

Package ‘gjam’

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Type Package

Title Generalized Joint Attribute Modeling

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Description Analyzes joint attribute data (e.g., species abundance) that are combinations of continuous and discrete data with Gibbs sampling. Full model and computation details are described in Clark et al. (2018) <doi:10.1002/ecm.1241>.

License GPL (>= 2)

Imports Rcpp (>= 0.11.5), MASS, RANN

Depends R (>= 2.10)

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VignetteBuilder knitr

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R topics documented:

gjam-package	2
gjam	4
gjamCensorY	7
gjamDeZero	9
gjamFillMissingTimes	11
gjamIIE	12
gjamIIEplot	14
gjamOrdination	15

gjamPlot	17
gjamPoints2Grid	19
gjamPredict	20
gjamPriorTemplate	22
gjamReZero	24
gjamSensitivity	25
gjamSimData	27
gjamSpec2Trait	29
gjamTrimY	31

Index	33
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gjam-package	<i>Generalized Joint Attribute Modeling</i>
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Description

Inference and prediction for jointly distributed responses that are combinations of continuous and discrete data. Functions begin with 'gjam' to avoid conflicts with other packages.

Details

Package: gjam
 Type: Package
 Version: 2.2.7
 Date: 2019-4-17
 License: GPL (>= 2)
 URL: <http://sites.nicholas.duke.edu/clarklab/code/>

The generalized joint attribute model (gjam) analyzes multivariate data that are combinations of presence-absence, ordinal, continuous, discrete, composition, zero-inflated, and censored. It does so as a joint distribution over response variables. gjam provides inference on sensitivity to input variables, correlations between responses on the data scale, model selection, and prediction.

Importantly, analysis is done on the observation scale. That is, coefficients and covariances are interpreted on the same scale as the data. Contrast this approach with standard Generalized Linear Models, where coefficients and covariances are difficult to interpret and cannot be compared across responses that are modeled on different scales.

gjam was motivated by species distribution and abundance data in ecology, but can provide an attractive alternative to traditional methods wherever observations are multivariate and combine multiple scales and mixtures of continuous and discrete data.

gjam can be used to model ecological trait data, where species traits are translated to locations as community-weighted means and modes.

Posterior simulation is done by Gibbs sampling. Analysis is done by these functions, roughly in order of how frequently they might be used:

[gjam](#) fits model with Gibbs sampling.

[gjamSimData](#) simulates data for analysis by [gjam](#).

[gjamPriorTemplate](#) sets up prior distribution for coefficients.

[gjamSensitivity](#) evaluates sensitivity to predictors from [gjam](#).

[gjamCensorY](#) defines censored values and intervals.

[gjamTrimY](#) trims the response matrix and aggregates rare types.

[gjamPlot](#) plots output from [gjam](#).

[gjamSpec2Trait](#) constructs plot by trait matrix.

[gjamPredict](#) does conditional prediction.

[gjamOrdination](#) ordines the response matrix.

[gjamDeZero](#) de-zeros response matrix for storage.

[gjamReZero](#) recovers response matrix from de-zeroed format.

[gjamIIE](#) evaluates indirect effects and interactions.

[gjamIIEplot](#) plots indirect effects and interactions.

[gjamSpec2Trait](#) generates trait values.

[gjamPoints2Grid](#) aggregates incidence data to counts on a lattice.

Author(s)

Author: James S Clark, <jimclark@duke.edu>, Daniel Taylor-Rodriguez

References

Clark, J.S., D. Nemergut, B. Seyednasrollah, P. Turner, and S. Zhang. 2017. Generalized joint attribute modeling for biodiversity analysis: Median-zero, multivariate, multifarious data. *Ecological Monographs* 87, 34-56.

Clark, J.S. 2016. Why species tell more about traits than traits tell us about species: Predictive models. *Ecology* 97, 1979-1993.

Taylor-Rodriguez, D., K. Kaufeld, E. M. Schliep, J. S. Clark, and A. E. Gelfand. 2016. Joint species distribution modeling: dimension reduction using Dirichlet processes. *Bayesian Analysis*, in press.

See Also

[gjam](#), [gjamSimData](#), [gjamSensitivity](#), [gjamCensorY](#), [gjamTrimY](#), [gjamPredict](#), [gjamSpec2Trait](#), [gjamPlot](#), [gjamDeZero](#), [gjamReZero](#)

A more detailed vignette is can be obtained with:

```
browseVignettes('gjam')
```

gjam

*Gibbs sampler for gjam data***Description**

Analyzes joint attribute data (e.g., species abundance) with Gibbs sampling. Input can be output from [gjamSimData](#). Returns a list of objects from Gibbs sampling that can be plotted by [gjamPlot](#).

Usage

```
gjam(formula, xdata, ydata, modelList)

## S3 method for class 'gjam'
print(x, ...)

## S3 method for class 'gjam'
summary(object, ...)
```

Arguments

formula	R formula for model, e.g., $\sim x_1 + x_2$.
xdata	data.frame containing predictors in formula. If not found in xdata variables, they must be available from the user's workspace.
ydata	n by S response matrix or data.frame. Column names are unique labels, e.g., species names. All columns will be included in the analysis.
modelList	list specifying inputs, including ng (number of Gibbs steps), burnin, and typeNames. Can include the number of holdouts for out-of-sample prediction, holdoutN. See Details .
x	object of class gjam .
object	currently, also an object of class gjam .
...	further arguments not used here.

Details

Note that formula begins with \sim , not $y \sim$. The response matrix is passed in the form of a n by S matrix or data.frame ydata.

Both predictors in xdata and responses in ydata can include missing values as NA. Factors in xdata should be declared using factor. For computational stability variables that are not factors are standardized by mean and variance, then transformed back to original scales in output. To retain a variable in its original scale during computation include it in the character string notStandard as part of the list modelList. (example shown in the vignette on traits).

modelList has these defaults and provides these options:

ng = 2000, number of Gibbs steps.

burnin = 500, no. initial steps, must be less than ng.

typeNameNames can be 'PA' (presenceAbsence), 'CON' (continuous on $(-\text{Inf}, \text{Inf})$), 'CA' (continuous abundance, zero censoring), 'DA' (discrete abundance), 'FC' (fractional composition), 'CC' (count composition), 'OC' (ordinal counts), 'CAT' (categorical classes). typeNameNames can be a single value that applies to all columns in ydata, or there can be one value for each column.

holdoutN = 0, number of observations to hold out for out-of-sample prediction.

holdoutIndex = numeric(0), numeric vector of observations (row numbers) to holdout for out-of-sample prediction.

censor = NULL, list specifying columns, values, and intervals for censoring, see [gjamCensorY](#).

effort = NULL, list containing 'columns', a vector of length $\leq S$ giving the names of columns in in y, and 'values', a length-n vector of effort or a n by S matrix (see Examples). effort can be plot area, search time, etc. for discrete count data 'DA'.

