

Package ‘bootcluster’

July 22, 2025

Type Package

Title Bootstrapping Estimates of Clustering Stability

Version 0.4.2

Description Implementation of the bootstrapping approach for the estimation of clustering stability and its application in estimating the number of clusters, as introduced by Yu et al (2016) <doi:10.1142/9789814749411_0007>. Implementation of the non-parametric bootstrap approach to assessing the stability of module detection in a graph, the extension for the selection of a parameter set that defines a graph from data in a way that optimizes stability and the corresponding visualization functions, as introduced by Tian et al (2021) <doi:10.1002/sam.11495>. Implemented out-of-bag stability estimation function and k-select Smin-based k-selection function as introduced by Liu et al (2022) <doi:10.1002/sam.11593>. Implemented ensemble clustering method based-on k-means clustering method, spectral clustering method and hierarchical clustering method.

Depends R (>= 3.5.1)

Imports cluster, mclust (>= 5.0.0), flexclust, fpc, plyr, dplyr, doParallel, foreach, igraph (>= 1.2.0), compiler, stats, parallel, grid, grDevices, ggplot2, gridExtra, intergraph, GGally, network, kernlab, sna, progress

License GPL-2

Encoding UTF-8

LazyData true

RoxygenNote 7.3.2

NeedsCompilation no

Author Han Yu [aut],
Mingmei Tian [aut],
Tianmou Liu [aut, cre] (ORCID: <<https://orcid.org/0000-0003-3584-0483>>)

Maintainer Tianmou Liu <tianmouliu@outlook.com>

Repository CRAN

Date/Publication 2025-06-17 23:00:02 UTC

Contents

agreement	2
agreement_nk	3
analyze_moc_datasets	3
compare_moc_results	4
ensemble.cluster.multi	5
ensemble_cluster_multi_combinations	6
esembl.stability	8
k.select	9
k.select_ref	10
load_moc_datasets	11
min_agreement	12
network.stability	12
network.stability.output	14
ob.stability	15
plot_moc_grid	16
plot_moc_results	17
ref_dist	18
ref_dist_bin	19
ref_dist_pca	19
stability	20
threshold.select	21
wine	22
Index	24

agreement	<i>Calculate agreement between two clustering results</i>
-----------	---

Description

Calculate agreement between two clustering results

Usage

agreement(clst1, clst2)

Arguments

- | | |
|-------|--------------------------|
| clst1 | First clustering result |
| clst2 | Second clustering result |

Value

Vector of agreement values

agreement_nk	<i>Calculate agreement between two clustering results with known number of clusters</i>
--------------	---

Description

Calculate agreement between two clustering results with known number of clusters

Usage

```
agreement_nk(clst1, clst2, nk)
```

Arguments

clst1	First clustering result
clst2	Second clustering result
nk	Number of clusters

Value

Vector of agreement values

analyze_moc_datasets	<i>Multi-Method Ensemble Clustering Analysis for Multiple-Objective Clustering (MOC) Datasets</i>
----------------------	---

Description

Performs ensemble clustering analysis on multiple datasets using different clustering methods and compares their performance.

Usage

```
analyze_moc_datasets(  
  datasets,  
  selected,  
  n_ref = 3,  
  B = 100,  
  plot = TRUE,  
  plot_file = NULL  
)
```

Arguments

datasets	List of datasets to analyze
selected	Indices of datasets to analyze
n_ref	Number of reference distributions (default: 3)
B	Number of bootstrap samples (default: 100)
plot	Whether to generate plots (default: TRUE)
plot_file	Output file for plots (default: NULL)

Value

- A list containing:
 - results** Results for each dataset
 - ari_table** Adjusted Rand Index comparison table
 - runtime_table** Runtime comparison table
 - plots** List of generated plots if plot=TRUE

compare_moc_results	<i>Compare MOC Results</i>
---------------------	----------------------------

Description

Compare MOC Results

Usage

```
compare_moc_results(results, metric = "ari", plot = TRUE)
```

Arguments

results	Results from analyze_moc_datasets
metric	Metric to compare ("ari", "runtime", or "modularity")
plot	Whether to generate comparison plot (default: TRUE)

`ensemble.cluster.multi`*Multi-Method Ensemble Clustering with Graph-based Consensus*

Description

Implements ensemble clustering by combining multiple clustering methods (k-means, hierarchical, and spectral clustering) using a graph-based consensus approach.

