

# Package ‘latrend’

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**Title** A Framework for Clustering Longitudinal Data

**Description** A framework for clustering longitudinal datasets in a standardized way. Provides an interface to existing R packages for clustering longitudinal univariate trajectories, facilitating reproducible and transparent analyses. Additionally, standard tools are provided to support cluster analyses, including repeated estimation, model validation, and model assessment. The interface enables users to compare results between methods, and to implement and evaluate new methods with ease.

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 'methodFeature.R' 'methodFlexmix.R' 'methodFlexmixGBTM.R'  
 'methodFunFEM.R' 'methodLMKM.R' 'methodGCKM.R' 'methodKML.R'  
 'methodLcmmGMM.R' 'methodLcmmGBTM.R' 'methodLongclust.R'  
 'methodMclustLLPA.R' 'methodMixAK\_GLMM.R' 'methodMixTVEM.R'  
 'methodMixtoolsGMM.R' 'methodMixtoolsNPRM.R' 'methodRandom.R'  
 'methodStratify.R' 'methods.R' 'metricsInternal.R'  
 'metricsExternal.R' 'model-evaluation.R' 'model-summary.R'  
 'model-transform.R' 'modelApprox.R' 'modelCrimCV.R'  
 'modelDtwclust.R' 'modelFeature.R' 'modelFlexmix.R'  
 'modelFunFEM.R' 'modelKML.R' 'modelPartition.R' 'modelLMKM.R'  
 'modelLcmmGMM.R' 'modelLcmmGBTM.R' 'modelLongclust.R'  
 'modelMclustLLPA.R' 'modelMixAK\_GLMM.R' 'modelMixAK\_GLMMlist.R'  
 'modelMixTVEM.R' 'modelMixtoolsGMM.R' 'modelMixtoolsRM.R'  
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latrend-package

*latrend: A Framework for Clustering Longitudinal Data***Description**

A framework for clustering longitudinal datasets in a standardized way. Provides an interface to existing R packages for clustering longitudinal univariate trajectories, facilitating reproducible and transparent analyses. Additionally, standard tools are provided to support cluster analyses, including repeated estimation, model validation, and model assessment. The interface enables users to compare results between methods, and to implement and evaluate new methods with ease.

**Features**

- Unified cluster analysis, independent of the underlying algorithms used. Enabling users to compare the performance of various longitudinal cluster methods on the case study at hand.
- Supports many different methods for longitudinal clustering out of the box (see the list of supported packages below).
- The framework consists of extensible S4 methods based on an abstract model class, enabling rapid prototyping of new cluster methods or model specifications.
- Standard plotting tools for model evaluation across methods (e.g., trajectories, cluster trajectories, model fit, metrics)
- Support for many cluster metrics through the packages clusterCrit, mclustcomp, and igraph.
- The structured and unified analysis approach enables simulation studies for comparing methods.
- Standardized model validation for all methods through bootstrapping or k-fold cross-validation.

## Getting started

The `latrendData` dataset is included with the package and is used in all examples. The `plotTrajectories()` function can be used to visualize any longitudinal dataset, given the `id` and `time` are specified.

```
data(latrendData)
head(latrendData)
options(latrend.id = "Id", latrend.time = "Time")
plotTrajectories(latrendData, response = "Y")
```

Discovering longitudinal clusters using the package involves the specification of the longitudinal cluster method that should be used.

```
kmMethod <- lcMethodKML("Y", nClusters = 3)
kmMethod
```

The specified method is then estimated on the data using the generic estimation procedure function `latrend()`:

```
model <- latrend(kmMethod, data = latrendData)
```

Analyze the fitted model

```
summary(model)
plot(model)
metric(model, c("WMAE", "BIC"))
qqPlot(model)
```

Create derivative method specifications for 1 to 5 clusters using the `lcMethods()` function. A series of methods can be estimated using `latrendBatch()`.

```
kmMethods <- lcMethods(kmMethod, nClusters = 1:5)
models <- latrendBatch(kmMethods, data = latrendData)
```

Determine the number of clusters through one or more internal cluster metrics. This can be done visually using the `plotMetric()` function.

```
plotMetric(models, c("WMAE", "BIC"))
```

## Vignettes

Further step-by-step instructions on how to use the package are described in the vignettes.

- See `vignette("demo", package = "latrend")` for an introduction to conducting a longitudinal cluster analysis on a example case study.
- See `vignette("simulation", package = "latrend")` for an example on conducting a simulation study.
- See `vignette("validation", package = "latrend")` for examples on applying internal cluster validation.
- See `vignette("implement", package = "latrend")` for examples on constructing your own cluster models.

**Useful pages**

Method specification: [lcMethod](#) [lcMethods](#)

Method estimation: [latrend](#) [latrendRep](#) [latrendBatch](#) [latrendBoot](#) [latrendCV](#) [latrend-parallel](#)

Model functions: [lcModel](#) [clusterTrajectories](#) [plotClusterTrajectories](#) [postprob](#) [trajectoryAssignments](#) [predictPostprob](#) [predictAssignments](#) [predict.lcModel](#) [predictForCluster](#) [fitted.lcModel](#) [fitted-Trajectories](#)

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**See Also**

Useful links:

- <https://github.com/philips-software/latrend>
- Report bugs at <https://github.com/philips-software/latrend/issues>

---

APPA

*Average posterior probability of assignment (APPA)*

---

**Description**

Computes the average posterior probability of assignment (APPA) for each cluster.

**Usage**

```
APPA(object)
```

**Arguments**

object            The model, of type `lcModel`.

**Value**

The APPA per cluster, as a numeric vector of length `nClusters(object)`. Empty clusters will output NA.

## References

Nagin DS (2005). *Group-based modeling of development*. Harvard University Press. ISBN 9780674041318, doi: [10.4159/9780674041318](https://doi.org/10.4159/9780674041318).

Klijn SL, Weijenberg MP, Lemmens P, van den Brandt PA, Passos VL (2017). “Introducing the fit-criteria assessment plot - A visualisation tool to assist class enumeration in group-based trajectory modelling.” *Statistical Methods in Medical Research*, **26**(5), 2424-2436. doi: [10.1177/0962280215598665](https://doi.org/10.1177/0962280215598665).

van der Nest G, Lima Passos V, Candel MJ, van Breukelen GJ (2020). “An overview of mixture modelling for latent evolutions in longitudinal data: Modelling approaches, fit statistics and software.” *Advances in Life Course Research*, **43**, 100323. ISSN 1040-2608, doi: [10.1016/j.alcr.2019.100323](https://doi.org/10.1016/j.alcr.2019.100323).

## See Also

[confusionMatrix](#) [OCC](#)

---

as.data.frame.lcMethod

*Convert lcMethod arguments to a list of atomic types*

---

## Description

Converts the arguments of a `lcMethod` to a named list of [atomic](#) types.

## Usage

```
## S3 method for class 'lcMethod'
as.data.frame(x, ..., eval = TRUE, nullValue = NA, envir = NULL)
```

## Arguments

<code>x</code>	lcMethod to be coerced to a character vector.
<code>...</code>	Additional arguments.
<code>eval</code>	Whether to evaluate the arguments in order to replace expression if the resulting value is of a class specified in <code>evalClasses</code> .
<code>nullValue</code>	Value to use to represent the NULL type. Must be of length 1.
<code>envir</code>	The environment in which to evaluate the arguments. If NULL, the environment associated with the object is used. If not available, the <code>parent.frame()</code> is used.

## Value

A single-row `data.frame` where each columns represents an argument call or evaluation.

## See Also

Other `lcMethod` functions: [\[\[,lcMethod-method](#), [as.data.frame.lcMethods\(\)](#), [as.lcMethods\(\)](#), [as.list.lcMethod\(\)](#), [evaluate.lcMethod\(\)](#), [formula.lcMethod\(\)](#), [lcMethod-class](#), [names,lcMethod-method](#), [update.lcMethod\(\)](#)



---

 as.data.frame.lcMethods

*Convert a list of lcMethod objects to a data.frame*


---

### Description

Converts a list of lcMethod objects to a data.frame.

### Usage

```
## S3 method for class 'lcMethods'
as.data.frame(x, ..., eval = TRUE, nullValue = NA, envir = parent.frame())
```

### Arguments

x	the lcMethods or list to be coerced to a data.frame.
...	Additional arguments.
eval	Whether to evaluate the arguments in order to replace expression if the resulting value is of a class specified in evalClasses.
nullValue	Value to use to represent the NULL type. Must be of length 1.
envir	The environment in which to evaluate the arguments. If NULL, the environment associated with the object is used. If not available, the parent.frame() is used.

### Value

A data.frame with each row containing the argument values of a method object.

### See Also

Other lcMethod functions: [\[\[,lcMethod-method](#), [as.data.frame.lcMethod\(\)](#), [as.lcMethods\(\)](#), [as.list.lcMethod\(\)](#), [evaluate.lcMethod\(\)](#), [formula.lcMethod\(\)](#), [lcMethod-class](#), [names.lcMethod-method](#), [update.lcMethod\(\)](#)

---

 as.data.frame.lcModels

*Generate a data.frame containing the argument values per method per row*


---

### Description

Generate a data.frame containing the argument values per method per row

### Usage

```
## S3 method for class 'lcModels'
as.data.frame(x, ..., excludeShared = FALSE, eval = TRUE)
```

**Arguments**

x	lcModels or a list of lcModel
...	Arguments passed to <a href="#">as.data.frame.lcMethod</a> .
excludeShared	Whether to exclude columns which have the same value across all methods.
eval	Whether to evaluate the arguments in order to replace expression if the resulting value is of a class specified in evalClasses.

**Value**

A data.frame.

---

as.lcMethods

*Convert a list of lcMethod objects to a lcMethods list*

---

**Description**

Convert a list of lcMethod objects to a lcMethods list

**Usage**

```
as.lcMethods(x)
```

**Arguments**

x	A list of lcMethod objects.
---	-----------------------------

**Value**

A lcMethods object.

**See Also**

Other lcMethod functions: [\[\[,lcMethod-method](#), [as.data.frame.lcMethods\(\)](#), [as.data.frame.lcMethod\(\)](#), [as.list.lcMethod\(\)](#), [evaluate.lcMethod\(\)](#), [formula.lcMethod\(\)](#), [lcMethod-class](#), [names.lcMethod-method](#), [update.lcMethod\(\)](#)

---

as.lcModels	<i>Convert a list of lcModels to a lcModels list</i>
-------------	--

---

**Description**

Convert a list of lcModels to a lcModels list

**Usage**

```
as.lcModels(x)
```

**Arguments**

x                    A list of lcModel objects, an lcModels object, or NULL.

