Package: iClusterVB (via r-universe)

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Type Package

Title Fast Integrative Clustering and Feature Selection for High Dimensional Data

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Description A variational Bayesian approach for fast integrative clustering and feature selection, facilitating the analysis of multi-view, mixed type, high-dimensional datasets with applications in fields like cancer research, genomics, and more.

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BugReports https://github.com/AbdalkarimA/iClusterVB/issues

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`chmap` *Generates a heat map based on an iClusterVB object*

Description

Generates a heat map based on an iClusterVB object

Usage

```
chmap(fit, rho = 0.5, cols = NULL, title = NULL, ...)
```

Arguments

`fit`	A fitted iClusterVB object.
`rho`	The minimum probability of inclusion for features shown on the heatmap. Default is 0.5. 0 would show all features. Only useful for VS_method = 1.
`cols`	A vector of colors to use for the clusters. The default is a random selection of colors.
`title`	A character vector or a single value. Title of the heat map. The default is "View 1 - Distribution 1", ..., "View R - Distribution R".
`...`	Additional arguments to be passed down to `pheatmap`

Value

Returns a heat map for each data view.

Examples

```
# Setting up the data
dat1 <- list(
  gauss_1 = sim_data$continuous1_data[c(1:20, 61:80, 121:140, 181:200), 1:75],
  gauss_2 = sim_data$continuous2_data[c(1:20, 61:80, 121:140, 181:200), 1:75],
  poisson_1 = sim_data$count_data[c(1:20, 61:80, 121:140, 181:200), 1:75])


dist <- c(
  "gaussian", "gaussian",
  "poisson")

fit_iClusterVB <- iClusterVB(
  mydata = dat1,
  dist = dist,
  K = 4,
  initial_method = "VarSelLCM",
  VS_method = 1,
  max_iter = 25
)


# We can set the colors, turn off scaling and set titles

chmap(fit_iClusterVB,
  cols = c("red", "blue", "green", "purple"),
  title = c("Gene Expression", "DNA Methylation", "Copy Number"),
  scale = "none"
)
```

`iClusterVB` *Fast Integrative Clustering for High-Dimensional Multi-View Data Using Variational Bayesian Inference*

Description

`iClusterVB` offers a novel, fast, and integrative approach to clustering high-dimensional, mixed-type, and multi-view data. By employing variational Bayesian inference, iClusterVB facilitates effective feature selection and identification of disease subtypes, enhancing clinical decision-making.

Usage

```
iClusterVB(
  mydata,
  dist,
  K = 10,
  initial_method = "VarSelLCM",
  VS_method = 0,
  initial_cluster = NULL,
```

```
  initial_vs_prob = NULL,
  initial_fit = NULL,
  initial_omega = NULL,
  input_hyper_parameters = NULL,
  max_iter = 200,
  early_stop = 1,
  per = 10,
  convergence_threshold = 1e-04
)
```

Arguments

mydata	A list of length R, where R is the number of datasets, containing the input data. • Note: For **categorical** data, 0's must be re-coded to another, non-0 value.
dist	A vector of length R specifying the type of data or distribution. Options include: 'gaussian' (for continuous data), 'multinomial' (for binary or categorical data), and 'poisson' (for count data).
K	The maximum number of clusters, with a default value of 10. The algorithm will converge to a model with dominant clusters, removing redundant clusters and automating the determination of the number of clusters.
initial_method	The initialization method for cluster allocation. Options include: "VarSelLCM" (default), "random", "kproto" (k-prototypes), "kmeans" (continuous data only), "mclust" (continuous data only), or "lca" (poLCA, categorical data only).
VS_method	The variable/feature selection method. Options are 0 for clustering without variable/feature selection (default) and 1 for clustering with variable/feature selection.
initial_cluster	The initial cluster membership. The default is NULL, which uses initial_method for initial cluster allocation. If not NULL, it will override the initial values setting for this parameter.
initial_vs_prob	The initial variable/feature selection probability, a scalar. The default is NULL, which assigns a value of 0.5.
initial_fit	Initial values based on a previously fitted iClusterVB model (an iClusterVB object). The default is NULL.
initial_omega	Customized initial values for feature inclusion probabilities. The default is NULL. If not NULL, it will override the initial values setting for this parameter. If VS_method = 1, initial_omega is a list of length R, with each element being an array with dimensions {dim=c(N, p[[r]])}. Here, N is the sample size and p[[r]] is the number of features for dataset r, where r = 1, ..., R.
input_hyper_parameters	A list of the initial hyper-parameters of the prior distributions for the model. The default is NULL, which assigns alpha_00 = 0.001, mu_00 = 0, s2_00 = 100, a_00 = 1, b_00 = 1,kappa_00 = 1, u_00 = 1, v_00 = 1.
max_iter	The maximum number of iterations for the VB algorithm. The default is 200.

