

Package ‘clustord’

May 29, 2025

Type Package

Title Cluster Ordinal Data via Proportional Odds or Ordered Stereotype

Version 1.3.4

Date 2025-05-21

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Description

Biclustering, row clustering and column clustering using the proportional odds model (POM), ordered stereotype model (OSM) or binary model for ordinal categorical data. Fernández, D., Arnold, R., Pledger, S., Liu, I., & Costilla, R. (2019) <[doi:10.1007/s11634-018-0324-3](https://doi.org/10.1007/s11634-018-0324-3)>.

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URL <https://vuw-clustering.github.io/clustord/>

Depends R (>= 3.5.0), stats, utils

Imports Rcpp (>= 1.0.1), MASS, nnet, flexclust, methods

LinkingTo Rcpp, RcppArmadillo, RcppClock

Suggests knitr, formatR, rmarkdown, testthat (>= 2.1.0), multgee, parallel

Encoding UTF-8

RoxygenNote 7.3.2

VignetteBuilder knitr, formatR

NeedsCompilation yes

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Repository CRAN
Date/Publication 2025-05-29 08:20:02 UTC

Contents

calc.cluster.comparisons	2
calc.SE.rowcluster	3
clustord	4
mat2df	19
osm	20
rerun	24
Index	26

calc.cluster.comparisons
<i>Calculate comparison measures between two sets of clustering results</i>

Description

Given two sets of posterior probabilities of membership for clusters, calculate three measures to compare the clustering memberships.

Usage

```
calc.cluster.comparisons(ppr1, ppr2)
```

Arguments

- ppr1 Posterior probabilities of cluster membership, named ppr_m or ppc_m in the output of [clustord](#). If you have performed biclustering, then ppr1 should be the clustering results for just one of the dimensions i.e. just the row clustering results, or just the column clustering results. The rows of ppr1 give the entries that have been clustered, and each column corresponds to one cluster.
- ppr2 Posterior probabilities of cluster membership from a different clustering run, which will be compared to ppr1.

Details

The three measures are the Adjusted Rand Index (ARI), the Normalised Variation of Information (NVI) and the Normalised Information Distance (NID).
The three measures are documented in

Value

A list with components:

ARI: Adjusted Rand Index.

NVI: Normalised Variation of Information.

NID: Normalised Information Distance.

References

Fernández, D., & Pledger, S. (2016). Categorising count data into ordinal responses with application to ecological communities. *Journal of agricultural, biological, and environmental statistics (JABES)*, 21(2), 348–362.

calc.SE.rowcluster	<i>Calculate standard errors of clustering parameters.</i>
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Description

Calculate SE of parameters fitted using [clustord](#).

Usage

```
calc.SE.rowcluster(long.df, clust.out, optim.control = default.optim.control())
```

```
calc.SE.biclust(long.df, clust.out, optim.control = default.optim.control())
```

Arguments

long.df	The data frame, in long format, as passed to clustord .
clust.out	A clustord object.
optim.control	control list for the optim call within the M step of the EM algorithm. See the control list Details in the optim manual for more info.

Details

Use `calc.SE.rowcluster` to calculate SE for row clustering and column clustering, or `calc.SE.biclust` to calculate SE for biclustering.

Calculates SE by running `optimHess` (see [optim](#)) on the incomplete-data log-likelihood to find the hessian at the fitted parameter values from [clustord](#). Then the square roots of the diagonal elements of the negative inverse of the hessian are the standard errors of the parameters i.e. `SE <- sqrt(diag(solve(-optim.hess)))`.

Note that SE values are **only** calculated for the independent parameters. For example, if the constraint on the row clustering parameters is set to `constraint_sum_zero = TRUE`, where the last row clustering parameter is the negative sum of the other parameters, SE values will only be calculated for the first RG-1 parameters, the independent ones. This applies similarly to individual column effect coefficients, etc.

The function requires an input which is the output of `clustord`, which includes the component `outvect`, the final vector of independent parameter values from the EM algorithm, which will correspond to a subset of the parameter values in `parlist.out`.

Value

The standard errors corresponding to the elements of `clust.out$outvect`.

Functions

- `calc.SE.rowcluster()`: SE for rowclustering
- `calc.SE.biccluster()`: SE for biclustering

clustord	<i>Likelihood-based clustering using Ordered Stereotype Models (OSM), Proportional Odds Models (POM) or Binary Models</i>
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Description

Likelihood-based clustering with parameters fitted using the EM algorithm. You can perform clustering on rows or columns of a data matrix, or biclustering on both rows and columns simultaneously. You can include any number of covariates for rows and covariates for columns. Ordinal models used in the package are Ordered Stereotype Model (OSM), Proportional Odds Model (POM) and a dedicated Binary Model for binary data.

Usage

```
clustord(
  formula,
  model,
  nclus.row = NULL,
  nclus.column = NULL,
  long.df,
  initvect = NULL,
  pi.init = NULL,
  kappa.init = NULL,
  EM.control = default.EM.control(),
  optim.method = "L-BFGS-B",
  optim.control = default.optim.control(),
  constraint_sum_zero = TRUE,
  start_from_simple_model = TRUE,
  parallel_starts = FALSE,
  nstarts = 5,
  verbose = FALSE
)
```

Arguments

formula	model formula (see 'Details').
model	"OSM" for Ordered Stereotype Model or "POM" for Proportional Odds Model or "Binary" for binary data model.
nclus.row	number of row clustering groups.
nclus.column	number of column clustering groups.
long.df	data frame with at least three columns, Y and ROW and COL. Each row in the data frame corresponds to a single cell in the original data matrix; the response value in that cell is given by Y, and the row and column indices of that cell in the matrix are given by ROW and COL. Use <code>mat2df</code> to create this data frame from your data matrix of responses. <code>mat2df</code> also allows you to supply data frames of row or column covariates which will be incorporated into <code>long.df</code> .
initvect	(default NULL) vector of starting parameter values for the model. Note: if the user enters an initial vector of parameter values, it is strongly recommend that the user also check the values of <code>parlist.init</code> in the output object, to make sure that the constructed parameters are as expected . If NULL, starting parameter values will be generated automatically. See 'Details' for definitions of the parameters used for different models.
pi.init	(default NULL) starting parameter values for the proportions of observations in the different row clusters. If NULL, starting values will be generated automatically. User-specified values of <code>pi.init</code> must be of length <code>(nclus.row-1)</code> because the final value will be automatically calculated so that the values of <code>pi</code> sum to 1.
kappa.init	(default NULL) starting parameter values for the proportions of observations in the different column clusters. If NULL, starting values will be generated automatically. User-specified values of <code>kappa.init</code> must be of length <code>(nclus.column-1)</code> because the final value will be automatically calculated so that the values of <code>kappa</code> sum to 1.
EM.control	(default = <code>list(EMcycles=50, EMlikelihoodtol=1e-4, EMparamtol=1e-2, paramstopping=TRUE, startEMcycles=10, keepallparams=FALSE, epsilon=1e-6)</code>) list of parameters controlling the EM algorithm. EMcycles controls how many EM iterations of the main EM algorithm are used to fit the chosen submodel. EMlikelihoodtol is the tolerance for the stopping criterion for the log-likelihood in the EM algorithm. The criterion is the absolute change in the incomplete log-likelihood since the previous iteration, scaled by the size of the dataset $n \times p$, where n is the number of rows in the data matrix and p is the number of columns in the data matrix. The scaling is applied because the incomplete log-likelihood is predominantly affected by the dataset size. EMparamtol is the tolerance for the stopping criterion for the parameters in the EM algorithm. This is a tolerance for the sum of the scaled parameter changes from the last iteration, i.e. the tolerance is not for any individual parameter but for the sum of changes in all the parameters. Thus the default tolerance is 1e-2.

