Package: BTIME (via r-universe)

May 26, 2026

Title Bayesian Hierarchical Models for Single-Cell Protein Data

Version 1.0.1

Description Bayesian Hierarchical beta-binomial models for modeling cell population to predictors/exposures. This package utilizes 'runjags' to run Gibbs sampling, parallelizing the chains. Options for different covariances/relationship structures between parameters of interest.

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Encoding UTF-8

RoxygenNote 7.3.2

Imports coda, runjags, VGAM, matlib

Depends rjags

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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Repository https://cran.r-universe.dev

Date/Publication 2026-02-24 22:30:08 UTC

RemoteUrl https://github.com/cran/BTIME

RemoteRef HEAD

RemoteSha f4471fa6f67511de53a6677f4bb72b6f6b0dd038

Contents

`BICAM` *Bayesian Immune Cell Abundance Model (BICAM)*

Description

Bayesian Immune Cell Abundance Model (BICAM)

Usage

```
BICAM(
  dat,
  M,
  adapt,
  burn,
  it,
  thin = 1,
  ran_eff = 1,
  chains = 4,
  cores = 4,
  v0_mu_logit = 0.01,
  ncov = 1,
  model = "Unstr",
  dis = NULL,
  tree = NULL,
  treelevels = NULL
)
```

Arguments

`dat`	data frame with dataset (proper setup displayed in tutorial)
`M`	number of cell types/parameters of interest
`adapt`	number of adaptation iterations (for compiling model)
`burn`	number of burn-in iterations
`it`	number of sampling iterations (after burn-in)
`thin`	number of thinning samples
`ran_eff`	indicate whether to use random subject effect (repeated measurements)
`chains`	number of chains to run
`cores`	number of cores
`v0_mu_logit`	anticipated proportion of cell types/parameters
`ncov`	number of covariates input into the model
`model`	covariance model selection
`dis`	distance matrix for Exp. Decay model
`tree`	tree-structured covariance matrix for Tree and Scaled Tree models
`treelevels`	list of matrices for multilevel, tree-structured covariance matrix for TreeLevels model

Value

A list of inputs and results

Index