**Value**

A lcModels object.

**See Also**

lcModels

Other lcModel list functions: [lcModels](#), [print.lcModels\(\)](#), [subset.lcModels\(\)](#)

---

as.list.lcMethod	<i>Extract the method arguments as a list</i>
------------------	---

---

**Description**

Extract the method arguments as a list

**Usage**

```
## S3 method for class 'lcMethod'
as.list(x, ..., args = names(x), eval = TRUE, expand = FALSE, envir = NULL)
```

**Arguments**

x                    The lcMethod object.

...                  Additional arguments.

args                A character vector of argument names to select. Only available arguments are returned. Alternatively, a function or list of functions, whose formal arguments will be selected from the method.

eval                Whether to evaluate the arguments.

expand	Whether to return all method arguments when "... " is present among the requested argument names.
envir	The environment in which to evaluate the arguments. If NULL, the environment associated with the object is used. If not available, the parent.frame() is used.

**Value**

A list with the argument calls or evaluated results depending on the value for eval.

**See Also**

Other lcMethod functions: [\[\[,lcMethod-method](#), [as.data.frame.lcMethods\(\)](#), [as.data.frame.lcMethod\(\)](#), [as.lcMethods\(\)](#), [evaluate.lcMethod\(\)](#), [formula.lcMethod\(\)](#), [lcMethod-class](#), [names,lcMethod-method](#), [update.lcMethod\(\)](#)

**Examples**

```
library(kml)
data(latrendData)
method <- lcMethodKML("Y", id = "Id", time = "Time")
as.list(method)

as.list(method, args = c('id', 'time'))

# select arguments used by kml()
as.list(method, args = kml::kml)

# select arguments used by either kml() or parALGO()
as.list(method, args = c(kml::kml, kml::parALGO))
```

---

clusterNames

*Get the cluster names*

---

**Description**

Get the cluster names

**Usage**

```
clusterNames(object, factor = FALSE)
```

**Arguments**

object	The lcModel object.
factor	Whether to return the cluster names as a factor.

**Value**

A character of the cluster names.

**Examples**

```
data(latrendData)
model <- latrend(lcMethodKML("Y", id = "Id", time = "Time"), latrendData)
clusterNames(model) # A, B
```

---

clusterNames<-            *Update the cluster names*

---

**Description**

Update the cluster names

**Usage**

```
clusterNames(object) <- value
```

**Arguments**

object	The lcModel object to update.
value	The character with the new names.

**Value**

The updated lcModel object.

**Examples**

```
data(latrendData)
model <- latrend(lcMethodKML("Y", id = "Id", time = "Time"), latrendData)
clusterNames(model) <- c("Group 1", "Group 2")
```

---

clusterProportions        *Proportional size of each cluster*

---

**Description**

Obtain the proportional size per cluster, with sizes between 0 and 1. By default, the cluster proportions are determined from the cluster-averaged posterior probabilities of the fitted data (as computed by the [postprob\(\)](#) function).

**Usage**

```
## S4 method for signature 'lcModel'
clusterProportions(object, ...)
```

**Arguments**

object            The lcModel to obtain the proportions from.  
 ...                Arguments passed on to [postprob](#)

**Value**

A named numeric vector of length nClusters(object) with the proportional size of each cluster.

**Implementation**

Classes extending lcModel can override this method to return, for example, the exact estimated mixture proportions based on the model coefficients.

```
setMethod("clusterProportions", "lcModelExt", function(object, ...) {
  # return cluster proportion vector
})
```

**See Also**

[clusterSizes](#) [postprob](#)

**Examples**

```
data(latrendData)
model <- latrend(lcMethodKML("Y", id = "Id", time = "Time"), latrendData)
clusterProportions(model)
```

---

clusterSizes	<i>Number of trajectories per cluster</i>
--------------	---

---

**Description**

Obtain the size of each cluster, where the size is determined by the number of assigned trajectories to each cluster.

**Usage**

```
clusterSizes(object, ...)
```

**Arguments**

object            The lcModel object.  
 ...                Arguments passed on to [trajectoryAssignments](#)

**Details**

The cluster sizes are computed from the trajectory cluster membership as decided by the `trajectoryAssignments()` function.

**Value**

A named integer vector of length `nClusters(object)` with the number of assigned trajectories per cluster.

**See Also**

[clusterProportions](#) [trajectoryAssignments](#)

**Examples**

```
data(latrendData)
model <- latrend(lcMethodKML("Y", id = "Id", time = "Time"), latrendData)
clusterSizes(model)
```

---

`clusterTrajectories`    *Extract the cluster trajectories*

---

**Description**

Extracts a data frame of all cluster trajectories.

**Usage**

```
## S4 method for signature 'lcModel'
clusterTrajectories(object, at = time(object), what = "mu", ...)
```

**Arguments**

<code>object</code>	The <code>lcModel</code> object.
<code>at</code>	An optional vector of the times at which to compute the cluster trajectory predictions.
<code>what</code>	The distributional parameter to predict. By default, the mean response 'mu' is predicted. The cluster membership predictions can be obtained by specifying <code>what = 'mb'</code> .
<code>...</code>	Additional arguments.

**Value**

A data.frame of the estimated values at the given times. The first column should be named "Cluster". The second column should be time, with the name matching the `timeVariable(object)`. The third column should be the expected value of the observations, named after the `responseVariable(object)`.

**See Also**

Other model-specific methods: `coef.lcModel()`, `converged()`, `deviance.lcModel()`, `df.residual.lcModel()`, `fitted.lcModel()`, `fittedTrajectories()`, `lcModel-class`, `logLik.lcModel()`, `model.frame.lcModel()`, `nobs.lcModel()`, `postprob()`, `predict.lcModel()`, `predictAssignments()`, `predictForCluster()`, `predictPostprob()`, `residuals.lcModel()`, `sigma.lcModel()`, `time.lcModel()`

**Examples**

```
model <- latrend(method = lcMethodLcmmGMM(fixed = Y ~ Time, mixture = ~ Time),
  id = "Id", time = "Time", data = latrendData)
clusterTrajectories(model)

clusterTrajectories(model, at = c(0, .5, 1))
```

---

<code>coef.lcModel</code>	<i>Extract lcModel coefficients</i>
---------------------------	-------------------------------------

---

**Description**

Extract the coefficients of the `lcModel` object, if defined. The returned set of coefficients depends on the underlying type of `lcModel`. The default implementation checks for the existence of a `coef()` function for the internal model as defined in the `@model` slot, returning the output if available.

**Usage**

```
## S3 method for class 'lcModel'
coef(object, ...)
```

**Arguments**

<code>object</code>	The <code>lcModel</code> object.
<code>...</code>	Additional arguments.

**Value**

A named numeric vector with all coefficients, or a matrix with each column containing the cluster-specific coefficients. If `coef()` is not defined for the given model, an empty numeric vector is returned.

**Implementation**

Classes extending `lcModel` can override this method to return model-specific coefficients.

```
coef.lcModelExt <- function(object, ...) {
  # return model coefficients
}
```



**See Also**

Other model-specific methods: `clusterTrajectories()`, `converged()`, `deviance.lcModel()`, `df.residual.lcModel()`, `fitted.lcModel()`, `fittedTrajectories()`, `lcModel-class`, `logLik.lcModel()`, `model.frame.lcModel()`, `nobs.lcModel()`, `postprob()`, `predict.lcModel()`, `predictAssignments()`, `predictForCluster()`, `predictPostprob()`, `residuals.lcModel()`, `sigma.lcModel()`, `time.lcModel()`

**Examples**

```
data(latrendData)
method <- lcMethodLcmmGBTM(fixed = Y ~ Time, mixture = ~ 1,
  id = "Id", time = "Time", nClusters = 3)
gbtm <- latrend(method, data = latrendData)
coef(gbtm)
```

---

compose

*lcMethod fit process: compose an lcMethod object*

---

**Description**

Note: this function should not be called directly, as it is part of the `lcMethod` fitting process. For fitting an `lcMethod` object to a dataset, see `latrend()`.

The `compose()` function of the `lcMethod` object evaluates and finalizes the `lcMethod` arguments.

The default implementation returns an updated object with all arguments having been evaluated.

**Usage**

```
## S4 method for signature 'lcMethod'
compose(method, envir = NULL)
```

**Arguments**

<code>method</code>	The <code>lcMethod</code> object.
<code>envir</code>	The environment in which the <code>lcMethod</code> should be evaluated

**Value**

The evaluated and finalized `lcMethod` object.

**Implementation**

In general, there is no need to extend this method for a specific method, as all arguments are automatically evaluated by the `compose,lcMethod` method.

However, in case there is a need to extend processing or to prevent evaluation of specific arguments (e.g., for handling errors), the method can be overridden for the specific `lcMethod` subclass.

```

setMethod("compose", "lcMethodExample", function(method, envir = NULL) {
  newMethod <- callNextMethod()
  # further processing
  return(newMethod)
})

```

### Fitting procedure

Each `lcMethod` subclass defines a type of methods in terms of a series of steps for estimating the method. These steps, as part of the fitting procedure, are executed by `latrend()` in the following order:

1. `compose()`: Evaluate and finalize the method argument values.
2. `validate()`: Check the validity of the method argument values in relation to the dataset.
3. `prepareData()`: Process the training data for fitting.
4. `prefit()`: Prepare environment for estimation, independent of training data.
5. `fit()`: Estimate the specified method on the training data, outputting an object inheriting from `lcModel`.
6. `postFit()`: Post-process the outputted `lcModel` object.

The result of the fitting procedure is an `lcModel` object that inherits from the `lcModel` class.

### See Also

[evaluate.lcMethod](#)

---

confusionMatrix	<i>Compute the posterior confusion matrix</i>
-----------------	---

---

### Description

Compute the posterior confusion matrix (PCM). The entry  $(i, j)$  represents the probability (or number, in case of `scale = TRUE`) of a trajectory belonging to cluster  $i$  is assigned to cluster  $j$  under the specified trajectory cluster assignment strategy.

### Usage

```
confusionMatrix(object, strategy = which.max, scale = TRUE, ...)
```

### Arguments

object	The model, of type <code>lcModel</code> .
strategy	The strategy for assigning trajectories to a specific cluster, see <a href="#">trajectoryAssignments()</a> . If <code>strategy = NULL</code> , the posterior probabilities are used as weights (analogous to a repeated evaluation of <code>strategy = which.weight</code> ).
scale	Whether to express the confusion in probabilities ( <code>scale = TRUE</code> ), or in terms of the number of trajectories.
...	Arguments passed on to <a href="#">trajectoryAssignments</a>

**Value**

A K-by-K confusion matrix with  $K = nClusters(object)$ .

