Package 'PLNmodels'

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Title Poisson Lognormal Models

Version 1.3.1

Description The Poisson-lognormal model and variants (Chiquet, Mariadassou and Robin, 2021 <doi:10.3389/fevo.2021.588292>) can be used for a variety of multivariate problems when count data are at play, including principal component analysis for count data, discriminant analysis, model-based clustering and network inference. Implements variational algorithms to fit such models accompanied with a set of functions for visualization and diagnostic.

URL https://pln-team.github.io/PLNmodels/

BugReports https://github.com/pln-team/PLNmodels/issues

License GPL (>= 3)

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'PLNnetworkfit-S3methods.R' 'PLNnetworkfit-class.R'
'RcppExports.R' 'ZIPLNfit-class.R' 'ZIPLN.R'
'ZIPLNfit-S3methods.R' 'ZIPLNnetwork.R' 'barents.R'
'import_utils.R' 'microcosm.R' 'mollusk.R' 'oaks.R'
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`AIC.PLNfit` *Akaike Information Criterion for a fitted PLN model*

Description

Computes the variational AIC as `loglik - nb_param` (larger is better). This follows the maximization convention used throughout PLNmodels.

Usage

```
## S3 method for class 'PLNfit'
AIC(object, ..., k = 2)
```

Arguments

`object`	an R6 object with class `PLNfit`
`...`	additional parameters for S3 compatibility. Not used
`k`	not used, present for S3 compatibility.

Value

A scalar: the variational AIC (larger is better).

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
model <- PLN(Abundance ~ 1, data = trichoptera)
AIC(model)
```

AIC.ZIPLNfit *Akaike Information Criterion for a fitted ZIPLN model*

Description

Computes the variational AIC as `loglik - nb_param` (larger is better). This follows the maximization convention used throughout PLNmodels.

Usage

```
## S3 method for class 'ZIPLNfit'
AIC(object, ..., k = 2)
```

Arguments

`object`	an R6 object with class `ZIPLNfit`
`...`	additional parameters for S3 compatibility. Not used
`k`	not used, present for S3 compatibility.

Value

A scalar: the variational AIC (larger is better).

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
model <- ZIPLN(Abundance ~ 1, data = trichoptera)
AIC(model)
```

barents *Barents fish data set*

Description

This data set gives the abundance of 30 fish species observed in 89 sites in the Barents sea. For each site, 4 additional covariates are known. Subsample of the original datasets studied by Fossheim et al, 2006.

Usage

```
barents
```

Format

A data frame with 6 variables:

- Abundance: A 30 fish species by 89 sites count matrix
- Offset: A 30 fish species by 89 samples offset matrix, measuring the sampling effort in each site
- 4 covariates for latitude, longitude, depth (in meters), temperature (in Celsius degrees).

Source

Data from M. Fossheim and coauthors.

References

Fossheim, Maria, Einar M. Nilssen, and Michaela Aschan. "Fish assemblages in the Barents Sea." Marine Biology Research 2.4 (2006). doi:10.1080/17451000600815698

Examples

```
data(barents)
```

BIC.PLNfit *Bayesian Information Criterion for a fitted PLN model*

Description

Computes the variational BIC as `loglik - 0.5 * log(n) * nb_param` (larger is better). This follows the maximization convention used throughout PLNmodels.

Usage

```
## S3 method for class 'PLNfit'
BIC(object, ...)
```

Arguments

`object`	an R6 object with class `PLNfit`
`...`	additional parameters for S3 compatibility. Not used

Value

A scalar: the variational BIC (larger is better).

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
model <- PLN(Abundance ~ 1, data = trichoptera)
BIC(model)
```

BIC.ZIPLNfit *Bayesian Information Criterion for a fitted ZIPLN model*

Description

Computes the variational BIC as `loglik - 0.5 * log(n) * nb_param` (larger is better). This follows the maximization convention used throughout PLNmodels.

Usage

```
## S3 method for class 'ZIPLNfit'
BIC(object, ...)
```

Arguments

`object`	an R6 object with class `ZIPLNfit`
`...`	additional parameters for S3 compatibility. Not used

Value

A scalar: the variational BIC (larger is better).

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
model <- ZIPLN(Abundance ~ 1, data = trichoptera)
BIC(model)
```

coef.PLNfit *Extract model coefficients*

Description

Extracts model coefficients from objects returned by `PLN()` and its variants

Usage

```
## S3 method for class 'PLNfit'
coef(object, type = c("main", "covariance"), ...)
```

Arguments

`object`	an R6 object with class `PLNfit`
`type`	type of parameter that should be extracted. Either "main" (default) for B or "covariance" for Σ
`...`	additional parameters for S3 compatibility. Not used

Value

A matrix of coefficients extracted from the PLNfit model.

See Also

`sigma.PLNfit()`, `vcov.PLNfit()`, `standard_error.PLNfit()`

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLN <- PLN(Abundance ~ 1 + offset(log(Offset)), data = trichoptera)
coef(myPLN) ## B
coef(myPLN, type = "covariance") ## Sigma
```

`coef.PLNLDAfit` *Extracts model coefficients from objects returned by* `PLNLDA()`

Description

The method for objects returned by `PLNLDA()` only returns coefficients associated to the Θ part of the model (see the PLNLDA vignette for mathematical details).

Usage

```
## S3 method for class 'PLNLDAfit'
coef(object, ...)
```

Arguments

`object`	an R6 object with class PLNLDAfit
`...`	additional parameters for S3 compatibility. Not used

Value

Either NULL or a matrix of coefficients extracted from the PLNLDAfit model.

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLNLDA <- PLNLDA(Abundance ~ Wind, grouping = Group, data = trichoptera)
coef(myPLNLDA)
```

`coef.PLNmixturefit` *Extract model coefficients*

Description

Extracts model coefficients from objects returned by `PLN()` and its variants

Usage

```
## S3 method for class 'PLNmixturefit'
coef(object, type = c("main", "means", "covariance", "mixture"), ...)
```

Arguments

`object`	an R6 object with class `PLNmixturefit`
`type`	type of parameter that should be extracted. Either "main" (default) for Θ, "means" for μ, "mixture" for π or "covariance" for Σ
`...`	additional parameters for S3 compatibility. Not used

Value

A matrix of coefficients extracted from the PLNfit model.

See Also

`sigma.PLNmixturefit()`

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLN <- PLNmixture(Abundance ~ 1 + offset(log(Offset)),
       data = trichoptera, control = PLNmixture_param(smoothing = "none")) %>% getBestModel()
coef(myPLN) ## Theta - empty here
coef(myPLN, type = "mixture") ## pi
coef(myPLN, type = "means") ## mu
coef(myPLN, type = "covariance") ## Sigma
```

---

coef.ZIPLNfit *Extract model coefficients*

Description

Extracts model coefficients from objects returned by ZIPLN() and its variants

Usage

```
## S3 method for class 'ZIPLNfit'
coef(object, type = c("count", "zero", "precision", "covariance"), ...)
```

Arguments

object	an R6 object with class ZIPLNfit
type	type of parameter that should be extracted. Either "count" (default) for B, "zero" for $B0$, "precision" for Ω, "covariance" for Σ
...	additional parameters for S3 compatibility. Not used

Value

A matrix of coefficients extracted from the ZIPLNfit model.

See Also

sigma.ZIPLNfit()

Examples

```
data(scRNA)
# data subsample: only 100 random cell and the 50 most varying transcript
subset <- sample.int(nrow(scRNA), 100)
myPLN  <- ZIPLN(counts[, 1:50] ~ 1 + offset(log(total_counts)), subset = subset, data = scRNA)
```

coefficient_path *Extract the regularization path of a PLNnetwork fit*

Description

Extract the regularization path of a PLNnetwork fit

Usage

```
coefficient_path(Robject, precision = TRUE, corr = TRUE)
```

Arguments

Robject	an object with class Networkfamily, i.e. an output from PLNnetwork()
precision	a logical, should the coefficients of the precision matrix Omega or the covariance matrix Sigma be sent back. Default is TRUE.
corr	a logical, should the correlation (partial in case precision = TRUE) be sent back. Default is TRUE.

Value

Sends back a tibble/data.frame.

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
fits <- PLNnetwork(Abundance ~ 1, data = trichoptera)
head(coefficient_path(fits))
```

compute_offset *Compute offsets from a count data using one of several normalization schemes*

Description

Computes offsets from the count table using one of several normalization schemes (TSS, CSS, RLE, GMPR, Wrench, TMM, etc) described in the literature.

Usage

```
compute_offset(
  counts,
  offset = c("TSS", "GMPR", "RLE", "CSS", "Wrench", "TMM", "none"),
  scale = c("none", "count"),
  ...
)
```

Arguments

counts	Required. An abundance count table, preferably with dimensions names and species as columns.
offset	Optional. Normalization scheme used to compute scaling factors used as offset during PLN inference. Available schemes are "TSS" (Total Sum Scaling, default), "CSS" (Cumulative Sum Scaling, used in metagenomeSeq), "RLE" (Relative Log Expression, used in DESeq2), "GMPR" (Geometric Mean of Pairwise Ratio, introduced in Chen et al., 2018), Wrench (introduced in Kumar et al., 2018) or "none". Alternatively the user can supply its own vector or matrix of offsets (see note for specification of the user-supplied offsets).
scale	Either "none" (default) or "count". Should the offset be normalized to be on the same scale as the counts ?
...	Additional parameters passed on to specific methods (for now CSS and RLE)

Details

RLE has additional pseudocounts and type arguments to add pseudocounts to the observed counts (defaults to 0L) and to compute offsets using only positive counts (if type == "poscounts"). This mimics the behavior of DESeq2::DESeq() when using sfType == "poscounts". CSS has an additional reference argument to choose the location function used to compute the reference quantiles (defaults to median as in the Nature publication but can be set to mean to reproduce behavior of functions cumNormStat* from metagenomeSeq). Wrench has two additional parameters: groups to specify sample groups and type to either reproduce exactly the default Wrench::wrench() behavior (type = "wrench", default) or to use simpler heuristics (type = "simple"). Note that (i) CSS normalization fails when the median absolute deviation around quantiles does not become instable for high quantiles (limited count variations both within and across samples) and/or one sample has less than two positive counts, (ii) RLE fails when there are no common species across all samples (unless type == "poscounts" has been specified) and (iii) GMPR fails if a sample does not share any species with all other samples. TMM code between two libraries is simplified and adapted from M. Robinson (edgeR:::.calcFactorTMM). The final output is however different from the one produced by edgeR:::.calcFactorTMM as they are intended to be used as such in the model (whereas they need to be multiplied by sequencing depths in edgeR)

Value

If offset = "none", NULL else a vector of length nrow(counts) with one offset per sample.

References

Chen, L., Reeve, J., Zhang, L., Huang, S., Wang, X. and Chen, J. (2018) GMPR: A robust normalization method for zero-inflated count data with application to microbiome sequencing data. PeerJ, 6, e4600 doi:10.7717/peerj.4600

Paulson, J. N., Colin Stine, O., Bravo, H. C. and Pop, M. (2013) Differential abundance analysis for microbial marker-gene surveys. Nature Methods, 10, 1200-1202 doi:10.1038/nmeth.2658

Anders, S. and Huber, W. (2010) Differential expression analysis for sequence count data. Genome Biology, 11, R106 doi:10.1186/gb20101110r106

Kumar, M., Slud, E., Okrah, K. et al. (2018) Analysis and correction of compositional bias in sparse sequencing count data. BMC Genomics 19, 799 doi:10.1186/s1286401851605

Robinson, M.D., Oshlack, A. (2010) A scaling normalization method for differential expression analysis of RNA-seq data. Genome Biol 11, R25 doi:10.1186/gb2010113r25

Examples

```
data(trichoptera)
counts <- trichoptera$Abundance
compute_offset(counts)
## Other normalization schemes
compute_offset(counts, offset = "RLE", pseudocounts = 1)
compute_offset(counts, offset = "Wrench", groups = trichoptera$Covariate$Group)
compute_offset(counts, offset = "GMPR")
compute_offset(counts, offset = "TMM")
## User supplied offsets
my_offset <- setNames(rep(1, nrow(counts)), rownames(counts))
compute_offset(counts, offset = my_offset)
```

---

compute_PLN_starting_point

Helper function for PLN initialization.

Description

Barebone function to compute starting points for B, M and S2 when fitting a PLN. Mostly intended for internal use.

Usage

```
compute_PLN_starting_point(Y, X, O, w, method = c("LM", "GLM"))
```

Arguments

`Y`	Response count matrix
`X`	Covariate matrix. Note that initialization will fail if the model matrix is singular.
`O`	Offset matrix (in log-scale)
`w`	Weight vector (defaults to 1)
`method`	character: strategy used to initialize B. Either `"LM"` (default, fast weighted log-linear regression) or `"GLM"` (p independent Poisson GLMs, more accurate for complex or unbalanced designs but slower).

Details

- **B**: estimated by weighted LM (`method = "LM"`, default) or p independent Poisson GLMs (`method = "GLM"`). The GLM option gives better B estimates for factorial or unbalanced designs at the cost of p IRLS fits.
- **M**: initialized to `log((1 + Y) / exp(O))` (M_full in the X*B + M_res parameterization).
- **S**: initialized element-wise to `1 / sqrt(2 + Y)`, the approximate VE-step optimum at Omega = I. This adapts automatically to count levels: high S for zero counts (high uncertainty), low S for large counts.

Value

a named list of starting values for model parameter B and variational parameters M and S2 used in the iterative optimization algorithm of `PLN()`

Examples

```
## Not run:
data(barents)
Y <- barents$Abundance
X <- model.matrix(Abundance ~ Latitude + Longitude + Depth + Temperature, data = barents)
O <- log(barents$Offset)
w <- rep(1, nrow(Y))
compute_PLN_starting_point(Y, X, O, w)
compute_PLN_starting_point(Y, X, O, w, method = "GLM")

## End(Not run)
```

`compute_ZIPLN_starting_point` *Helper function for ZIPLN initialization.*

Description

Fast LM-based starting point for ZIPLN: one multivariate `lm.fit` for the PLN component and empirical zero rates / binomial GLMs for the ZI component. Replaces the previous per-species `pscl::zeroinfl` loop.

Usage

```
compute_ZIPLN_starting_point(Y, X, X0, O, w = NULL)
```

Arguments

Y	Response count matrix (n × p)
X	Design matrix for the PLN component (n × d)
X0	Design matrix for the ZI component (n × d0, empty matrix(NA,0,0) when unused)
O	Offset matrix in log-scale (n × p)
w	Weight vector of length n (defaults to uniform weights)

Value

Named list: B (d × p), M (n × p), S2 (n × p), R (n × p), B0 (d0 × p)

---

extract_probs *Extract edge selection frequency in bootstrap subsamples*

Description

Extracts edge selection frequency in networks reconstructed from bootstrap subsamples during the stars stability selection procedure, as either a matrix or a named vector. In the latter case, edge names follow igraph naming convention.

Usage

```
extract_probs(
  Robject,
  penalty = NULL,
  index = NULL,
  crit = c("StARS", "BIC", "EBIC"),
  format = c("matrix", "vector"),
  tol = 1e-05
)
```

Arguments

Robject	an object with class PLNnetworkfamily, i.e. an output from PLNnetwork()
penalty	penalty used for the bootstrap subsamples
index	Integer index of the model to be returned. Only the first value is taken into account.
crit	a character for the criterion used to performed the selection. Either "BIC", "ICL", "EBIC", "StARS", "R_squared". Default is ICL for PLNPCA, and BIC for PLNnetwork. If StARS (Stability Approach to Regularization Selection) is chosen and stability selection was not yet performed, the function will call the method stability_selection() with default argument.
format	output format. Either a matrix (default) or a named vector.
tol	tolerance for rounding error when comparing penalties.

Value

Either a matrix or named vector of edge-wise probabilities. In the latter case, edge names follow igraph convention.

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
nets <- PLNnetwork(Abundance ~ 1 + offset(log(Offset)), data = trichoptera)
## Not run:
stability_selection(nets)
probs <- extract_probs(nets, crit = "StARS", format = "vector")
probs

## End(Not run)

## Not run:
## Add edge attributes to graph using igraph
net_stars <- getBestModel(nets, "StARS")
g <- plot(net_stars, type = "partial_cor", plot=F)
library(igraph)
E(g)$prob <- probs[as_ids(E(g))]
g

## End(Not run)
```

`fitted.PLNfit` *Extracts model fitted values from objects returned by* `PLN()` *and its variants*

Description

Extracts model fitted values from objects returned by `PLN()` and its variants

Usage

```
## S3 method for class 'PLNfit'
fitted(object, ...)
```

Arguments

`object`	an R6 object with class `PLNfit`
`...`	additional parameters for S3 compatibility. Not used

Value

A matrix of Fitted values extracted from the object object.

fitted.PLNmixturefit *Extracts model fitted values from objects returned by* PLNmixture() *and its variants*

Description

Extracts model fitted values from objects returned by PLNmixture() and its variants

Usage

```
## S3 method for class 'PLNmixturefit'
fitted(object, ...)
```

Arguments

object	an R6 object with class PLNmixturefit
...	additional parameters for S3 compatibility. Not used

Value

A matrix of Fitted values extracted from the object object.

fitted.ZIPLNfit *Extracts model fitted values from objects returned by* ZIPLN() *and its variants*

Description

Extracts model fitted values from objects returned by ZIPLN() and its variants

Usage

```
## S3 method for class 'ZIPLNfit'
fitted(object, ...)
```

Arguments

object	an R6 object with class ZIPLNfit
...	additional parameters for S3 compatibility. Not used

Value

A matrix of Fitted values extracted from the object object.

`getBestModel.PLNPCAfamily` *Best model extraction from a collection of models*

Description

Best model extraction from a collection of models

Usage

```
## S3 method for class 'PLNPCAfamily'
getBestModel(Robject, crit = c("ICL", "BIC"), ...)

getBestModel(Robject, crit, ...)

## S3 method for class 'PLNmixturefamily'
getBestModel(Robject, crit = c("ICL", "BIC"), ...)

## S3 method for class 'Networkfamily'
getBestModel(Robject, crit = c("BIC", "EBIC", "StARS"), ...)

## S3 method for class 'PLNnetworkfamily'
getBestModel(Robject, crit = c("BIC", "EBIC", "StARS"), ...)

## S3 method for class 'ZIPLNnetworkfamily'
getBestModel(Robject, crit = c("BIC", "EBIC", "StARS"), ...)
```

Arguments

`Robject`	an object with class PLNPCAfamilly ot PLNnetworkfamily
`crit`	a character for the criterion used to performed the selection. Either "BIC", "ICL", "EBIC", "StARS", "R_squared". Default is `ICL` for `PLNPCA`, and `BIC` for `PLNnetwork`. If StARS (Stability Approach to Regularization Selection) is chosen and stability selection was not yet performed, the function will call the method `stability_selection()` with default argument.
`...`	additional parameters for StARS criterion (only for `PLNnetwork`). `stability`, a scalar indicating the target stability (= 1 - 2 beta) at which the network is selected. Default is `0.9`.

Value

Send back an object with class `PLNPCAfit` or `PLNnetworkfit`

Methods (by class)

- `getBestModel(PLNPCAfamily)`: Model extraction for `PLNPCAfamily`

- `getBestModel(PLNmixturefamily)`: Model extraction for `PLNmixturefamily`
- `getBestModel(Networkfamily)`: Model extraction for `PLNnetworkfamily` or `ZIPLNnetworkfamily`
- `getBestModel(PLNnetworkfamily)`: Model extraction for `PLNnetworkfamily`
- `getBestModel(ZIPLNnetworkfamily)`: Model extraction for `ZIPLNnetworkfamily`

Examples

```
## Not run:
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPCA <- PLNPCA(Abundance ~ 1 + offset(log(Offset)), data = trichoptera, ranks = 1:4)
myModel <- getBestModel(myPCA)

## End(Not run)
```

`getModel.PLNPCAfamily` *Model extraction from a collection of models*

Description

Model extraction from a collection of models

Usage

```
## S3 method for class 'PLNPCAfamily'
getModel(Robject, var, index = NULL)

getModel(Robject, var, index)

## S3 method for class 'PLNmixturefamily'
getModel(Robject, var, index = NULL)

## S3 method for class 'Networkfamily'
getModel(Robject, var, index = NULL)

## S3 method for class 'PLNnetworkfamily'
getModel(Robject, var, index = NULL)

## S3 method for class 'ZIPLNnetworkfamily'
getModel(Robject, var, index = NULL)
```

Arguments

`Robject`	an R6 object with class `PLNPCAfamily` or `PLNnetworkfamily`
`var`	value of the parameter (`rank` for PLNPCA, `sparsity` for PLNnetwork) that identifies the model to be extracted from the collection. If no exact match is found, the model with closest parameter value is returned with a warning.
`index`	Integer index of the model to be returned. Only the first value is taken into account.

Value

Sends back an object with class PLNPCAfit or PLNnetworkfit.

Methods (by class)

- getModel(PLNPCAfamily): Model extraction for PLNPCAfamily
- getModel(PLNmixturefamily): Model extraction for PLNmixturefamily
- getModel(Networkfamily): Model extraction for PLNnetworkfamily or ZIPLNnetworkfamily
- getModel(PLNnetworkfamily): Model extraction for PLNnetworkfamily
- getModel(ZIPLNnetworkfamily): Model extraction for ZIPLNnetworkfamily

Examples

```
## Not run:
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPCA <- PLNPCA(Abundance ~ 1 + offset(log(Offset)), data = trichoptera, ranks = 1:5)
myModel <- getModel(myPCA, 2)

## End(Not run)
```

ICL *Integrated Classification Likelihood*

Description

Generic function to compute the Integrated Classification Likelihood (ICL) of a fitted model. ICL = BIC - entropy of the variational distribution (larger is better).

ICL.PLNfit: ICL for a fitted PLNfit.

ICL.ZIPLNfit: ICL for a fitted ZIPLNfit.

Usage

```
ICL(object, ...)

## S3 method for class 'PLNfit'
ICL(object, ...)

## S3 method for class 'ZIPLNfit'
ICL(object, ...)
```

Arguments

object	an R6 object with class ZIPLNfit
...	additional parameters passed to methods

Value

A scalar: the variational ICL (larger is better).

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
model <- PLN(Abundance ~ 1, data = trichoptera)
ICL(model)
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
model <- ZIPLN(Abundance ~ 1, data = trichoptera)
ICL(model)
```

---

logLik.PLNfit *Extract log-likelihood of a fitted PLN model*

Description

Returns the variational lower bound of the log-likelihood as a "logLik" object, compatible with stats::AIC() and stats::BIC().

Usage

```
## S3 method for class 'PLNfit'
logLik(object, ...)
```

Arguments

object	an R6 object with class PLNfit
...	additional parameters for S3 compatibility. Not used

Value

An object of class "logLik". The numeric value is the variational ELBO. Attributes df and nobs hold the number of parameters and observations.

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
model <- PLN(Abundance ~ 1, data = trichoptera)
logLik(model)
```

logLik.ZIPLNfit *Extract log-likelihood of a fitted ZIPLN model*

Description

Returns the variational lower bound of the log-likelihood as a "logLik" object, compatible with stats::AIC() and stats::BIC().

Usage

```
## S3 method for class 'ZIPLNfit'
logLik(object, ...)
```

Arguments

object	an R6 object with class ZIPLNfit
...	additional parameters for S3 compatibility. Not used

Value

An object of class "logLik". The numeric value is the variational ELBO. Attributes df and nobs hold the number of parameters and observations.

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
model <- ZIPLN(Abundance ~ 1, data = trichoptera)
logLik(model)
```

microcosm *Cow microbiome data set*

Description

This data gives the evolution of the microbiota of 45 lactating cows before and after calving in terms of counts of Amplicon Sequence Variants (ASV) in various body sites. Three body sites (vagina, mouth, nose) in addition to the milk of the 4 teats were sampled at 4 times points: 1 week before calving (except for the milk), 1 month, 3 months and 7 months after calving. We present a reduced version of the original data consisting of 880 samples with sequencing depths ranging from 1,001 to 71,881 reads per sample (see doi:10.1186/s4252302300252w for details). ASVs with prevalence in the dataset lower than 5% were filtered out and samples for which the total depth (after ASV filtering were removed), resulting in a count table of n = 880 samples with p = 259 ASV and a mean proportion of zeroes of 90.3%.

