

Package ‘MoEClust’

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Title Gaussian Parsimonious Clustering Models with Covariates

Version 1.2.1

Description

Clustering via parsimonious Gaussian Mixtures of Experts using the MoEClust models introduced by Murphy and Murphy (2017) <arXiv:1711.05632>. This package fits finite Gaussian mixture models with a formula interface for supplying gating and/or expert network covariates using a range of parsimonious covariance parameterisations via the EM/CEM algorithm. Visualisation of the results of such models using generalised pairs plots is also facilitated.

Depends R (>= 3.3.0)

License GPL (>= 2)

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URL <https://cran.r-project.org/package=MoEClust>

BugReports <https://github.com/Keefe-Murphy/MoEClust>

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MoEClust-package	<i>MoEClust: Gaussian Parsimonious Clustering Models with Covariates</i>
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Description

Clustering via parsimonious Gaussian Mixtures of Experts using the *MoEClust* models introduced by Murphy and Murphy (2017) <[arXiv:1711.05632](https://arxiv.org/abs/1711.05632)>. This package fits finite Gaussian mixture models with gating and/or expert network covariates using a range of parsimonious covariance parameterisations via the EM/CEM algorithm. Visualisation of the results of such models using generalised pairs plots is also facilitated.

Usage

The most important function in the **MoEClust** package is: `MoE_clust`, for fitting the model via EM/CEM with gating and/or expert network covariates, supplied via formula interfaces.

Other functions also exist, e.g. `MoE_control`, `MoE_crit`, `MoE_dens`, `MoE_estep`, `MoE_compare`, and `aitken`, which are all used within `MoE_clust` but are nonetheless made available for standalone use.

`MoE_compare` is provided for conducting model selection between different results from `MoE_clust` using different covariate combinations &/or initialisation strategies, etc.

A dedicated plotting function exists for visualising the results using generalised pairs plots, for examining the gating network, and/or log-likelihood, and/or clustering uncertainties, and/or graphing model selection criteria values. The generalised pairs plots (`MoE_gpairs`) visualise all pairwise relationships between clustered response variables and associated continuous, categorical, and/or ordinal covariates in the gating &/or expert networks, coloured according to the MAP classification, and also give the marginal distributions of each variable (incl. the covariates) along the diagonal.

An `as.Mclust` method is provided to coerce the output of class "MoEClust" from `MoE_clust` to the "Mclust" class, to facilitate use of plotting and other functions for the "Mclust" class within the `mclust` package. As per `mclust`, **MoEClust** also facilitates modelling with an additional noise component (with or without the mixing proportion for the noise component depending on covariates).

Finally, a `predict` method is provided for predicting the fitted response and probability of cluster membership (and by extension the MAP classification) for new data, in the form of new covariates and new response data, or new covariates only.

The package also contains two data sets: `ais` and `CO2data`.

Details

- Type: Package
- Package: MoEClust
- Version: 1.2.1
- Date: 2018-12-11 (this version), 2017-11-28 (original release)
- Licence: GPL (>=2)

See Also

Further details and examples are given in the associated vignette document:
`vignette("MoEClust", package = "MoEClust")`

Author(s)

Keefe Murphy [aut, cre], Thomas Brendan Murphy [ctb]

Maintainer: Keefe Murphy - <<keefe.murphy@ucd.ie>>

References

K. Murphy and T. B. Murphy (2017). Parsimonious Model-Based Clustering with Covariates. *To appear*. <[arXiv:1711.05632](https://arxiv.org/abs/1711.05632)>.

See Also

Useful links:

- <https://cran.r-project.org/package=MoEClust>
- Report bugs at <https://github.com/Keefe-Murphy/MoEClust>

Examples

```
## Not run:
data(ais)
res <- MoE_clust(ais[,3:7], G=2, gating=~BMI, expert=~sex,
                modelNames=c("EVE", "VVE", "VEE"), network.data=ais)
plot(res, what="gpairs")

data(CO2data)
GNP <- CO2data[,1]
CO2 <- CO2data[,2]
m1 <- MoE_clust(CO2, G=1:2)
m2 <- MoE_clust(CO2, G=2, gating= ~ GNP)
m3 <- MoE_clust(CO2, G=1:2, expert= ~ GNP)
m4 <- MoE_clust(CO2, G=2, gating= ~ GNP, expert= ~ GNP)
MoE_compare(m1, m2, m3, m4)
## End(Not run)
```

ais

Australian Institute of Sport data

Description

Data on 102 male and 100 female athletes collected at the Australian Institute of Sport, courtesy of Richard Telford and Ross Cunningham.

Usage

```
data(ais)
```

Format

A data frame with 202 observations on the following 13 variables:

- ,1 sex - categorical, levels = female, male
- ,2 sport - categorical, levels = B_Ball, Field, Gym, Netball, Row, Swim, T_400m, Tennis, T_Sprnt, W_Polo
- ,3 RCC - red cell count (numeric)
- ,4 WCC - white cell count (numeric)
- ,5 Hc - Hematocrit (numeric)
- ,6 Hg - Hemoglobin (numeric)

,7 Fe - plasma ferritin concentration (numeric)
 ,8 BMI - body mass index: $Wt/(Ht)^2$ (numeric)
 ,9 SSF - sum of skin folds (numeric)
 ,10 Bfat - body fat percentage (numeric)
 ,11 LBM - lean body mass (numeric)
 ,12 Ht - height, cm (numeric)
 ,13 Wt - weight, kg (numeric)

Details

The data have been made publicly available in connection with the book by Cook and Weisberg (1994).

References

Cook, R. D. and Weisberg, S. (1994), *An Introduction to Regression Graphics*. John Wiley & Sons, New York.

Examples

```
data(ais, package="MoEClust")
pairs(ais[,c(3:4, 10:13)], col=as.numeric(ais[,1]), main = "AIS data")
```

aitken

Aitken Acceleration

Description

Calculates the Aitken acceleration estimate of the final converged maximised log-likelihood under the EM/CEM framework.

Usage

```
aitken(loglik)
```

Arguments

loglik A vector of three consecutive log-likelihood values. These three values should be in ascending order, though this is not checked.

Details

The final converged maximised log-likelihood can be used to determine convergence of the EM/CEM algorithm within `MoE_clust`, i.e. by checking whether the absolute difference between the current log-likelihood estimate and the final converged maximised log-likelihood estimate is less than some tolerance.

Value

A list with the following named components:

ll	The most current estimate for the log-likelihood.
linf	The most current estimate of the final converged maximised log-likelihood.
a	The Aitken acceleration value where typically $0 \leq a \leq 1$. When $a < 0$, a numerical issue or bug has occurred; when $a > 1$, the algorithm is accelerating and should not be stopped.

When the "aitken" method is employed within `MoE_clust` (via `MoE_control`), `ll` at convergence gives the log-likelihood achieved by the estimated parameters, while `linf` at convergence estimates the log-likelihood that would be achieved after an infinite number of EM/CEM iterations.

Note

Within `MoE_clust`, as specified by the stopping argument of `MoE_control`, "aitken" is the default method used to assess convergence. The other option monitors the "relative" change in log-likelihood against some tolerance. See `MoE_control`.

Author(s)

Keefe Murphy - <<keefe.murphy@ucd.ie>>

References

Boehning, D., Dietz, E., Schaub, R., Schlattmann, P. and Lindsay, B. G. (1994). The distribution of the likelihood ratio for mixtures of densities from the one-parameter exponential family. *Annals of the Institute of Statistical Mathematics*, 46(2): 373-388.

See Also

[MoE_control](#)

Examples

```
(a1 <- aitken(-c(449.61534, 442.84221, 436.58999)))
a2 <- aitken(-c(442.84221, 436.58999, 436.58998))
abs(a2$linf - a1$linf) < 1e-05 #FALSE
a3 <- aitken(-c(436.58998, 436.58997, 436.58997))
abs(a3$linf - a2$linf) < 1e-05 #TRUE
(ll <- a3$linf)
(a <- a3$a)
```

`as.Mclust`*Convert MoEClust objects to the Mclust class*

Description

Converts an object of class "MoEClust" generated by `MoE_clust` and converts it to an object of class "Mclust" as generated by fitting `Mclust`, to facilitate use of plotting and other functions for the "Mclust" class within the **mclust** package.

Usage

```
as.Mclust(x,  
          signif = 0L,  
          ...)
```

Arguments

<code>x</code>	An object of class "MoEClust" generated by <code>MoE_clust</code> or an object of class "MoECompare" generated by <code>MoE_compare</code> . Models with a noise component are facilitated here too.
<code>signif</code>	Significance level for outlier removal. Must be a single number in the interval [0, 1). Corresponds to the percentage of data to be considered extreme and therefore removed (half of <code>signif</code> at each endpoint, on a column-wise basis). The default, 0, corresponds to no outlier removal. Only invoke this argument as an aid to visualisation via <code>plot.Mclust</code> .
<code>...</code>	Further arguments to be passed to other methods.

Details

Of course, the user is always encouraged to use the dedicated `plot` function for objects of the "MoEClust" class instead, but calling `plot` after converting via `as.Mclust` can be particularly useful for univariate mixtures.

In the presence of expert network covariates, the component-specific covariance matrices are modified for plotting purposes via the function `expert_covar`, in order to account for the extra variability of the means, usually resulting in bigger shapes & sizes for the MVN ellipses.

The `signif` argument is intended only to aid visualisation via `plot.Mclust`, as plots therein can be sensitive to outliers, particularly with regard to axis limits.

Value

An object of class "Mclust". See `methods(class="Mclust")` for a (non-exhaustive) list of functions which can be applied to this class.

Note

Of the functions which can be applied to the result of the conversion, `logLik.Mclust` shouldn't be trusted in the presence of either expert network covariates, or (for models with more than 1 component) gating network covariates.

Mixing proportions are averaged over observations in components in the presence of gating network covariates during the coercion.

Plots may be misleading in the presence of gating &/or expert covariates when the `what` argument is "density" within `plot.Mclust`; users are encouraged to use `MoE_gpairs` with `response.type="density"` instead.

The functions `clustCombi` and `clustCombiOptim` can be safely used (provided `as.Mclust(x)` is supplied as the object argument to `clustCombi`), as they only rely on `x$z` and `x$G` only. See the examples below.

Author(s)

Keefe Murphy - <<keefe.murphy@ucd.ie>>

References

C. Fraley and A. E. Raftery (2002). Model-based clustering, discriminant analysis, and density estimation. *Journal of the American Statistical Association*, 97:611-631.

See Also

`Mclust`, `plot.Mclust`, `MoE_clust`, `plot.MoEClust`, `expert_covar`

Examples

```
## Not run:
# Fit a gating network mixture of experts model to the ais data
data(ais)
mod <- MoE_clust(ais[,3:7], G=1:9, gating= ~ BMI + sex, network.data=ais)

# Convert to the "Mclust" class and examine the classification
mod2 <- as.Mclust(mod)
plot(mod2, what="classification")

# Examine the uncertainty
plot(mod2, what="uncertainty")

# Return the optimal number of clusters according to entropy
combi <- mclust::clustCombi(object=mod2)
optim <- mclust::clustCombiOptim(combi)
table(mod2$classification, ais$sex)
table(optim$cluster.combi, ais$sex)

# While we could have just used plot.MoEClust above,
# plot.Mclust is especially useful for univariate data
data(CO2data)
res <- MoE_clust(CO2data$CO2, G=2, expert = ~ GNP, network.data=CO2data)
```

```
plot(as.Mclust(res))  
## End(Not run)
```

CO2data

GNP and CO2 Data Set

Description

This data set gives the gross national product (GNP) per capita in 1996 for various countries as well as their estimated carbon dioxide (CO2) emission per capita for the same year.

Usage

```
data(CO2data)
```

Format

This data frame consists of 28 countries and the following variables:

- GNP - The gross product per capita in 1996.
- CO2 - The estimated carbon dioxide emission per capita in 1996.
- country - An abbreviation pertaining to the country measures (e.g. "GRC" = Greece and "CH" = Switzerland).