**See Also**

[postprob](#) [clusterProportions](#) [trajectoryAssignments](#) [APPA](#) [OCC](#)

**Examples**

```
data(latrendData)
model = latrend(lcMethodLcmmGMM(
  fixed = Y ~ Time, mixture = ~ Time, random = ~ 1,
  id = "Id", time = "Time"),
  data=latrendData)
confusionMatrix(model)
```

---

converged

*Check model convergence*

---

**Description**

Check convergence of the fitted `lcModel` object. The default implementation returns NA.

**Usage**

```
## S4 method for signature 'lcModel'
converged(object, ...)
```

**Arguments**

`object`            The `lcModel` to check for convergence.  
`...`                Additional arguments.

**Value**

Either logical indicating convergence, or a numeric status code.

**Implementation**

Classes extending `lcModel` can override this method to return a convergence status or code.

```
setMethod("converged", "lcModelExt", function(object, ...) {
  # return convergence code
})
```

**See Also**

Other model-specific methods: [clusterTrajectories\(\)](#), [coef.lcModel\(\)](#), [deviance.lcModel\(\)](#), [df.residual.lcModel\(\)](#), [fitted.lcModel\(\)](#), [fittedTrajectories\(\)](#), [lcModel-class](#), [logLik.lcModel\(\)](#), [model.frame.lcModel\(\)](#), [nobs.lcModel\(\)](#), [postprob\(\)](#), [predict.lcModel\(\)](#), [predictAssignments\(\)](#), [predictForCluster\(\)](#), [predictPostprob\(\)](#), [residuals.lcModel\(\)](#), [sigma.lcModel\(\)](#), [time.lcModel\(\)](#)

**Examples**

```
data(latrendData)
method <- lcMethodLcmmGBTM(fixed = Y ~ Time, mixture = ~ 1,
  id = "Id", time = "Time", nClusters = 3)
gbtm <- latrend(method, data = latrendData)
converged(gbtm)
```

---

`createTestDataFold`      *Create the test fold data for validation*

---

**Description**

Create the test fold data for validation

**Usage**

```
createTestDataFold(data, trainData, id = getOption("latrend.id"))
```

**Arguments**

<code>data</code>	A <code>data.frame</code> representing the complete dataset.
<code>trainData</code>	A <code>data.frame</code> representing the training data, which should be a subset of <code>data</code> .
<code>id</code>	The trajectory identifier variable.

**See Also**

[createTrainDataFolds](#)

Other validation methods: [createTestDataFolds\(\)](#), [createTrainDataFolds\(\)](#), [latrendBoot\(\)](#), [latrendCV\(\)](#), [lcModel-data-filters](#)

**Examples**

```
data(latrendData)
trainDataList <- createTrainDataFolds(latrendData, id = "Id", folds = 10)
testData1 <- createTestDataFold(latrendData, trainDataList[[1]], id = "Id")
```

---

createTestDataFolds    *Create all k test folds from the training data*

---

### Description

Create all k test folds from the training data

### Usage

```
createTestDataFolds(data, trainDataList, ...)
```

### Arguments

data	A data.frame representing the complete dataset.
trainDataList	A list of data.frame representing each of the data training folds. These should be derived from data.
...	Arguments passed to <a href="#">createTestDataFold</a> .

### See Also

Other validation methods: [createTestDataFold\(\)](#), [createTrainDataFolds\(\)](#), [latrendBoot\(\)](#), [latrendCV\(\)](#), [lcModel-data-filters](#)

### Examples

```
data(latrendData)
trainDataList <- createTrainDataFolds(latrendData, folds = 10, id = "Id")
testDataList <- createTestDataFolds(latrendData, trainDataList)
```

---

createTrainDataFolds    *Create the training data for each of the k models in k-fold cross validation evaluation*

---

### Description

Create the training data for each of the k models in k-fold cross validation evaluation

### Usage

```
createTrainDataFolds(
  data,
  folds = 10,
  id = getOption("latrend.id"),
  seed = NULL
)
```

**Arguments**

data	A data.frame representing the complete dataset.
folds	The number of folds. By default, a 10-fold scheme is used.
id	The trajectory identifier variable.
seed	The seed to use, in order to ensure reproducible fold generation at a later moment.

**Value**

A list of data.frame of the folds training datasets.

**See Also**

Other validation methods: [createTestDataFolds\(\)](#), [createTestDataFold\(\)](#), [latrendBoot\(\)](#), [latrendCV\(\)](#), [lcModel-data-filters](#)

**Examples**

```
data(latrendData)
trainFolds <- createTrainDataFolds(latrendData, folds = 10, id = "Id")

trainFolds <- createTrainDataFolds(latrendData, folds = 10, id = "Id", seed = 1)
```

---

dcastRepeatedMeasures *Cast a longitudinal data.frame to a matrix*

---

**Description**

Converts a longitudinal data.frame comprising trajectories with an equal number of observations, measured at identical moments in time, to a matrix. Each row of the matrix represents a trajectory.

**Usage**

```
dcastRepeatedMeasures(
  data,
  response,
  id = getOption("latrend.id"),
  time = getOption("latrend.time")
)
```

**Arguments**

data	The matrix containing a trajectory on each row.
response	The response column name.
id	The id column name.
time	The time column name.

**Value**

A matrix with a trajectory per row.

---

defineExternalMetric *Define an external metric for lcModels*

---

**Description**

Define an external metric for lcModels

**Usage**

```
defineExternalMetric(  
  name,  
  fun,  
  warnIfExists = getOption("latrend.warnMetricOverride", TRUE)  
)
```

**Arguments**

name	The name of the metric.
fun	The function to compute the metric, accepting a lcModel object as input.
warnIfExists	Whether to output a warning when the metric is already defined.

**See Also**

Other metric functions: [defineInternalMetric\(\)](#), [externalMetric](#), [lcModel](#), [lcModel-method](#), [getExternalMetricDefinition\(\)](#), [getExternalMetricNames\(\)](#), [getInternalMetricDefinition\(\)](#), [getInternalMetricNames\(\)](#), [metric\(\)](#)

---

defineInternalMetric *Define an internal metric for lcModels*

---

**Description**

Define an internal metric for lcModels

**Usage**

```
defineInternalMetric(  
  name,  
  fun,  
  warnIfExists = getOption("latrend.warnMetricOverride", TRUE)  
)
```

**Arguments**

name	The name of the metric.
fun	The function to compute the metric, accepting a lcModel object as input.
warnIfExists	Whether to output a warning when the metric is already defined.

**See Also**

Other metric functions: [defineExternalMetric\(\)](#), [externalMetric, lcModel, lcModel-method](#), [getExternalMetricDefinition\(\)](#), [getExternalMetricNames\(\)](#), [getInternalMetricDefinition\(\)](#), [getInternalMetricNames\(\)](#), [metric\(\)](#)

**Examples**

```
defineInternalMetric("BIC", fun = BIC)

mae <- function(object) {
  mean(abs(residuals(object)))
}
defineInternalMetric("MAE", fun = mae)
```

---

deviance.lcModel      *lcModel deviance*

---

**Description**

Get the deviance of the fitted lcModel object.

**Usage**

```
## S3 method for class 'lcModel'
deviance(object, ...)
```

**Arguments**

object	The lcModel object.
...	Additional arguments.

**Details**

The default implementation checks for the existence of the deviance() function for the internal model, and returns the output, if available.

**Value**

A numeric with the deviance value. If unavailable, NA is returned.



**See Also**

[stats::deviance metric](#)

Other model-specific methods: [clusterTrajectories\(\)](#), [coef.lcModel\(\)](#), [converged\(\)](#), [df.residual.lcModel\(\)](#), [fitted.lcModel\(\)](#), [fittedTrajectories\(\)](#), [lcModel-class](#), [logLik.lcModel\(\)](#), [model.frame.lcModel\(\)](#), [nobs.lcModel\(\)](#), [postprob\(\)](#), [predict.lcModel\(\)](#), [predictAssignments\(\)](#), [predictForCluster\(\)](#), [predictPostprob\(\)](#), [residuals.lcModel\(\)](#), [sigma.lcModel\(\)](#), [time.lcModel\(\)](#)

---

`df.residual.lcModel`     *Extract the residual degrees of freedom from a lcModel*

---

**Description**

Extract the residual degrees of freedom from a lcModel

**Usage**

```
## S3 method for class 'lcModel'
df.residual(object, ...)
```

**Arguments**

<code>object</code>	The lcModel object.
<code>...</code>	Additional arguments.

**Value**

A numeric with the residual degrees of freedom. If unavailable, NA is returned.

**See Also**

[stats::df.residual](#) [nobs](#) [residuals](#)

Other model-specific methods: [clusterTrajectories\(\)](#), [coef.lcModel\(\)](#), [converged\(\)](#), [deviance.lcModel\(\)](#), [fitted.lcModel\(\)](#), [fittedTrajectories\(\)](#), [lcModel-class](#), [logLik.lcModel\(\)](#), [model.frame.lcModel\(\)](#), [nobs.lcModel\(\)](#), [postprob\(\)](#), [predict.lcModel\(\)](#), [predictAssignments\(\)](#), [predictForCluster\(\)](#), [predictPostprob\(\)](#), [residuals.lcModel\(\)](#), [sigma.lcModel\(\)](#), [time.lcModel\(\)](#)

---

estimationTime	<i>Get the model estimation time</i>
----------------	--------------------------------------

---

### Description

Get the estimation time of the model, determined by the time taken for the associated `fit()` function to finish.

### Usage

```
## S4 method for signature 'lcModel'  
estimationTime(object, unit = "secs", ...)  
  
## S4 method for signature 'lcModels'  
estimationTime(object, unit = "secs", ...)  
  
## S4 method for signature 'list'  
estimationTime(object, unit = "secs", ...)
```

### Arguments

object	The list of <code>lcModel</code> objects.
unit	The time unit in which the estimation time should be outputted. By default, estimation time is in seconds. For accepted units, see <a href="#">base::difftime</a> .
...	Additional arguments.

### Value

A numeric representing the model estimation time, in the specified unit.

