Math 640 Final Paper

Max Kearns and Tommy Jones

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1 Introduction

The analysis of text data is an area of vital research in both frequentist and Bayesian statistics. Text can, and indeed does, store a vast amount of information that is not easily evaluated with well-understood statistical methods. While text analysis is used throughout our economy, it does not have nearly as much research and knowledge behind it as does numerical data. This paper attempts to slightly further the bank of techniques for text analysis, in the hopes that text data will someday be as understood as numerical data is today.

One method that researchers currently use to model text frequencies is with a Dirichlet prior on a Multinomial likelihood. The prior provides uncertainty on $\vec{\theta}$, which is the vector of word probabilities. The usual model then assumes a non-informative uniform prior on the Dirichlet parameter ($\vec{\alpha}$). In a Bayesian setting, however, this approach seems overly simplistic, and MCMC methods provide a simple solution to sample from a more complex distribution. This research intends to start to answer the question as to whether more uncertainty on $\vec{\alpha}$ would improve the model. Zipf's law provides a basis for how to vary $\vec{\alpha}$ in a way that is consistent with knowledge about human language.

Zipf's law is an empirical property of natural language. It states that the word frequencies of any corpus of text follows a power law distribution, regardless of context or language. This means that the most common word will be twice as frequent as the second most common word, and n times as frequent as the nth most common word. (citations needed) Based on what Zipf's law dictates, this research tests the viability of placing a Pareto(γ, β) prior on $\vec{\alpha}$, where γ is fixed at a sufficiently small value. This Pareto distribution is a power-law that should provide some uncertainty on $\vec{\alpha}$ that mirrors this inherent property of language.

In order to determine whether this prior merits further research on more complex models, we will begin by modeling a small data set using a simple model that features a multinomial likelihood, a Dirichlet prior, a Pareto hyper-prior, with a non-informative Jeffery's hyper-prior . We will compare this model to a control that does not allow for uncertainty on $\vec{\alpha}$. The data set is 100 randomly sampled NIH grant abstracts from 2014.

2 Methods

2.1 Models

For both the control and the experimental model, we assume that the word count $\vec{y}$ is Multinomial, so has the following likelihood.

$$\vec{y} \sim multinom(n, \vec{\theta}) \implies \mathcal{L}(\vec{y}|\vec{\theta}, \vec{\alpha}, \beta) \propto \prod_k \theta_k^{y_k} \tag{1}$$

On $\vec{\theta}$, the vector of word probabilities, we place a Dirichlet prior.

$$\vec{\theta} \sim Dir(\vec{\alpha}) \implies \pi(\vec{\theta}) = \mathcal{B}(\vec{\alpha}) \prod_k \theta_k^{\alpha_k - 1} \tag{2}$$

The control model will stop here, and assume a uniform distribution on α_k. The control model then has the simple form $\vec{\theta}|\vec{y}, \vec{\alpha} \sim Dir(\vec{y} + \vec{\alpha})$, and an unknown distribution for $\vec{\alpha}|\vec{y}, \vec{\beta}$; shown below (the full derivation can be found in Appendix B). We will sample from $\vec{\alpha}|\vec{y}, \vec{\beta}$ with an Inverse-Gaussian proposal.

$$p(\alpha_k|\theta_k, y_k) \propto \theta_k^{\alpha_k} \tag{3}$$

The candidate model, however, will assume a $Pareto(\gamma, \beta)$ prior on α_k, with Jeffery's prior on β.

$$\alpha_k \sim Pareto(\gamma, \beta) \implies \pi(\vec{\alpha}) = \prod_k \gamma^\beta \beta \alpha_k^{-(\beta+1)} \tag{4}$$

$$\pi(\beta) \propto \frac{1}{\beta} \tag{5}$$

This results in the unknown posterior below, and a full derivation of the model can be found in Appendix B.

$$P(\vec{\theta}, \vec{\alpha}, \beta | \vec{y}) \propto \beta^{(K-1)} \gamma^{k\beta} \mathcal{B}(\vec{\alpha}) \prod_k \theta_k^{y_k + \alpha_k - 1} \alpha_k^{-(\beta+1)} \tag{6}$$

This prior is unrecognizable, so we will proceed by making a Gibbs sampler of the full conditional posteriors, which can be found below.

$$P(\vec{\theta} | \vec{\alpha}, \beta, \vec{y}) \propto \prod_k \theta_k^{y_k + \alpha_k - 1} \tag{7}$$

$$P(\vec{\alpha} | \vec{\theta}, \beta, \vec{y}) \propto \mathcal{B}(\vec{\alpha}) \prod_k \theta_k^{y_k + \alpha_k - 1} \alpha_k^{-(\beta+1)} \tag{8}$$

$$P(\beta | \vec{\theta}, \vec{\alpha}, \vec{y}) \propto \beta^{K-1} \exp\left[-\beta \left(\sum_k \log(\alpha_k) - k \log(\gamma) \right) \right] \tag{9}$$

$$\tag{10}$$

Of these conditional posteriors, only $\vec{\alpha}|\vec{\theta}, \beta, \vec{y}$ is an unknown distribution. $\vec{\theta}|\vec{\alpha}, \beta, \vec{y}$ is a $Dir(\vec{y} + \vec{\alpha})$, and $\beta|\vec{\theta}, \vec{\alpha}, \vec{y}$ is a $\text{Gamma}\left(k, \sum_k \log(\alpha_k) - k \log(\gamma)\right)$. The other two conditionals will be sampled using a Metropolis-Hastings algorithm with another Inverse-Gaussian proposal.

2.2 Sampling

2.2.1 Data

The NIH provides grant abstracts to the public, and these documents provide a perfect data set upon which to test our model. The data set contains 5,542 unique words. Figure 1 shows the properties of Zipf's law in the data set. In the histogram, it is evident just how much mass is in the right tail of the distribution. It shows that the overwhelming majority of the words occur less than 100 times, despite the fact that the most frequent word, 'the', occurs 1,928 times. The right side of figure 1 shows a log transformation of the word count and the rank. When graphed in this way, power laws appear as a straight line. This shows that our data set does indeed follow a power law, despite some noise toward the lower end of the distribution. This is a common result, and given a larger sample, this noise would be reduced.

2.2.2 Samplers

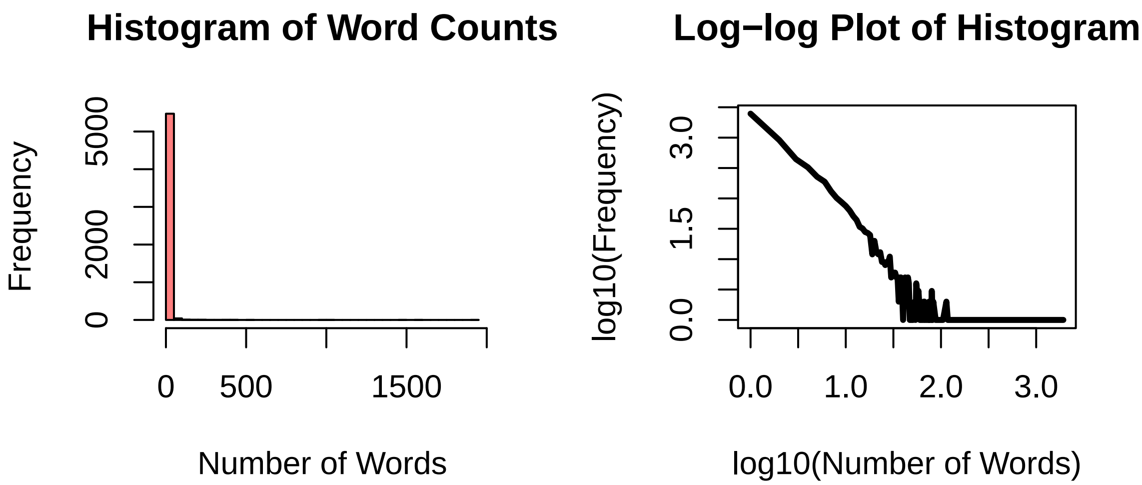

Figure 1: Histogram of Word counts (left) and Log-log plot of word counts, ordered by rank (right).