FULL = F in modelList will save full prediction chains in \$chains\$ygibbs.

notStandard = NULL, character vector of column names in xdata that should not be standardized.

reductList = list(N = 20, r = 3), list of dimension reduction parameters, invoked when reductList is included in modelList or automatically when ydata has too many columns. See vignette on Dimension Reduction.

random, character string giving the name of a column in xdata that will be used to specify random effects. The random group column should be declared as a factor. There should be replication, i.e., each group level occurs multiple times.

REDUCT = F in modelList overrides automatic dimension reduction.

FCgroups, CCgroups, are length-S vectors assigned to columns in ydata indicating composition 'FC' or 'CC' group membership. For example, if there are two 'CA' columns in ydata followed by two groups of fractional composition data, each having three columns, then typeNameNames = c('CA', 'CA', 'FC', 'FC', 'FC', 'FC') and FCgroups = c(0,0,1,1,1,2,2,2). note: gjamSimData is not currently set up to simulate multiple composition groups, but gjam will model it.

PREDICTX = T executes inverse prediction of x. Speed-up by setting PREDICTX = F.

ematAlpha = .5 is the probability assigned for conditional and marginal independence in the ematrix.

traitList = list(plotByTrait, traitTypes, specByTrait), list of trait objects. See vignette on Trait analysis.

More detailed vignettes can be obtained with:

```
browseVignettes('gjam')
```

Value

Returns an object of class "gjam", which is a list containing the following components:

call	function call
chains	list of MCMC matrices, each with ng rows; includes coefficients bgibbs(Q*S columns), bgibbsUn (unstandardized for x), sensitivity fgibbs (Q1 columns), and fbibbs (Q1 columns, where $Q1 = Q - 1$, unless there are multilevel factors); covariance sgibbs has $S*(S + 1)/2$ columns (REDUCT == F) or $N*r$ columns (REDUCT == T).

fit	list of diagnostics (DIC, rmspeAll, rmspeBySpec, xscore, yscore).
inputs	list of input summaries, including breakMat (partition matrix), classBySpec (interval assignment), designTable (summary of design matrix), [factorBeta, interBeta, intMat, I (factor and interaction information), other, notOther (response columns to exclude and not), [standMat, standRows, standX] means and variances to standardize x, [x, xdata, y] cleaned versions of data.
missing	list of missing objects, including locations for predictors xmiss and responses ymiss in xdata and ydata, respectively, predictor means xmissMu and standard errors xmissSe, response means ymissMu and standard errors ymissSe .
modellist	list of model specifications from input modellist.
parameters	list of parameter estimates, including coefficient matrices on standardized (betaMu, betaSe), unstandardized (betaMuUn, betaSeUn), and dimensionless (fBetaMu, fBetaSd) scales; correlation (corMu, corSe) and covariance (sigMu, sigSe) matrices; sensitivities to predictors (fmatrix, fMu, fSe); environmental response matrix (ematrix), with locations of zero elements, conditionally (whConZero) and marginally (whichZero), set at probability level modellist\$ematAlpha); and latent variables (wMu, wSd).
prediction	list of predicted values, including species richness (responses predicted > 0); inverse predicted x (xpredMu, xpredSd) and predicted y (ypredMu, ypredSd) matrices.

If **traits** are modeled, then parameters will additionally include betaTraitMu, betaTraitSe (coefficients), sigmaTraitMu, sigmaTraitSe (covariance). prediction will additionally include tMuOrd (ordinal trait means), tMu, tSe (trait predictions).

Author(s)

James S Clark, <jimclark@duke.edu>

References

Clark, J.S., D. Nemergut, B. Seyednasrollah, P. Turner, and S. Zhang. 2017. Generalized joint attribute modeling for biodiversity analysis: Median-zero, multivariate, multifarious data. *Ecological Monographs*, 87, 34-56.

See Also

[gjamSimData](#) simulates data

A more detailed vignette is can be obtained with:

```
browseVignettes('gjam')
```

website 'http://sites.nicholas.duke.edu/clarklab/code/'.

Examples

```
## Not run:
## combinations of scales
types <- c('DA', 'DA', 'OC', 'OC', 'OC', 'OC', 'CC', 'CC', 'CC', 'CC', 'CC', 'CA', 'CA', 'PA', 'PA')
```

```
f <- gjamSimData(S = length(types), typeNames = types)
m1 <- list(ng = 50, burnin = 5, typeNames = f$typeNames)
out <- gjam(f$formula, f$xdata, f$ydata, modelList = m1)
summary(out)

# repeat with ng = 5000, burnin = 500, then plot data:
p1 <- list(trueValues = f$trueValues, SMALLPLOTS=F)
gjamPlot(out, plotPars = p1)

## discrete abundance with heterogeneous effort
S <- 5
n <- 1000
eff <- list( columns = 1:S, values = round(runif(n,.5,5),1) )
f <- gjamSimData(n, S, typeNames='DA', effort=eff)
m1 <- list(ng = 500, burnin = 50, typeNames = f$typeNames, effort = eff)
out <- gjam(f$formula, f$xdata, f$ydata, modelList = m1)
summary(out)

# repeat with ng = 2000, burnin = 500, then plot data:
p1 <- list(trueValues = f$trueValues)
gjamPlot(out, plotPars = p1)

## End(Not run)
```

gjamCensorY

Censor gjam response data

Description

Returns a list with censored values, intervals, and censored response matrix y .

Usage

```
gjamCensorY(values, intervals, y, type='CA', whichcol = c(1:ncol(y)))
```

Arguments

values	Values in y that are censored, specified by intervals
intervals	matrix having two rows and one column for each value in values. The first row holds lower bounds. The second row holds upper bounds. See Examples .
y	Response matrix, n rows by S columns. All values within intervals will be replaced with values
type	Response type, see typeNames in gjam
whichcol	Columns in y that are censored (often not all responses are censored)

Details

Any values in y that fall within censored intervals are replaced with censored values. The example below simulates data collected on an 'octave scale': 0, 1, 2, 4, 8, ..., an approach to accelerate data collection with approximate bins.

Value

Returns a list containing two elements.

<code>y</code>	<code>n</code> by <code>S</code> matrix updated with censored values substituted for those falling within intervals.
<code>censor</code>	list containing <code>\$columns</code> that are censored and <code>\$partition</code> , a matrix with 3 rows used in <code>gjam</code> and <code>gjamPlot</code> , one column per censor interval. Rows are values, followed by lower and upper bounds.

Author(s)

James S Clark, <jimclark@duke.edu>

References

Clark, J.S., D. Nemergut, B. Seyednasrollah, P. Turner, and S. Zhang. 2017. Generalized joint attribute modeling for biodiversity analysis: Median-zero, multivariate, multifarious data. *Ecological Monographs* 87, 34-56.

See Also

`gjamSimData` simulates data `gjam` analyzes data
 A more detailed vignette is can be obtained with:
`browseVignettes('gjam')`
 website '<http://sites.nicholas.duke.edu/clarklab/code/>'.

