BayesianImportance example

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Contents

SIMULATE DATA

```
library(BayesianImp)
library(mnormt)
set.seed(1234)

n <- 100
nclass_gamma <- 10
nclass_eta <- 20

mu <- c(1, 2)
sigma <- matrix(c(1, 0, 0, 1), 2, 2)

# Sample a standardized correlated design matrix
X <- rmnorm(n, mu, sigma)

# Add random effects
gamma <- rep(rnorm(nclass_gamma, 0, sqrt(1)), each = n/nclass_gamma)
eta <- rep(rnorm(nclass_eta, 0, sqrt(1)), each = n/nclass_eta)
epsilon = rnorm(n, mean = 0, sd = 1)

# Define some formula
Y <- 1 + 1 * X[, 1] + sqrt(2) * X[, 2] + gamma + eta + epsilon  # write epsilon as a random effect

# Collect as a dataframe
data_bayes = data.frame(cbind(Y, X = X))
data_bayes = data.frame(cbind(data_bayes, gamma = gamma))
data_bayes = data.frame(cbind(data_bayes, eta = eta))
```

USAGE

```
set.seed(1234)
model <- run_bayesian_imp(data_bayes, Y ~ V2 + V3 + (1 | gamma) + (1 |
    eta))
```

```
set.seed(1234)
samples_and_model <- run_bayesian_imp(data_bayes, Y ~ V2 + V3 + (1 |
    gamma) + (1 | eta), 5000, return_samples = TRUE)
samples = samples_and_model$samples
model_samps = samples_and_model$model
```

```
set.seed(1234)
summary(model_samps)
```

```
##
## Call:
##    c("inla.core(formula = formula, family = family, contrasts = contrasts, ", " data = data, quantil
##    offset, ", " scale = scale, weights = weights, Ntrials = Ntrials, strata = strata, ", " lp.scale
##    link.covariates, verbose = verbose, ", " lincomb = lincomb, selection = selection, control.comput
##    control.predictor = control.predictor, control.family = control.family, ", " control.inla = contr
##    control.fixed, ", " control.mode = control.mode, control.expert = control.expert, ", " control.ha
##    control.lincomb = control.lincomb, ", " control.update = control.update, control.lp.scale = contr
##    control.pardiso = control.pardiso, only.hyperparam = only.hyperparam, ", " inla.call = inla.call,
##    num.threads = num.threads, ", " blas.num.threads = blas.num.threads, keep = keep, working.directo
##    silent = silent, inla.mode = inla.mode, safe = FALSE, debug = debug, ", " .parent.frame = .parent
## Time used:
##     Pre = 4.47, Running = 0.325, Post = 0.0444, Total = 4.84
## Fixed effects:
##              mean    sd 0.025quant 0.5quant 0.975quant  mode kld
## (Intercept) 0.000 0.175     -0.350    0.000      0.350 0.000   0
## V2          0.435 0.039      0.359    0.434      0.511 0.434   0
## V3          0.579 0.043      0.495    0.579      0.663 0.579   0
##
## Random effects:
##   Name     Model
##     gamma IID model
##    eta IID model
##
## Model hyperparameters:
##                                          mean   sd 0.025quant 0.5quant 0.975quant mode
## Precision for the Gaussian observations 7.62 1.21       5.48     7.55      10.22 7.42
## Precision for gamma                     7.06 5.31       1.77     5.58      21.16 3.73
## Precision for eta                       9.85 5.70       2.70     8.60      24.39 6.34
##
## Marginal log-Likelihood:  -89.55
##  is computed
## Posterior summaries for the linear predictor and the fitted values are computed
## (Posterior marginals needs also 'control.compute=list(return.marginals.predictor=TRUE)')
```