As discussed above, to sample from these conditional distributions, we had to create Gibb's samplers using metropolis-hastings components. For both the control and the man model, we used an Inverse-Gaussian to sample from the conditional posterior on α, and sampled directly from the conditional posteriors of the other parameters. Table 1 provides a summary of the distributions of the acceptance rates. While the acceptance rates are diverse for each element of α, they all fall within an acceptable range.

Table 1: Acceptance Rates

	Main	Control
min.	0.1078625	0.2806000
25%	0.1838250	0.4704125
50%	0.1997438	0.4895000
75%	0.2159844	0.5044875
max.	0.3817375	0.5123000

In order to asses the convergence of the samplers, we found the Geweke statistic for the log transformed likelihood of each model. The control model shows convergence with this statistic (p=.02), but the main model is well outside the typical range for a convergent sample(p=-2.5). Convergence for this sampler is extremely difficult to achieve, and may be impossible. Many proposal densities were attempted, and none allowed this sample to converge. This is but one of the flaws of our main model. We also have inspected some visual convergence diagnostics (Appendix C), but they all indicate that the control has converged and the main model has not.

2.3 Comparison

For the comparison of the models, we calculated the deviance information criterion for each estimate of α, creating a distribution of DICs. This distribution is shown in figure 2. We also provide the plot of the densities of the log-likelihood of each estimate of α (Figure 2).

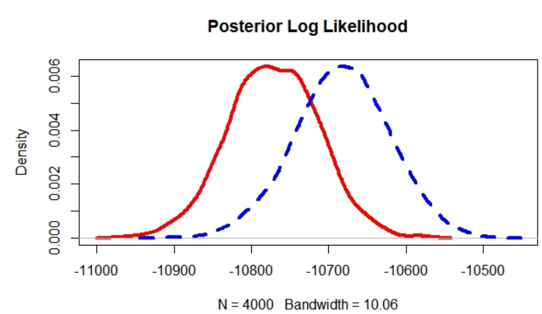

Figure 2: Distribution of log-likelihoods.

3 Results

Figures 2 and 3 provide fairly conclusive evidence that the main model does is not better than the control. Figure XX DIC plot shows that the control model has a much

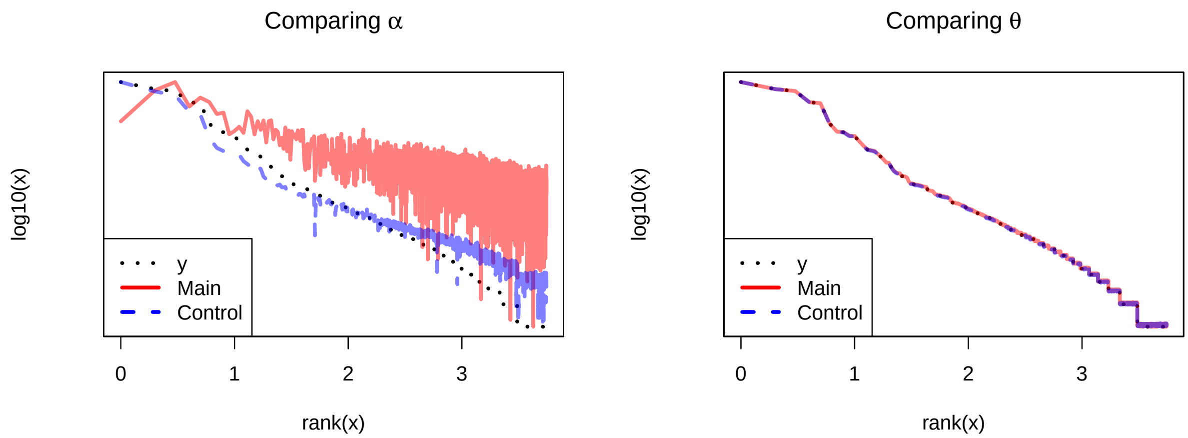

Figure 4: Histogram of Word counts (left) and Log-log plot of word counts, ordered by rank (right).

lower DIC, and the credible intervals for these estimates do not overlap. This suggests that the control is a better model. The log-likelihood plot also shows that the control model is more likely, although with some overlap of distribution.

4 Discussion

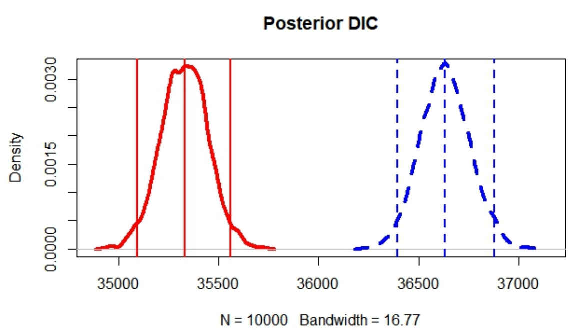

Figure 3: Distribution of DICs; vertical lines indicate the median and credible intervals.

The main model did not significantly improve upon the control. Indeed, the main model drastically increased the complexity of the process, without improving the estimation. Both the DIC distribution, and the distribution of the log-likelihood show that this model does not improve the fit of the predictions. In conjunction with the convergence issues, this model seems to have no redeeming features despite its increased complexity. The lesson of this experiment seems to be that increased complexity does not necessarily mean better estimation.

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5 References

5.1 make sure to cite the data source

5.2 Cite info on Zipf's law

6 Appendix A

```
# load and prepare the data
dtm <- CreateDtm(doc_vec = nih_sample$ABSTRACT_TEXT, # nih_sample from textmineR
                 doc_names = nih_sample$APPLICATION_ID,
                 ngram_window = c(1,1),
                 stopword_vec = c(),
                 verbose = FALSE)

y <- colSums(dtm) # nih_sample_dtm from the textmineR package

y <- y[order(y, decreasing = TRUE)]

# Histogram of y
hist(y, breaks = 50, col = rgb(1,0,0,0.5),
     main = "Histogram of Word Counts",
     ylab = "Frequency",
     xlab = "Number of Words")
```

Describe Zipf's law plot here

```
# log-log plot of y
f <- as.data.frame(table(y), stringsAsFactors = FALSE)

plot(log10(as.numeric(f$y)), log10(f$Freq), type = "l", lwd = 3,
     main = "Log-log Plot of Histogram",
     xlab = "log10(Number of Words)", ylab = "log10(Frequency)")
```