### Examples

```
data(latrendData)  
model <- latrend(lcMethodKML("Y", id = "Id", time = "Time"), latrendData)  
estimationTime(model)  
estimationTime(model, unit = 'mins')  
estimationTime(model, unit = 'days')
```

---

evaluate.lcMethod      *Substitute the call arguments for their evaluated values*

---

### Description

Substitutes the call arguments if they can be evaluated without error.

### Usage

```
## S3 method for class 'lcMethod'
evaluate(
  object,
  classes = "ANY",
  try = TRUE,
  exclude = character(),
  envir = NULL
)
```

### Arguments

object	The lcMethod object.
classes	Substitute only arguments with specific class types. By default, all types are substituted.
try	Whether to try to evaluate arguments and ignore errors (the default), or to fail on any argument evaluation error.
exclude	Arguments to exclude from evaluation.
envir	The environment in which to evaluate the arguments. If NULL, the environment associated with the object is used. If not available, the <code>parent.frame()</code> is used.

### Value

A new lcMethod object with the substituted arguments.

### See Also

[compose](#)

Other lcMethod functions: [\[\[,lcMethod-method](#), [as.data.frame.lcMethods\(\)](#), [as.data.frame.lcMethod\(\)](#), [as.lcMethods\(\)](#), [as.list.lcMethod\(\)](#), [formula.lcMethod\(\)](#), [lcMethod-class](#), [names,lcMethod-method](#), [update.lcMethod\(\)](#)

---

```
externalMetric,lcModel,lcModel-method
      Compute external model metric(s)
```

---

## Description

Compute one or more external metrics for two or more `lcModel` objects.

Note that there are many external metrics available, and there exists no external metric that works best in all scenarios. It is recommended to carefully consider which metric is most appropriate for your use case.

Many of the external metrics depend on implementations in other packages:

- `clusterCrit` (Desgraupes 2018)
- `mclustcomp` (You 2018)
- `igraph` (Csardi and Nepusz 2006)
- `psych` (Revelle 2019)

See `mclustcomp::mclustcomp()` for a grouped overview of similarity metrics.

Call `getInternalMetricNames()` to retrieve the names of the defined internal metrics. Call `getExternalMetricNames()` to retrieve the names of the defined external metrics.

## Usage

```
## S4 method for signature 'lcModel,lcModel'
externalMetric(
  object,
  object2,
  name = getOption("latrend.externalMetric"),
  ...
)

## S4 method for signature 'lcModels,missing'
externalMetric(object, object2, name = "adjustedRand")

## S4 method for signature 'lcModels,character'
externalMetric(object, object2 = "adjustedRand")

## S4 method for signature 'lcModels,lcModel'
externalMetric(object, object2, name, drop = TRUE)

## S4 method for signature 'list,lcModel'
externalMetric(object, object2, name, drop = TRUE)
```

**Arguments**

object	The lcModel, lcModels, or list of lcModel objects to compute the metrics for.
object2	The other lcModel to compare with.
name	The name(s) of the external metric(s) to compute. If no names are given, the names specified in the latrend.externalMetric option (none by default) are used.
...	Additional arguments.
drop	Whether to return a numeric vector instead of a data.frame in case of a single metric.

**Details**

List of currently supported external metrics:

<b>Metric name</b>	<b>Description</b>
adjustedRand	<b>Adjusted Rand index</b>
CohensKappa	<b>Cohen's kappa</b>
F	<b>F-score</b>
F1	<b>F1-score</b> , also referred to as the <b>Sørensen–Dice Coefficient</b> , or Dice similarity coefficient
FolkesMallows	<b>Fowlkes-Mallows index</b>
Hubert	Hubert index
Jaccard	<b>Jaccard index</b>
jointEntropy	<b>Joint entropy</b> between model assignments
Kulczynski	Kulczynski index
MaximumMatch	Maximum match measure
McNemar	McNemar statistic
MeilaHeckerman	Meila-Heckerman measure
Mirkin	Mirkin metric
MI	<b>Mutual information</b>
NMI	Normalized mutual information
NSJ	Normalized version of splitJoin. The proportion of edits relative to the maximum changes (twice the number of edits)
NVI	Normalized variation of information
Overlap	<b>Overlap coefficient</b> , also referred to as the Szymkiewicz–Simpson coefficient
PD	Partition difference
Phi	<b>Phi coefficient</b> .
precision	<b>precision</b>
Rand	<b>Rand index</b>
recall	<b>recall</b>
RogersTanimoto	Rogers-Tanimoto dissimilarity
RusselRao	Russell-Rao dissimilarity
SMC	<b>Simple matching coefficient</b>
splitJoin	total split-join index
splitJoin.ref	Split-join index of the first model to the second model
SokalSneath1	Type-1 Sokal-Sneath dissimilarity
SokalSneath2	Type-2 Sokal-Sneath dissimilarity
VI	<b>Variation of information</b>

Wallace1	Type-1 Wallace criterion
Wallace2	Type-2 Wallace criterion
WMSSE	Weighted minimum sum of squared errors between cluster trajectories
WMMSE	Weighted minimum mean of squared errors between cluster trajectories
WMAE	Weighted minimum mean of absolute errors between cluster trajectories

## Value

For `externalMetric(lcModel,lcModel)`: A numeric vector of the computed metrics.

A named numeric vector containing the computed model metrics.

For `externalMetric(lcModels)`: A distance matrix of class `dist` representing the pairwise comparisons.

For `externalMetric(lcModels,name)`: A distance matrix of class `dist` representing the pairwise comparisons.

For `externalMetric(lcModels,lcModel)`: A named numeric vector or `data.frame` containing the computed model metrics.

For `externalMetric(list,lcModel)`: A named numeric vector or `data.frame` containing the computed model metrics.

## Implementation

See the documentation of the `defineExternalMetric()` function for details on how to define your own external metrics.

## References

Cohen J (1960). “A Coefficient of Agreement for Nominal Scales.” *Educational and Psychological Measurement*, **20**(1), 37-46. doi: [10.1177/001316446002000104](https://doi.org/10.1177/001316446002000104), <https://doi.org/10.1177/001316446002000104>.

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Desgraupes B (2018). *clusterCrit: Clustering Indices*. R package version 1.2.8, <https://CRAN.R-project.org/package=clusterCrit>.

Hubert L, Arabie P (1985). “Comparing Partitions.” *Journal of Classification*, **2**(1), 193–218. ISSN 1432-1343, doi: [10.1007/BF01908075](https://doi.org/10.1007/BF01908075).

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Revelle W (2019). *psych: Procedures for Psychological, Psychometric, and Personality Research*. Northwestern University, Evanston, Illinois. R package version 1.9.12, <https://CRAN.R-project.org/package=psych>.

You K (2018). *mclustcomp: Measures for Comparing Clusters*. R package version 0.3.1, <https://CRAN.R-project.org/package=mclustcomp>.

**See Also**[metric](#)

Other metric functions: [defineExternalMetric\(\)](#), [defineInternalMetric\(\)](#), [getExternalMetricDefinition\(\)](#), [getExternalMetricNames\(\)](#), [getInternalMetricDefinition\(\)](#), [getInternalMetricNames\(\)](#), [metric\(\)](#)

**Examples**

```
data(latrendData)
model1 <- latrend(lcMethodKML("Y", id = "Id", time = "Time"), latrendData)
model2 <- latrend(lcMethodLcmmGMM(fixed = Y ~ Time, mixture = ~ Time,
  id = "Id", time = "Time"), latrendData)
ari <- externalMetric(model1, model2, 'adjustedRand')
```

---

*fit**lcMethod fit process: logic for fitting the method to the processed data*

---

**Description**

Note: this function should not be called directly, as it is part of the `lcMethod` fitting process. For fitting an `lcMethod` object to a dataset, see [latrend\(\)](#).

The `fit()` function of the `lcMethod` object estimates the model with the evaluated method specification, processed training data, and prepared environment.

**Usage**

```
## S4 method for signature 'lcMethod'
fit(method, data, envir, verbose)
```

**Arguments**

<code>method</code>	An object inheriting from <code>lcMethod</code> with all its arguments having been evaluated and finalized.
<code>data</code>	A <code>data.frame</code> representing the transformed training data.
<code>envir</code>	The environment containing variables generated by <a href="#">prepareData()</a> and <a href="#">preFit()</a> .
<code>verbose</code>	A <a href="#">R.utils::Verbose</a> object indicating the level of verbosity.

**Value**

The fitted object inheriting from `lcModel`.

### Implementation

This method should be implemented for all lcMethod subclasses.

```
setMethod("fit", "lcMethodExample", function(method, data, envir, verbose) {
  # estimate the model or cluster parameters
  coefs <- FIT_CODE

  # create the lcModel object
  new("lcModelExample",
    method = method,
    data = data,
    model = coefs,
    clusterNames = make.clusterNames(method$nClusters)
  )
})
```

### Fitting procedure

Each lcMethod subclass defines a type of methods in terms of a series of steps for estimating the method. These steps, as part of the fitting procedure, are executed by `latrend()` in the following order:

1. `compose()`: Evaluate and finalize the method argument values.
2. `validate()`: Check the validity of the method argument values in relation to the dataset.
3. `prepareData()`: Process the training data for fitting.
4. `preFit()`: Prepare environment for estimation, independent of training data.
5. `fit()`: Estimate the specified method on the training data, outputting an object inheriting from lcModel.
6. `postFit()`: Post-process the outputted lcModel object.

The result of the fitting procedure is an `lcModel` object that inherits from the lcModel class.

---

fitted.lcModel

*Extract lcModel fitted values*

---

### Description

Returns the cluster-specific fitted values for the given lcModel object. The default implementation calls `predict()` with `newdata = NULL`.

### Usage

```
## S3 method for class 'lcModel'
fitted(object, ..., clusters = trajectoryAssignments(object))
```



**Arguments**

<code>object</code>	The <code>lcModel</code> object.
<code>...</code>	Additional arguments.
<code>clusters</code>	Optional cluster assignments per id. If unspecified, a matrix is returned containing the cluster-specific predictions per column.

**Value**

A numeric vector of the fitted values for the respective class, or a matrix of fitted values for each cluster.

**Implementation**

Classes extending `lcModel` can override this method to adapt the computation of the predicted values for the training data. Note that the implementation of this function is only needed when `predict()` and `predictForCluster()` are not defined for the `lcModel` subclass.

```
fitted.lcModelExt <- function(object, ..., clusters = trajectoryAssignments(object)) {
  pred = predict(object, newdata = NULL)
  transformFitted(pred = pred, model = object, clusters = clusters)
}
```

The `transformFitted()` function takes care of transforming the prediction input to the right output format.