References

Hurn, M., Justel, A. and Robert, C. P. (2003) Estimating Mixtures of Regressions, *Journal of Computational and Graphical Statistics*, 12(1): 55-79.

drop_constants

Drop constant variables from a formula

Description

Drops constant variables from the RHS of a formula taking the data set (dat), the formula (formula), and an optional subset vector (sub) as arguments.

Usage

```
drop_constants(dat,  
              formula,  
              sub = NULL)
```

Arguments

dat	A data.frame where rows correspond to observations and columns correspond to variables. Ideally column names should be present.
formula	An object of class " formula ": a symbolic description of the model to be fitted. Variables in the formula not present in the columns of dat will automatically be discarded. The formula may include interactions or higher order terms.
sub	An optional vector specifying a subset of observations to be used in the fitting process.

Value

The updated formula with constant variables removed.

Note

Formulas with and without intercepts are accommodated.

Author(s)

Keefe Murphy - <<keefe.murphy@ucd.ie>>

See Also

[drop_levels](#)

Examples

```
data(ais)
hema <- as.matrix(ais[,3:7])
sex <- ais$sex
BMI <- ais$BMI

# Set up a no-intercept regression formula with constant column 'sex'
form1 <- as.formula(hema ~ sex + BMI - 1)
sub <- ais$sex == "male"

# Try fitting a linear model
mod1 <- try(lm(form1, data=ais, subset=sub), silent=TRUE)
inherits(mod1, "try-error") # TRUE

# Remove redundant variables from formula & try again
form2 <- drop_constants(ais, form1, sub)
mod2 <- try(lm(form2, data=ais, subset=sub), silent=TRUE)
inherits(mod2, "try-error") # FALSE
```

drop_levels	<i>Drop unused factor levels to predict from unseen data</i>
-------------	--

Description

Drops unseen factor levels in `newdata` for which predictions are required from a `lm` model fit.

Usage

```
drop_levels(fit,  
            newdata)
```

Arguments

<code>fit</code>	A fitted <code>lm</code> model.
<code>newdata</code>	A <code>data.frame</code> containing variables with which to predict.

Value

A `data.frame` like `newdata` with unseen factor levels replaced by NA.

Note

This function is untested for models other than `lm`.

Author(s)

Keefe Murphy - <<keefe.murphy@ucd.ie>>

See Also

[drop_constants](#)

Examples

```
data(ais)
hema <- as.matrix(ais[,3:7])
BMI <- ais$BMI
sport <- ais$sport
sub <- ais$sport != "Row"

# Fit a linear model
mod <- lm(hema ~ BMI + sport, data=ais, subset=sub)

# Make predictions
pred1 <- try(predict(mod, newdata=ais), silent=TRUE)
inherits(pred1, "try-error") #TRUE

# Remove unused levels and try again
```

```
pred2 <- try(predict(mod, newdata=drop_levels(mod, ais)), silent=TRUE)
inherits(pred2, "try-error") #FALSE
anyNA(pred2)                 #TRUE
```

expert_covar	<i>Account for extra variability in covariance matrices with expert covariates</i>
--------------	--

Description

In the presence of expert network covariates, this helper function modifies the component-specific covariance matrices of a "MoEClust" object, in order to account for the extra variability of the means, usually resulting in bigger shapes & sizes for the MVN ellipses. The function also works for univariate response data.

Usage

```
expert_covar(x)
```

Arguments

x An object of class "MoEClust" generated by [MoE_clust](#), or an object of class "MoECompare" generated by [MoE_compare](#). Models with a noise component are facilitated here too.

Details

This function is used internally by [plot.MoEClust](#) and [as.Mclust](#), for visualisation purposes.

Value

The variance component only from the parameters list from the output of a call to [MoE_clust](#), modified accordingly.

Note

The modelName of the resulting variance object may not correspond to the model name of the "MoEClust" object, in particular scale, shape, &/or orientation may no longer be constrained across clusters. Usually, the modelName of the transformed variance object will be "VVV".

Author(s)

Keefe Murphy - <<keefe.murphy@ucd.ie>>

References

K. Murphy and T. B. Murphy (2017). Parsimonious Model-Based Clustering with Covariates. *To appear*. <[arXiv:1711.05632](#)>.

See Also

[MoE_clust](#), [MoE_gpairs](#), [plot.MoEClust](#), [as.Mclust](#)

Examples

```
data(ais)
res <- MoE_clust(ais[,3:7], G=2, gating= ~ BMI, expert= ~ sex,
               network.data=ais, modelNames="EVE")

# Extract the variance object
res$parameters$variance

# Modify the variance object
expert_covar(res)
```

force_posiDiag	<i>Force diagonal elements of a triangular matrix to be positive</i>
----------------	--

Description

This function ensures that the triangular matrix in a QR (or other) decomposition has positive values along its diagonal.

Usage

```
force_posiDiag(x)
```

Arguments

x A matrix, which must be either upper-triangular or lower-triangular.

Value

An upper or lower triangular matrix with positive diagonal entries such that the matrix is still a valid decomposition of the matrix the input x is a decomposition of.

Author(s)

Keefe Murphy - <<keefe.murphy@ucd.ie>>

Examples

```
data(ais)
res <- MoE_clust(ais[,3:7], G=3, modelNames="EEE")
sig <- res$parameters$variance
a <- force_posiDiag(sig$cholSigma)
b <- chol(sig$Sigma)
round(sum(a - b), 10) == 0            #TRUE
sum(crossprod(a) != sig$Sigma) == 0 #TRUE
sum(crossprod(b) != sig$Sigma) == 0 #TRUE
```

MoE_clust

*MoEClust: Gaussian Parsimonious Clustering Models with Covariates***Description**

Fits MoEClust models: Gaussian Mixture of Experts models with GPCM/**mclust**-family covariance structures. In other words, performs model-based clustering via the EM/CEM algorithm where covariates are allowed to enter neither, either, or both the mixing proportions (gating network) and/or component densities (expert network) of a Gaussian Parsimonious Clustering Model.

Usage

```
MoE_clust(data,
           G = 1:9,
           modelNames = NULL,
           gating = NULL,
           expert = NULL,
           network.data = NULL,
           control = MoE_control(...),
           ...)
```

```
## S3 method for class 'MoEClust'
print(x,
      digits = 3L,
      ...)
```

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

Arguments

<code>data</code>	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
<code>G</code>	An integer vector specifying the numbers of mixture components (clusters) to fit. Defaults to $G=1:9$. Must be a strictly positive integer, unless a noise component is included in the estimation, in which case $G=0$ is allowed and included by default. (see MoE_control).
<code>modelNames</code>	A vector of character strings indicating the models to be fitted in the EM/CEM phase of clustering. With n observations and d variables, the defaults are:
for univariate data	<code>c("E", "V")</code>
for multivariate data $n > d$	<code>mclust.options("emModelNames")</code>
for high-dimensional multivariate data $n \leq d$	<code>c("EII", "VII", "EEI", "EVI", "VEI", "VVI")</code>

For single-component models these options reduce to:

for univariate data	"E"
for multivariate data $n > d$	c("EII", "EEI", "EEE")
for high-dimensional multivariate data $n \leq d$	c("EII", "EEI")

For zero-component models with a noise component only the "E" and "EII" models will be fit for univariate and multivariate data, respectively. The help file for [mclustModelNames](#) further describes the available models (though the "X" in the single-component models will be coerced to "E" if supplied that way). For single-component models, other model names equivalent to those above can be supplied, but will be coerced to those above.

gating	A formula for determining the model matrix for the multinomial logistic regression in the gating network when fixed covariates enter the mixing proportions. This will be ignored where $G=1$. Continuous, categorical, and/or ordinal covariates are allowed. Logical covariates will be coerced to factors. Interactions and higher order terms are permitted. The specification of the LHS of the formula is ignored. Intercept terms are included by default.
expert	A formula for determining the model matrix for the (multivariate) WLS in the expert network when fixed covariates are included in the component densities. Continuous, categorical, and/or ordinal covariates are allowed. Logical covariates will be coerced to factors. Interactions & higher order terms are permitted. The specification of the LHS of the formula is ignored. Intercept terms are included by default.
network.data	An optional data frame in which to look for the covariates in the gating &/or expert network formulas, if any. If not found in network.data, any supplied gating &/or expert covariates are taken from the environment from which MoE_clust is called. Try to ensure the names of variables in network.data do not match any of those in data.
control	A list of control parameters for the EM/CEM and other aspects of the algorithm. The defaults are set by a call to MoE_control .
...	An alternative means of passing control parameters directly via the named arguments of MoE_control . Do not pass the output from a call to MoE_control here! This argument is only relevant for the MoE_clust function and will be ignored for the associated print and summary functions.
x, object, digits	Arguments required for the print and summary functions: x and object are objects of class "MoEClust" resulting from a call to MoE_clust , while digits gives the number of decimal places to round to for printing purposes (defaults to 3).

Details

The function effectively allows 4 different types of Gaussian Mixture of Experts model (as well as the different models in the GPCM/[mclust](#) family, for each): i) the standard finite Gaussian mixture with no covariates, ii) fixed covariates only in the gating network, iii) fixed covariates only in the expert network, iv) the full Mixture of Experts model with fixed covariates entering both the mixing

proportions and component densities. Note that having the same covariates in both networks is allowed. So too are interactions and higher order terms (see [formula](#)). Covariates can be continuous, categorical, logical, or ordinal, but the response must always be continuous.

While model selection in terms of choosing the optimal number of components and the GPCM/**mclust** model type is performed within [MoE_clust](#), using one of the [criterion](#) options within [MoE_control](#), choosing between multiple fits with different combinations of covariates or different initialisation settings can be done by supplying objects of class "MoEClust" to [MoE_compare](#).

Value

A list (of class "MoEClust") with the following named entries, mostly corresponding to the chosen optimal model (as determined by the [criterion](#) within [MoE_control](#)):

call	The matched call.
data	The input data, as a <code>data.frame</code> .
modelName	A character string denoting the GPCM/ mclust model type at which the optimal criterion occurs.
n	The number of observations in the data.
d	The dimension of the data.
G	The optimal number of mixture components.
BIC	A matrix of <i>all</i> BIC values with <code>length{G}</code> rows and <code>length(modelNames)</code> columns. May include missing entries: NA represents models which were not visited, <code>-Inf</code> represents models which were terminated due to error, for which a log-likelihood could not be estimated. Inherits the classes "MoECriterion" and "mclustBIC", for which dedicated printing and plotting functions exist, respectively.
ICL	A matrix of <i>all</i> ICL values with <code>length{G}</code> rows and <code>length(modelNames)</code> columns. May include missing entries: NA represents models which were not visited, <code>-Inf</code> represents models which were terminated due to error, for which a log-likelihood could not be estimated. Inherits the classes "MoECriterion" and "mclustICL", for which dedicated printing and plotting functions exist, respectively.
AIC	A matrix of <i>all</i> AIC values with <code>length{G}</code> rows and <code>length(modelNames)</code> columns. May include missing entries: NA represents models which were not visited, <code>-Inf</code> represents models which were terminated due to error, for which a log-likelihood could not be estimated. Inherits the classes "MoECriterion" and "mclustAIC", for which dedicated printing and plotting functions exist, respectively.
bic	The BIC value corresponding to the optimal model. May not necessarily be the optimal BIC.
icl	The ICL value corresponding to the optimal model. May not necessarily be the optimal ICL.
aic	The AIC value corresponding to the optimal model. May not necessarily be the optimal AIC.

