

Bayesian Stock-Recruit Methods

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Hierarchical Ricker Model

- Spawner-recruit data
 - spatially structured, by populations exposed to salmon farms (Broughton Archipelago) and reference regions (Areas 7-11)
- Effects
 - year & management area w/in year as random & nested random effects respectively
 - density-dependent mortality was treated as a fixed factor per population (i.e. different for even- and odd-year populations within the same river)
 - growth rate is fixed factor
 - average lice per wild juvenile salmon (estimated from the GLMM) was included as covariate

That gave a model of:

$$R_{i,t} = N_{i,t-2} \exp [r - b_i N_{i,t-2} - c W_{a,t-1} + \theta_t + \theta_{a,t} + \epsilon_{i,t}]$$

- Variables:
 - $R_{i,t}$ is the recruitment of population i in year t
 - $N_{i,t}$ is the abundance of spawners of population i in year $t - 2$
 - r is the growth rate
 - b_i is the density-dependence parameter for each population
 - $W_{a,t-1}$ is the average lice per wild juvenile salmon the previous year
 - c is the strength of the relationship between salmon survival and lice on wild juvenile salmon
 - θ_t environmental stochasticity, spatially coherent among all populations for year
 - $\theta_{a,t}$ spatially coherent variation for population within a management area
 - $\epsilon_{i,t}$ random annual variation that is independent among populations

The linear version of the Ricker model is then fit:

$$\ln \frac{R_{i,t}}{N_{i,t-2}} = r - b_i N_{i,t-2} - c W_{a,t-1} + \theta_t + \theta_{a,t} + \epsilon_{i,t}$$