

N-mixture models in NIMBLE

Introduction

The purpose of this document is to showcase how N-mixture models (Royle, 2004) may be used with the NABat data pipeline to model colony counts and capture records.

Model description

N-mixture model

The following is a condensed description of the model discussed by Royle (2004). Let N_i denote the number of individuals *available for capture* at site i and p_{ij} denote the probability of detecting an individual on visit j to site i . Then,

$$N_i \sim \text{Poisson}(\lambda_i)$$

$$y_{ij} \sim \text{Binomial}(N_i, p_{ij})$$

Alternatively, a negative binomial sampling model can be placed on the the latent number of individuals available for capture.

$$N_i \sim \text{Negative binomial}(\mu_i, \phi)$$

$$y_{ij} \sim \text{Binomial}(N_i, p_{ij})$$

Zero-inflated N-mixture model

In some cases, some sites may not be tenable for the target species. To account for the extra zeros induced by habitat insuitability, an occupancy layer can be added, resulting in a zero-inflated N-mixture model.

$$Z_i \sim \text{Bernoulli}(\psi_i)$$

$$N_i|z_i \sim \text{Negative binomial}(z_i * \mu_i, \phi)$$

$$y_{ij}|N_i \sim \text{Binomial}(N_i, p_{ij})$$

Simulated experiments

Poisson N-mixture model

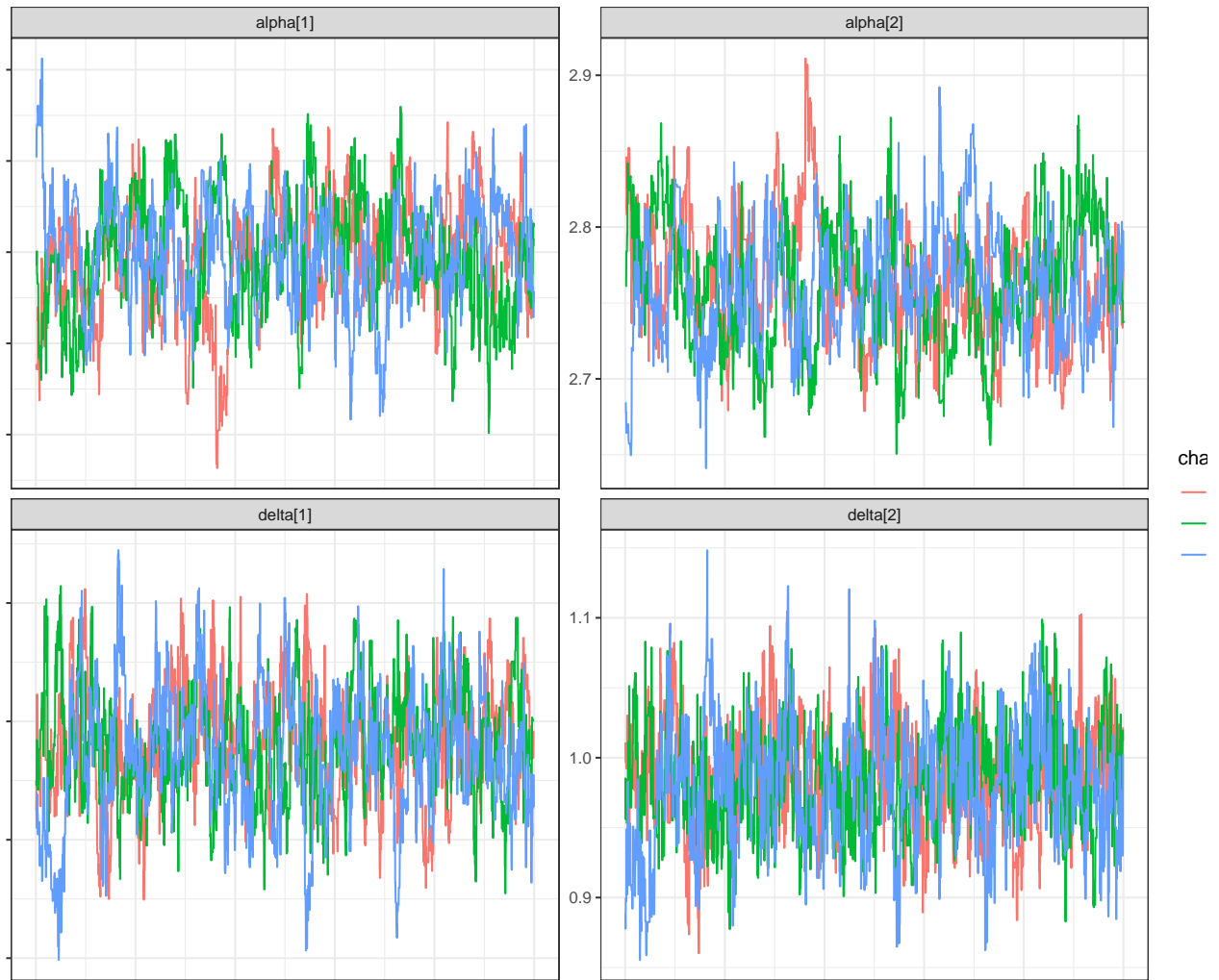
```
{
  for (site in 1:nsites) {
    log(lambda[site]) <- inprod(alpha[1:p_alpha], W[site,
      1:p_alpha])
    N[site] ~ dpois(lambda = lambda[site])
  }
  for (row in 1:nrows) {
    logit(p[row]) <- inprod(delta[1:p_delta], V[row, 1:p_delta])
    y[row] ~ dbinom(prob = p[row], size = N[site_ndx[row]])
  }
  for (i in 1:p_alpha) {
    alpha[i] ~ dnorm(0, sd = 2)
  }
  for (i in 1:p_delta) {
    delta[i] ~ dnorm(0, sd = 2)
  }
}
```