gating	An object of class "MoE_gating" and either "multinom" or "glm" (for single-component models) giving the <code>multinom</code> regression coefficients of the gating network. If gating covariates were <i>NOT</i> supplied (or the best model has just one component), this corresponds to a RHS of ~1, otherwise the supplied gating formula. As such, a fitted gating network is always returned even in the absence of supplied covariates. The number of parameters to penalise by for <code>MoE_crit</code> is given by <code>length(coef(gating))</code> , and the gating formula used is stored here as an attribute. If there is a noise component, its coefficients are those for the <i>last</i> component. Users are cautioned against making inferences about statistical significance from summaries of the coefficients in the gating network.
expert	An object of class "MoE_expert" and "lm" giving the (multivariate) WLS regression coefficients of the expert network. If expert covariates were NOT supplied, this corresponds to a RHS of ~1, otherwise the supplied expert formula. As such, a fitted expert network is always returned even in the absence of supplied covariates. The number of parameters to penalise by for <code>MoE_crit</code> is given by <code>G * length(coef(expert[[1]]))</code> , and the expert formula used is stored here as an attribute. Users are cautioned against making inferences about statistical significance from summaries of the coefficients in the expert network.
LOGLIK	A matrix of <i>all</i> maximal log-likelihood values with <code>length{G}</code> rows and <code>length(modelNames)</code> columns. May include missing entries: NA represents models which were not visited, <code>-Inf</code> represents models which were terminated due to error, for which a log-likelihood could not be estimated. Inherits the classes "MoECriterion" and "mclustLoglik", for which dedicated printing and plotting functions exist, respectively.
loglik	The vector of increasing log-likelihood values for every EM/CEM iteration under the optimal model. The last element of this vector is the maximum log-likelihood achieved by the parameters returned at convergence.
linf	An asymptotic estimate of the final converged maximised log-likelihood. Returned when <code>stopping="aitken"</code> and <code>G > 1</code> (see <code>MoE_control</code> and <code>aitken</code>), otherwise the last element of <code>loglik</code> is returned instead.
df	The number of estimated parameters in the optimal model (i.e. the number of 'used' degrees of freedom). Subtract this number from <code>n</code> to get the degrees of freedom. The number of parameters due to the gating network, expert network, and covariance matrices are also stored here as attributes of <code>df</code> .
iters	The total number of EM/CEM iterations for the optimal model.
hypvol	The hypervolume parameter for the noise component if required, otherwise set to NA (see <code>MoE_control</code>).
parameters	A list with the following named components: <ul style="list-style-type: none"> <code>pro</code> The mixing proportions: either a vector of length <code>G</code> or, if gating covariates were supplied, a matrix with an entry for each observation (rows) and component (columns). <code>mean</code> The means of each component. If there is more than one component, this is a matrix whose <i>k</i>-th column is the mean of the <i>k</i>-th component of the mixture model.

For models with expert network covariates, this is given by the posterior mean of the fitted values, otherwise the posterior mean of the response is reported. For models with expert network covariates, the *observation-specific* means can be accessed by calling `predict` on each object in the list given by `expert`.

<code>variance</code>	A list of variance parameters of each component of the model. The components of this list depend on the model type specification. See the help file for <code>mclustVariance</code> for details. Also see <code>expert_covar</code> for an alternative approach to summarising the variance parameters in the presence of expert network covariates.
<code>Vinv</code>	The inverse of the hypervolume parameter for the noise component if required, otherwise set to <code>NULL</code> (see <code>MoE_control</code>).
<code>z</code>	The final responsibility matrix whose $[i, k]$ -th entry is the probability that observation i belongs to the k -th component. If there is a noise component, its values are found in the <i>last</i> column.
<code>classification</code>	The vector of cluster labels for the chosen model corresponding to <code>z</code> , i.e. <code>max.col(z)</code> . Observations belonging to the noise component will belong to component \emptyset .
<code>uncertainty</code>	The uncertainty associated with the <code>classification</code> .
<code>net.covs</code>	A data frame gathering the unique set of covariates used in the gating and expert networks, if any. Will contain zero columns in the absence of gating or expert network covariates. Supplied gating covariates will be excluded if the optimal model has only one component. May have fewer columns than covariates supplied via the <code>network.data</code> argument also, as only the included covariates are gathered here.
<code>resid.data</code>	In the presence of expert network covariates, this is the augmented data actually used in the clustering at convergence, as a list of G matrices of WLS residuals of dimension $n * d$. Will contain zero columns in the absence of expert network covariates.
<code>DF</code>	A matrix giving the numbers of estimated parameters (i.e. the number of 'used' degrees of freedom) for <i>all</i> visited models, with <code>length{G}</code> rows and <code>length(modelNames)</code> columns. Subtract these numbers from n to get the degrees of freedom. May include missing entries: <code>NA</code> represents models which were not visited, <code>-Inf</code> represents models which were terminated due to error, for which parameters could not be estimated. Inherits the classes "MoECriterion" and "mclustDF", for which dedicated printing and plotting functions exist, respectively.
<code>ITERS</code>	A matrix giving the total number of EM/CEM iterations for <i>all</i> visited models, with <code>length{G}</code> rows and <code>length(modelNames)</code> columns. May include missing entries: <code>NA</code> represents models which were not visited, <code>Inf</code> represents models which were terminated due to singularity/error and thus would never have converged. Inherits the classes "MoECriterion" and "mclustITERS", for which dedicated printing and plotting functions exist, respectively.

Dedicated `plot`, `predict`, `print` and `summary` functions exist for objects of class "MoEClust". The results can be coerced to the "Mclust" class to access other functions from the `mclust` package via `as.Mclust`.

Note

Where BIC, ICL, AIC, LOGLIK, DF and ITTERS contain NA entries, this corresponds to a model which was not run; for instance a VVV model is never run for single-component models as it is equivalent to EEE. As such, one can consider the value as not really missing, but equivalent to the EEE value. BIC, ICL, AIC, LOGLIK, DF and ITTERS all inherit the classes "MoECriterion" and "mclustBIC", "mclustICL", etc., for which dedicated printing and plotting functions exist, respectively.

Author(s)

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References

K. Murphy and T. B. Murphy (2017). Parsimonious Model-Based Clustering with Covariates. *To appear*. <[arXiv:1711.05632](https://arxiv.org/abs/1711.05632)>.

C. Fraley and A. E. Raftery (2002). Model-based clustering, discriminant analysis, and density estimation. *Journal of the American Statistical Association*, 97:611-631.

See Also

[MoE_compare](#), [plot.MoEClust](#), [predict.MoEClust](#), [MoE_control](#), [as.Mclust](#), [MoE_crit](#), [MoE_estep](#), [MoE_cstep](#), [MoE_dens](#), [mclustModelNames](#), [mclustVariance](#), [expert_covar](#) [aitken](#)

Examples

```
## Not run:
data(ais)
hema <- ais[,3:7]
sex <- ais$sex
BMI <- ais$BMI

# Fit a standard finite mixture model
m1 <- MoE_clust(hema, G=2:3)

# Allow covariates to enter the mixing proportions
m2 <- MoE_clust(hema, G=2:3, gating= ~ sex + BMI)

# Allow covariates to enter the component densities
m3 <- MoE_clust(hema, G=2:3, expert= ~ sex)

# Allow covariates to enter both the gating & expert network
m4 <- MoE_clust(hema, G=2:3, gating= ~ BMI, expert= ~ sex)

# Extract the model with highest ICL
(comp <- MoE_compare(m1, m2, m3, m4, criterion="icl"))
(best <- comp$optimal)
(summ <- summary(best))

# Examine the gating and expert networks in greater detail
# (but refrain from inferring statistical significance!)
```

```

summary(best$gating)
summary(best$expert)

# Visualise the results, incl. the gating network and log-likelihood
plot(best, what="gpairs")
plot(best, what="gating")
plot(best, what="loglik")

# Visualise the results using the 'lattice' library
require("lattice")
z <- factor(best$classification, labels=paste0("Cluster", seq_len(best$G)))
splom(~ hema | sex, groups=z)
splom(~ hema | z, groups=sex)
## End(Not run)

```

MoE_compare

Choose the best MoEClust model

Description

Takes one or more sets of MoEClust models fitted by [MoE_clust](#) and ranks them according to the BIC, ICL, or AIC. It's possible to respect the internal ranking within each set of models, or to discard models within each set which were already deemed sub-optimal.

Usage

```

MoE_compare(...,
             criterion = c("bic", "icl", "aic"),
             pick = 3L,
             optimal.only = FALSE)

## S3 method for class 'MoECompare'
print(x,
      index = seq_len(x$pick),
      noise = TRUE,
      digits = 3L,
      ...)

```

Arguments

...	One or more objects of class "MoEClust" outputted by MoE_clust . All models must have been fit to the same data set. A single <i>named</i> list of such objects can also be supplied. This argument is only relevant for the MoE_compare function and will be ignored for the associated print function.
criterion	The criterion used to determine the ranking. Defaults to "bic".
pick	The (integer) number of models to be ranked and compared. Defaults to 3L. Will be constrained by the number of models within the "MoEClust" objects supplied via ... if optimal.only is FALSE, otherwise constrained simply by

- the number of "MoEClust" objects supplied. Setting `pick=Inf` is a valid way to select all models.
- `optimal.only` Logical indicating whether to only rank models already deemed optimal within each "MoEClust" object (TRUE), or to allow models which were deemed suboptimal enter the final ranking (FALSE, the default). See details
- `x`, `index`, `noise`, `digits`
- Arguments required for the associated print function:
- `x` An object of class "MoECompare" resulting from a call to [MoE_compare](#).
 - `index` A logical or numeric vector giving the indices of the rows of the table of ranked models to print. This defaults to the full set of ranked models. It can be useful when the table of ranked models is large to examine a subset via this `index` argument, for display purposes.
 - `noise` A logical which determines whether presence of a noise-component should be indicated by the method employed to estimate the hypervolume (defaults to TRUE) or, if FALSE, simply by TRUE. In the absence of a noise component, FALSE will be printed regardless. Only relevant if at least one of the models being compared has a noise component.
If any of the compared models do have a noise component, this switch also controls whether the influence (or not) of gating covariates on the noise component's mixing proportion is indicated (either by TRUE or FALSE for models with a noise component, or else a blank entry for those without), for the models among those being compared which have gating covariates.
 - `digits` The number of decimal places to round model selection criteria to (defaults to 3).

Details

The purpose of this function is to conduct model selection on "MoEClust" objects, fit to the same data set, with different combinations of gating/expert network covariates or different initialisation settings.

Model selection will have already been performed in terms of choosing the optimal number of components and GPCM/**mclust** model type within each supplied set of results, but [MoE_compare](#) will respect the internal ranking of models when producing the final ranking if `optimal.only` is FALSE: otherwise only those models already deemed optimal within each "MoEClust" object will be ranked.

As such if two sets of results are supplied when `optimal.only` is FALSE, the 1st, 2nd and 3rd best models could all belong to the first set of results, meaning a model deemed suboptimal according to one set of covariates could be superior to one deemed optimal under another set of covariates.

Value

A list of class "MoECompare", for which a dedicated print function exists, containing the following elements (each of length `pick`, and ranked according to `criterion`, where appropriate):

- `optimal` The single optimal model (an object of class "MoEClust") among those supplied, according to the chosen `criterion`.
- `pick` The final number of ranked models. May be different (i.e. less than) the supplied `pick` value.

MoENames	The names of the supplied "MoEClust" objects.
modelNameNames	The mclustModelNames .
G	The optimal numbers of components.
df	The numbers of estimated parameters.
iters	The numbers of EM/CEM iterations.
bic	BIC values, ranked according to criterion.
icl	TCL values, ranked according to criterion.
aic	AIC values, ranked according to criterion.
loglik	Maximal log-likelihood values, ranked according to criterion.
gating	The gating formulas.
expert	The expert formulas.
equalPro	Logical indicating whether mixing proportions were constrained to be equal across components.
hypvol	Hypervolume parameters for the noise component if required, otherwise set to NA (see MoE_control).
noise	Either a logical indicating the presence/absence of a noise component, or the type of noise component fitted (if any). Depends on the supplied value of noise. Only displayed if at least one of the compared models has a noise component.
noise.gate	Logical indicating whether gating covariates were allowed to influence the noise component's mixing proportion. Only printed for models with a noise component, when at least one of the compared models has gating covariates, and even then only when noise is supplied as TRUE.

Note

The criterion argument here need not comply with the criterion used for model selection within each "MoEClust" object, but be aware that a mismatch in terms of criterion *may* require the optimal model to be re-fit in order to be extracted, thereby slowing down [MoE_compare](#).

