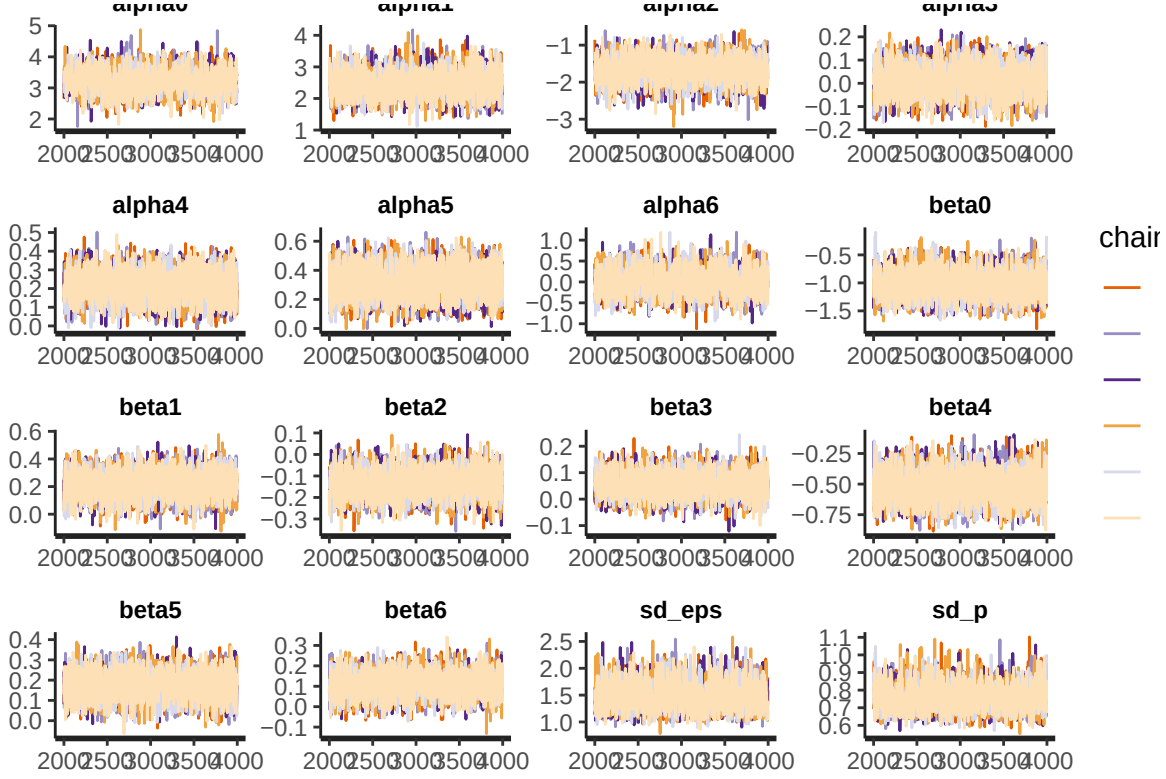
HMC Diagnostics

Script for checking MCMC/HMC diagnostics - this might be better as an Rmd to just have one output for supplemental publication