Simulated data

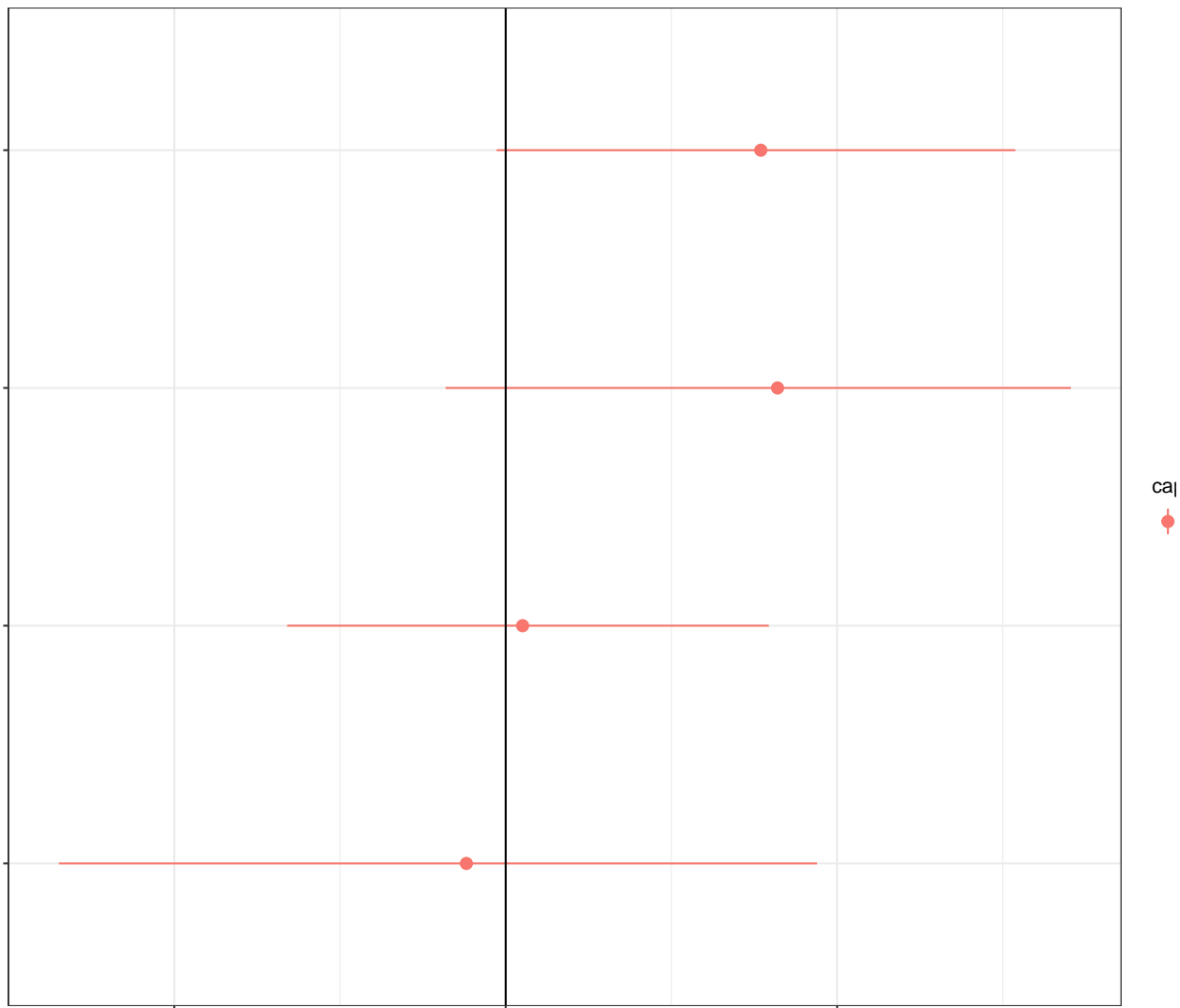


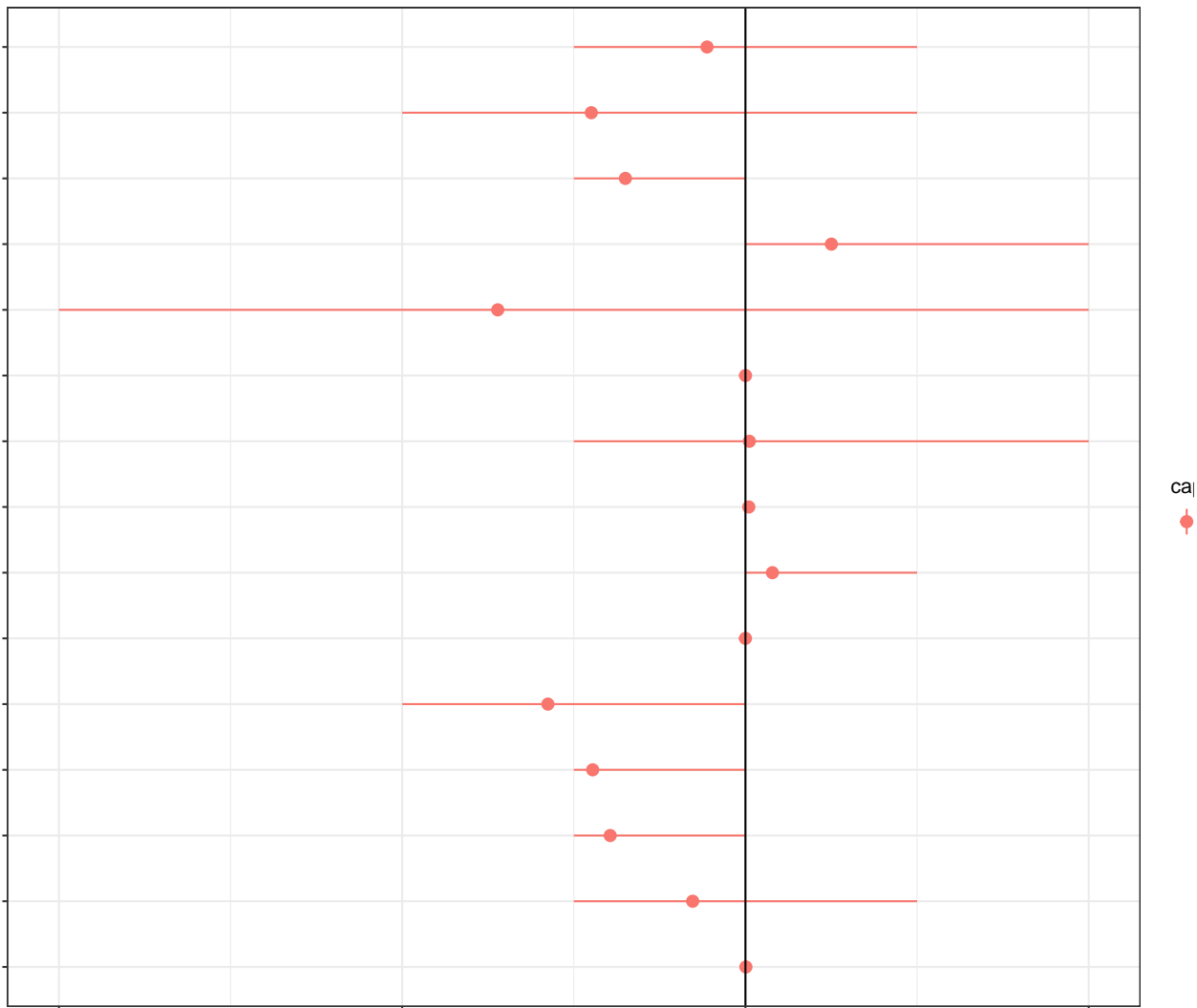
Fit model

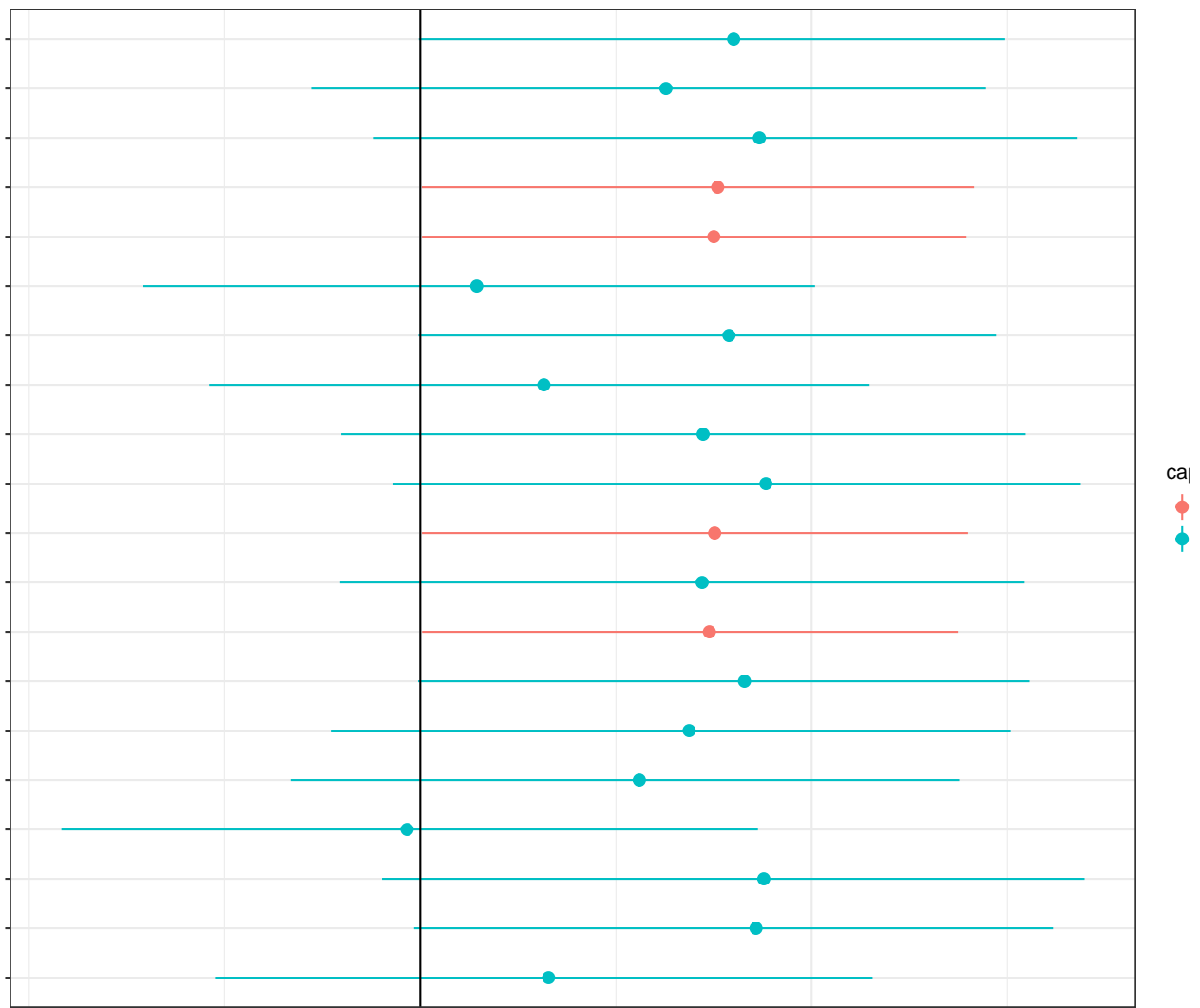
Diagnostics



Posterior summaries

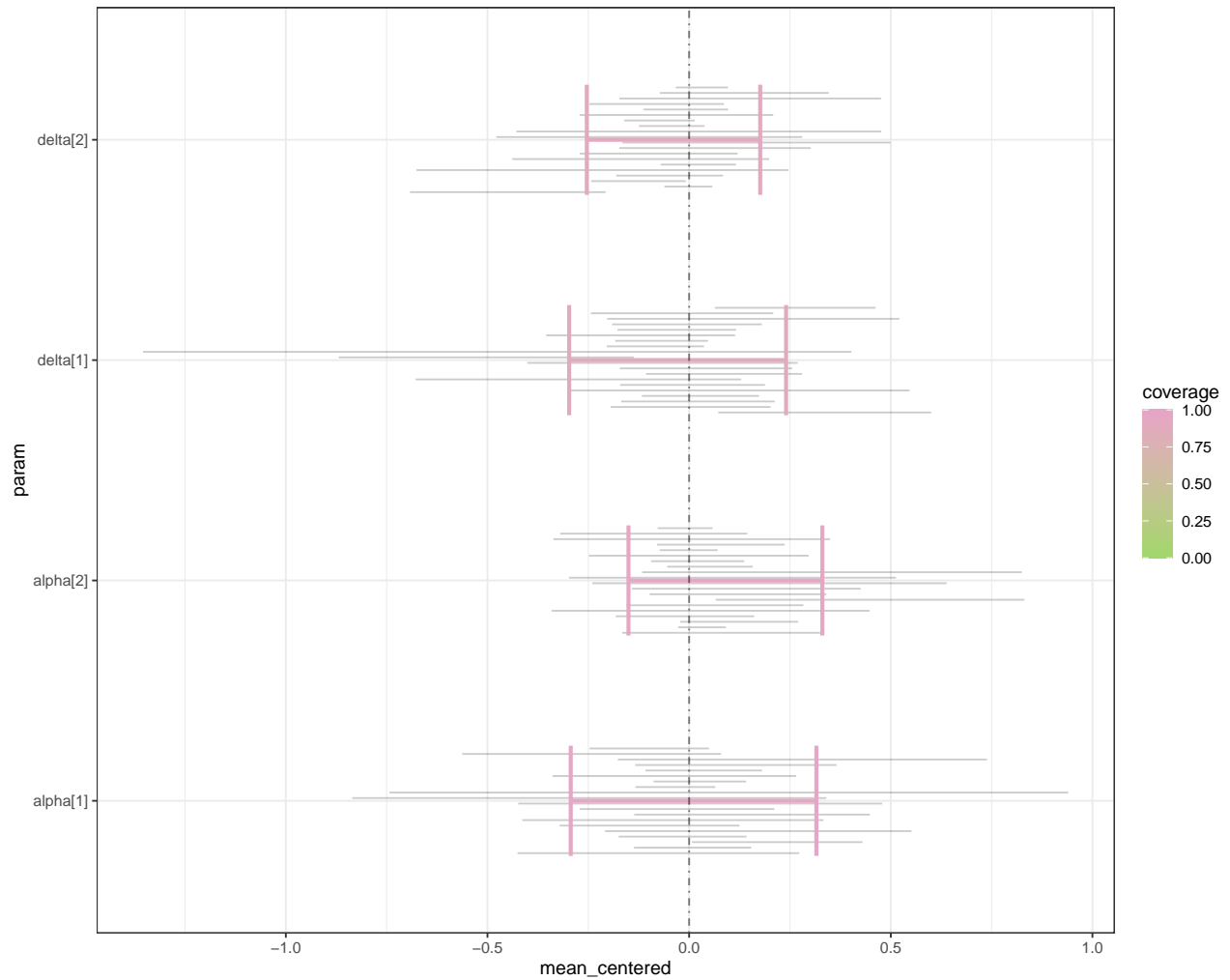






Baby simulation study

Twenty simulated data sets with random generating values.



Negative binomial N-mixture model

```
{
  for (site in 1:nsites) {
    log(lambda[site]) <- inprod(alpha[1:p_alpha], W[site,
      1:p_alpha])
    nbp[site] <- phi/(phi + lambda[site])
    N[site] ~ dnegbin(prob = nbp[site], size = phi)
  }
  for (row in 1:nrows) {
    logit(p[row]) <- inprod(delta[1:p_delta], V[row, 1:p_delta])
    y[row] ~ dbinom(prob = p[row], size = N[site_ndx[row]])
  }
  for (i in 1:p_alpha) {
    alpha[i] ~ dnorm(0, sd = 2)
  }
  for (i in 1:p_delta) {
    delta[i] ~ dnorm(0, sd = 2)
  }
}
```