6.0.1 Sampling the control model

```
# declare a function for the control sampler
control_sampler <- function(y, B, seed, theta0, alpha0) {

  # set up sampling functions for M-H
  f_alpha_k <- function(alpha_k, theta_k) {
    theta_k ^ alpha_k
  }

  j_alpha <- function(mu = 1, prob = FALSE, n = NULL, x = NULL, rate = 0.1) {
    # if prob is false, draw a sample, otherwise find p(x)
    if (! prob) {
      # out <- rexp(n = n, rate = rate)
      out <- rinvgauss(n = n, mean = mu, shape = rate)
      # out <- rpareto(n = n, location = mu, shape = rate)
    } else {
```

```r
    # out <- dexp(x, rate)
    out <- dinvgauss(x, mean = mu, shape = rate)
    # out <- dpareto(x, location = mu, shape = rate)
  }

  out
}

# set up constants
k <- length(y)

theta <- matrix(0, nrow = B, ncol = k)

theta[1,] <- theta0

alpha <- matrix(0, nrow = B, ncol = k)

alpha[1,] <- alpha0

acc_alpha <- numeric(ncol(alpha))

# run the sampler
for (j in 2:B) {
  # sample theta
  theta[j,] <- rdirichlet(1, y + alpha[j-1,])

  # sample alpha
  alpha_star <- j_alpha(n = k)

  r <- (f_alpha_k(alpha_k = alpha_star, theta_k = theta[j-1,]) /
          f_alpha_k(alpha[j-1,],theta[j-1,])) /
    (j_alpha(prob = TRUE, x = alpha_star) /
       j_alpha(prob = TRUE, x = alpha[j-1,]))

  u <- runif(1)

  keep <- pmin(r,1) > u

  alpha[j,keep] <- alpha_star[keep]

  alpha[j,!keep] <- alpha[j-1,!keep]

  # acc_alpha[j] <- sum(keep) / k

  acc_alpha <- acc_alpha + keep

}

acc_alpha <- acc_alpha / B

# return the result
list(theta = theta, alpha = alpha, acc_alpha = acc_alpha, seed = seed,
     theta0 = theta0, alpha0 = alpha0)
```

```r
}

# run 4 chains of 20,000 iterations each

B <- 20000

control_chains <- list(list(seed = 1020,
                            theta0 = y / sum(y),
                            alpha0 = rep(0.01, length(y))),
                       list(seed = 6,
                            theta0 = c(100, rep(1, length(y) - 1)) /
                              sum(c(100, rep(1, length(y) - 1))),
                            alpha0 = rep(0.1, length(y))),
                       list(seed = 74901,
                            theta0 = rep(1/length(y), length(y)),
                            alpha0 = rep(0.5, length(y))),
                       list(seed = 481,
                            theta0 = c(rep(100, 100), rep(10, length(y) - 100)) /
                               sum(c(rep(1, 100), rep(0, length(y) - 100))),
                            alpha0 = rep(0.9, length(y))))

control_chains <- TmParallelApply(control_chains, function(x){
  # run sampler
  result <- control_sampler(y, B, seed = x$seed, theta0 = x$theta0, alpha0 = x$alpha0)

  # remove 50% burn-in itertions and check convergence
  result$alpha <- result$alpha[(B/2):B,]

  result$theta <- result$theta[(B/2):B,]

  result$geweke_alpha <- apply(result$alpha,2,function(k){
    out <- try(geweke.diag(k)$z)

    if (class(out) == "try-error")
      return(NA)

    out
  })

  result$geweke_theta <- apply(result$theta,2,function(k){
    out <- try(geweke.diag(k)$z)

    if (class(out) == "try-error")
      return(NA)

    out
  })

  # thin every 10th interation
  result$alpha <- result$alpha[seq(10, nrow(result$alpha), by=10),]

  result$theta <- result$theta[seq(10, nrow(result$theta), by=10),]
```

```r
  # return full result
  result

}, cpus = 2, export = c("y", "B", "control_sampler"),
   libraries = c("gtools", "EnvStats", "coda", "statmod"))

# check acceptance rate
control_alpha_acc <- sapply(control_chains, function(x) mean(x$acc_alpha))

# check convergence with Geweke statistic
control_theta_conv <- sapply(control_chains, function(x){
  mean(abs(x$geweke_theta) >= 1.96 | is.na(x$geweke_theta))
})

control_alpha_conv <- sapply(control_chains, function(x){
  mean(abs(x$geweke_alpha) >= 1.96 | is.na(x$geweke_alpha))
})
```

6.0.2 Sampling the main model

```r
# declare a sampling function for the main model

main_sampler <- function(y, B, seed, theta0, alpha0, beta0, gamma) {

  # set up functions for M-H sampler for alpha

  # these functions are just for a single alpha_k
  f_alpha_k <- function(alpha_k, theta_k, beta) {
    alpha_k ^ (-beta - 1) * theta_k ^ alpha_k
  }

  j_alpha <- function(mu = 1, prob = FALSE, n = NULL, x = NULL, rate = 0.1) {
    # if prob is false, draw a sample, otherwise find p(x)
    if (! prob) {
      # out <- rexp(n = n, rate = rate)
      out <- rinvgauss(n = n, mean = mu, shape = rate)
      # out <- rpareto(n = n, location = mu, shape = rate)
      # out <- rhalfcauchy(n = n, scale = rate)
    } else {
      # out <- dexp(x, rate)
      out <- dinvgauss(x, mean = mu, shape = rate)
      # out <- dpareto(x, location = mu, shape = rate)
      # out <- dhalfcauchy(x, scale = rate)
    }

    out
  }

  # set up sampler
  k <- length(y)

  theta <- matrix(0, nrow = B, ncol = k)
```

```r
theta[ 1, ] <- theta0

alpha <- matrix(0, nrow = B, ncol = k)

alpha[ 1, ] <- alpha0

acc_alpha <- numeric(ncol(alpha))

beta <- numeric(B)

beta[ 1 ] <- 2

a <- 0; b <- 0 # reduces to non-informative prior for beta

g <- gamma

# run the sampler
# run sampler
for (j in 2:B) {

  # sample theta
  theta[j,] <- rdirichlet(1, y + alpha[j-1,])

  # sample beta
  beta[j] <- rgamma(1, k + a, sum(log(alpha[j-1,]) - k * log(g)) + b)

  # sample alpha
  alpha_star <- j_alpha(n = k)

  r <- (f_alpha_k(alpha_k = alpha_star, theta_k = theta[j-1,], beta = beta[j-1]) /
          f_alpha_k(alpha[j-1,],theta[j-1,],beta[j-1])) /
    (j_alpha(prob = TRUE, x = alpha_star) / j_alpha(prob = TRUE, x = alpha[j-1,]))

  u <- runif(1)

  keep <- pmin(r,1) > u

  alpha[j,keep] <- alpha_star[keep]

  alpha[j,!keep] <- alpha[j-1,!keep]

  # acc_alpha[j] <- sum(keep) / k

  acc_alpha <- acc_alpha + keep

}

acc_alpha <- acc_alpha / B

# return the result
list(theta = theta, alpha = alpha, acc_alpha = acc_alpha, beta = beta,
     seed = seed, theta0 = theta0, alpha0 = alpha0)
```

```
}
# run 4 chains of 20,000 iterations each

B <- 20000

main_chains <- list(list(seed = 1020,
                         theta0 = y / sum(y),
                         alpha0 = rep(0.01, length(y)),
                         beta0 = 2),
                    list(seed = 6,
                         theta0 = c(100, rep(1, length(y) - 1)) /
                           sum(c(100, rep(1, length(y) - 1))),
                         alpha0 = rep(0.1, length(y)),
                         beta0 = 1),
                    list(seed = 74901,
                         theta0 = rep(1/length(y), length(y)),
                         alpha0 = rep(0.5, length(y)),
                         beta0 = 0.01),
                    list(seed = 481,
                         theta0 = c(rep(100, 100), rep(10, length(y) - 100)) /
                           sum(c(rep(1, 100), rep(0, length(y) - 100))),
                         alpha0 = rep(0.9, length(y)),
                         beta0 = 0.5))

main_chains <- TmParallelApply(main_chains, function(x){
  # run sampler
  result <- main_sampler(y, B, seed = x$seed, theta0 = x$theta0,
                         alpha0 = x$alpha0, beta0 = x$beta0, gamma = 0.01)

  # remove 50% burn-in itertions and check convergence
  result$alpha <- result$alpha[(B/2):B,]

  result$theta <- result$theta[(B/2):B,]

  result$beta <- result$beta[(B/2):B]

  result$geweke_alpha <- apply(result$alpha,2,function(k){
    out <- try(geweke.diag(k)$z)

    if (class(out) == "try-error")
      return(NA)

    out
  })

  result$geweke_theta <- apply(result$theta,2,function(k){
    out <- try(geweke.diag(k)$z)

    if (class(out) == "try-error")
      return(NA)

    out
  })
```

```r
  result$geweke_beta <- try(geweke.diag(result$beta)$z)


  # thin every 10th interation
  result$alpha <- result$alpha[seq(10, nrow(result$alpha), by=10),]

  result$theta <- result$theta[seq(10, nrow(result$theta), by=10),]

  result$beta <- result$beta[seq(10, length(result$beta), 10)]

  # return full result
  result

}, cpus = 2, export = c("y", "B", "main_sampler"),
   libraries = c("gtools", "EnvStats", "coda", "statmod"))

# check acceptance rate
main_alpha_acc <- sapply(main_chains, function(x) mean(x$acc_alpha))

# check convergence with Geweke statistic
main_theta_conv <- sapply(main_chains, function(x){
  mean(abs(x$geweke_theta) >= 1.96 | is.na(x$geweke_theta))
})

main_alpha_conv <- sapply(main_chains, function(x){
  mean(abs(x$geweke_alpha) >= 1.96 | is.na(x$geweke_alpha))
})

main_beta_conv <- sapply(main_chains, function(x) x$geweke_beta)

save.image('.RData')
```