Usage

```
microcosm
```

Format

A data frame with 6 variables:

- Abundance: A 880 samples by 259 taxa count matrix
- sample: Unique sample id
- Offset: sequencing depth
- site: sampling site (`O`: oral; `N`: nasal; `V`: vaginal; `M`: milk)
- time: sampling time (`-1W`: 1 week before calving; `1M`: 1 month after calving; `3M`: 3 months after calving; `7M`: 7 months after calving)
- site_time: factor of possible pairs of (site, time). The combination `M -1W` is absent.

Source

Data from M. Mariadassou and coauthors.

References

Mariadassou, M., Nouvel, L.X., Constant, F. et al. Microbiota members from body sites of dairy cows are largely shared within individual hosts throughout lactation but sharing is limited in the herd. anim microbiome 5, 32 (2023). doi:10.1186/s4252302300252w

See Also

`prepare_data()`

Examples

```
data(microcosm)
## Not run:
my_ZIPLN <- ZIPLN(formula = Abundance ~ 0 + site + offset(log(Offset)) | 1, data = microcosm)

## End(Not run)
```

---

mollusk *Mollusk data set*

Description

This data set gives the abundance of 32 mollusk species in 163 samples. For each sample, 4 additional covariates are known.

Usage

```
mollusk
```

Format

A list with 2 two data frames:

Abundance a 163 x 32 data frame of abundancies/counts (163 samples and 32 mollusk species)

Covariate a 163 x 4 data frame of covariates:

- **site** a factor with 8 levels indicating the sampling site
- **season** a factor with 4 levels indicating the season
- **method** a factor with 2 levels for the method of sampling - wood or string
- **duration** a numeric with 3 levels for the time of exposure in week

In order to prepare the data for using formula in multivariate analysis (multiple outputs and inputs), use `prepare_data()`. Original data set has been extracted from ade4.

Source

Data from Richardot-Coulet, Chessel and Bournaud.

References

Richardot-Coulet, M., Chessel D. and Bournaud M. (1986) Typological value of the benthos of old beds of a large river. Methodological approach. Archiv fùr Hydrobiologie, 107, 363–383.

See Also

`prepare_data()`

Examples

```
data(mollusk)
mollusc <- prepare_data(mollusk$Abundance, mollusk$Covariate)
```

Networkfamily *An R6 Class to virtually represent a collection of network fits*

Description

The functions `PLNnetwork()` and `ZIPLNnetwork()` both produce an instance of this class, which can be thought of as a vector of `PLNnetworkfit`s `ZIPLNfit_sparse`s (indexed by penalty parameter)

This class comes with a set of methods mostly used to compare network fits (in terms of goodness of fit) or extract one from the family (based on penalty parameter and/or goodness of it). See the documentation for `getBestModel()`, `getModel()` and plot() for the user-facing ones.

Super class

`PLNfamily` -> `Networkfamily`

Active bindings

`penalties` the sparsity level of the network in the successively fitted models

`stability_path` the stability path of each edge as returned by the stars procedure

`stability` mean edge stability along the penalty path

`criteria` a data frame with the values of some criteria (variational log-likelihood, (E)BIC, ICL and R2, stability) for the collection of models / fits BIC, ICL and EBIC are defined so that they are on the same scale as the model log-likelihood, i.e. with the form, loglik - 0.5 penalty

Methods

Public methods:

- `Networkfamily$new()`
- `Networkfamily$optimize()`
- `Networkfamily$coefficient_path()`
- `Networkfamily$getBestModel()`
- `Networkfamily$plot()`
- `Networkfamily$plot_stars()`
- `Networkfamily$plot_objective()`
- `Networkfamily$show()`
- `Networkfamily$clone()`

`Networkfamily$new()`: Initialize all models in the collection

Usage:

```
Networkfamily$new(penalties, data, control)
```

Arguments:

`penalties` a vector of positive real number controlling the level of sparsity of the underlying network.

`data` a named list used internally to carry the data matrices

`control` a list for controlling the optimization.

Returns: Update all network fits in the family with smart starting values

`Networkfamily$optimize()`: Call to the C++ optimizer on all models of the collection

Usage:

```
Networkfamily$optimize(data, config)
```

Arguments:

`data` a named list used internally to carry the data matrices

`config` a list for controlling the optimization.

`Networkfamily$coefficient_path()`: Extract the regularization path of a `Networkfamily`

Usage:

```
Networkfamily$coefficient_path(precision = TRUE, corr = TRUE)
```

Arguments:

`precision` Logical. Should the regularization path be extracted from the precision matrix Omega (`TRUE`, default) or from the variance matrix Sigma (`FALSE`)

`corr` Logical. Should the matrix be transformed to (partial) correlation matrix before extraction? Defaults to `TRUE`

`Networkfamily$getBestModel()`: Extract the best network in the family according to some criteria

Usage:

```
Networkfamily$getBestModel(crit = c("BIC", "EBIC", "StARS"), stability = 0.9)
```

Arguments:

`crit` character. Criterion used to perform the selection. If "StARS" is chosen but `$stability` field is empty, will compute stability path.

`stability` Only used for "StARS" criterion. A scalar indicating the target stability (= 1 - 2 beta) at which the network is selected. Default is `0.9`.

Details: For BIC and EBIC criteria, higher is better.

`Networkfamily$plot()`: Display various outputs (goodness-of-fit criteria, robustness, diagnostic) associated with a collection of network fits (a `Networkfamily`)

Usage:

```
Networkfamily$plot(
  criteria = c("loglik", "pen_loglik", "BIC", "EBIC"),
  reverse = FALSE,
  log.x = TRUE
)
```

Arguments:

`criteria` vector of characters. The criteria to plot in `c("loglik", "pen_loglik", "BIC", "EBIC")`. Defaults to all of them.

`reverse` A logical indicating whether to plot the value of the criteria in the "natural" direction (loglik - 0.5 penalty) or in the "reverse" direction (-2 loglik + penalty). Default to FALSE, i.e use the natural direction, on the same scale as the log-likelihood.

`log.x` logical: should the x-axis be represented in log-scale? Default is `TRUE`.

Returns: a `ggplot2::ggplot` graph

`Networkfamily$plot_stars()`: Plot stability path

Usage:

```
Networkfamily$plot_stars(stability = 0.9, log.x = TRUE)
```

Arguments:

`stability` scalar: the targeted level of stability using stability selection. Default is `0.9`.

`log.x` logical: should the x-axis be represented in log-scale? Default is `TRUE`.

Returns: a `ggplot2::ggplot` graph

`Networkfamily$plot_objective()`: Plot objective value of the optimization problem along the penalty path

Usage:

`Networkfamily$plot_objective()`

Returns: a `ggplot2::ggplot` graph

`Networkfamily$show()`: User friendly print method

Usage:

```
Networkfamily$show()
```

`Networkfamily$clone()`: The objects of this class are cloneable with this method.

Usage:

```
Networkfamily$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

The functions `PLNnetwork()`, `ZIPLNnetwork()` and the classes `PLNnetworkfit`, `ZIPLNfit_sparse`

`oaks` *Oaks amplicon data set*

Description

This data set gives the abundance of 114 taxa (66 bacterial OTU, 48 fungal OTUs) in 116 samples. For each sample, 11 additional covariates are known.

Usage

```
oaks
```

Format

A data frame with 13 variables:

- Abundance: A 114 taxa by 116 samples count matrix
- Offset: A 114 taxa by 116 samples offset matrix
- Sample: Unique sample id
- tree: Tree status with respect to the pathogen (susceptible, intermediate or resistant)
- branch: Unique branch id in each tree (4 branches were sampled in each tree, with 10 leaves per branch)
- leafNO: Unique leaf id in each tree (40 leaves were sampled in each tree)
- distTObase: Distance of the sampled leaf to the base of the branch
- distTOtrunk: Distance of the sampled leaf to the base of the tree trunk
- distTOground: Distance of the sampled leaf to the base of the ground

- pmInfection: Powdery mildew infection, proportion of the upper leaf area displaying mildew symptoms
- orientation: Orientation of the branch (South-West SW or North-East NE)
- readsTOTfun: Total number of ITS1 reads for that leaf
- readsTOTbac: Total number of 16S reads for that leaf

Source

Data from B. Jakuschkin and coauthors.

References

Jakuschkin, B., Fievet, V., Schwaller, L. et al. Deciphering the Pathobiome: Intra- and Interkingdom Interactions Involving the Pathogen Erysiphe alphitoides . Microb Ecol 72, 870–880 (2016). doi:10.1007/s002480160777x

See Also

`prepare_data()`

Examples

```
data(oaks)
## Not run:
oaks_networks <- PLNnetwork(formula = Abundance ~ 1 + offset(log(Offset)), data = oaks)

## End(Not run)
```

PLN *Poisson lognormal model*

Description

Fit the multivariate Poisson lognormal model with a variational algorithm. Use the (g)lm syntax for model specification (covariates, offsets, weights).

Usage

```
PLN(formula, data, subset, weights, control = PLN_param())
```

Arguments

`formula`	an object of class "formula": a symbolic description of the model to be fitted.
`data`	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula), typically the environment from which the model is called.

subset	an optional vector specifying a subset of observations to be used in the fitting process.
weights	an optional vector of observation weights to be used in the fitting process.
control	a list-like structure for controlling the optimization, with default generated by PLN_param(). See the associated documentation for details.

Value

an R6 object with class PLNfit

See Also

The class PLNfit and the configuration function PLN_param()

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLN <- PLN(Abundance ~ 1, data = trichoptera)
```

PLNfamily *An R6 Class to represent a collection of PLNfit*

Description

super class for PLNPCAfamily and PLNnetworkfamily.

Public fields

`responses` the matrix of responses common to every models

`covariates` the matrix of covariates common to every models

`offsets` the matrix of offsets common to every models

`weights` the vector of observation weights

`inception` a PLNfit object, obtained when no sparsifying penalty is applied.

`models` a list of PLNfit object, one per penalty.

Active bindings

`criteria` a data frame with the values of some criteria (approximated log-likelihood, BIC, ICL, etc.) for the collection of models / fits BIC and ICL are defined so that they are on the same scale as the model log-likelihood, i.e. with the form, loglik - 0.5 penalty

`convergence` sends back a data frame with some convergence diagnostics associated with the optimization process (method, optimal value, etc)

Methods

Public methods:

- PLNfamily$new()
- PLNfamily$postTreatment()
- PLNfamily$getModel()
- PLNfamily$plot()
- PLNfamily$show()
- PLNfamily$print()
- PLNfamily$clone()

PLNfamily$new(): Create a new PLNfamily object.

Usage:

```
PLNfamily$new(responses, covariates, offsets, weights, control)
```

Arguments:

`responses` the matrix of responses common to every models

`covariates` the matrix of covariates common to every models

`offsets` the matrix of offsets common to every models

`weights` the vector of observation weights

`control` list controlling the optimization and the model

Returns: A new PLNfamily object

PLNfamily$postTreatment(): Update fields after optimization

Usage:

```
PLNfamily$postTreatment(config_post, config_optim)
```

Arguments:

`config_post` a list for controlling the post-treatments (optional bootstrap, jackknife, R2, etc.).

`config_optim` a list for controlling the optimization parameters used during post_treatments

PLNfamily$getModel(): Extract a model from a collection of models

Usage:

```
PLNfamily$getModel(var, index = NULL)
```

Arguments:

`var` value of the parameter (`rank` for PLNPCA, `sparsity` for PLNnetwork) that identifies the model to be extracted from the collection. If no exact match is found, the model with closest parameter value is returned with a warning.

`index` Integer index of the model to be returned. Only the first value is taken into account.

Returns: A PLNfit object

PLNfamily$plot(): Lineplot of selected criteria for all models in the collection

Usage:

```
PLNfamily$plot(criteria, reverse)
```

Arguments:

`criteria` A valid model selection criteria for the collection of models. Includes loglik, BIC (all), ICL (PLNPCA) and pen_loglik, EBIC (PLNnetwork)

`reverse` A logical indicating whether to plot the value of the criteria in the "natural" direction (loglik - penalty) or in the "reverse" direction (-2 loglik + penalty). Default to FALSE, i.e use the natural direction, on the same scale as the log-likelihood.

Returns: A `ggplot2::ggplot` object

`PLNfamily$show()`: User friendly print method

Usage:

```
PLNfamily$show()
```

`PLNfamily$print()`: User friendly print method

Usage:

```
PLNfamily$print()
```

`PLNfamily$clone()`: The objects of this class are cloneable with this method.

Usage:

```
PLNfamily$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

`getModel()`

`PLNfit` *An R6 Class to represent a PLNfit in a standard, general framework*

Description

The function `PLN()` fit a model which is an instance of a object with class `PLNfit`. Objects produced by the functions `PLNnetwork()`, `PLNPCA()`, `PLNmixture()` and `PLNLDA()` also enjoy the methods of `PLNfit()` by inheritance.

This class comes with a set of R6 methods, some of them being useful for the user and exported as S3 methods. See the documentation for `coef()`, `sigma()`, `predict()`, `vcov()` and `standard_error()`.

Fields are accessed via active binding and cannot be changed by the user.

Active bindings

`n` number of samples

`q` number of dimensions of the latent space

`p` number of species

`d` number of covariates

`nb_param` number of parameters in the current PLN model

`model_par` a list with the matrices of the model parameters: B (covariates), Sigma (covariance), Omega (precision matrix), plus some others depending on the variant)

`var_par` a list with the matrices of the variational parameters: M (means) and S2 (variances)

`optim_par` a list with parameters useful for monitoring the optimization

`latent` a matrix: values of the latent vector (Z in the model)

`latent_pos` a matrix: values of the latent position vector (Z) without covariates effects or offset

`fitted` a matrix: fitted values of the observations (A in the model)

`vcov_coef` matrix of sandwich estimator of the variance-covariance of B (need fixed -ie known- covariance at the moment)

`vcov_model` character: the model used for the residual covariance

`weights` observational weights

`loglik` (weighted) variational lower bound of the loglikelihood

`loglik_vec` element-wise variational lower bound of the loglikelihood

`AIC` variational lower bound of the AIC

`BIC` variational lower bound of the BIC

`entropy` Entropy of the variational distribution

`ICL` variational lower bound of the ICL

`R_squared` approximated goodness-of-fit criterion

`criteria` a vector with loglik, BIC, ICL and number of parameters

Methods

Public methods:

- `PLNfit$new()`
- `PLNfit$update()`
- `PLNfit$optimize()`
- `PLNfit$optimize_vestep()`
- `PLNfit$postTreatment()`
- `PLNfit$predict()`
- `PLNfit$predict_cond()`
- `PLNfit$show()`
- `PLNfit$print()`
- `PLNfit$clone()`

`PLNfit$new()`: Initialize a `PLNfit` model

Usage:

```
PLNfit$new(responses, covariates, offsets, weights, formula, control)
```

Arguments:

`responses` the matrix of responses (called Y in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`covariates` design matrix (called X in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`offsets` offset matrix (called O in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`weights` an optional vector of observation weights to be used in the fitting process.

`formula` model formula used for fitting, extracted from the formula in the upper-level call

`control` a list-like structure for controlling the fit, see `PLN_param()`.

`PLNfit$update()`: Update a `PLNfit` object

Usage:

```
PLNfit$update(
  B = NA,
  Sigma = NA,
  Omega = NA,
  M = NA,
  S2 = NA,
  Ji = NA,
  R2 = NA,
  Z = NA,
  A = NA,
  monitoring = NA
)
```

Arguments:

`B` matrix of regression matrix

`Sigma` variance-covariance matrix of the latent variables

`Omega` precision matrix of the latent variables. Inverse of Sigma.

`M` matrix of variational parameters for the mean

`S2` matrix of variational parameters for the variance

`Ji` vector of variational lower bounds of the log-likelihoods (one value per sample)

`R2` approximate R^2 goodness-of-fit criterion

`Z` matrix of latent vectors (includes covariates and offset effects)

`A` matrix of fitted values

`monitoring` a list with optimization monitoring quantities

Returns: Update the current `PLNfit` object

`PLNfit$optimize()`: Call to the NLopt or TORCH optimizer and update of the relevant fields

Usage:

```
PLNfit$optimize(responses, covariates, offsets, weights, config)
```

Arguments:

`responses` the matrix of responses (called Y in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`covariates` design matrix (called X in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`offsets` offset matrix (called O in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`weights` an optional vector of observation weights to be used in the fitting process.

`config` part of the `control` argument which configures the optimizer

`PLNfit$optimize_vestep()`: Result of one call to the VE step of the optimization procedure: optimal variational parameters (M, S2) and corresponding log likelihood values for fixed model parameters (Sigma, B). Intended to position new data in the latent space.

Usage:

```
PLNfit$optimize_vestep(
  covariates,
  offsets,
  responses,
  weights,
  B = self$model_par$B,
  Omega = self$model_par$Omega,
  control = PLN_param(backend = "nlopt")
)
```

Arguments:

`covariates` design matrix (called X in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`offsets` offset matrix (called O in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`responses` the matrix of responses (called Y in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`weights` an optional vector of observation weights to be used in the fitting process.

`B` Optional fixed value of the regression parameters

`Omega` precision matrix of the latent variables. Inverse of Sigma.

`control` a list-like structure for controlling the fit, see `PLN_param()`.

`Sigma` variance-covariance matrix of the latent variables

Returns: A list with three components:

- the matrix `M` of variational means,
- the matrix `S2` of variational variances
- the vector `log.lik` of (variational) log-likelihood of each new observation

`PLNfit$postTreatment()`: Update R2, fisher and std_err fields after optimization

Usage:

```
PLNfit$postTreatment(
  responses,
```

```
  covariates,
  offsets,
  weights = rep(1, nrow(responses)),
  config_post,
  config_optim,
  nullModel = NULL
)
```

Arguments:

`responses` the matrix of responses (called Y in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`covariates` design matrix (called X in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`offsets` offset matrix (called O in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`weights` an optional vector of observation weights to be used in the fitting process.

`config_post` a list for controlling the post-treatments (optional bootstrap, jackknife, R2, etc.). See details

`config_optim` a list for controlling the optimization (optional bootstrap, jackknife, R2, etc.). See details

`nullModel` null model used for approximate R2 computations. Defaults to a GLM model with same design matrix but not latent variable.

Details: The list of parameters `config` controls the post-treatment processing, with the following entries:

- jackknife boolean indicating whether jackknife should be performed to evaluate bias and variance of the model parameters. Default is FALSE.
- bootstrap integer indicating the number of bootstrap resamples generated to evaluate the variance of the model parameters. Default is 0 (inactivated).
- variational_var boolean indicating whether variational Fisher information matrix should be computed to estimate the variance of the model parameters (highly underestimated). Default is FALSE.
- sandwich_var boolean indicating whether sandwich estimator should be computed to estimate the variance of the model parameters (highly underestimated). Default is FALSE.
- trace integer for verbosity. should be > 1 to see output in post-treatments

`PLNfit$predict()`**:** Predict position, scores or observations of new data.

Usage:

```
PLNfit$predict(
  newdata,
  responses = NULL,
  type = c("link", "response"),
  level = 1,
  envir = parent.frame()
)
```

Arguments:

`newdata` A data frame in which to look for variables with which to predict. If omitted, the fitted values are used.

`responses` Optional data frame containing the count of the observed variables (matching the names of the provided as data in the PLN function), assuming the interest is in testing the model.

`type` Scale used for the prediction. Either `link` (default, predicted positions in the latent space) or `response` (predicted counts).

`level` Optional integer value the level to be used in obtaining the predictions. Level zero corresponds to the population predictions (default if `responses` is not provided) while level one (default) corresponds to predictions after evaluating the variational parameters for the new data.

`envir` Environment in which the prediction is evaluated

Details: Note that `level = 1` can only be used if responses are provided, as the variational parameters can't be estimated otherwise. In the absence of responses, `level` is ignored and the fitted values are returned

Returns: A matrix with predictions scores or counts.

`PLNfit$predict_cond()`**:** Predict position, scores or observations of new data, conditionally on the observation of a (set of) variables

Usage:

```
PLNfit$predict_cond(
  newdata,
  cond_responses,
  type = c("link", "response"),
  var_par = FALSE,
  envir = parent.frame()
)
```

Arguments:

`newdata` a data frame containing the covariates of the sites where to predict

`cond_responses` a data frame containing the count of the observed variables (matching the names of the provided as data in the PLN function)

`type` Scale used for the prediction. Either `link` (default, predicted positions in the latent space) or `response` (predicted counts).

`var_par` Boolean. Should new estimations of the variational parameters of mean and variance be sent back, as attributes of the matrix of predictions. Default to `FALSE`.

`envir` Environment in which the prediction is evaluated

Returns: A matrix with predictions scores or counts.

`PLNfit$show()`**:** User friendly print method

Usage:

```
PLNfit$show(
  model = paste("A multivariate Poisson Lognormal fit with", self$vcov_model,
    "covariance model.\n")
)
```

Arguments:

`model` First line of the print output

`PLNfit$print()`: User friendly print method

Usage:

```
PLNfit$print()
```

`PLNfit$clone()`: The objects of this class are cloneable with this method.

Usage:

```
PLNfit$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
## Not run:
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLN <- PLN(Abundance ~ 1, data = trichoptera)
class(myPLN)
print(myPLN)

## End(Not run)
```

`PLNfit_diagonal` *An R6 Class to represent a PLNfit in a standard, general framework, with diagonal residual covariance*

Description

The function `PLNLDA()` produces an instance of an object with class `PLNLDAfit`.

This class comes with a set of methods, some of them being useful for the user: See the documentation for the methods inherited by `PLNfit()`, the `plot()` method for LDA visualization and `predict()` method for prediction

Super class

`PLNfit` -> `PLNfit_diagonal`

Active bindings

`nb_param` number of parameters in the current PLN model

`vcov_model` character: the model used for the residual covariance

Methods

Public methods:

- PLNfit_diagonal$new()
- PLNfit_diagonal$clone()

PLNfit_diagonal$new(): Initialize a PLNfit model

Usage:

```
PLNfit_diagonal$new(responses, covariates, offsets, weights, formula, control)
```

Arguments:

`responses` the matrix of responses (called Y in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`covariates` design matrix (called X in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`offsets` offset matrix (called O in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`weights` an optional vector of observation weights to be used in the fitting process.

`formula` model formula used for fitting, extracted from the formula in the upper-level call

`control` a list for controlling the optimization. See details.

PLNfit_diagonal$clone(): The objects of this class are cloneable with this method.

Usage:

```
PLNfit_diagonal$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Super classes

PLNfit -> PLNLDAfit -> PLNLDAfit_spherical

Active bindings

`vcov_model` character: the model used for the residual covariance

`nb_param` number of parameters in the current PLN model

Methods

Public methods:

- PLNLDAfit_spherical$new()
- PLNLDAfit_spherical$clone()

PLNLDAfit_spherical$new(): Initialize a PLNfit model

Usage:

```
PLNLDAfit_spherical$new(
  grouping,
  responses,
  covariates,
  offsets,
  weights,
  formula,
  control
)
```

Arguments:

`grouping` a factor specifying the class of each observation used for discriminant analysis.