**See Also**

[fittedTrajectories](#) [plotFittedTrajectories](#) [stats::fitted](#) [predict.lcModel](#) [trajectoryAssignments](#) [transformFitted](#)

Other model-specific methods: [clusterTrajectories\(\)](#), [coef.lcModel\(\)](#), [converged\(\)](#), [deviance.lcModel\(\)](#), [df.residual.lcModel\(\)](#), [fittedTrajectories\(\)](#), [lcModel-class](#), [logLik.lcModel\(\)](#), [model.frame.lcModel\(\)](#), [nobs.lcModel\(\)](#), [postprob\(\)](#), [predict.lcModel\(\)](#), [predictAssignments\(\)](#), [predictForCluster\(\)](#), [predictPostprob\(\)](#), [residuals.lcModel\(\)](#), [sigma.lcModel\(\)](#), [time.lcModel\(\)](#)

**Examples**

```
data(latrendData)
model <- latrend(lcMethodKML("Y", id = "Id", time = "Time"), latrendData)
fitted(model)
```

---

fittedTrajectories      *Extract the fitted trajectories for all strata*

---

## Description

Extract the fitted trajectories for all strata

## Usage

```
## S4 method for signature 'lcModel'
fittedTrajectories(
  object,
  at = time(object),
  what = "mu",
  clusters = trajectoryAssignments(object),
  ...
)
```

## Arguments

object	The model.
at	The time points at which to compute the id-specific trajectories. The default implementation merely filters the output of <code>fitted()</code> , so fitted values can only be outputted for times at which the model was trained.
what	The distributional parameter to compute the response for.
clusters	The cluster assignments for the strata to base the trajectories on.
...	Additional arguments.

## Details

The default implementation uses the output of `fitted()` of the respective model.

## Value

A `data.frame` representing the fitted response per trajectory per moment in time for the respective cluster.

## See Also

Other model-specific methods: [clusterTrajectories\(\)](#), [coef.lcModel\(\)](#), [converged\(\)](#), [deviance.lcModel\(\)](#), [df.residual.lcModel\(\)](#), [fitted.lcModel\(\)](#), [lcModel-class](#), [logLik.lcModel\(\)](#), [model.frame.lcModel\(\)](#), [nobs.lcModel\(\)](#), [postprob\(\)](#), [predict.lcModel\(\)](#), [predictAssignments\(\)](#), [predictForCluster\(\)](#), [predictPostprob\(\)](#), [residuals.lcModel\(\)](#), [sigma.lcModel\(\)](#), [time.lcModel\(\)](#)

**Examples**

```

data(latrendData)
m <- lcMethodKML("Y", id = "Id", time = "Time")
model <- latrend(method = m, data = latrendData)
fittedTrajectories(model)

fittedTrajectories(model, at = time(model)[c(1, 2)])

```

---

formula.lcMethod	<i>Extract formula</i>
------------------	------------------------

---

**Description**

Extracts the associated formula for the given distributional parameter.

**Usage**

```

## S3 method for class 'lcMethod'
formula(x, what = "mu", envir = NULL, ...)

```

**Arguments**

x	The lcMethod object.
what	The distributional parameter to which this formula applies. By default, the formula specifies "mu".
envir	The environment in which to evaluate the arguments. If NULL, the environment associated with the object is used. If not available, the parent.frame() is used.
...	Additional arguments.

**Value**

The formula for the given distributional parameter.

**See Also**

Other lcMethod functions: [\[\[,lcMethod-method](#), [as.data.frame.lcMethods\(\)](#), [as.data.frame.lcMethod\(\)](#), [as.lcMethods\(\)](#), [as.list.lcMethod\(\)](#), [evaluate.lcMethod\(\)](#), [lcMethod-class](#), [names.lcMethod-method](#), [update.lcMethod\(\)](#)

**Examples**

```

m <- lcMethodMixtoolsGMM(formula = Y ~ Time + (1 | Id))
formula(m) # Y ~ Time + (1 | Id)

```

---

formula.lcModel	<i>Extract the formula of a lcModel</i>
-----------------	---

---

### Description

Get the formula associated with the fitted lcModel object. This is determined by the formula argument of the lcMethod specification that was used to fit the model.

### Usage

```
## S3 method for class 'lcModel'  
formula(x, what = "mu", ...)
```

### Arguments

x	The lcModel object.
what	The distributional parameter.
...	Additional arguments.

### Value

Returns the associated formula, or response  $\sim \emptyset$  if not specified.

### See Also

[stats::formula](#)

### Examples

```
data(latrendData)  
method <- lcMethodLMKM(Y ~ Time, id = "Id", time = "Time", nClusters = 3)  
lmkm <- latrend(method, data = latrendData)  
formula(lmkm) # Y ~ Time  
  
kml <- latrend(lcMethodKML("Y", id = "Id", time = "Time"), latrendData)  
formula(kml) # Y ~  $\emptyset$ 
```

---

generateLongData	<i>Generate longitudinal test data</i>
------------------	--

---

## Description

Generate longitudinal test data

## Usage

```
generateLongData(
  sizes = c(40, 60),
  fixed = Value ~ 1 + Time,
  cluster = ~1 + Time,
  random = ~1,
  id = getOption("latrend.id"),
  data = data.frame(Time = seq(0, 1, by = 0.1)),
  fixedCoefs = c(0, 0),
  clusterCoefs = cbind(c(-2, 1), c(2, -1)),
  randomScales = cbind(0.1, 0.1),
  rrandom = rnorm,
  noiseScales = c(0.1, 0.1),
  rnoise = rnorm,
  clusterNames = LETTERS[seq_along(sizes)],
  shuffle = FALSE,
  seed = NULL
)
```

## Arguments

sizes	Number of strata per cluster.
fixed	Fixed effects formula.
cluster	Cluster effects formula.
random	Random effects formula.
id	Name of the strata.
data	Data with covariates to use for generation. Stratified data may be specified by adding a grouping column.
fixedCoefs	Coefficients matrix for the fixed effects.
clusterCoefs	Coefficients matrix for the cluster effects.
randomScales	Standard deviations matrix for the size of the variance components (random effects).
rrandom	Random sampler for generating the variance components at location 0.
noiseScales	Scale of the random noise passed to rnoise. Either scalar or defined per cluster.
rnoise	Random sampler for generating noise at location 0 with the respective scale.

clusterNames	A character vector denoting the names of the generated clusters.
shuffle	Whether to randomly reorder the strata in which they appear in the data.frame.
seed	Optional seed to set for the PRNG. The set PRNG state persists after the function completes.

### Examples

```
longdata <- generateLongData(sizes = c(40, 70), id = "Id",
                             cluster = ~poly(Time, 2, raw = TRUE),
                             clusterCoefs = cbind(c(1, 2, 5), c(-3, 4, .2)))
plotTrajectories(longdata, response = "Value", id = "Id", time = "Time")
```

---

getArgumentDefaults     *Default argument values for lcMethod subclass*

---

### Description

Returns the default arguments associated with the respective `lcMethod` subclass. These arguments are automatically included into the `lcMethod` object during initialization.

### Usage

```
## S4 method for signature 'lcMethod'
getArgumentDefaults(object)
```

### Arguments

object                    The `lcMethod` object.

### Value

A named list of argument values.

### Implementation

Although implementing this method is optional, it prevents users from having to specify all arguments every time they want to create a method specification.

In this example, most of the default arguments are defined as arguments of the function `lcMethodExample`, which we can include in the list by calling `formals`. Copying the arguments from functions is especially useful when your method implementation is based on an existing function.

```
setMethod("getArgumentDefaults", "lcMethodExample", function(object) {
  list(
    formals(lcMethodExample),
    formals(funFEM::funFEM),
    extra = Value ~ 1,
    tol = 1e-4,
```

```

        callNextMethod()
    )
})

```

It is recommended to add `callNextMethod()` to the end of the list. This enables inheriting the default arguments from superclasses.

### See Also

[lcMethod getArgumentExclusions](#)

Other `lcMethod` implementations: [getArgumentExclusions\(\)](#), [lcMethod-class](#), [lcMethodAkmedoids](#), [lcMethodCrimCV](#), [lcMethodCustom](#), [lcMethodDtwclust](#), [lcMethodFeature](#), [lcMethodFunFEM](#), [lcMethodGCKM](#), [lcMethodKML](#), [lcMethodLMKM](#), [lcMethodLcmmGBTM](#), [lcMethodLcmmGMM](#), [lcMethodLongclust](#), [lcMethodMclustLLPA](#), [lcMethodMixAK\\_GLMM](#), [lcMethodMixtoolsGMM](#), [lcMethodMixtoolsNPRM](#), [lcMethodRandom](#), [lcMethodStratify](#)

---

`getArgumentExclusions` *Arguments to be excluded for lcMethod subclass*

---

### Description

Returns the names of arguments that should be excluded during instantiation of the `lcMethod`.

### Usage

```

## S4 method for signature 'lcMethod'
getArgumentExclusions(object)

```

### Arguments

`object`            The `lcMethod` object.

### Value

A character vector of argument names.

### Implementation

This function only needs to be implemented if you want to avoid users from specifying redundant arguments or arguments that are set automatically or conditionally on other arguments.

```

setMethod("getArgumentExclusions", "lcMethodExample", function(object) {
  c(
    "doPlot",
    "verbose",
    callNextMethod()
  )
})

```

Adding ``callNextMethod()`` to the end of the return vector enables inheriting exclusions from superclasses.

**See Also**

[lcMethod getArgumentsExclusions](#)

Other lcMethod implementations: [getArgumentDefaults\(\)](#), [lcMethod-class](#), [lcMethodAkmedoids](#), [lcMethodCrimCV](#), [lcMethodCustom](#), [lcMethodDtwclust](#), [lcMethodFeature](#), [lcMethodFunFEM](#), [lcMethodGCKM](#), [lcMethodKML](#), [lcMethodLMKM](#), [lcMethodLcmmGBTM](#), [lcMethodLcmmGMM](#), [lcMethodLongclust](#), [lcMethodMclustLLPA](#), [lcMethodMixAK\\_GLMM](#), [lcMethodMixtoolsGMM](#), [lcMethodMixtoolsNPRM](#), [lcMethodRandom](#), [lcMethodStratify](#)

`getExternalMetricDefinition`

*Get the external metric definition*

**Description**

Get the external metric definition

**Usage**

```
getExternalMetricDefinition(name)
```

**Arguments**

name	The name of the metric.
------	-------------------------

**Value**

The metric function, or NULL if not defined.