6.1 Comparison

We should put some posterior plots here, maybe

```r
# Combine the results from the chains
control_posterior <- list(theta = do.call(rbind, lapply(control_chains, function(x) x$theta)),
                          alpha = do.call(rbind, lapply(control_chains, function(x) x$alpha)))

main_posterior <- list(theta = do.call(rbind, lapply(main_chains, function(x) x$theta)),
                          alpha = do.call(rbind, lapply(main_chains, function(x) x$alpha)),
                          beta = do.call(c, lapply(main_chains, function(x) x$beta)))
```

```r
# check acceptance rates
main_alpha_acc <- sapply(main_chains, function(x) x$acc_alpha)

control_alpha_acc <- sapply(control_chains, function(x) x$acc_alpha)

plot(density(rowMeans(control_alpha_acc)), lwd = 4, col = "blue", lty = 2,
     main = expression(paste("Acceptance rates of ", alpha, " parameters in both models")),
     xlab = "Acceptance rate",
     xlim = range(control_alpha_acc, main_alpha_acc))
```

```r
lines(density(rowMeans(main_alpha_acc)), lwd = 4, lty = 1, col = "red")
legend("topright", legend = c("Main", "Control"), lwd = 4, lty = c(1,3),
       col = c("red", "blue"))

alpha_acc_table <- data.frame(Main = quantile(rowMeans(main_alpha_acc), c(0,0.25,0.5,0.75,1)),
                              Control = quantile(rowMeans(control_alpha_acc), c(0,0.25,0.5,0.75,1)),
                              stringsAsFactors = FALSE)

rownames(alpha_acc_table) <- c("min.", "25%", "50%", "75%", "max.")

knitr::kable(alpha_acc_table, digits = 2)
```

Convergence is based on log likelihood of both models

```r
# check convergence

conv <- parallel::mclapply(list(main = main_posterior, control = control_posterior),
                           function(x){
                             apply(x$theta,1,function(z) dmultinom(y, prob = z, log = T))
                           })

par(mfrow = c(2,1), mar = c(2.1,4.1,2.1,2.1))
plot(conv$main, type = "l",
     main = "Main model", col = "red", xaxt = "n", xlab = "",
     ylab = expression(paste("log[P(y|",theta,")]")))
abline(v = c(1000,2000,3000))
plot(conv$control, type = "l",
     main = "Control model", col = "blue", xaxt = "n", xlab = "",
     ylab = expression(paste("log[P(y|",theta,")]")))
abline(v = c(1000,2000,3000))

g <- lapply(conv, geweke.diag)

g <- data.frame(Main = g[[1]]$z, Control = g[[2]]$z)

rownames(g) <- ""

knitr::kable(data.frame(g),digits = 2, caption = "Geweke statistic of log likelihoods")
```

MCMC plots of selected words

```r
# MCMC plots

# get indices of max, median, 3rd quartile words
q <- quantile(y, c(1,0.95, 0.75))

ind <- sapply(q, function(x) which(y == x)[1])

# look at ACF/mcmcplot

capture <- lapply(ind, function(k){
  a <- matrix(main_posterior$alpha[,k], ncol = 1)
  colnames(a) <- "alpha"
  mcmcplot1(a, greek = TRUE, col = "red")
```

```r
  a <- matrix(control_posterior$alpha[,k], ncol = 1)
  colnames(a) <- "alpha"
  mcmcplot1(a, greek = TRUE)

})

capture <- lapply(ind, function(k){
  a <- matrix(main_posterior$theta[,k], ncol = 1)
  colnames(a) <- "theta"
  mcmcplot1(a, greek = TRUE, col = "red")

  a <- matrix(control_posterior$theta[,k], ncol = 1)
  colnames(a) <- "theta"
  mcmcplot1(a, greek = TRUE)
})

b <- matrix(main_posterior$beta, ncol = 1)
colnames(b) <- "beta"
mcmcplot1(b, greek = TRUE, col = "red")
```

log posterior

```r
# log posterior comparison
main_p <- apply(main_posterior$theta,1,function(x) dmultinom(y, prob = x, log = TRUE))

control_p <- apply(control_posterior$theta,1,function(x) dmultinom(y, prob = x, log = TRUE))

d1 <- density(main_p)
d2 <- density(control_p)

plot(d1, col = "red", lwd = 4,
     main = "Posterior Log Likelihood",
     xlim = range(c(d1$x, d2$x)))
lines(d2, col = "blue", lwd = 4, lty = 2)
```