`responses` the matrix of responses (called Y in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`covariates` design matrix (called X in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`offsets` offset matrix (called O in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`weights` an optional vector of observation weights to be used in the fitting process.

`formula` model formula used for fitting, extracted from the formula in the upper-level call

`control` a list for controlling the optimization. See details.

`PLNLDAfit_spherical$clone()`: The objects of this class are cloneable with this method.

Usage:

```
PLNLDAfit_spherical$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
## Not run:
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLN <- PLN(Abundance ~ 1, data = trichoptera)
class(myPLN)
print(myPLN)

## End(Not run)
## Not run:
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLNLDA <- PLNLDA(Abundance ~ 1, data = trichoptera, control = PLN_param(covariance = "spherical"))
class(myPLNLDA)
print(myPLNLDA)

## End(Not run)
```

PLNfit_fixedcov *An R6 Class to represent a PLNfit in a standard, general framework, with fixed (inverse) residual covariance*

Description

An R6 Class to represent a PLNfit in a standard, general framework, with fixed (inverse) residual covariance

Super class

PLNfit -> PLNfit_fixedcov

Active bindings

nb_param number of parameters in the current PLN model

vcov_model character: the model used for the residual covariance

vcov_coef matrix of sandwich estimator of the variance-covariance of B (needs known covariance at the moment)

Methods

Public methods:

- PLNfit_fixedcov$new()
- PLNfit_fixedcov$optimize()
- PLNfit_fixedcov$clone()

PLNfit_fixedcov$new(): Initialize a PLNfit model

Usage:

```
PLNfit_fixedcov$new(responses, covariates, offsets, weights, formula, control)
```

Arguments:

responses the matrix of responses (called Y in the model). Will usually be extracted from the corresponding field in PLNfamily-class

covariates design matrix (called X in the model). Will usually be extracted from the corresponding field in PLNfamily-class

offsets offset matrix (called O in the model). Will usually be extracted from the corresponding field in PLNfamily-class

weights an optional vector of observation weights to be used in the fitting process.

formula model formula used for fitting, extracted from the formula in the upper-level call

control a list for controlling the optimization. See details.

PLNfit_fixedcov$optimize(): Call to the NLopt or TORCH optimizer and update of the relevant fields

Usage:

```
PLNfit_fixedcov$optimize(responses, covariates, offsets, weights, config)
```

Arguments:

`responses` the matrix of responses (called Y in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`covariates` design matrix (called X in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`offsets` offset matrix (called O in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`weights` an optional vector of observation weights to be used in the fitting process.

`config` part of the `control` argument which configures the optimizer

`PLNfit_fixedcov$clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
PLNfit_fixedcov$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
## Not run:
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLN <- PLN(Abundance ~ 1, data = trichoptera)
class(myPLN)
print(myPLN)

## End(Not run)
```

`PLNfit_genpop` *An R6 Class to represent a PLNfit with a residual covariance structured by a fixed correlation matrix (e.g. a genetic relationship matrix), motivated by population genetics*

Description

Sigma = sigma2 * (rho * C + (1 - rho) * I_p), where C is a fixed p x p correlation matrix supplied by the user (`control$C`) and (sigma2, rho) are estimated. See `GeneticCovTraits` in `src/covariance_pln.h` for the C++ side.

Super class

`PLNfit` -> `PLNfit_genpop`

Active bindings

`nb_param` number of parameters in the current PLN model

`vcov_model` character: the model used for the residual covariance

`gen_par` a list with the two extra parameters of the genpop covariance model: sigma2 (variance scale) and rho (mixing weight / heritability), decoded from Sigma and C.

Methods

Public methods:

- `PLNfit_genpop$new()`
- `PLNfit_genpop$optimize()`
- `PLNfit_genpop$clone()`

`PLNfit_genpop$new()`: Initialize a `PLNfit_genpop` model

Usage:

```
PLNfit_genpop$new(responses, covariates, offsets, weights, formula, control)
```

Arguments:

`responses` the matrix of responses (called Y in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`covariates` design matrix (called X in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`offsets` offset matrix (called O in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`weights` an optional vector of observation weights to be used in the fitting process.

`formula` model formula used for fitting, extracted from the formula in the upper-level call

`control` a list for controlling the optimization, must include a field `C` (the fixed p x p correlation matrix). See details.

`PLNfit_genpop$optimize()`: Call to the NLopt or builtin optimizer and update of the relevant fields

Usage:

```
PLNfit_genpop$optimize(responses, covariates, offsets, weights, config)
```

Arguments:

`responses` the matrix of responses (called Y in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`covariates` design matrix (called X in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`offsets` offset matrix (called O in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`weights` an optional vector of observation weights to be used in the fitting process.

`config` part of the `control` argument which configures the optimizer

`PLNfit_genpop$clone()`: The objects of this class are cloneable with this method.

Usage:

```
PLNfit_genpop$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

Examples

```
## Not run:
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
p <- ncol(trichoptera$Abundance)
C <- 0.5^abs(outer(1:p, 1:p, "-")); diag(C) <- 1
myPLN <- PLN(Abundance ~ 1, data = trichoptera, control = PLN_param(covariance = "genpop", C = C))
class(myPLN)
print(myPLN)

## End(Not run)
```

PLNfit_spherical *An R6 Class to represent a PLNfit in a standard, general framework, with spherical residual covariance*

Description

An R6 Class to represent a PLNfit in a standard, general framework, with spherical residual covariance

Super class

PLNfit -> PLNfit_spherical

Active bindings

nb_param number of parameters in the current PLN model

vcov_model character: the model used for the residual covariance

Methods

Public methods:

- PLNfit_spherical$new()
- PLNfit_spherical$clone()

PLNfit_spherical$new(): Initialize a PLNfit model

Usage:

```
PLNfit_spherical$new(responses, covariates, offsets, weights, formula, control)
```

Arguments:

`responses` the matrix of responses (called Y in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`covariates` design matrix (called X in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`offsets` offset matrix (called O in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`weights` an optional vector of observation weights to be used in the fitting process.

`formula` model formula used for fitting, extracted from the formula in the upper-level call

`control` a list for controlling the optimization. See details.

`PLNfit_spherical$clone()`: The objects of this class are cloneable with this method.

Usage:

```
PLNfit_spherical$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
## Not run:
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLN <- PLN(Abundance ~ 1, data = trichoptera)
class(myPLN)
print(myPLN)

## End(Not run)
```

`PLNLDA` *Poisson lognormal model towards Linear Discriminant Analysis*

Description

Fit the Poisson lognormal for LDA with a variational algorithm. Use the (g)lm syntax for model specification (covariates, offsets).

Usage

```
PLNLDA(formula, data, subset, weights, grouping, control = PLNLDA_param())
```

Arguments

`formula`	an object of class "formula": a symbolic description of the model to be fitted.
`data`	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula), typically the environment from which the model is called.

subset	an optional vector specifying a subset of observations to be used in the fitting process.
weights	an optional vector of observation weights to be used in the fitting process.
grouping	a factor specifying the class of each observation used for discriminant analysis.
control	a list-like structure for controlling the optimization, with default generated by PLNLDA_param(). See the associated documentation.

Details

See PLNLDA_param() for a full description of the optimization parameters. Note that unlike PLN_param(), PLNLDA_param() does not expose the "fixed" covariance option or the Omega parameter, which are not meaningful in the LDA context.

Value

an R6 object with class PLNLDAfit()

See Also

The class PLNLDAfit

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLNLDA <- PLNLDA(Abundance ~ 1, grouping = Group, data = trichoptera)
```

PLNLDAfit *An R6 Class to represent a PLNfit in a LDA framework*

Description

The function PLNLDA() produces an instance of an object with class PLNLDAfit.

This class comes with a set of methods, some of them being useful for the user: See the documentation for the methods inherited by PLNfit(), the plot() method for LDA visualization and predict() method for prediction

Super class

PLNfit -> PLNLDAfit

Active bindings

`rank` the dimension of the current model

`nb_param` number of parameters in the current PLN model

`model_par` a list with the matrices associated with the estimated parameters of the PLN model: B (covariates), Sigma (latent covariance), C (latent loadings), P (latent position) and Mu (group means)

`percent_var` the percent of variance explained by each axis

`corr_map` a matrix of correlations to plot the correlation circles

`scores` a matrix of scores to plot the individual factor maps

`group_means` a matrix of group mean vectors in the latent space.

Methods

Public methods:

- `PLNLDAfit$new()`
- `PLNLDAfit$optimize()`
- `PLNLDAfit$postTreatment()`
- `PLNLDAfit$setVisualization()`
- `PLNLDAfit$plot_individual_map()`
- `PLNLDAfit$plot_correlation_map()`
- `PLNLDAfit$plot_LDA()`
- `PLNLDAfit$predict()`
- `PLNLDAfit$show()`
- `PLNLDAfit$clone()`

`PLNLDAfit$new()`: Initialize a `PLNLDAfit` object

Usage:

```
PLNLDAfit$new(
  grouping,
  responses,
  covariates,
  offsets,
  weights,
  formula,
  control
)
```

Arguments:

`grouping` a factor specifying the class of each observation used for discriminant analysis.

`responses` the matrix of responses (called Y in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`covariates` design matrix (called X in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`offsets` offset matrix (called O in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`weights` an optional vector of observation weights to be used in the fitting process.

`formula` model formula used for fitting, extracted from the formula in the upper-level call

`control` list controlling the optimization and the model

`PLNLDAfit$optimize()`: Compute group means and axis of the LDA (noted B in the model) in the latent space, update corresponding fields

Usage:

```
PLNLDAfit$optimize(grouping, responses, covariates, offsets, weights, config)
```

Arguments:

`grouping` a factor specifying the class of each observation used for discriminant analysis.

`responses` the matrix of responses (called Y in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`covariates` design matrix. Automatically built from the covariates and the formula from the call

`offsets` offset matrix (called O in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`weights` an optional vector of observation weights to be used in the fitting process.

`config` list controlling the optimization

`X` Abundance matrix.

`PLNLDAfit$postTreatment()`: Update R2, fisher and std_err fields and visualization

Usage:

```
PLNLDAfit$postTreatment(
  grouping,
  responses,
  covariates,
  offsets,
  weights = rep(1, nrow(responses)),
  config_post,
  config_optim
)
```

Arguments:

`grouping` a factor with group memberships

`responses` the matrix of responses (counts)

`covariates` the matrix of covariates

`offsets` the matrix of offsets

`weights` an optional vector of observation weights. Default is uniform weights.

`config_post` a list for controlling the post-treatments (optional bootstrap, jackknife, R2, etc.).

`config_optim` list controlling the optimization parameters

`PLNLDAfit$setVisualization()`: Compute LDA scores in the latent space and update corresponding fields.

Usage:

```
PLNLDAfit$setVisualization(scale.unit = FALSE)
```

Arguments:

`scale.unit` Logical. Should LDA scores be rescaled to have unit variance

`PLNLDAfit$plot_individual_map()`: Plot the factorial map of the LDA

Usage:

```
PLNLDAfit$plot_individual_map(
  axes = 1:min(2, self$rank),
  main = "Individual Factor Map",
  plot = TRUE
)
```

Arguments:

`axes` numeric, the axes to use for the plot when map = "individual" or "variable". Default it c(1,min(rank))

`main` character. A title for the single plot (individual or variable factor map). If NULL (the default), an hopefully appropriate title will be used.

`plot` logical. Should the plot be displayed or sent back as ggplot object

Returns: a `ggplot2::ggplot` graphic

`PLNLDAfit$plot_correlation_map()`: Plot the correlation circle of a specified axis for a `PLNLDAfit` object

Usage:

```
PLNLDAfit$plot_correlation_map(
  axes = 1:min(2, self$rank),
  main = "Variable Factor Map",
  cols = "default",
  plot = TRUE
)
```

Arguments:

`axes` numeric, the axes to use for the plot when map = "individual" or "variable". Default it c(1,min(rank))

`main` character. A title for the single plot (individual or variable factor map). If NULL (the default), an hopefully appropriate title will be used.

`cols` a character, factor or numeric to define the color associated with the variables. By default, all variables receive the default color of the current palette.

`plot` logical. Should the plot be displayed or sent back as ggplot object

Returns: a `ggplot2::ggplot` graphic

`PLNLDAfit$plot_LDA()`: Plot a summary of the `PLNLDAfit` object

Usage:

```
PLNLDAfit$plot_LDA(
  nb_axes = min(3, self$rank),
  var_cols = "default",
  plot = TRUE
)
```

Arguments:

`nb_axes` scalar: the number of axes to be considered when map = "both". The default is min(3,rank).

`var_cols` a character, factor or numeric to define the color associated with the variables. By default, all variables receive the default color of the current palette.

`plot` logical. Should the plot be displayed or sent back as ggplot object

Returns: a `grob` object

`PLNLDAfit$predict()`**:** Predict group of new samples

Usage:

```
PLNLDAfit$predict(
  newdata,
  type = c("posterior", "response", "scores"),
  scale = c("log", "prob"),
  prior = NULL,
  control = PLN_param(backend = "nlopt"),
  envir = parent.frame()
)
```

Arguments:

`newdata` A data frame in which to look for variables, offsets and counts with which to predict.

`type` The type of prediction required. The default are posterior probabilities for each group (in either unnormalized log-scale or natural probabilities, see "scale" for details), "response" is the group with maximal posterior probability and "scores" is the average score along each separation axis in the latent space, with weights equal to the posterior probabilities.

`scale` The scale used for the posterior probability. Either log-scale ("log", default) or natural probabilities summing up to 1 ("prob").

`prior` User-specified prior group probabilities in the new data. If NULL (default), prior probabilities are computed from the learning set.

`control` a list for controlling the optimization. See `PLN()` for details.

`envir` Environment in which the prediction is evaluated

`PLNLDAfit$show()`**:** User friendly print method

Usage:

```
PLNLDAfit$show()
```

`PLNLDAfit$clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
PLNLDAfit$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

The function `PLNLDA`.

Examples

```
## Not run:
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLNLDA <- PLNLDA(Abundance ~ 1, grouping = Group, data = trichoptera)
class(myPLNLDA)
print(myPLNLDA)

## End(Not run)
```

`PLNLDAfit_diagonal` *An R6 Class to represent a PLNfit in a LDA framework with diagonal covariance*

Description

The function `PLNLDA()` produces an instance of an object with class `PLNLDAfit`.

This class comes with a set of methods, some of them being useful for the user: See the documentation for the methods inherited by `PLNfit()`, the `plot()` method for LDA visualization and `predict()` method for prediction

Super classes

`PLNfit` -> `PLNLDAfit` -> `PLNLDAfit_diagonal`

Active bindings

`vcov_model` character: the model used for the residual covariance

`nb_param` number of parameters in the current PLN model

Methods

Public methods:

- `PLNLDAfit_diagonal$new()`
- `PLNLDAfit_diagonal$clone()`

`PLNLDAfit_diagonal$new()`**:** Initialize a `PLNfit` model

Usage:

```
PLNLDAfit_diagonal$new(
  grouping,
  responses,
  covariates,
  offsets,
  weights,
  formula,
  control
)
```

Arguments:

`grouping` a factor specifying the class of each observation used for discriminant analysis.

`responses` the matrix of responses (called Y in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`covariates` design matrix (called X in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`offsets` offset matrix (called O in the model). Will usually be extracted from the corresponding field in PLNfamily-class

`weights` an optional vector of observation weights to be used in the fitting process.

`formula` model formula used for fitting, extracted from the formula in the upper-level call

`control` a list for controlling the optimization. See details.

`PLNLDAfit_diagonal$clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
PLNLDAfit_diagonal$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
## Not run:
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLNLDA <- PLNLDA(Abundance ~ 1, data = trichoptera, control = PLN_param(covariance = "diagonal"))
class(myPLNLDA)
print(myPLNLDA)

## End(Not run)
```

`PLNLDA_param` *Control of a PLNLDA fit*

Description

Helper to define list of parameters to control the PLNLDA fit. All arguments have defaults.

Usage

```
PLNLDA_param(
  backend = c("builtin", "nlopt", "torch"),
  trace = 1,
  covariance = c("full", "diagonal", "spherical"),
  config_post = list(),
  config_optim = list(),
  inception = NULL
)
```

Arguments

backend	optimization back used, either "nlopt" or "torch". Default is "nlopt"
trace	a integer for verbosity.
covariance	character setting the model for the covariance matrix. Either "full", "diagonal" or "spherical". Default is "full".
config_post	a list for controlling the post-treatments (optional bootstrap, jackknife, R2, etc.). See details
config_optim	a list for controlling the optimizer (either "nlopt" or "torch" backend). See details
inception	Set up the parameters initialization: by default, the model is initialized with a multivariate linear model applied on log-transformed data, and with the same formula as the one provided by the user. However, the user can provide a PLNfit (typically obtained from a previous fit), which sometimes speeds up the inference.

Details

The list of parameters `config_optim` controls the optimizers. When "nlopt" is chosen the following entries are relevant

- "algorithm" the optimization method used by NLOPT among LD type, e.g. "CCSAQ", "MMA", "LBFGS". See NLOPT documentation for further details. Default is "CCSAQ".
- "maxeval" stop when the number of iteration exceeds maxeval. Default is 10000
- "ftol_rel" stop when an optimization step changes the objective function by less than ftol multiplied by the absolute value of the parameter. Default is 1e-8
- "xtol_rel" stop when an optimization step changes every parameters by less than xtol multiplied by the absolute value of the parameter. Default is 1e-6
- "ftol_abs" stop when an optimization step changes the objective function by less than ftol_abs. Default is 0.0 (disabled)
- "xtol_abs" stop when an optimization step changes every parameters by less than xtol_abs. Default is 0.0 (disabled)
- "maxtime" stop when the optimization time (in seconds) exceeds maxtime. Default is -1 (disabled)
- "profiled" (full covariance only) if TRUE, profile both B and Omega at every nlopt evaluation instead of running an EM loop (Omega fixed for the duration of each inner nlopt solve, B profiled in closed form at every evaluation). Despite the extra `O(n*p^2 + p^3)` cost per evaluation, benchmarks found it consistently faster than the EM loop (and with a slightly better loglik) across a range of problem sizes. Default is TRUE; set to FALSE to recover the EM loop.

When "torch" backend is used (only for PLN and PLNLDA for now), the following entries are relevant:

- "algorithm" the optimizer used by torch among RPROP (default), RMSPROP, ADAM and ADAGRAD

- "maxeval" stop when the number of iteration exceeds maxeval. Default is 10 000
- "numepoch" stop training once this number of epochs exceeds numepoch. Set to -1 to enable infinite training. Default is 1 000
- "num_batch" number of batches to use during training. Defaults to 1 (use full dataset at each epoch)
- "ftol_rel" stop when an optimization step changes the objective function by less than ftol multiplied by the absolute value of the parameter. Default is 1e-8
- "xtol_rel" stop when an optimization step changes every parameters by less than xtol multiplied by the absolute value of the parameter. Default is 1e-6
- "lr" learning rate. Default is 0.1.
- "momentum" momentum factor. Default is 0 (no momentum). Only used in RMSPROP
- "weight_decay" Weight decay penalty. Default is 0 (no decay). Not used in RPROP
- "step_sizes" pair of minimal (default: 1e-6) and maximal (default: 50) allowed step sizes. Only used in RPROP
- "etas" pair of multiplicative increase and decrease factors. Default is (0.5, 1.2). Only used in RPROP
- "centered" if TRUE, compute the centered RMSProp where the gradient is normalized by an estimation of its variance weight_decay (L2 penalty). Default to FALSE. Only used in RMSPROP

When "builtin" backend is used, the following entries are relevant

- "maxeval" stop when the number of Newton steps in the inner loop exceeds maxeval. Default is 10000
- "ftol_in" stop the inner loop when the objective changes by less than ftol_in (relative). Default is 1e-8
- "maxit_em" stop the EM outer loop when the number of EM iterations exceeds maxit_em. Default is 50
- "ftol_em" stop the EM outer loop when the ELBO changes by less than ftol_em (relative). Default is 1e-8

The list of parameters `config_post` controls the post-treatment processing (for most `PLN*()` functions), with the following entries (defaults may vary depending on the specific function, check `config_post_default_*` for defaults values):

- jackknife boolean indicating whether jackknife should be performed to evaluate bias and variance of the model parameters. Default is FALSE.
- bootstrap integer indicating the number of bootstrap resamples generated to evaluate the variance of the model parameters. Default is 0 (inactivated).
- variational_var boolean indicating whether variational Fisher information matrix should be computed to estimate the variance of the model parameters (highly underestimated). Default is FALSE.
- sandwich_var boolean indicating whether sandwich estimation should be used to estimate the variance of the model parameters (highly underestimated). Default is FALSE.
- rsquared boolean indicating whether approximation of R2 based on deviance should be computed. Default is TRUE

Value

list of parameters configuring the fit.

`PLNmixture` *Poisson lognormal mixture model*

Description

Fit the mixture variants of the Poisson lognormal with a variational algorithm. Use the (g)lm syntax for model specification (covariates, offsets).

Usage

```
PLNmixture(formula, data, subset, clusters = 1:5, control = PLNmixture_param())
```

Arguments

`formula`	an object of class "formula": a symbolic description of the model to be fitted.
`data`	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula), typically the environment from which the model is called.
`subset`	an optional vector specifying a subset of observations to be used in the fitting process.
`clusters`	a vector of integer containing the successive number of clusters (or components) to be considered
`control`	a list-like structure for controlling the optimization, with default generated by `PLNmixture_param()`. See the associated documentation for details.

Value

an R6 object with class `PLNmixturefamily`, which contains a collection of models with class `PLNmixturefit`

See Also

The classes `PLNmixturefamily`, `PLNmixturefit` and `PLNmixture_param()`

Examples

```
## Use parallel to dispatch the computations on 2 workers
## Not run:
options(mc.cores = 2)

## End(Not run)

data(trichoptera)
```

```
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myMixtures <- PLNmixture(Abundance ~ 1 + offset(log(Offset)), clusters = 1:4, data = trichoptera,
                         control = PLNmixture_param(smoothing = 'none'))

## Not run:
options(mc.cores = 1)

## End(Not run)
```

PLNmixturefamily *An R6 Class to represent a collection of PLNmixturefit*

Description

The function PLNmixture() produces an instance of this class.

This class comes with a set of methods, some of them being useful for the user: See the documentation for getBestModel(), getModel() and plot().

Super class

PLNfamily -> PLNmixturefamily

Active bindings

clusters vector indicating the number of clusters considered is the successively fitted models

Methods

Public methods:

- PLNmixturefamily$new()
- PLNmixturefamily$optimize()
- PLNmixturefamily$smooth()
- PLNmixturefamily$plot()
- PLNmixturefamily$plot_objective()
- PLNmixturefamily$getBestModel()
- PLNmixturefamily$show()
- PLNmixturefamily$print()
- PLNmixturefamily$clone()

PLNmixturefamily$new(): helper function for forward smoothing: split a group

Initialize all models in the collection.

Usage:

```
PLNmixturefamily$new(
  clusters,
  responses,
  covariates,
  offsets,
  formula,
  control
)
```

Arguments:

`clusters` the dimensions of the successively fitted models

`responses` the matrix of responses common to every models

`covariates` the matrix of covariates common to every models

`offsets` the matrix of offsets common to every models

`formula` model formula used for fitting, extracted from the formula in the upper-level call

`control` a list for controlling the optimization. See details.

`control` a list for controlling the optimization. See details.