Plethodon jordani

View Traceplots



Check Domain Specific Expectations

Check N for Truncation

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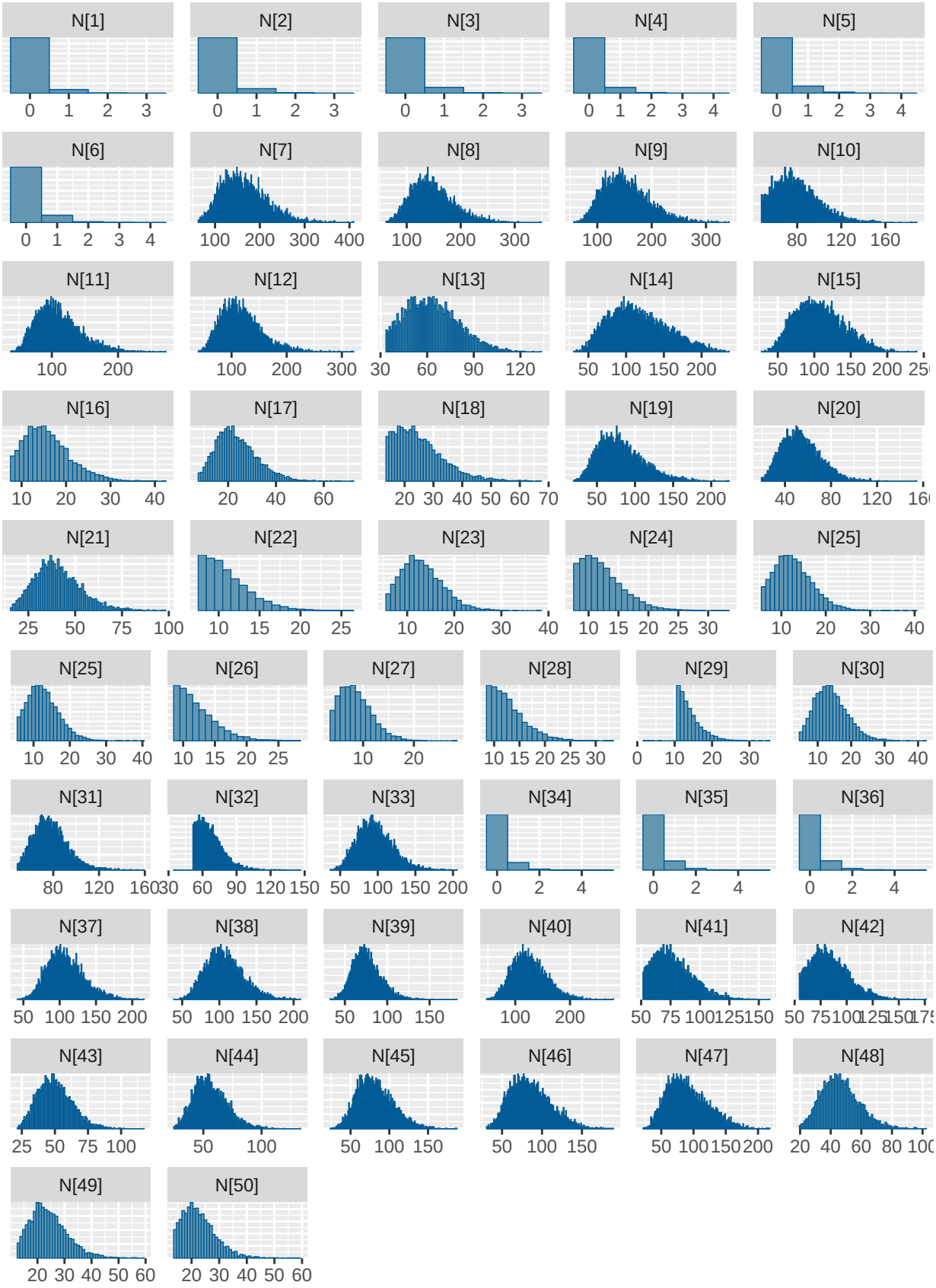
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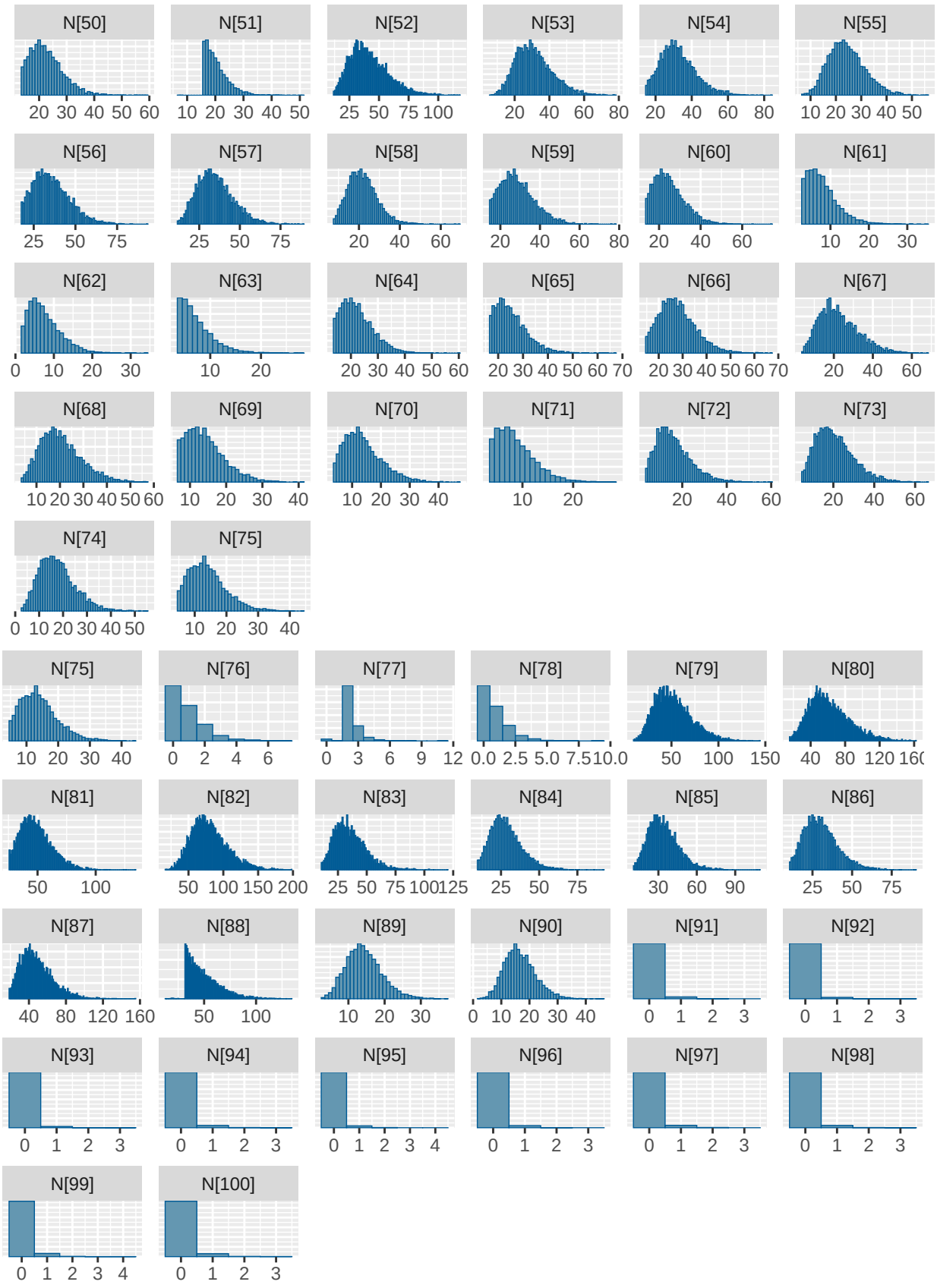
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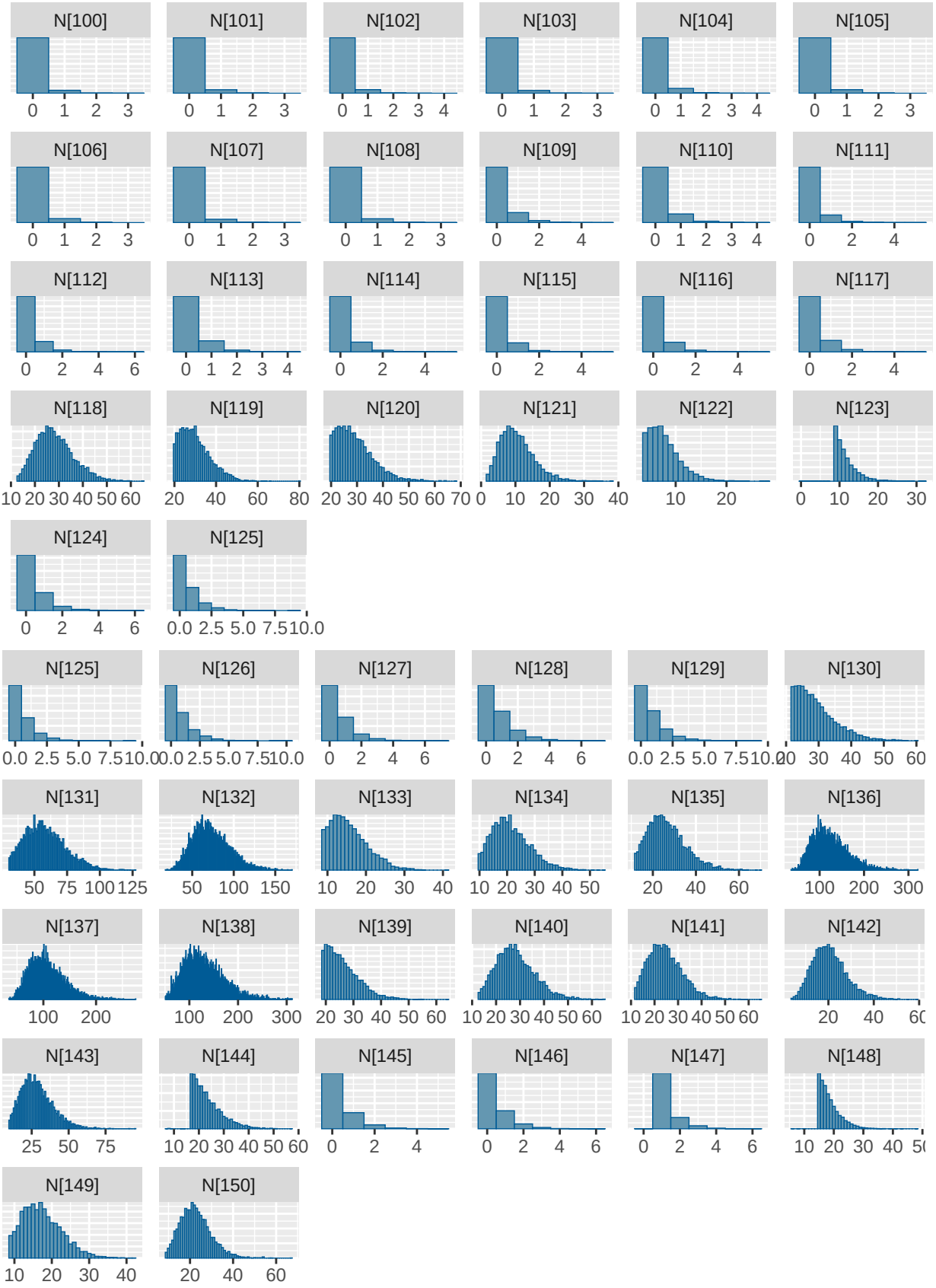
N[99]
0 1 2 3 4
N[100]
0 1 2 3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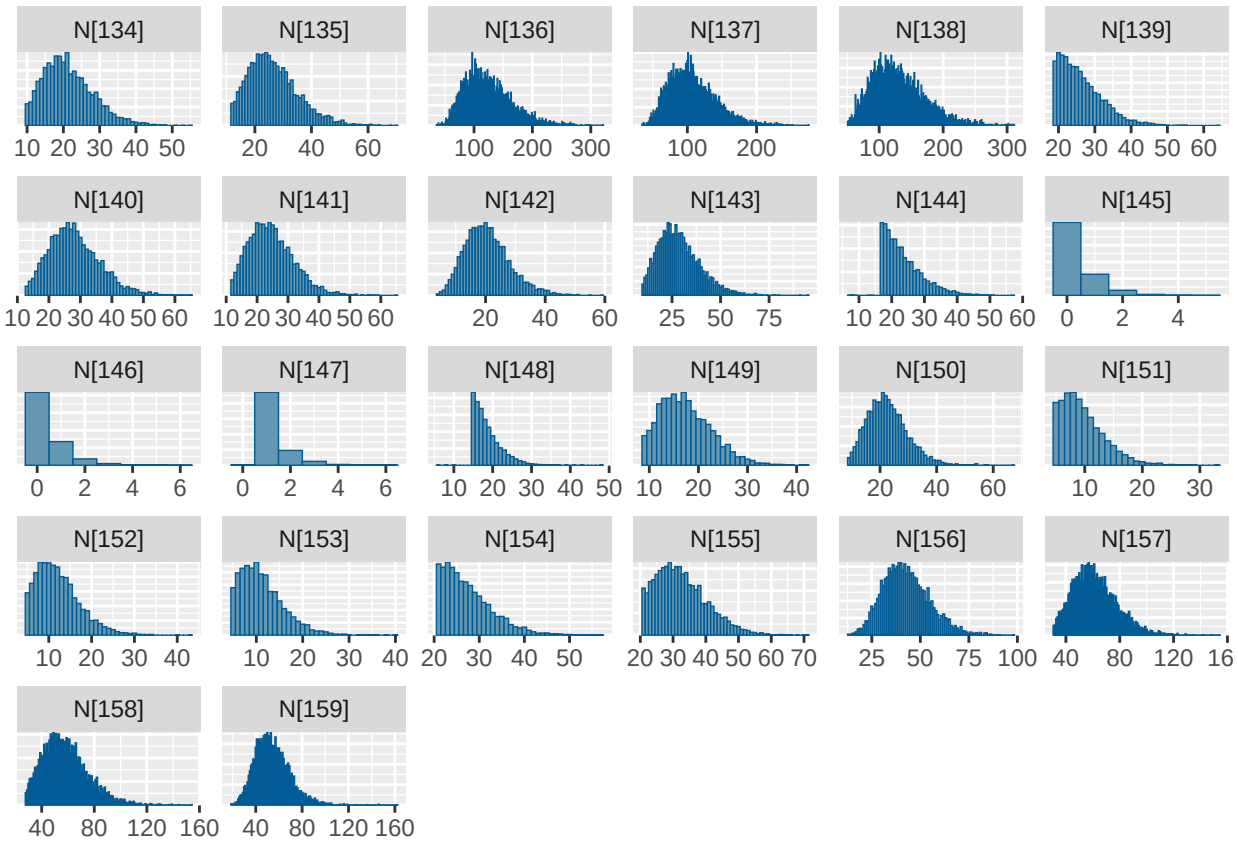
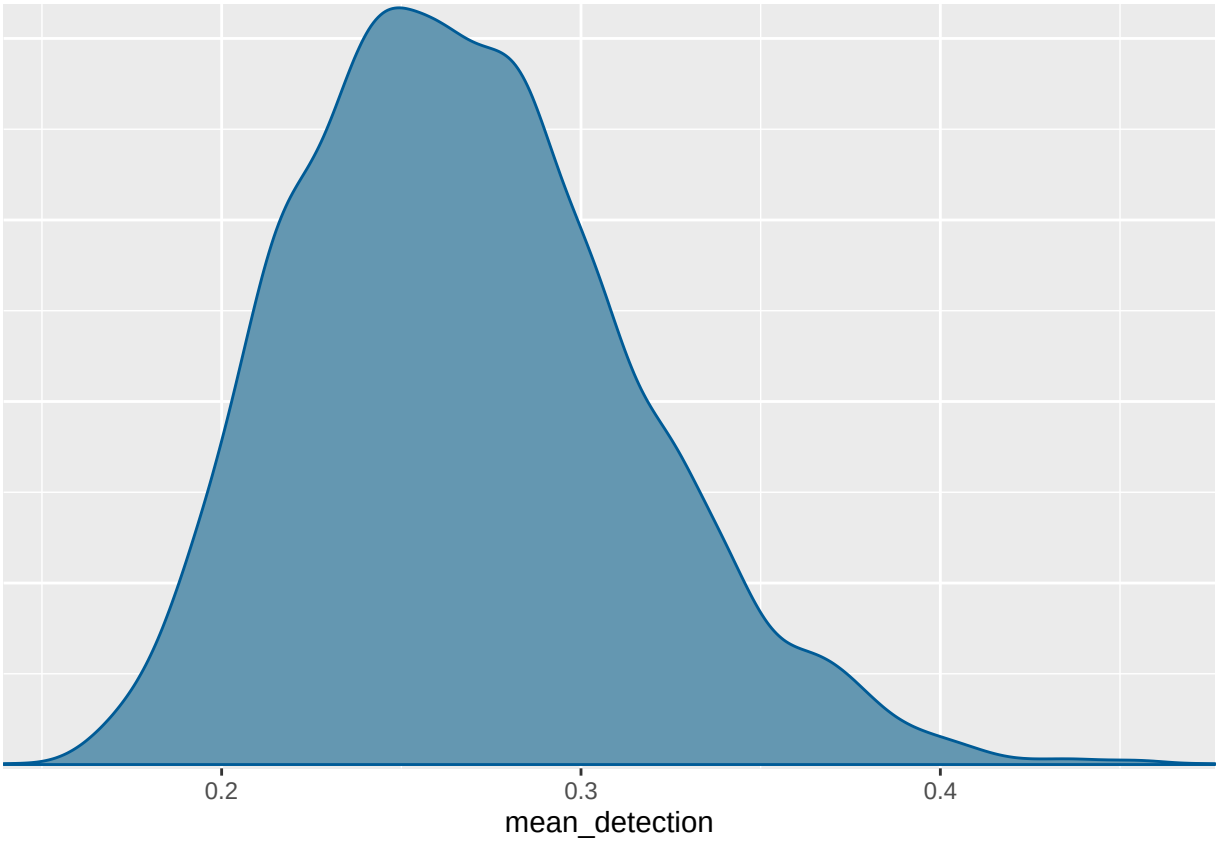


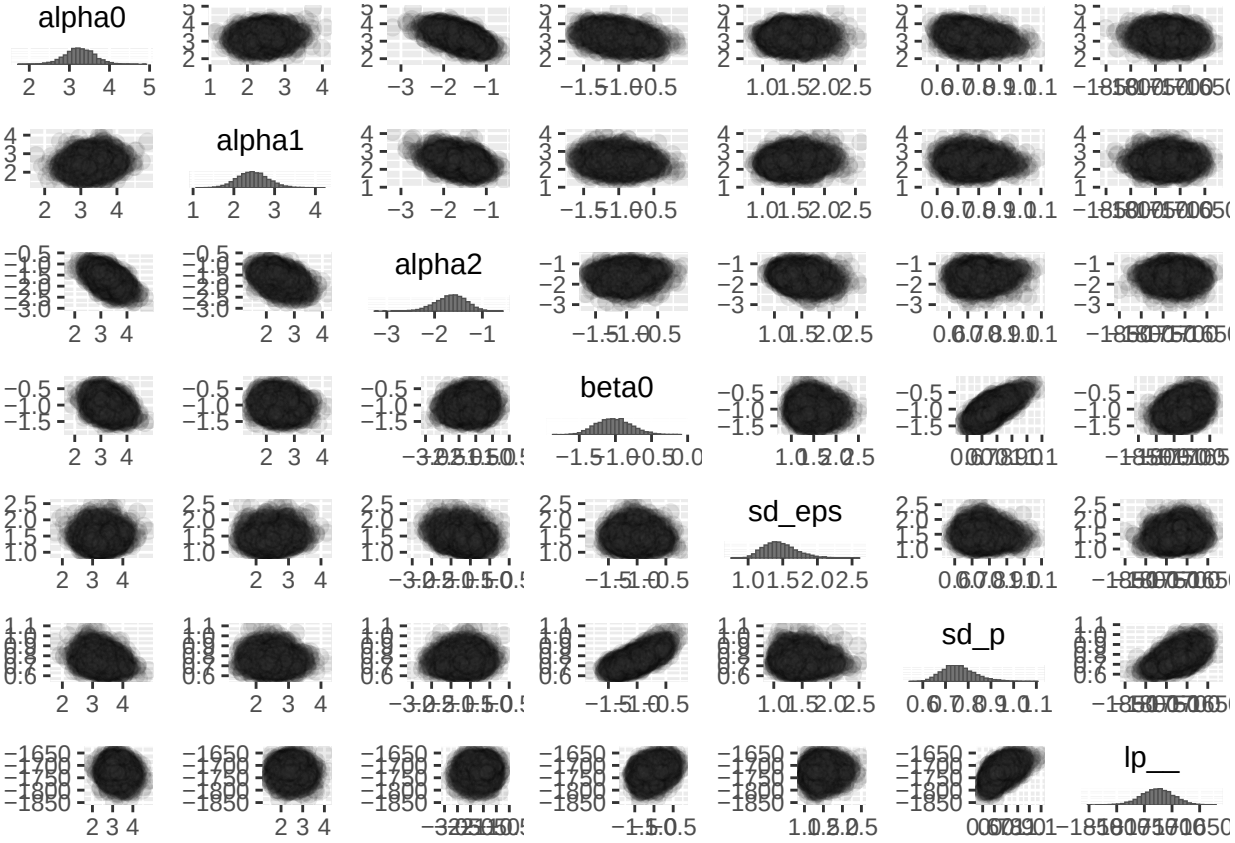

```
## null device
##           1
```

Check detection

In simulations abundance esimates are unreliable when detection gets below 20%



Check Divergences and Pairwise Correlations



Check Energy and Treedepth

Summarize Samples Sizes and Mixing

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effective sample sizes (should be > 100) - Aki Vehtari, Andrew Gelman, Daniel Simpson, Bob Carpenter, and Paul-Christian Bürkner (2019). Rank-normalization, folding, and localization: An improved R-hat for assessing convergence of MCMC. arXiv preprint arXiv:1903.08008.