`early_stop` Whether to stop the algorithm upon convergence or to continue until `max_iter` is reached. Options are 1 (default) to stop when the algorithm converges, and 0 to stop only when `max_iter` is reached.

`per` Print information every "per" iterations. The default is 10.

`convergence_threshold`
The convergence threshold for the change in ELBO. The default is 0.0001.

Value

The `iClusterVB` function creates an object (list) of class `iClusterVB`. Relevant outputs include:

`elbo:` The evidence lower bound for each iteration.

`cluster:` The cluster assigned to each individual.

`initial_values:`
A list of the initial values.

`hyper_parameters:`
A list of the hyper-parameters.

`model_parameters:`
A list of the model parameters after the algorithm is run.

- Of particular interest is `rho`, a list of the posterior inclusion probabilities for the features in each of the data views. This is the probability of including a certain predictor in the model, given the observations. This is only available if `VS_method = 1`.

Note

If any of the data views are "gaussian", please include them **first**, both in the input data `mydata` and correspondingly in the distribution vector `dist`. For example, `dist <- c("gaussian","gaussian", "poisson", "multinomial")`, and **not** `dist <- c("poisson", "gaussian","gaussian", "multinomial")` or `dist <- c("gaussian", "poisson", "gaussian", "multinomial")`

Examples

```
# sim_data comes with the iClusterVB package.
dat1 <- list(
  gauss_1 = sim_data$continuous1_data[c(1:20, 61:80, 121:140, 181:200), 1:75],
  gauss_2 = sim_data$continuous2_data[c(1:20, 61:80, 121:140, 181:200), 1:75],
  poisson_1 = sim_data$count_data[c(1:20, 61:80, 121:140, 181:200), 1:75])

dist <- c(
  "gaussian", "gaussian",
  "poisson")

# Note: `max_iter` is a time-intensive step.
# For the purpose of testing the code, use a small value (e.g. 10).
# For more accurate results, use a larger value (e.g. 200).

fit_iClusterVB <- iClusterVB(
  mydata = dat1,
  dist = dist,
```

```
  K = 4,
  initial_method = "VarSelLCM",
  VS_method = 1,
  max_iter = 10
)

# We can obtain a summary using the summary() function
summary(fit_iClusterVB)
```

---

laml *LAML (Acute Myeloid Leukemia) Data*

Description

This is a subset of the LAML (Acute Myeloid Leukemia) data (TCGA, 2013). The Acute Myeloid Leukemia (laml_tcga) datasets were download using the cBioPortal for Cancer Genomics tool (Cerami et al., 2012; Gao et al., 2013). The 170 samples with gene expression data and mutation data were included. Only a subset of the genes was selected, as desribed below. To access the data containing all the genes, please visit: https://github.com/AbdalkarimA/iClusterVB

Usage

```
data(laml)
```

Value

Within the data file, there is:

`laml.cli:`	A dataframe of clinical information for the 170 samples.
`laml.exp:`	A matrix of 170 samples and the gene expression values of the 500 genes chosen by Zainul Abidin and Westhead (2016) based on having the highest ranked-based coefficients of variation and standard deviation across the samples. Some names may have been updated or corrected from the supplementary material.
`laml.mut:`	A matrix of 170 samples and the mutation status of 156 genes that had >=2 mutations. 1 indicates the presence of mutation, and 0 indicates the absence of mutation.

References

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Zainul Abidin, F. N., & Westhead, D. R. (2017). Flexible model-based clustering of mixed binary and continuous data: application to genetic regulation and cancer. Nucleic acids research, 45(7), e53. https://doi.org/10.1093/nar/gkw1270

`piplot` *Generates a probability inclusion plot based on an iClusterVB object*

Description

Generates a probability inclusion plot based on an iClusterVB object

Usage

```
piplot(
  fit,
  plot_grid = TRUE,
  ylab = "Probability of Inclusion",
  title = NULL,
  ...
)
```

Arguments

`fit`	A fitted iClusterVB object.
`plot_grid`	LOGICAL. Whether to use the `plot_grid` function from the **cowplot** package. The default is TRUE.
`ylab`	The y-axis label. The default is "Probability of Inclusion".
`title`	The title of the plots. It can be a character vector or a single value. The default output is "View 1 - Distribution 1", ..., "View R - Distribution R".
`...`	Additional arguments to add to the `plot_grid` function.

Value

Returns a probability inclusion plot or plots.