`PLNmixturefamily$optimize()`: Call to the optimizer on all models of the collection

Usage:

```
PLNmixturefamily$optimize(config)
```

Arguments:

`config` a list for controlling the optimization

`PLNmixturefamily$smooth()`: function to restart clustering to avoid local minima by smoothing the loglikelihood values as a function of the number of clusters

Usage:

```
PLNmixturefamily$smooth(control)
```

Arguments:

`control` a list to control the smoothing process

`PLNmixturefamily$plot()`: Lineplot of selected criteria for all models in the collection

Usage:

```
PLNmixturefamily$plot(criteria = c("loglik", "BIC", "ICL"), reverse = FALSE)
```

Arguments:

`criteria` A valid model selection criteria for the collection of models. Any of "loglik", "BIC" or "ICL" (all).

`reverse` A logical indicating whether to plot the value of the criteria in the "natural" direction (loglik - 0.5 penalty) or in the "reverse" direction (-2 loglik + penalty). Default to FALSE, i.e use the natural direction, on the same scale as the log-likelihood..

Returns: A `ggplot2::ggplot` object

`PLNmixturefamily$plot_objective()`: Plot objective value of the optimization problem along the penalty path

Usage:

```
PLNmixturefamily$plot_objective()
```

Returns: a ggplot2::ggplot graph

`PLNmixturefamily$getBestModel()`: Extract best model in the collection

Usage:

```
PLNmixturefamily$getBestModel(crit = c("BIC", "ICL", "loglik"))
```

Arguments:

`crit` a character for the criterion used to performed the selection. Either "BIC", "ICL" or "loglik". Default is `ICL`

Returns: a `PLNmixturefit` object

`PLNmixturefamily$show()`: User friendly print method

Usage:

```
PLNmixturefamily$show()
```

`PLNmixturefamily$print()`: User friendly print method

Usage:

```
PLNmixturefamily$print()
```

`PLNmixturefamily$clone()`: The objects of this class are cloneable with this method.

Usage:

```
PLNmixturefamily$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

The function `PLNmixture`, the class `PLNmixturefit`

`PLNmixturefit` *An R6 Class to represent a PLNfit in a mixture framework*

Description

The function `PLNmixture` produces a collection of models which are instances of object with class `PLNmixturefit`. A `PLNmixturefit` (say, with k components) is itself a collection of k `PLNfit`.

This class comes with a set of methods, some of them being useful for the user: See the documentation for ...

Active bindings

`n` number of samples

`p` number of dimensions of the latent space

`k` number of components

`d` number of covariates

`components` components of the mixture (PLNfits)

`latent` a matrix: values of the latent vector (Z in the model)

`latent_pos` a matrix: values of the latent position vector (Z) without covariates effects or offset

`posteriorProb` matrix ofposterior probability for cluster belonging

`memberships` vector for cluster index

`mixtureParam` vector of cluster proportions

`optim_par` a list with parameters useful for monitoring the optimization

`nb_param` number of parameters in the current PLN model

`entropy_clustering` Entropy of the variational distribution of the cluster (multinomial)

`entropy_latent` Entropy of the variational distribution of the latent vector (Gaussian)

`entropy` Full entropy of the variational distribution (latent vector + clustering)

`loglik` variational lower bound of the loglikelihood

`loglik_vec` element-wise variational lower bound of the loglikelihood

`BIC` variational lower bound of the BIC

`ICL` variational lower bound of the ICL (include entropy of both the clustering and latent distributions)

`R_squared` approximated goodness-of-fit criterion

`criteria` a vector with loglik, BIC, ICL, and number of parameters

`model_par` a list with the matrices of parameters found in the model (Theta, Sigma, Mu and Pi)

`vcov_model` character: the model used for the covariance (either "spherical", "diagonal" or "full")

`fitted` a matrix: fitted values of the observations (A in the model)

`group_means` a matrix of group mean vectors in the latent space.

Methods

Public methods:

- `PLNmixturefit$new()`
- `PLNmixturefit$optimize()`
- `PLNmixturefit$predict()`
- `PLNmixturefit$plot_clustering_data()`
- `PLNmixturefit$plot_clustering_pca()`
- `PLNmixturefit$postTreatment()`
- `PLNmixturefit$show()`
- `PLNmixturefit$print()`

- PLNmixturefit$clone()

PLNmixturefit$new(): Optimize a the
Initialize a PLNmixturefit model

Usage:

```
PLNmixturefit$new(
  responses,
  covariates,
  offsets,
  posteriorProb,
  formula,
  control
)
```

Arguments:

responses the matrix of responses common to every models

covariates the matrix of covariates common to every models

offsets the matrix of offsets common to every models

posteriorProb matrix ofposterior probability for cluster belonging

formula model formula used for fitting, extracted from the formula in the upper-level call

control a list for controlling the optimization.

PLNmixturefit$optimize(): Optimize a PLNmixturefit model

Usage:

```
PLNmixturefit$optimize(responses, covariates, offsets, config)
```

Arguments:

responses the matrix of responses common to every models

covariates the matrix of covariates common to every models

offsets the matrix of offsets common to every models

config a list for controlling the optimization

PLNmixturefit$predict(): Predict group of new samples

Usage:

```
PLNmixturefit$predict(
  newdata,
  type = c("posterior", "response", "position"),
  prior = matrix(rep(1/self$k, self$k), nrow(newdata), self$k, byrow = TRUE),
  control = PLNmixture_param(),
  envir = parent.frame()
)
```

Arguments:

newdata A data frame in which to look for variables, offsets and counts with which to predict.

type The type of prediction required. The default posterior are posterior probabilities for each group , response is the group with maximal posterior probability and latent is the averaged latent coordinate (without offset and nor covariate effects), with weights equal to the posterior probabilities.

`prior` User-specified prior group probabilities in the new data. The default uses a uniform prior.

`control` a list-like structure for controlling the fit. See `PLNmixture_param()` for details.

`envir` Environment in which the prediction is evaluated

`PLNmixturefit$plot_clustering_data()`: Plot the matrix of expected mean counts (without offsets, without covariate effects) reordered according the inferred clustering

Usage:

```
PLNmixturefit$plot_clustering_data(
  main = "Expected counts reorder by clustering",
  plot = TRUE,
  log_scale = TRUE
)
```

Arguments:

`main` character. A title for the plot. An hopefully appropriate title will be used by default.

`plot` logical. Should the plot be displayed or sent back as `ggplot2::ggplot` object

`log_scale` logical. Should the color scale values be log-transform before plotting? Default is `TRUE`.

Returns: a `ggplot2::ggplot` graphic

`PLNmixturefit$plot_clustering_pca()`: Plot the individual map of a PCA performed on the latent coordinates, where individuals are colored according to the memberships

Usage:

```
PLNmixturefit$plot_clustering_pca(
  main = "Clustering labels in Individual Factor Map",
  plot = TRUE
)
```

Arguments:

`main` character. A title for the plot. An hopefully appropriate title will be used by default.

`plot` logical. Should the plot be displayed or sent back as `ggplot2::ggplot` object

Returns: a `ggplot2::ggplot` graphic

`PLNmixturefit$postTreatment()`: Update fields after optimization

Usage:

```
PLNmixturefit$postTreatment(
  responses,
  covariates,
  offsets,
  weights,
  config_post,
  config_optim,
  nullModel
)
```

Arguments:

`responses` the matrix of responses common to every models

`covariates` the matrix of covariates common to every models

`offsets` the matrix of offsets common to every models

`weights` an optional vector of observation weights to be used in the fitting process.

`config_post` a list for controlling the post-treatment

`config_optim` a list for controlling the optimization during the post-treatment computations

`nullModel` null model used for approximate R2 computations. Defaults to a GLM model with same design matrix but not latent variable.

`PLNmixturefit$show()`: User friendly print method

Usage:

```
PLNmixturefit$show()
```

`PLNmixturefit$print()`: User friendly print method

Usage:

```
PLNmixturefit$print()
```

`PLNmixturefit$clone()`: The objects of this class are cloneable with this method.

Usage:

```
PLNmixturefit$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

The function `PLNmixture`, the class `PLNmixturefamily`

`PLNmixture_param` *Control of a PLNmixture fit*

Description

Helper to define list of parameters to control the PLNmixture fit. All arguments have defaults.

Usage

```
PLNmixture_param(
  backend = c("builtin", "nlopt", "torch"),
  trace = 1,
  covariance = "spherical",
  init_cl = "kmeans",
  smoothing = "both",
  config_optim = list(),
  config_post = list(),
  inception = NULL
)
```

Arguments

backend	optimization back used, either "builtin", "nlopt" or "torch". Default is "builtin".
trace	a integer for verbosity.
covariance	character setting the model for the covariance matrices of the mixture components. Either "full", "diagonal" or "spherical". Default is "spherical".
init_cl	The initial clustering to apply. Either, 'kmeans', CAH' or a user defined clustering given as a list of clusterings, the size of which is equal to the number of clusters considered. Default is 'kmeans'.
smoothing	The smoothing to apply. Either, 'none', forward', 'backward' or 'both'. Default is 'both'.
config_optim	a list for controlling the optimizer (either "nlopt" or "torch" backend). See details
config_post	a list for controlling the post-treatments (optional bootstrap, jackknife, R2, etc.). See details
inception	Set up the parameters initialization: by default, the model is initialized with a multivariate linear model applied on log-transformed data, and with the same formula as the one provided by the user. However, the user can provide a PLNfit (typically obtained from a previous fit), which sometimes speeds up the inference.

Details

The list of parameters `config_optim` controls the optimizers. When "nlopt" is chosen the following entries are relevant

- "algorithm" the optimization method used by NLOPT among LD type, e.g. "CCSAQ", "MMA", "LBFGS". See NLOPT documentation for further details. Default is "CCSAQ".
- "maxeval" stop when the number of iteration exceeds maxeval. Default is 10000
- "ftol_rel" stop when an optimization step changes the objective function by less than ftol multiplied by the absolute value of the parameter. Default is 1e-8
- "xtol_rel" stop when an optimization step changes every parameters by less than xtol multiplied by the absolute value of the parameter. Default is 1e-6
- "ftol_abs" stop when an optimization step changes the objective function by less than ftol_abs. Default is 0.0 (disabled)
- "xtol_abs" stop when an optimization step changes every parameters by less than xtol_abs. Default is 0.0 (disabled)
- "maxtime" stop when the optimization time (in seconds) exceeds maxtime. Default is -1 (disabled)
- "profiled" (full covariance only) if TRUE, profile both B and Omega at every nlopt evaluation instead of running an EM loop (Omega fixed for the duration of each inner nlopt solve, B profiled in closed form at every evaluation). Despite the extra `O(n*p^2 + p^3)` cost per evaluation, benchmarks found it consistently faster than the EM loop (and with a slightly better loglik) across a range of problem sizes. Default is TRUE; set to FALSE to recover the EM loop.

When "torch" backend is used (only for PLN and PLNLDA for now), the following entries are relevant:

- "algorithm" the optimizer used by torch among RPROP (default), RMSPROP, ADAM and ADAGRAD
- "maxeval" stop when the number of iteration exceeds maxeval. Default is 10 000
- "numepoch" stop training once this number of epochs exceeds numepoch. Set to -1 to enable infinite training. Default is 1 000
- "num_batch" number of batches to use during training. Defaults to 1 (use full dataset at each epoch)
- "ftol_rel" stop when an optimization step changes the objective function by less than ftol multiplied by the absolute value of the parameter. Default is 1e-8
- "xtol_rel" stop when an optimization step changes every parameters by less than xtol multiplied by the absolute value of the parameter. Default is 1e-6
- "lr" learning rate. Default is 0.1.
- "momentum" momentum factor. Default is 0 (no momentum). Only used in RMSPROP
- "weight_decay" Weight decay penalty. Default is 0 (no decay). Not used in RPROP
- "step_sizes" pair of minimal (default: 1e-6) and maximal (default: 50) allowed step sizes. Only used in RPROP
- "etas" pair of multiplicative increase and decrease factors. Default is (0.5, 1.2). Only used in RPROP
- "centered" if TRUE, compute the centered RMSProp where the gradient is normalized by an estimation of its variance weight_decay (L2 penalty). Default to FALSE. Only used in RMSPROP

When "builtin" backend is used, the following entries are relevant

- "maxeval" stop when the number of Newton steps in the inner loop exceeds maxeval. Default is 10000
- "ftol_in" stop the inner loop when the objective changes by less than ftol_in (relative). Default is 1e-8
- "maxit_em" stop the EM outer loop when the number of EM iterations exceeds maxit_em. Default is 50
- "ftol_em" stop the EM outer loop when the ELBO changes by less than ftol_em (relative). Default is 1e-8

The list of parameters `config_post` controls the post-treatment processing (for most `PLN*()` functions), with the following entries (defaults may vary depending on the specific function, check `config_post_default_*` for defaults values):

- jackknife boolean indicating whether jackknife should be performed to evaluate bias and variance of the model parameters. Default is FALSE.
- bootstrap integer indicating the number of bootstrap resamples generated to evaluate the variance of the model parameters. Default is 0 (inactivated).

- variational_var boolean indicating whether variational Fisher information matrix should be computed to estimate the variance of the model parameters (highly underestimated). Default is FALSE.
- sandwich_var boolean indicating whether sandwich estimation should be used to estimate the variance of the model parameters (highly underestimated). Default is FALSE.
- rsquared boolean indicating whether approximation of R2 based on deviance should be computed. Default is TRUE

Value

list of parameters configuring the fit.

Outer-loop optimization parameters

`PLNmixture_param()` adds parameters controlling the EM and smoothing outer loops:

- "ftol_em" outer EM solver stops when the objective changes by less than ftol_em (relative). Default is 1e-3
- "maxit_em" outer EM solver stops when the number of iterations exceeds maxit_em. Default is 50
- "it_smooth" number of the iterations of the smoothing procedure. Default is 1.

See Also

`PLN_param()`

PLNnetwork *Sparse Poisson lognormal model for network inference*

Description

Perform sparse inverse covariance estimation for the Zero Inflated Poisson lognormal model using a variational algorithm. Iterate over a range of logarithmically spaced sparsity parameter values. Use the (g)lm syntax to specify the model (including covariates and offsets).

Usage

```
PLNnetwork(
  formula,
  data,
  subset,
  weights,
  penalties = NULL,
  control = PLNnetwork_param()
)
```

Arguments

formula	an object of class "formula": a symbolic description of the model to be fitted.
data	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula), typically the environment from which the model is called.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
weights	an optional vector of observation weights to be used in the fitting process.
penalties	an optional vector of positive real number controlling the level of sparsity of the underlying network. if NULL (the default), will be set internally. See PLNnetwork_param() for additional tuning of the penalty.
control	a list-like structure for controlling the optimization, with default generated by PLNnetwork_param(). See the corresponding documentation for details;

Value

an R6 object with class PLNnetworkfamily, which contains a collection of models with class PLNnetworkfit

See Also

The classes PLNnetworkfamily and PLNnetworkfit, and the and the configuration function PLNnetwork_param().

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
fits <- PLNnetwork(Abundance ~ 1, data = trichoptera)
```

PLNnetworkfamily *An R6 Class to represent a collection of* PLNnetworkfits

---

Description

The function PLNnetwork() produces an instance of this class.

This class comes with a set of methods mostly used to compare network fits (in terms of goodness of fit) or extract one from the family (based on penalty parameter and/or goodness of it). See the documentation for getBestModel(), getModel() and plot() for the user-facing ones.

Super classes

PLNfamily -> Networkfamily -> PLNnetworkfamily

Methods

Public methods:

- PLNnetworkfamily$new()
- PLNnetworkfamily$stability_selection()
- PLNnetworkfamily$clone()

`PLNnetworkfamily$new()`: Initialize all models in the collection

Usage:

```
PLNnetworkfamily$new(penalties, data, control)
```

Arguments:

`penalties` a vector of positive real number controlling the level of sparsity of the underlying network.

`data` a named list used internally to carry the data matrices

`control` a list for controlling the optimization.

Returns: Update current `PLNnetworkfit` with smart starting values

`PLNnetworkfamily$stability_selection()`: Compute the stability path by stability selection

Usage:

```
PLNnetworkfamily$stability_selection(
  subsamples = NULL,
  control = PLNnetwork_param()
)
```

Arguments:

`subsamples` a list of vectors describing the subsamples. The number of vectors (or list length) determines the number of subsamples used in the stability selection. Automatically set to 20 subsamples with size `10*sqrt(n)` if `n >= 144` and `0.8*n` otherwise following Liu et al. (2010) recommendations.

`control` a list controlling the main optimization process in each call to `PLNnetwork()`. See `PLNnetwork()` and `PLN_param()` for details.

`PLNnetworkfamily$clone()`: The objects of this class are cloneable with this method.

Usage:

```
PLNnetworkfamily$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

The function `PLNnetwork()`, the class `PLNnetworkfit`

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
fits <- PLNnetwork(Abundance ~ 1, data = trichoptera)
class(fits)
```

PLNnetworkfit *An R6 Class to represent a PLNfit in a sparse inverse covariance framework*

Description

The function PLNnetwork() produces a collection of models which are instances of object with class PLNnetworkfit. This class comes with a set of methods, some of them being useful for the user: See the documentation for plot() and methods inherited from PLNfit.

Super classes

PLNfit -> PLNfit_fixedcov -> PLNnetworkfit

Active bindings

vcov_model character: the model used for the residual covariance

penalty the global level of sparsity in the current model

penalty_weights a matrix of weights controlling the amount of penalty element-wise.

n_edges number of edges if the network (non null coefficient of the sparse precision matrix)

nb_param number of parameters in the current PLN model

pen_loglik variational lower bound of the l1-penalized loglikelihood

EBIC variational lower bound of the EBIC

density proportion of non-null edges in the network

criteria a vector with loglik, penalized loglik, BIC, EBIC, ICL, R_squared, number of parameters, number of edges and graph density

Methods

Public methods:

- PLNnetworkfit$new()
- PLNnetworkfit$optimize()
- PLNnetworkfit$latent_network()
- PLNnetworkfit$plot_network()
- PLNnetworkfit$show()
- PLNnetworkfit$clone()

PLNnetworkfit$new(): Initialize a PLNnetworkfit object

Usage:

```
PLNnetworkfit$new(data, control)
```

Arguments:

data a named list used internally to carry the data matrices

`control` a list for controlling the optimization.

`PLNnetworkfit$optimize()`: Call to the C++ optimizer and update of the relevant fields

Usage:

```
PLNnetworkfit$optimize(data, config)
```

Arguments:

`data` a named list used internally to carry the data matrices

`config` a list for controlling the optimization

`PLNnetworkfit$latent_network()`: Extract interaction network in the latent space

Usage:

```
PLNnetworkfit$latent_network(type = c("partial_cor", "support", "precision"))
```

Arguments:

`type` edge value in the network. Can be "support" (binary edges), "precision" (coefficient of the precision matrix) or "partial_cor" (partial correlation between species)

Returns: a square matrix of size `PLNnetworkfit$n`

`PLNnetworkfit$plot_network()`: plot the latent network.

Usage:

```
PLNnetworkfit$plot_network(
  type = c("partial_cor", "support"),
  output = c("igraph", "corrplot"),
  edge.color = c("#F8766D", "#00BFC4"),
  remove.isolated = FALSE,
  node.labels = NULL,
  layout = layout_in_circle,
  plot = TRUE
)
```

Arguments:

`type` edge value in the network. Either "precision" (coefficient of the precision matrix) or "partial_cor" (partial correlation between species).

`output` Output type. Either `igraph` (for the network) or `corrplot` (for the adjacency matrix)

`edge.color` Length 2 color vector. Color for positive/negative edges. Default is `c("#F8766D", "#00BFC4")`. Only relevant for igraph output.

`remove.isolated` if `TRUE`, isolated node are remove before plotting. Only relevant for igraph output.

`node.labels` vector of character. The labels of the nodes. The default will use the column names ot the response matrix.

`layout` an optional igraph layout. Only relevant for igraph output.

`plot` logical. Should the final network be displayed or only sent back to the user. Default is `TRUE`.

`PLNnetworkfit$show()`: User friendly print method

Usage:

```
PLNnetworkfit$show()
```

`PLNnetworkfit$clone()`: The objects of this class are cloneable with this method.

Usage:

```
PLNnetworkfit$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

The function `PLNnetwork()`, the class `PLNnetworkfamily`

Examples

```
## Not run:
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
nets <- PLNnetwork(Abundance ~ 1, data = trichoptera)
myPLNnet <- getBestModel(nets)
class(myPLNnet)
print(myPLNnet)

## End(Not run)
```

`PLNnetwork_param` *Control of PLNnetwork fit*

Description

Helper to define list of parameters to control the PLN fit. All arguments have defaults.

Usage

```
PLNnetwork_param(
  backend = c("builtin", "nlopt", "torch"),
  inception_cov = c("full", "spherical", "diagonal"),
  inception_backend = NULL,
  inception_niter = NULL,
  maxit_ve = NULL,
  trace = 1,
  n_penalties = 30,
  min_ratio = 0.1,
  penalize_diagonal = TRUE,
  penalty_weights = NULL,
  config_post = list(),
  config_optim = list(),
  inception = NULL
)
```

Arguments

backend	optimization backend, either "builtin" (Newton, default) or "nlopt" (CCSAQ) or "torch". The default combines "builtin" with maxit_ve = 1 and inception_niter = 5 (see maxit_ve and inception_backend): this consistently finds a better ELBO than plain "nlopt", at essentially the same speed. Without a good inception, "builtin" alone (maxit_ve = NULL) can converge to a poor basin on large datasets — use "nlopt" if you want to opt out of the whole combination.
inception_cov	Covariance structure used for the inception PLN: "full" (default), "diagonal" or "spherical". Non-full structures are now fully supported: when inception_cov != "full", the penalty grid is built from the empirical covariance of latent residuals $M - XB$ (a full-rank proxy for Σ), avoiding the broken max_pen = 0 that previously occurred with diagonal/spherical.
inception_backend	character or NULL (default, i.e. same as backend). Backend for the inception PLN only; the penalty grid models always use backend. Ignored when inception is supplied by the user.
inception_niter	integer or NULL. Limits the inception PLN to at most this many iterations (EM iterations for "builtin", function evaluations × 10 for "nlopt"). Default is 5L when backend = "builtin" (NULL, i.e. full convergence, otherwise): fewer iterations keep the latent mean M from over-converging toward the unconstrained optimum, which would make it harder to warm-start the sparse penalty models. Values above ~20 typically hurt. When inception_cov != "full" or inception_niter is set, the penalty grid uses the empirical residual covariance $crossprod(M - XB)/n$ for max_pen.
maxit_ve	integer or NULL. Maximum number of inner VE-step iterations per outer GLASSO alternation turn. Default is 1L when backend = "builtin" (NULL, i.e. full convergence — maxit_em for "builtin", maxeval for "nlopt" — otherwise). maxit_ve = 1 implements a **partial E-step** (generalized EM): one Newton step per outer turn prevents over-convergence that causes oscillations with the GLASSO M-step — see backend for the full default combination and its benchmark.
trace	a integer for verbosity.
n_penalties	an integer that specifies the number of values for the penalty grid when internally generated. Ignored when penalties is non NULL
min_ratio	the penalty grid ranges from the minimal value that produces a sparse to this value multiplied by min_ratio. Default is 0.1.
penalize_diagonal	boolean: should the diagonal terms be penalized in the graphical-Lasso? Default is TRUE
penalty_weights	either a single or a list of p x p matrix of weights (default: all weights equal to 1) to adapt the amount of shrinkage to each pairs of node. Must be symmetric with positive values.
config_post	a list for controlling the post-treatments (optional bootstrap, jackknife, R2, etc.). See details

`config_optim` a list for controlling the optimizer (either "nlopt" or "torch" backend). See details

`inception` Set up the parameters initialization: by default, the model is initialized with a multivariate linear model applied on log-transformed data, and with the same formula as the one provided by the user. However, the user can provide a PLNfit (typically obtained from a previous fit), which sometimes speeds up the inference.

