therefore must specify priors for all parameters, i.e., $\sigma_\rho \sim \text{Uniform}(0, 10)$, $\sigma_\eta \sim \text{Uniform}(0, 10)$, $\varphi \sim \text{Uniform}(0, 1)$, and $\ln(\mu_\rho) \sim \text{Uniform}(-5, 5)$. The model was implemented in JAGS (Plummer 2003) called from *R* (R Core Development Team 2012) using the *R2jags* package (Su and Yajima 2012). We ran three sampling chains, each with 100,000 discarded samples followed by 100,000 monitored samples and a thinning rate of 100, resulting in 3,000 retained samples from the posterior distribution. We checked for evidence of non-convergence using trace plots, the Gelman-Rubin R -statistic, and estimated effective sample sizes, and confirmed that the effective samples size was >100 for all parameters (corresponding to a Gelman-Rubin generally <1.02).

LITERATURE CITED

Plummer, M. 2003. JAGS: A program for analysis of Bayesian graphical models using Gibbs sampling. Proceedings of the 3rd International Workshop on Distributed Statistical Computing (DSC 2003). Vienna, Austria.

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Su, Y.-S., and M. Yajima. 2012. R2jags: A Package for Running jags from R.