### Homework 6

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```
rm(list = ls())
library(rjags)
## Loading required package: coda
## Linked to JAGS 4.3.0
## Loaded modules: basemod, bugs
library(dplyr)
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##
       filter, lag
## The following objects are masked from 'package:base':
##
       intersect, setdiff, setequal, union
##
library(ggplot2)
library(rethinking)
## Loading required package: rstan
## Loading required package: StanHeaders
## rstan (Version 2.21.3, GitRev: 2e1f913d3ca3)
## For execution on a local, multicore CPU with excess RAM we recommend calling
## options(mc.cores = parallel::detectCores()).
## To avoid recompilation of unchanged Stan programs, we recommend calling
## rstan_options(auto_write = TRUE)
##
## Attaching package: 'rstan'
## The following object is masked from 'package:coda':
##
##
       traceplot
## Loading required package: cmdstanr
## This is cmdstanr version 0.5.1.9000
## - CmdStanR documentation and vignettes: mc-stan.org/cmdstanr
## - CmdStan path: /Users/alexziyujiang/.cmdstan/cmdstan-2.29.2
## - CmdStan version: 2.29.2
```

```
## Loading required package: parallel
## rethinking (Version 2.21)
##
## Attaching package: 'rethinking'
## The following object is masked from 'package:rstan':
##
## stan
## The following object is masked from 'package:stats':
##
## rstudent
library(betareg)
```

# **Data Preprocessing**

```
# read data
d <- read.csv(file = "qog_jan16.csv")

# transform variables
d$wdi_mortinftot <- d$wdi_mortinftot/1000
d$epi_watsup <- d$epi_watsup - mean(d$epi_watsup)

# y and x for jags
y <- d$wdi_mortinftot
x <- d$epi_watsup</pre>
```

# Jags Code

```
linear_model_code <- "</pre>
  model{
   for(i in 1:n){
      # likelihood
      y[i] ~ dbeta(a[i], b[i])
      # conditional mean (logit link)
      logit(mu[i]) <- beta0 + beta1*x[i]</pre>
      # transform back to a and b
      a[i] <- mu[i] * phi
      b[i] <- (1-mu[i]) * phi
      # compute partial derivative numerically
      ## plus 0.001
      logit(mup[i]) \leftarrow beta0 + beta1*(x[i]+0.001)
      ## minus 0.001
      logit(mum[i]) \leftarrow beta0 + beta1*(x[i]-0.001)
      ## difference
      apdx[i] \leftarrow ((mup[i] - mum[i])/(2*0.001))
```

```
# posterior predictive
    ynew[i] ~ dbeta(a[i], b[i])
}

# priors
beta0 ~ dnorm(0, 1)
beta1 ~ dnorm(0, 1)
phi ~ dunif(0, 500)
}
```

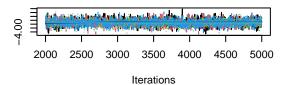
# Jags model compilation

```
# fit model, 4 chains
model <- jags.model(file = textConnection(linear_model_code),</pre>
                     data = list(x = x,
                                 y = y,
                                 n = length(y)), n.chains = 4)
## Compiling model graph
##
      Resolving undeclared variables
##
      Allocating nodes
## Graph information:
      Observed stochastic nodes: 184
##
      Unobserved stochastic nodes: 187
##
##
      Total graph size: 3058
##
## Initializing model
# burn-in 1e3
update(model, n.iter = 1e3)
\# sample betas + phi
betas <- coda.samples(model,</pre>
                       variable.names = c("beta0", "beta1", "phi"),
                       n.iter = 3e3)
```

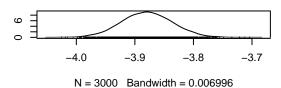
# model diagnostics

```
# check trace plot
plot(betas)
```

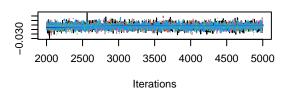
#### Trace of beta0



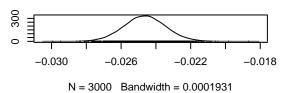
# Density of beta0



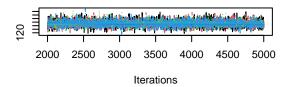
#### Trace of beta1



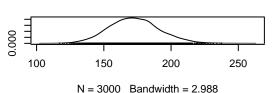
#### Density of beta1



#### Trace of phi



#### Density of phi



# # effective sample size effectiveSize(betas)

```
## beta0 beta1 phi
## 3124.312 3572.105 4872.169
# Rhat
```

#### # nnaı

gelman.diag(betas)

```
## Potential scale reduction factors:
##
##
         Point est. Upper C.I.
## beta0
                   1
                           1.01
                            1.01
## beta1
                   1
                            1.00
## phi
##
## Multivariate psrf
##
## 1
```

#### model results

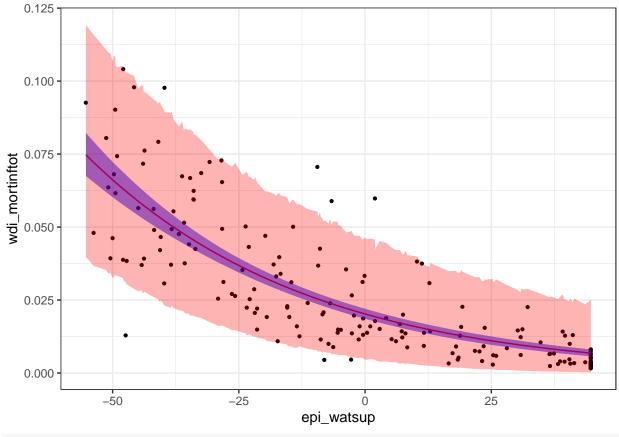
```
# posterior mean + credible intervals
precis(as.data.frame(betas[[1]]), digits = 4, prob = .95) %>% data.frame %>% dplyr::select(c(-histogram

