Package ‘banocc’

May 24, 2024

Type Package

Title Bayesian ANalysis Of Compositional Covariance

Version 1.28.0

Date 2022-04-20

Maintainer George Weingart <george.weingart@gmail.com>, Curtis Huttenhower <chuttenh@hsph.harvard.edu>

Description BAnOCC is a package designed for compositional data, where each sample sums to one. It infers the approximate covariance of the unconstrained data using a Bayesian model coded with `rstan`. It provides as output the `stanfit` object as well as posterior median and credible interval estimates for each correlation element.

License MIT + file LICENSE

Depends R (>= 3.5.1), rstan (>= 2.17.4)

Imports coda (>= 0.18.1), mvtnorm, stringr

Suggests knitr, rmarkdown, methods, testthat, BiocStyle

VignetteBuilder knitr

RoxygenNote 5.0.1

biocViews ImmunoOncology, Metagenomics, Software, Bayesian

git_url https://git.bioconductor.org/packages/banocc

git_branch RELEASE_3_19

git_last_commit 12c9e57

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-05-24

Author Emma Schwager [aut, cre], Curtis Huttenhower [aut]
Contents

banocc .................................................. 2
banocc_model ......................................... 2
compositions_hard_null .......................... 3
compositions_neg_spike .......................... 4
compositions_null ................................. 4
compositions_pos_spike .......................... 5
counts_hard_null ................................. 5
counts_neg_spike ................................. 6
counts_null ......................................... 6
counts_pos_spike ................................. 7
get_banocc_output ............................... 7
run_banocc .......................................... 8

Index 11

banocc

banocc: A package for Bayesian ANalysis of Compositional Correlation

Description

BAnOCC is a package for inferring correlations between features in compositional data, where each sample sums to one. It provides one object, banocc_model and one function, run_banocc

banocc objects

banocc_model has the stan model code to be compiled using rstan::stan.

banocc functions

run_banocc takes a compiled model, and returns the 'stanfit' object resulting from a call to rstan::sampling
get_banocc_output takes a 'stanfit' object or the output of run_banocc and returns a list with the posterior median and credible interval estimates

banocc_model

The stan model used in the Bayesian fit

Description

This is the literal model used for fitting in Stan

Usage

banocc_model
compositions_hard_null

Format

An object of class character of length 1.

Value

The BAnOCC model as a string to be compiled with rstan::stan_model.

Examples

data(compositions_null)
## Not run:
compiled_banocc_model <- rstan::stan_model(model_code = banocc_model)
## End(Not run)

compositions_hard_null

Simulated compositional data with no feature correlations

Description

These are the normalized samples corresponding to counts_hard_null. They should have a very different correlation structure from the counts. In particular, there should be one strong, positive association which is not present in the count correlation structure.

Usage

compositions_hard_null

Format

A data frame with 1000 rows (compositional samples) and 9 variables (the features).

Value

A data frame with 1000 compositional samples from 9 features, generated by dividing each row of counts_hard_null by its sum.
compositions_neg_spike

Simulated compositional data with a negative count correlation

Description
These are the normalized data corresponding to counts_neg_spike. The count data have one negative feature correlation, but the compositional correlation structure should be different.

Usage
compositions_neg_spike

Format
A data frame with 1000 rows (compositional samples) and 9 variables (the features)

Value
A data frame with 1000 compositional samples from 9 features, generated by dividing each row of counts_neg_spike by its sum.

compositions_null
Simulated compositional data with no feature correlations

Description
These are the normalized samples corresponding to counts_null. They should have a similar (but not identical) correlation structure.

Usage
compositions_null

Format
A data frame with 1000 rows (compositional samples) and 9 variables (the features)

Value
A data frame with 1000 compositional samples from 9 features, generated by dividing each row of counts_null by its sum.
\textit{compositions\_pos\_spike}

Simulated compositional data with a positive count correlation

\underline{Description}

These are the normalized data corresponding to counts\_pos\_spike. The count data have one positive feature correlation, but the compositional correlation structure should be different.