**See Also**

Other metric functions: [defineExternalMetric\(\)](#), [defineInternalMetric\(\)](#), [externalMetric](#), [lcModel](#), [lcModel-metric](#), [getExternalMetricNames\(\)](#), [getInternalMetricDefinition\(\)](#), [getInternalMetricNames\(\)](#), [metric\(\)](#)

`getExternalMetricNames`

*Get the names of the available external metrics*

**Description**

Get the names of the available external metrics

**Usage**

```
getExternalMetricNames()
```



**See Also**

Other metric functions: [defineExternalMetric\(\)](#), [defineInternalMetric\(\)](#), [externalMetric, lcModel, lcModel-metric\(\)](#), [getExternalMetricDefinition\(\)](#), [getInternalMetricDefinition\(\)](#), [getInternalMetricNames\(\)](#), [metric\(\)](#)

---

`getInternalMetricDefinition`

*Get the internal metric definition*

---

**Description**

Get the internal metric definition

**Usage**

`getInternalMetricDefinition(name)`

**Arguments**

name                    The name of the metric.

**Value**

The metric function, or NULL if not defined.

**See Also**

Other metric functions: [defineExternalMetric\(\)](#), [defineInternalMetric\(\)](#), [externalMetric, lcModel, lcModel-metric\(\)](#), [getExternalMetricDefinition\(\)](#), [getExternalMetricNames\(\)](#), [getInternalMetricNames\(\)](#), [metric\(\)](#)

---

`getInternalMetricNames`

*Get the names of the available internal metrics*

---

**Description**

Get the names of the available internal metrics

**Usage**

`getInternalMetricNames()`

**See Also**

Other metric functions: [defineExternalMetric\(\)](#), [defineInternalMetric\(\)](#), [externalMetric, lcModel, lcModel-metric\(\)](#), [getExternalMetricDefinition\(\)](#), [getExternalMetricNames\(\)](#), [getInternalMetricDefinition\(\)](#), [metric\(\)](#)

---

getLabel	<i>Extract the method label.</i>
----------	----------------------------------

---

### Description

Extracts the assigned label from the given lcMethod or lcModel object. By default, the label is determined from the "label" argument of the lcMethod object. The label of an lcModel object is set upon estimation by [latrend\(\)](#) to the label of its associated lcMethod object.

### Usage

```
## S4 method for signature 'lcMethod'
getLabel(object, ...)
```

```
## S4 method for signature 'lcModel'
getLabel(object, ...)
```

### Arguments

object	The lcMethod or lcModel object.
...	Additional arguments.

### Value

The extracted label, as character.

### See Also

[getName](#) [getShortName](#)

### Examples

```
getLabel(lcMethodKML()) # ""
getLabel(lcMethodKML(label = "v2")) # "v2"
```

---

getLcMethod	<i>Get the method specification of a lcModel</i>
-------------	--

---

### Description

Get the lcMethod specification object that was used for fitting the given lcModel object.

### Usage

```
getLcMethod(object)
```

**Arguments**

object            The lcModel object.

**Value**

An lcMethod object.

**See Also**

[getCall.lcModel](#)

**Examples**

```
model = latrend(method=lcMethodKML("Y", id = "Id", time = "Time"), data=latrendData)
getLcMethod(model)
```

---

getName

*Get the (short) name of the lcMethod or Model*

---

**Description**

Extract the full or shortened name of the given lcMethod or lcModel object. The name of the fitted lcModel is determined by its associated lcMethod name and label, unless specified otherwise.

**Usage**

```
## S4 method for signature 'lcMethod'
getName(object, ...)
```

```
## S4 method for signature 'lcMethod'
getShortName(object, ...)
```

```
## S4 method for signature 'lcModel'
getName(object)
```

```
## S4 method for signature 'lcModel'
getShortName(object)
```

**Arguments**

object            The lcMethod or lcModel object.

...                Additional arguments.

**Value**

A character name.

**Implementation**

When implementing your own `lcMethod` subclass, override these methods to provide full and abbreviated names.

```
setMethod("getName", "lcMethodExample", function(object) "example name")
```

```
setMethod("getShortName", "lcMethodExample", function(object) "EX")
```

Similar methods can be implemented for your `lcModel` subclass, however in practice this is not needed as the names are determined by default from the `lcMethod` object that was used to fit the `lcModel` object.

**See Also**

[getLabel](#)

**Examples**

```
getName(lcMethodKML()) # "longitudinal k-means"
getShortName(lcMethodKML()) # "KML"
```

---

<code>ids</code>	<i>Get the trajectory ids on which the model was fitted</i>
------------------	---

---

**Description**

Get the trajectory ids on which the model was fitted

**Usage**

```
ids(object)
```

**Arguments**

`object`            The `lcModel` object.

**Details**

The order returned by `ids(object)` determines the id order for any output involving id-specific values, such as in [trajectoryAssignments\(\)](#) or [postprob\(\)](#).

**Value**

A character vector or integer vector of the identifier for every fitted trajectory.

**Examples**

```
data(latrendData)
model = latrend(lcMethodKML("Y", id = "Id", time = "Time"), latrendData)
ids(model) # 1, 2, ..., 200
```

---

idVariable	<i>Extract the trajectory identifier variable</i>
------------	---

---

**Description**

Extracts the trajectory identifier variable (i.e., column name) from the given object.

**Usage**

```
## S4 method for signature 'lcMethod'
idVariable(object, ...)
```

```
## S4 method for signature 'lcModel'
idVariable(object)
```

**Arguments**

object	The object to extract the variable from.
...	Not used.

**Value**

The trajectory identifier name, as character.

**See Also**

Other lcModel variables: [responseVariable\(\)](#), [timeVariable\(\)](#)

**Examples**

```
method <- lcMethodKML(id = "Traj")
idVariable(method) # "Traj"

model <- latrend(lcMethodKML("Y", id = "Id", time = "Time"), latrendData)
idVariable(model) # "Id"
```

---

initialize,lcMethod-method	<i>lcMethod initialization</i>
----------------------------	--------------------------------

---

**Description**

Initialization of lcMethod objects, converting arbitrary arguments to arguments as part of an lcMethod object.

**Usage**

```
## S4 method for signature 'lcMethod'
initialize(.Object, ...)
```

**Arguments**

.Object	The newly allocated lcMethod object.
...	Other method arguments.

**Examples**

```
new("lcMethodKML", response = "Value")
```

---

latrend

---

*Cluster longitudinal data*


---

**Description**

Fit a longitudinal cluster method to the given training data, according to the specification provided by the lcMethod object.

This function runs all steps as part of the [method fitting procedure](#).

**Usage**

```
latrend(
  method,
  data,
  ...,
  envir = NULL,
  verbose = getOption("latrend.verbose")
)
```

**Arguments**

method	An lcMethod object specifying the longitudinal cluster method to apply, or the name (as character) of an lcMethod subclass. See <a href="#">lcMethod</a> for details.
data	The data.frame to which to apply the method. Inputs supported by <a href="#">trajectories()</a> can also be used.
...	Any other arguments to update the lcMethod definition with.
envir	The environment in which to evaluate the method arguments (by <a href="#">compose()</a> ). This environment is also used to evaluate the data argument if it is of type call.
verbose	The level of verbosity. Either an object of class Verbose (see <a href="#">R.utils::Verbose</a> for details), a logical indicating whether to show basic computation information, a numeric indicating the verbosity level (see <a href="#">Verbose</a> ), or one of c('info', 'fine', 'finest').

## Details

If a seed value is specified in the `lcMethod` object or arguments to `latrend`, this seed is set using `set.seed` prior to the cluster preparation step.

## Value

A `lcModel` object representing the fitted model.

## See Also

Other longitudinal cluster fit functions: [latrendBatch\(\)](#), [latrendBoot\(\)](#), [latrendCV\(\)](#), [latrendRep\(\)](#)

## Examples

```
data(latrendData)
model <- latrend(lcMethodKML("Y", id = "Id", time = "Time"), data = latrendData)

model <- latrend("lcMethodKML", response = "Y", id = "Id", time = "Time", data = latrendData)

method <- lcMethodKML("Y", id = "Id", time = "Time")
model <- latrend(method, data = latrendData, nClusters = 3)

model <- latrend(method, data = latrendData, nClusters = 3, seed = 1)
```

---

latrend-parallel      *Parallel computing using latrend*

---

## Description

The model estimation functions support parallel computation through the use of the [foreach](#) mechanism. In order to make use of parallel execution, a parallel back-end must be registered.

## Windows

On Windows, the [parallel-package](#) can be used to define parallel socket workers.

```
nCores <- parallel::detectCores(logical = FALSE)
cl <- parallel::makeCluster(nCores)
```

Then, register the cluster as the parallel back-end using the `doParallel` package:

```
doParallel::registerDoParallel(cl)
```

If you defined your own `lcMethod` or `lcModel` extension classes, make sure to load them on the workers as well. This can be done, for example, using:

```
parallel::clusterEvalQ(cl,
  expr = setClass('lcMethodMyImpl', contains = "lcMethod"))
```

**Unix**

On Unix systems, it is easier to setup parallelization as the R process is forked. In this example we use the doMC package:

```
nCores <- parallel::detectCores(logical = FALSE)
doMC::registerDoMC(nCores)
```

**See Also**

[latrendRep](#), [latrendBatch](#), [latrendBoot](#), [latrendCV](#)

**Examples**

```
data(latrendData)

# parallel latrendRep()
method <- lcMethodKML(response = "Y")
models <- latrendRep(method, data = latrendData, .rep = 5, parallel = TRUE)

# parallel latrendBatch()
methods <- lcMethods(method, nClusters = 1:3)
models <- latrendBatch(methods, data = latrendData, parallel = TRUE)
```

---

latrendBatch

---

*Cluster longitudinal data for a list of method specifications*


---

**Description**

Fit a list of longitudinal cluster methods on one or more datasets.