Details

The list of parameters `config_optim` controls the optimizers. When "nlopt" is chosen the following entries are relevant

- "algorithm" the optimization method used by NLOPT among LD type, e.g. "CCSAQ", "MMA", "LBFGS". See NLOPT documentation for further details. Default is "CCSAQ".
- "maxeval" stop when the number of iteration exceeds maxeval. Default is 10000
- "ftol_rel" stop when an optimization step changes the objective function by less than ftol multiplied by the absolute value of the parameter. Default is 1e-8
- "xtol_rel" stop when an optimization step changes every parameters by less than xtol multiplied by the absolute value of the parameter. Default is 1e-6
- "ftol_abs" stop when an optimization step changes the objective function by less than ftol_abs. Default is 0.0 (disabled)
- "xtol_abs" stop when an optimization step changes every parameters by less than xtol_abs. Default is 0.0 (disabled)
- "maxtime" stop when the optimization time (in seconds) exceeds maxtime. Default is -1 (disabled)
- "profiled" (full covariance only) if TRUE, profile both B and Omega at every nlopt evaluation instead of running an EM loop (Omega fixed for the duration of each inner nlopt solve, B profiled in closed form at every evaluation). Despite the extra `O(n*p^2 + p^3)` cost per evaluation, benchmarks found it consistently faster than the EM loop (and with a slightly better loglik) across a range of problem sizes. Default is TRUE; set to FALSE to recover the EM loop.

When "torch" backend is used (only for PLN and PLNLDA for now), the following entries are relevant:

- "algorithm" the optimizer used by torch among RPROP (default), RMSPROP, ADAM and ADAGRAD
- "maxeval" stop when the number of iteration exceeds maxeval. Default is 10 000
- "numepoch" stop training once this number of epochs exceeds numepoch. Set to -1 to enable infinite training. Default is 1 000
- "num_batch" number of batches to use during training. Defaults to 1 (use full dataset at each epoch)
- "ftol_rel" stop when an optimization step changes the objective function by less than ftol multiplied by the absolute value of the parameter. Default is 1e-8

- "xtol_rel" stop when an optimization step changes every parameters by less than xtol multiplied by the absolute value of the parameter. Default is 1e-6
- "lr" learning rate. Default is 0.1.
- "momentum" momentum factor. Default is 0 (no momentum). Only used in RMSPROP
- "weight_decay" Weight decay penalty. Default is 0 (no decay). Not used in RPROP
- "step_sizes" pair of minimal (default: 1e-6) and maximal (default: 50) allowed step sizes. Only used in RPROP
- "etas" pair of multiplicative increase and decrease factors. Default is (0.5, 1.2). Only used in RPROP
- "centered" if TRUE, compute the centered RMSProp where the gradient is normalized by an estimation of its variance weight_decay (L2 penalty). Default to FALSE. Only used in RMSPROP

When "builtin" backend is used, the following entries are relevant

- "maxeval" stop when the number of Newton steps in the inner loop exceeds maxeval. Default is 10000
- "ftol_in" stop the inner loop when the objective changes by less than ftol_in (relative). Default is 1e-8
- "maxit_em" stop the EM outer loop when the number of EM iterations exceeds maxit_em. Default is 50
- "ftol_em" stop the EM outer loop when the ELBO changes by less than ftol_em (relative). Default is 1e-8

The list of parameters `config_post` controls the post-treatment processing (for most `PLN*()` functions), with the following entries (defaults may vary depending on the specific function, check `config_post_default_*` for defaults values):

- jackknife boolean indicating whether jackknife should be performed to evaluate bias and variance of the model parameters. Default is FALSE.
- bootstrap integer indicating the number of bootstrap resamples generated to evaluate the variance of the model parameters. Default is 0 (inactivated).
- variational_var boolean indicating whether variational Fisher information matrix should be computed to estimate the variance of the model parameters (highly underestimated). Default is FALSE.
- sandwich_var boolean indicating whether sandwich estimation should be used to estimate the variance of the model parameters (highly underestimated). Default is FALSE.
- rsquared boolean indicating whether approximation of R2 based on deviance should be computed. Default is TRUE

Value

list of parameters configuring the fit.

Outer-loop optimization parameters

`PLNnetwork_param()` adds two parameters controlling the alternating GLASSO/VEM loop:

- "ftol_em" outer alternating solver stops when the objective changes by less than ftol_em (relative). Default is 1e-5
- "maxit_em" outer alternating solver stops when the number of iterations exceeds maxit_em. Default is 20

See Also

`PLN_param()`

PLNPCA *Poisson lognormal model towards Principal Component Analysis*

Description

Fit the PCA variants of the Poisson lognormal with a variational algorithm. Use the (g)lm syntax for model specification (covariates, offsets).

Usage

```
PLNPCA(formula, data, subset, weights, ranks = 1:5, control = PLNPCA_param())
```

Arguments

`formula`	an object of class "formula": a symbolic description of the model to be fitted.
`data`	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula), typically the environment from which the model is called.
`subset`	an optional vector specifying a subset of observations to be used in the fitting process.
`weights`	an optional vector of observation weights to be used in the fitting process.
`ranks`	a vector of integer containing the successive ranks (or number of axes to be considered)
`control`	a list-like structure for controlling the optimization, with default generated by `PLNPCA_param()`. See the associated documentation. for details.

Value

an R6 object with class `PLNPCAfamily`, which contains a collection of models with class `PLNPCAfit`

See Also

The classes `PLNPCAfamily` and `PLNPCAfit`, and the configuration function `PLNPCA_param()`.

Examples

```
## Use parallel to dispatch the computations on 2 workers
## Not run:
options(mc.cores = 2)

## End(Not run)

data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPCA <- PLNPCA(Abundance ~ 1 + offset(log(Offset)), data = trichoptera, ranks = 1:5)

## Not run:
options(mc.cores = 1)

## End(Not run)
```

PLNPCAfamily *An R6 Class to represent a collection of PLNPCAfit*

Description

The function PLNPCA() produces an instance of this class.

This class comes with a set of methods, some of them being useful for the user: See the documentation for getBestModel(), getModel() and plot().

Super class

PLNfamily -> PLNPCAfamily

Active bindings

ranks the dimensions of the successively fitted models

Methods

Public methods:

- PLNPCAfamily$new()
- PLNPCAfamily$optimize()
- PLNPCAfamily$getModel()
- PLNPCAfamily$getBestModel()
- PLNPCAfamily$plot()
- PLNPCAfamily$show()
- PLNPCAfamily$clone()

PLNPCAfamily$new(): Initialize all models in the collection. A single SVD of the residual matrix M - X*B is computed once and shared across all ranks. M and B come from either a user-provided PLNfit inception or a fast LM on log-transformed counts (default, controlled by init_method).

Usage:

```
PLNPCAfamily$new(
  ranks,
  responses,
  covariates,
  offsets,
  weights,
  formula,
  control
)
```

Arguments:

`ranks` the dimensions of the successively fitted models

`responses` the matrix of responses common to every models

`covariates` the matrix of covariates common to every models

`offsets` the matrix of offsets common to every models

`weights` the vector of observation weights

`formula` model formula used for fitting, extracted from the formula in the upper-level call

`control` list controlling the optimization and the model

`PLNPCAfamily$optimize()`**:** Call to the C++ optimizer on all models of the collection

Usage:

```
PLNPCAfamily$optimize(config)
```

Arguments:

`config` list controlling the optimization.

`PLNPCAfamily$getModel()`**:** Extract model from collection and add "PCA" class for compatibility with `factoextra::fviz()`

Usage:

```
PLNPCAfamily$getModel(var, index = NULL)
```

Arguments:

`var` value of the parameter (rank for PLNPCA, sparsity for PLNnetwork) that identifies the model to be extracted from the collection. If no exact match is found, the model with closest parameter value is returned with a warning.

`index` Integer index of the model to be returned. Only the first value is taken into account.

Returns: a `PLNPCAfit` object

`PLNPCAfamily$getBestModel()`**:** Extract best model in the collection

Usage:

```
PLNPCAfamily$getBestModel(crit = c("ICL", "BIC"))
```

Arguments:

`crit` a character for the criterion used to performed the selection. Either "ICL", "BIC". Default is `ICL`

Returns: a `PLNPCAfit` object

`PLNPCAfamily$plot()`: Lineplot of selected criteria for all models in the collection

Usage:

```
PLNPCAfamily$plot(criteria = c("loglik", "BIC", "ICL"), reverse = FALSE)
```

Arguments:

`criteria` A valid model selection criteria for the collection of models. Any of "loglik", "BIC" or "ICL" (all).

`reverse` A logical indicating whether to plot the value of the criteria in the "natural" direction (loglik - penalty) or in the "reverse" direction (-2 loglik + penalty). Default to FALSE, i.e use the natural direction, on the same scale as the log-likelihood.

Returns: A `ggplot2::ggplot` object

`PLNPCAfamily$show()`: User friendly print method

Usage:

```
PLNPCAfamily$show()
```

`PLNPCAfamily$clone()`: The objects of this class are cloneable with this method.

Usage:

```
PLNPCAfamily$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

The function `PLNPCA()`, the class `PLNPCAfit()`

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPCAs <- PLNPCA(Abundance ~ 1 + offset(log(Offset)), data = trichoptera, ranks = 1:5)
class(myPCAs)
```

PLNPCAfit *An R6 Class to represent a PLNfit in a PCA framework*

Description

The function `PLNPCA()` produces a collection of models which are instances of object with class `PLNPCAfit`. This class comes with a set of methods, some of them being useful for the user: See the documentation for the methods inherited by `PLNfit` and the `plot()` methods for PCA visualization

Super class

`PLNfit` -> `PLNPCAfit`

Active bindings

`var_par` variational parameters (M, S2) in the rank-q latent space

`rank` the dimension of the current model

`vcov_model` character: the model used for the residual covariance

`nb_param` number of parameters in the current PLN model

`entropy` entropy of the variational distribution

`latent_pos` a matrix: values of the latent position vector (Z) without covariates effects or offset

`model_par` a list with the matrices associated with the estimated parameters of the pPCA model: B (covariates), Sigma (covariance), Omega (precision) and C (loadings)

`percent_var` the percent of variance explained by each axis

`corr_circle` a matrix of correlations to plot the correlation circles

`scores` a matrix of scores to plot the individual factor maps (a.k.a. principal components)

`rotation` a matrix of rotation of the latent space

`eig` description of the eigenvalues, similar to percent_var but for use with external methods

`var` a list of data frames with PCA results for the variables: `coord` (coordinates of the variables), `cor` (correlation between variables and dimensions), `cos2` (Cosine of the variables) and `contrib` (contributions of the variable to the axes)

`ind` a list of data frames with PCA results for the individuals: `coord` (coordinates of the individuals), `cos2` (Cosine of the individuals), `contrib` (contributions of individuals to an axis inertia) and `dist` (distance of individuals to the origin).

`call` Hacky binding for compatibility with factoextra functions

Methods

Public methods:

- `PLNPCAfit$new()`
- `PLNPCAfit$warm_start_from()`
- `PLNPCAfit$update()`
- `PLNPCAfit$optimize()`
- `PLNPCAfit$optimize_vestep()`
- `PLNPCAfit$project()`
- `PLNPCAfit$setVisualization()`
- `PLNPCAfit$postTreatment()`
- `PLNPCAfit$plot_individual_map()`
- `PLNPCAfit$plot_correlation_circle()`
- `PLNPCAfit$plot_PCA()`
- `PLNPCAfit$show()`
- `PLNPCAfit$clone()`

`PLNPCAfit$new()`: Initialize a `PLNPCAfit` object. Uses the shared SVD from `control$svdM` (computed once in `PLNPCAfamily`) to set the starting loadings `C` and scores `M`. The regression coefficients `B` are initialised by the parent `PLNfit` constructor (LM or user-provided inception).

Usage:

```
PLNPCAfit$new(rank, responses, covariates, offsets, weights, formula, control)
```

Arguments:

`rank` rank of the PCA (or equivalently, dimension of the latent space)

`responses` the matrix of responses (called Y in the model). Will usually be extracted from the corresponding field in `PLNfamily`

`covariates` design matrix (called X in the model). Will usually be extracted from the corresponding field in `PLNfamily`

`offsets` offset matrix (called O in the model). Will usually be extracted from the corresponding field in `PLNfamily`

`weights` an optional vector of observation weights to be used in the fitting process.

`formula` model formula used for fitting, extracted from the formula in the upper-level call

`control` a list for controlling the optimization. See details.

`PLNPCAfit$warm_start_from()`: Reinitialize parameters for sequential warm-starting from a lower-rank fit. Fitted loadings C, scores M, variances S, and regression coefficients B from `prev_fit` are carried over; new columns are padded using the inception SVD (C) or zeros/0.1 (M/S).

Usage:

```
PLNPCAfit$warm_start_from(prev_fit, svdM)
```

Arguments:

`prev_fit` a converged `PLNPCAfit` of rank `self$rank - k` (k >= 1)

`svdM` the inception SVD (from `PLNPCAfamily`)

`PLNPCAfit$update()`: Update a `PLNPCAfit` object

Usage:

```
PLNPCAfit$update(
  B = NA,
  Sigma = NA,
  Omega = NA,
  C = NA,
  M = NA,
  S2 = NA,
  Z = NA,
  A = NA,
  Ji = NA,
  R2 = NA,
  monitoring = NA
)
```

Arguments:

`B` matrix of regression matrix

`Sigma` variance-covariance matrix of the latent variables

`Omega` precision matrix of the latent variables. Inverse of Sigma.

`C` matrix of PCA loadings (in the latent space)

`M` matrix of mean vectors for the variational approximation

`S2` matrix of variational variances (n × q)

`Z` matrix of latent vectors (includes covariates and offset effects)

`A` matrix of fitted values

`Ji` vector of variational lower bounds of the log-likelihoods (one value per sample)

`R2` approximate R^2 goodness-of-fit criterion

`monitoring` a list with optimization monitoring quantities

Returns: Update the current `PLNPCAfit` object

`PLNPCAfit$optimize()`**:** Call to the C++ optimizer and update of the relevant fields

Usage:

```
PLNPCAfit$optimize(responses, covariates, offsets, weights, config)
```

Arguments:

`responses` the matrix of responses (called Y in the model). Will usually be extracted from the corresponding field in `PLNfamily`

`covariates` design matrix (called X in the model). Will usually be extracted from the corresponding field in `PLNfamily`

`offsets` offset matrix (called O in the model). Will usually be extracted from the corresponding field in `PLNfamily`

`weights` an optional vector of observation weights to be used in the fitting process.

`config` part of the `control` argument which configures the optimizer

`PLNPCAfit$optimize_vestep()`**:** Result of one call to the VE step of the optimization procedure: optimal variational parameters (M, S) and corresponding log likelihood values for fixed model parameters (C, B). Intended to position new data in the latent space for further use with PCA.

Usage:

```
PLNPCAfit$optimize_vestep(
  covariates,
  offsets,
  responses,
  weights = rep(1, self$n),
  control = PLNPCA_param(backend = "nlopt")
)
```

Arguments:

`covariates` design matrix (called X in the model). Will usually be extracted from the corresponding field in `PLNfamily`

`offsets` offset matrix (called O in the model). Will usually be extracted from the corresponding field in `PLNfamily`

`responses` the matrix of responses (called Y in the model). Will usually be extracted from the corresponding field in `PLNfamily`

`weights` an optional vector of observation weights to be used in the fitting process.

`control` a list for controlling the optimization. See details.

Returns: A list with three components:

- the matrix M of variational means,
- the matrix S2 of variational variances
- the vector log.lik of (variational) log-likelihood of each new observation

`PLNPCAfit$project()`: Project new samples into the PCA space using one VE step

Usage:

```
PLNPCAfit$project(newdata, control = PLNPCA_param(), envir = parent.frame())
```

Arguments:

`newdata` A data frame in which to look for variables, offsets and counts with which to predict.

`control` a list for controlling the optimization. See `PLN()` for details.

`envir` Environment in which the projection is evaluated

Returns:

- the named matrix of scores for the newdata, expressed in the same coordinate system as `self$scores`

`PLNPCAfit$setVisualization()`: Compute PCA scores in the latent space and update corresponding fields.

Usage:

```
PLNPCAfit$setVisualization(scale.unit = FALSE)
```

Arguments:

`scale.unit` Logical. Should PCA scores be rescaled to have unit variance

`PLNPCAfit$postTreatment()`: Update R2, fisher, std_err fields and set up visualization

Usage:

```
PLNPCAfit$postTreatment(
  responses,
  covariates,
  offsets,
  weights = rep(1, nrow(responses)),
  config_post,
  config_optim,
  nullModel = NULL
)
```

Arguments:

`responses` the matrix of responses (called Y in the model). Will usually be extracted from the corresponding field in `PLNfamily`

`covariates` design matrix (called X in the model). Will usually be extracted from the corresponding field in `PLNfamily`

`offsets` offset matrix (called O in the model). Will usually be extracted from the corresponding field in `PLNfamily`

`weights` an optional vector of observation weights to be used in the fitting process.

`config_post` a list for controlling the post-treatments (optional bootstrap, jackknife, R2, etc.). See details

`config_optim` a list for controlling the optimizer (either "nlopt" or "torch" backend). See details

`nullModel` null model used for approximate R2 computations. Defaults to a GLM model with same design matrix but not latent variable.

Details: The list of parameters `config_post` controls the post-treatment processing, with the following entries:

- jackknife boolean indicating whether jackknife should be performed to evaluate bias and variance of the model parameters. Default is FALSE.
- bootstrap integer indicating the number of bootstrap resamples generated to evaluate the variance of the model parameters. Default is 0 (inactivated).
- variational_var boolean indicating whether variational Fisher information matrix should be computed to estimate the variance of the model parameters (highly underestimated). Default is FALSE.
- rsquared boolean indicating whether approximation of R2 based on deviance should be computed. Default is TRUE
- trace integer for verbosity. should be > 1 to see output in post-treatments

`PLNPCAfit$plot_individual_map()`: Plot the factorial map of the PCA

Usage:

```
PLNPCAfit$plot_individual_map(
  axes = 1:min(2, self$rank),
  main = "Individual Factor Map",
  plot = TRUE,
  cols = "default"
)
```

Arguments:

`axes` numeric, the axes to use for the plot when map = "individual" or "variable". Default it c(1,min(rank))

`main` character. A title for the single plot (individual or variable factor map). If NULL (the default), an hopefully appropriate title will be used.

`plot` logical. Should the plot be displayed or sent back as ggplot object

`cols` a character, factor or numeric to define the color associated with the individuals. By default, all individuals receive the default color of the current palette.

Returns: a `ggplot2::ggplot` graphic

`PLNPCAfit$plot_correlation_circle()`: Plot the correlation circle of a specified axis for a `PLNLDAfit` object

Usage:

```
PLNPCAfit$plot_correlation_circle(
  axes = 1:min(2, self$rank),
  main = "Variable Factor Map",
  cols = "default",
  plot = TRUE
)
```

Arguments:

`axes` numeric, the axes to use for the plot when map = "individual" or "variable". Default it c(1,min(rank))

`main` character. A title for the single plot (individual or variable factor map). If NULL (the default), an hopefully appropriate title will be used.

`cols` a character, factor or numeric to define the color associated with the variables. By default, all variables receive the default color of the current palette.

`plot` logical. Should the plot be displayed or sent back as ggplot object

Returns: a `ggplot2::ggplot` graphic

`PLNPCAfit$plot_PCA()`: Plot a summary of the `PLNPCAfit` object

Usage:

```
PLNPCAfit$plot_PCA(
  nb_axes = min(3, self$rank),
  ind_cols = "ind_cols",
  var_cols = "var_cols",
  plot = TRUE
)
```

Arguments:

`nb_axes` scalar: the number of axes to be considered when map = "both". The default is min(3,rank).

`ind_cols` a character, factor or numeric to define the color associated with the individuals. By default, all variables receive the default color of the current palette.

`var_cols` a character, factor or numeric to define the color associated with the variables. By default, all variables receive the default color of the current palette.

`plot` logical. Should the plot be displayed or sent back as ggplot object

Returns: a `grob` object

`PLNPCAfit$show()`: User friendly print method

Usage:

```
PLNPCAfit$show()
```

`PLNPCAfit$clone()`: The objects of this class are cloneable with this method.

Usage:

```
PLNPCAfit$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

The function `PLNPCA`, the class `PLNPCAfamily`

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPCAs <- PLNPCA(Abundance ~ 1 + offset(log(Offset)), data = trichoptera, ranks = 1:5)
myPCA <- getBestModel(myPCAs)
class(myPCA)
print(myPCA)
```

PLNPCA_param *Control of PLNPCA fit*

Description

Helper to define list of parameters to control the PLNPCA fit. All arguments have defaults.

Usage

```
PLNPCA_param(
  backend = c("nlopt", "builtin", "torch"),
  trace = 1,
  config_optim = list(),
  config_post = list(),
  inception = NULL,
  init_method = c("LM", "GLM", "EM"),
  init_niter = 5L,
  sequential = FALSE
)
```

Arguments

backend	optimization backend, either "nlopt" (default, NLOPT/CCSAQ, recommended for PLNPCA: conservative per-variable steps reliably find the global basin even when the singular-value ratio d1/sqrt(n) is large), "builtin" (the home-made optimizer, a profiled trust-region Newton), or "torch" (**experimental**: automatic differentiation via the torch package; tends to find lower loglik than "nlopt" and "builtin" on most datasets — not recommended). The "builtin" backend profiles out the variational parameters (M, S) with a per-observation Newton VE-step and optimises the loadings (B, C) with a saddle-aware trust-region Newton on the resulting objective (analytic Schur Hessian-vector products, Jacobi-preconditioned Steihaug-CG). It reliably reaches a higher variational bound than "nlopt" on small/moderate data at comparable speed, and is faster on large data; tuning keys in config_optim: cg_maxit, maxit_out, ftol_out, gtol, delta0. On large data (many samples and variables) the reduced-Hessian landscape is indefinite and the outer trust-region iteration converges slowly but keeps improving the bound, so it is capped by maxit_out (default 150) rather than by the gradient tolerance: the higher ranks then trade quality for time. For the best variational bound on large data, raise it, e.g. config_optim = list(maxit_out = 300).

`trace` a integer for verbosity.

`config_optim` a list for controlling the optimizer (either "nlopt" or "torch" backend). See details

`config_post` a list for controlling the post-treatments (optional bootstrap, jackknife, R2, etc.). See details

`inception` an optional pre-fitted `PLNfit` object. When provided, its variational means `M` and regression coefficients `B` are used to compute the shared SVD `svd(M - X*B)` that initialises all ranks simultaneously. This replaces the default LM-based starting point and gives the highest-quality initialisation for large ranks. When `NULL` (default), see `init_method`. `init_method` is ignored when `inception` is set. **Recommendation**: for large ranks (`rank > sqrt(p)`) on complex datasets, prefer `init_method = "EM"` (cheap, most gains) or `inception = PLN(formula, data)` (maximum quality, full convergence cost).

`init_method` character: strategy used to compute the starting point for the shared SVD.

- `"LM"` (default): fast multivariate `lm.fit` on log-transformed counts. Good for small to moderate ranks (`rank <= sqrt(p)`). Recommended default.
- `"GLM"`: p independent Poisson GLMs. Rarely better than `"LM"` for PLNPCA; not recommended.
- `"EM"`: run `init_niter` variational EM iterations of a full PLN (builtin backend) before computing the SVD, giving a latent mean M closer to the true posterior. **Recommended for large ranks** (`rank > sqrt(p)`), where it noticeably improves the loglik at negligible extra cost. Caution: hurts for small ranks, because an over-converged M reduces low-rank SVD discriminability. Ignored when `inception` is provided.