A dedicated print function exists for objects of class "MoECompare".

[plot.MoEClust](#) and [as.Mclust](#) can both also be called on objects of class "MoECompare".

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References

K. Murphy and T. B. Murphy (2017). Parsimonious Model-Based Clustering with Covariates. *To appear*. <[arXiv:1711.05632](#)>.

See Also

[MoE_clust](#), [mclustModelNames](#), [plot.MoEClust](#), [as.Mclust](#)

Examples

```

data(CO2data)
GNP  <- CO2data[,1]
CO2  <- CO2data[,2]
m1   <- MoE_clust(CO2, G=1:2)
m2   <- MoE_clust(CO2, G=1:2, gating= ~ GNP)
m3   <- MoE_clust(CO2, G=1:2, expert= ~ GNP)
m4   <- MoE_clust(CO2, G=1:2, gating= ~ GNP, expert= ~ GNP)
m5   <- MoE_clust(CO2, G=1:2, equalPro=TRUE)
m6   <- MoE_clust(CO2, G=1:2, expert= ~ GNP, equalPro=TRUE)

# Rank only the optimal models and examine the best model
(comp <- MoE_compare(m1, m2, m3, m4, m5, m6, pick=6, optimal.only=TRUE))
(best <- comp$optimal)
(summ <- summary(best))

# Examine all models visited, including those already deemed suboptimal
# Only print models with expert covariates & more than one component
comp2 <- MoE_compare(m1, m2, m3, m4, m5, m6, pick=18)
print(comp2, comp2$expert != "None" & comp2$G > 1)

```

MoE_control

Set control values for use with MoEClust

Description

Supplies a list of arguments (with defaults) for use with `MoE_clust`.

Usage

```

MoE_control(algo = c("EM", "CEM", "cemEM"),
            criterion = c("bic", "icl", "aic"),
            stopping = c("aitken", "relative"),
            init.z = c("hc", "quantile", "kmeans", "mclust", "random"),
            nstarts = 1L,
            exp.init = list(...),
            eps = .Machine$double.eps,
            tol = c(1e-05, sqrt(.Machine$double.eps), 1e-08),
            itmax = c(.Machine$integer.max, .Machine$integer.max, 100L),
            equalPro = FALSE,
            noise.args = list(...),
            hc.args = list(...),
            km.args = list(...),
            init.crit = c("bic", "icl"),
            warn.it = 0L,
            verbose = interactive(),
            ...)

```

Arguments

algo	Switch controlling whether models are fit using the "EM" (the default) or "CEM" algorithm. The option "cemEM" allows running the EM algorithm starting from convergence of the CEM algorithm.
criterion	When either G or modelNames is a vector, criterion determines whether the "bic" (Bayesian Information Criterion), "icl" (Integrated Complete Likelihood), "aic" (Akaike Information Criterion) is used to determine the 'best' model when gathering output. Note that all criteria will be returned in any case.
stopping	The criterion used to assess convergence of the EM/CEM algorithm. The default ("aitken") uses Aitken's acceleration method via aitken , otherwise the "relative" change in log-likelihood is monitored (which may be less strict). Both stopping rules are ultimately governed by <code>tol[1]</code> . When the "aitken" method is employed, the asymptotic estimate of the final converged maximised log-likelihood is also returned as <code>linf</code> for models with 2 or more components, though the largest element of the returned vector <code>loglik</code> still gives the log-likelihood value achieved by the parameters returned at convergence, under both stopping methods (see MoE_clust).
init.z	<p>The method used to initialise the cluster labels. Defaults to a model-based agglomerative hierarchical clustering tree as per "hc" for multivariate data (see <code>hc.args</code>), or "quantile"-based clustering as per quant_clust for univariate data (unless there are expert network covariates incorporated via <code>exp.init\$joint</code> &/or <code>exp.init\$clustMD</code>, in which case the default is again "hc"). The "quantile" option is thus only available for univariate data when expert network covariates are not incorporated via <code>exp.init\$joint</code> &/or <code>exp.init\$clustMD</code>, or when expert network covariates are not supplied.</p> <p>Other options include "kmeans" (see <code>km.args</code>), "random" initialisation, and a full run of Mclust (itself initialised via a model-based agglomerative hierarchical clustering tree, again see <code>hc.args</code>), although this last option "mclust" will be coerced to "hc" if there are no gating &/or expert covariates within MoE_clust (in order to better reproduce Mclust output).</p> <p>When <code>isTRUE(exp.init\$clustMD)</code> and the <code>clustMD</code> library is loaded, the <code>init.z</code> argument instead governs the method by which a call to <code>clustMD</code> is initialised. In this instance, "quantile" will instead default to "hc", and the arguments to <code>hc.args</code> and <code>km.args</code> will be ignored (unless all <code>clustMD</code> model types fail for a given number of components).</p> <p>When <code>init.z="mclust"</code> or <code>clustMD</code> is successfully invoked (via <code>exp.init\$clustMD</code>), the argument <code>init.crit</code> (see below) specifies the model-selection criterion ("bic" or "icl") by which the optimal Mclust or <code>clustMD</code> model type to initialise with is determined, and <code>criterion</code> remains unaffected.</p>
nstarts	The number of random initialisations to use when <code>init.z="random"</code> . Defaults to 1. Results will be based on the random start yielding the highest estimated log-likelihood. Note that all <code>nstarts</code> random initialisations are affected by <code>exp.init\$mahalanobis</code> , if invoked in the presence of expert network covariates, which may remove some of the randomness.
exp.init	A list supplying select named parameters to control the initialisation routine in the presence of <i>expert</i> network covariates (otherwise ignored):

`joint` A logical indicating whether the initial partition is obtained on the joint distribution of the response and expert network covariates (defaults to TRUE) or just the response variables (FALSE). By default, only continuous expert network covariates are considered (see `exp.init$clustMD` below). Only relevant when `init.z` is not "random" (unless `isTRUE(exp.init$clustMD)`, in which case `init.z` specifies the initialisation routine for a call to `clustMD`). This will render the "quantile" option to `init.z` for univariate data unusable if continuous expert network covariates are supplied &/or categorical/ordinal expert network covariates are supplied when `isTRUE(exp.init$clustMD)` and the `clustMD` library is loaded.

`clustMD` A logical indicating whether categorical/ordinal covariates should be incorporated when using the joint distribution of the response and expert network covariates for initialisation (defaults to FALSE). Only relevant when `isTRUE(exp.init$joint)`. Requires the use of the `clustMD` library. Note that initialising in this manner involves fitting all `clustMD` model types in parallel for all numbers of components considered, and may fail (especially) in the presence of nominal expert network covariates.

Supplying this argument as TRUE when the `clustMD` library is loaded has the effect of superseding the `init.z` argument: this argument now governs instead how the call to `clustMD` is initialised (unless all `clustMD` model types fail for a given number of components, in which case `init.z` is invoked *instead* to initialise for G values for which all `clustMD` model types failed). Similarly, the arguments `hc.args` and `km.args` will be ignored (again, unless all `clustMD` model types fail for a given number of components).

`mahalanobis` A logical indicating whether to iteratively reallocate observations during the initialisation phase to the component corresponding to the expert network regression to which it's closest to the fitted values of in terms of Mahalanobis distance (defaults to TRUE). This will ensure that each component can be well modelled by a single expert prior to running the EM/CEM algorithm.

`max.init` The maximum number of iterations for the Mahalanobis distance-based reallocation procedure when `exp.init$mahalanobis` is TRUE. Defaults to 100.

`drop.break` When `isTRUE(exp.init$mahalanobis)` observations will be completely in or out of a component during the initialisation phase. As such, it may occur that constant columns will be present when building a given component's expert regression (particularly for categorical covariates). It may also occur, due to this partitioning, that "unseen" data, when calculating the residuals, will have new factor levels. When `isTRUE(exp.init$drop.break)`, the Mahalanobis distance based initialisation phase will explicitly fail in either of these scenarios.

Otherwise, `drop_constants` and `drop_levels` will be invoked when `exp.init$drop.break` is FALSE (the default) to *try* to remedy the situation. In any case, only a warning that the initialisation step failed will be printed, regardless of the value of `exp.init$drop.break`.

`eps`

A scalar tolerance associated with deciding when to terminate computations due to computational singularity in covariances. Smaller values of `eps` allow computations to proceed nearer to singularity. The default is the relative machine preci-

	<p>sion <code>.Machine\$double.eps</code>, which is approximately $2e-16$ on IEEE-compliant machines.</p>
<code>tol</code>	<p>A vector of length three giving relative convergence tolerances for 1) the log-likelihood of the EM/CEM algorithm, 2) parameter convergence in the inner loop for models with iterative M-step ("<code>VEI</code>", "<code>EVE</code>", "<code>VEE</code>", "<code>VVE</code>", "<code>VEV</code>"), and 3) optimisation in the multinomial logistic regression in the gating network, respectively. The default is <code>c(1e-05, sqrt(.Machine\$double.eps), 1e-08)</code>. If only one number is supplied, it is used as the tolerance for all three cases given.</p>
<code>itmax</code>	<p>A vector of length three giving integer limits on the number of iterations for 1) the EM/CEM algorithm, 2) the inner loop for models with iterative M-step ("<code>VEI</code>", "<code>EVE</code>", "<code>VEE</code>", "<code>VVE</code>", "<code>VEV</code>"), and 3) the multinomial logistic regression in the gating network, respectively.</p> <p>The default is <code>c(.Machine\$integer.max, .Machine\$integer.max, 100)</code> allowing termination to be completely governed by <code>tol</code> for the inner and outer loops of the EM. If only one number is supplied, it is used as the iteration limit for the outer loop only.</p>
<code>equalPro</code>	<p>Logical variable indicating whether or not the mixing proportions are to be constrained to be equal in the model. Default: <code>equalPro = FALSE</code>. Only relevant when gating covariates are <i>not</i> supplied within <code>MoE_clust</code>, otherwise ignored. In the presence of a noise component (see <code>noise.args</code>), only the mixing proportions for the non-noise components are constrained to be equal, after accounting for the noise component.</p>
<code>noise.args</code>	<p>A list supplying select named parameters to control inclusion of a noise component in the estimation of the mixture:</p> <p><code>noise.init</code> A logical or numeric vector indicating an initial guess as to which observations are noise in the data. If numeric, the entries should correspond to row indices of the data. If supplied, a noise term will be added to the model in the estimation. This argument can be used in conjunction with <code>tau0</code> below, or can be replaced by that argument also.</p> <p><code>tau0</code> Prior mixing proportion for the noise component. This provides an alternative to <code>noise.init</code> as a means to invoke a noise component, by instead specifying the prior probability of belonging to the noise component for <i>all</i> observations. If supplied, must be a scalar in the interval (0, 1). Additionally, both <code>noise.init</code> and <code>tau0</code> can be supplied together, in which case observations corresponding to <code>noise.init</code> have probability <code>tau0</code> (rather than 1) of belonging to the noise component.</p> <p><code>noise.gate</code> A logical indicating whether gating network covariates influence the mixing proportion for the noise component, if any. Defaults to <code>TRUE</code>, but leads to greater parsimony if <code>FALSE</code>. Only relevant in the presence of a noise component; only effects estimation in the presence of gating covariates.</p> <p><code>noise.meth</code> The method used to estimate the volume when a noise component is invoked. Defaults to <code>hypvol</code>. For univariate data, this argument is ignored and the range of the data is used instead. The options "<code>convexhull</code>" and "<code>ellipsoidhull</code>" require loading the <code>geometry</code> and <code>cluster</code> libraries, respectively.</p>