\underline{Usage}

compositions\_pos\_spike

\underline{Format}

A data frame with 1000 rows (compositional samples) and 9 variables (the features)

\underline{Value}

A data frame with 1000 compositional samples from 9 features, generated by dividing each row of counts\_pos\_spike by its sum.

\textit{counts\_hard\_null}

Simulated count data with no feature correlations

\underline{Description}

Nine features are draw independently from very different log-normal distributions whose means and variances are positively correlated. This means that the compositions generated from this dataset (see compositions\_hard\_null) should be have a correlation structure very different from that of these counts.

\underline{Usage}

counts\_hard\_null

\underline{Format}

A data frame with 1000 rows (samples) and 9 variables (the features)

\underline{Value}

A data frame with 1000 unconstrained samples from 9 features.
counts_neg_spike  
*Simulated count data with one negative feature correlation*

**Description**

Nine features are drawn from a log-normal distribution with one negative correlation. The resulting compositions are in compositions_neg_spike.

**Usage**

counts_neg_spike

**Format**

A data frame with 1000 rows (samples) and 9 variables (the features)

**Value**

A data frame with 1000 unconstrained samples from 9 features.

_____________

counts_null  
*Simulated count data with no feature correlations*

**Description**

Nine features are drawn independently from similar log-normal distributions to generate null count data. Because the feature distributions are very similar, the compositions generated from this dataset (see compositions_null), should have a correlation structure similar to that of the counts.

**Usage**

counts_null

**Format**

A data frame with 1000 rows (the samples) and 9 variables (the features)

**Value**

A data frame with 1000 unconstrained samples from 9 features.
counts_pos_spike

Simulated count data with one positive feature correlation

**Description**

Nine features are drawn from a log-normal distribution with one positive correlation. The resulting compositions are in compositions_pos_spike.

**Usage**

`counts_pos_spike`

**Format**

A data frame with 1000 rows (samples) and 9 variables (the features)

**Value**

A data frame with 1000 unconstrained samples from 9 features.

get_banocc_output

Takes a model fit from BAnOCC, evaluates convergence and generates appropriate convergence metrics and inference

**Description**

Takes a model fit from BAnOCC, evaluates convergence and generates appropriate convergence metrics and inference

**Usage**

`get_banocc_output(banoccfit, conf_alpha = 0.05, get_min_width = FALSE, calc_snc = TRUE, eval_convergence = TRUE, verbose = FALSE, num_level = 0)`

**Arguments**

- `banoccfit` Either a stanfit object (the Fit element returned by run_banocc), or the list returned by a call to run_banocc.
- `conf_alpha` The percentage of the posterior density outside the credible interval. That is, a 1-conf_alpha * 100% credible interval will be returned.
- `get_min_width` A boolean value: should the minimum CI width that includes zero be calculated?
- `calc_snc` Boolean: should the scaled neighborhood criterion be calculated?
eval_convergence

Boolean: if ‘TRUE’, convergence will be evaluated using the Rhat statistic, and the fit output (estimates, credible intervals, etc.) will be missing if this statistic does not indicate convergence.

verbose

Print informative statements as the function executes?

num_level

The number of indentations to add to the output when verbose = TRUE.

Value

Returns a named list with the following elements:

CI

The 1-conf_alpha * 100% credible intervals

Estimates.median

The correlation estimates, which are the marginal posterior medians

Min.width

Only present if the get_min_width argument is TRUE. The minimum CI width that includes zero for each correlation.

SNC

Only present if the calc_snc argument is TRUE. The scaled neighborhood criterion for each correlation.

Fit

The stanfit object returned by the call to run_banocc.

Data

Only present if the banoccfit argument is specified as the output of a call to run_banocc. It will be missing if banoccfit is specified as a stanfit object.

See Also

vignette("banocc-vignette") for more examples.