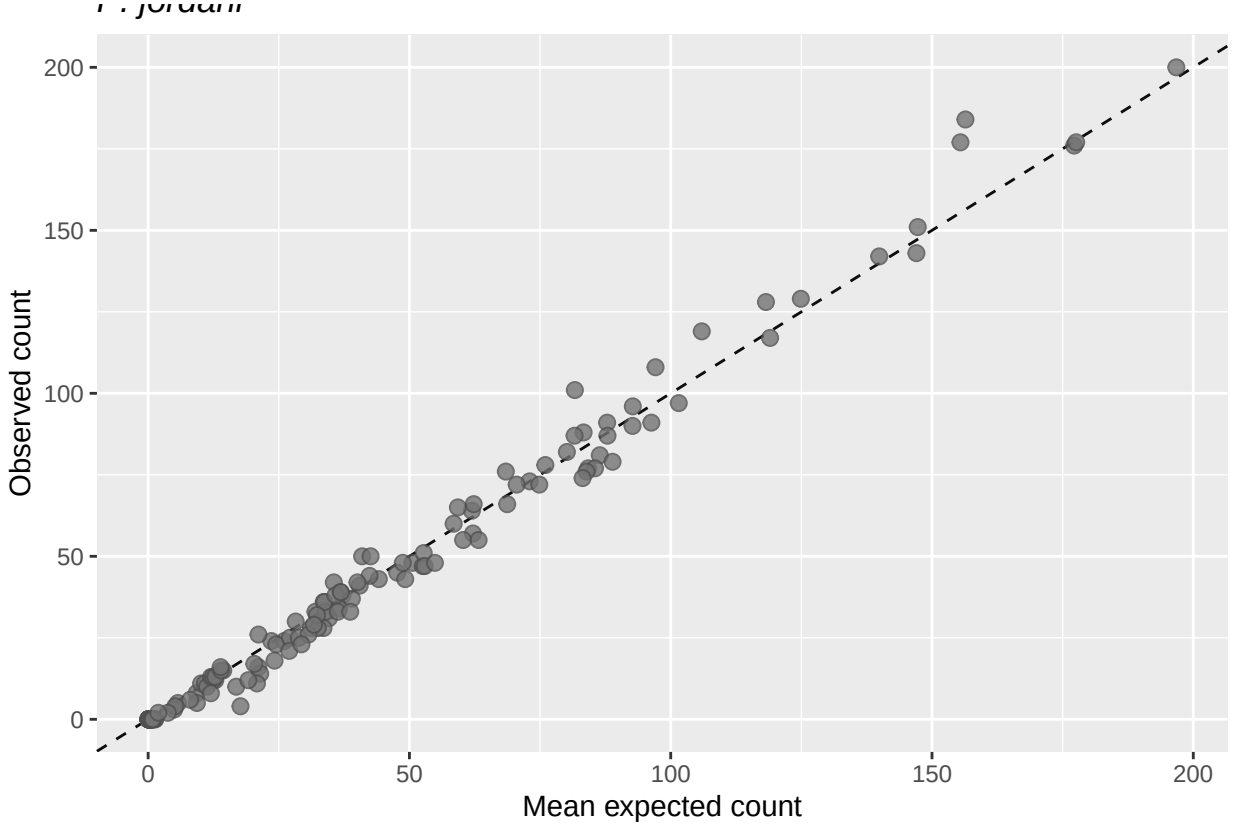
```
## [1] 1.003609
```

```
## [1] 1675
```

```
## [1] 2564
```

Posterior Predictive Checks

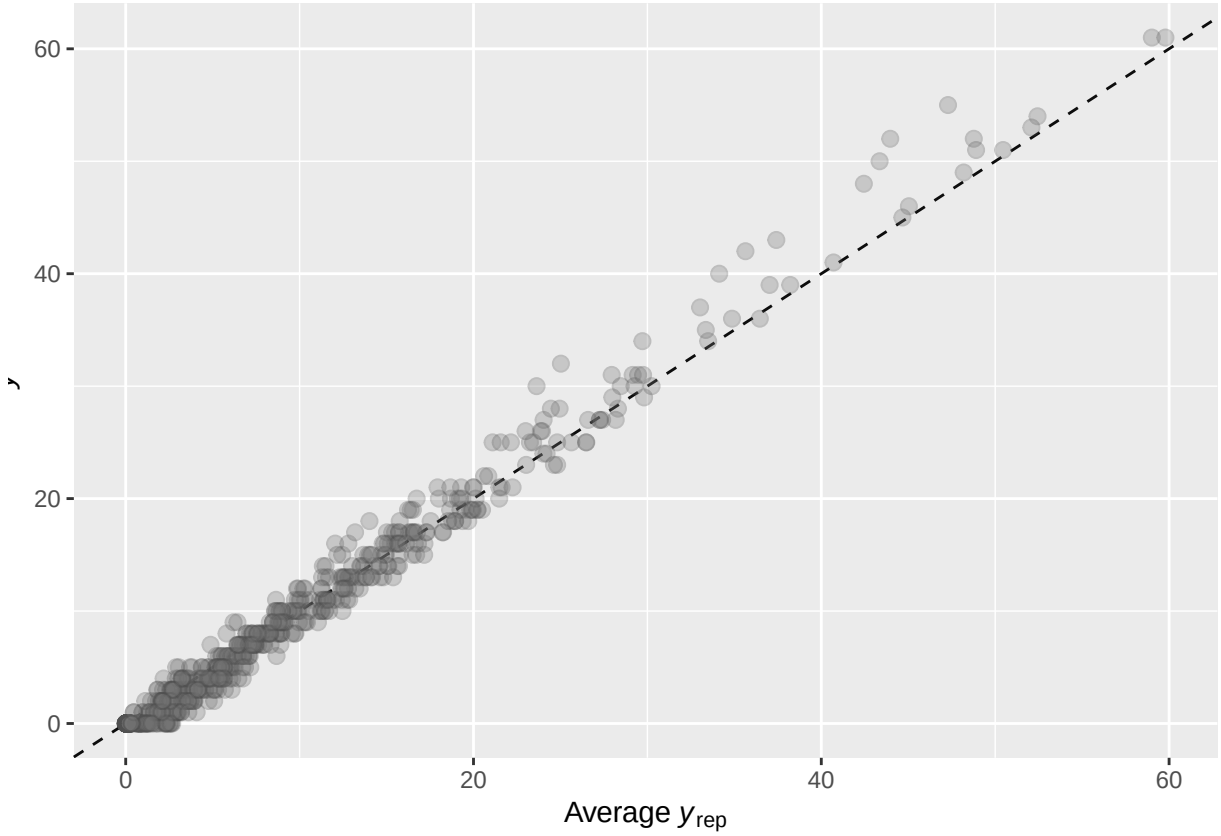
Examine posterior prredictions of total counts across all 5 visits