hc.args	<p>A list supplying select named parameters to control the initialisation of the cluster allocations when <code>init.z="hc"</code> (or when <code>init.z="mclust"</code>, which itself relies on <code>hc</code>), unless <code>isTRUE(exp.init\$clustMD)</code>, the <code>clustMD</code> library is loaded, and none of the <code>clustMD</code> model types fail (otherwise irrelevant):</p> <p><code>hcUse</code> A string specifying the type of input variables to be used. Unlike <code>Mclust</code>, this defaults to "VARS" here.</p> <p><code>hc.meth</code> A character string indicating the model to be used when hierarchical clustering (see <code>hc</code>) is employed for initialisation (either when <code>init.z="hc"</code> or <code>init.z="mclust"</code>). Defaults to "EII" for high-dimensional data, or "VVV" otherwise.</p>
km.args	<p>A list supplying select named parameters to control the initialisation of the cluster allocations when <code>init.z="kmeans"</code>, unless <code>isTRUE(exp.init\$clustMD)</code>, the <code>clustMD</code> library is loaded, and none of the <code>clustMD</code> model types fail (otherwise irrelevant):</p> <p><code>kstarts</code> The number of random initialisations to use. Defaults to 10.</p> <p><code>kriters</code> The maximum number of K-Means iterations allowed. Defaults to 10.</p>
init.crit	The criterion to be used to determine the optimal model type to initialise with, when <code>init.z="mclust"</code> or when <code>isTRUE(exp.init\$clustMD)</code> and the <code>clustMD</code> library is loaded (one of "bic" or "icl"). Defaults to "icl" when <code>criterion="icl"</code> , otherwise defaults to "bic". The <code>criterion</code> argument remains unaffected.
warn.it	A single number giving the iteration count at which a warning will be printed if the EM/CEM algorithm has failed to converge. Defaults to 0, i.e. no warning (which is true for any <code>warn.it</code> value less than 3), otherwise the message is printed regardless of the value of <code>verbose</code> . If non-zero, <code>warn.it</code> should be moderately large, but obviously less than <code>itmax[1]</code> . A warning will always be printed if one of more models fail to converge in <code>itmax[1]</code> iterations.
verbose	Logical indicating whether to print messages pertaining to progress to the screen during fitting. By default is TRUE if the session is interactive, and FALSE otherwise. If FALSE, warnings and error messages will still be printed to the screen, but everything else will be suppressed.
...	Catches unused arguments.

Details

`MoE_control` is provided for assigning values and defaults within `MoE_clust`.

While the `criterion` argument controls the choice of the optimal number of components and GPCM/`mclust` model type, `MoE_compare` is provided for choosing between fits with different combinations of covariates or different initialisation settings.

Value

A named list in which the names are the names of the arguments and the values are the values supplied to the arguments.

Note

Note that successfully invoking `exp.init$clustMD` (though it defaults to `FALSE`) effects the role of the arguments `init.z`, `hc.args`, and `km.args`. Please read the documentation above carefully in this instance.

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See Also

[MoE_clust](#), [aitken](#), [hc](#), [mclust.options](#), [quant_clust](#), [clustMD](#), [hypvol](#), [convhulln](#), [ellipsoidhull](#), [MoE_compare](#)

Examples

```
## Not run:
ctrl1 <- MoE_control(criterion="icl", itmax=100, warn.it=15, init.z="random")

data(CO2data)
GNP <- CO2data$GNP
res <- MoE_clust(CO2data$CO2, G=2, expert = ~ GNP, control=ctrl1)

# Alternatively, specify control arguments directly
res2 <- MoE_clust(CO2data$CO2, G=2, expert = ~ GNP, stopping="relative")

# Supplying ctrl1 without naming it as control throws an error,
# when any of {modelName, gating, expert} are not supplied
res3 <- MoE_clust(CO2data$CO2, G=2, expert = ~ GNP, ctrl1)

# Initialise via the mixed-type joint distribution of response & covariates
# Let the ICL criterion determine the optimal clustMD model type
ctrl2 <- MoE_control(exp.init=list(clustMD=TRUE, mahalanobis=FALSE), init.crit="icl")
data(ais)
library(clustMD)
res4 <- MoE_clust(ais[,3:7], G=2, modelName="EVE", expert=~sex,
                 network.data=ais, control=ctrl2)

# Include a noise component by specifying its prior mixing proportion
res5 <- MoE_clust(ais[,3:7], G=2, modelName="EVE", tau0=0.1)
## End(Not run)
```

Description

Computes the BIC (Bayesian Information Criterion), ICL (Integrated Complete Likelihood), and AIC (Akaike Information Criterion) for parsimonious mixture of experts models given the log-likelihood, the dimension of the data, the number of mixture components in the model, the numbers of parameters in the gating and expert networks respectively, and, for the ICL, the numbers of observations in each component.

Usage

```
MoE_crit(modelName,
         loglik,
         n,
         d,
         G,
         gating.pen = G - 1L,
         expert.pen = G * d,
         z = NULL,
         df = NULL)
```

Arguments

modelName	A character string indicating the model. The help file for <code>mclustModelNames</code> describes the available models.
loglik	The log-likelihood for a data set with respect to the Gaussian mixture model specified in the <code>modelName</code> argument.
n, d, G	The number of observations in the data, dimension of the data, and number of components in the Gaussian mixture model, respectively, used to compute <code>loglik</code> . <code>d</code> & <code>G</code> are not necessary if <code>df</code> is supplied.
gating.pen	The number of parameters of the <i>gating</i> network of the MoEClust model. Defaults to <code>G - 1</code> , which corresponds to no gating covariates. If covariates are included, this should be the number of regression coefficients in the fitted <i>gating</i> object. If there are no covariates and mixing proportions are further assumed to be present in equal proportion, <code>gating.pen</code> should be <code>0</code> . The number of parameters used in the estimation of the noise component, if any, should also be included. Not necessary if <code>df</code> is supplied.
expert.pen	The number of parameters of the <i>expert</i> network of the MoEClust model. Defaults to <code>G * d</code> , which corresponds to no expert covariates. If covariates are included, this should be the number of regression coefficients in the fitted <i>expert</i> object. Not necessary if <code>df</code> is supplied.
z	The <code>n</code> times <code>G</code> responsibility matrix whose <code>[i,k]</code> -th entry is the probability that observation <code>i</code> belongs to the <code>k</code> -th component. If supplied the ICL is also computed and returned, otherwise only the BIC and AIC.
df	An alternative way to specify the number of estimated parameters (or 'used' degrees of freedom) exactly. If supplied, the arguments <code>d</code> , <code>G</code> , <code>gating.pen</code> and <code>expert.pen</code> , which are used to calculate the number of parameters, will be ignored. The number of parameters used in the estimation of the noise component, if any, should also be included.

Details

The function is vectorized with respect to the arguments `modelName` and `loglik`.

If `model` is an object of class "MoEClust" with `G` components, the number of parameters for the `gating.pen` and `expert.pen` are `length(coef(model$gating))` and `G * length(coef(model$expert[[1]]))`, respectively.

Models with a noise component are facilitated here too provided the extra number of parameters are accounted for by the user.

Value

A simplified array containing the BIC, AIC, number of estimated parameters (df) and, if `z` is supplied, also the ICL, for each of the given input arguments.

Note

In order to speed up repeated calls to the function inside `MoE_clust`, no checks take place.

Author(s)

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References

Biernacki, C., Celeux, G., Govaert, G. (2000). Assessing a mixture model for clustering with the integrated completed likelihood. *IEEE Trans. Pattern Analysis and Machine Intelligence*, 22(7): 719-725.

See Also

[MoE_clust](#), [nVarParams](#), [mclustModelNames](#)

Examples

```
MoE_crit(modelName=c("VVI", "VVE", "VVV"), n=120, d=8,
          G=3, loglik=c(-4036.99, -3987.12, -3992.45))

data(CO2data)
GNP <- CO2data$GNP
model <- MoE_clust(CO2data$CO2, G=1:2, expert= ~ GNP)
G <- model$G
name <- model$modelName
ll <- max(model$loglik)
n <- length(CO2data$CO2)
z <- model$z

# Compare BIC from MoE_crit to the BIC of the model
(bic2 <- MoE_crit(modelName=name, loglik=ll, n=n, d=1, G=G, z=z,
                  expert.pen=G * length(coef(model$expert[[1]])))["bic",])
identical(bic2, unname(model$bic)) #TRUE
```

```
# Make the same comparison with the known number of estimated parameters
(bic3 <- MoE_crit(modelName=name, loglik=ll, n=n, G=G, df=model$df, z=z)["bic",])
identical(bic3, bic2)           #TRUE
```

MoE_cstep

C-step for MoEClust Models

Description

Function to compute the assignment matrix z and the conditional log-likelihood for MoEClust models, with the aid of [MoE_dens](#).

Usage

```
MoE_cstep(data,
           mus,
           sigs,
           log.tau = 0L,
           Vinv = NULL,
           Dens = NULL)
```

Arguments

- | | |
|---------|--|
| data | If there are no expert network covariates, data should be a numeric matrix or data frame, wherein rows correspond to observations (n) and columns correspond to variables (d). If there are expert network covariates, this should be a list of length G containing matrices/data.frames of (multivariate) WLS residuals for each component. |
| mus | The mean for each of G components. If there is more than one component, this is a matrix whose k -th column is the mean of the k -th component of the mixture model. For the univariate models, this is a G -vector of means. In the presence of expert network covariates, all values should be equal to \emptyset . |
| sigs | The variance component in the parameters list from the output to eg. MoE_clust . The components of this list depend on the specification of <code>modelName</code> (see mclustVariance for details). The number of components G , the number of variables d , and the <code>modelName</code> are inferred from <code>sigs</code> . |
| log.tau | If covariates enter the gating network, an n times G matrix of mixing proportions, otherwise a G -vector of mixing proportions for the components of the mixture. Must be on the log-scale in both cases. The default of \emptyset effectively means densities (or log-densities) aren't scaled by the mixing proportions. |
| Vinv | An estimate of the reciprocal hypervolume of the data region. The default is determined by applying the function hypvol to the data. Used only if an initial guess as to which observations are noise is supplied. Mixing proportion(s) must be included for the noise component also. |

Dens (Optional) A numeric matrix whose $[i, k]$ -th entry is the **log**-density of observation i in component k , scaled by the mixing proportions, to which the function is to be applied, typically obtained by [MoE_dens](#) but this is not necessary. If this is supplied, all other arguments are ignored, otherwise [MoE_dens](#) is called according to the other supplied arguments.

Value

A list containing two elements:

z A matrix with n rows and G columns containing 1 where the observation belongs to the cluster indicated by the column number, and 0 otherwise.

loglik The estimated conditional log-likelihood.

Note

This function is intended for joint use with [MoE_dens](#), using the **log**-densities. Caution is advised using this function without explicitly naming the arguments. Models with a noise component are facilitated here too.

The C-step can be replaced by an E-step, see [MoE_estep](#) and the `algo` argument to [MoE_control](#).

Author(s)

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See Also

[MoE_dens](#), [MoE_clust](#), [MoE_estep](#), [MoE_control](#), [mclustVariance](#)

Examples

```
# MoE_cstep can be invoked for fitting MoEClust models via the CEM algorithm
# via the 'algo' argument to MoE_control:
data(ais)
hema <- ais[,3:7]
model <- MoE_clust(hema, G=3, gating= ~ BMI + sex, modelNames="EEE", network.data=ais, algo="CEM")
Dens <- MoE_dens(data=hema, mus=model$parameters$mean,
                 sigs=model$parameters$variance, log.tau=log(model$parameters$pro))

# Construct the z matrix and compute the conditional log-likelihood
Cstep <- MoE_cstep(Dens=Dens)
(l1 <- Cstep$loglik)

# Check that the z matrix & classification are the same as those from the model
identical(max.col(Cstep$z), as.integer(unname(model$classification))) #TRUE
identical(Cstep$z, model$z) #TRUE

# Call MoE_cstep directly
Cstep2 <- MoE_cstep(data=hema, sigs=model$parameters$variance,
                  mus=model$parameters$mean, log.tau=log(model$parameters$pro))
identical(Cstep2$loglik, l1) #TRUE
```

MoE_dens

*Density for MoEClust Mixture Models***Description**

Computes densities (or log-densities) of observations in MoEClust mixture models.