The individual parameter criteria are the absolute differences between the exponentiated absolute parameter value at the current timestep and the exponentiated absolute parameter value at the previous timestep, as a proportion of the exponentiated absolute parameter value at the current timestep. The exponentiation is to rescale parameter values that are close to zero.

there are around 5 independent parameter values, then at the point of convergence using default tolerances for the log-likelihood and the parameters, each parameter will have a scaled absolute change since the previous iteration of about $1e-4$; if there are 20 or 30 independent parameters, then each will have a scaled absolute change of about $1e-6$.

paramstopping: if FALSE, indicates that the EM algorithm should only check convergence based on the change in incomplete-data log-likelihood, relative to the current difference between the complete-data and incomplete-data log-likelihoods, i.e. $\text{abs}(\text{delta_lli})/\text{abs}(\text{llc}[\text{iter}] - \text{lli}[\text{iter}])$; if TRUE, indicates that as well as checking the likelihood criterion, the EM algorithm should also check whether the relative change in the exponentials of the absolute values of the current parameters is below the tolerance EMstoppingpar, to see whether the parameters and the likelihood have both converged.

startEMcycles controls how many EM iterations are used when fitting the simpler submodels to get starting values for fitting models with interaction.

keepallparams: if TRUE, keep a record of parameter values (including π_r and κ_c) for every EM iteration.

rerunestepbeforelli: if TRUE, and only when using biclustering, rerun the E-step before calculating the incomplete-data log-likelihood. The EM algorithm runs the E-step to estimate the cluster membership probabilities and then runs the M-step to estimate the parameters by maximising the complete-data log-likelihood (LLC), and then recalculates the estimated incomplete-data log-likelihood (LLI) to check for convergence. The biclustering LLI approximation uses the cluster membership probabilities so will be slightly more accurate if these cluster membership probabilities are recalculated using the very latest parameter estimates. So the TRUE setting for this control recalculates the cluster memberships before calculating the LLI approx.

uselatestlli: Kept for backwards compatibility with original version of clustord algorithm. Original version of the algorithm had this set to FALSE, which keeps the best LLI from any previous iteration rather than the latest LLI. The default, TRUE, instead keeps the latest LLI even if there was a better LLI in a previous iteration. This is appropriate: In row clustering the exact LLI is used and the EM algorithm creators proved the LLI should always not decrease with each iteration. In biclustering the approximation to the LLI may be very inaccurate when the algorithm is a long way from convergence, so even when the value of LLI appears to be very high in early iterations this may not be accurate, so it is better to take the latest value.

For columnclustering, the parameters saved from each iteration will NOT be converted to column clustering format, and will be in the row clustering format, so alpha in EM.status\$params.every.iteration will correspond to β_c and π will correspond to κ .

epsilon: default $1e-6$, small value used to adjust values of π , κ and θ that are too close to zero so that taking logs of them does not create infinite

- values.
- optim.method** (default "L-BFGS-B") method to use in optim within the M step of the EM algorithm. Must be one of 'L-BFGS-B', 'BFGS', 'CG' or 'Nelder-Mead' (i.e. not the SANN method).
- optim.control** control list for the optim call within the M step of the EM algorithm. See the control list Details in the optim manual for more info. Please note that although optim, by default, uses `pgtol=0` and `factr=1e7` in the L-BFGS-B method, clustord, by default, alters these to `pgtol=1e-4` and `factr=1e11`, but you can use this `optim.control` argument in clustord to revert them to the defaults if you want. The reason for the change is that the chosen values in clustord reduce the tolerance on the log-likelihood function optimization in order to speed up the algorithm, and because the log-likelihood is on the scale of $1e4$ for <100 rows in the data matrix and $1e6$ for 5000 rows in the data matrix, tolerance at the default optim scale is not as important as the choice of model type and structure or the number of starting points. If one model is better than another, it will probably have a likelihood that is better by about the size of the data matrix, which is far larger than the tolerance in the optimization. If one starting point is better than another, it will probably have a likelihood that is better on about 1/10th or 1/100th the size of the data matrix, which is still far larger than the tolerance in the optimization. If you need accurate parameter estimates, firstly make sure to try more starting points, then perform model selection first, and then finally rerun the chosen model with finer tolerance, e.g. the optim defaults, `pgtol=0` and `factr=1e7`.
- constraint_sum_zero** (default TRUE) if TRUE, use constraints that cluster effects sum to zero; if FALSE, use constraints that the cluster effect for the first cluster will be 0. Both versions have the same constraints for joint row-column cluster effects: these effects are described by a matrix of parameters `gamma_rc`, indexed by row cluster and column cluster indices, and the constraints are that the final column of `gamma_rc` is equal to the negative sum of the other columns (so gamma columns sum to zero) and first row of `gamma_rc` is equal to the negative sum of the other rows (so gamma rows sum to zero).
- start_from_simple_model** (default TRUE) if TRUE, fit a simpler clustering model first and use that to provide starting values for all parameters for the model with interactions; if FALSE, use the more basic models to provide starting values only for `pi.init` and `kappa.init`. If the full model has interaction terms, then simpler models are ones without the interactions. If the model has individual row/column effects alongside the clusters, then simpler models are ones without the individual row/column effects. If the full model has covariates, then simpler models are ones without the covariates (to get starting values for the cluster parameters), and ones with the covariates but no clustering (to get starting values for the covariates).
- parallel_starts** (default FALSE) if TRUE, by generating multiple random starts, those random starts will be parallelised over as many cores as are available. For example, on a personal computer this will be one fewer than the number of cores in the machine, to make sure one is left for system tasks external to R.

nstarts	(default 5) number of random starts to generate, if generating random starting points for the EM algorithm.
verbose	(default FALSE) changes how much is reported to the console during the algorithm's progress. If TRUE, reports the incomplete-data log-likelihood at every EM algorithm iteration and the trace information from <code>nnet::multinom()</code> during the process of fitting initial values for the μ parameters. If FALSE, the incomplete log-likelihood is only reported every 10 iterations of the EM algorithm and the initial fitting reporting is suppressed. Regardless of the verbosity setting the algorithm reports each of the random starts and whenever it finds a better log-likelihood than all previous starts, and it also reports when it is fitting simpler models to find starting values for the parameters vs fitting the final, more complex model. If wanting the detailed output from <code>optim()</code> , use <code>optim.control=list(trace=X)</code> , where X is 1 to 6, with 6 being the highest level of verbosity for the L-BFGS-B algorithm.

Details

You can select your own input parameters, or starting values will be generated by running `kmeans` or by fitting simpler models and feeding the outputs into the final model as starting values.

The starting point for clustering is a data matrix of response values that are binary or categorical. You may also have a data frame of covariates that are linked to the rows of the data matrix, and may also have a data frame of covariates that are linked to the columns of the data matrix.

For example, if clustering data from fishing trawls, where the rows are trawl events and columns are species caught, then you could also supply a gear covariate linked to the rows, representing gear used on each trawl event, and could additionally supply species covariates linked to the columns, representing auxiliary information about each species. There is no requirement to provide any covariates, and you can provide only row covariates, or only column covariates.

Before running `clustord`, you need to run `mat2df` to convert the data matrix into a long form data frame. The data frame needs to have at least three columns, Y and ROW and COL. Each row in the data frame corresponds to a single cell in the original data matrix; the response value in that cell is given by Y, and the row and column indices of that cell in the matrix are given by ROW and COL.

`mat2df` also allows you to supply data frames of row or column covariates which will be incorporated into `long.df`.

Then, to run the `clustord` function, you need to enter your chosen formula and model, and the number of clusters you want to fit. The formula `model_structure` is akin to that for `glm`, but with a few restrictions. You can include any number of covariates in the same way as for a multiple regression model, though unlike for `glm`, you can include both row and column covariates.