Examples

```
## Not run:
# data in octaves
v <- up <- c(0, 2^c(0:4), Inf)
dn <- c(-Inf, v[-length(v)])
i <- rbind( dn, up ) # intervals

f <- gjamSimData(n = 2000, S = 15, Q = 3, typeNames='CA')
y <- f$y
cc <- c(3:6) # censored columns
g <- gjamCensorY(values = v, intervals = i, y = y, whichcol = cc)
y[,cc] <- g$y # replace columns
ml <- list(ng = 50, burnin = 10, censor = g$censor, typeNames = f$typeNames)
output <- gjam(f$formula, xdata = f$xdata, ydata = y, modelList = ml)

#repeat with ng = 2000, burnin = 500, then:
```



```

pl <- list(trueValues = f$trueValues, width = 3, height = 3)
gjamPlot(output, pl)

# upper detection limit
up <- 5
v <- up
i <- matrix(c(up,Inf),2)
rownames(i) <- c('down','up')

f <- gjamSimData(typeNames='CA')
g <- gjamCensorY(values = v, intervals = i, y = f$y)
ml <- list(ng = 50, burnin = 10, censor = g$censor, typeNames = f$typeNames)
out <- gjam(f$formula, xdata = f$xdata, ydata = g$y, modelList = ml)

#repeat with ng = 2000, burnin = 500, then:
pl <- list(trueValues = f$trueValues, width = 3, height = 3)
gjamPlot(out, pl)

# lower detection limit
lo <- .001
values <- upper <- lo
intervals <- matrix(c(-Inf,lo),2)
rownames(intervals) <- c('lower','upper')

## End(Not run)

```

gjamDeZero

Compress (de-zero) gjam data

Description

Returns a de-zeroed (sparse matrix) version of matrix `yamat` with objects needed to re-zero it.

Usage

```
gjamDeZero(yamat)
```

Arguments

`yamat` n by S response matrix

Details

Many abundance data sets are mostly zeros. [gjamDeZero](#) extracts non-zero elements for storage.

Value

Returns a list containing the de-zeroed ymat as a vector yvec.

yvec	non-zero elements of ymat
n	no. rows of ymat
S	no. cols of ymat
index	index for non-zeros
ynames	column names of ymat

Author(s)

James S Clark, <jimclark@duke.edu>

References

Clark, J.S., D. Nemergut, B. Seyednasrollah, P. Turner, and S. Zhang. 2016. Generalized joint attribute modeling for biodiversity analysis: Median-zero, multivariate, multifarious data. *Ecological Monographs* 87, 34-56.

See Also

[gjamReZero](#) to recover ymat
 browseVignettes('gjam')
 website 'http://sites.nicholas.duke.edu/clarklab/code/'.

Examples

```
## Not run:
library(repmis)
source_data("https://github.com/jimclarkatduke/gjam/blob/master/fungEnd.RData?raw=True")

ymat <- gjamReZero(fungEnd$yDeZero) # OTUs stored without zeros
length(fungEnd$yDeZero$yvec)      # size of stored version
length(ymat)                      # full size
yDeZero <- gjamDeZero(ymat)
length(yDeZero$yvec)              # recover de-zeroed vector

## End(Not run)
```

`gjamFillMissingTimes` *Fill out data for time series (state-space) gjam*

Description

Fills in predictor, response, and effort matrices for time series data where there are multiple multivariate time series. Time series gjam is still under development.

Usage

```
gjamFillMissingTimes(xdata, ydata, edata, groups, times,
                    sequences=NULL, fillNA=T, fillTimes=T)
```

Arguments

<code>xdata</code>	<code>n</code> by <code>Q</code> data.frame holding predictor variables
<code>ydata</code>	<code>n</code> by <code>S</code> matrix holding response variables
<code>edata</code>	<code>n</code> by <code>S</code> matrix holding effort
<code>groups</code>	column name in <code>xdata</code> holding group indicator
<code>times</code>	column name in <code>xdata</code> holding time indicator
<code>sequences</code>	column name in <code>xdata</code> holding sequence indicator
<code>fillNA</code>	fill new rows in <code>ydata</code> with NA; otherwise interpolated value
<code>fillTimes</code>	insert rows for missing times: integers values in column <code>times</code>

Details

Fills missing times in `xdata`, `ydata`, `edata`. If `fillTimes = TRUE` insert rows for missing times, including a `times = 0`, which serves as a prior mean for `times = 1`. `groups` must be uniquely defined. Within groups can be sequences, as when there is a time series for groups for each year.

Value

A list containing the following:

<code>xdata</code>	filled version of <code>xdata</code>
<code>ydata</code>	filled version of <code>ydata</code>
<code>edata</code>	filled version of <code>edata</code>
<code>timeZero</code>	row numbers in new data where each time series begins, with <code>times = 0</code>
<code>timeLast</code>	row numbers in new data where each time series ends
<code>rowInserts</code>	row numbers for all inserted rows
<code>noEffort</code>	rows for which effort is zero, except <code>times = 0</code>

Author(s)

James S Clark, <jimclark@duke.edu>

References

Clark, J.S., D. Nemergut, B. Seyednasrollah, P. Turner, and S. Zhang. 2016. Generalized joint attribute modeling for biodiversity analysis: Median-zero, multivariate, multifarious data. *Ecological Monographs*, 87, 34-56.

See Also

[gjam](#) for more on xdata, ydata, and effort.

A more detailed vignette is can be obtained with:

```
browseVignettes('gjam')
```

web site 'http://sites.nicholas.duke.edu/clarklab/code/'.

Examples

```
## Not run:
# under construction

## End(Not run)
```

gjamIIE

Indirect effects and interactions for gjam data

Description

Evaluates direct, indirect, and interactions from a [gjam](#) object. Returns a list of objects that can be plotted by [gjamIIEplot](#).

Usage

```
gjamIIE(output, xvector, MEAN = T, keepNames = NULL, omitY = NULL,
        sdScaleX = T, sdScaleY = F)
```

Arguments

output	object of class inheriting from "gjam".
xvector	vector of predictor values, with names, corresponding to columns in output\$x.
MEAN	logical, if false, then median used.
omitY	character vector of columns in output\$y to omit from calculations.
keepNames	character vector of columns in output\$y. If omitted, all columns used.
sdScaleX	standardize coefficients to X scale.
sdScaleY	standardize coefficients to correlation scale.

Details

For plotting or recovering effects. The list `fit$IIE` has matrices for main effects (`mainEffect`), interactions (`intEffect`), direct effects (`dirEffect`), indirect effects (`indEffectTo`), and standard deviations for each. The direct effects are the sum of main effects and interactions. The indirect effects include main effects and interactions that come through other species, determined by covariance matrix `sigma`.

If `sdScaleX = T` effects are standardized from the Y/X to Y scale. This is the typical standardization for predictor variables. If `sdScaleY = T` effects are given on the correlation scale. If both are true effects are dimensionless. See the `gjam` vignette on dimension reduction.

Value

A list of objects for plotting by `gjamIIEplot`.

