

# BTRR\_demo

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```
source('BTRR.R')
```

```
##
```

```
## 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
```

```
## Loading required package: proto
```

```
## Warning in doTryCatch(return(expr), name, parentenv, handler): unable to load shared object '/Library
```

```
##   dlopen(/Library/Frameworks/R.framework/Resources/modules//R_X11.so, 6): Library not loaded: /opt/X
```

```
##   Referenced from: /Library/Frameworks/R.framework/Resources/modules//R_X11.so
```

```
##   Reason: image not found
```

```
## Warning in system2("/usr/bin/otool", c("-L", shQuote(DSO)), stdout = TRUE):
```

```
## running command ''/usr/bin/otool' -L '/Library/Frameworks/R.framework/Resources/
```

```
## library/tcltk/libs//tcltk.so'' had status 1
```

```
## Could not load tcltk. Will use slower R code instead.
```

```
##
```

```
## Attaching package: 'MASS'
```

```
## The following object is masked from 'package:dplyr':
```

```
##
```

```
##     select
```

```
## Loading required package: lme4
```

```
## Loading required package: Matrix
```

```
##
```

```
## Attaching package: 'Matrix'
```

```
## The following objects are masked from 'package:tidyr':
```

```
##
```

```
##     expand, pack, unpack
```

```
##
```

```
## Attaching package: 'lmerTest'
```

```
## The following object is masked from 'package:lme4':
```

```
##
```

```
##     lmer
```

```
## The following object is masked from 'package:stats':
##
##      step
library(plot.matrix)
```

## Simulate data

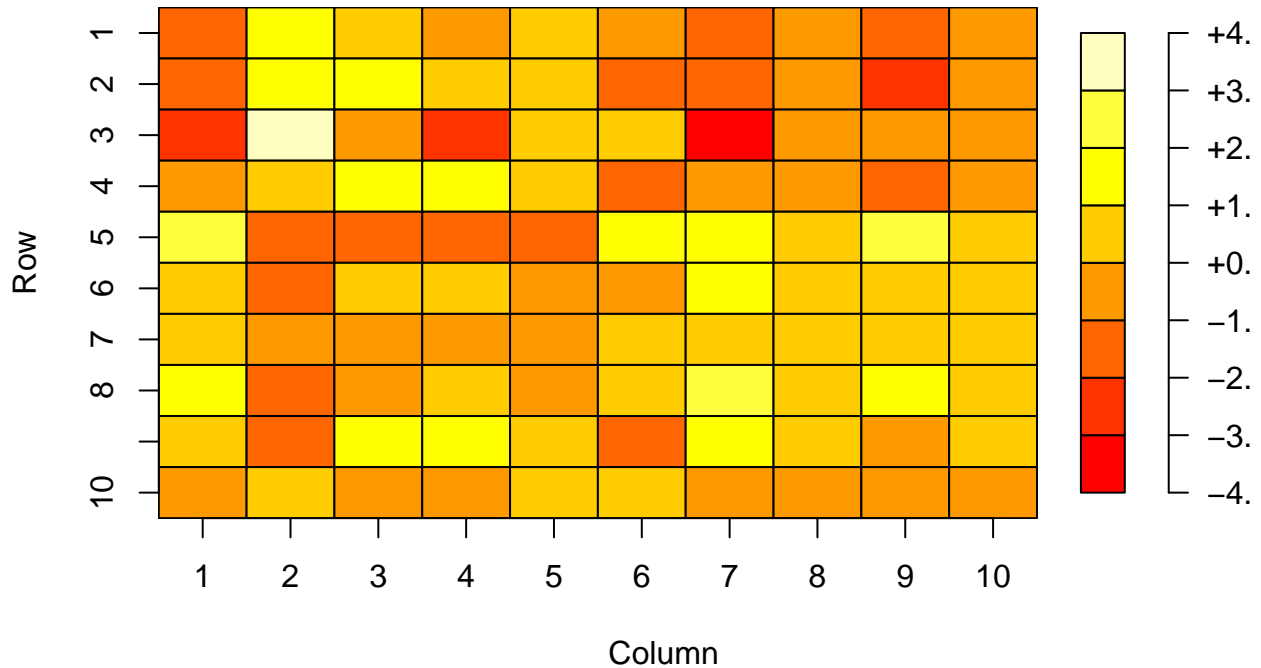
```
set.seed(1234)
N <- 50 # sample size (BTRR preferable to OLS if N is small)
K <- 3 # number of covariates
p <- c(10,10) # dimensions of each tensor outcome (BTRR preferable to OLS if prod(p) is large)
X.train <- array(rnorm(N*K), dim=c(N,K)) # simulated covariates
nIDs <- 3
ID <- sample(1:nIDs, N, replace=T) # ID index (for subjects 1-10)
table(ID) # make sure each subject has >=2 observations

## ID
## 1 2 3
## 18 19 13
# Note: for one overall intercept, set ID=NA and add a column of 1s to X.train

R.true <- 2 # true rank
# main effect coefficients: each a matrix generated from low-rank tensor decomposition,
# with normally-distributed tensor margins
Gamma.true <- t(sapply(1:K, function(x) c(TP.rankR(list(array(rnorm(p[1]*R.true), dim=c(p[1], R.true)),
array(rnorm(p[2]*R.true), dim=c(p[2], R.true))))))