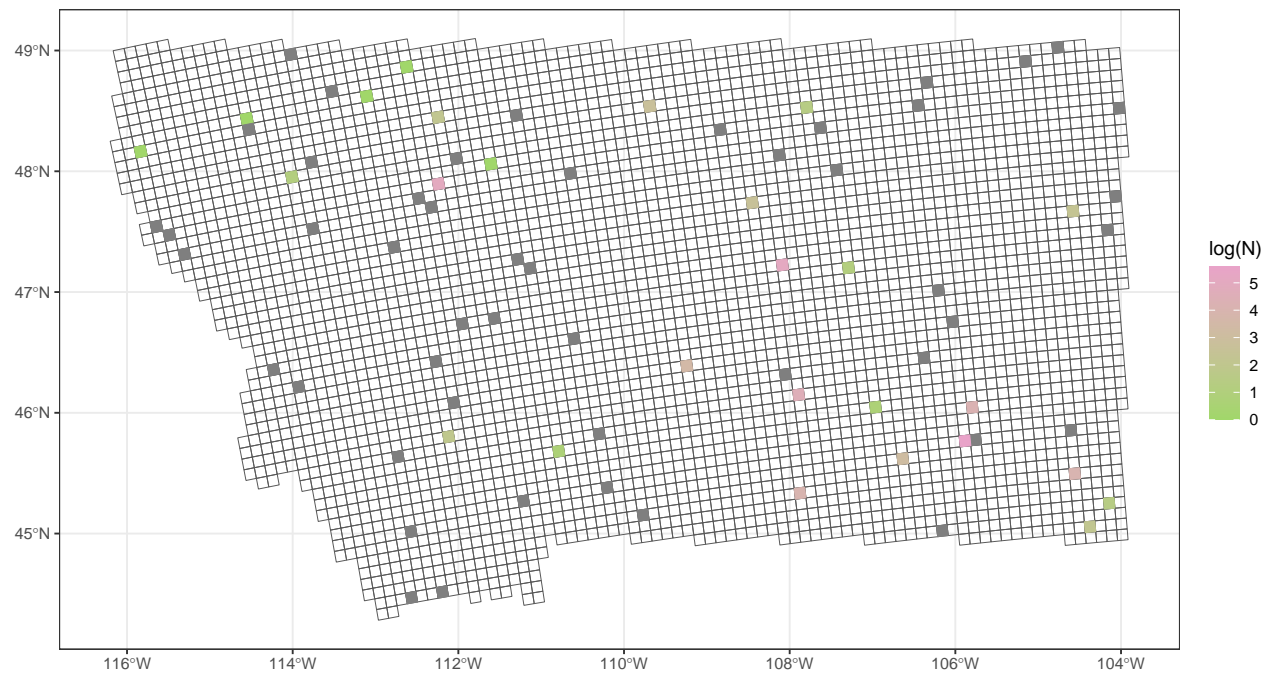


```

    phi ~ T(dnorm(0, 1), 0, Inf)
  }

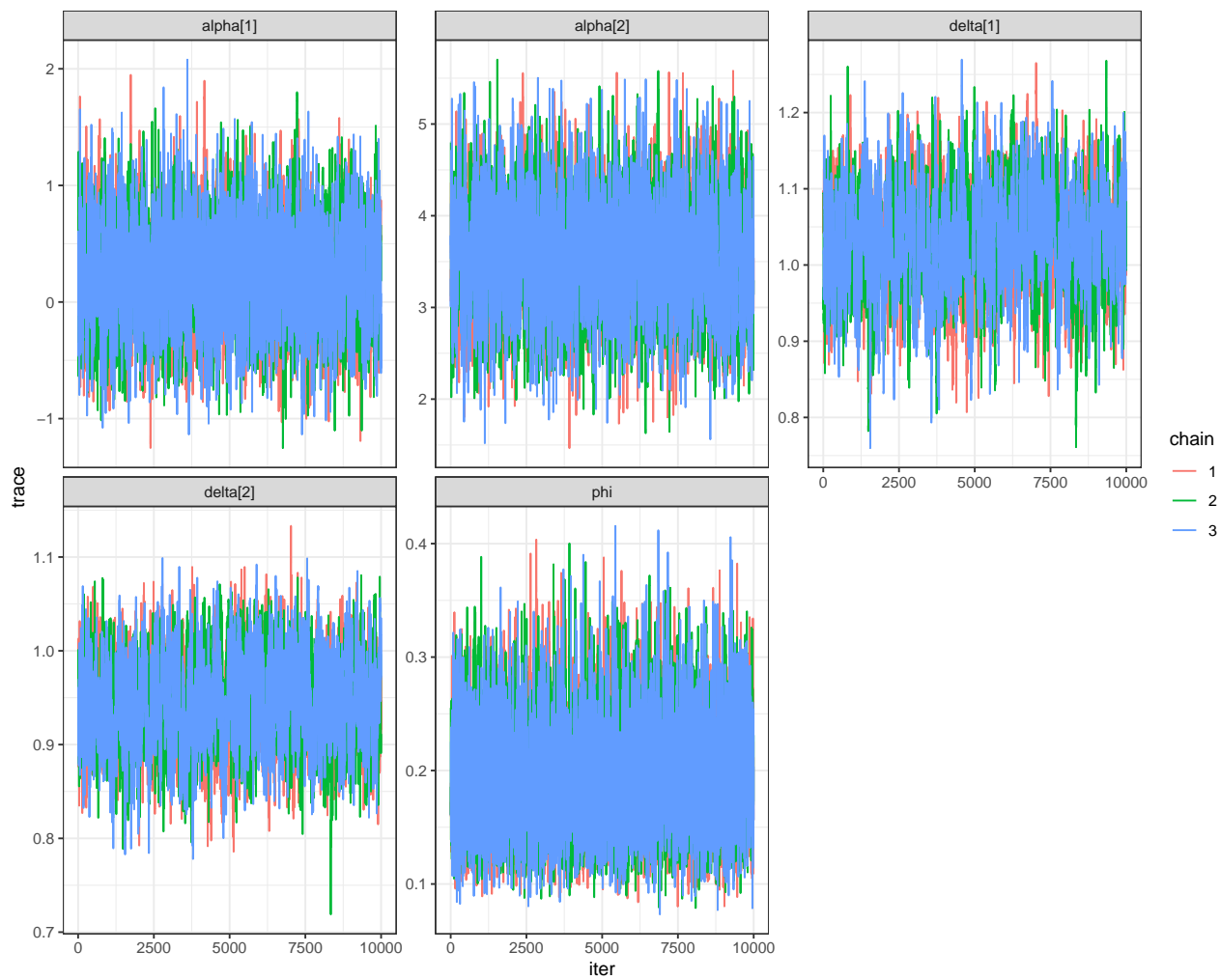
```