Author(s)

James S Clark, <jimclark@duke.edu>

References

Clark, J.S., D. Nemergut, B. Seyednasrollah, P. Turner, and S. Zhang. 2016. Generalized joint attribute modeling for biodiversity analysis: Median-zero, multivariate, multifarious data. *Ecological Monographs* 87, 34-56.

See Also

`gjamIIEplot` plots output from `gjamIIE`

A more detailed vignette is can be obtained with:

```
browseVignettes('gjam')
```

web site '<http://sites.nicholas.duke.edu/clarklab/code/>'.

Examples

```
## Not run:
sim <- gjamSimData(S = 12, Q = 5, typeNames = 'CA')
m1 <- list(ng = 50, burnin = 5, typeNames = sim$typeNames)
out <- gjam(sim$formula, sim$xdata, sim$ydata, modelList = m1)

xvector <- colMeans(out$inputs$x) #predict at mean values for data
xvector[1] <- 1

fit <- gjamIIE(output = out, xvector)

gjamIIEplot(fit, response = 'S1', effectMu = c('main','ind'),
            effectSd = c('main','ind'), legLoc = 'topleft')

## End(Not run)
```

gjamIIEplot

*Plots indirect effects and interactions for gjam data***Description**

Using the object returned by `gjamIIEplot` generates a plot for a response variable.

Usage

```
gjamIIEplot(fit, response, effectMu, effectSd = NULL,
            ylim = NULL, col='black', legLoc = 'topleft', cex = 1)
```

Arguments

<code>fit</code>	object from <code>gjamIIE</code> .
<code>response</code>	name of a column in <code>fit\$y</code> to plot.
<code>effectMu</code>	character vector of mean effects to plot, can include 'main', 'int', 'direct', 'ind'.
<code>effectSd</code>	character vector can include all or some of <code>effectMu</code> .
<code>ylim</code>	vector of two values defines vertical axis range.
<code>col</code>	vector of colors for barplot.
<code>legLoc</code>	character for legend location.
<code>cex</code>	font size.

Details

For plotting direct effects, interactions, and indirect effects from an object `fit` generated by `gjamIIE`. The character vector supplied as `effectMu` can include main effects ('main'), interactions ('int'), main effects plus interactions ('direct'), and/or indirect effects ('ind'). The list `effectSd` draws 0.95 predictive intervals for all or some of the effects listed in `effectMu`. Bars are contributions of each effect to the response.

For factors, effects are plotted relative to the mean over all factor levels.

Author(s)

James S Clark, <jimclark@duke.edu>

References

Clark, J.S., D. Nemergut, B. Seyednasrollah, P. Turner, and S. Zhang. 2017. Generalized joint attribute modeling for biodiversity analysis: Median-zero, multivariate, multifarious data. *Ecological Monographs* 87, 34-56.

See Also

`gjamIIE` generates output for `gjamIIEplot`

A more detailed vignette is can be obtained with:

```
browseVignettes('gjam')
```

web site '<http://sites.nicholas.duke.edu/clarklab/code/>'.

Examples

```
## Not run:
sim <- gjamSimData(S = 10, Q = 6, typeNames = 'OC')
m1 <- list(ng = 50, burnin = 5, typeNames = sim$typeNames)
out <- gjam(sim$formula, sim$xdata, sim$ydata, modelList = m1)

xvector <- colMeans(out$inputs$x) #predict at mean values for data
xvector[1] <- 1

fit <- gjamIIE(out, xvector)

gjamIIEplot(fit, response = 'S1', effectMu = c('main','ind'),
            effectSd = c('main','ind'), legLoc = 'topleft')

## End(Not run)
```

gjamOrdination	<i>Ordinate gjam data</i>
----------------	---------------------------

Description

Ordinate data from a `gjam` object using correlation corresponding to reponse matrix E.

Usage

```
gjamOrdination(output, specLabs = NULL, col = NULL, cex = 1,
               PLOT=T, method = 'PCA')
```

Arguments

output	object of <code>class</code> "gjam".
specLabs	character vector of variable names in <code>colnames(output\$y)</code> .
col	character vector of columns in <code>output\$y</code> to label in plots.
cex	text size in plot.
PLOT	logical, if true, draw plots.
method	character variable can specify 'NMDS'.

Details

Ordinates the response correlation ematrix contained in `output$parameterTables`. If `method = 'PCA'` returns eigenvalues and eigenvectors. If `method = 'PCA'` returns three NMDS dimensions. If `PLOT`, then plots will be generated. Uses principle components analysis or non-metric multidimensional scale (NMDS).

Value

<code>eVecs</code>	$S \times S$ or, if there is an other response variable to be excluded, $S-1 \times S-1$ matrix of eigenvectors for species (rows) by eigenvectors (columns).
<code>eValues</code>	If <code>method = 'PCA'</code> returns length- S or, there is an other response variable to be excluded, length- $S-1$ vector of eigenvalues. If <code>method = 'NMDS'</code> this variable is NULL.

Author(s)

James S Clark, <jimclark@duke.edu>

References

Clark, J.S., D. Nemergut, B. Seyednasrollah, P. Turner, and S. Zhang. 2017. Generalized joint attribute modeling for biodiversity analysis: Median-zero, multivariate, multifarious data. *Ecological Monographs* 87, 34-56.

See Also

[gjam](#) fits the data

A more detailed vignette is can be obtained with:

```
browseVignettes('gjam')
```

website '<http://sites.nicholas.duke.edu/clarklab/code/>'.

Examples

```
## Not run:
f      <- gjamSimData(S = 30, typeNames = 'CA')
m1     <- list(ng = 30, burnin = 5, typeNames = f$typeNames, holdoutN = 10)
output <- gjam(f$formula, f$xdata, f$ydata, modelList = m1)
ePCA   <- gjamOrdination(output, PLOT=FALSE)
eNMDS  <- gjamOrdination(output, PLOT=FALSE, method='NMDS')

## End(Not run)
```


gjamPlot

*Plot gjam analysis***Description**

Constructs plots of posterior distributions, predictive distributions, and additional analysis from output of [gjam](#).

Usage

```
gjamPlot(output, plotPars)
```

Arguments

output	object of <code>class</code> "gjam"
plotPars	list having default values described in Details

Details

plotPars a list that can contain the following, listed with default values:

PLOTY = T	plot predicted y.
PLOTX = T	plot inverse predicted x.
PREDICTX = T	inverse prediction of x; does not work if PREDICTX = F in <code>link{gjam}</code> .
ncluster	number of clusters to highlight in cluster diagrams, default based on S.
CORLINES = T	draw grid lines on grid plots of R and E.
cex = 1	text size for grid plots, see par .
BETAGRID = T	draw grid of beta coefficients.
PLOTALLY = F	an individual plot for each column in y.
SMALLPLOTS = T	avoids plot margin error on some devices, better appearance if FALSE.
GRIDPLOTS = F	cluster and grid plots derived from parameters; matrices R and E are discussed in Clark et al.
SAVEPLOTS = F	plots saved in pdf format.
outfolder = 'gjamOutput'	folder for plot files if SAVEPLOTS = T.
width, height = 4	can be small values, in inches, to avoid plot margin error on some devices.
specColor = 'black'	color for posterior box-and-whisker plots.
ematAlpha = .95	prob threshold used to infer that a covariance value in Emat is not zero.
ncluster = 4	number of clusters to identify in ematrix.