# plot tensor (matrix) coefficient to see spatial patterns
plot(array(Gamma.true[1,], dim=p), main='True Tensor Coefficient 1')
```

## True Tensor Coefficient 1



```
# random intercepts: generated from low-rank tensor decomposition
Bi.true <- t(sapply(1:nIDs, function(x) c(TP.rankR(list(array(rnorm(p[1]*R.true),dim=c(p[1],R.true)),
                                                    array(rnorm(p[2]*R.true),dim=c(p[2],R.true)))))))

# set noise variance in simulated data
true.noise.var <- .5

# generate outcome data
Y.train <- t(sapply(1:N, function(x) X.train[x,] %*% Gamma.true + Bi.true[ID[x],]))
Y.train <- Y.train + array(rnorm(N*prod(p), sd=sqrt(true.noise.var), dim=c(N,prod(p)))
Y.train <- array(Y.train, dim=c(N,p)) # make into N x p1 x p2 array

# set ~5% of values to be missing
p.missing <- 0.05
missing.inds <- array(rbinom(N*prod(p),1,p.missing),dim=c(N,p))
Y.train[missing.inds==1] <- NA
sum(is.na(Y.train)) / (N*prod(p))
```

```
## [1] 0.0476
```

## Fit model using BTRR (tensor.reg function)

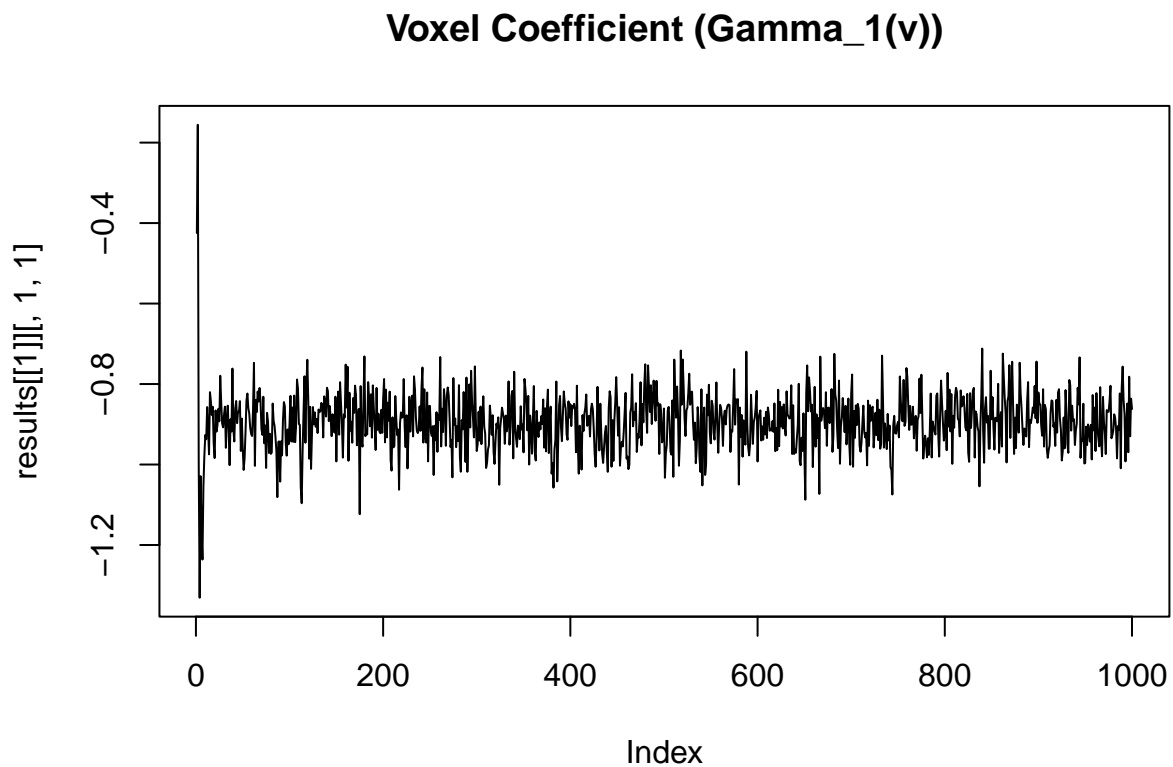
```
nsweep <- 1000 # number of MCMC iterations
R <- 2 # chosen rank for Gamma's and Bi's (tensor coefficients/intercepts)
# Note: can specify R<-c(R1,R2) for Gamma's rank R1 and Bi's rank R2
results <- tensor.reg(Y.train, X.train, ID, nsweep=nsweep, R=R, show.prog=T,prog.count=50)
```

