

Package: MergeKmeans (via r-universe)

July 19, 2026

Type Package

Title Clustering Large Datasets by Merging K-Means Solutions

Version 0.2.0

Description Fast clustering of large datasets by hierarchically merging components of a K-means solution based on the pairwise overlap between the Gaussian mixture components implied by the K-means partition, as proposed by Melnykov and Michael (2020) <[doi:10.1007/s00357-019-09314-8](https://doi.org/10.1007/s00357-019-09314-8)>. Implements the DEMP-K merging algorithm with single, Ward's, average, and complete linkages, the overlap map display for selecting the number of clusters, four K-means variants corresponding to Gaussian mixtures with spherical or elliptical, homoscedastic or heteroscedastic components, and a tool for selecting the number of K-means components.

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Encoding UTF-8

Imports stats, graphics, grDevices, utils, parallel

Suggests CompQuadForm, MixSim, mclust, broom, tibble, testthat (>= 3.0.0), knitr, rmarkdown

VignetteBuilder knitr

Config/testthat/edition 3

RoxygenNote 7.3.3

NeedsCompilation no

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Repository <https://cran.r-universe.dev>

Date/Publication 2026-07-19 13:20:07 UTC

RemoteUrl <https://github.com/cran/MergeKmeans>

RemoteRef HEAD

RemoteSha 6b68405dde09dc6d8dac6bf115111f13ff4d4dba

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chooseK	<i>Choose the number of K-means components</i>
---------	--

Description

Computes the proportion of the total variability explained by the between-cluster variability (SSB/SSTO) of K-means solutions over a grid of K values, plots it, and reports a recommended K for `MergeKmeans()`.

Usage

```
chooseK(  
  x,  
  K = seq(5, 50, by = 5),  
  nstart = 10,  
  iter.max = 100,  
  plot = TRUE,  
  cores = 1,  
  ...  
)
```

Arguments

x	numeric data matrix or data frame with observations in rows.
K	integer vector of candidate numbers of components.
nstart	number of K-means restarts per candidate.
iter.max	maximum number of K-means iterations.
plot	logical; plot SSB/SSTO against K with the recommendation marked.
cores	number of CPU cores used to evaluate the grid in parallel (POSIX systems only).
...	further arguments passed to <code>stats::kmeans()</code> .

Details

Following Melnykov and Michael (2020), a suitable number of components is found at or somewhat *beyond* the elbow of the curve — the point at which the increase in the explained proportion becomes marginal. Over-estimating K is safe (the merging procedure is robust to it), but K must exceed the number of clusters sought: setting K equal to the anticipated cluster count defeats the merging step. The reported recommendation is therefore one grid step beyond the detected elbow.

Value

Invisibly, a data frame with columns `K` and `ssb.ssto`, with the recommended K in `attr(, "recommended")`.

References

Melnykov, V. and Michael, S. (2020) Clustering large datasets by merging K-means solutions. *Journal of Classification*, 37, 97-123. doi:[10.1007/s00357019093148](https://doi.org/10.1007/s00357019093148)

See Also

[MergeKmeans\(\)](#)

Examples

```
set.seed(5)
x <- rbind(matrix(rnorm(400), ncol = 2),
             matrix(rnorm(400, mean = 5), ncol = 2))
out <- chooseK(x, K = 2:12, nstart = 5)
attr(out, "recommended")
```

MergeKmeans

Clustering by merging K-means solutions (DEMP-K)

Description

Fits the DEM-P-K clustering procedure of Melnykov and Michael (2020). A K-means solution with K components (chosen larger than the anticipated number of clusters) is interpreted as a Gaussian mixture fitted by the classification EM algorithm; the pairwise overlap between all component pairs is computed in closed form; and components are merged by hierarchical clustering with 1 - overlap as the dissimilarity. The merge tree is cut at a requested number of clusters G, at an overlap threshold `omega.star`, or automatically (`G = "auto"`).