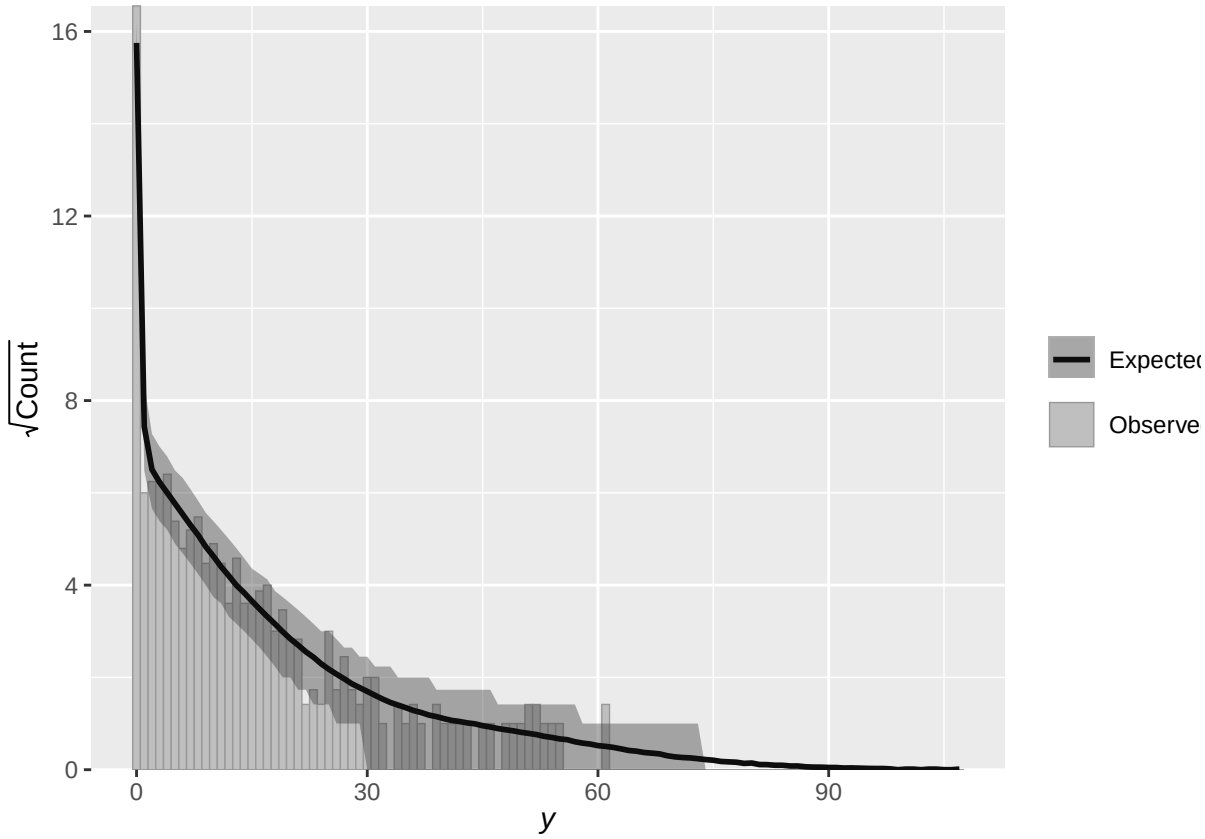


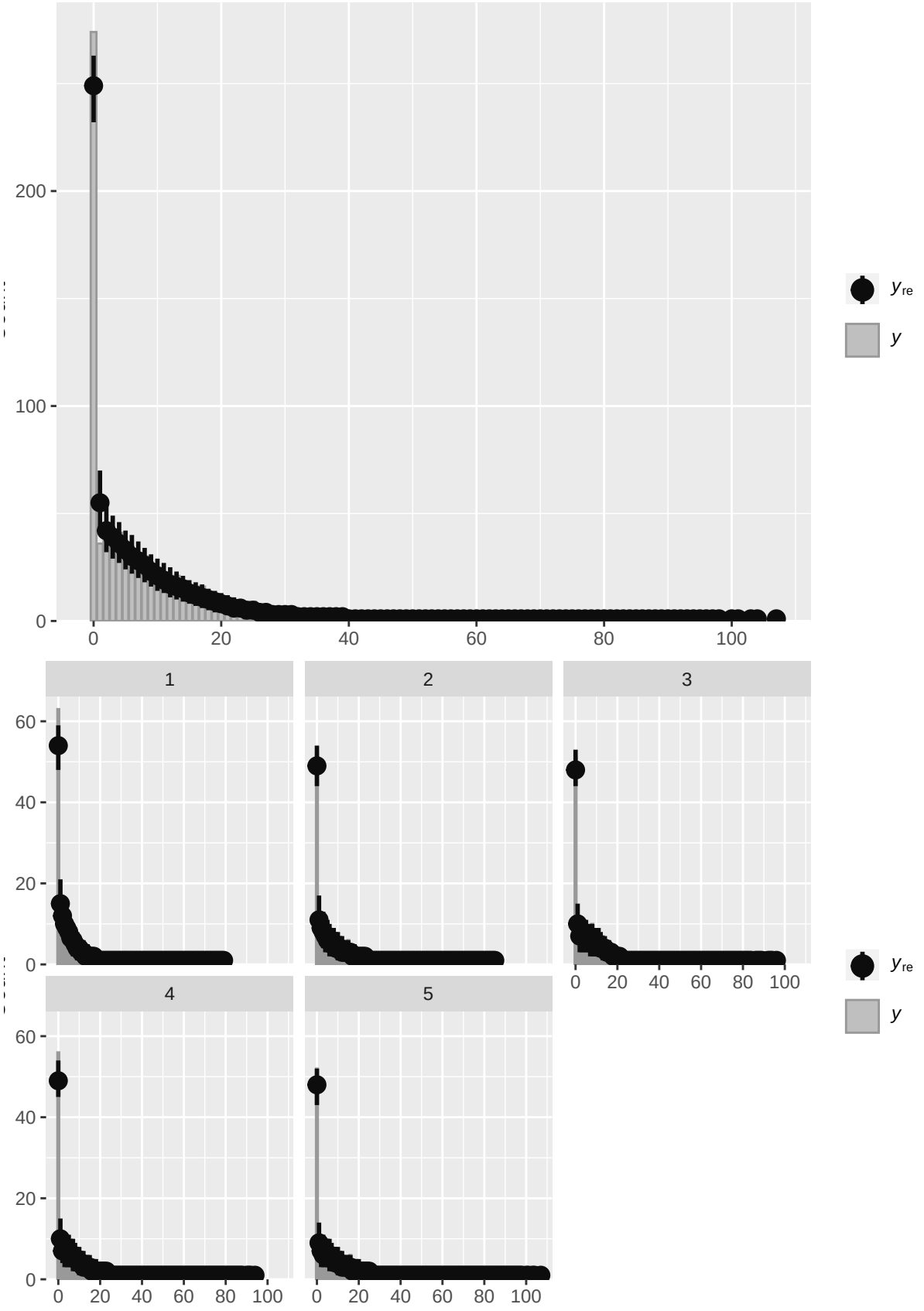
RMSE of posterior predictive

```
## [1] 5.070722
```

Posterior predictive check for each visit


60
40
20
0
y
0
20
40
60
Average y_{rep}


16
12
8
4
0
√Count
0
30
60
90
y
Expecte
Observe


200
100
0
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20
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60
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100
y_{re}
y
1
2
3
4
5
60
40
20
0
0
20
40
60
80
100
y_{re}
y