Usage

```
ensemble.cluster.multi(  
  x,  
  k_km,  
  k_hc,  
  k_sc,  
  n_ref = 3,  
  B = 100,  
  hc.method = "ward.D",  
  dist_method = "euclidean"  
)
```

Arguments

<code>x</code>	data.frame or matrix where rows are observations and columns are features
<code>k_km</code>	number of clusters for k-means clustering
<code>k_hc</code>	number of clusters for hierarchical clustering
<code>k_sc</code>	number of clusters for spectral clustering
<code>n_ref</code>	number of reference distributions for stability assessment (default: 3)
<code>B</code>	number of bootstrap samples for stability estimation (default: 100)
<code>hc.method</code>	hierarchical clustering method (default: "ward.D")
<code>dist_method</code>	distance method for spectral clustering (default: "euclidean")

Details

This function implements a multi-method ensemble clustering approach that: 1. Applies multiple clustering methods (k-means, hierarchical, spectral) 2. Assesses stability of each clustering through bootstrapping 3. Constructs a weighted bipartite graph representing all clusterings 4. Uses fast greedy community detection for final consensus

Value

A list containing:

membership Final cluster assignments from ensemble consensus

k_consensus Number of clusters found in consensus
individual_results List of results from individual clustering methods
stability_measures Stability measures for each method
graph igraph object of the ensemble graph

Examples

```
data(iris)
df <- iris[,1:4]
result <- ensemble.cluster.multi(df, k_km=3, k_hc=3, k_sc=3)
plot(df[,1:2], col=result$membership, pch=16)
```

ensemble_cluster_multi_combinations

Multi-Method Ensemble Clustering with Multiple Stability Combinations

Description

Implements ensemble clustering using multiple methods for combining stability measures, generating separate consensus results for each combination method.

Usage

```
ensemble_cluster_multi_combinations(
  x,
  k_km,
  k_hc,
  k_sc,
  n_ref = 3,
  B = 100,
  hc.method = "ward.D",
  dist_method = "euclidean",
  alpha = 0.25
)
```

Arguments

x	data.frame or matrix where rows are observations and columns are features
k_km	number of clusters for k-means clustering
k_hc	number of clusters for hierarchical clustering
k_sc	number of clusters for spectral clustering
n_ref	number of reference distributions for stability assessment (default: 3)

B	number of bootstrap samples for stability estimation (default: 100)
hc.method	hierarchical clustering method (default: "ward.D")
dist_method	distance method for spectral clustering (default: "euclidean")
alpha	weight for weighted combination (default: 0.5)

Value

A list containing results for each combination method:

product Results using product combination
arithmetic Results using arithmetic mean
geometric Results using geometric mean
harmonic Results using harmonic mean
weighted Results using weighted combination

Each method's results contain:

fastgreedy Results from fast greedy community detection
metis Results from METIS (leading eigenvector) community detection
hmetis Results from hMETIS (Louvain) community detection
graph igraph object of the ensemble graph
edge_weights Edge weights of the graph
individual_results Results from individual clustering methods
stability_measures Stability measures
incidence_matrix Incidence matrix used for graph construction

Each community detection method's results contain:

membership Final cluster assignments
k_consensus Number of clusters found

The function also returns comparison statistics for each community detection method:

comparison\$fastgreedy Comparison stats for fast greedy results
comparison\$metis Comparison stats for METIS results
comparison\$hmetis Comparison stats for hMETIS results

Examples

```
data(iris)
df <- iris[,1:4]
results <- ensemble_cluster_multi_combinations(df, k_km=3, k_hc=3, k_sc=3)
# Compare cluster assignments from different methods
table(product = results$product$membership,
      arithmetic = results$arithmetic$membership)
```

esembl.stability	<i>Estimate the stability of a clustering based on non-parametric bootstrap out-of-bag scheme, with option for subsampling scheme</i>
------------------	---

Description

Estimate the stability of a clustering based on non-parametric bootstrap out-of-bag scheme, with option for subsampling scheme

Usage

```
esembl.stability(
  x,
  k,
  scheme = "kmeans",
  B = 100,
  hc.method = "ward.D",
  cut_ratio = 0.5,
  dist_method = "euclidean"
)
```

Arguments

x	data.frame of the data set where rows are observations and columns are features
k	number of clusters for which to estimate the stability
scheme	clustering method to use ("kmeans", "hc", or "spectral")
B	number of bootstrap re-samples
hc.method	hierarchical clustering method (default: "ward.D")
cut_ratio	ratio for subsampling (default: 0.5)
dist_method	distance method for spectral clustering (default: "euclidean")

Details

This function estimates the stability through out-of-bag observations. It estimates the stability at the (1) observation level, (2) cluster level, and (3) overall.