Usage

```
MoE_dens(data,
         mus,
         sigs,
         log.tau = 0L,
         Vinv = NULL,
         logarithm = TRUE)
```

Arguments

- | | |
|-----------|--|
| data | If there are no expert network covariates, data should be a numeric matrix or data frame, wherein rows correspond to observations (n) and columns correspond to variables (d). If there are expert network covariates, this should be a list of length G containing matrices/data.frames of (multivariate) WLS residuals for each component. |
| mus | The mean for each of G components. If there is more than one component, this is a matrix whose k-th column is the mean of the k-th component of the mixture model. For the univariate models, this is a G-vector of means. In the presence of expert network covariates, all values should be equal to 0. |
| sigs | The variance component in the parameters list from the output to eg. MoE_clust . The components of this list depend on the specification of modelName (see mclustVariance for details). The number of components G, the number of variables d, and the modelName are inferred from sigs. |
| log.tau | If covariates enter the gating network, an n times G matrix of mixing proportions, otherwise a G-vector of mixing proportions for the components of the mixture. Must be on the log-scale in both cases. The default of 0 effectively means densities (or log-densities) aren't scaled by the mixing proportions. |
| Vinv | An estimate of the reciprocal hypervolume of the data region. The default is determined by applying the function hypvol to the data. Used only if an initial guess as to which observations are noise is supplied. Mixing proportion(s) must be included for the noise component also. |
| logarithm | A logical value indicating whether or not the logarithm of the component densities should be returned. This defaults to TRUE, otherwise component densities are returned, obtained from the component log-densities by exponentiation. The log-densities can be passed to MoE_estep or MoE_cstep . |

Value

A numeric matrix whose $[i, k]$ -th entry is the density or log-density of observation i in component k , scaled by the mixing proportions. These densities are unnormalised.

Note

This function is intended for joint use with [MoE_estep](#) or [MoE_cstep](#), using the **log**-densities. Note that models with a noise component are facilitated here too.

Author(s)

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See Also

[MoE_estep](#), [MoE_cstep](#), [MoE_clust](#), [mclustVariance](#)

Examples

```
data(ais)
hema <- ais[,3:7]
model <- MoE_clust(hema, G=3, gating= ~ BMI + sex, modelNames="EEE", network.data=ais)
Dens <- MoE_dens(data=hema, mus=model$parameters$mean,
                 sigs=model$parameters$variance, log.tau=log(model$parameters$pro))

# Construct the z matrix and compute the log-likelihood
Estep <- MoE_estep(Dens=Dens)
(ll <- Estep$loglik)

# Check that the z matrix & classification are the same as those from the model
identical(max.col(Estep$z), as.integer(unname(model$classification))) #TRUE
identical(Estep$z, model$z) #TRUE

# The same can be done for models with expert covariates
m2 <- MoE_clust(hema, G=2, expert= ~ sex, modelNames="EVE", network.data=ais)
Dens2 <- MoE_dens(data=m2$resid.data, sigs=m2$parameters$variance,
                 mus=0, log.tau=log(m2$parameters$pro))
```

MoE_estep

E-step for MoEClust Models

Description

Softmax function to compute the responsibility matrix z and the log-likelihood for MoEClust models, with the aid of [MoE_dens](#).

Usage

```
MoE_estep(data,
           mus,
           sigs,
           log.tau = 0L,
           Vinv = NULL,
           Dens = NULL)
```

Arguments

data	If there are no expert network covariates, data should be a numeric matrix or data frame, wherein rows correspond to observations (n) and columns correspond to variables (d). If there are expert network covariates, this should be a list of length G containing matrices/data.frames of (multivariate) WLS residuals for each component.
mus	The mean for each of G components. If there is more than one component, this is a matrix whose k-th column is the mean of the k-th component of the mixture model. For the univariate models, this is a G-vector of means. In the presence of expert network covariates, all values should be equal to 0.
sigs	The variance component in the parameters list from the output to eg. MoE_clust . The components of this list depend on the specification of modelName (see mclustVariance for details). The number of components G, the number of variables d, and the modelName are inferred from sigs.
log.tau	If covariates enter the gating network, an n times G matrix of mixing proportions, otherwise a G-vector of mixing proportions for the components of the mixture. Must be on the log-scale in both cases. The default of 0 effectively means densities (or log-densities) aren't scaled by the mixing proportions.
Vinv	An estimate of the reciprocal hypervolume of the data region. The default is determined by applying the function hypvol to the data. Used only if an initial guess as to which observations are noise is supplied. Mixing proportion(s) must be included for the noise component also.
Dens	(Optional) A numeric matrix whose [i,k]-th entry is the log -density of observation i in component k, scaled by the mixing proportions, to which the softmax function is to be applied, typically obtained by MoE_dens but this is not necessary. If this is supplied, all other arguments are ignored, otherwise MoE_dens is called according to the other supplied arguments.

Value

A list containing two elements:

z	A matrix with n rows and G columns containing the probability of cluster membership for each of n observations and G clusters.
loglik	The estimated log-likelihood, computed efficiently via rowLogSumExps .

Note

This softmax function is intended for joint use with `MoE_dens`, using the **log**-densities. Caution is advised using this function without explicitly naming the arguments. Models with a noise component are facilitated here too.

The E-step can be replaced by a C-step, see `MoE_cstep` and the `algo` argument to `MoE_control`.

Author(s)

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See Also

`MoE_dens`, `MoE_clust`, `MoE_cstep`, `MoE_control`, `mclustVariance`, `rowLogSumExps`

Examples

```
data(ais)
hema <- ais[,3:7]
model <- MoE_clust(hema, G=3, gating= ~ BMI + sex, modelNames="EEE", network.data=ais)
Dens <- MoE_dens(data=hema, mus=model$parameters$mean,
                 sigs=model$parameters$variance, log.tau=log(model$parameters$pro))

# Construct the z matrix and compute the log-likelihood
Estep <- MoE_estep(Dens=Dens)
(l1 <- Estep$loglik)

# Check that the z matrix & classification are the same as those from the model
identical(max.col(Estep$z), as.integer(unname(model$classification))) #TRUE
identical(Estep$z, model$z) #TRUE

# Call MoE_estep directly
Estep2 <- MoE_estep(data=hema, sigs=model$parameters$variance,
                   mus=model$parameters$mean, log.tau=log(model$parameters$pro))
identical(Estep2$loglik, l1) #TRUE

# The same can be done for models with expert covariates
m2 <- MoE_clust(hema, G=2, expert= ~ sex, modelNames="EVE", network.data=ais)
Estep3 <- MoE_estep(data=m2$resid.data, sigs=m2$parameters$variance,
                  mus=0, log.tau=log(m2$parameters$pro))
```

Description

Produces a matrix of plots showing pairwise relationships between continuous response variables and continuous/categorical/logical/ordinal associated covariates, as well as the clustering achieved, according to fitted MoEClust mixture models.

Usage

```
MoE_gpairs(res,
  response.type = c("points", "uncertainty", "density"),
  subset = list(...),
  scatter.type = c("lm", "points"),
  conditional = c("stripplot", "boxplot"),
  addEllipses = c("outer", "yes", "no", "inner", "both"),
  border.col = c("purple", "black", "brown", "brown", "navy"),
  bg.col = c("cornsilk", "white", "palegoldenrod", "palegoldenrod", "cornsilk"),
  outer.margins = list(bottom = grid::unit(2, "lines"),
    left = grid::unit(2, "lines"),
    top = grid::unit(2, "lines"),
    right = grid::unit(2, "lines")),
  outer.labels = NULL,
  outer.rot = c(0, 90),
  gap = 0.05,
  buffer = 0.02,
  scatter.pars = list(...),
  density.pars = list(...),
  stripplot.pars = list(...),
  barcode.pars = list(...),
  mosaic.pars = list(...),
  axis.pars = list(...),
  diag.pars = list(...),
  ...)
```

Arguments

- | | |
|---------------|--|
| res | An object of class "MoEClust" generated by MoE_clust , or an object of class "MoECompare" generated by MoE_compare . Models with a noise component are facilitated here too. |
| response.type | The type of plot desired for the scatter plots comparing continuous response variables. Defaults to "points".

Points can also be sized according to their associated clustering uncertainty with the option "uncertainty". In so doing, the transparency of the points will also be proportional to their clustering uncertainty, provided the device supports transparency. See also MoE_Uncertainty for an alternative means of visualising observation-specific cluster uncertainties (especially for univariate data).

Alternatively, the bivariate "density" contours can be displayed (see <code>density.pars</code>). Caution is advised when producing density plots for models with covariates in the expert network, the required number of evaluations of the (multivariate) Gaussian density for each panel (<code>res\$G * prod(density.pars\$grid.size)</code>) increases by a factor of <code>res\$n</code> , thus plotting may be slow. |
| subset | A list giving named arguments for producing only a subset of panels:

<code>show.map</code> Logical indicating whether to show panels involving the MAP classification (defaults to TRUE, unless there is only one component, in which case the MAP classification is never plotted.). |

	<p><code>data.ind</code> For subsetting response variables: a vector of column indices corresponding to the variables in the columns of <code>res\$data</code> which should be shown. Defaults to all. Can be \emptyset, in order to suppress plotting the response variables.</p> <p><code>cov.ind</code> For subsetting covariates: a vector of column indices corresponding to the covariates in the columns <code>res\$net.covs</code> which should be shown. Defaults to all. Can be \emptyset, in order to suppress plotting the covariates.</p> <p>The subsetting must include at least two variables, whether they be the MAP, a response variable, or a covariate, in order to be valid for plotting purposes.</p>
<code>scatter.type</code>	<p>A vector of length 2 (or 1) giving the plot type for the upper and lower triangular portions of the plot, respectively, pertaining to the associated covariates. Defaults to "lm" for covariate vs. response panels and "points" otherwise. Only relevant for models with continuous covariates in the gating &/or expert network. "ci" and "lm" type plots are only produced for plots pairing covariates with response, and never response vs. response or covariate vs. covariate. Note that lines &/or confidence intervals will only be drawn for continuous covariates included in the expert network; to include covariates included only in the gating network also, use the options "lm2" or "ci2".</p>
<code>conditional</code>	<p>A vector of length 2 (or 1) giving the plot type for the upper and lower triangular portions of the plot, respectively, for plots involving a mix of categorical and continuous variables. Defaults to "stripplot" in the upper triangle and "boxplot" in the lower triangle (see panel.stripplot and panel.bwplot). "barcode" and "violin" plots can also be produced. Only relevant for models with categorical covariates in the gating &/or expert network. Comparisons of two categorical variables (which can only ever be covariates) are always displayed via mosaic plots (see strucplot).</p>
<code>addEllipses</code>	<p>Controls whether to add MVN ellipses with axes corresponding to the within-cluster covariances for the response data ("yes" or "no"). The options "inner" and "outer" (the default) will colour the axes or the perimeter of those ellipses, respectively, according to the cluster they represent (according to <code>scatter.pars\$lci.col</code>). The option "both" will obviously colour both the axes and the perimeter. Ellipses are only ever drawn for multivariate data, and only when <code>response.type</code> is "points" or "uncertainty".</p> <p>Ellipses are centered on the posterior mean of the fitted values when there are expert network covariates, otherwise on the posterior mean of the response variables. In the presence of expert network covariates, the component-specific covariance matrices are also modified for plotting purposes via the function expert_covar, in order to account for the extra variability of the means, usually resulting in bigger shapes & sizes for the MVN ellipses.</p>
<code>border.col</code>	<p>A vector of length 5 (or 1) containing <i>border</i> colours for plots against the MAP classification, response vs. response, covariate vs. response, response vs. covariate, and covariate vs. covariate panels, respectively.</p> <p>Defaults to <code>c("purple", "black", "brown", "brown", "navy")</code>.</p>
<code>bg.col</code>	<p>A vector of length 5 (or 1) containing <i>background</i> colours for plots against the MAP classification, response vs. response, covariate vs. response, response vs. covariate, and covariate vs. covariate panels, respectively.</p> <p>Defaults to <code>c("cornsilk", "white", "palegoldenrod", "palegoldenrod", "cornsilk")</code>.</p>

