

# Something like Martin et al. 2015 in Stan

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## Reformat data for Stan

The first thing we have to do is put the simulated data in a format Stan can read. Stan requires data in lists, so we have to do the following manipulation. Note each of the objects in the list correspond to a data element defined in the stan programs.

```
source("data_sim.R")
dat_stan <- list(N = length(dat$year),
               sets = dat$sets,
               inter = dat$inter,
               mort = dat$mort)
```

## Estimate the Poisson model for bycatch interactions

First, we'll estimate the rate of interaction per set using the Poisson model specification.

```
pois_fit <- stan(file = "poisson_model.stan",
               data = dat_stan,
               iter = 1000,
               chains = 4,
               seed = 1234)
```

```
## Warning in readLines(file, warn = TRUE): incomplete final line found
## on '/Users/Jon/Dropbox/Documents/NOAA_postdoc/groundfish_bycatch/
## poisson_model.stan'
```

Now, let's check out the fit parameter to see if it comes close to what we know as the true rate parameter of 0.002.

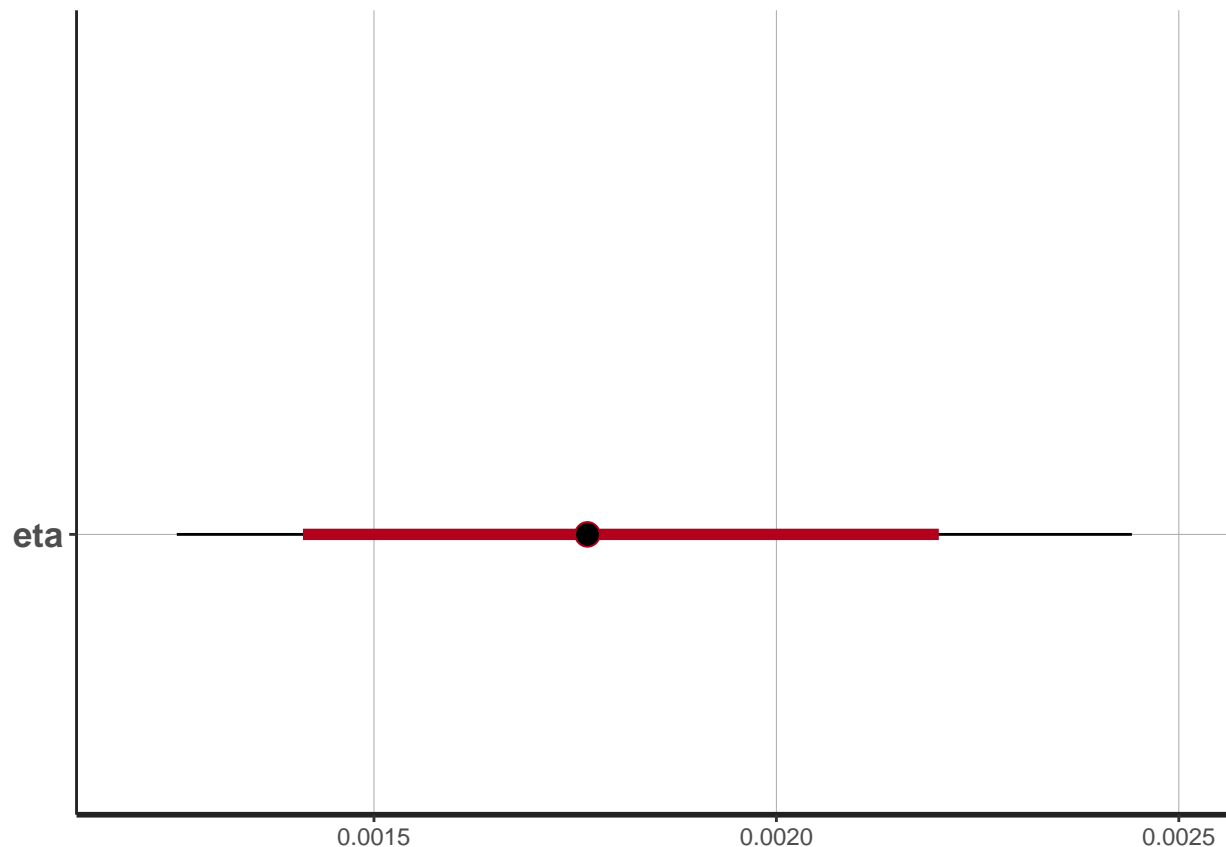
```
print(pois_fit)
```

```
## Inference for Stan model: poisson_model.
## 4 chains, each with iter=1000; warmup=500; thin=1;
## post-warmup draws per chain=500, total post-warmup draws=2000.
##
##      mean se_mean  sd  2.5%   25%   50%   75%  97.5% n_eff Rhat
## eta    0.00    0.00 0.00   0.0   0.00   0.00   0.00   0.00   751 1.01
## lp__ -41.79    0.02 0.74 -43.8 -41.95 -41.53 -41.32 -41.26   901 1.00
##
## Samples were drawn using NUTS(diag_e) at Thu Oct  4 12:08:59 2018.
## For each parameter, n_eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor on split chains (at
## convergence, Rhat=1).
```

```
plot(pois_fit)
```

```
## ci_level: 0.8 (80% intervals)
```

```
## outer_level: 0.95 (95% intervals)
```



Although we can't see the parameter estimate because it's being masked by 0 because of rounding, the Rhat close to 1 indicates we got model convergence. In the plot of the parameter we can see the posterior distribution for eta. Looks pretty good!