Note that, unlike `glm`, you should not specify a `family` argument; the `model` argument is used instead.

formula argument details

In the following description of different models, the Binary model is used for simplicity when giving the mathematical descriptions of the models, but you can use any of the following models with the Ordered Stereotype or Proportional Odds Models as well.

In the formula argument, the response must be exactly Y. You cannot use any functions of Y as the response, nor can you include Y in any terms on the right hand side of the formula. Y is the name in `clustord` of the response values in the original data matrix.

The formula argument has 4 special variables: ROWCLUST, COLCLUST, ROW and COL. There are some restrictions on how these can be used in the formula, as they are not covariates, but instead act as indicators of the clustering model_structure you want to use.

All other variables in the formula will be any covariates that you want to include in the model, and these are unrestricted, and can be used in the same way as in glm.

ROWCLUST and COLCLUST are used to indicate what row clustering model_structure you want, and what column clustering model_structure you want, respectively. The inclusion of ROWCLUST as a single term indicates that you want to include a row clustering effect in the model. In the simplest row clustering model, for Binary data with **row clustering** effects only, the basic function call would be

```
clustord(Y ~ ROWCLUST, model="Binary", long.df=long.df)
```

and the model fitted would have the form:

$$\text{Logit}(P(Y = 1)) = \mu + \text{rowc_coef_r}$$

where μ is the intercept term, and rowc_coef_r is the row cluster effect that will be applied to every row from the original data matrix that is a member of row cluster r. The inclusion of ROWCLUST corresponds to the inclusion of rowc_coef_r.

Note that we are not using notation involving greek letters, because (a) we ran out of letters for all the different types of parameters in the model and (b) with this many parameters, it would be difficult to remember which ones are which.

Similarly to row clustering, the formula $Y \sim \text{COLCLUST}$ would perform **column clustering**, with model $\text{Logit}(P(Y = 1)) = \mu + \text{colc_coef_c}$, where colc_coef_c is the column cluster effect that will be applied to every column from the original data matrix that is a member of column cluster c.

Including both ROWCLUST and COLCLUST in the same formula indicates that you want to perform biclustering, i.e. you want to cluster the rows and the columns of the original data matrix simultaneously. If included without interaction, then the terms just correspond to including rowc_coef_r and colc_coef_c in the model:

The formula

$$Y \sim \text{ROWCLUST} + \text{COLCLUST}$$

is the simplest possible **biclustering** model, $\text{Logit}(P(Y = 1)) = \mu + \text{rowc_coef_r} + \text{colc_coef_c}$

If you want to include interaction between the rows and columns, i.e. you want to perform block biclustering where each block corresponds to a row cluster r and a column cluster c, then that model has a matrix of parameters indexed by r and c.

`clustord(Y ~ ROWCLUST*COLCLUST, model="Binary", ...)` has the model $\text{Logit}(P(Y = 1)) = \mu + \text{rowc_colc_coef_rc}$

This model can instead be called using the equivalent formula $Y \sim \text{ROWCLUST} + \text{COLCLUST} + \text{ROWCLUST}:\text{COLCLUST}$.

You can instead use the formula $Y \sim \text{ROWCLUST}:\text{COLCLUST}$. Mathematically, this is equivalent to the previous two. In regression, the models would not be equivalent but in clustering, they are equivalent, and have the same number of independent parameters overall. If you include the main effects, then that reduces the number of independent parameters in the interaction term compared to if you just use the interaction term (see below section about `initvect`).

You cannot include just one of the main effects alongside the interaction term, i.e. you cannot use $Y \sim \text{ROWCLUST} + \text{ROWCLUST}:\text{COLCLUST}$ or $Y \sim \text{COLCLUST} + \text{ROWCLUST}:\text{COLCLUST}$. This is for simplicity in the code, and to avoid confusion when interpreting the results.

However, *clustord* allows a lot more flexibility than this. The variables ROW and COL are used to indicate that you want to also include **individual row or column effects**, respectively.

For example, if you are clustering binary data that indicates the presence/ absence of different species (columns) at different trawl events (rows), and you know that one particular species is incredibly common, then you can include column effects in the model, which will allow for the possibility that two columns may correspond to species with different probabilities of appearing in the trawl.

You can add individual column effects along with row clustering, or you can add individual row effects along with column clustering. The formula for row clustering with individual column effects (without interaction) is

$Y \sim \text{ROWCLUST} + \text{COL}$

which corresponds to Binary model

$\text{Logit}(P(Y = 1)) = \mu + \text{rowc_coef_r} + \text{col_coef_j}$

So if two cells from the data matrix are in the same row cluster, but in different columns, they will not have the same probability of $Y = 1$.

You can also add interaction between the individual row/column effects and the clustering effects.

If you still want to be able to see the row cluster and column effects separately, then you use $Y \sim \text{ROWCLUST} * \text{COL}$ or $Y \sim \text{ROWCLUST} + \text{COL} + \text{ROWCLUST} : \text{COL}$ (these are both the same), which have model

$\text{Logit}(P(Y = 1)) = \mu + \text{rowc_coef_r} + \text{col_coef_j} + \text{rowc_col_coef_rj}$

As before, *rowc_coef_r* and *col_coef_j* are the row cluster effects and individual column effects, and *rowc_col_coef_rj* are the interaction terms.

Alternatively, you can use the mathematically-equivalent formula

$Y \sim \text{ROWCLUST} : \text{COL}$ which has model

$\text{Logit}(P(Y = 1)) = \mu + \text{rowc_col_coef_rj}$

where the row cluster effects and individual column effects are absorbed into the matrix *rowc_col_coef_rj*.

These models are the same mathematically, the only differences between them are in how they are constrained (see below in the section about the *initvect* argument) and how they should be interpreted.

Note that if you were using covariates, then it would not be equivalent to leave out the main effects and just use the interaction terms, but the clustering models don't work quite the same as regression models with covariates.

Equivalently, if you want to cluster the columns, you can include individual row effects alongside the column clusters, i.e.

$Y \sim \text{COLCLUST} + \text{ROW}$ or $Y \sim \text{COLCLUST} + \text{ROW} + \text{COLCLUST} : \text{ROW}$,

depending on whether you want the interaction terms or not.

You are **not** able to include individual row effects with row clusters, or include individual column effects with column clusters, because there is not enough information in ordinal or binary data to fit these models. As a consequence, you cannot include individual row or column effects if you are doing biclustering, e.g.

$Y \sim \text{ROWCLUST} + \text{COLCLUST} + \text{ROW}$ or $Y \sim \text{ROWCLUST} + \text{COLCLUST} + \text{COL}$

are not permitted.

From version 1 of the package, you can now also include **covariates** alongside the clustering patterns. The basic way to do this is include them as additions to the clustering model_structure. For example, including one row covariate *xr* to a row clustering model would have the formula

$$Y \sim \text{ROWCLUST} + xr$$

with Binary model $\text{Logit}(P(Y = 1)) = \mu + \text{rowc_coef_r} + \text{row_coef_1} * xr_i$

where *row_coef_1* is the coefficient of *xr_i*, just as in a typical regression model.

Additional row covariates can also be included, and you can include interactions between them, and functions of them, as in regression models, e.g.

$$Y \sim \text{ROWCLUST} + xr1 * \log(xr2)$$

which would have the Binary model

$$\text{Logit}(P(Y = 1)) = \mu + \text{rowc_coef_r} + \text{row_coef1} * xr1_i + \text{row_coef2} * \log(xr2_i) + \text{row_coef3} * xr1_i * \log(xr2_i)$$

If instead you want to add column covariates to the model, they work in the same way after they've been added to the `long.df` data frame using `mat2df`, but they are indexed by *j* instead of *i*. Simplest model, with one single column covariate *xc*, would have formula

$$Y \sim \text{ROWCLUST} + xc$$

with Binary model $\text{Logit}(P(Y = 1)) = \mu + \text{rowc_coef_r} + \text{col_coef1} * xc_j$

You can use any functions of or interactions between column covariates, just as with row covariates. You can similarly add row or column covariates to column clustering or biclustering models.