`init_niter` integer: number of PLN EM iterations when `init_method = "EM"`. Default is 5. The sweet spot is 2–10: beyond ~10 the M over-converges toward the full PLN optimum, degrading the low-rank SVD and hurting small-rank models. Ignored for `"LM"` and `"GLM"`.

`sequential` logical. If `TRUE`, ranks are fitted in ascending order and each model is warm-started from the converged solution of the previous rank: loadings C are augmented with new columns from the inception SVD, while latent scores M and variances S2 are padded with zeros / 0.01 respectively. Disables parallel fitting across ranks. Default is `FALSE`.

Details

The list of parameters `config_optim` controls the optimizers. When "nlopt" is chosen the following entries are relevant

- "algorithm" the optimization method used by NLOPT among LD type, e.g. "CCSAQ", "MMA", "LBFGS". See NLOPT documentation for further details. Default is "CCSAQ".
- "maxeval" stop when the number of iteration exceeds maxeval. Default is 10000
- "ftol_rel" stop when an optimization step changes the objective function by less than ftol multiplied by the absolute value of the parameter. Default is 1e-8
- "xtol_rel" stop when an optimization step changes every parameters by less than xtol multiplied by the absolute value of the parameter. Default is 1e-6

- "ftol_abs" stop when an optimization step changes the objective function by less than ftol_abs. Default is 0.0 (disabled)
- "xtol_abs" stop when an optimization step changes every parameters by less than xtol_abs. Default is 0.0 (disabled)
- "maxtime" stop when the optimization time (in seconds) exceeds maxtime. Default is -1 (disabled)
- "profiled" (full covariance only) if TRUE, profile both B and Omega at every nlopt evaluation instead of running an EM loop (Omega fixed for the duration of each inner nlopt solve, B profiled in closed form at every evaluation). Despite the extra `O(n*p^2 + p^3)` cost per evaluation, benchmarks found it consistently faster than the EM loop (and with a slightly better loglik) across a range of problem sizes. Default is TRUE; set to FALSE to recover the EM loop.

When "torch" backend is used (only for PLN and PLNLDA for now), the following entries are relevant:

- "algorithm" the optimizer used by torch among RPROP (default), RMSPROP, ADAM and ADAGRAD
- "maxeval" stop when the number of iteration exceeds maxeval. Default is 10 000
- "numepoch" stop training once this number of epochs exceeds numepoch. Set to -1 to enable infinite training. Default is 1 000
- "num_batch" number of batches to use during training. Defaults to 1 (use full dataset at each epoch)
- "ftol_rel" stop when an optimization step changes the objective function by less than ftol multiplied by the absolute value of the parameter. Default is 1e-8
- "xtol_rel" stop when an optimization step changes every parameters by less than xtol multiplied by the absolute value of the parameter. Default is 1e-6
- "lr" learning rate. Default is 0.1.
- "momentum" momentum factor. Default is 0 (no momentum). Only used in RMSPROP
- "weight_decay" Weight decay penalty. Default is 0 (no decay). Not used in RPROP
- "step_sizes" pair of minimal (default: 1e-6) and maximal (default: 50) allowed step sizes. Only used in RPROP
- "etas" pair of multiplicative increase and decrease factors. Default is (0.5, 1.2). Only used in RPROP
- "centered" if TRUE, compute the centered RMSProp where the gradient is normalized by an estimation of its variance weight_decay (L2 penalty). Default to FALSE. Only used in RMSPROP

When "builtin" backend is used, the following entries are relevant

- "maxeval" stop when the number of Newton steps in the inner loop exceeds maxeval. Default is 10000
- "ftol_in" stop the inner loop when the objective changes by less than ftol_in (relative). Default is 1e-8

- "maxit_em" stop the EM outer loop when the number of EM iterations exceeds maxit_em. Default is 50
- "ftol_em" stop the EM outer loop when the ELBO changes by less than ftol_em (relative). Default is 1e-8

The list of parameters `config_post` controls the post-treatment processing (for most `PLN*()` functions), with the following entries (defaults may vary depending on the specific function, check `config_post_default_*` for defaults values):

- jackknife boolean indicating whether jackknife should be performed to evaluate bias and variance of the model parameters. Default is FALSE.
- bootstrap integer indicating the number of bootstrap resamples generated to evaluate the variance of the model parameters. Default is 0 (inactivated).
- variational_var boolean indicating whether variational Fisher information matrix should be computed to estimate the variance of the model parameters (highly underestimated). Default is FALSE.
- sandwich_var boolean indicating whether sandwich estimation should be used to estimate the variance of the model parameters (highly underestimated). Default is FALSE.
- rsquared boolean indicating whether approximation of R2 based on deviance should be computed. Default is TRUE

Value

list of parameters configuring the fit.

`PLN_param` *Control of a PLN fit*

Description

Helper to define list of parameters to control the PLN fit. All arguments have defaults.

Usage

```
PLN_param(
  backend = c("nlopt", "builtin", "torch"),
  trace = 1,
  covariance = c("full", "diagonal", "spherical", "fixed", "genpop"),
  Omega = NULL,
  C = NULL,
  config_post = list(),
  config_optim = list(),
  inception = NULL,
  init_method = c("LM", "GLM")
)
```

Arguments

backend	optimization backend, either "nlopt" (default), "builtin" or "torch". "nlopt" (CCSAQ, with config_optim$profiled = TRUE) is consistently faster than "builtin". "builtin" is the built-in envelope-theorem Newton optimizer; it can reach a slightly better optimum, an advantage that tends to grow with p — prefer it when the last bit of ELBO matters more than speed, typically for large p. "torch" is **experimental**: it may converge to suboptimal solutions or fail on some datasets.
trace	a integer for verbosity.
covariance	character setting the model for the covariance matrix. Either "full", "diagonal", "spherical", "fixed" or "genpop". Default is "full".
Omega	precision matrix of the latent variables. Inverse of Sigma. Must be specified if covariance is "fixed"
C	a fixed p x p correlation matrix (e.g. a genetic relationship matrix). Must be specified if covariance is "genpop": the residual covariance is then modeled as Sigma = sigma2 * (rho * C + (1 - rho) * I), with sigma2 and rho estimated.
config_post	a list for controlling the post-treatments (optional bootstrap, jackknife, R2, etc.). See details
config_optim	a list for controlling the optimizer (either "nlopt" or "torch" backend). See details
inception	Set up the parameters initialization: by default, the model is initialized with a multivariate linear model applied on log-transformed data, and with the same formula as the one provided by the user. However, the user can provide a PLNfit (typically obtained from a previous fit), which sometimes speeds up the inference.
init_method	character: strategy for the starting-point computation (ignored when inception is a PLNfit). Either "LM" (default) or "GLM" (p independent Poisson GLMs, better for complex or unbalanced designs). See compute_PLN_starting_point().

Details

The list of parameters config_optim controls the optimizers. When "nlopt" is chosen the following entries are relevant

- "algorithm" the optimization method used by NLOPT among LD type, e.g. "CCSAQ", "MMA", "LBFGS". See NLOPT documentation for further details. Default is "CCSAQ".
- "maxeval" stop when the number of iteration exceeds maxeval. Default is 10000
- "ftol_rel" stop when an optimization step changes the objective function by less than ftol multiplied by the absolute value of the parameter. Default is 1e-8
- "xtol_rel" stop when an optimization step changes every parameters by less than xtol multiplied by the absolute value of the parameter. Default is 1e-6
- "ftol_abs" stop when an optimization step changes the objective function by less than ftol_abs. Default is 0.0 (disabled)
- "xtol_abs" stop when an optimization step changes every parameters by less than xtol_abs. Default is 0.0 (disabled)

- "maxtime" stop when the optimization time (in seconds) exceeds maxtime. Default is -1 (disabled)
- "profiled" (full covariance only) if TRUE, profile both B and Omega at every nlopt evaluation instead of running an EM loop (Omega fixed for the duration of each inner nlopt solve, B profiled in closed form at every evaluation). Despite the extra `O(n*p^2 + p^3)` cost per evaluation, benchmarks found it consistently faster than the EM loop (and with a slightly better loglik) across a range of problem sizes. Default is TRUE; set to FALSE to recover the EM loop.

When "torch" backend is used (only for PLN and PLNLDA for now), the following entries are relevant:

- "algorithm" the optimizer used by torch among RPROP (default), RMSPROP, ADAM and ADAGRAD
- "maxeval" stop when the number of iteration exceeds maxeval. Default is 10 000
- "numepoch" stop training once this number of epochs exceeds numepoch. Set to -1 to enable infinite training. Default is 1 000
- "num_batch" number of batches to use during training. Defaults to 1 (use full dataset at each epoch)
- "ftol_rel" stop when an optimization step changes the objective function by less than ftol multiplied by the absolute value of the parameter. Default is 1e-8
- "xtol_rel" stop when an optimization step changes every parameters by less than xtol multiplied by the absolute value of the parameter. Default is 1e-6
- "lr" learning rate. Default is 0.1.
- "momentum" momentum factor. Default is 0 (no momentum). Only used in RMSPROP
- "weight_decay" Weight decay penalty. Default is 0 (no decay). Not used in RPROP
- "step_sizes" pair of minimal (default: 1e-6) and maximal (default: 50) allowed step sizes. Only used in RPROP
- "etas" pair of multiplicative increase and decrease factors. Default is (0.5, 1.2). Only used in RPROP
- "centered" if TRUE, compute the centered RMSProp where the gradient is normalized by an estimation of its variance weight_decay (L2 penalty). Default to FALSE. Only used in RMSPROP

When "builtin" backend is used, the following entries are relevant

- "maxeval" stop when the number of Newton steps in the inner loop exceeds maxeval. Default is 10000
- "ftol_in" stop the inner loop when the objective changes by less than ftol_in (relative). Default is 1e-8
- "maxit_em" stop the EM outer loop when the number of EM iterations exceeds maxit_em. Default is 50
- "ftol_em" stop the EM outer loop when the ELBO changes by less than ftol_em (relative). Default is 1e-8

The list of parameters `config_post` controls the post-treatment processing (for most `PLN*()` functions), with the following entries (defaults may vary depending on the specific function, check `config_post_default_*` for defaults values):

- jackknife boolean indicating whether jackknife should be performed to evaluate bias and variance of the model parameters. Default is FALSE.
- bootstrap integer indicating the number of bootstrap resamples generated to evaluate the variance of the model parameters. Default is 0 (inactivated).
- variational_var boolean indicating whether variational Fisher information matrix should be computed to estimate the variance of the model parameters (highly underestimated). Default is FALSE.
- sandwich_var boolean indicating whether sandwich estimation should be used to estimate the variance of the model parameters (highly underestimated). Default is FALSE.
- rsquared boolean indicating whether approximation of R2 based on deviance should be computed. Default is TRUE

Value

list of parameters configuring the fit.

`plot.Networkfamily` *Display various outputs (goodness-of-fit criteria, robustness, diagnostic) associated with a collection of network fits (either* `PLNnetworkfamily` *or* `ZIPLNnetworkfamily`*)*

Description

Display various outputs (goodness-of-fit criteria, robustness, diagnostic) associated with a collection of network fits (either `PLNnetworkfamily` or `ZIPLNnetworkfamily`)

Usage

```
## S3 method for class 'Networkfamily'
plot(
  x,
  type = c("criteria", "stability", "diagnostic"),
  criteria = c("loglik", "pen_loglik", "BIC", "EBIC"),
  reverse = FALSE,
  log.x = TRUE,
  stability = 0.9,
  ...
)

## S3 method for class 'PLNnetworkfamily'
plot(
  x,
```

```
  type = c("criteria", "stability", "diagnostic"),
  criteria = c("loglik", "pen_loglik", "BIC", "EBIC"),
  reverse = FALSE,
  log.x = TRUE,
  stability = 0.9,
  ...
)

## S3 method for class 'ZIPLNnetworkfamily'
plot(
  x,
  type = c("criteria", "stability", "diagnostic"),
  criteria = c("loglik", "pen_loglik", "BIC", "EBIC"),
  reverse = FALSE,
  log.x = TRUE,
  stability = 0.9,
  ...
)
```

Arguments

x	an R6 object with class PLNnetworkfamily or ZIPLNnetworkfamily
type	a character, either "criteria", "stability" or "diagnostic" for the type of plot.
criteria	Vector of criteria to plot, to be selected among "loglik" (log-likelihood), "BIC", "ICL", "R_squared", "EBIC" and "pen_loglik" (penalized log-likelihood). Default is c("loglik", "pen_loglik", "BIC", "EBIC"). Only used when type = "criteria".
reverse	A logical indicating whether to plot the value of the criteria in the "natural" direction (loglik - 0.5 penalty) or in the "reverse" direction (-2 loglik + penalty). Default to FALSE, i.e use the natural direction, on the same scale as the log-likelihood.
log.x	logical: should the x-axis be represented in log-scale? Default is TRUE.
stability	scalar: the targeted level of stability in stability plot. Default is .9.
...	additional parameters for S3 compatibility. Not used

Details

The BIC and ICL criteria have the form 'loglik - 1/2 * penalty' so that they are on the same scale as the model log-likelihood. You can change this direction and use the alternate form '-2*loglik + penalty', as some authors do, by setting reverse = TRUE.

Value

Produces either a diagnostic plot (with type = 'diagnostic'), a stability plot (with type = 'stability') or the evolution of the criteria of the different models considered (with type = 'criteria', the default).

Functions

- `plot(PLNnetworkfamily)`: Display various outputs associated with a collection of network fits
- `plot(ZIPLNnetworkfamily)`: Display various outputs associated with a collection of network fits

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
fits <- PLNnetwork(Abundance ~ 1, data = trichoptera)
## Not run:
plot(fits)

## End(Not run)
```

---

plot.PLNfamily *Display the criteria associated with a collection of PLN fits (a PLNfamily)*

Description

Display the criteria associated with a collection of PLN fits (a PLNfamily)

Usage

```
## S3 method for class 'PLNfamily'
plot(x, criteria = c("loglik", "BIC", "ICL"), reverse = FALSE, ...)
```

Arguments

`x`	an R6 object with class `PLNfamily`
`criteria`	vector of characters. The criteria to plot in c("loglik", "BIC", "ICL"). Default is c("loglik", "BIC", "ICL").
`reverse`	A logical indicating whether to plot the value of the criteria in the "natural" direction (loglik - 0.5 penalty) or in the "reverse" direction (-2 loglik + penalty). Default to FALSE, i.e use the natural direction, on the same scale as the log-likelihood.
`...`	additional parameters for S3 compatibility. Not used

Details

The BIC and ICL criteria have the form 'loglik - 1/2 * penalty' so that they are on the same scale as the model log-likelihood. You can change this direction and use the alternate form '-2*loglik + penalty', as some authors do, by setting `reverse = TRUE`.

Value

Produces a plot representing the evolution of the criteria of the different models considered, highlighting the best model in terms of BIC and ICL (see details).

See Also

`plot.PLNPCAfamily()` and `plot.PLNnetworkfamily()`

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPCAs <- PLNPCA(Abundance ~ 1 + offset(log(Offset)), data = trichoptera, ranks = 1:5)
## Not run:
plot(myPCAs)

## End(Not run)
```

---

plot.PLNLDAfit *LDA visualization (individual and/or variable factor map(s)) for a* `PLNPCAfit` *object*

Description

LDA visualization (individual and/or variable factor map(s)) for a `PLNPCAfit` object

Usage

```
## S3 method for class 'PLNLDAfit'
plot(
  x,
  map = c("both", "individual", "variable"),
  nb_axes = min(3, x$rank),
  axes = seq.int(min(2, x$rank)),
  var_cols = "var_colors",
  plot = TRUE,
  main = NULL,
  ...
)
```

Arguments

x	an R6 object with class PLNPCAfit
map	the type of output for the PCA visualization: either "individual", "variable" or "both". Default is "both".
nb_axes	scalar: the number of axes to be considered when map = "both". The default is min(3,rank).

axes	numeric, the axes to use for the plot when map = "individual" or "variable". Default it c(1,min(rank))
var_cols	a character or factor to define the color associated with the variables. By default, all variables receive the default color of the current palette.
plot	logical. Should the plot be displayed or sent back as ggplot2::ggplot object
main	character. A title for the single plot (individual or variable factor map). If NULL (the default), an hopefully appropriate title will be used.
...	Not used (S3 compatibility).

Value

displays an individual and/or variable factor maps for the corresponding axes, and/or sends back a ggplot2::ggplot or gtable object

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLNLDA <- PLNLDA(Abundance ~ 1, grouping = Group, data = trichoptera)
## Not run:
plot(myPLNLDA, map = "individual", nb_axes = 2)

## End(Not run)
```

---

plot.PLNmixturefamily *Display the criteria associated with a collection of PLNmixture fits (a PLNmixturefamily)*

Description

Display the criteria associated with a collection of PLNmixture fits (a PLNmixturefamily)

Usage

```
## S3 method for class 'PLNmixturefamily'
plot(
  x,
  type = c("criteria", "diagnostic"),
  criteria = c("loglik", "BIC", "ICL"),
  reverse = FALSE,
  ...
)
```

Arguments

x	an R6 object with class PLNmixturefamily
type	a character, either "criteria" or "diagnostic" for the type of plot.
criteria	vector of characters. The criteria to plot in c("loglik", "BIC", "ICL"). Default is c("loglik", "BIC", "ICL").
reverse	A logical indicating whether to plot the value of the criteria in the "natural" direction (loglik - 0.5 penalty) or in the "reverse" direction (-2 loglik + penalty). Default to FALSE, i.e use the natural direction, on the same scale as the log-likelihood.
...	additional parameters for S3 compatibility. Not used

Details

The BIC and ICL criteria have the form 'loglik - 1/2 * penalty' so that they are on the same scale as the model log-likelihood. You can change this direction and use the alternate form '-2*loglik + penalty', as some authors do, by setting reverse = TRUE.

Value

Produces either a diagnostic plot (with type = 'diagnostic') or the evolution of the criteria of the different models considered (with type = 'criteria', the default).

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myMixtures <- PLNmixture(Abundance ~ 1 + offset(log(Offset)),
           data = trichoptera, control = PLNmixture_param(smoothing = "none"))
plot(myMixtures, reverse = TRUE)
```

---

plot.PLNmixturefit *Mixture visualization of a* PLNmixturefit *object*

Description

Represent the result of the clustering either by coloring the individual in a two-dimension PCA factor map, or by representing the expected matrix of count reorder according to the clustering.

Usage

```
## S3 method for class 'PLNmixturefit'
plot(x, type = c("pca", "matrix"), main = NULL, plot = TRUE, ...)
```

Arguments

x	an R6 object with class PLNmixturefit
type	character for the type of plot, either "pca", for or "matrix". Default is "pca".
main	character. A title for the plot. If NULL (the default), an hopefully appropriate title will be used.
plot	logical. Should the plot be displayed or sent back as ggplot2::ggplot object
...	Not used (S3 compatibility).

Value

a ggplot2::ggplot graphic

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLN <- PLNmixture(Abundance ~ 1 + offset(log(Offset)),
       data = trichoptera, control = PLNmixture_param(smoothing = "none")) %>% getBestModel()
## Not run:
plot(myPLN, "pca")
plot(myPLN, "matrix")

## End(Not run)
```

---

plot.PLNnetworkfit *Extract and plot the network (partial correlation, support or inverse covariance) from a PLNnetworkfit object*

Description

Extract and plot the network (partial correlation, support or inverse covariance) from a PLNnetworkfit object

Usage

```
## S3 method for class 'PLNnetworkfit'
plot(
  x,
  type = c("partial_cor", "support"),
  output = c("igraph", "corrplot"),
  edge.color = c("#F8766D", "#00BFC4"),
  remove.isolated = FALSE,
  node.labels = NULL,
  layout = layout_in_circle,
  plot = TRUE,
  ...
)
```

Arguments

x	an R6 object with class PLNnetworkfit
type	character. Value of the weight of the edges in the network, either "partial_cor" (partial correlation) or "support" (binary). Default is "partial_cor".
output	the type of output used: either 'igraph' or 'corrplot'. Default is 'igraph'.
edge.color	Length 2 color vector. Color for positive/negative edges. Default is c("#F8766D", "#00BFC4"). Only relevant for igraph output.
remove.isolated	if TRUE, isolated node are remove before plotting. Only relevant for igraph output.
node.labels	vector of character. The labels of the nodes. The default will use the column names ot the response matrix.
layout	an optional igraph layout. Only relevant for igraph output.
plot	logical. Should the final network be displayed or only sent back to the user. Default is TRUE.
...	Not used (S3 compatibility).

Value

Send back an invisible object (igraph or Matrix, depending on the output chosen) and optionally displays a graph (via igraph or corrplot for large ones)

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
fits <- PLNnetwork(Abundance ~ 1, data = trichoptera)
myNet <- getBestModel(fits)
## Not run:
plot(myNet)

## End(Not run)
```

---

plot.PLNPCAfamily *Display the criteria associated with a collection of PLNPCA fits (a PLNPCAfamily)*

Description

Display the criteria associated with a collection of PLNPCA fits (a PLNPCAfamily)

Usage

```
## S3 method for class 'PLNPCAfamily'
plot(x, criteria = c("loglik", "BIC", "ICL"), reverse = FALSE, ...)
```

Arguments

x	an R6 object with class PLNPCAfamily
criteria	vector of characters. The criteria to plot in c("loglik", "BIC", "ICL"). Default is c("loglik", "BIC", "ICL").
reverse	A logical indicating whether to plot the value of the criteria in the "natural" direction (loglik - 0.5 penalty) or in the "reverse" direction (-2 loglik + penalty). Default to FALSE, i.e use the natural direction, on the same scale as the log-likelihood.
...	additional parameters for S3 compatibility. Not used

Details

The BIC and ICL criteria have the form 'loglik - 1/2 * penalty' so that they are on the same scale as the model log-likelihood. You can change this direction and use the alternate form '-2*loglik + penalty', as some authors do, by setting `reverse = TRUE`.

Value

Produces a plot representing the evolution of the criteria of the different models considered, highlighting the best model in terms of BIC and ICL (see details).