DIC, now in distribution form!

```r
# calculate DIC for each model
calc_dic <- function(y, theta_mat, B = NULL) {

  llik <- apply(theta_mat, 1, function(x) dmultinom(y, prob = x, log = TRUE))

  pdic <- 2 * var(llik)


  if (! is.null(B)) {
    dic <- sapply(seq_len(B), function(th){
      -2 * dmultinom(y, prob = theta_mat[ sample(seq_len(nrow(theta_mat)), 1) , ], log = TRUE)
    })

    dic <- dic + 2 * pdic
  } else {
    dic <- -2 * dmultinom(y, prob = colMeans(theta_mat), log = TRUE) + 2 * pdic
  }
```

```
  dic

}

main_dic <- calc_dic(y, main_posterior$theta, B = 10000)

control_dic <- calc_dic(y, control_posterior$theta, B = 10000)

d1 <- density(main_dic)

d2 <- density(control_dic)

plot(d1, col = "red", lwd = 4,
     main = "Posterior DIC",
     xlim = range(c(d1$x, d2$x)))
lines(d2, col = "blue", lwd = 4, lty = 2)
abline(v = quantile(main_dic, probs = c(0.025, 0.5, 0.975)), col = "red", lwd = 2)
abline(v = quantile(control_dic, probs = c(0.025, 0.5, 0.975)), col = "blue", lwd = 2, lty = 2)


# barplot(c(Main = main_dic, Control = control_dic), col = c("red", "blue"),
#         density = c(-1,25))
```

full circle: zipfs law and our models

```
# log-log plots of alpha and theta vs. y

# alpha
plot(log10(seq_along(y)), log10(y),
     lwd = 3, yaxt = "n", ylab = "log10(x)", xlab = "rank(x)", type = "l",
     lty = 3, main = expression(paste("Comparing ", alpha)))
par(new = TRUE)
plot(log10(seq_along(y)), log10(colMeans(main_posterior$alpha)),
     lwd = 3, yaxt = "n", ylab = "", xaxt = "n", xlab = "", type = "l", lty = 1,
     col = rgb(1,0,0,0.5))
par(new = TRUE)
plot(log10(seq_along(y)), log10(colMeans(control_posterior$alpha)),
     lwd = 3, yaxt = "n", ylab = "", xaxt = "n", xlab = "", type = "l", lty = 2,
     col = rgb(0,0,1,0.5))
legend("bottomleft", legend = c("y", "Main", "Control"),
       lwd = 3, lty = c(3,1,2), col = c("black", "red", "blue"))

# theta
plot(log10(seq_along(y)), log10(y),
     lwd = 3, yaxt = "n", ylab = "log10(x)", xlab = "rank(x)", type = "l",
     lty = 3, main = expression(paste("Comparing ", theta)))
par(new = TRUE)
plot(log10(seq_along(y)), log10(colMeans(main_posterior$theta)),
     lwd = 3, yaxt = "n", ylab = "", xaxt = "n", xlab = "", type = "l", lty = 1,
     col = rgb(1,0,0,0.5))
par(new = TRUE)
plot(log10(seq_along(y)), log10(colMeans(control_posterior$theta)),
     lwd = 3, yaxt = "n", ylab = "", xaxt = "n", xlab = "", type = "l", lty = 2,
     col = rgb(0,0,1,0.5))
```

```r
legend("bottomleft", legend = c("y", "Main", "Control"),
       lwd = 3, lty = c(3,1,2), col = c("black", "red", "blue"))
```

7 Appendix B

7.1 Control Posterior Derivations

$$
\begin{aligned}
P(\vec{\theta}, \vec{\alpha} | \vec{y}) &\propto \left[\prod_k \theta_k^{y_k}\right] \left[\mathcal{B}(\vec{\alpha}) \prod_k \theta_k^{\alpha_k - 1}\right] \times 1 && (11)\\
&= \left[\prod_k \theta_k^{y_k}\right] \left[\mathcal{B}(\vec{\alpha}) \prod_k \theta_k^{\alpha_k - 1}\right] && (12)\\
P(\vec{\theta} | \vec{\alpha}, \vec{y}) &\propto \prod_k \theta_k^{y_k + \alpha_k - 1} && (13)\\
&\implies \vec{\theta} | \vec{\alpha}, \vec{y} \sim Dir(\vec{y} + \vec{\alpha}) && (14)\\
P(\vec{\alpha} | \vec{\theta}, \vec{y}) &\propto \mathcal{B}(\vec{\alpha}) \prod_k \theta_k^{\alpha_k} && (15)\\
P(\alpha_k | \theta_k, y_k) &\propto \theta_k^{\alpha_k} && (16)
\end{aligned}
$$

7.2 Main Posterior Derivations

$$
\begin{aligned}
P(\vec{\theta}, \vec{\alpha}, \beta | \vec{y}) &\propto \left[\prod_k \theta_k^{y_k}\right] \left[\mathcal{B}(\vec{\alpha}) \prod_k \theta_k^{\alpha_k - 1}\right] \left[\prod_k \gamma^{\beta} \beta \alpha_k^{-(\beta+1)}\right] && (17)\\
&= \beta^{K-1} \gamma^{\beta k} \mathcal{B}(\vec{\alpha}) \prod_k \theta_k^{y_k + \alpha_k - 1} \alpha_k^{-(\beta+1)} && (18)\\
P(\vec{\theta} | \vec{\alpha}, \beta, \vec{y}) &\propto \prod_k \theta_k^{y_k + \alpha_k - 1} && (19)\\
&\implies \vec{\theta} | \vec{\alpha}, \beta, y \sim Dir(\vec{y} + \vec{\alpha}) && (20)\\
P(\vec{\alpha} | \vec{\theta}, \beta, \vec{y}) &\propto \mathcal{B}(\vec{\alpha}) \prod_k \theta_k^{y_k + \alpha_k - 1} \alpha_k^{-(\beta+1)} && (21)\\
&\implies \text{unknown distribution} && (22)\\
P(\beta | \vec{\theta}, \vec{\alpha}, \vec{y}) &\propto \beta^{K-1} \gamma^{\beta k} (\prod_k \alpha_k)^{-(\beta+1)} && (23)\\
&\propto \beta^{K-1} \gamma^{\beta k} (\prod_k \alpha_k)^{-\beta} && (24)\\
&\propto \beta^{K-1} \exp\left[-\beta \Big(\sum_k \log(\alpha_k) - k \log(\gamma) \Big) \right] && (25)\\
&\implies \beta | \vec{\theta}, \vec{\alpha}, \vec{y} \sim Gamma\Big(k, \sum_k \log(\alpha_k) - k \log(\gamma)\Big) && (26)
\end{aligned}
$$

7.3 Jeffrey's prior on β

$$p(\beta) \propto \prod_k \beta \alpha_k^{-(\beta+1)} \tag{27}$$

$$p(\beta) \propto \beta^k (\prod_k \alpha_k)^{-(\beta+1)} \tag{28}$$

$$\log\big(p(\beta)\big) \propto k\log(\beta) - \beta\log(\prod_k \alpha_k) - \log(\prod_k \alpha_k) \tag{29}$$