Value

membership vector of membership for each observation from the reference clustering

obs_wise vector of estimated observation-wise stability

clust_wise vector of estimated cluster-wise stability

overall numeric estimated overall stability

Smin numeric estimated Smin through out-of-bag scheme

Author(s)

Tianmou Liu

Examples

```
set.seed(123)
data(iris)
df <- iris[,1:4]
result <- esmbl.stability(df, k=3, scheme="kmeans")
```

k.select

*Estimate number of clusters***Description**

Estimate number of clusters by bootstrapping stability

Usage

```
k.select(x, range = 2:7, B = 20, r = 5, threshold = 0.8, scheme_2 = TRUE)
```

Arguments

x	a data.frame of the data set
range	a vector of integer values, of the possible numbers of clusters k
B	number of bootstrap re-samplings
r	number of runs of k-means
threshold	the threshold for determining k
scheme_2	logical TRUE if scheme 2 is used, FALSE if scheme 1 is used

Details

This function estimates the number of clusters through a bootstrapping approach, and a measure S_{min} , which is based on an observation-wise similarity among clusterings. The number of clusters k is selected as the largest number of clusters, for which the S_{min} is greater than a threshold. The threshold is often selected between 0.8 ~ 0.9. Two schemes are provided. Scheme 1 uses the clustering of the original data as the reference for stability calculations. Scheme 2 searches across the clustering samples that gives the most stable clustering.

Value

profile a vector of S_{min} measures for determining k
 k integer estimated number of clusters

Author(s)

Han Yu

References

Bootstrapping estimates of stability for clusters, observations and model selection. Han Yu, Brian Chapman, Arianna DiFlorio, Ellen Eischen, David Gotz, Matthews Jacob and Rachael Hageman Blair.

Examples

```
set.seed(1)
data(wine)
x0 <- wine[,2:14]
x <- scale(x0)
k.select(x, range = 2:10, B=20, r=5, scheme_2 = TRUE)
```

k.select_ref	<i>Estimate number of clusters</i>
--------------	------------------------------------

Description

Estimate number of clusters by bootstrapping stability

Usage

```
k.select_ref(df, k_range = 2:7, n_ref = 5, B = 100, B_ref = 50, r = 5)
```

Arguments

df	data.frame of the input dataset
k_range	integer valued vector of the numbers of clusters k to be tested upon
n_ref	number of reference distribution to be generated
B	number of bootstrap re-samples
B_ref	number of bootstrap resamples for the reference distributions
r	number of runs of k-means

Details

This function uses the out-of-bag scheme to estimate the number of clusters in a dataset. The function calculate the Smin of the dataset and at the same time, generate a reference dataset with the same range as the original dataset in each dimension and calculate the Smin_ref. The differences between Smin and Smin_ref at each k, Smin_diff(k), is taken into consideration as well as the standard deviation of the differences. We choose the k to be the argmax of (Smin_diff(k) - (Smin_diff(k+1) + (Smin_diff(k+1)))). If Smin_diff(k) less than 0.1 for all k in k_range, we say k = 1

Value

profile vector of $(S_{min_diff}(k) - (S_{min_diff}(k+1) + se(S_{min_diff}(k+1))))$ measures for researchers's inspection

k estimated number of clusters

Author(s)

Tianmou Liu

References

Bootstrapping estimates of stability for clusters, observations and model selection. Han Yu, Brian Chapman, Arianna DiFlorio, Ellen Eischen, David Gotz, Matthews Jacob and Rachael Hageman Blair.

Examples

```
set.seed(1)
data(iris)
df <- data.frame(iris[,1:4])
df <- scale(df)
k.select_ref(df, k_range = 2:7, n_ref = 5, B=500, B_ref = 500, r=5)
```

load_moc_datasets

Load Multiple-Objective Clustering (MOC) Datasets

Description

Loads and processes datasets for multiple-objective clustering analysis. The function loads CSV files from a specified directory and processes them by removing NA columns.