## mean sd X2.5. X97.5.
## beta0 -3.87687146 0.043187710 -3.96167833 -3.79340665
## beta1 -0.02460657 0.001181068 -0.02696522 -0.02223647
## phi 172.49675252 19.161328668 137.46313917 212.38878593
```

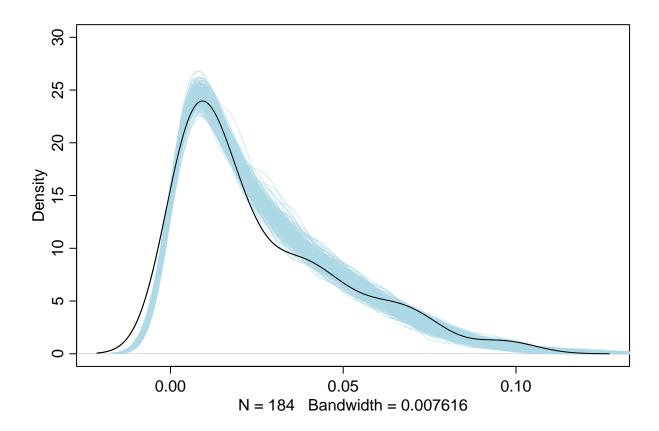
```
# compare with betareq
breg <- betareg(wdi_mortinftot ~ epi_watsup, data = d)</pre>
summary(breg)
##
## Call:
## betareg(formula = wdi_mortinftot ~ epi_watsup, data = d)
## Standardized weighted residuals 2:
##
                10 Median
                                3Q
      Min
                                       Max
## -4.9881 -0.5567 -0.0691 0.6217 2.3326
##
## Coefficients (mean model with logit link):
                Estimate Std. Error z value Pr(>|z|)
##
                           0.043278 -89.78
## (Intercept) -3.885477
                                              <2e-16 ***
## epi_watsup -0.024754
                           0.001207 -20.51
                                              <2e-16 ***
## Phi coefficients (precision model with identity link):
        Estimate Std. Error z value Pr(>|z|)
          173.67
                      18.71
                              9.281
                                       <2e-16 ***
## (phi)
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Type of estimator: ML (maximum likelihood)
## Log-likelihood:
                    603 on 3 Df
## Pseudo R-squared: 0.7595
## Number of iterations: 85 (BFGS) + 2 (Fisher scoring)
```

# posterior predictive checks

```
# sample mu and ynew
ymu.samples <- jags.samples(model,</pre>
                            variable.names = c("mu", "ynew"),
                            n.iter = 1e3)
# add posterior mean and quantiles to data.frame
d$mu.mean <- apply(ymu.samples$mu, 1, mean)
d$mu.lwr
          <- apply(ymu.samples$mu, 1, quantile, .025)</pre>
d$mu.upr
          <- apply(ymu.samples$mu, 1, quantile, .975)</pre>
d$ynew.lwr <- apply(ymu.samples$ynew,1, quantile, .025)
d$ynew.upr <- apply(ymu.samples$ynew,1, quantile, .975)
# ggplot
ggplot(d, aes(y = wdi_mortinftot, x = epi_watsup)) +
  geom_point(col = alpha("black", 1), cex = .8) +
  geom_line(aes(y = mu.mean), col = "red") +
  geom_ribbon(aes(ymin = mu.lwr, ymax = mu.upr), fill = alpha("blue", .5)) +
  geom_ribbon(aes(ymin = ynew.lwr, ymax = ynew.upr), fill = alpha("red", .3)) +
  theme_bw()
```



```
# density overlay
dens(y, ylim = c(0, 30), adj = 1, col = "black")
for(i in 1:200){
  dens(ymu.samples$ynew[,i,], adj = 1, col = alpha("lightblue", alpha = 0.5), add = T)
}
dens(y, adj = 1, col = "black", add = T)
```



## APD

```
# apd
apdx <- coda.samples(model, "apdx", n.iter = 1e3)</pre>
apdx <- do.call("rbind", apdx)</pre>
library(gtools)
##
## Attaching package: 'gtools'
## The following object is masked from 'package:rethinking':
##
##
       logit
bb_weights <- rdirichlet(nrow(apdx), alpha = rep(1, ncol(apdx)))</pre>
apd <- apply(bb_weights*apdx, 1, sum)</pre>
apd <- apd*1000
precis(apd) %>% data.frame %>% dplyr::select(c(-histogram))
                                    X5.5.
                                              X94.5.
             mean
                           sd
## apd -0.6280232 0.04891955 -0.7102447 -0.5531013
```