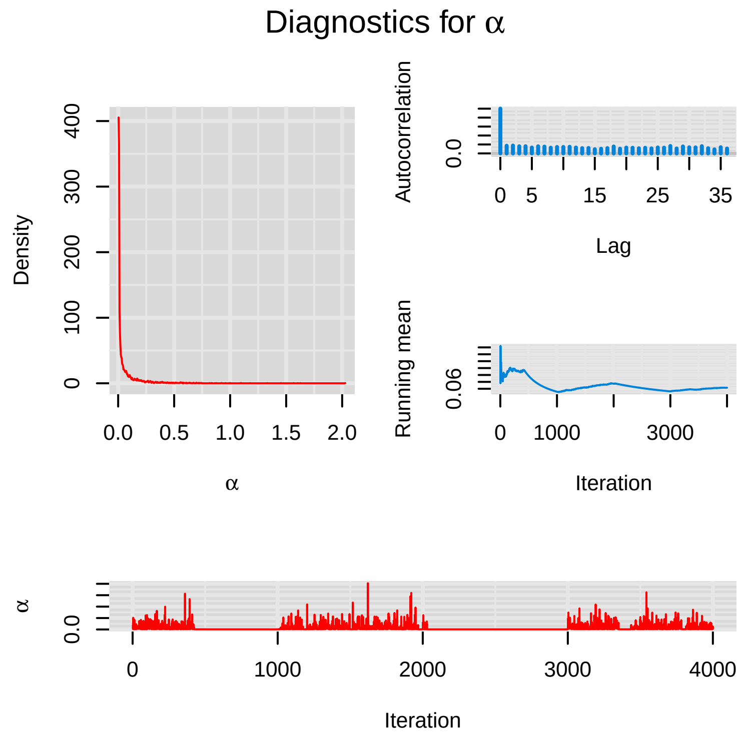
$$\frac{\partial}{\partial\beta}\log\big(p(\beta)\big) \propto \frac{k}{\beta} - \log(\prod_k \alpha_k) \tag{30}$$

$$\frac{\partial^2}{\partial\beta^2}\log\big(p(\beta)\big) \propto \frac{-k}{\beta^2} \tag{31}$$

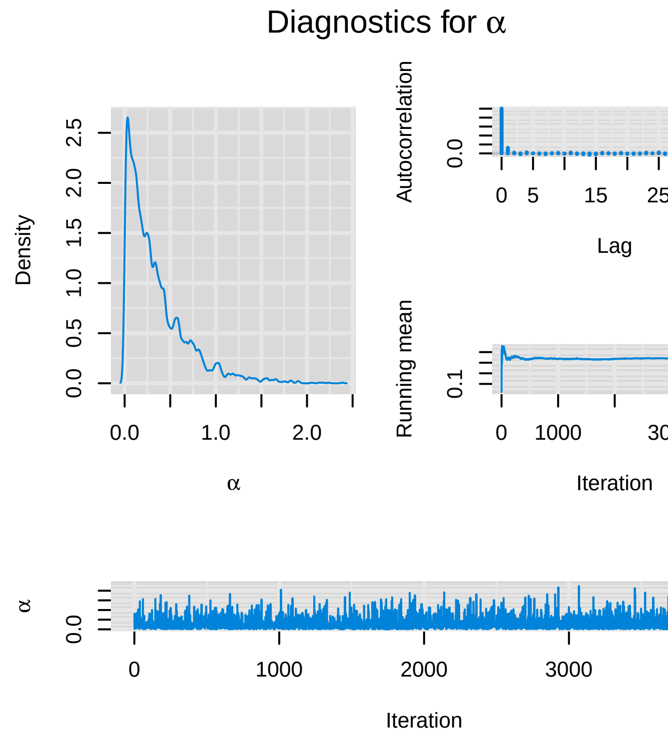
$$-E\Big[\frac{\partial^2}{\partial\beta^2}\log\big(p(\beta)\big)\Big] \propto \frac{k}{\beta^2} \tag{32}$$

$$\pi(\beta) \propto \frac{1}{\beta} \tag{33}$$

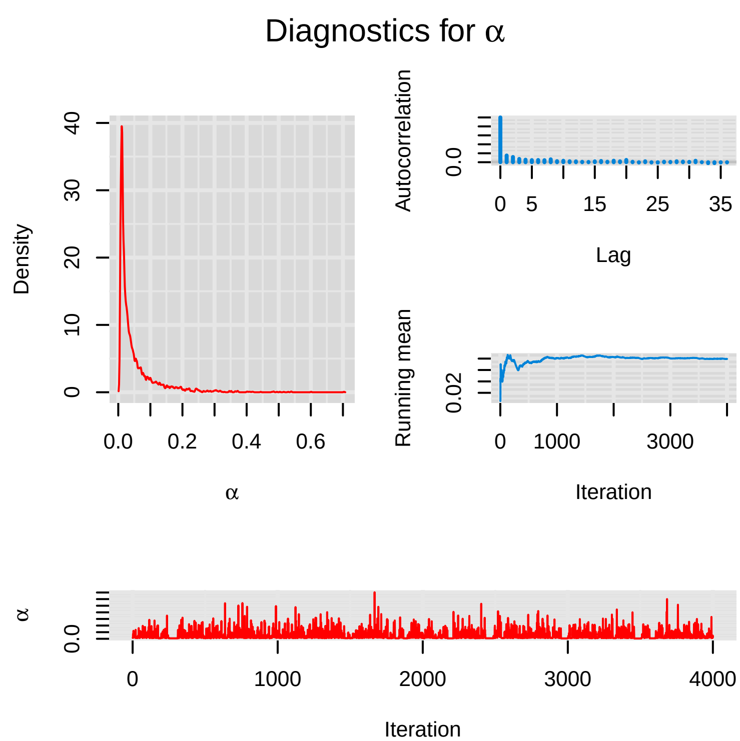
8 Appendix C



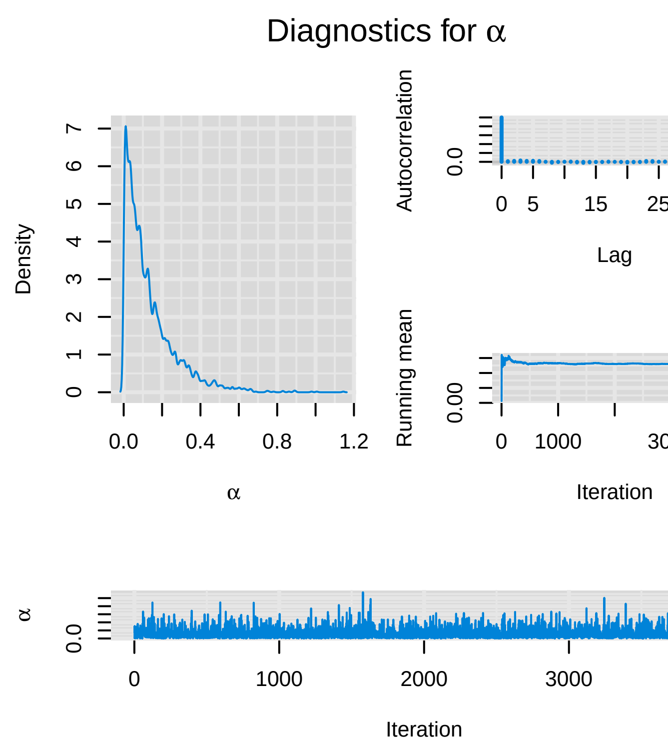
Diagnostics for α
Density
Autocorrelation
Lag
Running mean
Iteration
α
Iteration