**Usage**

```
latrendBatch(
  methods,
  data,
  cartesian = TRUE,
  seed = NULL,
  parallel = FALSE,
  errorHandling = "stop",
  envir = NULL,
  verbose = getOption("latrend.verbose")
)
```



**Arguments**

methods	A list of lcMethod objects.
data	The dataset(s) to which to fit the respective lcMethod on. Either a data.frame, matrix, list or an expression evaluating to one of the supported types. Multiple datasets can be supplied by encapsulating the datasets using data = .(df1, df2, ..., dfN). Doing this results in a more readable call associated with each fitted lcModel object.
cartesian	Whether to fit the provided methods on each of the datasets. If cartesian=FALSE, only a single dataset may be provided or a list of data matching the length of methods.
seed	Sets the seed for generating the respective seed for each of the method fits. Seeds are only set for methods without a seed argument.
parallel	Whether to enable parallel evaluation. See <a href="#">latrend-parallel</a> . Method evaluation and dataset transformation is done on the calling thread.
errorHandling	Whether to "stop" on an error, or to "remove" evaluations that raised an error.
envir	The environment in which to evaluate the lcMethod arguments.
verbose	The level of verbosity. Either an object of class Verbose (see <a href="#">R.utils::Verbose</a> for details), a logical indicating whether to show basic computation information, a numeric indicating the verbosity level (see <a href="#">Verbose</a> ), or one of c('info', 'fine', 'finest').

**Details**

Methods and datasets are evaluated and validated prior to any fitting. This ensures that the batch estimation fails as early as possible in case of errors.

**Value**

A lcModels object. In case of a model fit error under errorHandling = pass, a list is returned.

**See Also**

lcMethods

Other longitudinal cluster fit functions: [latrendBoot\(\)](#), [latrendCV\(\)](#), [latrendRep\(\)](#), [latrend\(\)](#)

**Examples**

```
data(latrendData)
refMethod <- lcMethodLMKM(Y ~ Time, id = "Id", time = "Time")
methods <- lcMethods(refMethod, nClusters = 1:3)
models <- latrendBatch(methods, data = latrendData)

# different dataset per method
models <- latrendBatch(lcMethods(refMethod, nClusters = 1:2),
  data = .(
    subset(latrendData, Time > .5),
    subset(latrendData, Time < .5)
  )
)
```

)

latrendBoot

*Cluster longitudinal data using bootstrapping***Description**

Performs bootstrapping, generating samples from the given data at the id level, fitting a lcModel to each sample.

**Usage**

```
latrendBoot(
  method,
  data,
  samples = 50,
  seed = NULL,
  parallel = FALSE,
  errorHandling = "stop",
  envir = NULL,
  verbose = getOption("latrend.verbose")
)
```

**Arguments**

method	An lcMethod object specifying the longitudinal cluster method to apply, or the name (as character) of an lcMethod subclass. See <a href="#">lcMethod</a> for details.
data	A data.frame.
samples	The number of bootstrap samples to evaluate.
seed	The seed to use. Optional.
parallel	Whether to enable parallel evaluation. See <a href="#">latrend-parallel</a> . Method evaluation and dataset transformation is done on the calling thread.
errorHandling	Whether to "stop" on an error, or to "remove" evaluations that raised an error.
envir	The environment in which to evaluate the method arguments (by <a href="#">compose()</a> ). This environment is also used to evaluate the data argument if it is of type call.
verbose	The level of verbosity. Either an object of class Verbose (see <a href="#">R.utils::Verbose</a> for details), a logical indicating whether to show basic computation information, a numeric indicating the verbosity level (see <a href="#">Verbose</a> ), or one of c('info', 'fine', 'finest').

**Value**

A lcModels object of length samples.

**See Also**

Other longitudinal cluster fit functions: [latrendBatch\(\)](#), [latrendCV\(\)](#), [latrendRep\(\)](#), [latrend\(\)](#)

Other validation methods: [createTestDataFolds\(\)](#), [createTestDataFold\(\)](#), [createTrainDataFolds\(\)](#), [latrendCV\(\)](#), [lcModel-data-filters](#)

**Examples**

```
data(latrendData)
method <- lcMethodLMKM(Y ~ Time, id = "Id", time = "Time")
model <- latrendBoot(method, latrendData, samples = 10)
```

---

latrendCV

---

*Cluster longitudinal data over k folds*


---

**Description**

Apply k-fold cross validation for internal cluster validation. Creates k random subsets ("folds") from the data, estimating a model for each of the k-1 combined folds.

**Usage**

```
latrendCV(
  method,
  data,
  folds = 10,
  seed = NULL,
  parallel = FALSE,
  errorHandling = "stop",
  envir = NULL,
  verbose = getOption("latrend.verbose")
)
```

**Arguments**

method	An lcMethod object specifying the longitudinal cluster method to apply, or the name (as character) of an lcMethod subclass. See <a href="#">lcMethod</a> for details.
data	A data.frame.
folds	The number of folds. Ten folds by default.
seed	The seed to use. Optional.
parallel	Whether to enable parallel evaluation. See <a href="#">latrend-parallel</a> . Method evaluation and dataset transformation is done on the calling thread.
errorHandling	Whether to "stop" on an error, or to "remove" evaluations that raised an error.
envir	The environment in which to evaluate the method arguments (by <a href="#">compose()</a> ). This environment is also used to evaluate the data argument if it is of type call.
verbose	The level of verbosity. Either an object of class Verbose (see <a href="#">R.utils::Verbose</a> for details), a logical indicating whether to show basic computation information, a numeric indicating the verbosity level (see <a href="#">Verbose</a> ), or one of c('info', 'fine', 'finest').

**Value**

A `lcModels` object of containing the folds training models.

**See Also**

Other longitudinal cluster fit functions: [latrendBatch\(\)](#), [latrendBoot\(\)](#), [latrendRep\(\)](#), [latrend\(\)](#)

Other validation methods: [createTestDataFolds\(\)](#), [createTestDataFold\(\)](#), [createTrainDataFolds\(\)](#), [latrendBoot\(\)](#), [lcModel-data-filters](#)

**Examples**

```
data(latrendData)
method <- lcMethodLMKM(Y ~ Time, id = "Id", time = "Time")
model <- latrendCV(method, latrendData, folds = 5)

model <- latrendCV(method, subset(latrendData, Time < .5), folds = 5, seed = 1)
```

---

latrendData	<i>Artificial longitudinal dataset comprising three classes</i>
-------------	---

---

**Description**

An artificial longitudinal dataset comprising 200 trajectories belonging to one of 3 classes. Each trajectory deviates in intercept and slope from its respective class trajectory.

**Usage**

```
latrendData
```

**Format**

A `data.frame` comprising longitudinal observations from 200 trajectories. Each row represents the observed value of a trajectory at a specific moment in time.

**Id** integer: The trajectory identifier.

**Time** numeric: The measurement time, between 0 and 2.

**Y** numeric: The observed value at the respective time `Time` for trajectory `Id`.

**Class** factor: The reference class.

**Source**

This dataset was generated using [generateLongData](#).

**See Also**

[generateLongData](#)

**Examples**

```

data(latrendData)
plotTrajectories(latrendData, id = "Id", time = "Time", response = "Y")

# plot according to the reference class
plotTrajectories(latrendData, id = "Id", time = "Time", response = "Y", cluster = "Class")

```

latrendRep

*Cluster longitudinal data repeatedly***Description**

Performs a repeated fit of the specified latrend model on the given data.

**Usage**

```

latrendRep(
  method,
  data,
  .rep = 10,
  ...,
  .errorHandling = "stop",
  .seed = NULL,
  .parallel = FALSE,
  envir = NULL,
  verbose = getOption("latrend.verbose")
)

```

**Arguments**

method	An lcMethod object specifying the longitudinal cluster method to apply, or the name (as character) of an lcMethod subclass. See <a href="#">lcMethod</a> for details.
data	The data.frame to which to apply the method. Inputs supported by <a href="#">trajectories()</a> can also be used.
.rep	The number of repeated fits.
...	Any other arguments to update the lcMethod definition with.
.errorHandling	Whether to "stop" on an error, or to "remove" evaluations that raised an error.
.seed	Set the seed for generating the respective seed for each of the repeated fits.
.parallel	Whether to use parallel evaluation. See <a href="#">latrend-parallel</a> .
envir	The environment in which to evaluate the method arguments (by <a href="#">compose()</a> ). This environment is also used to evaluate the data argument if it is of type call.
verbose	The level of verbosity. Either an object of class Verbose (see <a href="#">R.utils::Verbose</a> for details), a logical indicating whether to show basic computation information, a numeric indicating the verbosity level (see <a href="#">Verbose</a> ), or one of c('info', 'fine', 'finest').

**Details**

This method is faster than repeatedly calling `latrend` as it only prepares the data via `prepareData()` once.

**Value**

A `lcModels` object containing the resulting models.

**See Also**

Other longitudinal cluster fit functions: `latrendBatch()`, `latrendBoot()`, `latrendCV()`, `latrend()`

**Examples**

```
data(latrendData)
method <- lcMethodLMKM(Y ~ Time, id = "Id", time = "Time")
models <- latrendRep(method, data = latrendData, .rep = 5) # 5 repeated runs

models <- latrendRep(method, data = latrendData, .seed = 1, .rep = 3)
```

---

`lcApproxModel-class`    *lcApproxModel class*

---

**Description**

approx models have defined cluster trajectories at fixed moments in time, which should be interpolated. For a correct implementation, `lcApproxModel` requires the extending class to implement `clusterTrajectories(at=NULL)` to return the fixed cluster trajectories.

**Usage**

```
## S3 method for class 'lcApproxModel'
fitted(object, ..., clusters = trajectoryAssignments(object))

## S4 method for signature 'lcApproxModel'
predictForCluster(
  object,
  newdata,
  cluster,
  what = "mu",
  approxFun = approx,
  ...
)
```

**Arguments**

object	The lcModel object.
...	Additional arguments.
clusters	Optional cluster assignments per id. If unspecified, a matrix is returned containing the cluster-specific predictions per column.
newdata	Optional data.frame for which to compute the model predictions. If omitted, the model training data is used. Cluster trajectory predictions are made when ids are not specified.
cluster	The cluster name (as character) to predict for.
what	The distributional parameter to predict. By default, the mean response 'mu' is predicted. The cluster membership predictions can be obtained by specifying what = 'mb'.
approxFun	Function to interpolate between measurement moments, <a href="#">approx()</a> by default.

---

lcMethod-class	<i>lcMethod class</i>
----------------	-----------------------

---

**Description**

lcMethod objects represent the specification of a method for longitudinal clustering. Furthermore, the object class contains the logic for estimating the respective method.

You can specify a longitudinal cluster method through one of the method-specific constructor functions, e.g., `lcMethodKML()`, `lcMethodLcmmGBTM()`, or `lcMethodDtwclust()`. Alternatively, you can instantiate methods through `methods::new()`, e.g., by calling `new("lcMethodKML", response = "Value")`. In both cases, default values are specified for omitted arguments.