You can include **interactions between covariates** and ROWCLUST or COLCLUST in the formula. But these are **not quite** the same as interactions between covariates. The formula

$$Y \sim \text{ROWCLUST} * xr$$

where *xr* is some row covariate, corresponds to the Binary model

$$\text{Logit}(P(Y = 1)) = \mu + \text{rowc_coef_r} + \text{cov_coef} * xr_i + \text{rowc_row_coef_r1} * xr_i$$

What this means is that there is a term in the linear predictor that involves the row covariate *xr* (which has the index *i* because it is a row covariate), and each cluster (indexed by *r*) has a different coefficient for that covariate (as distinct from the non-interaction covariate models above, which have the same coefficients for the covariates regardless of which cluster the row is in).

This is different from interaction terms involving only covariates, where two or more covariates appear multiplied together in the model and then have a shared coefficient term attached to them. In a clustering/covariate interaction, the row or column clustering pattern controls the coefficients rather than adding a different type of covariate.

Note that the pure cluster effect *rowc_coef_r* is also included in the model automatically, in the same way that a regression formula $Y \sim x1 * x2$ would include the individual *x1* and *x2* effects as well as the interaction between *x1* and *x2*.

The coefficients for row clusters interacting with row coefficients are named *row_cluster_row_coef* in the output of `clustord` because you can also have coefficients for interactions between row clustering and column covariates, or column clustering and row covariates, or column clustering and column covariates. Row clustering interacting with column covariates would look something like

$$Y \sim \text{ROWCLUST} * xc$$

with Binary model $\text{Logit}(P(Y = 1)) = \mu + \text{rowc_coef_r} + \text{rowc_col_coef_r1} * xc_j$

The other combinations of clustering and covariates work similarly. *rowc_col_coef_r1* and the other similar coefficients have two indices. Their first index is the index of the cluster, and their

second index is the index of the covariate among the list of covariates interacting with that direction of clustering. So if there are two row covariates `xr1` and `xr2` interacting with three row clusters, that gives you 6 coefficients:

```
rowc_col_coef_11, rowc_col_coef_12, rowc_col_coef_21, rowc_col_coef_22, rowc_col_coef_31,
rowc_col_coef_32.
```

and you can also have a three-way interaction between row cluster and those two covariates, which would add the coefficients `rowc_col_coef_r3` for the `xr1:xr2` term.

You can instead add covariates that interact with column clusters, which will have parameters `colc_row_coef_cm`, where `m` here indexes just the covariates interacting with column cluster.

If you have covariates interacting with row clusters and other covariates interacting with column clusters, then you will have parameters `rowc_cov_coef_r1` **and** `colc_cov_coef_cm`.

An example of this is the model

```
Y ~ ROWCLUST + xr1 + ROWCLUST:xr1 + xc1 + COLCLUST + COLCLUST:log(xc1)
```

This has main effects for row clusters and column clusters, i.e. `ROWCLUST` and `COLCLUST`. It also has two covariate terms not interacting with clusters, `xr1` and `xc1`. It also has 1 covariate term interacting with row clusters, `xr1`, with coefficients `rowc_cov_coef_r1`, and 1 covariate term interacting with column clusters, `log(xc1)`, with coefficients `colc_cov_coef_c1`.

Restrictions on formula

The primary restriction on the formula argument is that that you **cannot** use functions of `ROW`, `COL`, `ROWCLUST` or `COLCLUST`, such as `log(ROW)` or `I(COLCLUST^2)`. That is because they are not covariates, and cannot be manipulated like that; instead, they are indicators for particular elements of the clustering model structure.

If performing biclustering, i.e. if `ROWCLUST` and `COLCLUST` are both in the model, and you want to include the interaction between them, then you can use the interaction between them on its own, or you can include both main effects, but you are not allowed to use just one main effect alongside the interaction. That is, you can use

```
Y ~ ROWCLUST + COLCLUST + ROWCLUST:COLCLUST or Y ~ ROWCLUST*COLCLUST,
```

or you can use `Y ~ ROWCLUST:COLCLUST`, and these two types of biclustering model will have different parameter constraints (see below under `initvect` details), but you **cannot** use

```
Y ~ ROWCLUST + ROWCLUST:COLCLUST or Y ~ COLCLUST + ROWCLUST:COLCLUST
```

As stated above, you also cannot include individual row effects alongside row clustering, and you cannot use individual column effects alongside column clustering, i.e. if `ROWCLUST` is in the formula, then `ROW` **cannot** be in the formula, and if `COLCLUST` is in the formula then `COL` **cannot** be in the formula.

If you are including `COL` with `ROWCLUST`, then you can include the interaction between them but that is the **only** permitted interaction term that involves `COL`, and similarly the interaction between `ROW` and `COLCLUST` is the **only** permitted interaction term that involves `ROW`. But you can include those interactions in the form

```
Y ~ ROWCLUST + COL + ROWCLUST:COL or as Y ~ ROWCLUST*COL, or as Y ~ ROWCLUST:COL.
```

These are the only permitted uses of the `COL` term, and there are equivalent constraints on the inclusion of `ROW`.

As stated above, you can include interactions between `ROWCLUST` or `COLCLUST` and covariates, but you **cannot** include three-way interactions between `ROWCLUST`, `COLCLUST` and one or more covariates are **not permitted** in `clustord`, mostly because of the prohibitive number of parameter values

that would need to be fitted, and the difficulty of interpreting such a model. That is, you cannot use formulae such as $Y \sim \text{ROWCLUST} * \text{COLCLUST} * x_r$, which would have Binary model $\text{Logit}(P(Y = 1)) = \mu + \text{bi_cluster_row_coef_rc1} * x_{r_i}$.

model argument details

The three models available in `clustord` are the Binary model, which is a Bernoulli model equivalent to the binary model in the package `clustglm`, the Proportional Odds Model (POM) and the Ordered Stereotype Model (OSM).

Many Binary model examples have been given above, which have the general form

$$\text{logit}(P(Y = 1)) = \mu + \text{«linear terms»}$$

where the linear terms can include row or column clustering effects, individual row or column effects, and row or column covariates, with or without interactions with row or column clustering.

The Proportional Odds Model and the Ordered Stereotype Model have the same `model_structure` for the linear terms, but the overall model equation is different.

The Proportional Odds Model (`model = "POM"`) has the form

$$\text{logit}(P(Y \leq k)) = \log(P(Y \leq k)/P(Y > k)) = \mu_k - \text{«linear terms»}$$

So the simplest POM for row clustering would be

$$\text{logit}(P(Y \leq k)) = \mu_k - \text{rowc_coef_r}$$

and the model including individual column effects and no interactions would be

$$\text{logit}(P(Y \leq k)) = \mu_k - \text{rowc_coef_r} - \text{col_coef_j}$$

Note that the linear-term coefficients have negative signs for the Proportional Odds Models. This is so that as the row cluster index increases, or as the column index increases, Y is more likely to fall at higher values (see Ch4 of Agresti, 2010).