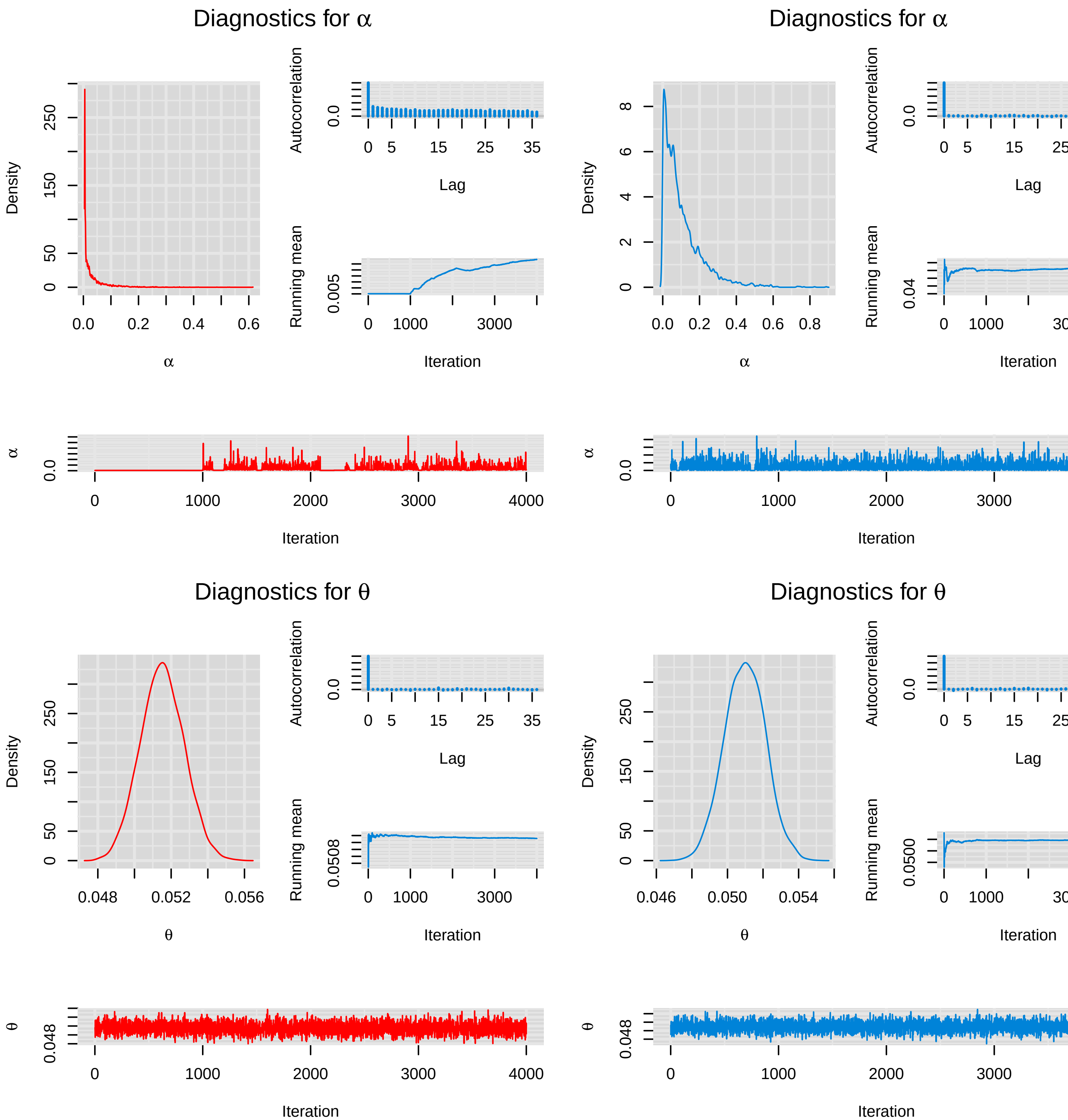
Diagnostics for α
Density
Autocorrelation
Lag
Running mean
Iteration
α
Iteration

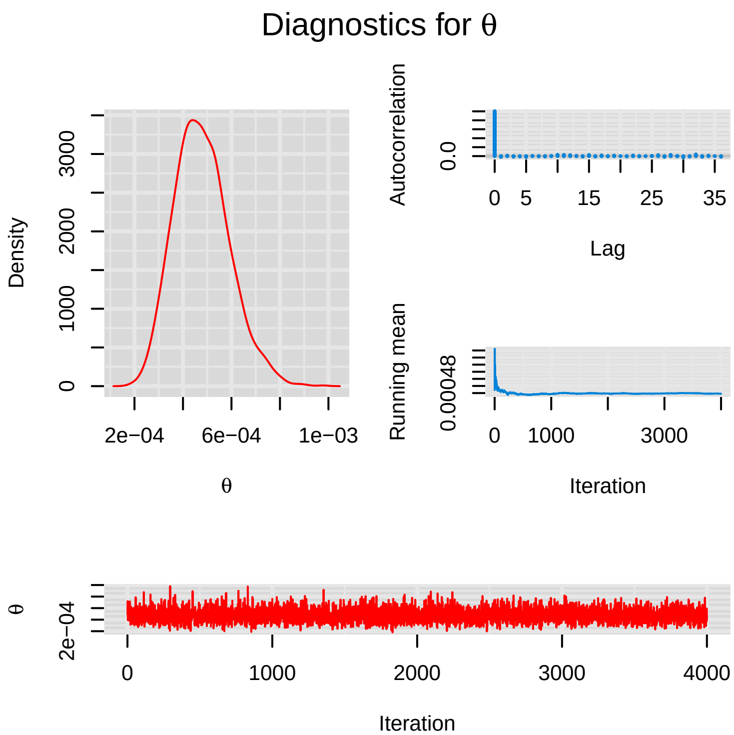


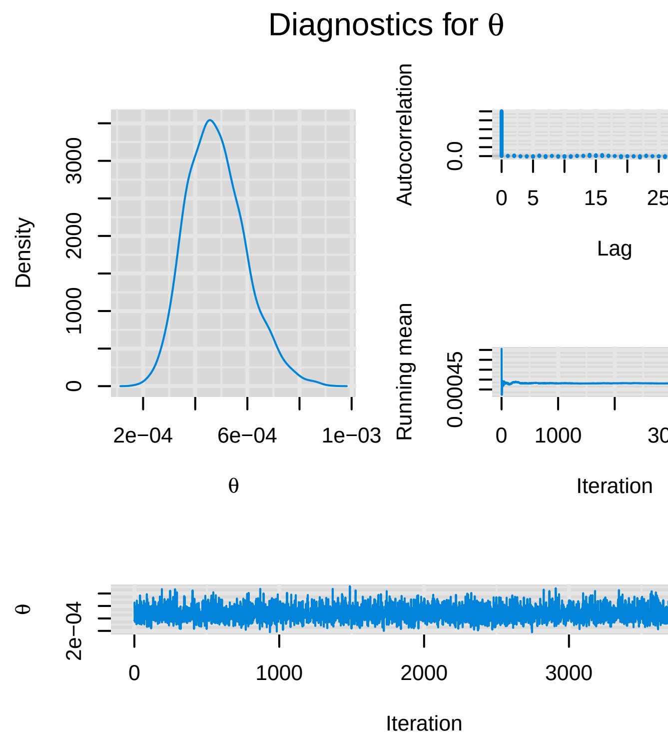
Diagnostics for α
Density
Autocorrelation
Lag
Running mean
Iteration
α
Iteration