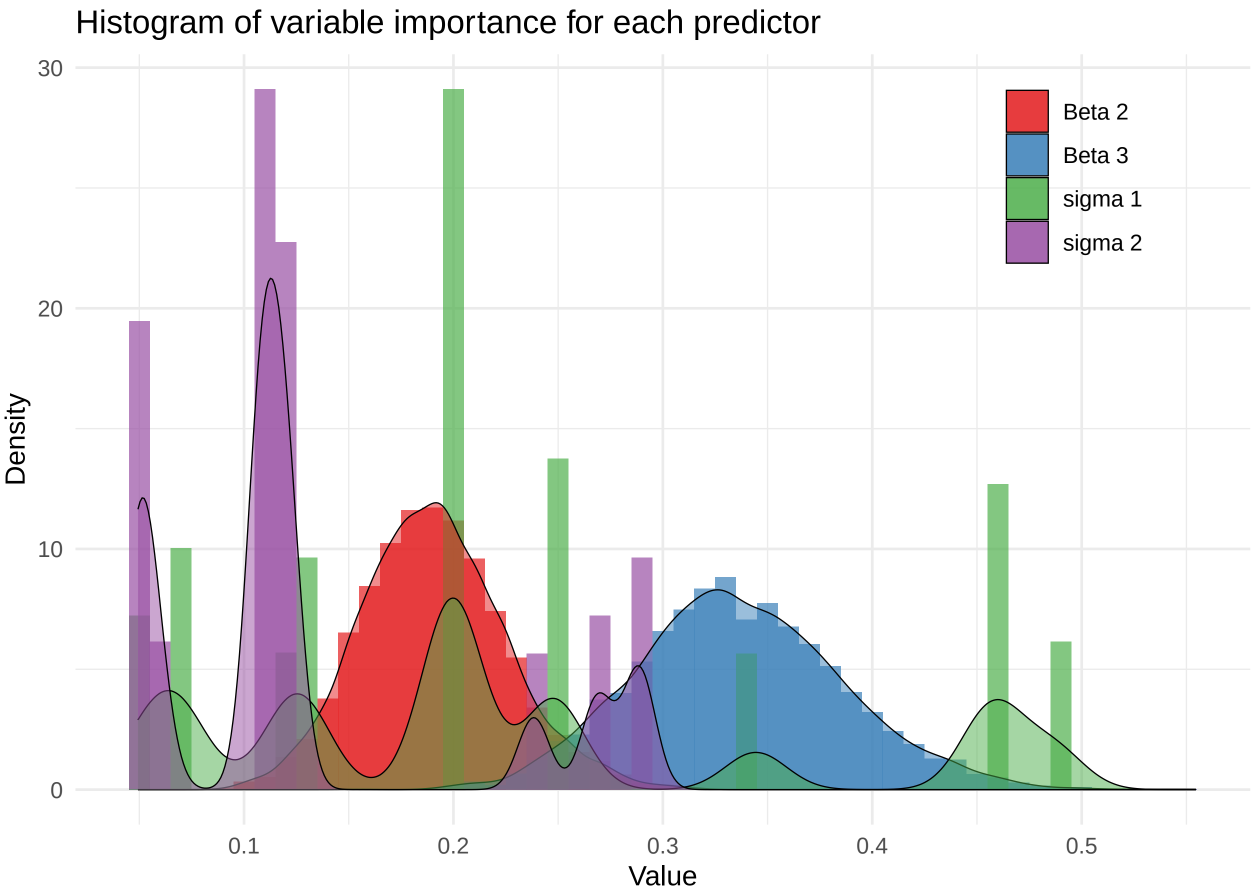
```
summary_importances(model_samps)
```

```
## Fixed Effects:
##    Predictor   Estimate Importance Std_Error
##  (Intercept) -3.239e-12  1.049e-23   0.17540
##           V2  4.345e-01  1.889e-01   0.03861
##           V3  5.788e-01  3.348e-01   0.04263
##
## Random Effects:
##          Random_Effect Precision Variance Std_Error
##  Gaussian Observations     7.624   0.1312     1.206
##                    gamma     7.056   0.1417     5.312
##                      eta     9.848   0.1015     5.704
##
##
## Total variance captured by the model: 0.7670
```