RMSE of posterior predictive for observations per visit

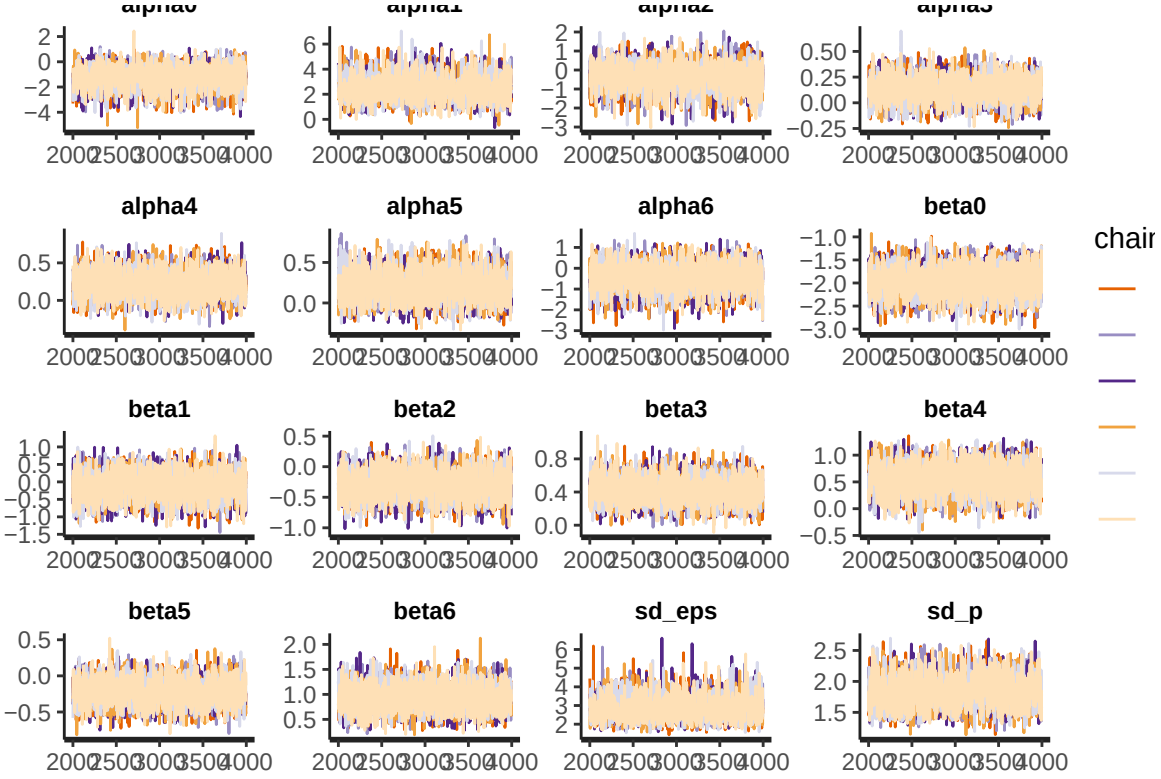
```
## [1] 2.956443
```

RMSE of posterior predictive

```
## [1] 1.322162
```

Desmognathus wrighti

View Traceplots



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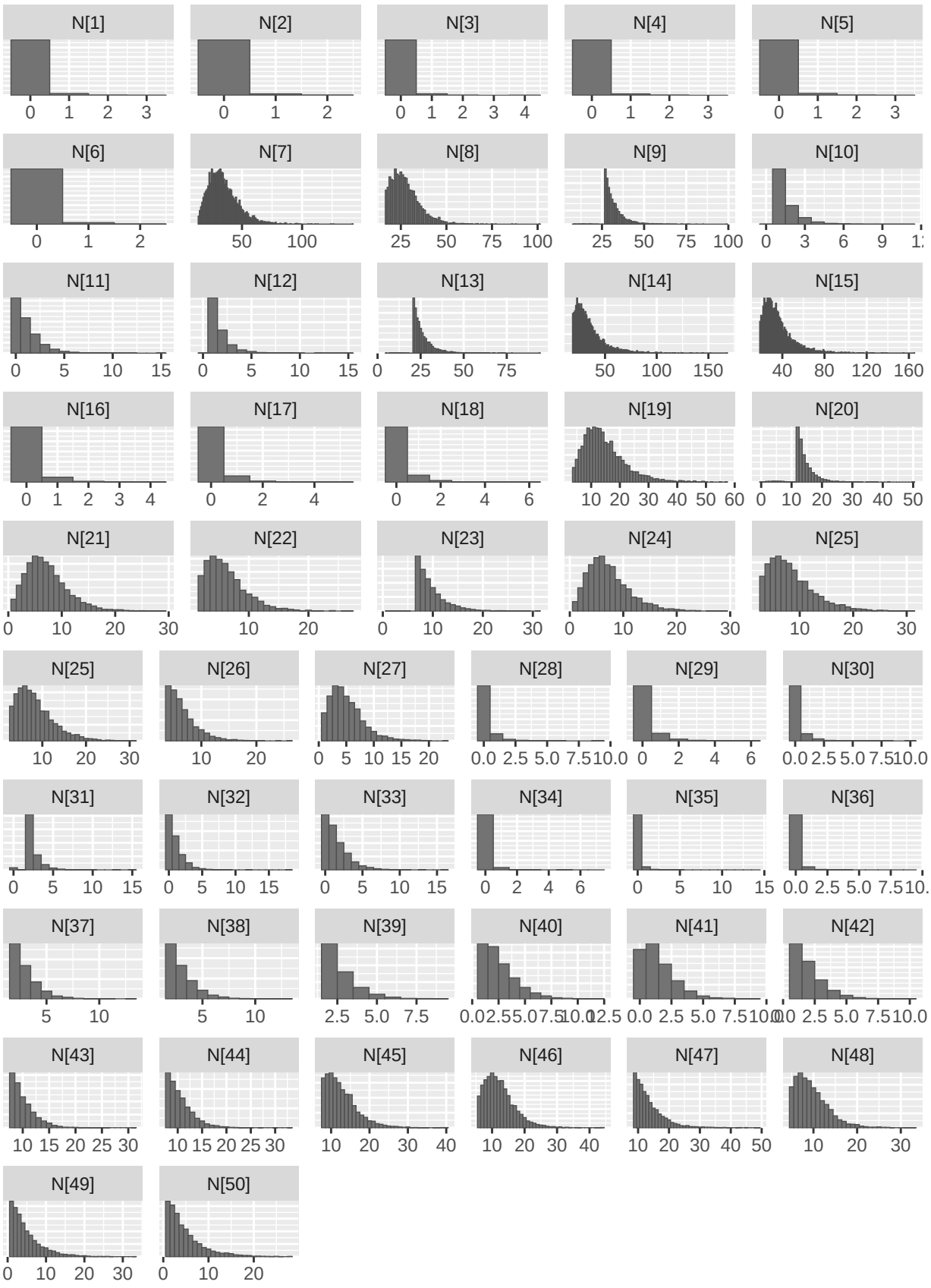
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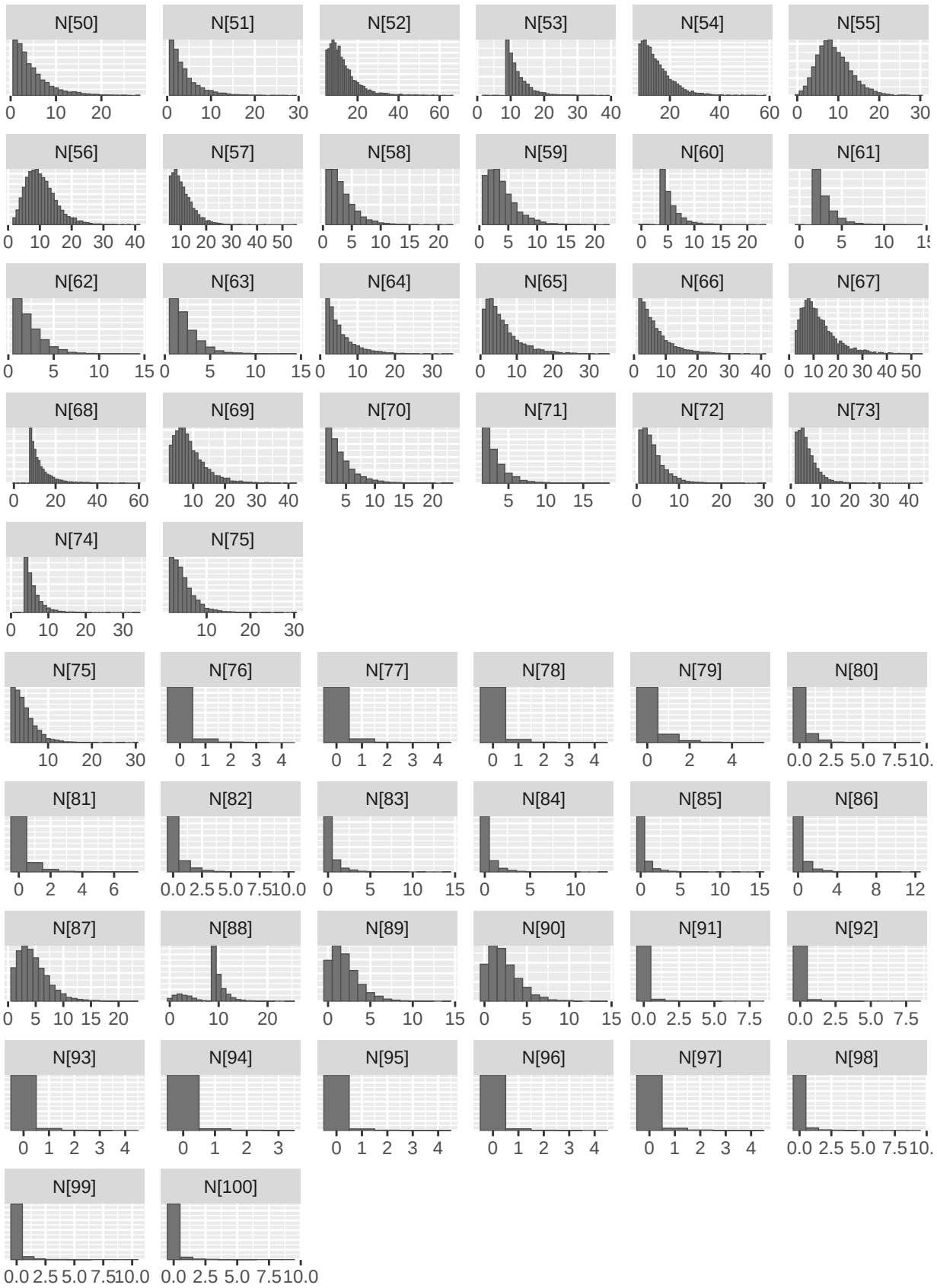
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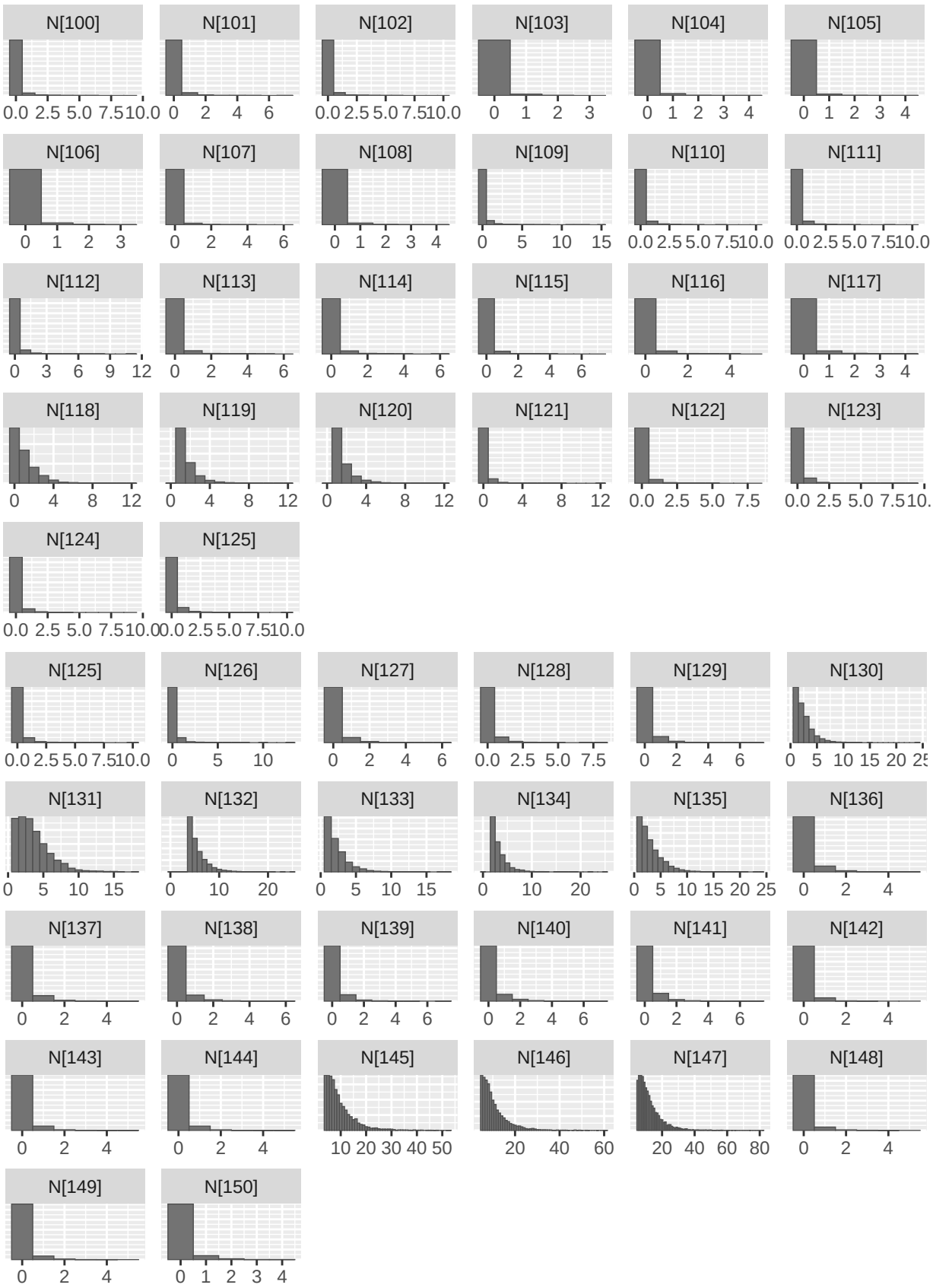
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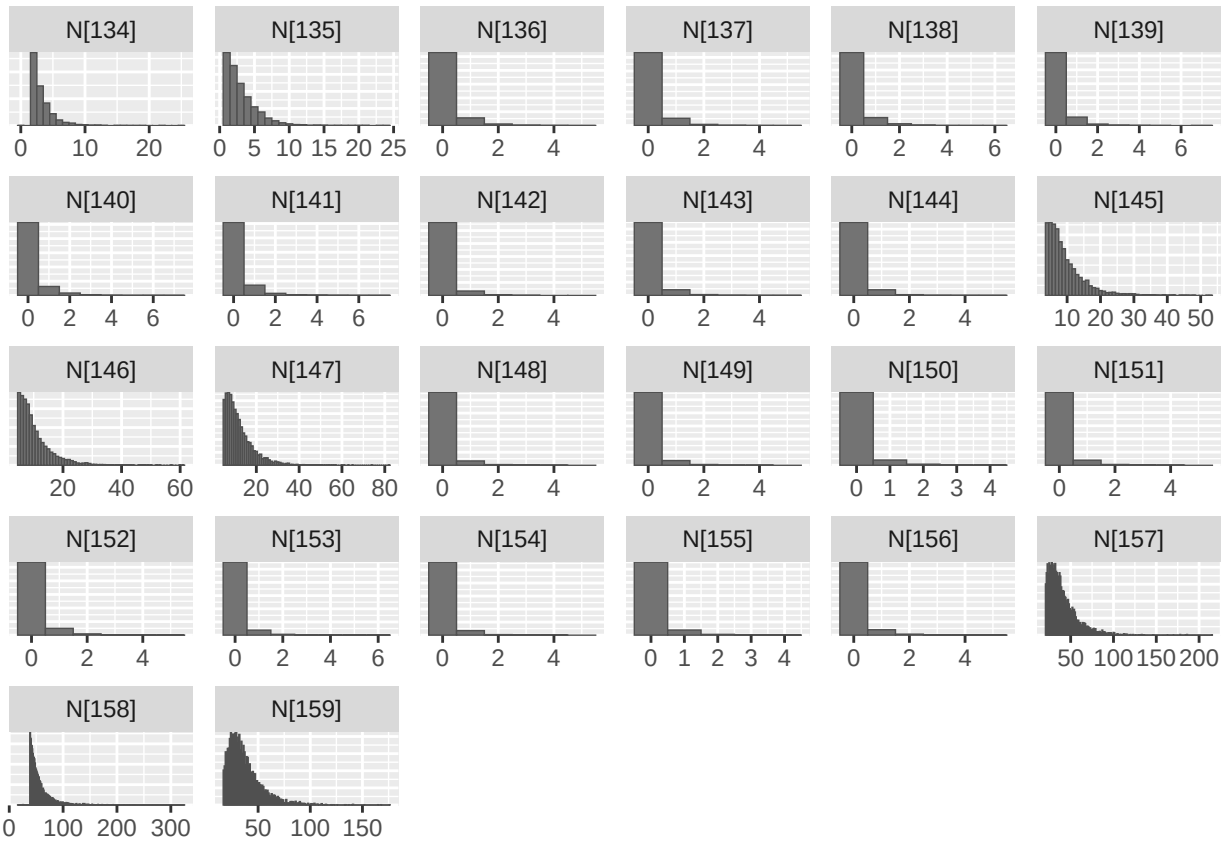