Usage

```
MergeKmeans(
  x,
  K = NULL,
  G = NULL,
  omega.star = NULL,
```

```

variant = c("HoSC", "HoEC", "HeSC", "HeEC"),
linkage = NULL,
nstart = 10,
iter.max = 100,
cem.iter.max = 50,
init = c("kmeans++", "random"),
start = NULL,
cores = 1,
keep.data = TRUE,
...
)

```

Arguments

<code>x</code>	numeric data matrix or data frame with observations in rows.
<code>K</code>	number of K-means components; choose it comfortably <i>larger</i> than the number of clusters <code>G</code> you expect, so that small spherical components can fill clusters of arbitrary shape (this is the opposite of the <code>centers</code> argument of <code>stats::kmeans()</code> , which is the final cluster count). If <code>NULL</code> (default), <code>K</code> is selected automatically with <code>chooseK()</code> and reported in a message.
<code>G</code>	requested number of clusters after merging, between 1 and <code>K</code> , or "auto" to cut at the largest gap (on the log scale) in the single-linkage merge sequence of the overlap matrix. The automatic suggestion can only return values in 2: (<code>K</code> -1): it cannot detect the single-cluster case (use <code>recut(fit, G = 1)</code> explicitly), and on structureless data it can suggest a large spurious value - always confirm with the overlap map.
<code>omega.star</code>	overlap threshold in (0, 1): merging stops when no pair of merged groups attains this overlap. Supply at most one of <code>G</code> and <code>omega.star</code> . Not meaningful with Ward's linkage.
<code>variant</code>	K-means variant (case-insensitive; aliases in Details).
<code>linkage</code>	linkage for the hierarchical merging, passed to <code>stats::hclust()</code> : one of "ward.D", "single", "average", "complete". The default (<code>NULL</code>) uses "ward.D", except for univariate data where "single" is used; see Details.
<code>nstart</code>	number of K-means restarts.
<code>iter.max</code>	maximum number of K-means iterations.
<code>cem.iter.max</code>	maximum number of classification EM iterations for the non-spherical variants.
<code>init</code>	initialization of the K-means restarts: "kmeans++" (default; Arthur and Vassilvitskii, 2007) or "random" (the <code>stats::kmeans()</code> default seeding).
<code>start</code>	optional precomputed partition to be merged instead of running K-means: an object of class "kmeans", a ClusterR-style list with a <code>clusters</code> element, a list with a <code>cluster</code> element, or a bare integer vector of component labels. <code>K</code> , <code>init</code> , and <code>nstart</code> are then ignored. The supplied labels are kept as is (component means are recomputed from the data), so <code>predict.MergeKmeans()</code> - which assigns by nearest component - reproduces them only if the supplied partition is itself nearest-center consistent.

cores	number of CPU cores for the K-means restarts (forked via parallel ; POSIX systems only, ignored on Windows). With cores > 1 results are not reproducible by <code>set.seed()</code> unless <code>RNGkind("L'Ecuyer-CMRG")</code> is set.
keep.data	logical; store the data in the returned object (needed only for <code>plot(..., what = "classification")</code> without a data argument). Set to FALSE for very large datasets.
...	further arguments passed to <code>stats::kmeans()</code> .

Details

Four variants of K-means are supported, each corresponding to a Gaussian mixture with specific restrictions (Melnykov and Michael, 2020, Section 3 and Appendix A):

- "HoSC" (default; alias "spherical"): homoscedastic spherical components - the traditional K-means algorithm based on Euclidean distances. The fastest variant and the one recommended for large datasets.
- "HoEC" (alias "elliptical"): homoscedastic elliptical components - K-means with Mahalanobis distances and a common covariance matrix.
- "HeSC" (alias "spherical-unequal"): heteroscedastic spherical components - per-component spherical variances.
- "HeEC" (alias "elliptical-unequal"): heteroscedastic elliptical components - unrestricted per-component covariance matrices (requires the **CompQuadForm** package for the overlap computation).

Variant names are matched case-insensitively. The non-spherical variants are initialized from the K-means partition and refined by classification EM iterations.

The choice of linkage should be driven by the cluster characteristics sought: single linkage is appropriate for detecting well-separated clusters of arbitrary shape, while Ward's linkage (`"ward.D"`, the default for $p \geq 2$) targets compact clusters. Two situations where Ward's linkage is unreliable and single linkage should be preferred: univariate data (the components form a chain in which only adjacent pairs overlap, so the default there is `"single"`), and severely unequal cluster sizes (the homoscedastic overlap does not weight components by mass, and Ward merges can then cross a genuine gap). When clusters are genuinely overlapping *Gaussian* ellipsoids, classical model-based clustering (e.g. **mclust**) remains the better tool; DEMP-K is at its best for non-Gaussian or arbitrarily shaped clusters and for sample sizes where model-based clustering is impractical.

Robustness limits worth knowing (established by simulation): single linkage can chain two clusters together through even small amounts of uniform background contamination – the breakdown level depends on the geometry, with failures observed between 1\ Ward's linkage was stable to at least 10\ heavy-tailed clusters (e.g. multivariate t with 1-2 degrees of freedom, or strong exponential tails) create bridge points that defeat overlap-based merging - "skewed" clusters are handled well, but "heavy-tailed" ones are not. The heteroscedastic variants ("HeSC", "HeEC") inherit unstable fixed points from their implied mixing proportions and may drop components or stop at the last stable iteration (with a warning) for larger p or K ; "HoSC" is the robust default.