The 'plot margin' errors mentioned above are device-dependent. They can be avoided by specifying small width, height (in inches) and by omitting the grid plots (GRIDPLOTS = F). If plotting does not produce a 'plot margin error', better appearance is obtained with SMALLPLOTS = F.

Names will not be legible for large numbers of species. Specify `specLabs = F` and use a character vector for `specColor` to identify species groups (see the [gjam vignette](#) on dimension reduction).

Box and whisker plots bound 0.68 and 0.95 credible and predictive intervals.

Value

Summary tables of parameter estimates are:

betaEstimates	Posterior summary of beta coefficients.
clusterIndex	cluster index for responses in grid/cluster plots.
clusterOrder	order for responses in grid/cluster plots.
eComs	groups based on clustering ematrix.
ematrix	$S \times S$ response correlation matrix for E.
eValues	eigenvalues of ematrix.
eVecs	eigenvectors of ematrix.
fit	list containing DIC, score, and rmspe.

Author(s)

James S Clark, <jimclark@duke.edu>

References

Clark, J.S., D. Nemergut, B. Seyednasrollah, P. Turner, and S. Zhang. 2017. Generalized joint attribute modeling for biodiversity analysis: Median-zero, multivariate, multifarious data. *Ecological Monographs* 87, 34-56.

See Also

[gjam](#) A more detailed vignette is can be obtained with:

```
browseVignettes('gjam')
```

website 'http://sites.nicholas.duke.edu/clarklab/code/'.

Examples

```
## Not run:
## ordinal data
f <- gjamSimData(S = 15, Q = 3, typeNames = 'OC')
m1 <- list(ng = 200, burnin = 50, typeNames = f$typeNames, holdoutN = 10)
out <- gjam(f$formula, f$xdata, f$ydata, modelList = m1)

# repeat with ng = 2000, burnin = 500, then plot data here:
p1 <- list(trueValues = f>trueValues, width=3, height=2)
fit <- gjamPlot(output = out, plotPars = p1)

## End(Not run)
```

<code>gjamPoints2Grid</code>	<i>Incidence point pattern to grid counts</i>
------------------------------	---

Description

From point pattern data in (x, y) generates counts on a lattice supplied by the user or specified by lattice size or density. For analysis in `gjam` as counts (known effort) or count composition (unknown effort) data.

Usage

```
gjamPoints2Grid(specs, xy, nxy = NULL, dxy = NULL,
                predGrid = NULL, effortOnly = TRUE)
```

Arguments

<code>specs</code>	character vector of species names or codes.
<code>xy</code>	matrix with rows = <code>length(specs)</code> and columns for (x, y) .
<code>nxy</code>	length-2 numeric vector with numbers of points evenly spaced on (x, y) .
<code>dxy</code>	length-2 numeric vector with distances for points evenly spaced on (x, y) .
<code>predGrid</code>	matrix with 2 columns for (x, y) .
<code>effortOnly</code>	logical to return only points where counts are positive (e.g., effort is unknown).

Details

For incidence data with species names `specs` and locations (x, y) constructs a lattice based a prediction grid `predGrid`, at a density of (dx, dy) , or with numbers of lattice points (nx, ny) . If `effortOnly = T`, returns only points with non-zero values.

A prediction grid `predGrid` would be passed when counts by locations of known effort are required or where multiple groups should be assign to the same lattice points.

The returned `gridBySpec` can be analyzed in `gjam` with known effort as count data "DA" or with unknown effort as count composition data "CC".

Value

<code>gridBySpec</code>	matrix with rows for grid locations, columns for counts by species.
<code>predGrid</code>	matrix with columns for (x, y) and rows matching <code>gridBySpec</code> .

Author(s)

James S Clark, <jimclark@duke.edu>

References

Clark, J.S., D. Nemergut, B. Seyednasrollah, P. Turner, and S. Zhang. 2016. Generalized joint attribute modeling for biodiversity analysis: Median-zero, multivariate, multifarious data. *Ecological Monographs* 87, 34-56.

See Also

[gjam](#) A more detailed vignette is can be obtained with:

```
browseVignettes('gjam')
```

Examples

```
## Not run:
## random data
n <- 100
s <- sample( letters[1:3], n, replace = TRUE)
xy <- cbind( rnorm(n,0,.2), rnorm(n,10,2) )

nx <- ny <- 5                                # uniform 5 X 5 lattice
f <- gjamPoints2Grid(s, xy, nxy = c(nx, ny))
plot(f$predGrid[,1], f$predGrid[,2], cex=.1, xlim=c(-1,1), ylim=c(0,20),
     xlab = 'x', ylab = 'y')
text(f$predGrid[,1], f$predGrid[,2], rowSums(f$gridBySpec))

dx <- .2                                       # uniform density
dy <- 1.5
g <- gjamPoints2Grid(s, xy, dxy = c(dx, dy))
text(g$predGrid[,1], g$predGrid[,2], rowSums(g$gridBySpec), col='brown')

p <- cbind( runif(30, -1, 1), runif(30, 0, 20) ) # irregular lattice
h <- gjamPoints2Grid(s, xy, predGrid = p)
text(h$predGrid[,1], h$predGrid[,2], rowSums(h$gridBySpec), col='blue')

## End(Not run)
```

gjamPredict

Predict gjam data

Description

Predicts data from a gjam object, including conditional and out-of-sample prediction.

Usage

```
gjamPredict(output, newdata = NULL, y2plot = NULL, ylim = NULL,
            FULL = FALSE)
```

Arguments

output	object of <code>class</code> "gjam".
newdata	a list of data for prediction, see Details .
y2plot	character vector of columns in <code>output\$y</code> to plot.
ylim	vector of lower and upper bounds for prediction plot
FULL	will return full chains for predictions as <code>output\$ychains</code>

Details

If `newdata` is not specified, the response is predicted from `xdata` as an in-sample prediction. If `newdata` is specified, prediction is either conditional or out-of-sample.

Conditional prediction on a new set of `y` values is done if `newdata` includes the matrix `ycondData`, which holds columns to condition on. `ycondData` must be a matrix and have column names matching those in `y` that it will replace. `ycondData` must have at least one column, but fewer than `ncol(y)` columns. Columns not included in `ycondData` will be predicted conditionally.

Alternatively, the list `newdata` can include a new version of `xdata` for out-of-sample prediction. The version of `xdata` passed in `newdata` has the columns with the same names and variable types as `xdata` passed to `gjam`. Note that factor levels must also match those included when fitting the model. All columns in `y` will be predicted out-of-sample.

For count composition data the effort (total count) is 1000.

Because there is no out-of-sample effort for 'CC' data, values are predicted on the [0, 1] scale.