```
## [1] 50
## [1] 100
## [1] 150
```

```
## [1] 200
## [1] 250
## [1] 300
## [1] 350
## [1] 400
## [1] 450
## [1] 500
## [1] 550
## [1] 600
## [1] 650
## [1] 700
## [1] 750
## [1] 800
## [1] 850
## [1] 900
## [1] 950
## [1] 1000
```

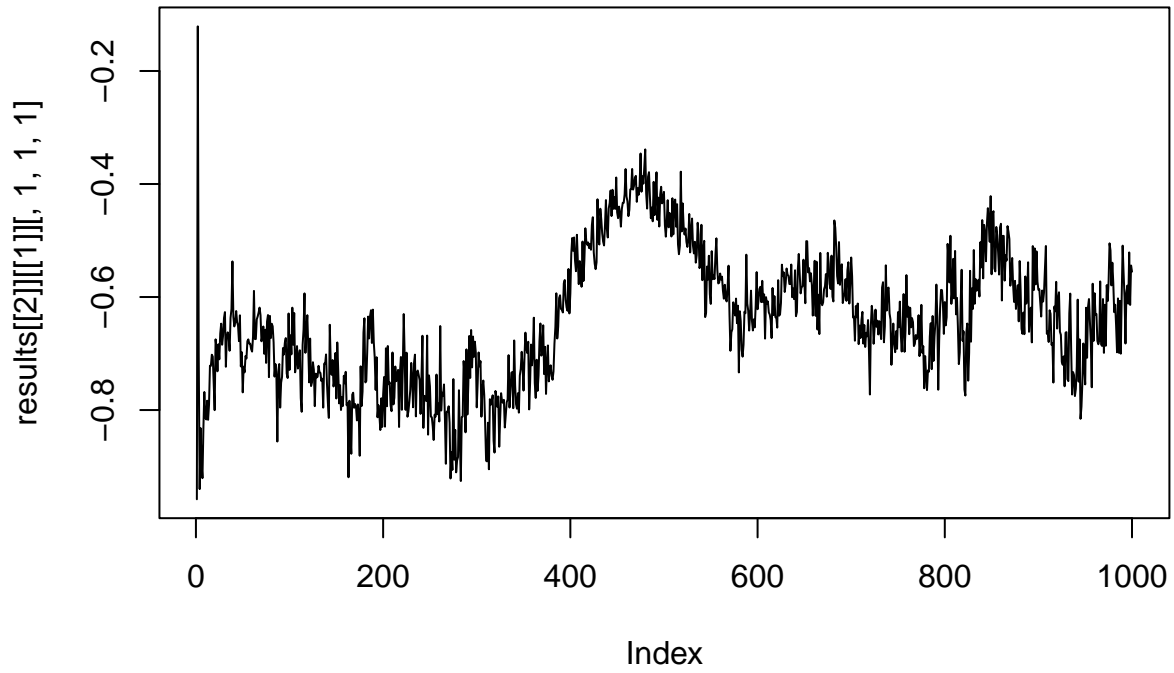
MCMC Traceplots: Plotted for each model parameter. Expected convergence for tensor coefficients and noise variance terms.