The Ordered Stereotype model (`model = "OSM"`) has the form

$$\log(P(Y = k)/P(Y = 1)) = \mu_k + \phi_k(\text{«linear terms»})$$

So the simplest OSM for row clustering would be

$$\log(P(Y = k)/P(Y = 1)) = \mu_k + \phi_k * \text{rowc_coef_r}$$

and the model including individual column effects and no interactions would be

$$\log(P(Y = k)/P(Y = 1)) = \mu_k + \phi_k(\text{rowc_coef_r} + \text{col_coef_j})$$

Note that the OSM is **not** a cumulative logit model, unlike the POM. The model describes the log of the k th level relative to the first level, which is the baseline category, but the patterns for $k = 2$ may be different than the patterns for $k = 3$. They are linked, because the linear terms will be the same, but they may not have the same shape. In this sense, the OSM is more flexible/less restrictive than the POM.

See Anderson (1984) for the original definition of the ordered stereotype model, and see Fernández et al. (2016) for the application to clustering.

The ϕ_k parameters may be treated as "score" parameters. After fitting the OSM, the fitted ϕ_k values can give some indication of what the true separation is between the categories. Even if the default labelling of the categories is from 1 to n , that doesn't mean that the categories are actually equally spaced in reality. But the fitted ϕ_k values from the OSM can be treated as data-derived numerical labels for the categories. Moreover, if two categories have very similar fitted ϕ_k values, e.g. if $\phi_2 = 0.11$ and $\phi_3 = 0.13$, that suggests that there is not enough information

in the data to distinguish between categories 2 and 3, and so you might as well merge them into a single category to simplify the model-fitting process and the interpretation of the results.

initvect argument details

Initvect is the vector of starting values for the parameters, made up of sections for each different type of parameter in the model. Note that the length of each section of initvect is the number of **independent** parameter values, not the overall number of parameter values of that type.

If you want to supply a vector of starting values for the EM algorithm, you need to be careful how many values you supply, and the order in which you include them in initvect, and you should **CHECK** the output list of parameters (which is the full set of parameter values, including dependent ones, broken up into each type of parameter) to check that your initvect model_structure is correct for the formula you have specified.

For example, the number of mu values will always be 1 fewer than the number of categories in the data, and the remaining value of mu is dependent on those q-1 values. In the OSM for data with 3 categories, the first value of mu for category 1 will be 0, and then the other 2 values of mu for categories 2 and 3 will be the independent values of mu. For the POM for data with 5 categories, the first 4 values of mu will be the independent values and then the last value of mu is infinity, because the probability of Y being in category 5 is defined as 1 minus the sum of the probabilities for the other 4 levels.

q is the number of levels in the values of y, n is the number of rows in the original data matrix, and p is the number of columns in the original data matrix.

For Binary, There is one independent value for mu, i.e. q = 2.

Ignore phi, which is not used in the Binary model.

For OSM, The starting values for mu_k are length q-1, and the model has mu_1 = 0 always, so the initvect values for mu will become mu_2, mu_3, etc. up to mu_q.

The starting values for phi_k are length q-2.

Note that the starting values for phi do not correspond directly to phi, because phi is restricted to being increasing and between 0 and 1, so instead the starting values are treated as elements u[2:q-1] of a vector u which can be between -Inf and +Inf, and then

```
phi[2] <- expit(u[2]) and
```

```
phi[k] <- expit(u[2] + sum(exp(u[3:k]))) for k between 3 and q-1
```

```
(phi[1] = 0 and phi[q] = 1).
```

For POM, The starting values for mu_k are length q-1, but the starting values do not correspond directly to mu_k, because mu_k is restricted to being increasing, i.e. the model has to have mu_1 <= mu_2 <= ... mu_q = +Inf

So instead of using the initvect values directly for mu_k, the 2nd to (q-1)th elements of initvect are used to construct mu_k as follows:

```
mu_1 <- initvect[1]
```

```
mu_2 <- initvect[1] + exp(initvect[2])
```

```
mu_3 <- initvect[1] + exp(initvect[2]) + exp(initvect[3])
```

... and so on up to mu_{k-1}, and mu_k is infinity, because it is not used directly to construct the probability of Y = q.

Thus the values that are used to construct μ_k can be unconstrained, which makes it easier to specify `initvect` and easier to optimize the parameter values.

Ignore ϕ_i , which is not used in POM.

For **all three models**,

The starting values for `rowc_coef_r` are length `nclus.row-1`, where `nclus.row` is the number of row clusters. The final row cluster parameter is dependent on the others (see the input parameter info for `constraint_sum_zero`), whereas if it were independent it would be colinear with the μ_k parameters and thus not identifiable.

Similarly the starting values for `colc_coef_c` are length `nclus.column-1`, where `nclus.column` is the number of column clusters, to avoid problems of colinearity and nonidentifiability.

If you have biclustering with an interaction term between row clusters and column clusters, then the number of independent values in the matrix of interaction terms depends on whether you include the main effects of row and column clusters separately. That is, if you use the biclustering model

$Y \sim \text{ROWCLUST} + \text{COLCLUST} + \text{ROWCLUST}:\text{COLCLUST}$, or equivalently

$Y \sim \text{ROWCLUST}*\text{COLCLUST}$,

then the main effect term `ROWCLUST` has `nclus.row-1` independent parameters in `initvect`, and `COLCLUST` has `nclus.column-1` independent parameters in `initvect`, and `ROWCLUST:COLCLUST` will have $(\text{nclus.row} - 1) * (\text{nclus.column} - 1)$ independent parameter values. The final matrix of interaction terms will be constrained to have its last row equal to the negative sum of the other rows, and the last column equal to the negative sum of the other columns.

On the other hand, if you want to use only the interaction term and not the main effects (which for the clustering model is mathematically equivalent), i.e.

$Y \sim \text{ROWCLUST}:\text{COLCLUST}$,

then that matrix of interaction terms will have $\text{nclus.row} * \text{nclus.column} - 1$ independent parameters, i.e. more independent parameters than if you included the main effects.

If you have column effects alongside row clusters (they are not permitted alongside column clusters), without interactions, i.e. the formula $Y \sim \text{ROWCLUST} + \text{COL}$ with Binary model $\text{Logit}(P(Y = 1)) = \mu + \text{rowc_coef_r} + \text{col_coef_j}$ then the row cluster coefficients have `nclus.row - 1` independent parameters, and the column effect coefficients have $p - 1$ independent parameters, where p is the number of columns in the original data matrix, i.e. the maximum value of `long.df$COL`.

If you include the interaction term, then the number of independent parameters again depends on whether you just use the interaction term, or include the main effects.

In the formula $Y \sim \text{ROWCLUST} + \text{COL} + \text{ROWCLUST}:\text{COL}$ or its equivalent with `"*"`, the interaction term will have $(\text{nclus.row} - 1) * (p - 1)$ independent parameters.

If you instead use the formula $Y \sim \text{ROWCLUST}:\text{COL}$, then the interaction term will have $\text{nclus.row} * p - 1$ independent parameters. Either way, the total number of independent parameters in the model will be $\text{nclus.row} * p$.

Similarly, if you have row effects alongside column clusters, without interactions, i.e. the formula

$Y \sim \text{COLCLUST} + \text{ROW}$,

with Binary model $\text{Logit}(P(Y = 1)) = \mu + \text{colc_coef_c} + \text{row_coef_i}$

then the column cluster coefficients will have `nclus.column - 1` independent parameters, and the row coefficients will have $n - 1$ independent parameters, where n is the number of rows in the original data matrix, i.e. the maximum value of `long.df$ROW`.

If you include the interaction term alongside the main effects, i.e.

$Y \sim \text{COLCLUST} + \text{ROW} + \text{COLCLUST}:\text{ROW}$, or its equivalent with "*", the interaction term will have $(\text{nclus.column} - 1) * (\text{n} - 1)$ independent parameters.

If you instead use the formula $Y \sim \text{COLCLUST}:\text{ROW}$, that interaction coefficient matrix will have $\text{nclus.column} * \text{n} - 1$ independent parameters.