- `outer.margins` A list of length 4 with units as components named bottom, left, top, and right, giving the outer margins; the defaults uses two lines of text. A vector of length 4 with units (ordered properly) will work, as will a vector of length 4 with numeric variables (interpreted as lines).
- `outer.labels` The default is NULL, for alternating labels around the perimeter. If "all", all labels are printed, and if "none", no labels are printed.
- `outer.rot` A 2-vector (x, y) rotating the top/bottom outer labels x degrees and the left/right outer labels y degrees. Only works for categorical labels of boxplot and mosaic panels. Defaults to `c(0, 90)`.
- `gap` The gap between the tiles; defaulting to 0.05 of the width of a tile.
- `buffer` The fraction by which to expand the range of quantitative variables to provide plots that will not truncate plotting symbols. Defaults to 2 percent of range currently.
- `scatter.pars` A list supplying select parameters for the continuous vs. continuous scatter plots.
 NULL is equivalent to:

```
list(scatter.pch=if(response.type == "uncertainty") 19 else res$classification,
      scatter.size=unit(0.25, "char"), scatter.col=res$classification, lci.col=res$classification)
```

 where `lci.col` gives the colour of the fitted lines &/or confidence intervals when `scatter.type` is one of "ci" or "lm" and the colour of the ellipses when `addEllipses` is one of "outer", "inner", or "both". Note that `scatter.pars$scatter.size` will be modified on an observation by observation level when `response.type` is "uncertainty". Note also that the default for `scatter.pars$scatter.pch` changes depending on whether `response.type` is given as "points" or "uncertainty", though it can of course be modified in both cases.
- `density.pars` A list supplying select parameters for visualising the bivariate density contours, only when `response.type` is "density".
 NULL is equivalent to:

```
list(grid.size=c(100, 100), dcol="grey50",
      nlevels=11, show.labels=TRUE),
```

 where `density.pars$grid.size` is a vector of length two giving the number of points in the x & y direction of the grid over which the density is evaluated, respectively, and `density.pars$dcol` is either a single colour or a vector of length `density.pars$nlevels` colours, although note that `density.pars$dcol`, when *not* specified, will be adjusted for transparency.
- `stripplot.pars` A list supplying select parameters for continuous vs. categorical panels when one of the entries of `conditional` is "stripplot".
 NULL is equivalent to:

```
list(strip.pch=res$classification, strip.size=unit(0.5, "char"),
      strip.col=res$classification, jitter=TRUE).
```
- `barcode.pars` A list supplying select parameters for continuous vs. categorical panels when one of the entries of `conditional` is "boxplot". See the help file for `barcode::barcode`.
 NULL is equivalent to:

	<code>list(nint=0, psize=unit(0.25, "char"), ptpch=1, bcspace=NULL, use.points=FALSE).</code>
<code>mosaic.pars</code>	A list supplying select parameters for categorical vs. categorical panels. NULL. Currently <code>shade</code> , <code>gp_labels</code> , <code>gp</code> , and <code>gp_args</code> are passed through to <code>strucplot</code> for producing mosaic tiles.
<code>axis.pars</code>	A list supplying select parameters for controlling axes. NULL is equivalent to: <code>list(n.ticks=5, axis.fontsize=9).</code> The argument <code>n.ticks</code> will be overwritten for categorical variables with fewer than 5 levels.
<code>diag.pars</code>	A list supplying select parameters for panels along the diagonal. NULL is equivalent to: <code>list(diag.fontsize=9, show.hist=TRUE, diagonal=TRUE, hist.color=hist.color, show.counts=TRUE),</code> where <code>hist.color</code> is a vector of length 4, giving the colours for the response variables, gating covariates, expert covariates, and covariates entering both networks, respectively. By default, response variables are "black" and covariates of any kind are "grey". The MAP classification is always coloured by cluster membership. <code>show.counts</code> is only relevant for categorical variables. When <code>diagonal=TRUE</code> (the default), the diagonal from the top left to the bottom right is used for displaying the marginal distributions of variables. Specifying <code>diagonal=FALSE</code> will place the diagonal running from the top right down to the bottom left.
<code>...</code>	Catches unused arguments. Alternatively, named arguments can be passed directly here to any/all of <code>scatter.pars</code> , <code>barcode.pars</code> , <code>mosaic.pars</code> , <code>axis.pars</code> and <code>diag.pars</code> .

Value

A generalised pairs plot showing all pairwise relationships between clustered response variables and associated gating &/or expert network continuous &/or categorical variables, coloured according to the MAP classification, with the marginal distributions of each variable along the diagonal.

Note

For MoEClust models with more than one associated covariate (entering either network), fitted lines produced in continuous covariate vs. continuous response scatter plots via `scatter.type="lm"` or `scatter.type="ci"` will **NOT** correspond to the coefficients in the expert network (`res$expert`). `plot.MoEClust` is a wrapper to `MoE_gpairs` which accepts the default arguments, and also produces other types of plots. Caution is advised producing generalised pairs plots when the dimension of the data is large.

Author(s)

Keefe Murphy - <<keefe.murphy@ucd.ie>>

References

K. Murphy and T. B. Murphy (2017). Parsimonious Model-Based Clustering with Covariates. *To appear*. <[arXiv:1711.05632](https://arxiv.org/abs/1711.05632)>.

Emerson, J.W., Green, W.A., Schloerke, B., Crowley, J., Cook, D., Hofmann, H. and Wickham, H. (2013). The Generalized Pairs Plot. *Journal of Computational and Graphical Statistics*, 22(1):79-91.

See Also

[MoE_clust](#), [plot.MoEClust](#), [MoE_Uncertainty](#), [panel.stripplot](#), [panel.bwplot](#), [panel.violin](#), [strucplot](#)

Examples

```
## Not run:
data(ais)
res <- MoE_clust(ais[,3:7], G=2, gating= ~ BMI, expert= ~ sex,
                network.data=ais, modelNames="EVE")
MoE_gpairs(res)

# Produce the same plot, but with a violin plot in the lower triangle.
# Add fitted lines to the scatter plots. Don't show the "sex" covariate.
# Size points in the response vs. response panels by their clustering uncertainty.
MoE_gpairs(res, conditional=c("stripplot", "violin"), cov.ind=1,
           scatter.type=c("lm2", "points"), response.type="uncertainty")

# Instead show the bivariate density contours of the response variables.
# (Plotting may be slow when response.type="density" for models with expert covariates.)
# Use different colours for histograms of covariates in the gating/expert/both networks.
# Also use different colours for response vs. covariate & covariate vs. response panels.
MoE_gpairs(res, response.type="density", show.labels=FALSE,
           hist.color=c("black", "cyan", "hotpink", "chartreuse"),
           bg.col=c("whitesmoke", "white", "mintcream", "mintcream", "floralwhite"))
## End(Not run)
```

MoE_mahala

Mahalanobis Distance Outlier Detection for Multivariate Response

Description

Computes the Mahalanobis distance between the fitted values and residuals of linear regression models with multivariate or univariate responses.

Usage

```
MoE_mahala(fit,
           resids,
           squared = FALSE)
```

Arguments

<code>fit</code>	A fitted <code>lm</code> model, inheriting either the <code>"mlm"</code> or <code>"lm"</code> class.
<code>resids</code>	The residuals. Can be residuals for observations included in the model, or residuals arising from predictions on unseen data.
<code>squared</code>	A logical. By default (<code>FALSE</code>), the generalized interpoint distance is computed. Set this flag to <code>TRUE</code> for the squared value.

Value

A vector giving the Mahalanobis distance (or squared Mahalanobis distance) between fitted values and residuals for each observation.

Author(s)

Keefe Murphy - <<keefe.murphy@ucd.ie>>

Examples

```
data(ais)
hema <- as.matrix(ais[,3:7])
mod <- lm(hema ~ sex + BMI, data=ais)
res <- hema - predict(mod)
MoE_mahala(mod, res)
```

MoE_news

Show the NEWS file

Description

Show the NEWS file of the MoEClust package.

Usage

```
MoE_news()
```

Value

The MoEClust NEWS file, provided the session is interactive.

Examples

```
MoE_news()
```

MoE_plotCrit *Model Selection Criteria Plot for MoEClust Mixture Models*

Description

Plots the BIC, ICL, AIC, or log-likelihood values of a fitted MoEClust object.

Usage

```
MoE_plotCrit(res,  
             criterion = c("bic", "icl", "aic", "loglik"),  
             ...)
```

Arguments

res	An object of class "MoEClust" generated by MoE_clust , or an object of class "MoECompare" generated by MoE_compare . Models with a noise component are facilitated here too.
criterion	The criterion to be plotted. Defaults to "bic".
...	Catches other arguments, or additional arguments to be passed to plot.mclustBIC (or equivalent functions for the other criterion arguments).

Value

A plot of the values of the chosen criterion. The values themselves can also be returned invisibly.

Note

[plot.MoEClust](#) is a wrapper to [MoE_plotCrit](#) which accepts the default arguments, and also produces other types of plots.

Author(s)

Keefe Murphy - <<keefe.murphy@ucd.ie>>

See Also

[MoE_clust](#), [plot.MoEClust](#), [plot.mclustBIC](#)

Examples

```
## Not run:  
data(ais)  
res <- MoE_clust(ais[,3:7], expert= ~ sex, network.data=ais)  
(crit <- MoE_plotCrit(res))  
## End(Not run)
```

MoE_plotGate

*Plot MoEClust Gating Network***Description**

Plots the gating network for fitted MoEClust models, i.e. the observation index against the mixing proportions for that observation, coloured by cluster.

Usage

```
MoE_plotGate(res,
             x.axis = NULL,
             type = "l",
             xlab = "Observation",
             ylab = expression(widehat(tau)[g]),
             ylim = c(0, 1),
             col = NULL,
             ...)
```

Arguments

<code>res</code>	An object of class "MoEClust" generated by MoE_clust , or an object of class "MoECompare" generated by MoE_compare . Models with a noise component are facilitated here too.
<code>x.axis</code>	Optional argument for the x-axis against which the mixing proportions are plotted. Defaults to <code>1:res\$n</code> if missing.
<code>type, xlab, ylab, ylim, col</code>	These graphical parameters retain their definitions from matplot .
<code>...</code>	Catches unused arguments, or additional arguments to be passed to matplot .

Value

A plot of the gating network of the fitted MoEClust model. The parameters of the gating network can also be returned invisibly.

Note

[plot.MoEClust](#) is a wrapper to [MoE_plotGate](#) which accepts the default arguments, and also produces other types of plots.

By default, the noise component (if any) will be coloured "grey65".

Author(s)

Keefe Murphy - <<keefe.murphy@ucd.ie>>

See Also

[MoE_clust](#), [plot.MoEClust](#), [matplot](#)

Examples

```
data(ais)
res  <- MoE_clust(ais[,3:7], gating= ~ BMI, G=3, modelNames="EEE",
                 network.data=ais, noise.gate=FALSE, tau0=0.1)

# Plot against the observation index and examine the gating network coefficients
(gate <- MoE_plotGate(res))

# Plot against BMI
MoE_plotGate(res, x.axis=ais$BMI, type="p", xlab="BMI", pch=1)
```

MoE_plotLogLik

Plot the Log-Likelihood of a MoEClust Mixture Model

Description

Plots the log-likelihood at every iteration of the EM/CEM algorithm used to fit a MoEClust mixture model.

Usage

```
MoE_plotLogLik(res,
               type = "l",
               xlab = "Iteration",
               ylab = "Log-Likelihood",
               xaxt = "n",
               ...)
```

Arguments

res An object of class "MoEClust" generated by [MoE_clust](#), or an object of class "MoECompare" generated by [MoE_compare](#). Models with a noise component are facilitated here too.

type, xlab, ylab, xaxt These graphical parameters retain their usual definitions from [plot](#).

... Catches unused arguments, or additional arguments to be passed to [plot](#).

Value

A plot of the log-likelihood versus the number EM iterations. A list with the vector of log-likelihood values and the final value at convergence can also be returned invisibly.

Note

`plot.MoEClust` is a wrapper to `MoE_plotLogLik` which accepts the default arguments, and also produces other types of plots.

`res$LOGLIK` can also be plotted, to compare maximal log-likelihood values for all fitted models.