Like K-means itself, the component solution depends on the scaling of the variables; consider standardizing (e.g. `scale(x)`) when variables are measured on very different scales. The merging step is fairly robust to scaling provided K is large enough.

For very large datasets the K-means step is the only material cost (the merging operates on the $K \times K$ overlap matrix). Two escape hatches are provided: `cores` forks the restarts on POSIX systems, and `start` accepts a partition computed by any external engine - for example `ClusterR::MiniBatchKmeans + predict, biganalytics::bigkmeans()`, or a previous `stats::kmeans()` run - so that `MergeKmeans()` only performs the merging. Component means are recomputed from the data, so only the labels of the supplied partition are used. The default Hartigan-Wong algorithm may emit "Quick-TRANSfer" warnings on some starts for very large n ; results are unaffected, but `algorithm = "MacQueen"` can be passed through `...` to silence them.

If neither `G` nor `omega.star` is supplied, the fit is returned uncut and a message reports the number of clusters suggested by the largest gap in the merge heights: inspect the overlap map with `plot(fit, what = "overlap")` and then call `recut()`. `G = "auto"` accepts that suggestion directly. The threshold `omega.star` is interpretable as a minimum pairwise overlap for merging only with single, average, or complete linkage, and is therefore not accepted with Ward's linkage.

Value

An object of class "MergeKmeans": a list with components

`cluster` integer vector of final cluster labels (NULL if the tree has not been cut).

`G` number of clusters after merging.

`components` integer vector of K-means component labels.

`component.map` integer vector mapping each component to its merged cluster.

`K` effective number of components.

`centers` $K \times p$ matrix of component means.

`cov` estimated covariance parameter(s); form depends on the variant.

`tau` mixing proportions implied by the variant.

`overlap` $K \times K$ matrix of pairwise overlaps.

`tree` the merge tree, an `stats::hclust` object.

`variant, linkage` the settings used.

`kmeans` the underlying `stats::kmeans()` fit (NULL when `start` was supplied).

`cem` iteration details for non-spherical variants, or NULL.

`data` the data matrix if `keep.data = TRUE`, else NULL.

References

Melnykov, V. and Michael, S. (2020) Clustering large datasets by merging K-means solutions. *Journal of Classification*, 37, 97-123. doi:10.1007/s00357019093148

Arthur, D. and Vassilvitskii, S. (2007) k-means++: the advantages of careful seeding. *Proceedings of SODA 2007*, 1027-1035.

See Also

`recut()`, `chooseK()`, `overlap_map()`, `pairwise_overlap()`, `predict.MergeKmeans()`

Examples

```
## two well-separated half-circular clusters
set.seed(7)
th <- runif(500, 0, pi)
x <- rbind(
  cbind(cos(th[1:250]), sin(th[1:250])) + matrix(rnorm(500, 0, 0.1), 250),
  cbind(1 - cos(th[251:500]), 0.4 - sin(th[251:500])) +
    matrix(rnorm(500, 0, 0.1), 250))
fit <- MergeKmeans(x, K = 10, G = 2, linkage = "single", nstart = 20)
table(fit$cluster, rep(1:2, each = 250))
plot(fit, what = "overlap")

## automatic G, and merging a partition computed elsewhere
fit2 <- MergeKmeans(x, K = 10, G = "auto", linkage = "single")
km <- kmeans(x, 10, nstart = 20)
fit3 <- MergeKmeans(x, start = km, G = 2, linkage = "single")
```

MergeKmeans-tidiers	<i>Broom tidiers for MergeKmeans fits</i>
---------------------	---

Description

Methods for the **broom** generics, registered when **broom** is loaded: `tidy()` returns one row per K-means component (its merged cluster, size, and center coordinates), `glance()` returns a one-row model summary, and `augment()` appends `.component` and `.cluster` columns to the data.

Usage

```
## S3 method for class 'MergeKmeans'
tidy(x, ...)

## S3 method for class 'MergeKmeans'
glance(x, ...)

## S3 method for class 'MergeKmeans'
augment(x, data = NULL, ...)
```

Arguments

<code>x</code>	a "MergeKmeans" object.
<code>...</code>	ignored.
<code>data</code>	the original data, for <code>augment()</code> ; defaults to the data stored in the fit.

Value

A data frame (a tibble when available): per-component rows for `tidy()`, a single row for `glance()`, and data plus `.component` and `.cluster` columns for `augment()`.