```
plot(results[[1]][,1,1],type="l",main="Voxel Coefficient (Gamma_1(v))") # first variable, first voxel
```



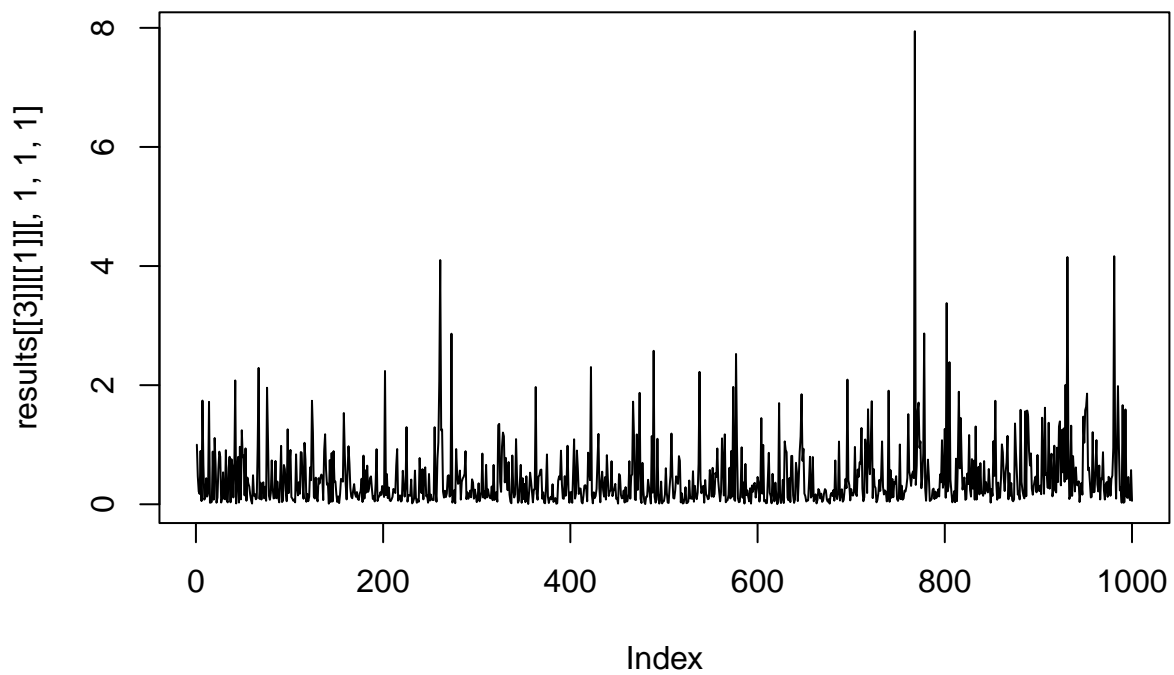
```
plot(results[[2]][[1]][,1,1,1],type="l", main="Tensor margin element (gamma_111)") # tensor margin element
```

**Tensor margin element (gamma\_111)**



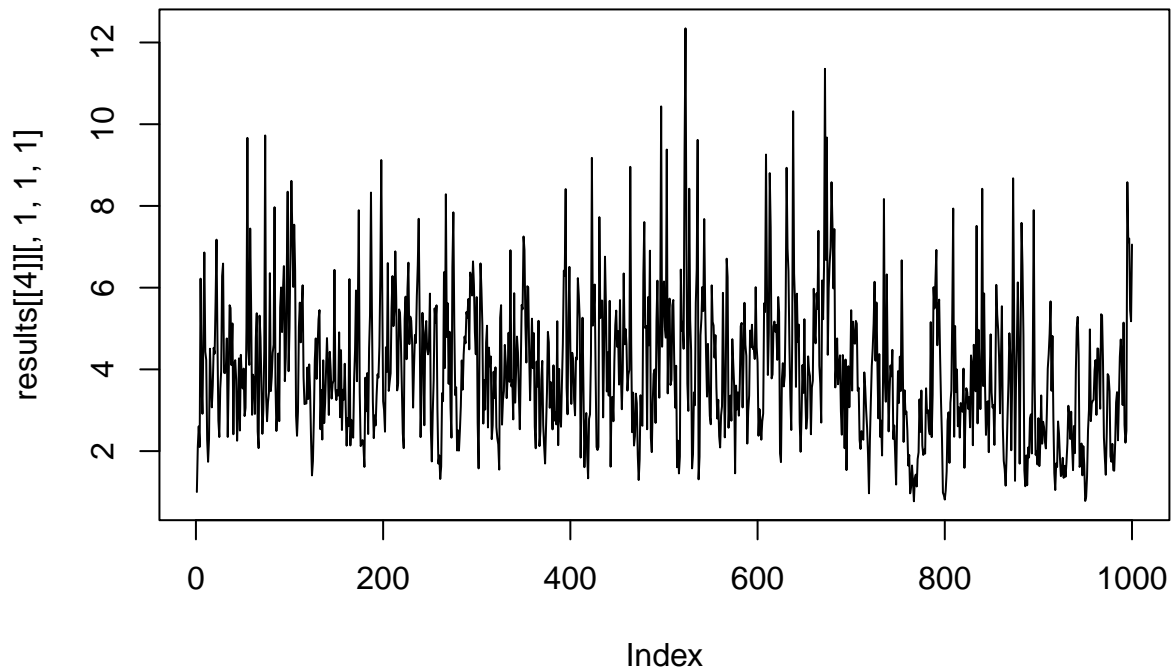
```
plot(results[[3]][[1]][,1,1,1],type="l", main="Tensor margin covariance (W_111)") # tensor margin cov d
```

**Tensor margin covariance (W\_111)**



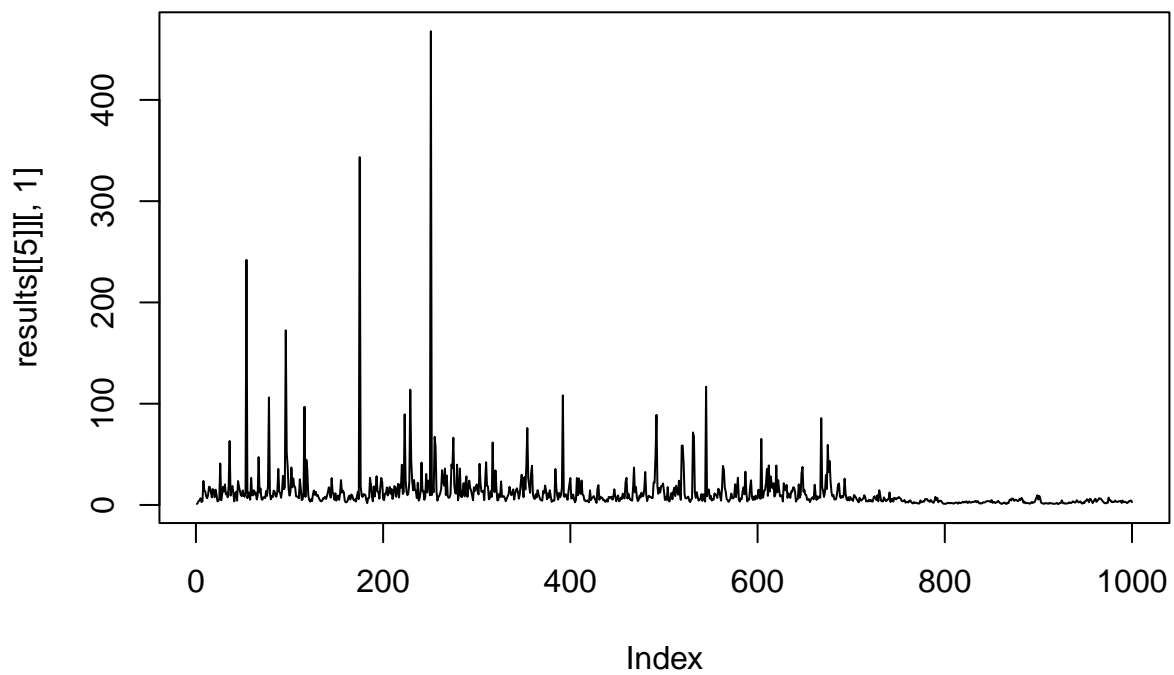
```
plot(results[[4]][,1,1,1],type="l", main="Rate parameter (lambda_111)") # lambda.drk
```

### Rate parameter (lambda\_111)



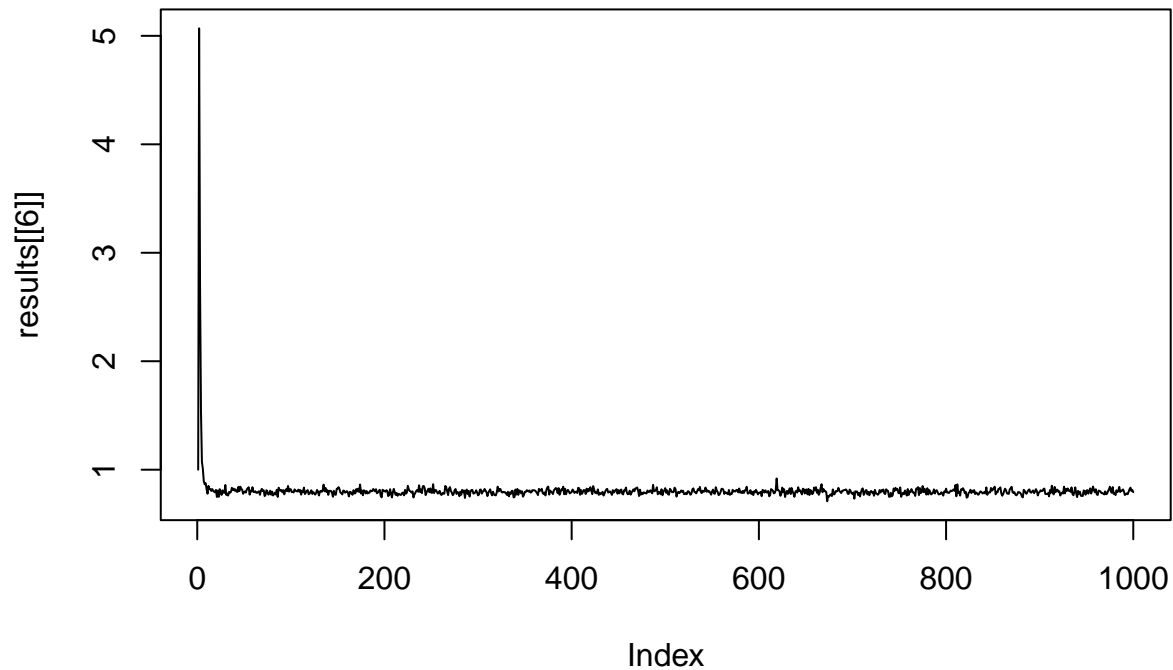
```
plot(results[[5]][,1], type="l", main="Global variance scaling (tau_1)") # tau.k
```

### Global variance scaling (tau\_1)