Author(s)

Keefe Murphy - <<keefe.murphy@ucd.ie>>

See Also

`MoE_clust`, `plot.MoEClust`,

Examples

```
data(ais)
res <- MoE_clust(ais[,3:7], gating= ~ BMI, expert= ~ sex,
                G=2, modelNames="EVE", network.data=ais)
(l1 <- MoE_plotLogLik(res))
```

MoE_Uncertainty

Plot Clustering Uncertainties

Description

Plots the clustering uncertainty for every observation from a fitted "MoEClust" model, including models with a noise component.

Usage

```
MoE_Uncertainty(res,
                type = c("barplot", "profile"),
                truth = NULL,
                decreasing = FALSE,
                ...)
```

Arguments

<code>res</code>	An object of class "MoEClust" generated by <code>MoE_clust</code> , or an object of class "MoECompare" generated by <code>MoE_compare</code> . Models with a noise component are facilitated here too.
<code>type</code>	The type of plot to be produced (defaults to "barplot"). The "profile" option instead displays uncertainties in increasing/decreasing order of magnitude (see decreasing).

truth	An optional argument giving the true classification of the data. When truth is supplied and type="barplot", misclassified observations are highlighted in a different colour, otherwise observations with uncertainty greater than 1/res\$G are given in a different colour. When truth is supplied and type="profile", the uncertainty of misclassified observations is marked by vertical lines on the plot.
decreasing	Logical indicating whether uncertainties should be ordered in decreasing order (defaults to FALSE). Only relevant when type="profile".
...	Catches unused arguments.

Details

The y-axis of this plot runs from 0 to $1 - 1/\text{res}\$G$, with a horizontal line also drawn at $1/\text{res}\$G$. When type="barplot", uncertainties greater than this value are given a different colour when truth is not supplied, otherwise misclassified observations are given a different colour. Note, however, that $G^{(0)} = \text{res}\$G + 1$ is used in place of res\$G for models with a noise component.

Value

A plot showing the clustering uncertainty of each observation (sorted in increasing/decreasing order when type="profile"). The (unsorted) vector of uncertainties can also be returned invisibly. When truth is supplied, the indices of the misclassified observations are also invisibly returned.

Note

`plot.MoEClust` is a wrapper to `MoE_Uncertainty` which accepts the default arguments, and also produces other types of plots.

An alternative means of visualising clustering uncertainties (at least for multivariate data) is provided by the functions `MoE_gpairs` and `plot.MoEClust`, specifically when their argument `response.type` is given as "uncertainty".

Author(s)

Keefe Murphy - <<keefe.murphy@ucd.ie>>

See Also

`MoE_clust`, `MoE_gpairs`, `plot.MoEClust`

Examples

```
data(ais)
res <- MoE_clust(ais[,3:7], gating= ~ sex, G=3, modelNames="EEE", network.data=ais)

# Produce an uncertainty barplot
MoE_Uncertainty(res)

# Produce an uncertainty profile plot
MoE_Uncertainty(res, type="profile")
```

```
# Let's assume the true clusters correspond to sex
(ub <- MoE_Uncertainty(res, truth=ais$sex))
(up <- MoE_Uncertainty(res, type="profile", truth=ais$sex))
```

noise_vol	<i>Approximate Hypervolume Estimate</i>
-----------	---

Description

Computes simple approximations to the hypervolume of univariate and multivariate data sets.

Usage

```
noise_vol(data,
          method = c("hypvol", "convexhull", "ellipsoidhull"),
          reciprocal = FALSE)
```

Arguments

data	A numeric vector, matrix, or data frame of observations. Categorical variables are not allowed. If a matrix or data frame, rows correspond to observations and columns correspond to variables.
method	The method used to estimate the hypervolume. The "convexhull" and "ellipsoidhull" options require loading the <code>geometry</code> and <code>cluster</code> libraries, respectively.
reciprocal	A logical variable indicating whether or not the reciprocal hypervolume is desired rather than the hypervolume itself. The default is to return the hypervolume.

Value

A hypervolume estimate (or its inverse), to be used as the hypervolume parameter for the noise component when observations are designated as noise in `MoE_clust`.

Author(s)

Keefe Murphy - <<keefe.murphy@ucd.ie>>

See Also

[hypvol](#), [convhulln](#), [ellipsoidhull](#)

Examples

```
data(ais)
noise_vol(ais[,3:7], reciprocal=TRUE)
```

plot.MoEClust	<i>Plot MoEClust Results</i>
---------------	------------------------------

Description

Plot results for fitted MoE_clust mixture models with gating &/or expert network covariates: generalised pairs plots, model selection criteria, the log-likelihood vs. the EM iterations, and the gating network are all currently visualisable.

Usage

```
## S3 method for class 'MoEClust'
plot(x,
     what = c("gpairs", "gating", "criterion", "loglik", "uncertainty"),
     ...)
```

Arguments

x	An object of class "MoEClust" generated by MoE_clust , or an object of class "MoECompare" generated by MoE_compare . Models with a noise component are facilitated here too.
what	The type of graph requested: gpairs A generalised pairs plot. To further customise this plot, arguments to MoE_gpairs can be supplied. gating The gating network. To further customise this plot, arguments to MoE_plotGate and matplot can be supplied. criterion The model selection criteria. To further customise this plot, arguments to MoE_plotCrit and plot.mclustBIC can be supplied. loglik The log-likelihood vs. the iterations of the EM algorithm. To further customise this plot, arguments to MoE_plotLogLik and plot can be supplied. uncertainty The clustering uncertainty for every observation. To further customise this plot, arguments to MoE_Uncertainty can be supplied. By default, all of the above graphs are produced.
...	Optional arguments to be passed to MoE_gpairs , MoE_plotGate , MoE_plotCrit , MoE_plotLogLik , MoE_Uncertainty , matplot , plot.mclustBIC and plot .

Details

For more flexibility in plotting, use [MoE_gpairs](#), [MoE_plotGate](#), [MoE_plotCrit](#), [MoE_plotLogLik](#) and [MoE_Uncertainty](#) directly.

Value

The visualisation according to "what" of the results of a fitted MoEClust model.

Note

Caution is advised producing generalised pairs plots when the dimension of the data is large.

Other types of plots are available by first calling `as.Mclust` on the fitted object, and then calling `plot.Mclust` on the results. These can be especially useful for univariate data.

Author(s)

Keefe Murphy - <keefe.murphy@ucd.ie>

References

K. Murphy and T. B. Murphy (2017). Parsimonious Model-Based Clustering with Covariates. *To appear*. <[arXiv:1711.05632](https://arxiv.org/abs/1711.05632)>.

See Also

`MoE_clust`, `MoE_gpairs`, `MoE_plotGate`, `MoE_plotCrit`, `MoE_plotLogLik`, `MoE_Uncertainty`, `as.Mclust`, `plot.Mclust`

Examples

```
## Not run:
data(ais)
res <- MoE_clust(ais[,3:7], gating= ~ BMI, expert= ~ sex,
               G=2, modelNames="EVE", network.data=ais)

# Plot the gating network
plot(res, what="gating")

# Plot the log-likelihood
plot(res, what="loglik")

# Plot the uncertainty profile
plot(res, what="uncertainty", type="profile")

# Produce a generalised pairs plot
plot(res, what="gpairs")

# Modify the gpairs plot by passing arguments to MoE_gpairs()
plot(res, what="gpairs", response.type="density",
     scatter.type="ci", jitter=FALSE, show.counts=FALSE)
## End(Not run)
```

predict.MoEClust *Predictions for MoEClust models*

Description

Predicts both cluster membership probability and fitted response values from a MoEClust model, using covariates and response data, or covariates only. The MAP classification is also reported in both cases.

Usage

```
## S3 method for class 'MoEClust'
predict(object,
        newdata,
        resid = FALSE,
        ...)

## S3 method for class 'MoEClust'
residuals(object,
          newdata,
          ...)
```

Arguments

object	An object of class "MoEClust" generated by <code>MoE_clust</code> , or an object of class "MoECompare" generated by <code>MoE_compare</code> . Predictions for models with a noise component are facilitated here too.
newdata	<p>A list with two <i>named</i> components, each of which must be a <code>data.frame</code> or <code>matrix</code> with named columns, giving the data for which predictions are desired.</p> <p><code>new.x</code> The new covariates for the gating &/or expert networks. Must be supplied when <code>newdata\$new.y</code> is supplied.</p> <p><code>new.y</code> (Optional) response data. When supplied, cluster and response prediction is based on both <code>newdata\$new.x</code> and <code>newdata\$new.y</code>, otherwise only on the covariates in <code>newdata\$new.x</code>.</p> <p>If supplied as a list with elements <code>new.x</code> and <code>new.y</code>, both must have the same number of rows.</p> <p>Alternatively, a single <code>data.frame</code> or <code>matrix</code> can be supplied and an attempt will be made to extract & separate covariate and response columns (<i>if any</i>) into <code>newdata\$new.x</code> and <code>newdata\$new.y</code> based on the variable names in <code>object\$data</code> and <code>object\$net.covs</code>.</p> <p>When <code>newdata</code> is not supplied in any way, the covariates and response variables used in the fitting of the model are used here.</p>
resid	A logical indicating whether to return the residuals also. Defaults to <code>FALSE</code> . Only allowed when response variables are supplied in some form. The function <code>residuals</code> is a wrapper to <code>predict</code> with the argument <code>resid</code> set to <code>TRUE</code> , with only the residuals returned.

... Catches unused arguments.

Value

A list with the following named components, regardless of whether `newdata$new.x` and `newdata$new.y` were used, or `newdata$new.x` only.

`y` Fitted values of the response variables.
`z` A matrix whose $[i, k]$ -th entry is the probability that observation i of the `newdata` belongs to the k -th component.
`classification` The vector of predicted cluster labels for the `newdata`.

When `residuals` is called, only the residuals are returned; when `predict` is called with `resid=TRUE`, the list above will also contain the element `resids`, containing the residuals.

Note

Predictions can also be made for models with noise components, in which case `z` will include the probability of belonging to "Cluster0" & `classification` will include labels with the value 0 for observations classified as noise (if any). Note that calculating `ystar` for models with a noise component involves renormalising the rows of `zstar` such that non-noise columns sum to 1, but the *unnormalised* `zstar` is what's reported.

Author(s)

Keefe Murphy - <<keefe.murphy@ucd.ie>>

References

K. Murphy and T. B. Murphy (2017). Parsimonious Model-Based Clustering with Covariates. *To appear*. <[arXiv:1711.05632](https://arxiv.org/abs/1711.05632)>.

See Also

[MoE_clust](#)

Examples

```
data(ais)

# Fit a MoEClust model and predict the same data
res <- MoE_clust(ais[,3:7], G=2, gating=~BMI, expert=~sex,
                modelNames="EVE", network.data=ais)
pred1 <- predict(res)
pred1$classification

# Remove some rows of the data for prediction purposes
ind <- sample(1:nrow(ais), 5)
dat <- ais[-ind,]

# Fit another MoEClust model to the retained data
```

```
res2 <- MoE_clust(dat[,3:7], G=3, gating=~BMI + sex,
                 modelNames="EEE", network.data=dat)

# Predict held back data using the covariates & response variables
pred2 <- predict(res2, newdata=ais[ind,])
# pred2 <- predict(res2, newdata=list(new.y=ais[ind,3:7],
#                                   new.x=ais[ind,c("BMI", "sex")]))
pred2$y

# Get the residuals
residuals(res2, newdata=ais[ind,])

# Predict held back data using only the covariates
pred3 <- predict(res2, newdata=list(new.x=ais[ind,c("BMI", "sex")]))
# pred3 <- predict(res2, newdata=ais[ind,c("BMI", "sex")])
pred3$z
```

quant_clust

Quantile-Based Clustering for Univariate Data

Description

Returns a quantile-based clustering for univariate data.

Usage

```
quant_clust(x,
            G)
```

Arguments

x A vector of numeric data.
G The desired number of clusters.

Value

The vector of cluster labels.

Examples

```
data(CO2data)
quant_clust(CO2data$CO2, G=2)
```

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