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPCAs <- PLNPCA(Abundance ~ 1 + offset(log(Offset)), data = trichoptera, ranks = 1:5)
## Not run:
plot(myPCAs)

## End(Not run)
```

---

plot.PLNPCAfit *PCA visualization (individual and/or variable factor map(s)) for a PLNPCAfit object*

Description

PCA visualization (individual and/or variable factor map(s)) for a PLNPCAfit object

Usage

```
## S3 method for class 'PLNPCAfit'
plot(
  x,
  map = c("both", "individual", "variable"),
  nb_axes = min(3, x$rank),
  axes = seq.int(min(2, x$rank)),
```

```
  ind_cols = "ind_colors",
  var_cols = "var_colors",
  plot = TRUE,
  main = NULL,
  ...
)
```

Arguments

x	an R6 object with class PLNPCAfit
map	the type of output for the PCA visualization: either "individual", "variable" or "both". Default is "both".
nb_axes	scalar: the number of axes to be considered when `map = "both"`. The default is `min(3,rank)`.
axes	numeric, the axes to use for the plot when `map = "individual"` or `map = "variable"`. Default it `c(1,min(rank))`
ind_cols	a character, factor or numeric to define the color associated with the individuals. By default, all variables receive the default color of the current palette.
var_cols	a character, factor or numeric to define the color associated with the variables. By default, all variables receive the default color of the current palette.
plot	logical. Should the plot be displayed or sent back as `ggplot2::ggplot` object
main	character. A title for the single plot (individual or variable factor map). If NULL (the default), an hopefully appropriate title will be used.
...	Not used (S3 compatibility).

Value

displays an individual and/or variable factor maps for the corresponding axes, and/or sends back a `ggplot2::ggplot` or gtable object

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPCAs <- PLNPCA(Abundance ~ 1 + offset(log(Offset)), data = trichoptera, ranks = 1:5)
myPCA <- getBestModel(myPCAs)
## Not run:
plot(myPCA, map = "individual", nb_axes=2, ind_cols = trichoptera$Group)
plot(myPCA, map = "variable", nb_axes=2)
plot(myPCA, map = "both", nb_axes=2, ind_cols = trichoptera$Group)

## End(Not run)
```

`plot.ZIPLNfit_sparse` *Extract and plot the network (partial correlation, support or inverse covariance) from a* `ZIPLNfit_sparse` *object*

Description

Extract and plot the network (partial correlation, support or inverse covariance) from a `ZIPLNfit_sparse` object

Usage

```
## S3 method for class 'ZIPLNfit_sparse'
plot(
  x,
  type = c("partial_cor", "support"),
  output = c("igraph", "corrplot"),
  edge.color = c("#F8766D", "#00BFC4"),
  remove.isolated = FALSE,
  node.labels = NULL,
  layout = layout_in_circle,
  plot = TRUE,
  ...
)
```

Arguments

`x`	an R6 object with class `ZIPLNfit_sparse`
`type`	character. Value of the weight of the edges in the network, either "partial_cor" (partial correlation) or "support" (binary). Default is `"partial_cor"`.
`output`	the type of output used: either 'igraph' or 'corrplot'. Default is `'igraph'`.
`edge.color`	Length 2 color vector. Color for positive/negative edges. Default is `c("#F8766D", "#00BFC4")`. Only relevant for igraph output.
`remove.isolated`	if `TRUE`, isolated node are remove before plotting. Only relevant for igraph output.
`node.labels`	vector of character. The labels of the nodes. The default will use the column names ot the response matrix.
`layout`	an optional igraph layout. Only relevant for igraph output.
`plot`	logical. Should the final network be displayed or only sent back to the user. Default is `TRUE`.
`...`	Not used (S3 compatibility).

Value

Send back an invisible object (igraph or Matrix, depending on the output chosen) and optionally displays a graph (via igraph or corrplot for large ones)

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
fit <- ZIPLN(Abundance ~ 1, data = trichoptera, control = ZIPLN_param(penalty = 0.1))
## Not run:
plot(fit)

## End(Not run)
```

`predict.PLNfit` *Predict counts of a new sample*

Description

Predict counts of a new sample

Usage

```
## S3 method for class 'PLNfit'
predict(
  object,
  newdata,
  responses = NULL,
  level = 1,
  type = c("link", "response"),
  ...
)
```

Arguments

`object`	an R6 object with class `PLNfit`
`newdata`	A data frame in which to look for variables and offsets with which to predict
`responses`	Optional data frame containing the count of the observed variables (matching the names of the provided as data in the PLN function), assuming the interest in in testing the model.
`level`	Optional integer value the level to be used in obtaining the predictions. Level zero corresponds to the population predictions (default if `responses` is not provided) while level one (default) corresponds to predictions after evaluating the variational parameters for the new data.
`type`	The type of prediction required. The default is on the scale of the linear predictors (i.e. log average count)
`...`	additional parameters for S3 compatibility. Not used

Value

A matrix of predicted log-counts (if `type = "link"`) or predicted counts (if `type = "response"`).

`predict.PLNLDAfit` *Predict group of new samples*

Description

Predict group of new samples

Usage

```
## S3 method for class 'PLNLDAfit'
predict(
  object,
  newdata,
  type = c("posterior", "response", "scores"),
  scale = c("log", "prob"),
  prior = NULL,
  control = PLN_param(backend = "nlopt"),
  ...
)
```

Arguments

`object`	an R6 object with class `PLNLDAfit`
`newdata`	A data frame in which to look for variables, offsets and counts with which to predict.
`type`	The type of prediction required. The default are posterior probabilities for each group (in either unnormalized log-scale or natural probabilities, see "scale" for details), "response" is the group with maximal posterior probability and "scores" is the average score along each separation axis in the latent space, with weights equal to the posterior probabilities.
`scale`	The scale used for the posterior probability. Either log-scale ("log", default) or natural probabilities summing up to 1 ("prob").
`prior`	User-specified prior group probabilities in the new data. If NULL (default), prior probabilities are computed from the learning set.
`control`	a list for controlling the optimization. See `PLN()` for details.
`...`	additional parameters for S3 compatibility. Not used

Value

A matrix of posterior probabilities for each group (if type = "posterior"), a matrix of (average) scores in the latent space (if type = "scores") or a vector of predicted groups (if type = "response").

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myLDA <- PLNLDA(Abundance ~ 0 + offset(log(Offset)),
                grouping = Group,
                data = trichoptera)
## Not run:
post_probs <- predict(myLDA, newdata = trichoptera, type = "posterior", scale = "prob")
head(round(post_probs, digits = 3))
predicted_group <- predict(myLDA, newdata = trichoptera, type = "response")
table(predicted_group, trichoptera$Group, dnn = c("predicted", "true"))

## End(Not run)
```

---

predict.PLNmixturefit *Prediction for a* PLNmixturefit *object*

Description

Predict either posterior probabilities for each group or latent positions based on new samples

Usage

```
## S3 method for class 'PLNmixturefit'
predict(
  object,
  newdata,
  type = c("posterior", "response", "position"),
 prior = matrix(rep(1/object$k, object$k), nrow(newdata), object$k, byrow = TRUE),
  control = PLNmixture_param(),
  ...
)
```

Arguments

object	an R6 object with class PLNmixturefit
newdata	A data frame in which to look for variables, offsets and counts with which to predict.
type	The type of prediction required. The default posterior are posterior probabilities for each group , response is the group with maximal posterior probability and latent is the averaged latent in the latent space, with weights equal to the posterior probabilities.
prior	User-specified prior group probabilities in the new data. The default uses a uniform prior.
control	a list-like structure for controlling the fit. See PLNmixture_param() for details.
...	additional parameters for S3 compatibility. Not used

Value

A matrix of posterior probabilities for each group (if type = "posterior"), a matrix of (average) position in the latent space (if type = "position") or a vector of predicted groups (if type = "response").

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLN <- PLNmixture(Abundance ~ 1 + offset(log(Offset)),
       data = trichoptera, control = PLNmixture_param(smoothing = "none")) %>% getBestModel()
predict(myPLN, trichoptera, "posterior")
predict(myPLN, trichoptera, "position")
predict(myPLN, trichoptera, "response")
```

---

predict.ZIPLNfit *Predict counts of a new sample*

Description

Predict counts of a new sample

Usage

```
## S3 method for class 'ZIPLNfit'
predict(
  object,
  newdata,
  responses = NULL,
  level = 1,
  type = c("link", "response", "deflated"),
  ...
)
```

Arguments

object	an R6 object with class ZIPLNfit
newdata	A data frame in which to look for variables and offsets with which to predict
responses	Optional data frame containing the count of the observed variables (matching the names of the provided as data in the PLN function), assuming the interest in in testing the model.
level	Optional integer value the level to be used in obtaining the predictions. Level zero corresponds to the population predictions (default if responses is not provided) while level one (default) corresponds to predictions after evaluating the variational parameters for the new data.

type	Scale used for the prediction. Either "link" (default, predicted positions in the latent space), "response" (predicted average counts, accounting for zero-inflation) or "deflated" (predicted average counts, not accounting for zero-inflation and using only the PLN part of the model).
...	additional parameters for S3 compatibility. Not used

Details

Note that level = 1 can only be used if responses are provided, as the variational parameters can't be estimated otherwise. In the absence of responses, level is ignored and the fitted values are returned

Note also that when type = "response" corresponds to predicting values with $(1 - \pi)A$, where A is the average count in the PLN part of the model and π the probability of zero-inflation, whereas type = "deflated" corresponds to A.

Value

A matrix of predicted log-counts (if type = "link") or predicted counts, accounting for zero-inflation (if type = "response") or not (if type = "deflated").

---

predict_cond *Predict counts conditionally*

Description

Predict counts of a new sample conditionally on a (set of) observed variables

Usage

```
predict_cond(
  object,
  newdata,
  cond_responses,
  type = c("link", "response"),
  var_par = FALSE
)

## S3 method for class 'PLNfit'
predict_cond(
  object,
  newdata,
  cond_responses,
  type = c("link", "response"),
  var_par = FALSE
)
```

Arguments

object	an R6 object with class PLNfit
newdata	A data frame in which to look for variables and offsets with which to predict
cond_responses	a data frame containing the counts of the observed variables (matching the names provided as data in the PLN function)
type	The type of prediction required. The default is on the scale of the linear predictors (i.e. log average count)
var_par	Boolean. Should new estimations of the variational parameters of mean and variance be sent back, as attributes of the matrix of predictions. Default to FALSE.

Value

A list containing:

pred	A matrix of predicted log-counts (if type = "link") or predicted counts (if type = "response")
M	A matrix containing E(Z_uncond | Y_c) for each given site.
S	A matrix containing Var(Z_uncond | Y_c) for each given site (sites are the third dimension of the array)

Methods (by class)

- predict_cond(PLNfit): Predict counts of a new sample conditionally on a (set of) observed variables for a PLNfit

Examples

```
data(trichoptera)
trichoptera_prep <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLN <- PLN(Abundance ~ Temperature + Wind, trichoptera_prep)
#Condition on the set of the first two species in the dataset (Hym, Hys) at the ten first sites
Yc <- trichoptera$Abundance[1:10, c(1, 2), drop=FALSE]
newX <- cbind(1, trichoptera$Covariate[1:10, c("Temperature", "Wind")])
pred <- predict_cond(myPLN, newX, Yc, type = "response")
```

---

prepare_data *Prepare data for use in PLN models*

Description

Prepare data in proper format for use in PLN model and its variants. The function (i) merges a count table and a covariate data frame in the most comprehensive way and (ii) computes offsets from the count table using one of several normalization schemes (TSS, CSS, RLE, GMPR, Wrench, etc). The function fails with informative messages when the heuristics used for sample matching fail.

Usage

```
prepare_data(
  counts,
  covariates,
  offset = "TSS",
  call = rlang::caller_env(),
  ...
)
```

Arguments

counts	Required. An abundance count table, preferably with dimensions names and species as columns.
covariates	Required. A covariates data frame, preferably with row names.
offset	Optional. Normalization scheme used to compute scaling factors used as offset during PLN inference. Available schemes are "TSS" (Total Sum Scaling, default), "CSS" (Cumulative Sum Scaling, used in metagenomeSeq), "RLE" (Relative Log Expression, used in DESeq2), "GMPR" (Geometric Mean of Pairwise Ratio, introduced in Chen et al., 2018), Wrench (introduced in Kumar et al., 2018) or "none". Alternatively the user can supply its own vector or matrix of offsets (see note for specification of the user-supplied offsets).
call	Optional. The execution environment in which to set the local error call.
...	Additional parameters passed on to compute_offset()

Value

A data.frame suited for use in PLN() and its variants with two specials components: an abundance count matrix (in component "Abundance") and an offset vector/matrix (in component "Offset", only if offset is not set to "none")

Note

User supplied offsets should be either vectors/column-matrices or have the same number of column as the original count matrix and either (i) dimension names or (ii) the same dimensions as the count matrix. Samples are trimmed in exactly the same way to remove empty samples.

References

Chen, L., Reeve, J., Zhang, L., Huang, S., Wang, X. and Chen, J. (2018) GMPR: A robust normalization method for zero-inflated count data with application to microbiome sequencing data. PeerJ, 6, e4600 doi:10.7717/peerj.4600

Paulson, J. N., Colin Stine, O., Bravo, H. C. and Pop, M. (2013) Differential abundance analysis for microbial marker-gene surveys. Nature Methods, 10, 1200-1202 doi:10.1038/nmeth.2658

Anders, S. and Huber, W. (2010) Differential expression analysis for sequence count data. Genome Biology, 11, R106 doi:10.1186/gb20101110r106

Kumar, M., Slud, E., Okrah, K. et al. (2018) Analysis and correction of compositional bias in sparse sequencing count data. BMC Genomics 19, 799 doi:10.1186/s1286401851605

Robinson, M.D., Oshlack, A. (2010) A scaling normalization method for differential expression analysis of RNA-seq data. Genome Biol 11, R25 doi:10.1186/gb2010113r25

See Also

`compute_offset()` for details on the different normalization schemes

Examples

```
data(trichoptera)
proper_data <- prepare_data(
 counts     = trichoptera$Abundance,
 covariates = trichoptera$Covariate,
 offset     = "GMPR",
 scale      = "count"
)
proper_data$Abundance
proper_data$Offset
```

---

rPLN *PLN RNG*

Description

Random generation for the PLN model with latent mean equal to mu, latent covariance matrix equal to Sigma and average depths (sum of counts in a sample) equal to depths

Usage

```
rPLN(
  n = 10,
  mu = rep(0, ncol(Sigma)),
  Sigma = diag(1, 5, 5),
  depths = rep(10000, n)
)
```

Arguments

`n`	the sample size
`mu`	vectors of means of the latent variable
`Sigma`	covariance matrix of the latent variable
`depths`	Numeric vector of target depths. The first is recycled if there are not `n` values

Details

The default value for mu and Sigma assume equal abundances and no correlation between the different species.

Value

a n * p count matrix, with row-sums close to depths, with an attribute "offsets" corresponding to the true generated offsets (in log-scale).

Examples

```
## 10 samples of 5 species with equal abundances, no covariance and target depths of 10,000
rPLN()
## 2 samples of 10 highly correlated species with target depths 1,000 and 100,000
## very different abundances
mu <- rep(c(1, -1), each = 5)
Sigma <- matrix(0.8, 10, 10); diag(Sigma) <- 1
rPLN(n=2, mu = mu, Sigma = Sigma, depths = c(1e3, 1e5))
```

---

scRNA *Single cell RNA-seq data*

Description

A dataset containing the counts of the 500 most varying transcripts in the mixtures of 5 cell lines in human liver (obtained with standard 10x scRNAseq Chromium protocol).

Usage

```
scRNA
```

Format

A data frame named 'scRNA' with 3918 rows (the cells) and 3 variables:

counts a 500 trancript by 3918 count matrix

cell_line factor, the cell line of the current row (among 5)

total_counts Total number of reads for that cell ...

Source

https://github.com/LuyiTian/sc_mixology/

`sigma.PLNfit` *Extract variance-covariance of residuals 'Sigma'*

Description

Extract the variance-covariance matrix of the residuals, usually noted

$$\Sigma$$

in PLN models. This captures the correlation between the species in the latent space.

Usage

```
## S3 method for class 'PLNfit'
sigma(object, ...)
```

Arguments

`object`	an R6 object with class `PLNfit`
`...`	additional parameters for S3 compatibility. Not used

Value

A semi definite positive matrix of size p, assuming there are p species in the model.

See Also

`coef.PLNfit()`, `standard_error.PLNfit()` and `vcov.PLNfit()` for other ways to access

$$\Sigma$$

.

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLN <- PLN(Abundance ~ 1 + offset(log(Offset)), data = trichoptera)
sigma(myPLN) ## Sigma
```

`sigma.PLNmixturefit` *Extract variance-covariance of residuals 'Sigma'*

Description

Extract the variance-covariance matrix of the residuals, usually noted

$$\Sigma$$

in PLN models. This captures the correlation between the species in the latent space. or PLNmixture, it is a weighted mean of the variance-covariance matrices of each component.

Usage

```
## S3 method for class 'PLNmixturefit'
sigma(object, ...)
```

Arguments

`object`	an R6 object with class `PLNmixturefit`
`...`	additional parameters for S3 compatibility. Not used

Value

A semi definite positive matrix of size p, assuming there are p species in the model.

See Also

`coef.PLNmixturefit()` for other ways to access

$$\Sigma$$

.

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLN <- PLNmixture(Abundance ~ 1 + offset(log(Offset)),
       data = trichoptera, control = PLNmixture_param(smoothing = "none")) %>% getBestModel()
sigma(myPLN) ## Sigma
```

sigma.ZIPLNfit *Extract variance-covariance of residuals 'Sigma'*

Description

Extract the variance-covariance matrix of the residuals, usually noted Σ in ZIPLN models.

Usage

```
## S3 method for class 'ZIPLNfit'
sigma(object, ...)
```

Arguments

object	an R6 object with class ZIPLNfit
...	additional parameters for S3 compatibility. Not used

Value

A semi definite positive matrix of size p, assuming there are p species in the model.

See Also

coef.ZIPLNfit()

stability_selection *Compute the stability path by stability selection*

Description

This function computes the StARS stability criteria over a path of penalties. If a path has already been computed, the functions stops with a message unless force = TRUE has been specified.

Usage

```
stability_selection(
  Robject,
  subsamples = NULL,
  control = PLNnetwork_param(),
  force = FALSE
)
```

Arguments

Robject	an object with class PLNnetworkfamily or ZIPLNnetworkfamily, i.e. an output from PLNnetwork() or ZIPLNnetwork()
subsamples	a list of vectors describing the subsamples. The number of vectors (or list length) determines th number of subsamples used in the stability selection. Automatically set to 20 subsamples with size 10*sqrt(n) if n >= 144 and 0.8*n otherwise following Liu et al. (2010) recommendations.
control	a list controlling the main optimization process in each call to PLNnetwork() or ZIPLNnetwork(). See PLN_param() or ZIPLN_param() for details.
force	force computation of the stability path, even if a previous one has been detected.

Value

the list of subsamples. The estimated probabilities of selection of the edges are stored in the fields stability_path of the initial Robject with class Networkfamily

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
fits <- PLNnetwork(Abundance ~ 1, data = trichoptera)
## Not run:
n <- nrow(trichoptera)
subs <- replicate(10, sample.int(n, size = n/2), simplify = FALSE)
stability_selection(nets, subsamples = subs)

## End(Not run)
```

---

standard_error.PLNPCAfit

Component-wise standard errors of B

Description

Extracts univariate standard errors for the estimated coefficient of B. Standard errors are computed from the (approximate) Fisher information matrix.

Usage

```
## S3 method for class 'PLNPCAfit'
standard_error(
  object,
  type = c("variational", "jackknife", "sandwich"),
  parameter = c("B", "Omega")
)
```

```
standard_error(
  object,
  type = c("sandwich", "variational", "jackknife"),
  parameter = c("B", "Omega")
)

## S3 method for class 'PLNfit'
standard_error(
  object,
  type = c("sandwich", "variational", "jackknife", "bootstrap"),
  parameter = c("B", "Omega")
)

## S3 method for class 'PLNfit_fixedcov'
standard_error(
  object,
  type = c("sandwich", "variational", "jackknife", "bootstrap"),
  parameter = c("B", "Omega")
)

## S3 method for class 'PLNmixturefit'
standard_error(
  object,
  type = c("variational", "jackknife", "sandwich"),
  parameter = c("B", "Omega")
)

## S3 method for class 'PLNnetworkfit'
standard_error(
  object,
  type = c("variational", "jackknife", "sandwich"),
  parameter = c("B", "Omega")
)
```

Arguments

`object`	an R6 object with class PLNfit
`type`	string describing the type of variance approximation: "variational", "jackknife", "sandwich". Default is "sandwich".
`parameter`	string describing the target parameter: either B (regression coefficients) or Omega (inverse residual covariance)

Value

A p * d positive matrix (same size as B) with standard errors for the coefficients of B

Methods (by class)

- `standard_error(PLNPCAfit)`: Component-wise standard errors of B in `PLNPCAfit` (not im-

plemented yet)

- `standard_error(PLNfit)`: Component-wise standard errors of B in `PLNfit`
- `standard_error(PLNfit_fixedcov)`: Component-wise standard errors of B in `PLNfit_fixedcov`
- `standard_error(PLNmixturefit)`: Component-wise standard errors of B in `PLNmixturefit` (not implemented yet)
- `standard_error(PLNnetworkfit)`: Component-wise standard errors of B in `PLNnetworkfit` (not implemented yet)

See Also

`vcov.PLNfit()` for the complete variance covariance estimation of the coefficient

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLN <- PLN(Abundance ~ 1 + offset(log(Offset)), data = trichoptera,
             control = PLN_param(config_post = list(sandwich_var = TRUE)))
standard_error(myPLN)
```

---

trichoptera *Trichoptera data set*

Description

Data gathered between 1959 and 1960 during 49 insect trapping nights. For each trapping night, the abundance of 17 Trichoptera species is recorded as well as 6 meteorological variables which may influence the abundance of each species. Finally, the observations (that is to say, the trapping nights), have been classified into 12 groups corresponding to contiguous nights between summer 1959 and summer 1960.

Usage

```
trichoptera
```

Format

A list with 2 two data frames:

Abundance a 49 x 17 matrix of abundancies/counts (49 trapping nights and 17 trichoptera species)

Covariate a 49 x 7 data frame of covariates:

Temperature Evening Temperature in Celsius

Wind Wind in m/s

Pressure Pressure in mm Hg

Humidity relative to evening humidity in percent

Cloudiness proportion of sky coverage at 9pm

Precipitation Nighttime precipitation in mm

Group a factor of 12 levels for the definition of the consecutive night groups

In order to prepare the data for using formula in multivariate analysis (multiple outputs and inputs), use `prepare_data()`. We only kept a subset of the original meteorological covariates for illustration purposes.

Source

Data from P. Usseglio-Polatera.

References

Usseglio-Polatera, P. and Auda, Y. (1987) Influence des facteurs météorologiques sur les résultats de piégeage lumineux. Annales de Limnologie, 23, 65–79. (code des espèces p. 76) See a data description at http://pbil.univ-lyon1.fr/R/pdf/pps034.pdf (in French)

See Also

`prepare_data()`

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
```

---

vcov.PLNfit *Calculate Variance-Covariance Matrix for a fitted* `PLN()` *model object*

Description

Returns the variance-covariance matrix of the main parameters of a fitted `PLN()` model object. The main parameters of the model correspond to

$$B$$

, as returned by `coef.PLNfit()`. The function can also be used to return the variance-covariance matrix of the residuals. The latter matrix can also be accessed via `sigma.PLNfit()`

Usage

```
## S3 method for class 'PLNfit'
vcov(object, type = c("main", "covariance"), ...)
```

Arguments

object	an R6 object with class PLNfit
type	type of parameter that should be extracted. Either "main" (default) for B or "covariance" for Σ
...	additional parameters for S3 compatibility. Not used

Value

A matrix of variance/covariance extracted from the PLNfit model. If type="main" and B is a matrix of size d * p, the result is a block-diagonal matrix with p (number of species) blocks of size d (number of covariates). if type="main", it is a symmetric matrix of size p. .