```
plot(results[[6]], type="l", main="Noise Variance (sigma^2)") # sigma^2
```

## Noise Variance ( $\sigma^2$ )



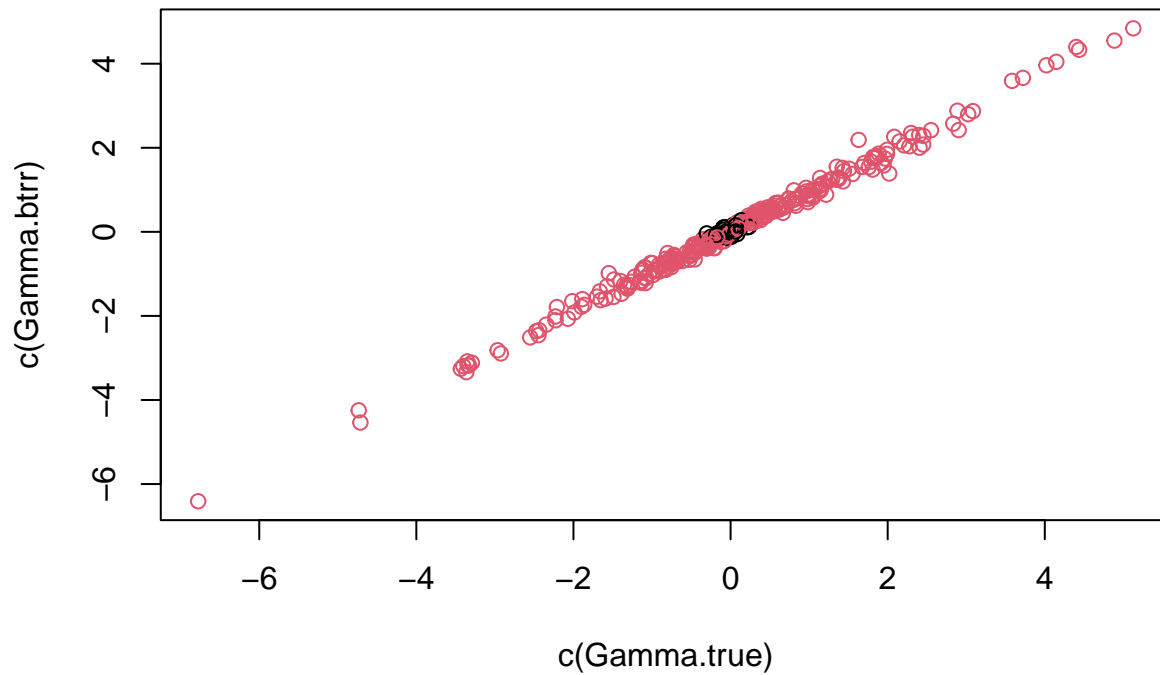
Get overall point and significance estimates (average over MCMC samples past burn in) from BTRR model