Examples

```
# Setting up the data
dat1 <- list(
  gauss_1 = sim_data$continuous1_data[c(1:20, 61:80, 121:140, 181:200), 1:75],
  gauss_2 = sim_data$continuous2_data[c(1:20, 61:80, 121:140, 181:200), 1:75],
  poisson_1 = sim_data$count_data[c(1:20, 61:80, 121:140, 181:200), 1:75])


dist <- c(
  "gaussian", "gaussian",
  "poisson")

fit_iClusterVB <- iClusterVB(
  mydata = dat1,
  dist = dist,
  K = 4,
  initial_cluster= c(rep(1, 20), rep(2, 20), rep(3, 20), rep(4, 20)),
  VS_method = 1,
  max_iter = 20
)

piplot(fit_iClusterVB, plot_grid = FALSE)
```

`plot.iClusterVB` *Generic plot method for 'iClusterVB' objects*

Description

Generic plot method for 'iClusterVB' objects

Usage

```
## S3 method for class 'iClusterVB'
plot(x, ...)
```

Arguments

`x`	A fitted iClusterVB object.
`...`	Potential further arguments (unused)

Value

Returns an evidence lower bound (ELBO) plot and a barplot of cluster percentages.

Examples

```
# Setting up the data
dat1 <- list(
  gauss_1 = sim_data$continuous1_data[c(1:20, 61:80, 121:140, 181:200), 1:75],
  gauss_2 = sim_data$continuous2_data[c(1:20, 61:80, 121:140, 181:200), 1:75],
  poisson_1 = sim_data$count_data[c(1:20, 61:80, 121:140, 181:200), 1:75])


dist <- c(
  "gaussian", "gaussian",
  "poisson")

fit_iClusterVB <- iClusterVB(
  mydata = dat1,
  dist = dist,
  K = 4,
  initial_method = "VarSelLCM",
  VS_method = 1,
  max_iter = 25
)

plot(fit_iClusterVB)
```

`sim_data` *Simulated Dataset*

Description

The dataset consists of $N = 240$ individuals and $R = 4$ data views with different data types. Two of the data views are continuous, one is count, and one is binary. The *true* number of clusters was set to $K = 4$, and the cluster proportions were set at $\pi_1 = 0.25, \pi_2 = 0.25, \pi_3 = 0.25, \pi_4 = 0.25$, such that we have balanced cluster proportions. Each of the data views had $p_r = 500$ features, $r = 1, \ldots, 4$, but only 50, or 10%, were relevant features that contributed to the clustering, and the rest were noise features that did not contribute to the clustering. In total, there were $p = \sum_{r=1}^{4} = 2000$ features.

For data view 1 (continuous), relevant features were generated from the following normal distributions: $\text{N}(10, 1)$ for Cluster 1, $\text{N}(5, 1)$ for Cluster 2, $\text{N}(-5, 1)$ for Cluster 3, and $\text{N}(-10, 1)$ for Cluster 4, while noise features were generated from $\text{N}(0, 1)$. For data view 2 (continuous), relevant features were generated from the following normal distributions: $\text{N}(-10, 1)$ for Cluster 1, $\text{N}(-5, 1)$ for Cluster 2, $\text{N}(5, 1)$ for Cluster 3, and $\text{N}(10, 1)$ for Cluster 4, while noise features were generated from $\text{N}(0, 1)$. For data view 3 (binary), relevant features were generated from the following Bernoulli distributions: $\text{Bernoulli}(0.05)$ for Cluster 1, $\text{Bernoulli}(0.2)$ for Cluster 2, $\text{Bernoulli}(0.4)$ for Cluster 3, and $\text{Bernoulli}(0.6)$ for Cluster 4, while noise features were generated from $\text{Bernoulli}(0.1)$. For data view 4 (count), relevant features were generated from the following Poisson distributions: $\text{Poisson}(50)$ for Cluster 1, $\text{Poisson}(35)$ for Cluster 2, $\text{Poisson}(20)$ for Cluster 3, and $\text{Poisson}(10)$ for Cluster 4, while noise features were generated from $\text{Poisson}(2)$.

Usage

```
data(sim_data)
```

Format

A list containing four datasets, and other elements of interest.

`summary.iClusterVB` *Generic summary method for 'iClusterVB' objects*

Description

Generic summary method for 'iClusterVB' objects

Usage

```
## S3 method for class 'iClusterVB'
summary(object, rho = 0.5, ...)
```

Arguments

`object`	A fitted iClusterVB object.
`rho`	The minimum posterior inclusion probability of interest to count the number of features that are >= `rho`. Default is 0.5. Only works for VS_method = 1.
`...`	Potential further arguments

Value

Returns a summary list for an 'agnes' object.

Examples

```
# Setting up the data
dat1 <- list(
  gauss_1 = sim_data$continuous1_data[c(1:20, 61:80, 121:140, 181:200), 1:75],
  gauss_2 = sim_data$continuous2_data[c(1:20, 61:80, 121:140, 181:200), 1:75],
  poisson_1 = sim_data$count_data[c(1:20, 61:80, 121:140, 181:200), 1:75])

dist <- c(
  "gaussian", "gaussian",
  "poisson")

fit_iClusterVB <- iClusterVB(
  mydata = dat1,
  dist = dist,
  K = 4,
  initial_method = "VarSelLCM",
  VS_method = 1,
```

```
  max_iter = 25
)

## S3 method for class 'iClusterVB'
summary(fit_iClusterVB, rho = 0.75)
```

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