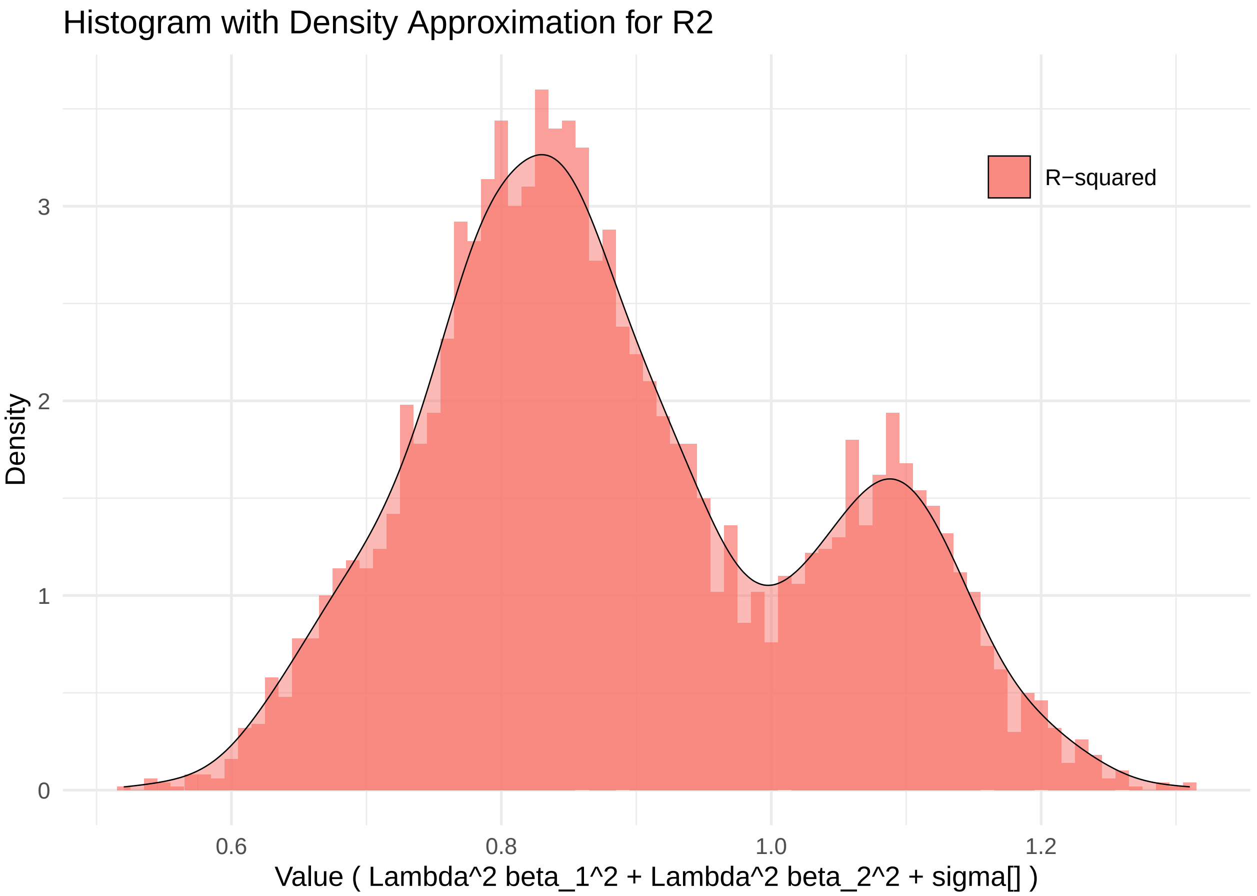
```
set.seed(1234)
samples_matrix <- extract_samples_info(samples, model_samps)
```

```
set.seed(1234)
plots <- plot_summary_info(samples_matrix)
```