Usage

```
load_moc_datasets(data_dir = getwd())
```

Arguments

data_dir Directory containing the CSV datasets (default: current working directory)

Value

A list containing:

datasets Named list of processed datasets

Examples

```
## Not run:
# Load datasets
result <- load_moc_datasets("path/to/MOC_Data")

# Access a specific dataset
spiral <- result$datasets$Spiral

## End(Not run)
```

min_agreement	<i>Calculate minimum agreement across clusters</i>
---------------	--

Description

Calculates the minimum average agreement value across all clusters

Usage

```
min_agreement(clst, agrmt)
```

Arguments

clst	clustering result vector
agrm	agreement values vector

Value

minimum average agreement value across clusters

network.stability	<i>Estimate of detect module stability</i>
-------------------	--

Description

Estimate of detect module stability

Usage

```
network.stability(
  data.input,
  threshold,
  B = 20,
  cor.method,
  large.size,
  PermuNo,
  scheme_2 = FALSE
)
```

Arguments

<code>data.input</code>	a <code>data.frame</code> of the data set where the rows are observations and columns are covariates
<code>threshold</code>	a numeric number of threshold for correlation matrix
<code>B</code>	number of bootstrap re-samplings
<code>cor.method</code>	the correlation method applied to the data set, three method are available: "pearson", "kendall", "spearman".
<code>large.size</code>	the smallest set of modules, the <code>large.size=0</code> is recommended to use right now.
<code>PermuNo</code>	number of random graphs for null
<code>scheme_2</code>	logical TRUE if scheme 2 is used, FALSE if scheme 1 is used. Right now, only FALSE is recommended.

Details

This function estimates the modules' stability through bootstrapping approach for the given threshold. The approach to stability estimation is to compare the module composition of the reference correlation graph to the various bootstrapped correlation graphs, and to assess the stability at the (1) node-level, (2) module-level, and (3) overall.

Value

`stabilityresult` a list of result for nodes-wise stability
`modularityresult` list of modularity information with the given threshold
`jaccardresult` list estimated unconditional observed stability and the estimates of expected stability under the null
`originalinformation` list information for original data, `igraph` object and adjacency matrix constructed with the given threshold

Author(s)

Mingmei Tian

References

A framework for stability-based module detection in correlation graphs. Mingmei Tian, Rachael Hageman Blair, Lina Mu, Matthew Bonner, Richard Browne and Han Yu.

Examples

```
set.seed(1)
data(wine)
x0 <- wine[1:50,]

mytest<-network.stability(data.input=x0,threshold=0.7, B=20,
cor.method='pearson',large.size=0,
PermuNo = 10,
```

```
scheme_2 = FALSE)
```

```
network.stability.output
```

Plot method for objects from threshold.select

Description

Plot method for objects from threshold.select

Usage

```
network.stability.output(input, optimal.only = FALSE)
```

Arguments

input	a list of results from function threshold.select
optimal.only	a logical value indicating whether only plot the network with optimal threshold or not. The default is False, generating all network figures with a large number of nodes could take some time.

Details

network.stability.output is used to generate a series of network plots based on the given threshold.seq, where the nodes are colored by the level of stability. The network with optimal threshold value selected by function threshold.select is colored as red.

Value

Plot of network figures

Author(s)

Mingmei Tian

References

A framework for stability-based module detection in correlation graphs. Mingmei Tian, Rachael Hageman Blair, Lina Mu, Matthew Bonner, Richard Browne and Han Yu.

Examples

```
set.seed(1)
data(wine)
x0 <- wine[1:50,]

mytest<-threshold.select(data.input=x0,threshold.seq=seq(0.1,0.5,by=0.05), B=20,
cor.method='pearson',large.size=0,
PermuNo = 10,
no_cores=1,
scheme_2 = FALSE)
network.stability.output(mytest)
```

ob.stability	<i>Estimate the stability of a clustering based on non-parametric bootstrap out-of-bag scheme, with option for subsampling scheme</i>
--------------	---

Description

Estimate the stability of a clustering based on non-parametric bootstrap out-of-bag scheme, with option for subsampling scheme

Usage

```
ob.stability(x, k, B = 500, r = 5, subsample = FALSE, cut_ratio = 0.5)
```

Arguments

x	data.frame of the data set where the rows as observations and columns as dimensions of features
k	number of clusters for which to estimate the stability
B	number of bootstrap re-samples
r	integer parameter in the kmeansCBI() funtion
subsample	logical parameter to use the subsampling scheme option in the resampling process (instead of bootstrap)
cut_ratio	numeric parameter between 0 and 1 for subsampling scheme training set ratio

Details

This function estimates the stability through out-of-bag observations It estimate the stability at the (1) observation level, (2) cluster level, and (3) overall.