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## null device
##           1
```

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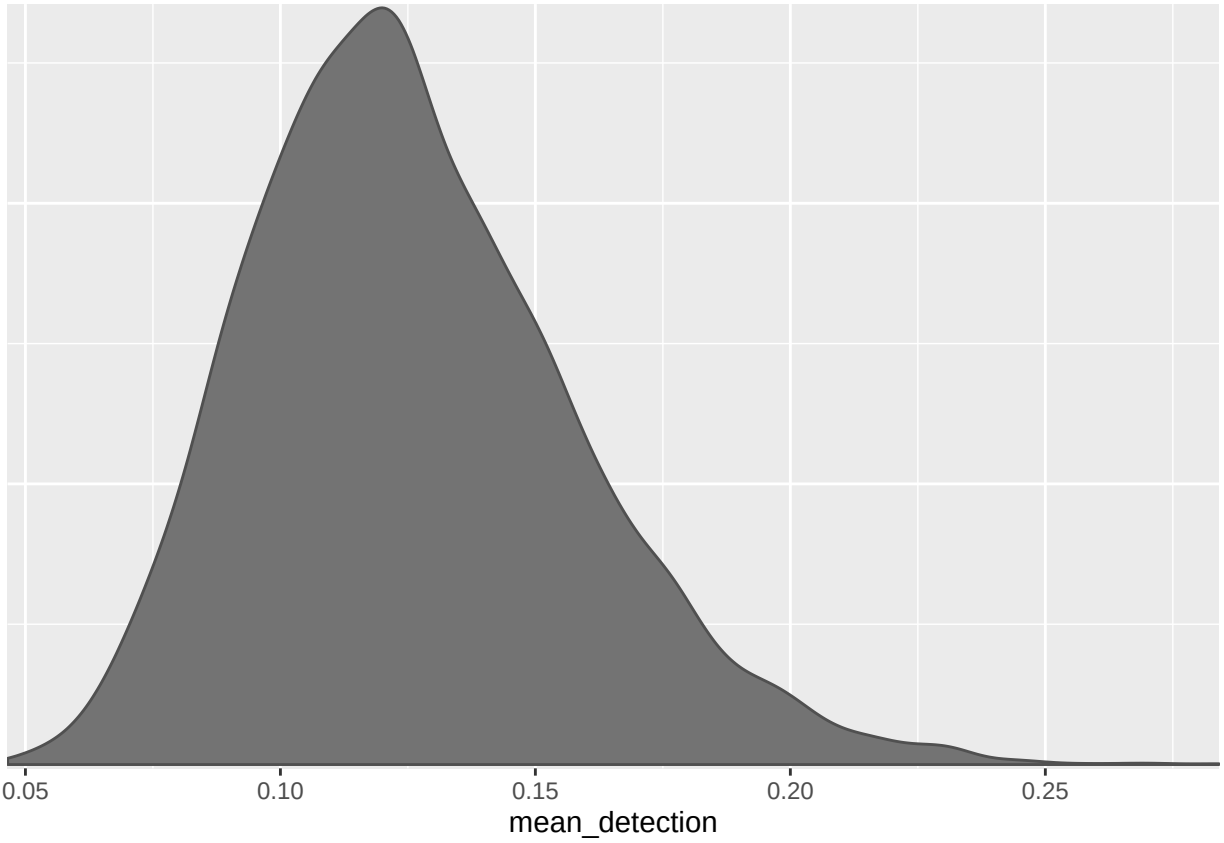

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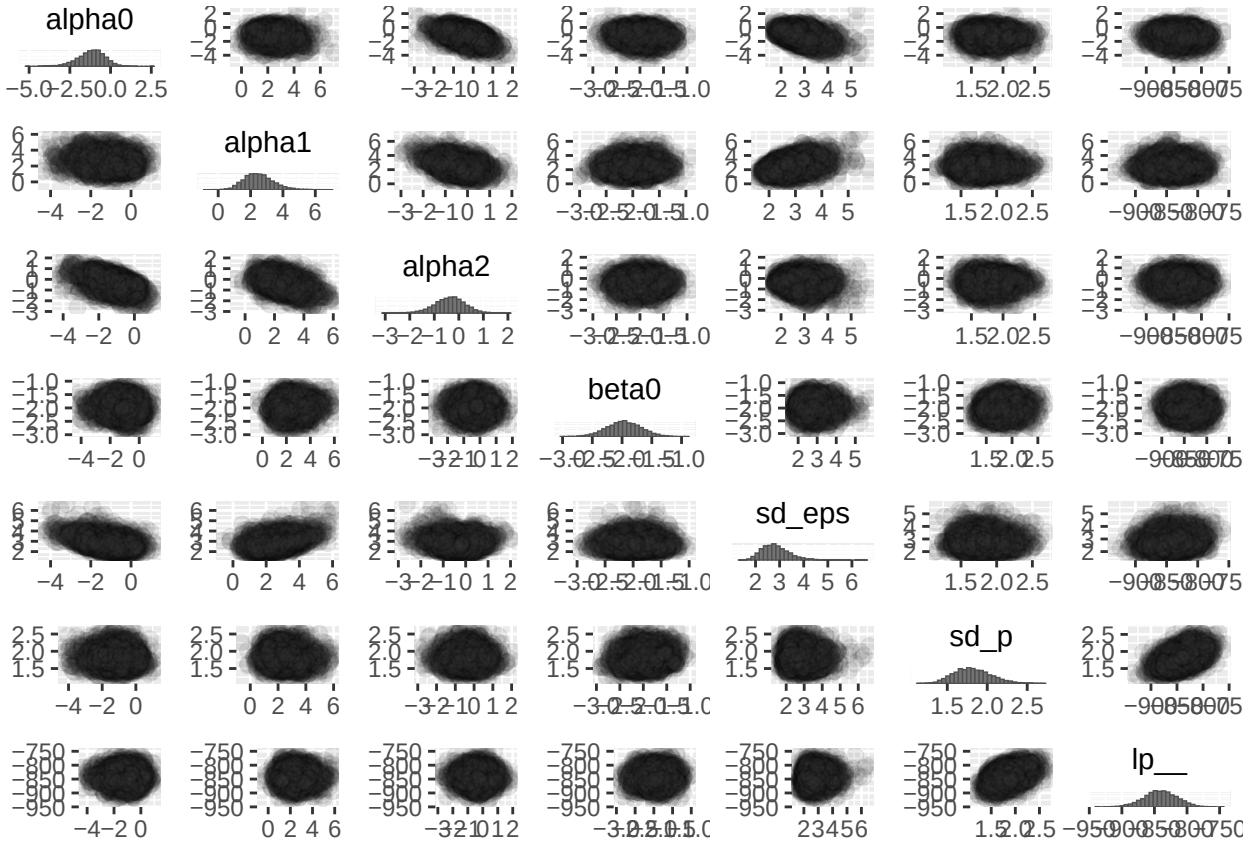

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```
## [1] 1.00399
```

```
## [1] 2346
```

```
## [1] 2987
```

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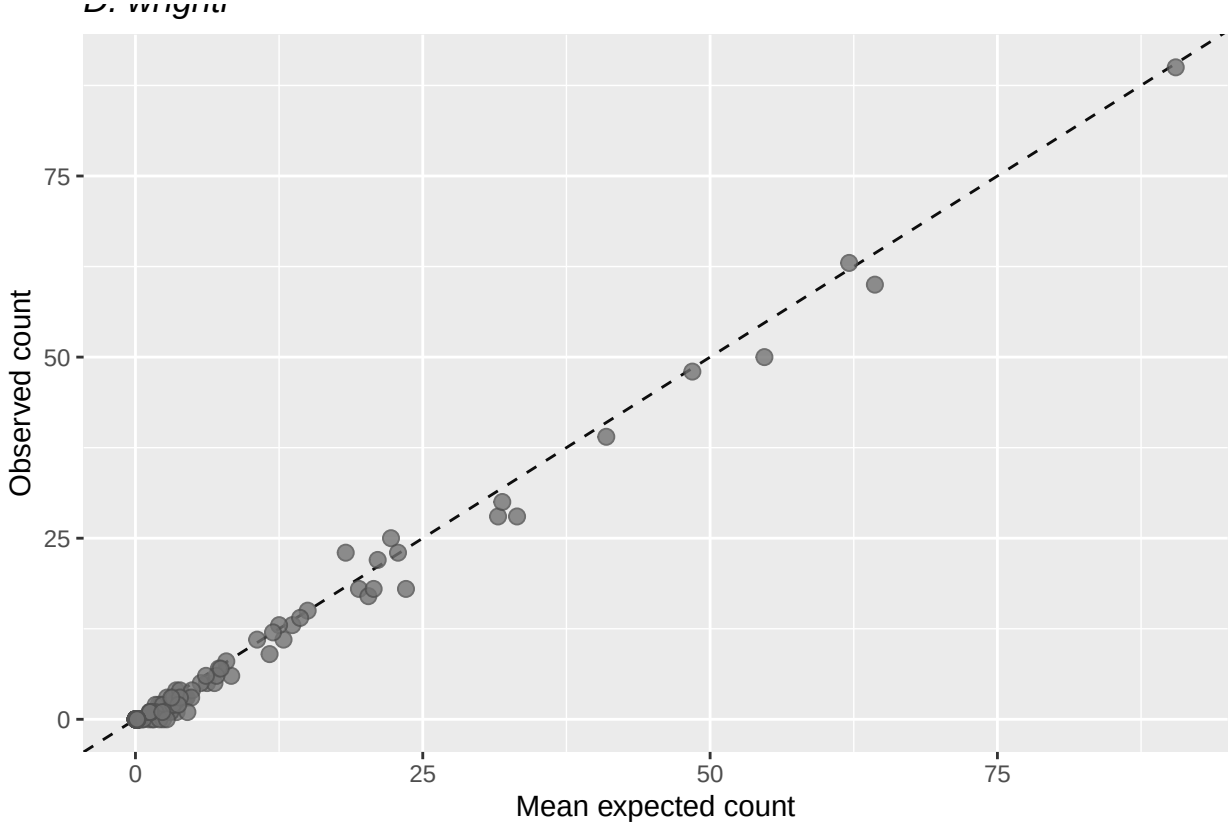
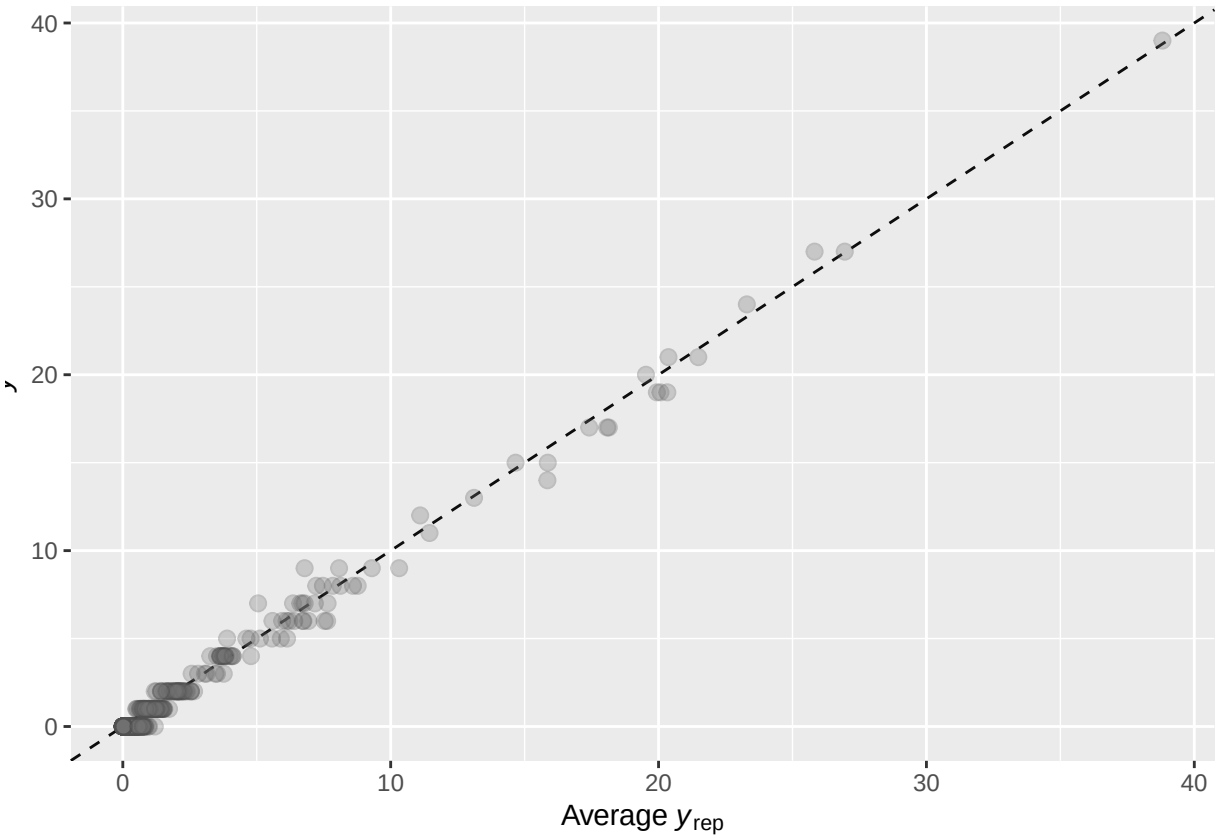