```
burn.in <- .3
Gamma.btrr <- apply(results[[1]][round(burn.in*nsweep):nsweep,,], c(2,3), mean)
Gamma.signif.btrr <- apply(results[[1]][round(burn.in*nsweep):nsweep,,], c(2,3), function(x) (quantile(x,
Bi.btrr <- apply(results[[7]][round(burn.in*nsweep):nsweep,,], c(2,3), mean)
Bi.signif.btrr <- apply(results[[7]][round(burn.in*nsweep):nsweep,,], c(2,3), function(x) (quantile(x,
```

Plot true vs. estimated coefficients (BTRR)

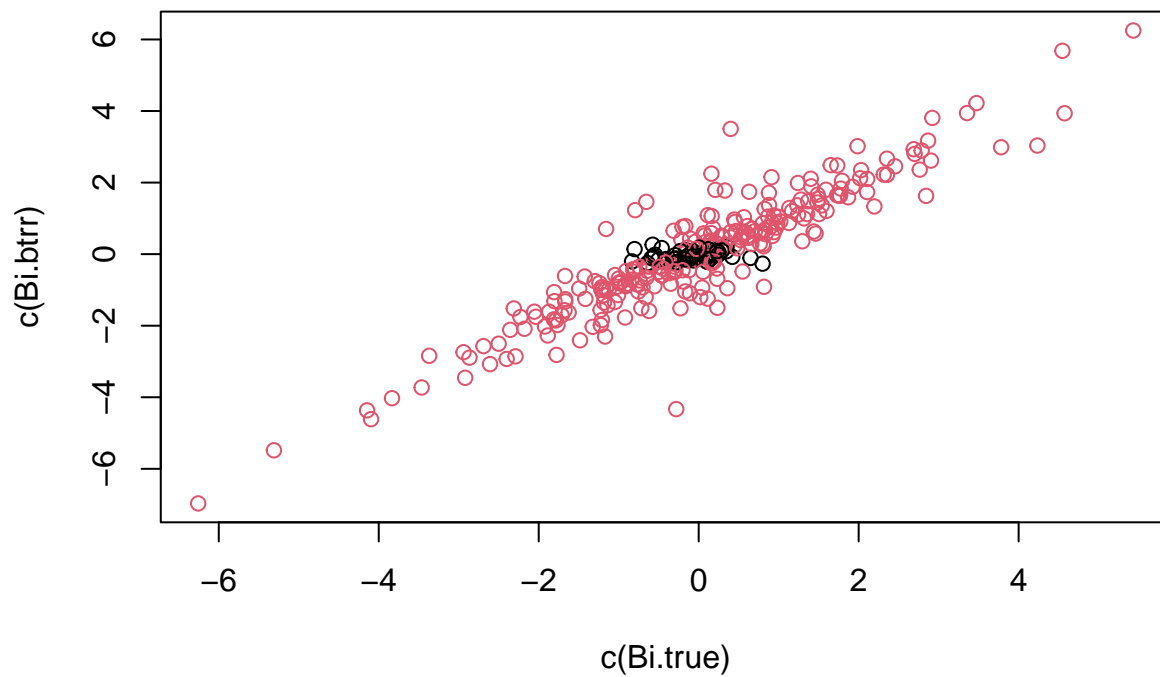
```
plot(c(Gamma.true), c(Gamma.btrr), col=factor(Gamma.signif.btrr),main="Estimated Coefficients (BTRR)")
```

## Estimated Coefficients (BTRR)



