# Package 'BayesVolcano'

March 31, 2026

**Title** Creating Volcano Plots from Bayesian Model Posteriors

**Version** 1.0.1

**URL** <https://github.com/KatjaDanielzik/BayesVolcano>

**BugReports** <https://github.com/KatjaDanielzik/BayesVolcano/issues>

**Description** Bayesian models are used to estimate effect sizes (e.g., gene expression changes, protein abundance differences, drug response effects) while accounting for uncertainty, small sample sizes, and complex experimental designs.
However, Bayesian posteriors of models with many parameters are often difficult to interpret at a glance.
One way to quickly identify important biological changes based on frequentist analysis are volcano plots (using fold-changes and p-values).
Bayesian volcano plots bring together the explicit treatment of uncertainty in Bayesian models and the familiar visualization of volcano plots.

**License** GPL (>= 3)

**Encoding** UTF-8

**RoxygenNote** 7.3.3

**Depends** R (>= 4.5)

**Imports** ggplot2, HDInterval, purrr, dplyr, magrittr, tidyr

**Suggests** brms, rstan, knitr, rmarkdown, testthat (>= 3.0.0)

**LazyData** true

**Config/testthat/edition** 3

**VignetteBuilder** knitr

**NeedsCompilation** no

**Author** Katja Danielzik [aut, cre, cph] (ORCID:
     <https://orcid.org/0009-0007-5021-6212>),
     Simo Kitanovski [aut, ctb] (ORCID:
     <https://orcid.org/0000-0003-2909-5376>),
     Daniel Hoffmann [aut] (ORCID: <https://orcid.org/0000-0003-2973-7869>)

**Maintainer** Katja Danielzik <katja.danielzik@uni-due.de>

**Repository** CRAN

**Date/Publication** 2026-03-31 09:50:15 UTC

## Contents

---

| annotation_df | *A posterior with parameter "delta_mu"* |
|---|---|

### Description

A data with two columns "parameter" and "label" corresponding to data("posterior")

### Usage

```
data("posterior")
```

### Format

"Parameter" refers to column names of posterior "Lable" are the biological entities corresponding to the parameters

### Source

**Script used to create simulated data** #BiocManager::install("MetaboDynamics") library(MetaboDynamics) data("longitudinalMetabolomics_df") library(BayesVolcano) data("posterior")

annotation_df <- as.data.frame(cbind(parameter=colnames(posterior), label=levels(as.factor(longitudinalMetabolomics_df$r group=rep(c("A","B")),value=rnorm(98,10,3)))) annotation_df$value <- as.numeric(annotation_df$value)

---

| extract_fit | *extract_fit* |
|---|---|

### Description

Wrapper function to extract parameter draws from two common Stan interfaces. This function requires the respective stan interface (rstan, brms) package to be installed.

### Usage

```
extract_fit(fit, parameter_name)
```

## Arguments

fit      A fitted Stan model object (stanfit, brmsfit).

parameter_name A character string of parameter name

## Value

A data frame with one row per MCMC draw and one column per parameter. If multiple parameters, columns are named after the parameter.

## Examples

```
# Not run:
# fit <- brms::brm(count ~ zAge + zBase * Trt + (1|patient),
#               data = brms::epilepsy[1:30,], family = poisson())

# posterior <- extract_stan_fit(fit, "b_Intercept")
# End(Not run)
```

---

plot_volcano     *Plot Bayesian Volcano plot*

---

## Description

Plot Bayesian Volcano plot

## Usage

```
plot_volcano(result, CrI = FALSE, CrI_width = FALSE, color = NULL)
```

## Arguments

result    from prepare_volcano_input() (a data frame).

CrI      Logical. Whether to display the CrI Interval of the parameter

CrI_width   Logical. Whether to display the CrI width as point size.

color     Column in 'result$result. Can be numerical or character.

## Value

a ggplot2 object

## Examples

```
data("posterior")
head(posterior)
data("annotation_df")
head(annotation_df)

result <- prepare_volcano_input(
  posterior = posterior,
  annotation = annotation_df,
)
plot_volcano(result,
  color = "group",
  CrI = TRUE,
  CrI_width = TRUE
)
```

---

posterior                    *A posterior with parameter "delta_mu"*

---

### Description

A data frame with 98 columns (each indicating posterior samples of the paramter "delta_mu" of one biological entity like e.g. a metabolite) and 1000 rows (the number of total samples (chains*iterations)) of the Bayesian model.

### Usage

```
data("posterior")
```

### Format

A data frame with 98 columns (each indicating posterior samples of the paramter "delta_mu" of one biological entity like e.g. a metabolite) and 1000 rows (the number of total samples (chains*iterations)) of the Bayesian model.

### Source

**Script used to create simulated data** #BiocManager::install("MetaboDynamics") library(MetaboDynamics) data("longitudinalMetabolomics_df") fit_dynamics_model(data=longitudinalMetabolomics_df) posterior <- as.data.frame(rstan::extract(fit,pars="euclidean_distance"))

library(stringr) cols <- colnames(posterior)[str_detect(pattern = ".1.2",string=colnames(posterior))] posterior <- posterior[,cols] posterior <- posterior[,-c(1:10,109:118)]

prepare_volcano_input    *Prepare volcano input*

---

### Description

This function has as input posterior draws, calculates pi-values and credible intervals (CrI), and annotates them with biological information (e.g., cell line, time point) based on parameter names and a user-provided annotation data frame. Returns a data frame that is ready for plotting.

### Usage

```
prepare_volcano_input(posterior, annotation, null.effect = 0, CrI_level = 0.95)
```

### Arguments

posterior       A data frame of posterior draws (one row per draw) [extract_fit()](#).

annotation      A data frame with at least one column:

- `parameter`: the parameter name (e.g., `doubling.1`, `logOR.treatment`)
- `label`: the biological label (e.g., `cell.line`, `time.point`)
- Optional: other columns (e.g., `group`, `condition`) for future coloring

null.effect     Central parameter value corresponding to no effect (default t=0).

CrI_level       a scalar between 0 and 1 specifying the mass within the credible interval (default=0.95, i.e. 95% credible interval (CrI)).

### Details

Only returns pi-values and credible intervals for parameters that are **in posterior and annotation**. For formula see README or Vignette

### Value

A list with:

- `result`: A data frame with columns:
    - `parameter`: original parameter name
    - `pi.value`: calculated pi.value
    - `null.effect`: set null effect by user
    - `parameter.median`: median posterior parameter value
    - `parameter.low`: lower boundary of CrI of parameter value
    - `paramter.high`: upper boundary of CrI of parameter value
    - `CrI.width`: the absolute distance between parameter.low and parameter.high
    - `CrI.level`: CrI_level set by user
    - `label`: biological label (e.g., `cell.line`)
    - Other columns from annotation (e.g., `group`, `condition`)

**See Also**

[extract_fit()](extract_fit())

**Examples**

```
# Example: Simulate posterior and annotation
posterior <- data.frame(
  doubling.1 = rnorm(1000),
  doubling.2 = rnorm(1000)
)

annotation <- data.frame(
  parameter = c("doubling.1", "doubling.2"),
  label = c("cell.line.A", "cell.line.B"),
  group = c("group1", "group1")
)

result <- prepare_volcano_input(
  posterior = posterior,
  annotation = annotation,
)

head(result$result)
```

# Index