RMSE of posterior predictive

```
## [1] 1.315241
```

Posterior predictive check for each visit



RMSE of posterior predictive for observations per visit

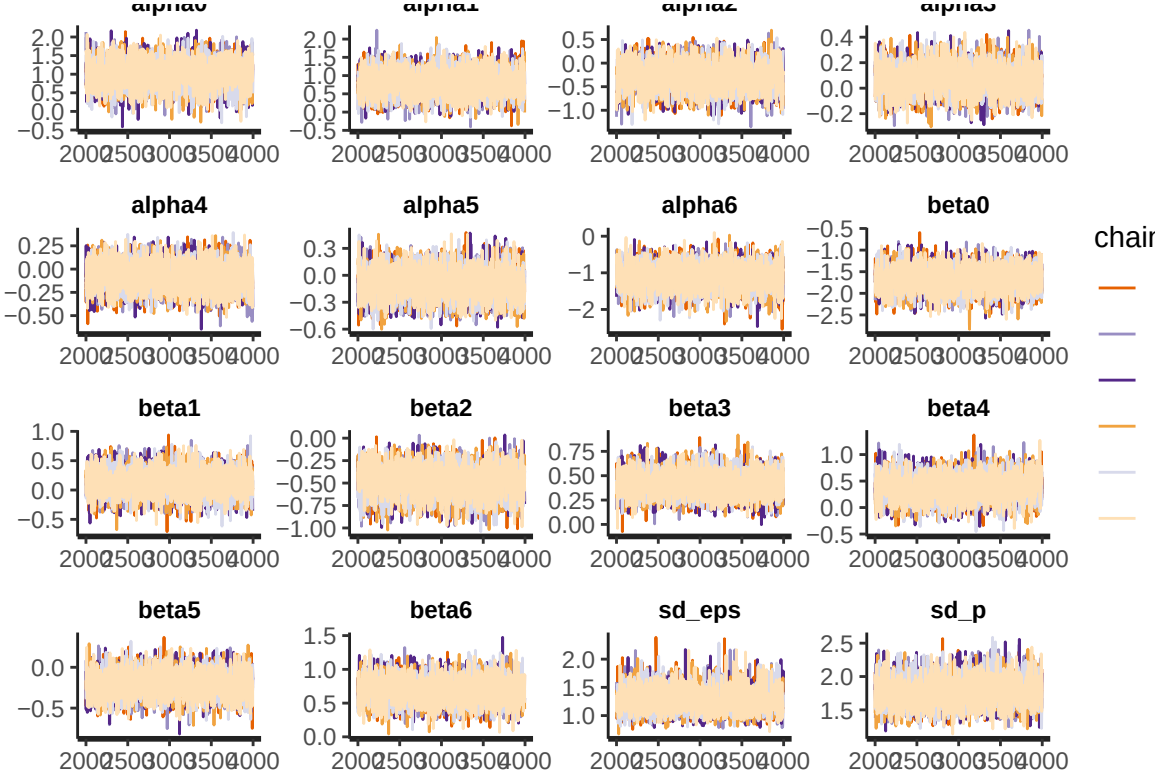
```
## [1] 0.7504749
```

RMSE of posterior predictive

```
## [1] 0.3356226
```

Eurycea wilderae

View Traceplots



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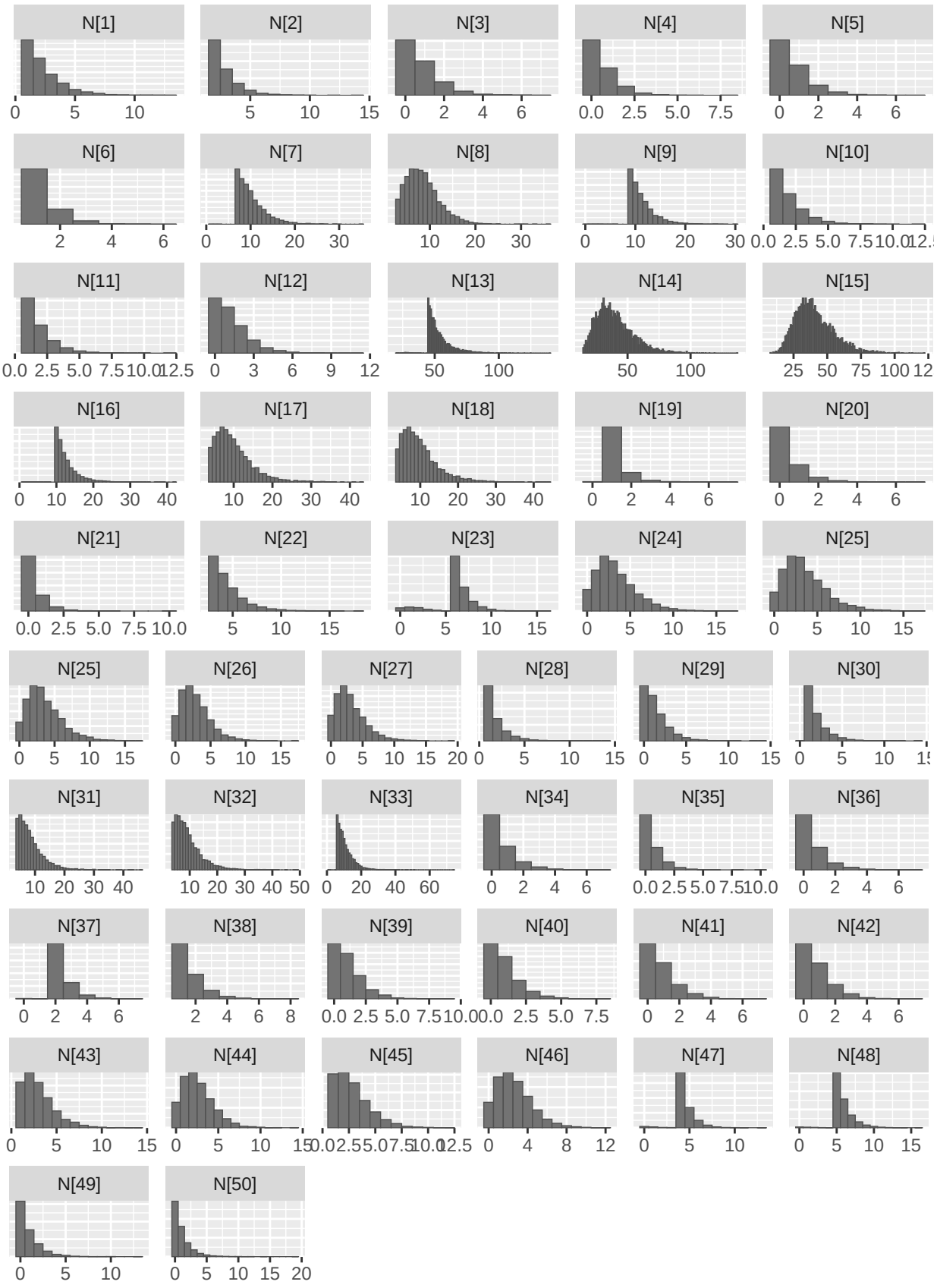
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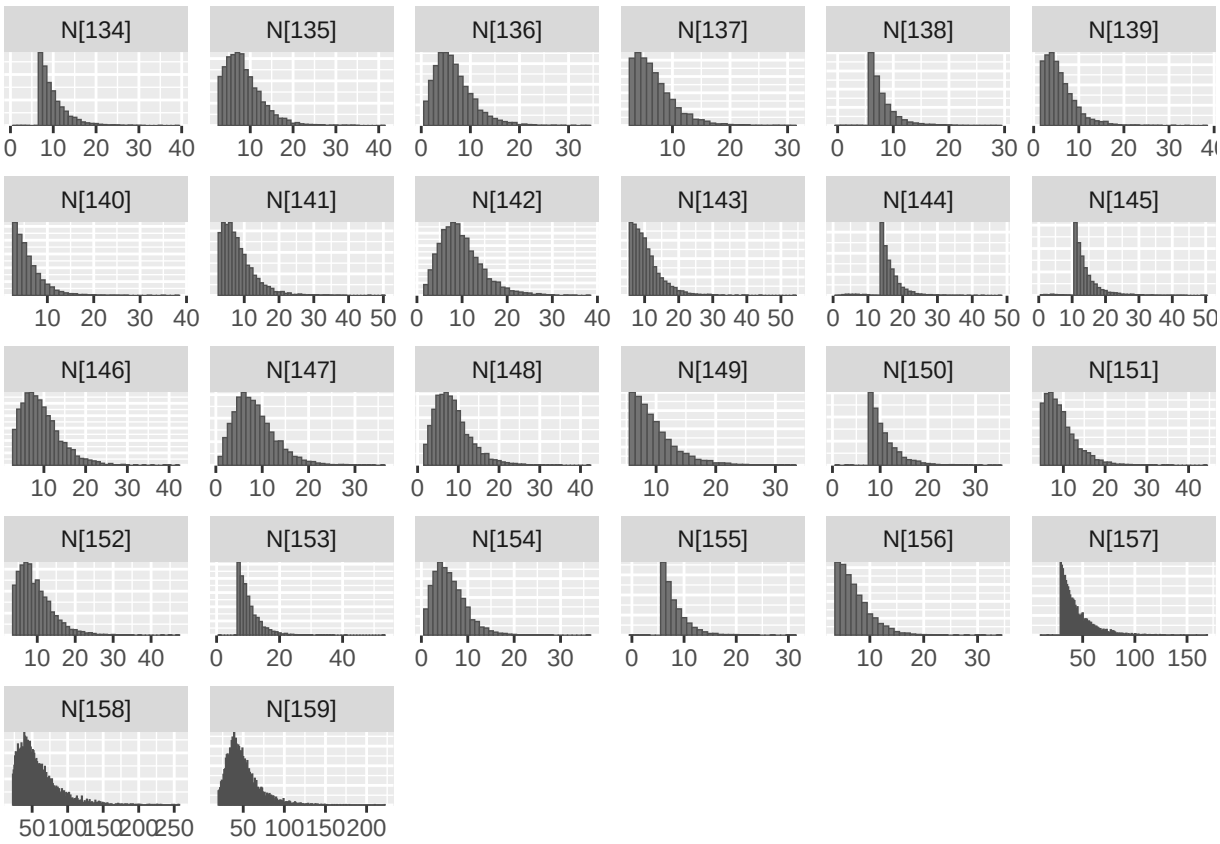


```
## null device
##           1
```

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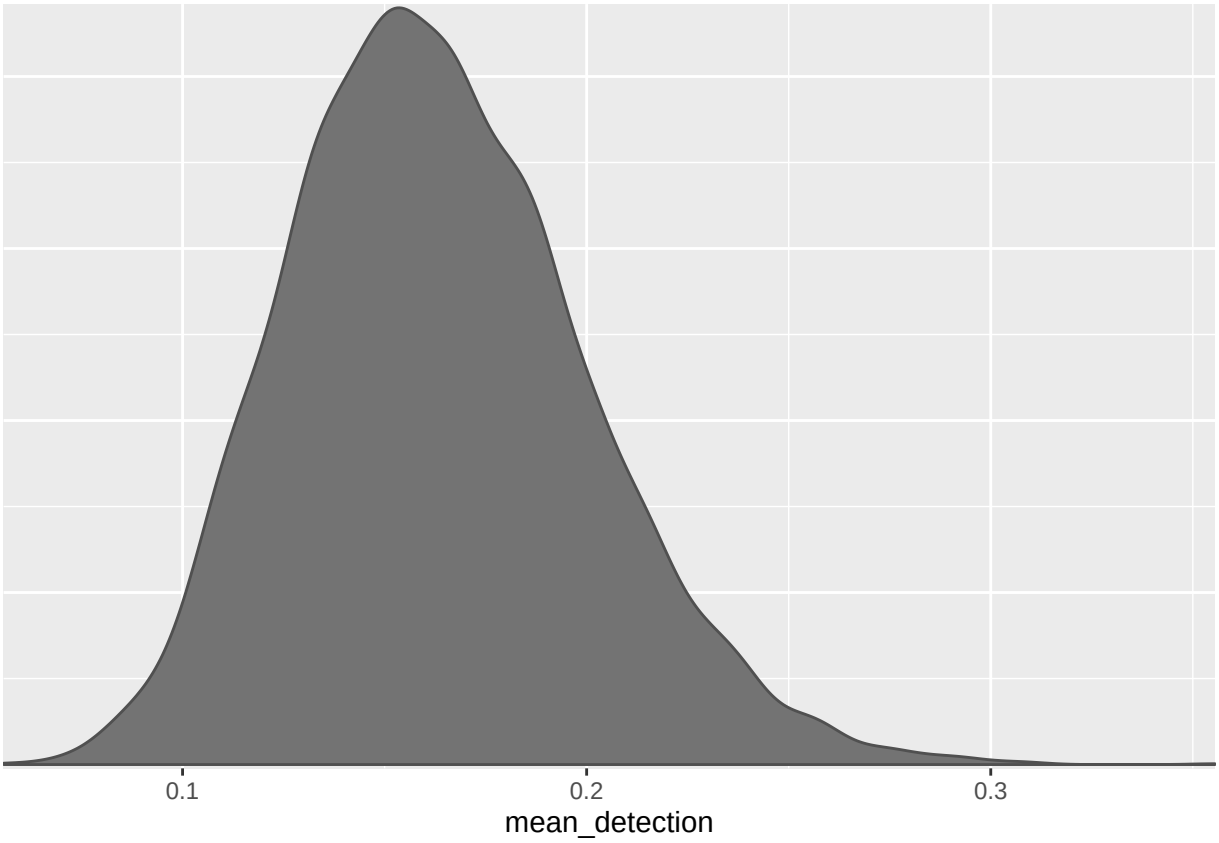