Value

membership vector of membership for each observation from the reference clustering

obs_wise vector of estimated observation-wise stability

clust_wise vector of estimated cluster-wise stability

overall numeric estimated overall stability

Smin numeric estimated Smin through out-of-bag scheme

Author(s)

Tianmou Liu

References

Bootstrapping estimates of stability for clusters, observations and model selection. Han Yu, Brian Chapman, Arianna DiFlorio, Ellen Eischen, David Gotz, Matthews Jacob and Rachael Hageman Blair.

Examples

```
set.seed(123)
data(iris)
df <- data.frame(iris[,1:4])
# You can choose to scale df before clustering by
# df <- scale(df)
ob.stability(df, k = 2, B=500, r=5)
```

plot_moc_grid

Create a Grid Plot of MOC Results

Description

Creates a grid plot with datasets as rows and clustering methods as columns. This function is designed to visualize multiple datasets and methods in a single plot.

Usage

```
plot_moc_grid(
  results,
  dataset_names = NULL,
  methods = c("kmeans", "hierarchical", "spectral", "fastgreedy", "metis", "hmetis"),
  plot_file = NULL,
  format = "pdf",
  mar = c(2, 2, 2, 1),
  cex = 0.7,
```

```

    point_size = 0.8,
    family = "serif",
    label_style = TRUE,
    maintain_aspect_ratio = TRUE
  )

```

Arguments

results	Results from analyze_moc_datasets
dataset_names	Names of datasets to plot (default: all datasets in results)
methods	Methods to plot (default: all available methods)
plot_file	Output file for plots (default: NULL)
format	Output format, either "pdf" or "eps" (default: "pdf")
mar	Margins for plots (default: c(2, 2, 2, 1))
cex	Text size multiplier (default: 0.7)
point_size	Point size for scatter plots (default: 0.8)
family	Font family (default: "serif" for Times New Roman)
label_style	Whether to add row/column labels (default: TRUE)
maintain_aspect_ratio	Whether to maintain aspect ratio in PDF (default: TRUE)

Value

Invisibly returns the layout information

plot_moc_results	<i>Plot MOC Results</i>
------------------	-------------------------

Description

Plot MOC Results

Usage

```

plot_moc_results(
  results,
  dataset_names,
  methods = c("kmeans", "hierarchical", "spectral", "fastgreedy", "metis", "hmetis"),
  plot_file = NULL,
  max_plots_per_page = 12,
  mar = c(2, 2, 2, 1)
)

```

Arguments

results	Results from analyze_moc_datasets
dataset_names	Name or vector of names of datasets to plot
methods	Methods to plot (default: c("fastgreedy", "metis", "hmetis"))
plot_file	Output file for plots (default: NULL)
max_plots_per_page	Maximum number of plots per page (default: 12)
mar	Margins for plots (default: c(2, 2, 2, 1))

ref_dist	<i>Generate reference distribution for stability assessment</i>
----------	---

Description

Generates a reference distribution by sampling from uniform distributions with ranges determined by the original data.

Usage

```
ref_dist(df)
```

Arguments

df	data.frame or matrix of the original dataset
----	--

Details

Generate Reference Distribution

Value

A scaled matrix containing the reference distribution

Examples

```
data(iris)
df <- iris[,1:4]
ref <- ref_dist(df)
```

ref_dist_bin	<i>Generate reference distribution for binary data</i>
--------------	--

Description

Generates a reference distribution by randomly permuting each column of the original binary dataset.

Usage

```
ref_dist_bin(df)
```

Arguments

df	data.frame or matrix of the original binary dataset
----	---

Details

Generate Binary Reference Distribution

Value

A matrix containing the permuted binary reference distribution

Examples

```
binary_data <- matrix(sample(0:1, 100, replace=TRUE), ncol=5)
ref <- ref_dist_bin(binary_data)
```

ref_dist_pca	<i>Generate PCA-based reference distribution</i>
--------------	--

Description

Generates a reference distribution in PCA space by sampling from uniform distributions with ranges determined by the PCA-transformed data.