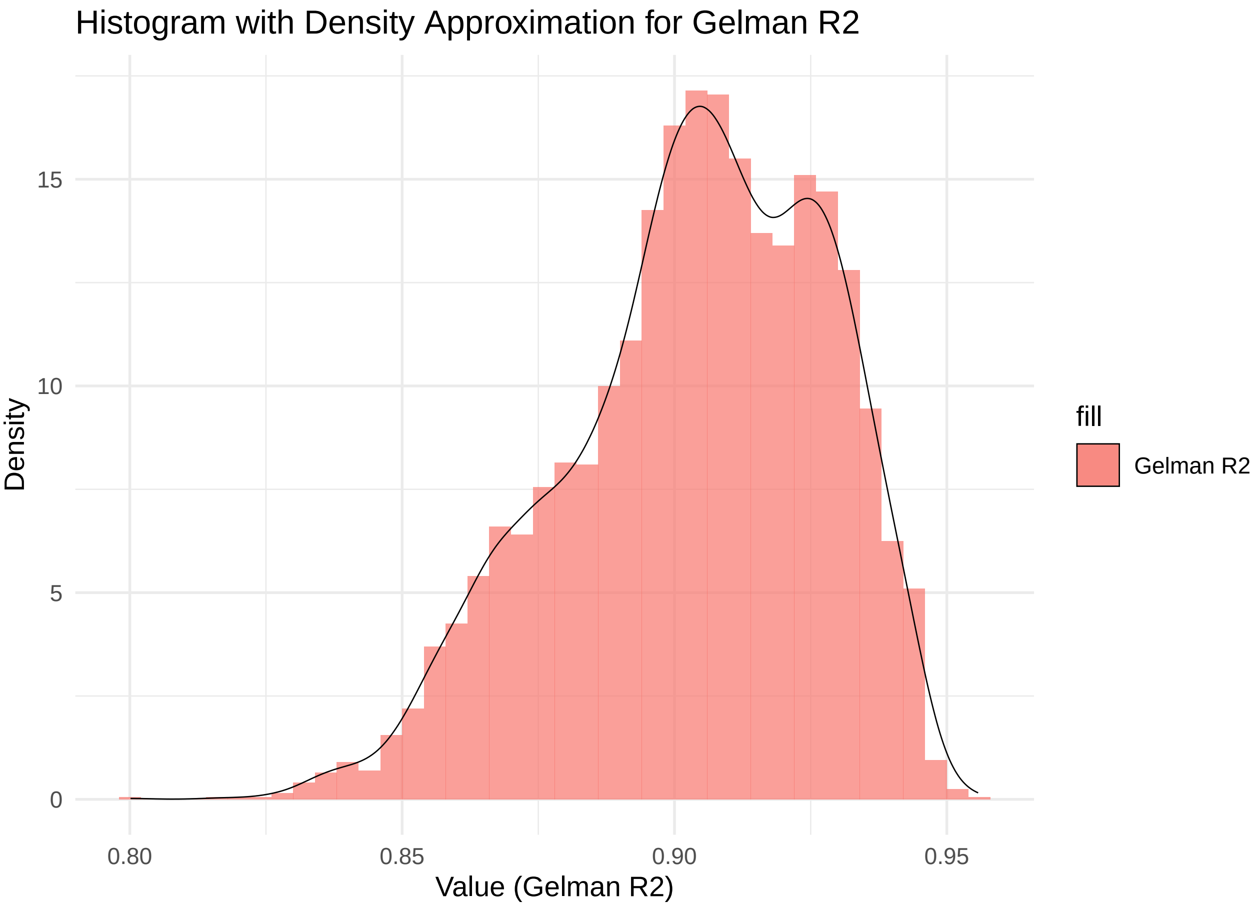
```
set.seed(1234)
plots$VariableImportancePlot
```



```
plots$RDistributionPlot
```



```
plots$GelmanR2DistributionPlot
```



```
rmarkdown::render(input = "BayesianImportanceExample.Rmd", output_format = "pdf_document")
```

How do I set up the design matrix for the random effects Z?

$$Y = X\beta + Z\gamma$$

Need help with this!

Am I right now just working with random intercepts? Is that what my gamma values truly represent?

In the run_INLA function I run INLA on the Z matrix(SVD approximation of X). Is it correct to run INLA on Z? Right now I transform right before plotting/giving the summary, keeping the beta coefficients from Z before that, since that is the output of the INLA model.

Struggling to make the priors work if they are not simply the default value. Now its just the basic version. This should probably be fixed as it is very limiting. In general I am a bit unsure if my script is efficient, as I have made it pretty quickly. Need a review of this.

In addition I need general comments on my package as there might be stuff missing that I am not aware of/could be improved.