Any covariate terms included in the formula will be split up by `clustord` into the covariates that interact with row clusters, the covariates that interact with column clusters, and the covariates that do not interact with row or column clusters.

The number of independent parameters for row-cluster-interacting covariates will be $\text{nclus.row} * L$, where L is the number of terms involving row clusters and covariates after any "*" terms have been expanded.

So in this formula, for example,

$Y \sim \text{ROWCLUST} * \text{xr1} + \text{xr2} + \text{ROWCLUST}:\log(\text{xc1})$

where xr1 and xr2 are row covariates, and xc1 is a column covariate, the fully expanded formula would be

$Y \sim \text{ROWCLUST} + \text{xr1} + \text{xr2} + \text{ROWCLUST}:\text{xr1} + \text{ROWCLUST}:\log(\text{xc1})$

and the terms interacting with `ROWCLUST` would be `ROWCLUST:xr1` and `ROWCLUST:log(xc1)`, so there would be $\text{nclus.row} * 2$ independent coefficients for those covariates.

The number of independent parameters for column-cluster-interacting covariates will be $\text{nclus.column} * M$, where M is the number of terms involving column clusters and covariates after any "*" terms have been expanded.

So this formula, for example,

$Y \sim I(\text{xr1}^2) + \text{COLCLUST} * \text{xc1} + \text{COLCLUST}:\text{xc2}:\text{xc3} + \text{COLCLUST} * \text{xr1}$

would be expanded as

$Y \sim \text{COLCLUST} + \text{xr1} + I(\text{xr1}^2) + \text{xc1} + \text{COLCLUST}:\text{xc1} + \text{COLCLUST}:\text{xc2}:\text{xc3} + \text{COLCLUST}:\text{xr1}$

and the terms interacting with `COLCLUST` would be `COLCLUST:xc1`, `COLCLUST:xc2:xc3` and `COLCLUST:xr1`, so there would be $\text{nclus.column} * 3$ independent coefficients for those covariates.

The number of independent parameters for covariates that do not interact with row or column clusters will be the same as the number of those covariate terms, after any "*" terms have been expanded.

So this formula, for example,

$Y \sim \text{ROWCLUST} * \text{xr1} + \text{xr2} + \text{ROWCLUST}:\log(\text{xc1}) + \text{COLCLUST} * \text{xc1}$

would be expanded as

$Y \sim \text{ROWCLUST} + \text{COLCLUST} + \text{xr1} + \text{xr2} + \text{xc1} + \text{ROWCLUST}:\text{xr1} + \text{ROWCLUST}:\log(\text{xc1}) + \text{COLCLUST}:\text{xc1}$,

so there would be 3 independent coefficients for the terms xr1 , xr2 , xc1 .

Note that there are **no intercept** terms for the coefficients, because those are incorporated into the parameters `mu_k`.

The **order of the** `initvect` **entries** is as follows, and any entries that are not included in the formula will be ignored and not included in `initvect`. That is, you should NOT provide values in `initvect` for components that are not included in the formula.

1) `mu` (or values used to construct `mu`, POM only) 2) values used to construct `phi` (OSM only) 3) row cluster coefficients 4) column cluster coefficients 5) [matrix] bicluster coefficients (i.e. interaction

between row and column clusters) 6) individual row coefficients 7) individual column coefficients 8) [matrix] interactions between row clusters and individual column coefficients 9) [matrix] interactions between column clusters and individual row coefficients 10) [matrix] row-cluster-specific coefficients for covariates interacting with row clusters 11) [matrix] column-cluster-specific coefficients for covariates interacting with column clusters 12) coefficients for covariates that do not interact with row or column clusters

Any entries marked as [matrix] will be constructed into matrices by filling those matrices row-wise, e.g. if you want starting values 1:6 for a matrix of 2 row clusters and 3 covariates interacting with those row clusters, the matrix of coefficients will become

```
1 2 3 4 5 6
```

For the formula $Y \sim \text{ROWCLUST} * \text{COLCLUST}$, where the matrix of interactions between row and column clusters has $(\text{nclus.row} - 1) * (\text{nclus.column} - 1)$ independent parameters, the last row and column of the matrix will be the negative sums of the rest, so e.g. if you have 2 row clusters and 3 column clusters, there will only be 2 independent values, so if you provide the starting values -0.5 and 1.2, the final matrix of parameters will be:

```
column cluster 1 column cluster 2 column cluster 3 row cluster 1 -0.5 1.2 -0.7 row cluster
2 0.5 -1.2 0.7
```

If the matrix is a matrix relating to row clusters, then the row clusters are in the rows, and if it's a matrix relating to column clusters but not row clusters, then the column clusters are in the rows, i.e. the matrix of coefficients for column clusters interacting with individual row effects will have the rows of the matrix corresponding to the clusters, i.e. the matrix would be indexed `colc_row_coef_ci`, `c` being the column cluster index and `i` being the row index.

Similarly, if the matrix is a matrix relating to column clusters and covariates, then the rows of the matrix will correspond to the column clusters, i.e. the matrix would be indexed `colc_cov_coef_cl`, `c` being the column cluster index and `l` being the covariate index.

If using biclustering with interaction between row and column clusters, then the row clusters will be the rows and the column clusters will be the columns, i.e. the matrix would be indexed `rowc_colc_coef_rc`, `r` being the row cluster index and `c` being the column cluster index.

Value

A `clustord` object, i.e. a list with components:

`info`: Basic info `n`, `p`, `q`, the number of parameters, the number of row clusters and the number of column clusters, where relevant.

`model`: The model used for fitting, "OSM" for Ordered Stereotype Model, "POM" for Proportional Odds Model, or "Binary" for Binary model.

`EM.status`: a list containing the latest iteration `iter`, latest incomplete-data and complete-data log-likelihoods `new.lli` and `new.llc`, the best incomplete-data log-likelihood `best.lli` and the corresponding complete-data log-likelihood, `llc.for.best.lli`, and the parameters for the best incomplete-data log-likelihood, `params.for.best.lli`, indicator of whether the algorithm converged `converged`, and if the user chose to keep all parameter values from every iteration, also `params.every.iteration`.

Note that for **biclustering**, i.e. when `ROWCLUST` and `COLCLUST` are both included in the model, the **incomplete** log-likelihood is calculated using the entropy approximation, and this may be **inaccurate** unless the algorithm has converged or is close to converging. So beware of using the incomplete log-likelihood and the corresponding AIC value **unless the EM algorithm has converged**.

`criteria`: the calculated values of AIC, BIC, etc. from the best incomplete-data log-likelihood.

`epsilon`: the very small value (default $1e-6$) used to adjust values of π and κ and θ that are too close to zero, so that taking logs of them does not produce infinite values. Use the `EM.control` argument to adjust `epsilon`.

`constraints_sum_zero`: the chosen value of `constraints_sum_zero`.

`param_lengths`: vector of total number of parameters/coefficients for each part of the model, labelled with the names of the components. The value is 0 for each component that is not included in the model, e.g. if there are no covariates interacting with row clusters then the `rowc_cov_coef` value will be 0. If the component is included, then the value given will include any dependent parameter/coefficient values, so if column clusters are included then the `colc_coef` value will be `nclus.column`, whereas the number of independent values will be `nclus.column - 1`.

`initvect`: the initial *vector* of parameter values, either specified by the user or generated automatically. This vector has only the **independent** values of the parameters, not the full set.

`outvect`: the final *vector* of parameter values, containing only the independent parameter values from `parlist.out`.

`parlist.init`: the initial list of parameters, constructed from the initial parameter vector `initvect`. Note that if the initial vector has been incorrectly specified, the values of `parlist.init` may not be as expected, and they should be checked by the user.

`parlist.out`: fitted values of parameters.

`pi`, `kappa`: fitted values of π and κ , where relevant.