See examples below.

Value

<code>x</code>	design matrix.
<code>sdList</code>	list of predictive means and standard errors includes <code>yMu</code> , <code>yPe</code> (predictive mean, SE), <code>wMu</code> , <code>wSe</code> (mean latent states and SEs)
<code>piList</code>	predictive intervals, only generated if <code>length(y) < 10000</code> , includes <code>yLo</code> , <code>yHi</code> (0.025, 0.975) prediction interval, <code>wLo</code> , <code>wHi</code> (0.025, 0.975) for latent states
<code>prPresent</code>	<code>n x S</code> matrix of probabilities of presence
<code>ematrix</code>	effort
<code>ychains</code>	full prediction chains if <code>FULL = T</code>

Author(s)

James S Clark, <jimclark@duke.edu>

References

Clark, J.S., D. Nemergut, B. Seyednasrollah, P. Turner, and S. Zhang. 2016. Generalized joint attribute modeling for biodiversity analysis: Median-zero, multivariate, multifarious data. *Ecological Monographs*, 87, 34-56.

See Also

[gjamSimData](#) simulates data

A more detailed vignette is can be obtained with:

```
browseVignettes('gjam')
```

web site '<http://sites.nicholas.duke.edu/clarklab/code/>'.

Examples

```

## Not run:
S <- 5
f <- gjamSimData(n = 200, S = S, Q = 3, typeNames = 'CC')
m1 <- list(ng = 50, burnin = 5, typeNames = f$typeNames, holdoutN = 10)
out <- gjam(f$formula, f$xdata, f$ydata, modelList = m1)

# predict data
par(mfrow=c(1,3),bty='n')
gjamPredict(out, y2plot = colnames(f$ydata)) #predict the data in-sample
title('full sample')

# out-of-sample prediction
xdata <- f$xdata[1:20,]
xdata[,3] <- mean(f$xdata[,3]) # mean for x[,3]
xdata[,2] <- seq(-2,2,length=20) # gradient x[,2]
newdata <- list(xdata = xdata, nsim = 50 )
p1 <- gjamPredict(out, newdata = newdata)

# plus/minus 1 prediction SE, default effort = 1000
x2 <- p1$x[,2]
ylim <- c(0, max(p1$sedList$yMu[,1] + p1$sedList$yPe[,1]))
plot(x2, p1$sedList$yMu[,1],type='l',lwd=2, ylim=ylim, xlab='x2',
     ylab = 'Predicted')
lines(x2, p1$sedList$yMu[,1] + p1$sedList$yPe[,1], lty=2)
lines(x2, p1$sedList$yMu[,1] - p1$sedList$yPe[,1], lty=2)

# .95 prediction error
lines(x2, p1$piList$yLo[,1], lty=3)
lines(x2, p1$piList$yHi[,1], lty=3)
title('SE and prediction, Sp 1')

# conditional prediction
ydataCond <- out$inputs$y[,1,drop=FALSE]*0 #set first column to zero
newdata <- list(ydataCond = ydataCond, nsim=50)
p0 <- gjamPredict(output = out, newdata = newdata)

ydataCond <- ydataCond + 20 #first column is 20
newdata <- list(ydataCond = ydataCond, nsim=50)
p1 <- gjamPredict(output = out, newdata = newdata)

plot(out$inputs$y[,4],p0$sedList$yMu[,4], cex=.4,col='orange'); abline(0,1,lty=2)
points(out$inputs$y[,4],p1$sedList$yMu[,4], cex=.4,col='blue')
title('Cond. on 1st Sp')

## End(Not run)

```

Description

Constructs coefficient matrices for low and high limits on the uniform prior distribution for beta.

Usage

```
gjamPriorTemplate(formula, xdata, ydata, lo = NULL, hi = NULL)
```

Arguments

formula	object of class formula, starting with ~, matches the formula passed to gjam
xdata	n x Q observation by predictor data.frame
ydata	n x Q observation by response data.frame
lo	list of lower limits
hi	list of upper limits

Details

The prior distribution for a coefficient $\beta[q, s]$ for predictor q and response s , is $\text{dunif}(\text{lo}[q, s], \text{hi}[q, s])$. `gjamPriorTemplate` generates these matrices. The default values are $(-\text{Inf}, \text{Inf})$, i.e., all values in `lo` equal to $-\text{Inf}$ and `hi` equal to Inf . These templates can be modified by changing specific values in `lo` and/or `hi`.

Alternatively, desired lower limits can be passed as the list `lo`, assigned to names in `xdata` (same limit for all species in `ydata`), in `ydata` (same limit for all predictors in `xdata`), or both, separating names in `xdata` and `ydata` by "_". The same convention is used for upper limits in `hi`.

These matrices are supplied in as list `betaPrior`, which is included in `modelList` passed to `gjam`. See examples and `browseVignettes('gjam')`.

Note that the informative prior slows computation.

Value

A list containing two matrices. `lo` is a $Q \times S$ matrix of lower coefficient limits. `hi` is a $Q \times S$ matrix of upper coefficient limits. Unless specied in `lo`, all values in `lo` = $-\text{Inf}$. Likewise, unless specied in `hi`, all values in `hiBeta` = $-\text{Inf}$.

Author(s)

James S Clark, <jimclark@duke.edu>

References

Clark, J.S., D. Nemergut, B. Seyednasrollah, P. Turner, and S. Zhang. 2017. Generalized joint attribute modeling for biodiversity analysis: Median-zero, multivariate, multifarious data. *Ecological Monographs* 87, 34-56.

See Also

[gjam](#)

Examples

```
## Not run:
library(repmis)
source_data("https://github.com/jimclarkatduke/gjam/blob/master/forestTraits.RData?raw=True")

xdata      <- forestTraits$xdata
plotByTree <- gjamReZero(forestTraits$treesDeZero) # re-zero
traitTypes <- forestTraits$traitTypes
specByTrait <- forestTraits$specByTrait

tmp <- gjamSpec2Trait(pbys = plotByTree, sbyt = specByTrait,
                     tTypes = traitTypes)
tTypes <- tmp$traitTypes
traity <- tmp$plotByCWM
censor <- tmp$censor

formula <- as.formula(~ temp + deficit)
lo <- list(temp_ring = 0, deficit_drought = 0) # positive combinations
b <- gjamPriorTemplate(formula, xdata, ydata = traity, lo = lo, hi = hi)
bp <- list(loBeta = b$lo, hiBeta = b$hi)

m1 <- list(ng=4000, burnin=1000, typeNames = tTypes, censor = censor,
          betaPrior = bp)
out <- gjam(formula, xdata, ydata = traity, modelList = m1)

S <- ncol(traity)
sc <- rep('black',S)
sc[colnames(traity)]
pl <- list(SMALLPLOTS=F, specColor=sc)
gjamPlot(output = out, plotPars = pl)

## End(Not run)
```

gjamReZero

Expand (re-zero) gjam data

Description

Returns a re-zeroed matrix `y` from the de-zeroed vector, a sparse matrix.