Examples

```
set.seed(6)
x <- rbind(matrix(rnorm(200), ncol = 2),
             matrix(rnorm(200, mean = 6), ncol = 2))
fit <- MergeKmeans(x, K = 6, G = 2, linkage = "single", nstart = 5)
if (requireNamespace("broom", quietly = TRUE)) {
  broom::tidy(fit)
  broom::glance(fit)
  head(broom::augment(fit, x))
}
```

overlap_map

Overlap map display

Description

Draws the overlap map of Melnykov and Michael (2020, Section 3.3): a lower-triangular heat map of all pairwise component overlaps, with components arranged so that strongly overlapping components are adjacent. Cells range from pale yellow (low overlap) to dark red (high overlap). The detached bottom row summarizes each column by its darkest hue: groups of adjacent dark cells indicate components that model a common cluster, while pale cells mark gaps between well-separated clusters, making the map an intuitive device for choosing the number of clusters.

Usage

```
overlap_map(
  omega,
  order = TRUE,
  zlim = NULL,
  col = NULL,
  legend = TRUE,
  main = "Overlap map",
  cex.axis = 0.8
)
```

Arguments

omega	a symmetric matrix of pairwise overlaps, typically the overlap entry of a MergeKmeans() fit.
order	TRUE (default) to order components by the algorithm described above, FALSE to keep the original order, or an integer permutation of 1:K.
zlim	numeric range mapped onto the color scale; defaults to the range of the off-diagonal overlaps.
col	vector of colors for the scale; defaults to a yellow-to-red ramp.
legend	logical; draw the color legend.
main	plot title.
cex.axis	expansion factor for the component labels.

Details

Components are ordered as in the paper: the first two are the pair with the highest overlap, and each subsequent component is the one with the highest overlap with any component already displayed.

Value

Invisibly, the integer ordering of the components used in the display.

References

Melnykov, V. and Michael, S. (2020) Clustering large datasets by merging K-means solutions. *Journal of Classification*, 37, 97-123. doi:10.1007/s00357019093148

See Also

`MergeKmeans()`, `plot.MergeKmeans()`

Examples

```
set.seed(2)
x <- rbind(matrix(rnorm(300, 0, 1), ncol = 2),
             matrix(rnorm(300, 7, 1), ncol = 2))
fit <- MergeKmeans(x, K = 8, linkage = "single")
overlap_map(fit$overlap)
```

pairwise_overlap	<i>Pairwise overlap between Gaussian components</i>
------------------	---

Description

Computes the matrix of pairwise overlaps between Gaussian mixture components, where the overlap between components k and k' is defined as the sum of the two misclassification probabilities $\omega_{k|k'} = \omega_{k'|k} + \omega_{k|k'}$ (Maitra and Melnykov, 2010). The covariance structure is inferred from the form of cov:

Usage

```
pairwise_overlap(centers, cov, tau = NULL, lim = 50000, acc = 1e-06)
```

Arguments

centers	numeric matrix of component means with one row per component ($K \times p$).
cov	covariance specification; see Details.
tau	optional vector of K mixing proportions (homoscedastic cases only); defaults to equal proportions.
lim, acc	accuracy settings passed to <code>CompQuadForm::davies()</code> for the heteroscedastic elliptical case.

Details

- a single number: homoscedastic spherical components $\Sigma_k = \sigma^2 I$ ("HoSC"),
- a $p \times p$ matrix: homoscedastic elliptical components $\Sigma_k = \Sigma$ ("HoEC"),
- a vector of length K : heteroscedastic spherical components $\Sigma_k = \sigma_k^2 I$ ("HeSC"),
- a $p \times p \times K$ array: heteroscedastic elliptical components ("HeEC").

For the homoscedastic cases the mixing proportions τ may be supplied (equal proportions by default). For the heteroscedastic cases the mixing proportions implied by the corresponding K-means variant are used: $\tau_k \propto \sigma_k^p$ for "HeSC" and $\tau_k \propto |\Sigma_k|^{1/2}$ for "HeEC", under which the log-ratio term in the misclassification probability vanishes (Melnykov and Michael, 2020, Appendix A). The "HeEC" case requires the **CompQuadForm** package, which evaluates the distribution of linear combinations of non-central chi-squared variables (Davies, 1980).

Value

A symmetric $K \times K$ matrix of pairwise overlaps with zero diagonal.