```
plot(c(Bi.true), c(Bi.btrr), col=factor(Bi.signif.btrr), main="Estimated Random Intercept (BTRR)")
```

## Estimated Random Intercept (BTRR)



```
paste0('Correlation for main coefficients (BTRR): ', signif(corr(c(Gamma.true), c(Gamma.btrr)),4))
```

```
## [1] "Correlation for main coefficients (BTRR): 0.9965"
```



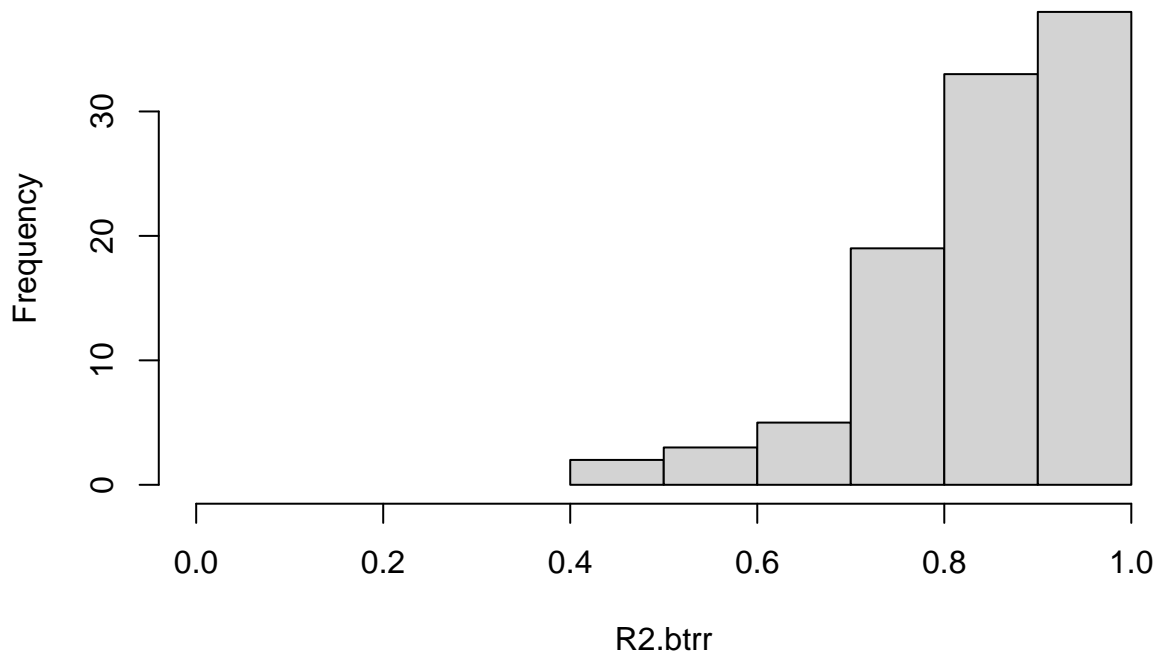
```
paste0('Correlation for random intercepts (BTRR): ', signif(cor(c(Bi.true), c(Bi.btrr)),4))

## [1] "Correlation for random intercepts (BTRR): 0.9209"
```

Find  $R^2$  for each voxel (BTRR)

```
R2.btrr <- getR2(Y.train, X.train, ID, Gamma.btrr, Bi.btrr)
hist(R2.btrr,5,xlim=c(0,1),main='Histogram of R^2 across voxels (BTRR)')
```

**Histogram of  $R^2$  across voxels (BTRR)**



```
paste0('Median R^2 across voxels (BTRR): ', signif(median(R2.btrr),4))