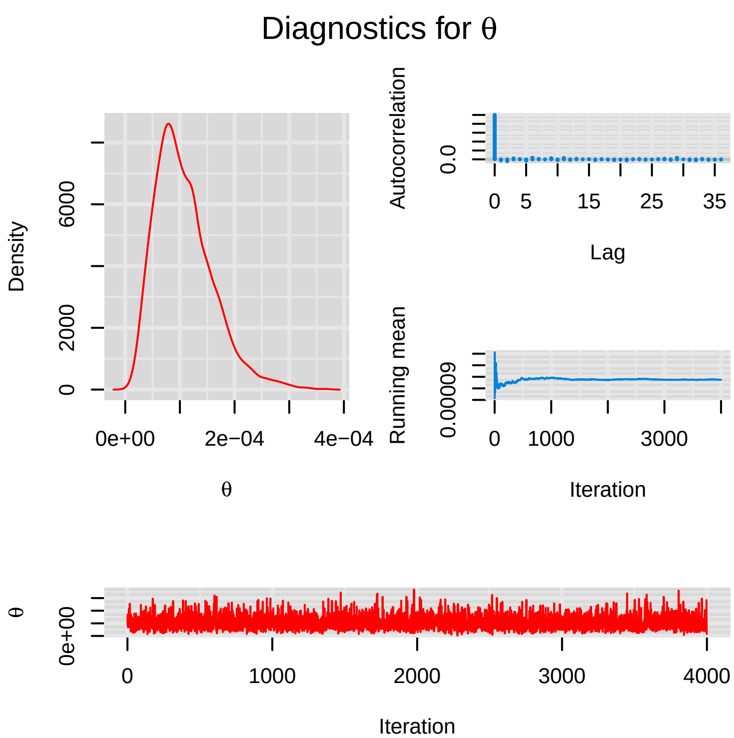


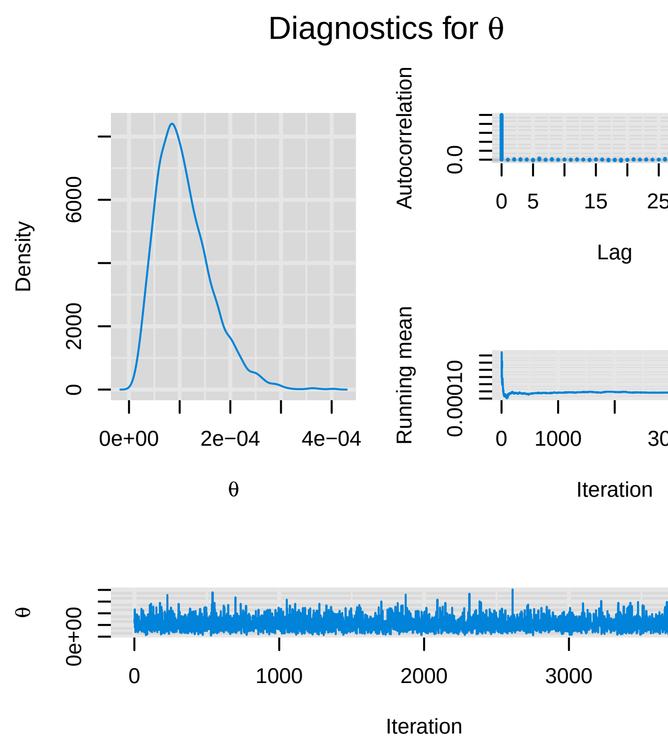
Diagnostics for α
Density
Autocorrelation
Lag
Running mean
Iteration
α
Iteration

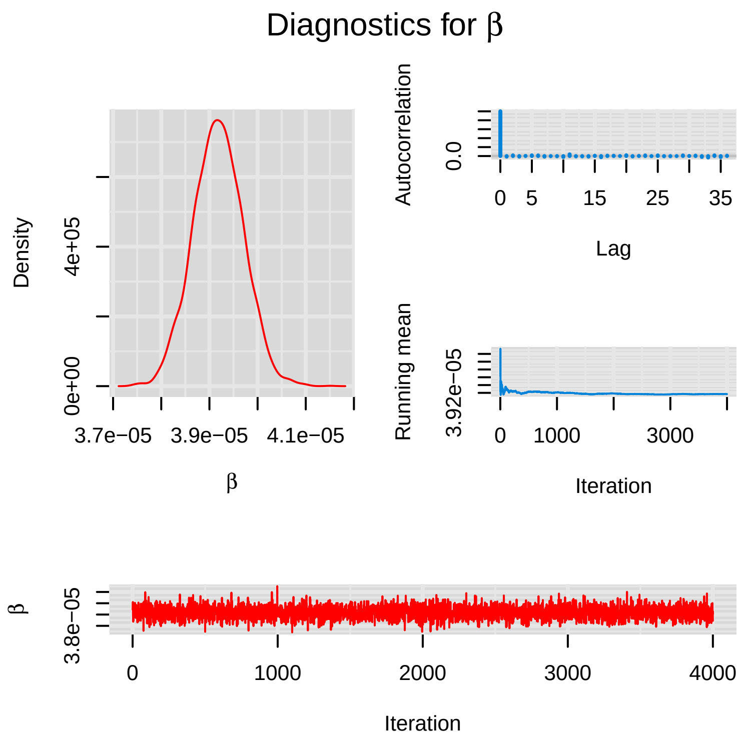

Diagnostics for α
Density
α
Autocorrelation
Lag
Running mean
Iteration
Diagnostics for α
Diagnostics for θ
θ
Diagnostics for θ


Diagnostics for θ
Density
θ
Autocorrelation
Lag
Running mean
Iteration
θ
Iteration

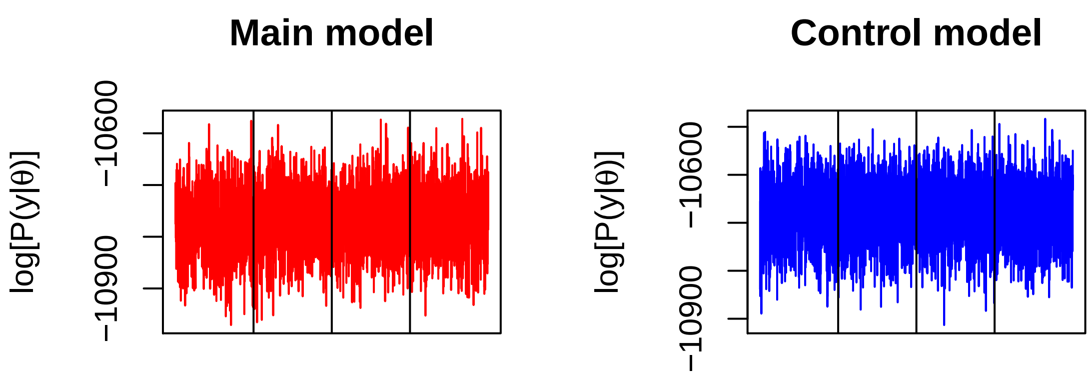

Diagnostics for θ
Density
θ
Autocorrelation
Lag
Running mean
Iteration
θ
Iteration


Diagnostics for θ
Density
θ
Autocorrelation
Lag
Running mean
Iteration
θ
Iteration


Diagnostics for θ
Density
θ
Autocorrelation
Lag
Running mean
Iteration
θ
Iteration



Diagnostics for β
Density
4e+05
0e+00
3.7e−05
3.9e−05
4.1e−05
β
Autocorrelation
0.0
0
5
15
25
35
Lag
Running mean
3.92e−05
0
1000
3000
Iteration
β
3.8e−05
0
1000
2000
3000
4000
Iteration



Main model
log[P(y|θ)]
−10600
−10900
Control model
log[P(y|θ)]
−10600
−10900