`ppr`, `ppc`: the posterior probabilities of membership of the row clusters and the column clusters, where relevant.

`rowc_mm`, `colc_mm`, `cov_mm`: the model matrices for, respectively, the covariates interacting with row clusters, the covariates interacting with column clusters, and the covariates not interacting with row or column clusters (i.e. the covariates with constant coefficients). Note that one row of each model matrix corresponds to one row of `long.df`.

`RowClusters`, `ColumnClusters`: the assigned row and column clusters, where relevant, where each row/column is assigned to a cluster based on maximum posterior probability of cluster membership (`ppr` and `ppc`).

`RowClusterMembers`, `ColumnClusterMembers`: vectors of assigned members of each row or column cluster, where each row/column is assigned to a cluster based on maximum posterior probability of cluster membership (`ppr` and `ppc`)

References

Fernandez, D., Arnold, R., & Pledger, S. (2016). Mixture-based clustering for the ordered stereotype model. *Computational Statistics & Data Analysis*, 93, 46-75.

Anderson, J. A. (1984). Regression and ordered categorical variables. *Journal of the Royal Statistical Society: Series B (Methodological)*, 46(1), 1-22.

Agresti, A. (2010). *Analysis of ordinal categorical data* (Vol. 656). John Wiley & Sons.

Examples

```
set.seed(1)
long.df <- data.frame(Y=factor(sample(1:3,5*20,replace=TRUE)),
```

```

ROW=factor(rep(1:20,times=5)),COL=rep(1:5,each=20))

# Model  $\text{Log}(P(Y=k)/P(Y=1))=\mu_k+\phi_k*\text{rowc\_coef\_r}$  with 3 row clustering groups:
clustord(Y~ROWCLUST,model="OSM",3,long.df=long.df,
        EM.control=list(EMcycles=2,startEMcycles=2), nstarts=2)

# Model  $\text{Log}(P(Y=k)/P(Y=1))=\mu_k+\phi_k*(\text{rowc\_coef\_r} + \text{col\_coef\_j})$  with 3 row clustering groups:
clustord(Y~ROWCLUST*COL,model="OSM",3,long.df=long.df,
        EM.control=list(EMcycles=2,startEMcycles=2), nstarts=2)

# Model  $\text{Logit}(P(Y \leq k))=\mu_k-\text{rowc\_coef\_r}-\text{col\_coef\_j}-\text{rowc\_col\_coef\_rj}$  with 2 row clustering groups:
clustord(Y~ROWCLUST*COL,model="POM",nclus.row=2,long.df=long.df,
        EM.control=list(EMcycles=2,startEMcycles=2), nstarts=2)

# Model  $\text{Log}(P(Y=k)/P(Y=1))=\mu_k+\phi_k*(\text{colc\_coef\_c})$  with 3 column clustering groups:
clustord(Y~COLCLUST,model="OSM",nclus.column=3,long.df=long.df,
        EM.control=list(EMcycles=2,startEMcycles=2), nstarts=2)

# Model  $\text{Log}(P(Y=k)/P(Y=1))=\mu_k+\phi_k*(\text{colc\_coef\_c} + \text{row\_coef\_i})$  with 3 column clustering groups:
clustord(Y~COLCLUST*ROW,model="OSM",nclus.column=3,long.df=long.df,
        EM.control=list(EMcycles=2,startEMcycles=2), nstarts=2)

# Model  $\text{Log}(P(Y=k)/P(Y=1))=\mu_k+\phi_k*(\text{rowc\_coef\_r} + \text{colc\_coef\_c})$ 
#   with 3 row clustering groups and 2 column clustering groups:
clustord(Y~ROWCLUST*COLCLUST,model="OSM",nclus.row=3,nclus.column=2,long.df=long.df,
        EM.control=list(EMcycles=2), nstarts=1)

# Model  $\text{Logit}(P(Y \leq k))=\mu_k-\text{rowc\_coef\_r}-\text{colc\_coef\_c}-\text{rowc\_colc\_coef\_rc}$ 
#   with 2 row clustering groups and 4 column clustering groups, and
#   interactions between them:
clustord(Y~ROWCLUST*COLCLUST, model="POM", nclus.row=2, nclus.column=4,
        long.df=long.df,EM.control=list(EMcycles=2), nstarts=1,
        start_from_simple_model=FALSE)

```

mat2df

Converting matrix of responses into a long-form data frame and incorporating covariates, if supplied.

Description

Converting matrix of responses into a long-form data frame and incorporating covariates, if supplied.

Usage

```
mat2df(mat, xr.df = NULL, xc.df = NULL)
```

Arguments

<code>mat</code>	matrix of responses to be clustered
<code>xr.df</code>	optional data frame of covariates corresponding to the rows of <code>mat</code> . Each row of <code>xr.df</code> corresponds to one row of <code>mat</code> , and each column of <code>xr.df</code> is a covariate.
<code>xc.df</code>	optional data frame of covariates corresponding to the columns of <code>mat</code> . Each row of <code>xc.df</code> corresponds to one column of <code>mat</code> , and each column of <code>xc.df</code> is a covariate.

Value

A data frame with columns `Y`, `ROW` and `COL`, and additional columns for covariates from `xr.df` and `xc.df`, if included.

The `Y` column of the output contains the entries in `mat`, with one row in the output per one cell in `mat`, and the `ROW` and `COL` entries indicate the row and column of the data matrix that correspond to the given cell. Any cells that were `NA` are left out of the output data frame.

If `xr.df` is supplied, then there are additional columns in the output corresponding to the columns of `xr.df`, and the values for each covariate are repeated for every entry that was in the corresponding row of the data matrix.

Similarly, if `xc.df` is supplied, there are additional columns in the output corresponding to the columns of `xc.df`, and the values for each covariate are repeated for every entry that was in the corresponding column of the data matrix.

osm

Ordinal data regression using the Ordered Stereotype Model (OSM).

Description

Fit a regression model to an ordered factor response. The model is NOT a logistic or probit model because the link function is not the logit, but the link function is log-based.

Usage

```
osm(
  formula,
  data,
  weights,
  start,
  ...,
  subset,
  na.action,
  Hess = FALSE,
  model = TRUE
)
```

Arguments

formula	a formula expression as for regression models, of the form response ~ predictors. The response should be a factor (preferably an ordered factor), which will be interpreted as an ordinal response, with levels ordered as in the factor. The model must have an intercept: attempts to remove one will lead to a warning and be ignored. An offset may be used. See the documentation of formula for other details.
data	a data frame, list or environment in which to interpret the variables occurring in formula.
weights	optional case weights in fitting. Default to 1.
start	initial values for the parameters. See the Details section for information about this argument.
...	additional arguments to be passed to optim, most often a control argument.
subset	expression saying which subset of the rows of the data should be used in the fit. All observations are included by default.
na.action	a function to filter missing data.
Hess	logical for whether the Hessian (the observed information matrix) should be returned.
model	logical for whether the model matrix should be returned.

Details

This function should be used in a very similar way to `MASS::polr`, and some of the arguments are the same as `polr`, but the ordinal model used here is less restrictive in its assumptions than the proportional odds model. However, it is still parsimonious i.e. it uses only a small number of additional parameters compared with the proportional odds model.

This model is the *ordered stereotype* model (Anderson 1984, Agresti 2010)

It is more flexible than the proportional odds model but only adds a handful of additional parameters. It is not a cumulative model, being instead defined in terms of the relationships between each of the higher categories and the lowest category that is treated as the reference category.

Each of the higher categories has its own intercept term, μ_k , which is similar to the zeta parameters in `polr`, but in the OSM each higher category also has its own scaling parameter, ϕ_k , which adjusts the effect of the covariates on the response. This allows the effect of the covariates on the response to be slightly different for each category of the response, thus making the model more flexible than the proportional odds model.