## [1] "Median R^2 across voxels (BTRR): 0.8759"
```

Fit model using OLS (not including random intercepts)

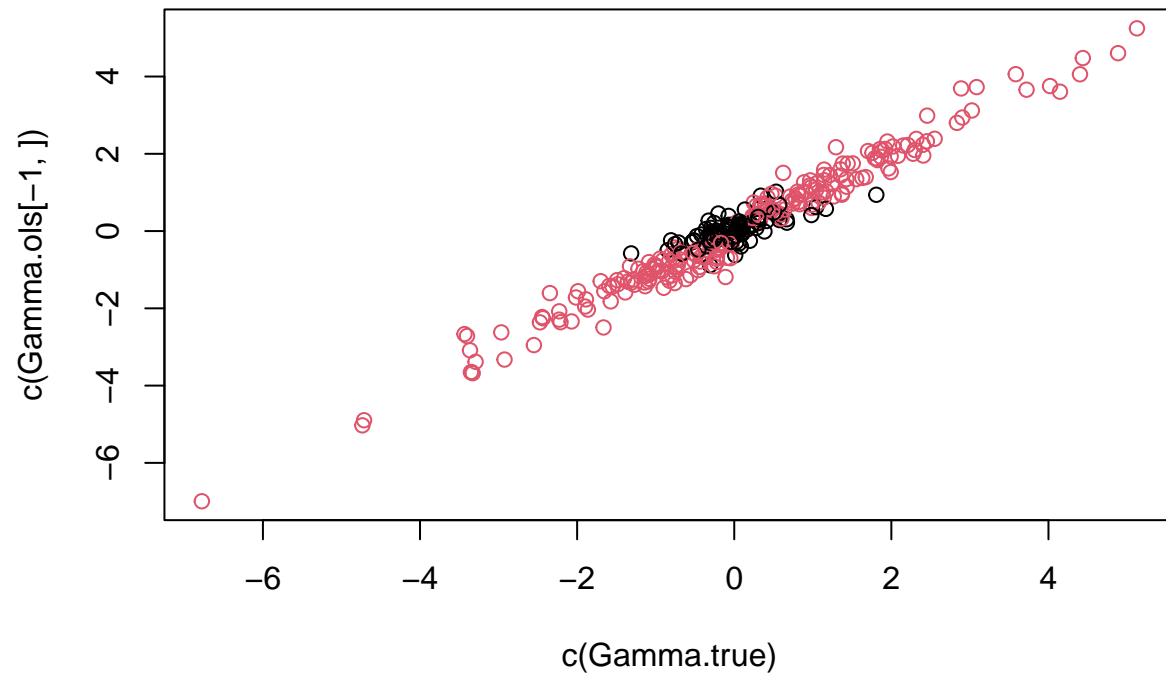
use `cbind(1,X.train)` to include overall intercept

```
ols_results <- vox.ols.reg(Y.train, cbind(1,X.train), find.signif=T)
Gamma.ols <- ols_results[[1]]
Gamma.signif.ols <- ols_results[[2]]
```

Plot estimated vs. true (OLS)

```
plot(c(Gamma.true), c(Gamma.ols[-1,]), col=factor(Gamma.signif.ols[-1,]),main="Estimated Coefficients (
```

## Estimated Coefficients (OLS)



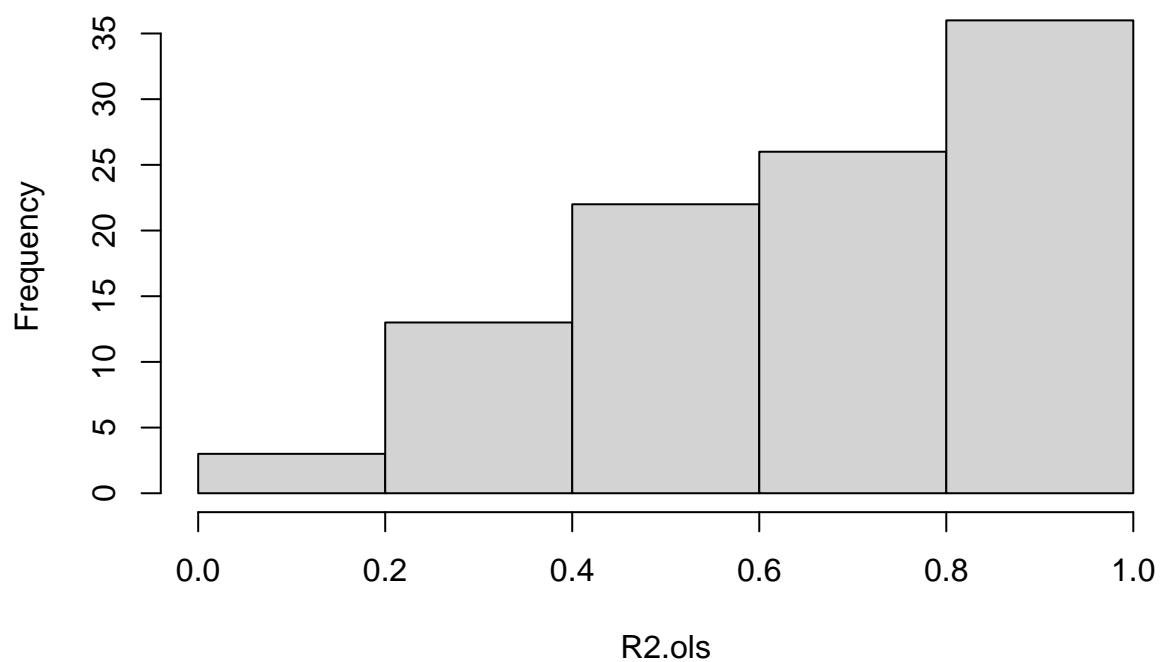
```
cor(c(Gamma.true), c(Gamma.ols[-1,]))
```

```
## [1] 0.9795621
```

Find  $R^2$  for each voxel (OLS)

```
R2.ols <- getR2(Y.train, cbind(1,X.train), ID=NA, Gamma.ols)
hist(R2.ols,5,main='Histogram of R^2 across voxels (OLS)')
```

## Histogram of $R^2$ across voxels (OLS)



```
paste0('Median  $R^2$  across voxels (OLS): ', signif(median(R2.ols),4))
```

```
## [1] "Median  $R^2$  across voxels (OLS): 0.6933"
```