Simulated data

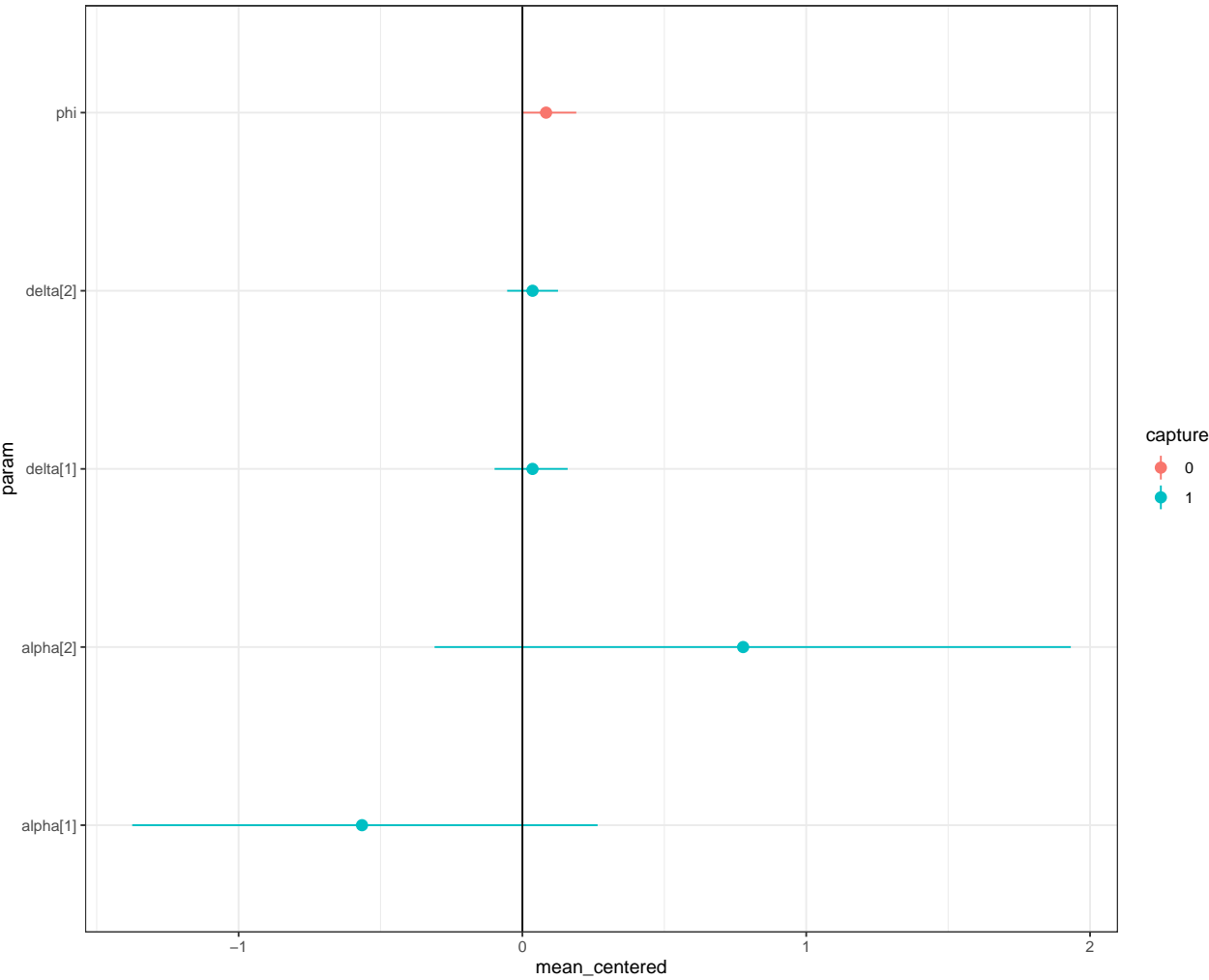


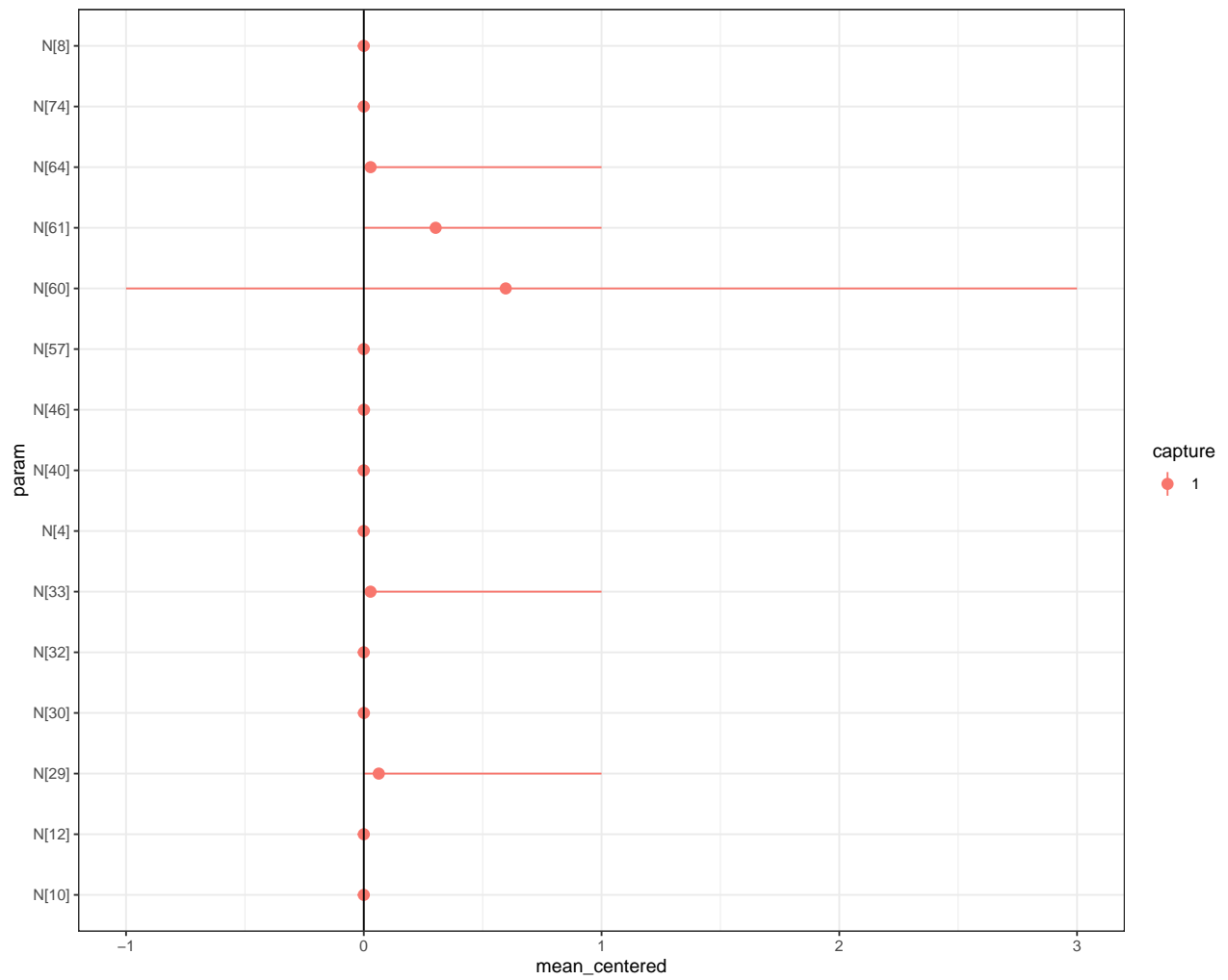
Fit model

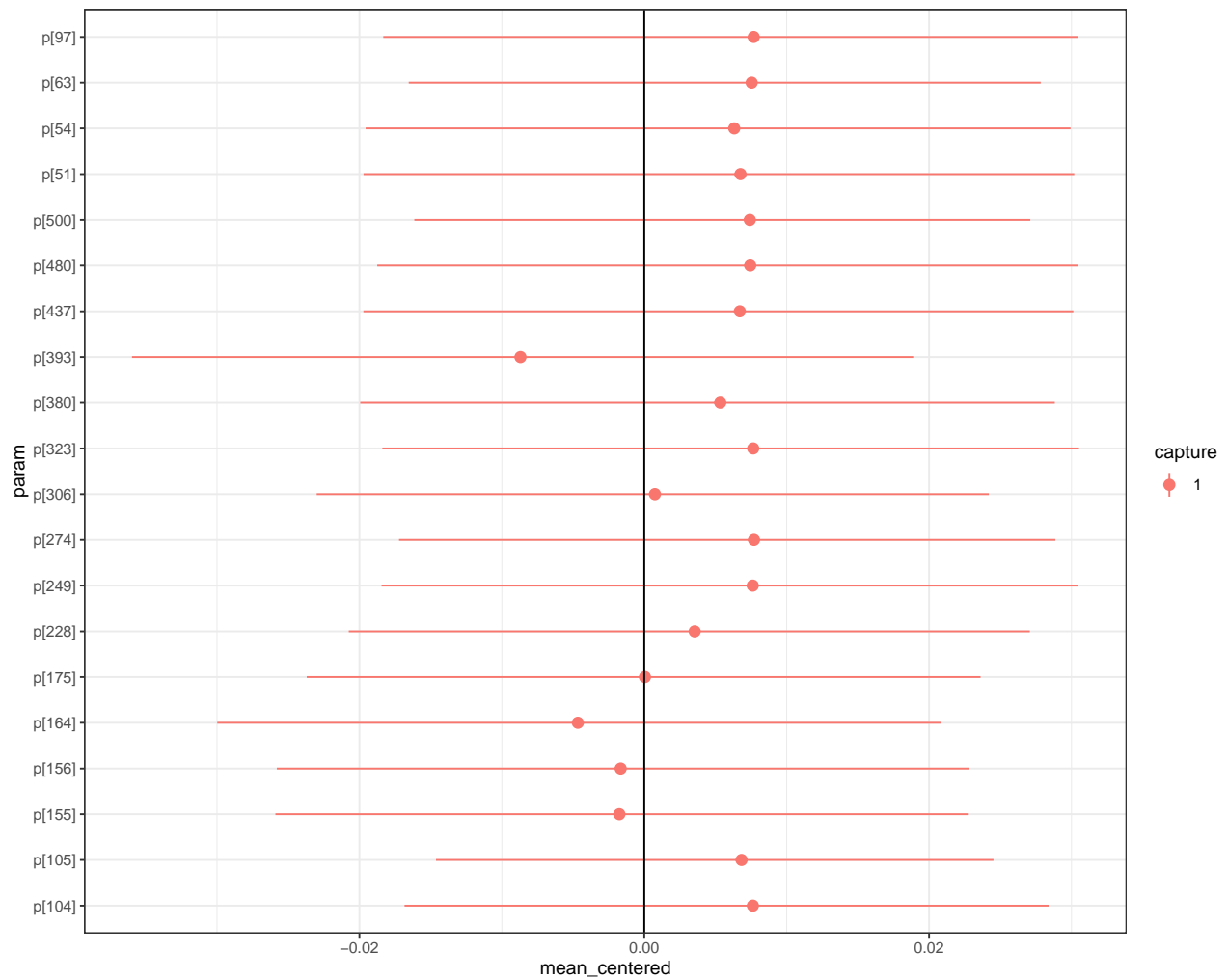