Usage

```
gjamReZero( yDeZero )
```

Arguments

`yDeZero` list created by `gjamReZero` containing number of rows `n`, number of columns `S`, index for non-zeros `index`, the vector of non-zero values `yvec`, and the column names `ynames`.

Details

Many abundance data sets are mostly zeros. `gjamReZero` recovers the full matrix from de-zeroed list `yDeZero` written by `gjamDeZero`

Value

`yamat` re-zeroed n by S matrix.

Author(s)

James S Clark, <jimclark@duke.edu>

References

Clark, J.S., D. Nemergut, B. Seyednasrollah, P. Turner, and S. Zhang. 2016. Generalized joint attribute modeling for biodiversity analysis: Median-zero, multivariate, multifarious data. *Ecological Monographs* 87, 34-56.

See Also

`gjamDeZero` to de-zero `yamat`
`browseVignettes('gjam')`
 website: `'http://sites.nicholas.duke.edu/clarklab/code/'`.

Examples

```
## Not run:
library(repmis)
source_data("https://github.com/jimclarkatduke/gjam/blob/master/fungEnd.RData?raw=True")
ymat <- gjamReZero(fungEnd$yDeZero) # OTUs stored without zeros
length(fungEnd$yDeZero$yvec)      # size of stored version
length(ymat)                      # full size

## End(Not run)
```

`gjamSensitivity` *Sensitivity coefficients for gjam*

Description

Evaluates sensitivity coefficients for full response matrix or subsets of it. Uses output from `gjam`. Returns a matrix of samples by predictors.

Usage

```
gjamSensitivity(output, group=NULL, nsim=100)
```

Arguments

output object fitted with gjam.
 group character vector of response-variable names from output\$inputs\$.
 nsim number of samples from posterior distribution.

Details

Sensitivity to predictors of entire response matrix or a subset of it, identified by the character string group. The equations for sensitivity are given here:

```
browseVignettes('gjam')
```

Value

Returns a nsim by predictor matrix of sensitivities to predictor variables.

Author(s)

James S Clark, <jimclark@duke.edu>

References

Clark, J.S., D. Nemergut, B. Seyednasrollah, P. Turner, and S. Zhang. 2017. Generalized joint attribute modeling for biodiversity analysis: Median-zero, multivariate, multifarious data. *Ecological Monographs*, 87, 34-56.

See Also

[gjamSimData](#) simulates data

A more detailed vignette is can be obtained with:

```
browseVignettes('gjam')
```

website '<http://sites.nicholas.duke.edu/clarklab/code/>'.

Examples

```
## Not run:
## combinations of scales
types <- c('DA', 'DA', 'OC', 'OC', 'OC', 'OC', 'CC', 'CC', 'CC', 'CC', 'CC', 'CA', 'CA', 'PA', 'PA')
f <- gjamSimData(S = length(types), typeNames = types)
m1 <- list(ng = 50, burnin = 5, typeNames = f$typeNames)
out <- gjam(f$formula, f$xdata, f$ydata, modelList = m1)

ynames <- colnames(f$y)
group <- ynames[types == 'OC']

full <- gjamSensitivity(out)
cc <- gjamSensitivity(out, group)

nt <- ncol(full)
```

```

boxplot( full, boxwex = 0.25, at = 1:nt - .21, col='blue', log='y',
         xaxt = 'n', xlab = 'Predictors', ylab='Sensitivity')
boxplot( cc, boxwex = 0.25, at = 1:nt + .2, col='forestgreen', add=T,
         xaxt = 'n')
axis(1,at=1:nt,labels=colnames(full))
legend('bottomright',c('full response','CC data'),
      text.col=c('blue','forestgreen'))

## End(Not run)

```

gjamSimData

*Simulated data for gjam analysis***Description**

Simulates data for analysis by [gjam](#).

Usage

```
gjamSimData(n = 1000, S = 10, Q = 5, x = NULL, nmiss = 0, typeNames, effort = NULL)
```

Arguments

n	Sample size
S	Number of response variables (columns) in y, typically less than n
Q	Number of predictors (columns) in design matrix $x \ll n$
x	design matrix, if supplied n and Q will be set to $nrow(x)$ and $ncol(x)$, respectively
nmiss	Number of missing values to in $x \ll n$
typeNames	Character vector of data types, see Details
effort	List containing 'columns' specifying columns to which effort applies, and 'values', a length-n vector of effort per observation.

Details

Generates simulated data and parameters for analysis by [gjam](#). Because both parameters and data are stochastic, not all simulations will give good results.

typeNames can be 'PA' (presenceAbsence), 'CA' (continuous), 'DA' (discrete), 'FC' (fractional composition), 'CC' (count composition), 'OC' (ordinal counts), and 'CAT' (categorical levels). If more than one 'CAT' is included, each defines a multilevel categorical response. One additional type, 'CON' (continuous), is not censored at zero by default.

If defined as a single character value typeNames applies to all columns in y. If not, typeNames is length-S character vector, identifying each response by column in y. If a column 'CAT' is included, a random number of levels will be generated, a, b, c, ...

A more detailed vignette is can be obtained with:

```
browseVignettes('gjam')
```

website 'http://sites.nicholas.duke.edu/clarklab/code/'.

Value

formula	R formula for model, e.g., $\sim x_1 + x_2$
xdata	data.frame includes columns for predictors in the design matrix
ydata	data.frame for the simulated response
y	response as a n by S matrix as assembled in gjam .
w	n by S latent states
typeY	vector of data types corresponding to columns in y, see Details
typeName	vector of data types corresponding to columns in ydata
trueValues	list containing true parameter values beta (regression coefficients), sigma (covariance matrix), corSpec (correlation matrix corresponding to sigma), and cuts (partition matrix for ordinal data).
effort	see Arguments .

Author(s)

James S Clark, <jimclark@duke.edu>

References

Clark, J.S., D. Nemergut, B. Seyedsrollah, P. Turner, and S. Zhang. 2016. Generalized joint attribute modeling for biodiversity analysis: Median-zero, multivariate, multifarious data. *Ecological Monographs* 87, 34-56.