Examples

data(compositions_null)

## Not run:
compiled_banocc_model <- rstan::stan_model(model_code=banocc_model)
b_fit <- run_banocc(C=compositions_null,
                    compiled_banocc_model=compiled_banocc_model)
b_output <- get_banocc_output(banoccfit=b_fit)

## End(Not run)

---

**run_banocc**

Runs BAnOCC to fit the model and generate appropriate convergence metrics and inference.

**Description**

Runs BAnOCC to fit the model and generate appropriate convergence metrics and inference.
Usage

```r
run_banocc(compiled_banocc_model, C, n = rep(0, ncol(C)), L = 10 *
    diag(ncol(C)), a = 0.5, b = 0.01, cores = getOption("mc.cores", 1L),
    chains = 4, iter = 50, warmup = floor(iter/2), thin = 1,
    init = NULL, control = NULL, verbose = FALSE, num_level = 0)
```

Arguments

- **compiled_banocc_model**
  - The compiled stan model (as with `stan_model(model_code = banocc_model)`).
- **C**
  - The dataset as a data frame or matrix. This should be N by P with N samples as the rows and P features as the columns.
- **n**
  - The prior mean for m; vectors of length less than P (the number of features/columns of C) will be recycled.
- **L**
  - The prior variance-covariance for m (must be positive-definite with dimension PxP where P=number of features/columns in C), or a vector of length p of variances for m. If a vector of length less than P is given, it will be recycled.
- **a**
  - The shape parameter of a gamma distribution (the prior on the shrinkage parameter lambda)
- **b**
  - The rate parameter of a gamma distribution (the prior on the shrinkage parameter lambda)
- **cores**
  - Number of cores to use when executing the chains in parallel, which defaults to 1 but we recommend setting the `mc.cores` option to be as many processors as the hardware and RAM allow (up to the number of chains).
- **chains**
  - A positive integer specifying the number of Markov chains. The default is 4.
- **iter**
  - A positive integer specifying the number of iterations for each chain (including warmup). The default is 2000.
- **warmup**
  - A positive integer specifying the number of warmup (aka burnin) iterations per chain. If step-size adaptation is on (which it is by default), this also controls the number of iterations for which adaptation is run (and hence these warmup samples should not be used for inference). The number of warmup iterations should not be larger than `iter` and the default is `iter/2`.
- **thin**
  - A positive integer specifying the period for saving samples. The default is 1, which is usually the recommended value.
- **init**
  - The initial values as a list (see `sampling` in the `rstan` package). Default value is `NULL`, which means that initial values are sampled from the priors for parameters m and lambda while 0 is set to the identity matrix.
- **control**
  - A named list of parameters to control the sampler’s behavior. See the details in the documentation for the `control` argument in `stan`.
- **verbose**
  - Print informative statements as the function executes?
- **num_level**
  - The number of indentations to add to the output when `verbose = TRUE`. 
Value

Returns a named list with the following elements:

**Data**  The data formatted as a named list that includes the input data (\(C\)) and the prior parameters (\(n, L, a, b\))

**Fit**  The stanfit object returned by the call to `sampling`

See Also

vignette("banocc-vignette") for more examples.

Examples

data(compositions_null)

```r
## Not run:
compiled_banocc_model <- rstan::stan_model(model_code=banocc_model)
b_stanfit <- run_banocc(C=compositions_null,
                         compiled_banocc_model=compiled_banocc_model)

## End(Not run)
```
Index

* datasets
  banocc_model, 2
  compositions_hard_null, 3
  compositions_neg_spike, 4
  compositions_null, 4
  compositions_pos_spike, 5
  counts_hard_null, 5
  counts_neg_spike, 6
  counts_null, 6
  counts_pos_spike, 7

banocc, 2
banocc-package (banocc), 2
banocc_model, 2

compositions_hard_null, 3
compositions_neg_spike, 4
compositions_null, 4
compositions_pos_spike, 5
counts_hard_null, 5
counts_neg_spike, 6
counts_null, 6
counts_pos_spike, 7

get_banocc_output, 7

run_banocc, 8

sampling, 9, 10
stan, 9