## Estimate the binomial model for mortality resulting from bycatch interaction

```
binom_fit <- stan(file = "binomial_model.stan",
  data = dat_stan,
  iter = 1000,
  chains = 4,
  seed = 1234)
```

```
## Warning in readLines(file, warn = TRUE): incomplete final line found
## on '/Users/Jon/Dropbox/Documents/NOAA_postdoc/groundfish_bycatch/
## binomial_model.stan'
```

```
print(binom_fit)
```

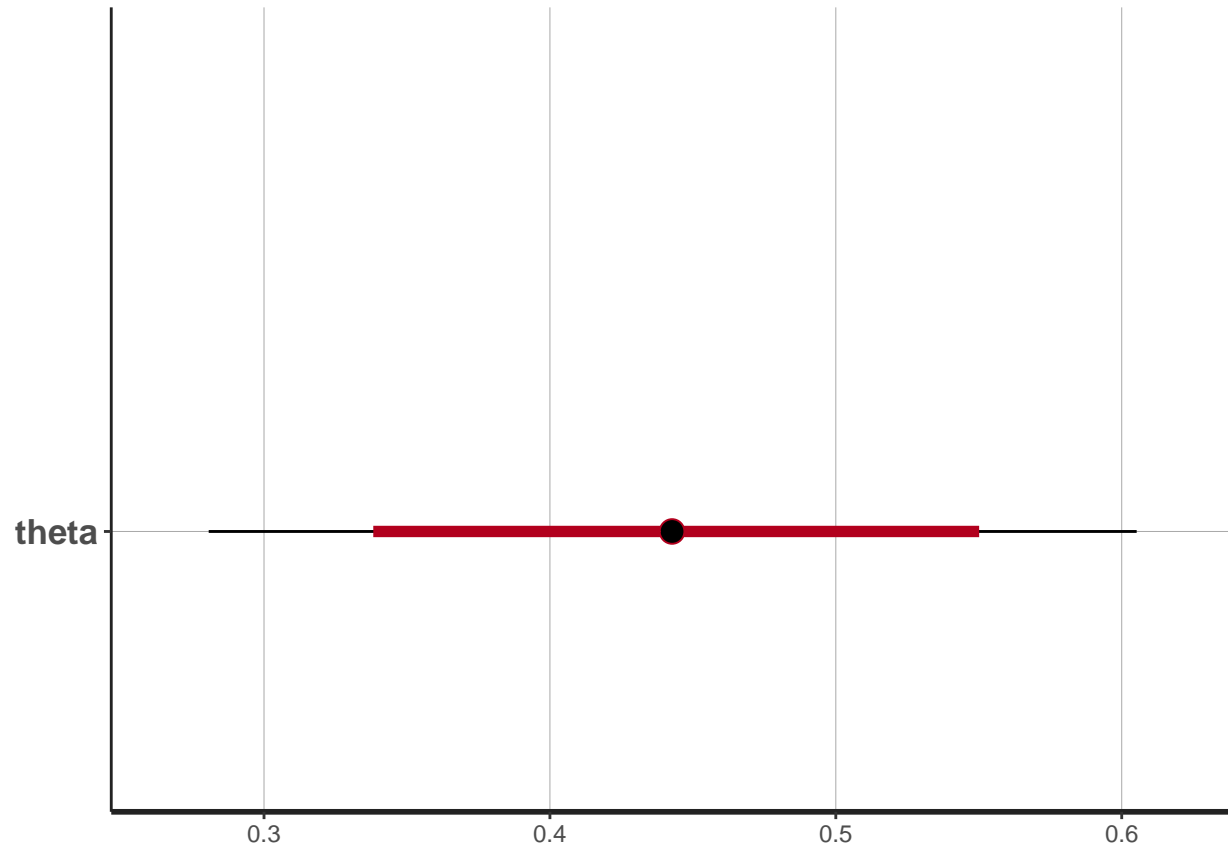
```
## Inference for Stan model: binomial_model.
## 4 chains, each with iter=1000; warmup=500; thin=1;
## post-warmup draws per chain=500, total post-warmup draws=2000.
##
##      mean se_mean  sd  2.5%   25%   50%   75%  97.5% n_eff Rhat
## theta   0.45    0.00 0.08   0.28   0.39   0.44   0.50   0.61   763 1.01
## lp__ -19.13    0.03 0.74 -21.27 -19.28 -18.84 -18.66 -18.61   820 1.00
##
## Samples were drawn using NUTS(diag_e) at Thu Oct  4 12:09:04 2018.
```

```
## For each parameter, n_eff is a crude measure of effective sample size,  
## and Rhat is the potential scale reduction factor on split chains (at  
## convergence, Rhat=1).
```

```
plot(binom_fit)
```

```
## ci_level: 0.8 (80% intervals)
```

```
## outer_level: 0.95 (95% intervals)
```



Again, given we only have 20 observations to estimate the model with, this looks pretty good to the known true value.