The final set of parameters are coefficients for each of the covariates, and these are equivalent to the coefs in `polr`. Higher or more positive values of the coefficients increases the probability of the response being in the higher categories, and lower or more negative values of the coefficients increase the probability of the response being in the lower categories.

The overall model takes the following form:

$$\log(P(Y = k | X)/P(Y = 1 | X)) = \mu_k + \phi_k * \beta_{\text{vec}}^T x_{\text{vec}}$$

for $k = 2, \dots, q$, where x_{vec} is the vector of covariates for the observation Y .

μ_1 is fixed at 0 for identifiability of the model, and the ϕ_k parameters are constrained to be ordered (giving the model its name) in the following way:

$0 = \text{phi}_1 \leq \text{phi}_2 \leq \dots \leq \text{phi}_k \leq \dots \leq \text{phi}_q = 1.$

(The unordered stereotype model restricts phi_1 and phi_q but allows the remaining phi_k to be in any order, and this is suitable for fitting the model for nominal data. However, this package does not provide that option, as it is already available in other packages which can fit the stereotype model.)

After fitting the model, the estimated values of the intermediate phi_k values indicate a suitable numerical spacing of the ordinal response categories that is based on the data. The spacings indicate how much distinct information each of the corresponding levels provide. For example, if you have five response categories and the fitted phi values are $(0, 0.04, 0.6, 0.62, 1)$ then this indicates that levels 1 and 2 provide very similar information about the effect of the covariates on the response, and levels 3 and 4 provide very similar information as each other. The meaning of this is that you could simplify the response by combining levels 1 and 2 and combining levels 3 and 4 (i.e. reduce the levels to 1, 3 and 5) and you would still be able to estimate the beta coefficients with similar accuracy.

Another use for the phi_k values is that if you want to carry out further analysis of the response, treating it as a numerical variable, then the phi values are a better choice of numerical values for the response categories than the default values 1 to q .

`start` argument values: `start` is a vector of start values for estimating the model parameters.

The first part of the `start` vector is starting values for the coefficients of the covariates, the second part is starting values for the μ values (per-category intercepts), and the third part is starting values for the raw parameters used to construct the phi values.

The length of the vector is [number of covariate terms] + [number of categories in response variable - 1] + [number of categories in response variable - 2]. Every one of the values can take any real value.

The second part is the starting values for the μ_k per-category intercept parameters, and since μ_1 is fixed at 0 for identifiability, the number of non-fixed μ_k parameters is one fewer than the number of categories.

The third part of the starting vector is a re-parametrization used to construct starting values for the estimated phi parameters such that the phi parameters observe the ordering restriction of the ordered stereotype model, but the raw parameters are not restricted which makes it easier to optimise over them. phi_1 is always 0 and phi_q is always 1 (where q is the number of response categories). If the raw parameters are u_2 up to $u_{(q-1)}$, then phi_2 is constructed as $\text{expit}(u_2)$, phi_3 is $\text{expit}(u_2 + \text{exp}(u_3))$, phi_4 is $\text{expit}(\text{exp}(u_3) + \text{exp}(u_4))$ etc. which ensures that the phi_k values are non-decreasing.

This code was adapted from file MASS/R/polr.R copyright (C) 1994-2013 W. N. Venables and B. D. Ripley Use of transformed intercepts contributed by David Firth The `osm` and `osm.fit` functions were written by Louise McMillan, 2020.

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Value

An object of class "osm". This has components

- beta the coefficients of the covariates, with NO intercept.
- mu the intercepts for the categories.
- phi the score parameters for the categories (restricted to be ordered).
- deviance the residual deviance.
- fitted.values a matrix of fitted values, with a column for each level of the response.
- lev the names of the response levels.
- terms the terms structure describing the model.
- df.residual the number of residual degrees of freedom, calculated using the weights.
- edf the (effective) number of degrees of freedom used by the model
- n, nobs the (effective) number of observations, calculated using the weights.
- call the matched call.
- convergence the convergence code returned by optim.
- niter the number of function and gradient evaluations used by optim.
- eta
- Hessian (if Hess is true). Note that this is a numerical approximation derived from the optimization proces.
- model (if model is true), the model used in the fitting.
- na.action the NA function used
- xlevels factor levels from any categorical predictors

References

Agresti, A. (2010). *Analysis of ordinal categorical data* (Vol. 656). John Wiley & Sons.

Anderson, J. A. (1984). Regression and ordered categorical variables. *Journal of the Royal Statistical Society: Series B (Methodological)*, 46(1), 1-22.

See Also

[MASS::polr()]

rerun

*Rerun clustord using the results of a previous run as the starting point.***Description**

This function is designed for two purposes. (1) You tried to run `clustord` and the results did not converge. You can supply this function with the previous results and the previous data object, and it will carry on running `clustord` from the endpoint of the previous run, which is quicker than starting the run again from scratch with more iterations.

Usage

```
rerun(
  results.original,
  long.df,
  EM.control = NULL,
  verbose = FALSE,
  optim.control = NULL
)
```

Arguments

<code>results.original</code>	The results of the previous run that you want to use as a starting point. The model, number of clusters, and final parameter values will be used, and the cluster controls such as <code>EMcycles</code> will be reused unless the user specifies new values. But the row cluster and/or column cluster memberships will NOT be reused, and nor will the dataset, so you can change the dataset slightly and the rest of the details will be applied to this new dataset.
<code>long.df</code>	The dataset to use for this run, which may be slightly different to the original. Please note that the only compatibility check performed is comparing the sizes of the original and new datasets, and it is up to the user to check that the new dataset is sufficiently similar to the old one.
<code>EM.control</code>	Options to use for this run such as <code>EMcycles</code> (number of EM iterations). Note that "startEMcycles" will not be relevant as this run will not generate random starts, it will run from the end parameters of the other run. See clustord documentation for more info.
<code>verbose</code>	(default FALSE) changes how much is reported to the console during the algorithm's progress. See clustord documentation for more info.
<code>optim.control</code>	Options to use for this run within <code>optim()</code> , which is used to estimate the parameters during each M-step. See clustord documentation for more info.

Details

(2) The previous result converged, but you have changed the dataset slightly, and want to rerun from the previous endpoint to save time.

Either way, you call the function in the same way, supplying the previous results object and a dataset, and optionally a new number of iterations ('EM.control=list(EMcycles=XXX)', where 'XXX' is the new number of iterations.)

The output parameters of the old result will be used as the new initial parameters.

Value

An object of class `clustord`. See [clustord](#) for more info.

Examples

```
set.seed(1)
long.df <- data.frame(Y=factor(sample(1:3,5*20,replace=TRUE)),
                      ROW=factor(rep(1:20,times=5)),COL=rep(1:5,each=20))
results.original <- clustord(Y ~ ROWCLUST, model="OSM", nclus.row=4,
                           long.df=long.df, EM.control=list(EMcycles=2))
results.original$EM.status$converged
# FALSE

## Since original run did not converge, rerun from that finishing point and
## allow more iterations this time
results.new <- rerun(results.original, long.df, EM.control=list(EMcycles=10))

## Alternatively, if dataset has changed slightly then rerun from the
## previous finishing point to give the new results a helping hand
long.df.new <- long.df[-c(4,25,140),]
results.new <- rerun(results.original, long.df.new)
```

Index

`calc.cluster.comparisons`, [2](#)
`calc.SE.biclust` (`calc.SE.rowcluster`),
 [3](#)
`calc.SE.rowcluster`, [3](#)
`clustord`, [2–4](#), [4](#), [24](#), [25](#)

`mat2df`, [5](#), [8](#), [11](#), [19](#)

`optim`, [3](#)
`osm`, [20](#)

`rerun`, [24](#)