References

- Melnykov, V. and Michael, S. (2020) Clustering large datasets by merging K-means solutions. *Journal of Classification*, 37, 97-123. doi:[10.1007/s00357019093148](https://doi.org/10.1007/s00357019093148)
- Maitra, R. and Melnykov, V. (2010) Simulating data to study performance of finite mixture modeling and clustering algorithms. *Journal of Computational and Graphical Statistics*, 19(2), 354-376.
- Davies, R. B. (1980) The distribution of a linear combination of chi-squared random variables. *Applied Statistics*, 29, 323-333.

See Also

[MergeKmeans\(\)](#), [overlap_map\(\)](#)

Examples

```
centers <- rbind(c(0, 0), c(3, 0), c(10, 10))
pairwise_overlap(centers, cov = 1)           # spherical, sigma^2 = 1
pairwise_overlap(centers, cov = c(1, 4, 1)) # heteroscedastic spherical
```

plot.MergeKmeans	<i>Plot method for MergeKmeans fits</i>
------------------	---

Description

Plot method for MergeKmeans fits

Usage

```
## S3 method for class 'MergeKmeans'
plot(x, what = c("overlap", "tree", "classification"), data = NULL, ...)
```

Arguments

x	a "MergeKmeans" object.
what	type of display: "overlap" for the overlap map (see overlap_map()), "tree" for the dendrogram of the hierarchical merging, or "classification" for a scatter plot of the data colored by the merged clusters (the first two principal components are shown when the data have more than two columns).
data	data matrix for what = "classification"; defaults to the data stored in the fit.
...	further arguments passed to overlap_map() , to plot.hclust() , or to plot() .

Value

For what = "overlap", invisibly the component ordering; otherwise NULL, invisibly.

See Also

[MergeKmeans\(\)](#), [overlap_map\(\)](#)

Examples

```
set.seed(3)
x <- rbind(matrix(rnorm(300), ncol = 2),
            matrix(rnorm(300, mean = 6), ncol = 2))
fit <- MergeKmeans(x, K = 8, G = 2, linkage = "single")
plot(fit, what = "overlap")
plot(fit, what = "tree")
plot(fit, what = "classification")
```

predict.MergeKmeans	<i>Predict cluster membership for new observations</i>
---------------------	--

Description

Assigns new observations to K-means components by the decision rule of the fitted variant (nearest center in the appropriate metric) and then maps components to merged clusters.

Usage

```
## S3 method for class 'MergeKmeans'
predict(object, newdata, ...)
```

Arguments

object	a "MergeKmeans" object.
newdata	numeric matrix or data frame of new observations with the same variables as the training data.
...	ignored.

Details

On the training data, the predicted components reproduce the fitted components exactly for K-means-based fits and for converged classification EM fits. The round-trip is not guaranteed when a user-supplied `start` partition was not nearest-center consistent or when the CEM iterations did not converge.

Value

A list with entries `component` (assigned K-means components) and `cluster` (merged cluster labels, or `NULL` if the merge tree has not been cut).

See Also

[MergeKmeans\(\)](#)

Examples

```
set.seed(4)
x <- rbind(matrix(rnorm(300), ncol = 2),
             matrix(rnorm(300, mean = 6), ncol = 2))
fit <- MergeKmeans(x, K = 8, G = 2, linkage = "single")
predict(fit, rbind(c(0, 0), c(6, 6)))
```

recut

Re-cut the merge tree of a MergeKmeans fit

Description

Produces a new partition from a fitted [MergeKmeans\(\)](#) object by cutting its merge tree at a different number of clusters or overlap threshold, without re-running K-means or the overlap computation.

Usage

```
recut(object, G = NULL, omega.star = NULL)
```

Arguments

<code>object</code>	a "MergeKmeans" object.
<code>G</code>	requested number of clusters, or "auto" to cut at the largest gap in merge heights.
<code>omega.star</code>	overlap threshold in (0, 1); meaningful with single, average, or complete linkage, where the merge heights are 1 - overlap (not accepted with Ward's linkage). Supply exactly one of <code>G</code> and <code>omega.star</code> .

Value

The input object with updated `cluster`, `G`, and `component.map` entries.

See Also[MergeKmeans\(\)](#)**Examples**

```
set.seed(1)
x <- rbind(matrix(rnorm(200), ncol = 2),
              matrix(rnorm(200, mean = 6), ncol = 2))
fit <- MergeKmeans(x, K = 8, G = 2, linkage = "single")
recut(fit, G = "auto")
```

summary.MergeKmeans	<i>Summary method for MergeKmeans fits</i>
---------------------	--

Description

Summary method for MergeKmeans fits

Usage

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

Arguments

object	a "MergeKmeans" object.
...	ignored.

Value

object, invisibly.

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