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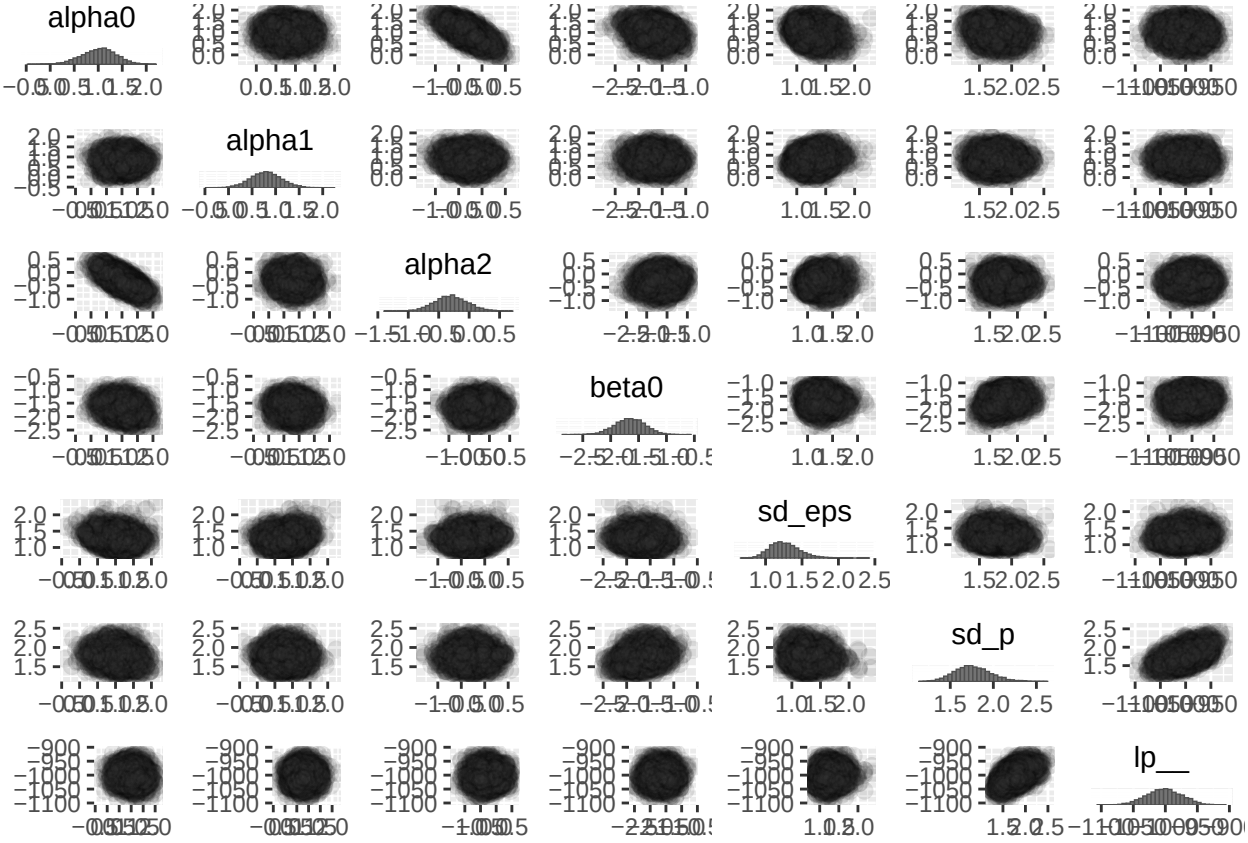

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```
## [1] 1.003496
```

```
## [1] 2495
```

```
## [1] 3415
```

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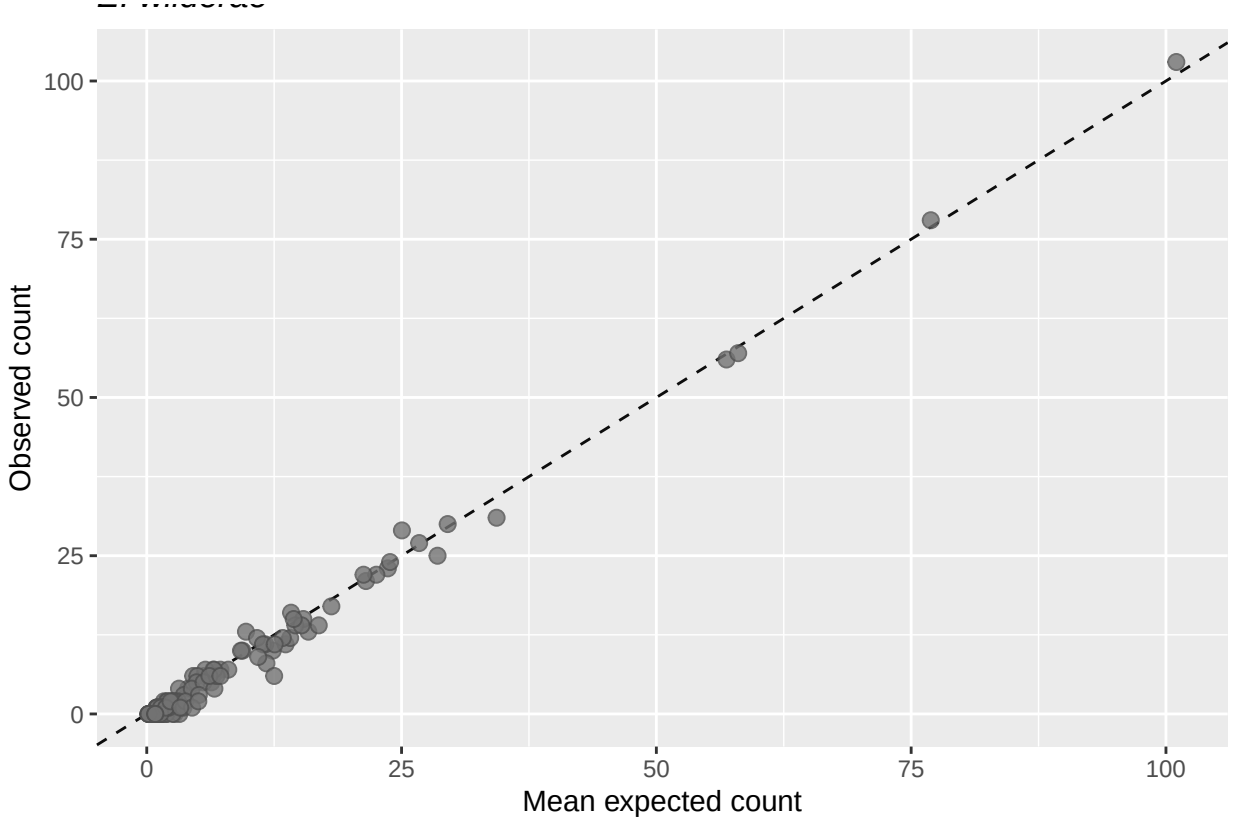
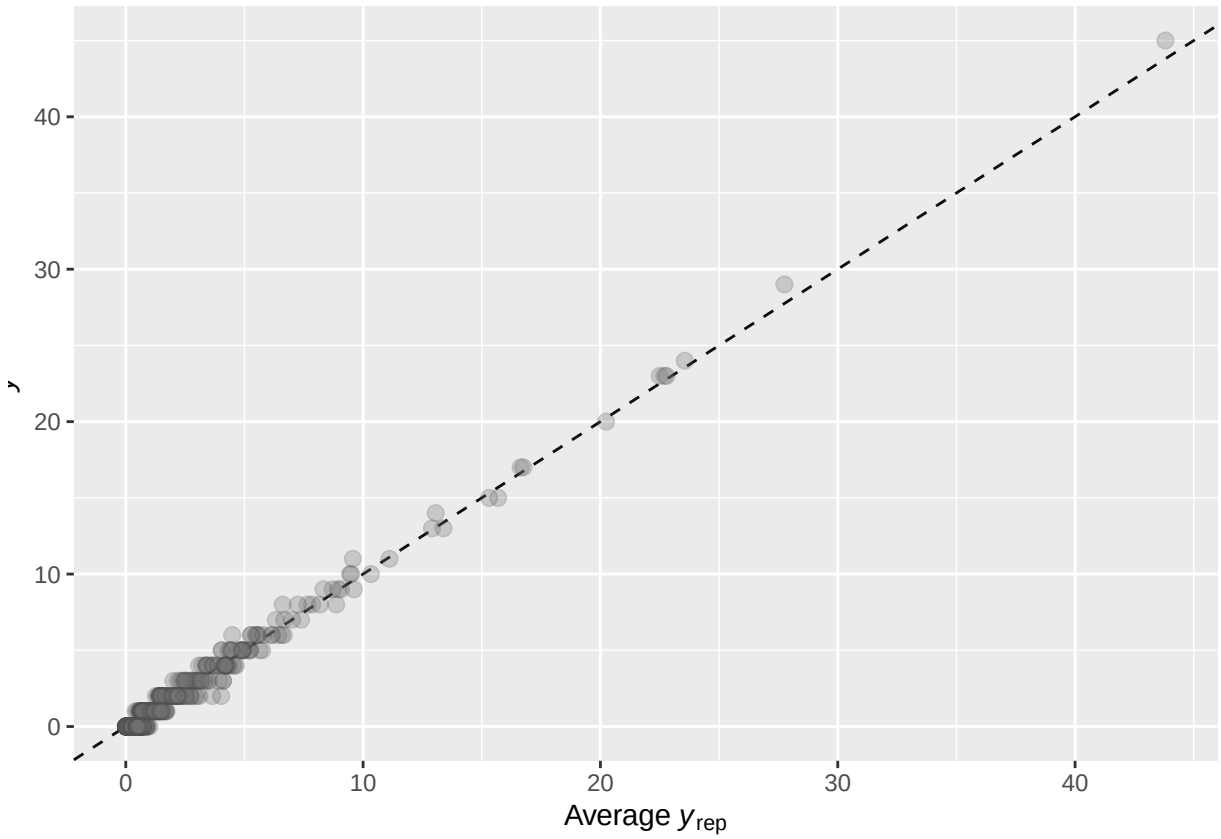


RMSE of posterior predictive

```
## [1] 1.404227
```

Posterior predictive check for each visit



RMSE of posterior predictive for observations per visit

```
## [1] 0.8349771
```

RMSE of posterior predictive

```
## [1] 0.3734131
```