Diagnostics



Posterior summaries

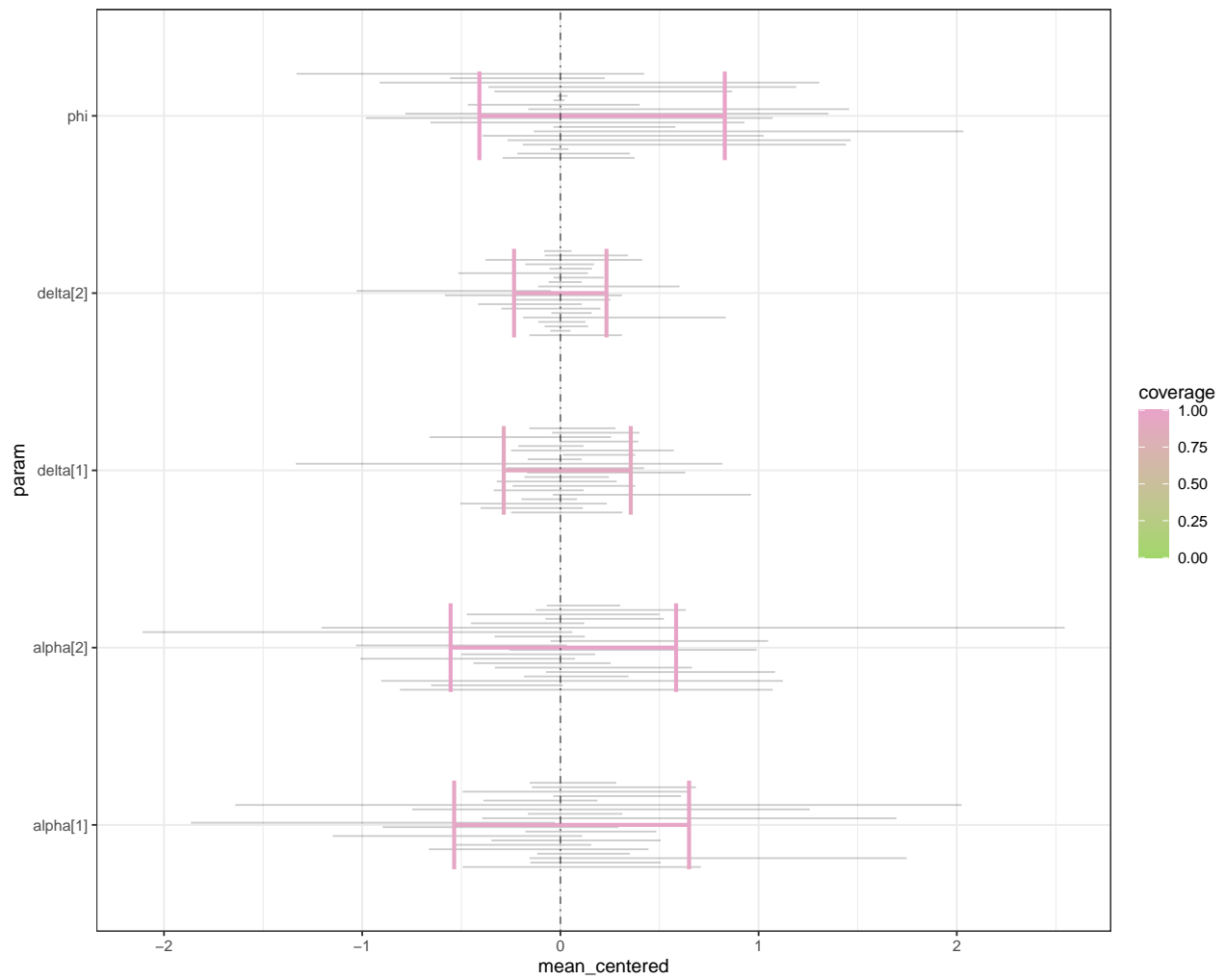






Baby simulation study

Twenty simulated data sets with random generating values.



References

- Royle, J.A. (2004) N-mixture models for estimating population size from spatially replicated counts. *Bio-metrics*, **60**, 108–115.