See Also

sigma.PLNfit(), coef.PLNfit(), standard_error.PLNfit()

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLN <- PLN(Abundance ~ 1 + offset(log(Offset)), data = trichoptera)
vcov(myPLN, type = "covariance") ## Sigma
```

ZIPLN *Zero Inflated Poisson lognormal model*

Description

Fit the multivariate Zero Inflated Poisson lognormal model with a variational algorithm. Use the (g)lm syntax for model specification (covariates, offsets, subset).

Usage

```
ZIPLN(
  formula,
  data,
  subset,
  zi = c("single", "row", "col"),
  control = ZIPLN_param()
)
```

Arguments

formula	an object of class "formula": a symbolic description of the model to be fitted.
data	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula), typically the environment from which the model is called.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
zi	a character describing the model used for zero inflation, either of • "single" (default, one parameter shared by all counts) • "col" (one parameter per variable / feature) • "row" (one parameter per sample / individual). If covariates are specified in the formula RHS (see details) this parameter is ignored.
control	a list-like structure for controlling the optimization, with default generated by ZIPLN_param(). See the associated documentation for details.

Details

Covariates for the Zero-Inflation parameter (using a logistic regression model) can be specified in the formula RHS using the pipe (`~ PLN effect | ZI effect`) to separate covariates for the PLN part of the model from those for the Zero-Inflation part. Note that different covariates can be used for each part.

Value

an R6 object with class ZIPLNfit

See Also

The class ZIPLNfit

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
## Use different models for zero-inflation...
myZIPLN_single <- ZIPLN(Abundance ~ 1, data = trichoptera, zi = "single")
## Not run:
myZIPLN_row    <- ZIPLN(Abundance ~ 1, data = trichoptera, zi = "row")
myZIPLN_col    <- ZIPLN(Abundance ~ 1, data = trichoptera, zi = "col")
## ...including logistic regression on covariates
myZIPLN_covar  <- ZIPLN(Abundance ~ 1 | 1 + Wind, data = trichoptera)

## End(Not run)
```

ZIPLNfit *An R6 Class to represent a ZIPLNfit*

Description

The function `ZIPLN()` fits a model which is an instance of an object with class `ZIPLNfit`.

This class comes with a set of R6 methods, some of which are useful for the end-user and exported as S3 methods. See the documentation for `coef()`, `sigma()`, `predict()`.

Fields are accessed via active binding and cannot be changed by the user.

Details

Covariates for the Zero-Inflation parameter (using a logistic regression model) can be specified in the formula RHS using the pipe (`~ PLN effect | ZI effect`) to separate covariates for the PLN part of the model from those for the Zero-Inflation part. Note that different covariates can be used for each part.

Active bindings

`n` number of samples/sites

`q` number of dimensions of the latent space

`p` number of variables/species

`d` number of covariates in the PLN part

`d0` number of covariates in the ZI part

`nb_param_zi` number of parameters in the ZI part of the model

`nb_param_pln` number of parameters in the PLN part of the model

`nb_param` number of parameters in the ZIPLN model

`model_par` a list with the matrices of parameters found in the model (B, Sigma, plus some others depending on the variant)

`var_par` a list with two matrices, M and S2, which are the estimated parameters in the variational approximation

`optim_par` a list with parameters useful for monitoring the optimization

`latent` a matrix: values of the latent vector (Z in the model)

`latent_pos` a matrix: values of the latent position vector (Z) without covariates effects or offset

`fitted` a matrix: fitted values of the observations (A in the model)

`vcov_model` character: the model used for the covariance (either "spherical", "diagonal", "full" or "sparse")

`zi_model` character: the model used for the zero inflation (either "single", "row", "col" or "covar")

`loglik` (weighted) variational lower bound of the loglikelihood

`loglik_vec` element-wise variational lower bound of the loglikelihood

`AIC` variational lower bound of the AIC

`BIC` variational lower bound of the BIC

`entropy` Entropy of the variational distribution

`entropy_ZI` Entropy of the variational distribution

`entropy_PLN` Entropy of the Gaussian variational distribution in the PLN component

`ICL` variational lower bound of the ICL

`criteria` a vector with loglik, BIC, ICL and number of parameters

Methods

Public methods:

- `ZIPLNfit$update()`
- `ZIPLNfit$new()`
- `ZIPLNfit$optimize()`
- `ZIPLNfit$optimize_vestep()`
- `ZIPLNfit$predict()`
- `ZIPLNfit$show()`
- `ZIPLNfit$print()`
- `ZIPLNfit$clone()`

`ZIPLNfit$update()`: Update a `ZIPLNfit` object

Usage:

```
ZIPLNfit$update(
  B = NA,
  B0 = NA,
  Pi = NA,
  Omega = NA,
  Sigma = NA,
  M = NA,
  S2 = NA,
  R = NA,
  Ji = NA,
  Z = NA,
  A = NA,
  monitoring = NA
)
```

Arguments:

`B` matrix of regression parameters in the Poisson lognormal component

`B0` matrix of regression parameters in the zero inflated component

`Pi` Zero inflated probability parameter (either scalar, row-vector, col-vector or matrix)

`Omega` precision matrix of the latent variables

`Sigma` covariance matrix of the latent variables

`M` matrix of mean vectors for the variational approximation

`S2` matrix of variance parameters for the variational approximation

`R` matrix of probabilities for the variational approximation

`Ji` vector of variational lower bounds of the log-likelihoods (one value per sample)

`Z` matrix of latent vectors (includes covariates and offset effects)

`A` matrix of fitted values

`monitoring` a list with optimization monitoring quantities

Returns: Update the current `ZIPLNfit` object

`ZIPLNfit$new()`**:** Initialize a `ZIPLNfit` model

Usage:

```
ZIPLNfit$new(data, control)
```

Arguments:

`data` a named list used internally to carry the data matrices

`control` a list for controlling the optimization. See details.

`ZIPLNfit$optimize()`**:** Call to the Cpp optimizer and update of the relevant fields

Usage:

```
ZIPLNfit$optimize(data, control)
```

Arguments:

`data` a named list used internally to carry the data matrices

`control` a list for controlling the optimization. See details.

`ZIPLNfit$optimize_vestep()`**:** Result of one call to the VE step of the optimization procedure: optimal variational parameters (M, S2, R) and corresponding log likelihood values for fixed model parameters (Sigma, B, B0). Intended to position new data in the latent space.

Usage:

```
ZIPLNfit$optimize_vestep(
  data,
  B = self$model_par$B,
  B0 = self$model_par$B0,
  Omega = self$model_par$Omega,
  control = ZIPLN_param(backend = "nlopt")$config_optim
)
```

Arguments:

`data` a named list used internally to carry the data matrices

`B` Optional fixed value of the regression parameters in the PLN component

`B0` Optional fixed value of the regression parameters in the ZI component

`Omega` inverse variance-covariance matrix of the latent variables

`control` a list for controlling the optimization. See details.

Returns: A list with three components:

- the matrix `M` of variational means,
- the matrix `S2` of variational variances
- the matrix `R` of variational ZI probabilities
- the vector `Ji` of (variational) log-likelihood of each new observation
- a list `monitoring` with information about convergence status

`ZIPLNfit$predict()`: Predict position, scores or observations of new data. See `predict.ZIPLNfit()` for the S3 method and additional details

Usage:

```
ZIPLNfit$predict(
  newdata,
  responses = NULL,
  type = c("link", "response", "deflated"),
  level = 1,
  envir = parent.frame()
)
```

Arguments:

`newdata` A data frame in which to look for variables with which to predict. If omitted, the fitted values are used.

`responses` Optional data frame containing the count of the observed variables (matching the names of the provided as data in the PLN function), assuming the interest in in testing the model.

`type` Scale used for the prediction. Either `"link"` (default, predicted positions in the latent space), `"response"` (predicted average counts, accounting for zero-inflation) or `"deflated"` (predicted average counts, not accounting for zero-inflation and using only the PLN part of the model).

`level` Optional integer value the level to be used in obtaining the predictions. Level zero corresponds to the population predictions (default if `responses` is not provided) while level one (default) corresponds to predictions after evaluating the variational parameters for the new data.

`envir` Environment in which the prediction is evaluated

Returns: A matrix with predictions scores or counts.

`ZIPLNfit$show()`: User friendly print method

Usage:

```
ZIPLNfit$show(
  model = paste("A multivariate Zero Inflated Poisson Lognormal fit with",
    self$vcov_model, "covariance model.\n")
)
```

Arguments:

`model` First line of the print output

`ZIPLNfit$print()`: User friendly print method

Usage:

```
ZIPLNfit$print()
```

`ZIPLNfit$clone()`: The objects of this class are cloneable with this method.

Usage:

```
ZIPLNfit$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
## Not run:
# See other examples in function ZIPLN
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLN <- ZIPLN(Abundance ~ 1, data = trichoptera)
class(myPLN)
print(myPLN)

## End(Not run)
```

`ZIPLNfit_diagonal` *An R6 Class to represent a ZIPLNfit in a standard, general framework, with diagonal residual covariance*

Description

An R6 Class to represent a ZIPLNfit in a standard, general framework, with diagonal residual covariance

Super class

`ZIPLNfit` -> `ZIPLNfit_diagonal`

Active bindings

`nb_param_pln` number of parameters in the PLN part of the current model

`vcov_model` character: the model used for the residual covariance

Methods

Public methods:

- `ZIPLNfit_diagonal$new()`
- `ZIPLNfit_diagonal$clone()`

`ZIPLNfit_diagonal$new()`**:** Initialize a `ZIPLNfit_diagonal` model

Usage:

```
ZIPLNfit_diagonal$new(data, control)
```

Arguments:

`data` a named list used internally to carry the data matrices

`control` a list for controlling the optimization. See details.

`ZIPLNfit_diagonal$clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ZIPLNfit_diagonal$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
## Not run:
# See other examples in function ZIPLN
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLN <- ZIPLN(Abundance ~ 1, data = trichoptera, control = ZIPLN_param(covariance = "diagonal"))
class(myPLN)
print(myPLN)

## End(Not run)
```

`ZIPLNfit_fixed` *An R6 Class to represent a ZIPLNfit in a standard, general framework, with fixed (inverse) residual covariance*

Description

An R6 Class to represent a ZIPLNfit in a standard, general framework, with fixed (inverse) residual covariance

Super class

`ZIPLNfit` -> `ZIPLNfit_fixed`

Active bindings

`nb_param_pln` number of parameters in the PLN part of the current model

`vcov_model` character: the model used for the residual covariance

Methods

Public methods:

- `ZIPLNfit_fixed$new()`
- `ZIPLNfit_fixed$clone()`

`ZIPLNfit_fixed$new()`: Initialize a `ZIPLNfit_fixed` model

Usage:

```
ZIPLNfit_fixed$new(data, control)
```

Arguments:

`data` a named list used internally to carry the data matrices

`control` a list for controlling the optimization. See details.

`ZIPLNfit_fixed$clone()`: The objects of this class are cloneable with this method.

Usage:

```
ZIPLNfit_fixed$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
## Not run:
# See other examples in function ZIPLN
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLN <- ZIPLN(Abundance ~ 1, data = trichoptera,
    control = ZIPLN_param(Omega = diag(ncol(trichoptera$Abundance))))
class(myPLN)
print(myPLN)

## End(Not run)
```

`ZIPLNfit_sparse` *An R6 Class to represent a ZIPLNfit in a standard, general framework, with sparse inverse residual covariance*

Description

An R6 Class to represent a ZIPLNfit in a standard, general framework, with sparse inverse residual covariance

Super class

`ZIPLNfit` -> `ZIPLNfit_sparse`

Active bindings

`penalty` the global level of sparsity in the current model

`penalty_weights` a matrix of weights controlling the amount of penalty element-wise.

`n_edges` number of edges if the network (non null coefficient of the sparse precision matrix)

`nb_param_pln` number of parameters in the PLN part of the current model

`vcov_model` character: the model used for the residual covariance

`pen_loglik` variational lower bound of the l1-penalized loglikelihood

`EBIC` variational lower bound of the EBIC

`density` proportion of non-null edges in the network

`criteria` a vector with loglik, penalized loglik, BIC, EBIC, ICL, R_squared, number of parameters, number of edges and graph density

Methods

Public methods:

- `ZIPLNfit_sparse$new()`
- `ZIPLNfit_sparse$latent_network()`
- `ZIPLNfit_sparse$plot_network()`

- ZIPLNfit_sparse$clone()

`ZIPLNfit_sparse$new()`: Initialize a `ZIPLNfit_fixed` model

Usage:

```
ZIPLNfit_sparse$new(data, control)
```

Arguments:

`data` a named list used internally to carry the data matrices

`control` a list for controlling the optimization. See details.

`ZIPLNfit_sparse$latent_network()`: Extract interaction network in the latent space

Usage:

```
ZIPLNfit_sparse$latent_network(type = c("partial_cor", "support", "precision"))
```

Arguments:

`type` edge value in the network. Can be "support" (binary edges), "precision" (coefficient of the precision matrix) or "partial_cor" (partial correlation between species)

Returns: a square matrix of size `ZIPLNfit_sparse$n`

`ZIPLNfit_sparse$plot_network()`: plot the latent network.

Usage:

```
ZIPLNfit_sparse$plot_network(
  type = c("partial_cor", "support"),
  output = c("igraph", "corrplot"),
  edge.color = c("#F8766D", "#00BFC4"),
  remove.isolated = FALSE,
  node.labels = NULL,
  layout = layout_in_circle,
  plot = TRUE
)
```

Arguments:

`type` edge value in the network. Either "precision" (coefficient of the precision matrix) or "partial_cor" (partial correlation between species).

`output` Output type. Either `igraph` (for the network) or `corrplot` (for the adjacency matrix)

`edge.color` Length 2 color vector. Color for positive/negative edges. Default is `c("#F8766D", "#00BFC4")`. Only relevant for igraph output.

`remove.isolated` if `TRUE`, isolated node are remove before plotting. Only relevant for igraph output.

`node.labels` vector of character. The labels of the nodes. The default will use the column names ot the response matrix.

`layout` an optional igraph layout. Only relevant for igraph output.

`plot` logical. Should the final network be displayed or only sent back to the user. Default is `TRUE`.

`ZIPLNfit_sparse$clone()`: The objects of this class are cloneable with this method.

Usage:

```
ZIPLNfit_sparse$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
## Not run:
# See other examples in function ZIPLN
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLN <- ZIPLN(Abundance ~ 1, data = trichoptera, control=  ZIPLN_param(penalty = 1))
class(myPLN)
print(myPLN)
plot(myPLN)

## End(Not run)
```

`ZIPLNfit_spherical` *An R6 Class to represent a ZIPLNfit in a standard, general framework, with spherical residual covariance*

Description

An R6 Class to represent a ZIPLNfit in a standard, general framework, with spherical residual covariance

Super class

`ZIPLNfit` -> `ZIPLNfit_spherical`

Active bindings

`nb_param_pln` number of parameters in the PLN part of the current model

`vcov_model` character: the model used for the residual covariance

Methods

Public methods:

- `ZIPLNfit_spherical$new()`
- `ZIPLNfit_spherical$clone()`

`ZIPLNfit_spherical$new()`: Initialize a `ZIPLNfit_spherical` model

Usage:

```
ZIPLNfit_spherical$new(data, control)
```

Arguments:

`data` a named list used internally to carry the data matrices

`control` a list for controlling the optimization. See details.

`ZIPLNfit_spherical$clone()`: The objects of this class are cloneable with this method.

Usage:

```
ZIPLNfit_spherical$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
## Not run:
# See other examples in function ZIPLN
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myPLN <- ZIPLN(Abundance ~ 1, data = trichoptera, control = ZIPLN_param(covariance = "spherical"))
class(myPLN)
print(myPLN)

## End(Not run)
```

`ZIPLNnetwork` *Zero Inflated Sparse Poisson lognormal model for network inference*

Description

Perform sparse inverse covariance estimation for the Zero Inflated Poisson lognormal model using a variational algorithm. Iterate over a range of logarithmically spaced sparsity parameter values. Use the (g)lm syntax to specify the model (including covariates and offsets).

Usage

```
ZIPLNnetwork(
  formula,
  data,
  subset,
  weights,
  zi = c("single", "row", "col"),
  penalties = NULL,
  control = ZIPLNnetwork_param()
)
```

Arguments

`formula`	an object of class "formula": a symbolic description of the model to be fitted.
`data`	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula), typically the environment from which the model is called.
`subset`	an optional vector specifying a subset of observations to be used in the fitting process.
`weights`	an optional vector of observation weights to be used in the fitting process.
`zi`	a character describing the model used for zero inflation, either of • "single" (default, one parameter shared by all counts) • "col" (one parameter per variable / feature)

- "row" (one parameter per sample / individual). If covariates are specified in the formula RHS (see details) this parameter is ignored.

`penalties` an optional vector of positive real number controlling the level of sparsity of the underlying network. if NULL (the default), will be set internally. See `PLNnetwork_param()` for additional tuning of the penalty.

`control` a list-like structure for controlling the optimization, with default generated by `ZIPLNnetwork_param()`. See the associated documentation for details.

Details

Covariates for the Zero-Inflation parameter (using a logistic regression model) can be specified in the formula RHS using the pipe (`~ PLN effect | ZI effect`) to separate covariates for the PLN part of the model from those for the Zero-Inflation part. Note that different covariates can be used for each part.

Value

an R6 object with class `ZIPLNnetworkfamily`

See Also

The classes `ZIPLNfit` and `ZIPLNnetworkfamily`

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
myZIPLNs <- ZIPLNnetwork(Abundance ~ 1, data = trichoptera, zi = "single")
```

ZIPLNnetworkfamily *An R6 Class to represent a collection of ZIPLNnetwork*

Description

The function `ZIPLNnetwork()` produces an instance of this class.

This class comes with a set of methods, some of them being useful for the user: See the documentation for `getBestModel()`, `getModel()` and `plot()`

Super classes

`PLNfamily` -> `Networkfamily` -> `ZIPLNnetworkfamily`

Public fields

`covariates0` the matrix of covariates included in the ZI component

Methods

Public methods:

- `ZIPLNnetworkfamily$new()`
- `ZIPLNnetworkfamily$stability_selection()`
- `ZIPLNnetworkfamily$clone()`

`ZIPLNnetworkfamily$new()`: Initialize all models in the collection

Usage:

```
ZIPLNnetworkfamily$new(penalties, data, control)
```

Arguments:

`penalties` a vector of positive real number controlling the level of sparsity of the underlying network.

`data` a named list used internally to carry the data matrices

`control` a list for controlling the optimization.

Returns: Update current `PLNnetworkfit` with smart starting values

`ZIPLNnetworkfamily$stability_selection()`: Compute the stability path by stability selection

Usage:

```
ZIPLNnetworkfamily$stability_selection(
  subsamples = NULL,
  control = ZIPLNnetwork_param()
)
```

Arguments:

`subsamples` a list of vectors describing the subsamples. The number of vectors (or list length) determines the number of subsamples used in the stability selection. Automatically set to 20 subsamples with size `10*sqrt(n)` if `n >= 144` and `0.8*n` otherwise following Liu et al. (2010) recommendations.

`control` a list controlling the main optimization process in each call to `PLNnetwork()`. See `ZIPLNnetwork()` and `ZIPLN_param()` for details.

`ZIPLNnetworkfamily$clone()`: The objects of this class are cloneable with this method.

Usage:

```
ZIPLNnetworkfamily$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

The function `ZIPLNnetwork()`, the class `ZIPLNfit_sparse`

Examples

```
data(trichoptera)
trichoptera <- prepare_data(trichoptera$Abundance, trichoptera$Covariate)
fits <- PLNnetwork(Abundance ~ 1, data = trichoptera)
class(fits)
```

`ZIPLNnetwork_param` *Control of ZIPLNnetwork fit*

Description

Helper to define list of parameters to control the ZIPLNnetwork fit. All arguments have defaults.

Usage

```
ZIPLNnetwork_param(
  backend = c("builtin", "nlopt"),
  inception_cov = c("full", "spherical", "diagonal"),
  trace = 1,
  n_penalties = 30,
  min_ratio = 0.1,
  penalize_diagonal = TRUE,
  penalty_weights = NULL,
  config_post = list(),
  config_optim = list(),
  inception = NULL
)
```

Arguments

`backend`	optimization backend, either `"builtin"` (default, joint Newton on (M,ψ,R), combined with the partial E-step `maxit_ve = 1`) or `"nlopt"` (CCSAQ). `"builtin"` consistently finds a better ELBO across the penalty path at the cost of being slower.
`inception_cov`	Covariance structure used for the inception PLN: `"full"` (default), `"diagonal"` or `"spherical"`. Non-full structures are now fully supported: when `inception_cov != "full"`, the penalty grid is built from the empirical covariance of latent residuals $M - XB$ (a full-rank proxy for Σ), avoiding the broken `max_pen = 0` that previously occurred with diagonal/spherical.
`trace`	a integer for verbosity.
`n_penalties`	an integer that specifies the number of values for the penalty grid when internally generated. Ignored when penalties is non `NULL`
`min_ratio`	the penalty grid ranges from the minimal value that produces a sparse to this value multiplied by `min_ratio`. Default is 0.1.
`penalize_diagonal`	boolean: should the diagonal terms be penalized in the graphical-Lasso? Default is `TRUE`
`penalty_weights`	either a single or a list of p x p matrix of weights (default: all weights equal to 1) to adapt the amount of shrinkage to each pairs of node. Must be symmetric with positive values.

config_post	a list for controlling the post-treatments (optional bootstrap, jackknife, R2, etc.). See details
config_optim	a list for controlling the optimizer (either "nlopt" or "torch" backend). See details
inception	Set up the parameters initialization: by default, the model is initialized with a multivariate linear model applied on log-transformed data, and with the same formula as the one provided by the user. However, the user can provide a PLNfit (typically obtained from a previous fit), which sometimes speeds up the inference.

Details

See PLNnetwork_param() for a full description of the optimization parameters. Note that some defaults values are different than those used in PLNnetwork_param():

- "ftol_out" (outer loop convergence tolerance the objective function) is set by default to 1e-6
- "maxit_out" (max number of iterations for the outer loop) is set by default to 50

Value

list of parameters configuring the fit.

See Also

PLNnetwork_param() and PLN_param()

ZIPLN_param *Control of a ZIPLN fit*

Description

Helper to define list of parameters to control the ZIPLN fit. All arguments have defaults.

Usage

```
ZIPLN_param(
  backend = c("builtin", "nlopt"),
  trace = 1,
  covariance = c("full", "diagonal", "spherical", "fixed", "sparse"),
  Omega = NULL,
  penalty = 0,
  penalize_diagonal = TRUE,
  penalty_weights = NULL,
  config_post = list(),
  config_optim = list(),
  inception = NULL
)
```

Arguments

backend	optimization backend, either "builtin" (default, built-in Newton optimizer for the joint VE step) or "nlopt" (NLOPT-based CCSAQ).
trace	a integer for verbosity.
covariance	character setting the model for the covariance matrix. Either "full", "diagonal", "spherical", "fixed" or "sparse". Default is "full".
Omega	precision matrix of the latent variables. Inverse of Sigma. Must be specified if covariance is "fixed"
penalty	a user-defined penalty to sparsify the residual covariance. Defaults to 0 (no sparsity).
penalize_diagonal	boolean: should the diagonal terms be penalized in the graphical-Lasso? Default is TRUE
penalty_weights	either a single or a list of p x p matrix of weights (default: all weights equal to 1) to adapt the amount of shrinkage to each pairs of node. Must be symmetric with positive values.
config_post	a list for controlling the post-treatments (optional bootstrap, jackknife, R2, etc.). See details
config_optim	a list for controlling the optimizer (either "nlopt" or "torch" backend). See details
inception	Set up the parameters initialization: by default, the model is initialized with a multivariate linear model applied on log-transformed data, and with the same formula as the one provided by the user. However, the user can provide a PLNfit (typically obtained from a previous fit), which sometimes speeds up the inference.

Details

See PLN_param() for a description of the generic config_optim entries (ftol_rel, xtol_rel, etc.). Like PLNnetwork_param(), ZIPLN_param() has two parameters controlling the outer EM loop:

- "ftol_out" outer solver stops when an optimization step changes the objective function by less than ftol_out multiplied by the absolute value of the parameter. Default is 1e-6
- "maxit_out" outer solver stops when the number of iteration exceeds maxit_out. Default is 200 for "builtin", 100 for "nlopt" and one additional parameter controlling the form of the variational approximation of the zero inflation:

Value

list of parameters used during the fit and post-processing steps

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