See Also

[gjam](#)

Examples

```
## Not run:
## ordinal data, show true parameter values
sim <- gjamSimData(S = 5, typeName = 'OC')
sim$ydata[1:5,]           # example data
sim>trueValues$cuts      # simulated partition
sim>trueValues$beta      # coefficient matrix

## continuous data censored at zero, note latent w for obs y = 0
sim <- gjamSimData(n = 5, S = 5, typeName = 'CA')
sim$w
sim$y

## continuous and discrete data
types <- c(rep('DA',5), rep('CA',4))
sim <- gjamSimData(n = 10, S = length(types), Q = 4, typeName = types)
sim$typeNames
sim$ydata

## composition count data
```

```

sim <- gjamSimData(n = 10, S = 8, typeNames = 'CC')
totalCount <- rowSums(sim$ydata)
cbind(sim$ydata, totalCount) # data with sample effort

## multiple categorical responses - compare matrix y and data.frqme ydata
types <- rep('CAT',2)
sim <- gjamSimData(S = length(types), typeNames = types)
head(sim$ydata)
head(sim$y)

## discrete abundance, heterogeneous effort
S <- 5
n <- 1000
ef <- list( columns = 1:S, values = round(runif(n,.5,5),1) )
sim <- gjamSimData(n, S, typeNames = 'DA', effort = ef)
sim$effort$values[1:20]

## combinations of scales, partition only for 'OC' columns
types <- c('OC', 'OC', 'OC', 'CC', 'CC', 'CC', 'CC', 'CA', 'CA', 'PA', 'PA')
sim <- gjamSimData(S = length(types), typeNames = types)
sim$typeNames
head(sim$ydata)
sim$trueValues$cuts

## End(Not run)

```

gjamSpec2Trait

Ecological traits for gjam analysis

Description

Constructs community-weighted mean-mode (CWMM) trait matrix for analysis with [gjam](#) for n observations, S species, P traits, and M total trait levels.

Usage

```
gjamSpec2Trait(pbys, sbyt, tTypes)
```

Arguments

pbys	$n \times S$ plot by species matrix (presence-absence, abundance)
sbyt	$S \times P$ species by trait matrix
tTypes	P data types for trait columns

Details

Generates the objects needed for a trait response model (TRM). As inputs the `sbyt` data.frame has P columns containing numeric values, ordinal scores, and categorical variables, identified by data type in `tTypes`. Additional trait columns can appear in the $n \times M$ output matrix `plotByCWMM`, because each level of a category becomes a new 'FC' column as a CWMM. Thus, M can exceed P , depending on the number of factors in `sbyt`. The exception is for categorical traits with only two levels, which can be treated as (0, 1) censored 'CA' data.

As output, the CWMM data types are given in `traitTypes`.

The list `sensor = NULL` unless some data types are censored. In the example below there are two censored columns.

A detailed vignette on trait analysis is obtained with:

```
browseVignettes('gjam')
```

Value

<code>plotByCWM</code>	$n \times M$ matrix of community-weight means (numeric) or modes (ordinal)
<code>traitTypes</code>	character vector of data types for traits
<code>specByTrait</code>	$S \times M$ matrix translates species to traits
<code>sensor</code>	list of censored columns, values, and intervals; see gjamCensorY

Author(s)

James S Clark, <jimclark@duke.edu>

References

Clark, J.S. 2016. Why species tell us more about traits than traits tell us about species: Predictive models. *Ecology* 97, 1979-1993.

Clark, J.S., D. Nemergut, B. Seyedsnasrollah, P. Turner, and S. Zhang. 2017. Generalized joint attribute modeling for biodiversity analysis: Median-zero, multivariate, multifarious data. *Ecological Monographs* 87, 34-56.

See Also

[gjam](#), [gjamCensorY](#)

Examples

```
## Not run:
library(repmis)
source_data("https://github.com/jimclarkatduke/gjam/blob/master/forestTraits.RData?raw=True")

xdata      <- forestTraits$xdata
plotByTree <- gjamReZero(forestTraits$treesDeZero) # re-zero
traitTypes <- forestTraits$traitTypes
specByTrait <- forestTraits$specByTrait
```

```

tmp <- gjamSpec2Trait(pbys = plotByTree, sbyt = specByTrait,
                    tTypes = traitTypes)
tTypes <- tmp$traitTypes
traity <- tmp$plotByCWM
censor <- tmp$censor

ml <- list(ng=2000, burnin=500, typeName = tTypes, censor = censor)
out <- gjam(~ temp + stdage + deficit, xdata, ydata = traity, modelList = ml)
pl <- list(SMALLPLOTS=F)
gjamPlot(output = out, plotPars = pl)

## End(Not run)

```

gjamTrimY

*Trim gjam response data***Description**

Returns a list that includes a subset of columns in *y*. Rare species can be aggregated into a single class.

Usage

```
gjamTrimY(y, minObs = 2, maxCols = NULL, OTHER = TRUE)
```

Arguments

<i>y</i>	n by S numeric response matrix
<i>minObs</i>	minimum number of non-zero observations
<i>maxCols</i>	maximum number of response variables
<i>OTHER</i>	logical or character string. If <i>OTHER</i> = TRUE, rare species are aggregated in a new column 'other'. A character vector contains the names of columns in <i>y</i> to be aggregated with rare species in the new column 'other'.

Details

Data sets commonly have many responses that are mostly zeros, large numbers of rare species, even singletons. Response matrix *y* can be trimmed to include only taxa having > *minObs* non-zero observations or to <= *maxCol* total columns. The option *OTHER* is recommended for composition data ('CC', 'FC'), where the 'other' column is taken as the reference class. If there are unidentified species they might be included in this class. [See [gjamSimData](#) for typeName codes].

Value

Returns a list containing three elements.

<i>y</i>	trimmed version of <i>y</i> .
<i>colIndex</i>	length-S vector of indices for new columns in <i>y</i> .
<i>nobs</i>	number of non-zero observations by column in <i>y</i> .

Author(s)

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References

Clark, J.S., D. Nemergut, B. Seyednasrollah, P. Turner, and S. Zhang. 2017. Generalized joint attribute modeling for biodiversity analysis: Median-zero, multivariate, multifarious data. *Ecological Monographs* 87, 34-56.

See Also

[gjamSimData](#) simulates data [gjam](#) analyzes data

A more detailed vignette is can be obtained with:

```
browseVignettes('gjam')
```

web site '<http://sites.nicholas.duke.edu/clarklab/code/>'.

Examples

```
## Not run:
library(repmis)
source_data("https://github.com/jimclarkatduke/gjam/blob/master/forestTraits.RData?raw=True")

y <- gjamReZero(fungEnd$yDeZero)      # re-zero data
dim(y)
y <- gjamTrimY(y, minObs = 200)$y     # species in >= 200 observations
dim(y)
tail(colnames(y))    # last column is 'other'

## End(Not run)
```


Index

*Topic **package**

gjam-package, 2

class, 5, 12, 15, 17, 20

GJAM (gjam-package), 2

gjam, 3, 4, 4, 7, 8, 12, 16–21, 23, 25, 27–30, 32

gjam-package, 2

gjamCensorY, 3, 5, 7, 30

gjamDeZero, 3, 9, 9, 25

gjamFillMissingTimes, 11

gjamIIE, 3, 12, 15

gjamIIEplot, 3, 12–14, 14

gjamOrdination, 3, 15

gjamPlot, 3, 4, 8, 17

gjamPoints2Grid, 3, 19

gjamPredict, 3, 20

gjamPriorTemplate, 3, 22

gjamReZero, 3, 10, 24, 24

gjamSensitivity, 3, 25

gjamSimData, 3, 4, 6, 8, 21, 26, 27, 31, 32

gjamSpec2Trait, 3, 29

gjamTrimY, 3, 31

par, 17

print.gjam (gjam), 4

summary.gjam (gjam), 4