Usage

```
ref_dist_pca(df)
```

Arguments

df	data.frame or matrix of the original dataset
----	--

Details

Generate Reference Distribution using PCA

Value

A scaled matrix containing the reference distribution in PCA space

Examples

```
data(iris)
df <- iris[,1:4]
ref <- ref_dist_pca(df)
```

stability

Estimate clustering stability of k-means

Description

Estimate of k-means bootstrapping stability

Usage

```
stability(x, k, B = 20, r = 5, scheme_2 = TRUE)
```

Arguments

x	a data.frame of the data set
k	a integer number of clusters
B	number of bootstrap re-samplings
r	number of runs of k-means
scheme_2	logical TRUE if scheme 2 is used, FALSE if scheme 1 is used

Details

This function estimates the clustering stability through bootstrapping approach. Two schemes are provided. Scheme 1 uses the clustering of the original data as the reference for stability calculations. Scheme 2 searches across the clustering samples that gives the most stable clustering.

Value

membership a vector of membership for each observation from the reference clustering
 obs_wise vector of estimated observation-wise stability
 overall numeric estimated overall stability

Author(s)

Han Yu

References

Bootstrapping estimates of stability for clusters, observations and model selection. Han Yu, Brian Chapman, Arianna DiFlorio, Ellen Eischen, David Gotz, Matthews Jacob and Rachael Hageman Blair.

Examples

```
set.seed(1)
data(wine)
x0 <- wine[,2:14]
x <- scale(x0)
stability(x, k = 3, B=20, r=5, scheme_2 = TRUE)
```

threshold.select	<i>Estimate of the overall Jaccard stability</i>
------------------	--

Description

Estimate of the overall Jaccard stability

Arguments

data.input	a data.frame of the data set where the rows are observations and columns are covariates
threshold.seq	a numeric sequence of candidate threshold
B	number of bootstrap re-samplings
cor.method	the correlation method applied to the data set,three method are available: "pearson", "kendall", "spearman".
large.size	the smallest set of modules, the large.size=0 is recommended to use right now.
PermuNo	number of random graphs for the estimation of expected stability
no_cores	a interger number of CPU cores on the current host (This function can't not be used yet).

Details

threshold.select is used to estimate of the overall Jaccard stability from a sequence of given threshold candidates, threshold.seq.

Value

`stabilityresult` a list of result for nodes-wise stability
`modularityresult` a list of modularity information with each candidate threshold
`jaccardresult` a list estimated unconditional observed stability and the estimates of expected stability under the nul
`originalinformation` a list information for original data, igraph object and adjacency matrix constructed with each candidate threshold
`threshold.seq` a list of candidate threshold given to the function

Author(s)

Mingmei Tian

References

A framework for stability-based module detection in correlation graphs. Mingmei Tian, Rachael Hageman Blair, Lina Mu, Matthew Bonner, Richard Browne and Han Yu.

Examples

```

set.seed(1)
data(wine)
x0 <- wine[1:50,]

mytest<-threshold.select(data.input=x0,threshold.seq=seq(0.5,0.8,by=0.05), B=20,
cor.method='pearson',large.size=0,
PermuNo = 10,
no_cores=1,
scheme_2 = FALSE)

```

wine

Wine Data Set

Description

These data are the results of a chemical analysis of wines grown in the same region in Italy but derived from three different cultivars. The analysis determined the quantities of 13 constituents found in each of the three types of wines.

Usage

```
data(wine)
```

Format

The data set wine contains a data.frame of 14 variables. The first variable is the types of wines. The other 13 variables are quantities of the constituents.

References

<https://archive.ics.uci.edu/ml/datasets/wine>

Index

agreement, [2](#)
agreement_nk, [3](#)
analyze_moc_datasets, [3](#)

compare_moc_results, [4](#)

ensemble.cluster.multi, [5](#)
ensemble_cluster_multi_combinations, [6](#)
esmb1.stability, [8](#)

k.select, [9](#)
k.select_ref, [10](#)

load_moc_datasets, [11](#)

min_agreement, [12](#)

network.stability, [12](#)
network.stability.output, [14](#)

ob.stability, [15](#)

plot_moc_grid, [16](#)
plot_moc_results, [17](#)

ref_dist, [18](#)
ref_dist_bin, [19](#)
ref_dist_pca, [19](#)

stability, [20](#)

threshold.select, [21](#)

wine, [22](#)