

# Package ‘BTIME’

February 24, 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.

**License** MIT + file LICENSE

**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** CRAN

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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

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