# Package ‘banocc’

April 25, 2017

**Type** Package  
**Title** Bayesian ANalysis Of Compositional Covariance  
**Version** 1.0.0  
**Date** 2015-04-14  
**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 (&gt;= 3.4), rstan (&gt;= 2.10.1)  
**Imports** coda (&gt;= 0.18.1), mvtnorm, stringr  
**Suggests** knitr, rmarkdown, methods, testthat  
**VignetteBuilder** knitr  
**RoxygenNote** 5.0.1  
**biocViews** Metagenomics, Software, Bayesian  
**NeedsCompilation** no  
**Author** Emma Schwager [aut, cre]  
**Maintainer** Emma Schwager &lt;emh146@mail.harvard.edu&gt;  

### R topics documented:

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

**Index** 10
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

Description

This is the literal model used for fitting in Stan

Usage

banocc_model

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.

compositions_pos_spike  |  Simulated compositional data with a positive count correlation

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.

Usage

compositions_pos_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_pos_spike by its sum.
counts_hard_null  
Simulated count data with no feature correlations

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.

Usage
counts_hard_null

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_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**

```r
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**

```r
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

```r
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.
run_banocc

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 \texttt{iter} and the default is \texttt{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 \texttt{sampling} in the \texttt{rstan} package). Default value is \texttt{NULL}, which means that initial values are sampled from the priors for parameters \(m\) and \(\lambda\) while \(O\) 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 \texttt{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 \texttt{stanfit} object returned by the call to \texttt{sampling}

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_stanfit <- run_banocc(C=compositions_null,
compilation_banocc_model=compiled_banocc_model)

## End(Not run)
Index

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

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

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

get_banocc_output, 7

run_banocc, 8

sampling, 9
stan, 9