Package 'banocc'

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Type Package

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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.

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`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

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`banocc_model` *The stan model used in the Bayesian fit*

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 strucutre 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

```
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

```
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 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 `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)
## 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)
```

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