**Details**

Because the lcMethod arguments may be unevaluated, argument retrieval functions such as `[[` accept an `envir` argument. A default environment can be assigned or obtained from a lcMethod object using the `environment()` function.

**Slots**

`arguments` A list representing the arguments of the lcMethod object. Arguments are not evaluated upon creation of the method object. Instead, arguments are stored similar to a call object, and are only evaluated when a method is fitted. Do not modify or access.

`sourceCalls` A list of calls for tracking the original call after substitution. Used for printing objects which require too many characters (e.g. function definitions, matrices). Do not modify or access.

### Method arguments

An lcMethod objects represent the specification of a method with a set of configurable parameters (referred to as arguments).

Arguments can be of any type. It is up to the lcMethod implementation of `validate()` to ensure that the required arguments are present and are of the expected type.

Arguments can have almost any name. Exceptions include the names "data", "envir", and "verbose". Furthermore, argument names may not start with a period (".").

Arguments cannot be directly modified, i.e., lcMethod objects are immutable. Modifying an argument involves creating an altered copy through the `update.lcMethod` method.

### Fitting procedure

Each lcMethod subclass defines a type of methods in terms of a series of steps for estimating the method. These steps, as part of the fitting procedure, are executed by `latrend()` in the following order:

1. `compose()`: Evaluate and finalize the method argument values.
2. `validate()`: Check the validity of the method argument values in relation to the dataset.
3. `prepareData()`: Process the training data for fitting.
4. `preFit()`: Prepare environment for estimation, independent of training data.
5. `fit()`: Estimate the specified method on the training data, outputting an object inheriting from lcModel.
6. `postFit()`: Post-process the outputted lcModel object.

The result of the fitting procedure is an `lcModel` object that inherits from the `lcModel` class.

### Implementation

The base class lcMethod provides the logic for storing, evaluating, and printing the method parameters.

Subclasses of lcMethod differ only in the fitting procedure logic (see above).

To implement your own lcMethod subclass, you'll want to implement at least the following functions:

- `fit()`: The main function for estimating your method.
- `getName()`: The name of your method.
- `getShortName()`: The abbreviated name of your method.
- `getArgumentDefaults()`: Sensible default argument values to your method.

For more complex methods, the additional functions as part of the fitting procedure (see the *Fitting procedure* section above) will be of use.



**See Also**

[environment](#)

Other lcMethod implementations: [getArgumentDefaults\(\)](#), [getArgumentExclusions\(\)](#), [lcMethodAkmedoids](#), [lcMethodCrimCV](#), [lcMethodCustom](#), [lcMethodDtwclust](#), [lcMethodFeature](#), [lcMethodFunFEM](#), [lcMethodGCKM](#), [lcMethodKML](#), [lcMethodLMKM](#), [lcMethodLcmmGBTM](#), [lcMethodLcmmGMM](#), [lcMethodLongclust](#), [lcMethodMclustLLPA](#), [lcMethodMixAK\\_GLMM](#), [lcMethodMixtoolsGMM](#), [lcMethodMixtoolsNPRM](#), [lcMethodRandom](#), [lcMethodStratify](#)

Other lcMethod functions: [\[\[,lcMethod-method,as.data.frame.lcMethods\(\),as.data.frame.lcMethod\(\),as.lcMethods\(\),as.list.lcMethod\(\),evaluate.lcMethod\(\),formula.lcMethod\(\),names,lcMethod-method,update.lcMethod\(\)](#)

**Examples**

```
kmlMethod <- lcMethodKML(response = "Value", nClusters = 2)
kmlMethod

kmlMethod <- new("lcMethodKML", response = "Value", nClusters = 2)

# create a copy with updated nClusters argument
kmlMethod3 <- update(kmlMethod, nClusters = 3)

# get argument names
names(kmlMethod)

# evaluate argument
kmlMethod$nClusters
```

---

lcMethodAkmedoids	<i>Specify AKMedoids method</i>
-------------------	---------------------------------

---

**Description**

Specify AKMedoids method

**Usage**

```
lcMethodAkmedoids(
  response,
  time = getOption("latrend.time"),
  id = getOption("latrend.id"),
  nClusters = 3,
  clusterCenter = median,
  crit = "Calinski_Harabasz",
  ...
)
```

**Arguments**

response	The name of the response variable.
time	The name of the time variable.
id	The name of the trajectory identification variable.
nClusters	The number of clusters to estimate.
clusterCenter	A function for computing the cluster center representation.
crit	Criterion to apply for internal model selection. Not applicable.
...	Arguments passed to <code>akmedoids::akclustr</code> . The following external arguments are ignored: <code>traj</code> , <code>id_field</code> , <code>k</code>

**References**

Adepeju M, Langton S, Bannister J (2020). *akmedoids: Anchored Kmedoids for Longitudinal Data Clustering*. R package version 0.1.5, <https://CRAN.R-project.org/package=akmedoids>.

**See Also**

Other lcMethod implementations: `getArgumentDefaults()`, `getArgumentExclusions()`, `lcMethod-class`, `lcMethodCrimCV`, `lcMethodCustom`, `lcMethodDtwclust`, `lcMethodFeature`, `lcMethodFunFEM`, `lcMethodGCKM`, `lcMethodKML`, `lcMethodLMKM`, `lcMethodLcmmGBTM`, `lcMethodLcmmGMM`, `lcMethodLongclust`, `lcMethodMclustLLPA`, `lcMethodMixAK_GLMM`, `lcMethodMixtoolsGMM`, `lcMethodMixtoolsNPRM`, `lcMethodRandom`, `lcMethodStratify`

**Examples**

```
library(akmedoids)
data(latrendData)
method <- lcMethodAkmedoids(response = "Y", time = "Time", id = "Id", nClusters = 3)
model <- latrend(method, data = latrendData)
```

---

lcMethodCrimCV

*Specify a zero-inflated repeated-measures GBTM method*


---

**Description**

Specify a zero-inflated repeated-measures GBTM method

**Usage**

```
lcMethodCrimCV(
  response,
  time = getOption("latrend.time"),
  id = getOption("latrend.id"),
  nClusters = 2,
  ...
)
```

**Arguments**

response	The name of the response variable.
time	The name of the time variable.
id	The name of the trajectory identifier variable.
nClusters	The number of clusters to estimate.
...	Arguments passed to <code>crimCV::crimCV</code> . The following external arguments are ignored: <code>Dat</code> , <code>ng</code> .

**References**

Nielsen JD (2018). *crimCV: Group-Based Modelling of Longitudinal Data*. R package version 0.9.6, <https://CRAN.R-project.org/package=crimCV>.

**See Also**

Other lcMethod implementations: `getArgumentDefaults()`, `getArgumentExclusions()`, `lcMethod-class`, `lcMethodAkmedoids`, `lcMethodCustom`, `lcMethodDtwclust`, `lcMethodFeature`, `lcMethodFunFEM`, `lcMethodGCKM`, `lcMethodKML`, `lcMethodLMKM`, `lcMethodLcmmGBTM`, `lcMethodLcmmGMM`, `lcMethodLongclust`, `lcMethodMclustLLPA`, `lcMethodMixAK_GLMM`, `lcMethodMixtoolsGMM`, `lcMethodMixtoolsNPRM`, `lcMethodRandom`, `lcMethodStratify`

**Examples**

```
library(crimCV)
data(latrendData)
method <- lcMethodCrimCV("Y", id = "Id", time = "Time", nClusters = 3, dpolyp = 1, init = 2)
model <- latrend(method, data = subset(latrendData, Time > .5))
plot(model)

data(T01adj)
method <- lcMethodCrimCV(response = "Offenses", time = "Offense", id = "Subject",
  nClusters = 2, dpolyp = 1, init = 2)
model <- latrend(method, data = T01adj[1:100, ])
```

---

lcMethodCustom

*Specify a custom method based on a model function*


---

**Description**

Specify a custom method based on a model function

**Usage**

```
lcMethodCustom(
  response,
  fun,
  center = meanNA,
  time = getOption("latrend.time"),
  id = getOption("latrend.id"),
  name = "custom"
)
```

**Arguments**

response	The name of the response variable.
fun	The cluster function with signature (method, data).
center	Optional function for computing the longitudinal cluster centers, with signature (x).
time	The name of the time variable.
id	The name of the trajectory identification variable.
name	The name of the method.

**See Also**

Other lcMethod implementations: [getArgumentDefaults\(\)](#), [getArgumentExclusions\(\)](#), [lcMethod-class](#), [lcMethodAkmedoids](#), [lcMethodCrimCV](#), [lcMethodDtwclust](#), [lcMethodFeature](#), [lcMethodFunFEM](#), [lcMethodGCKM](#), [lcMethodKML](#), [lcMethodLMKM](#), [lcMethodLcmmGBTM](#), [lcMethodLcmmGMM](#), [lcMethodLongclust](#), [lcMethodMclustLLPA](#), [lcMethodMixAK\\_GLMM](#), [lcMethodMixtoolsGMM](#), [lcMethodMixtoolsNPRM](#), [lcMethodRandom](#), [lcMethodStratify](#)

**Examples**

```
data(latrendData)
# Stratification based on the mean response level
clusfun <- function(data, response, id, time, ...) {
  clusters <- data.table::as.data.table(data)[, mean(Y) > 0, by = Id]$V1
  lcModelCustom(data = data,
    trajectoryAssignments = factor(clusters, levels = c(FALSE, TRUE), labels = c("Low", "High")),
    response = response,
    time = time,
    id = id)
}
method <- lcMethodCustom(response = "Y", fun = clusfun, id = "Id", time = "Time")
model <- latrend(method, data = latrendData)
```

---

lcMethodDtwclust      *Specify time series clustering via dtwclust*

---

### Description

Specify time series clustering via dtwclust

### Usage

```
lcMethodDtwclust(  
  response,  
  time = getOption("latrend.time"),  
  id = getOption("latrend.id"),  
  nClusters = 2,  
  ...  
)
```

### Arguments

response	The name of the response variable.
time	The name of the time variable.
id	The name of the trajectory identifier variable.
nClusters	Number of clusters.
...	Arguments passed to <code>dtwclust::tsclust</code> . The following arguments are ignored: series, k, trace.

### References

Sardá-Espinosa A (2019). "Time-Series Clustering in R Using the dtwclust Package." *The R Journal*. doi: [10.32614/RJ2019023](https://doi.org/10.32614/RJ2019023).

### See Also

Other lcMethod implementations: [getArgumentDefaults\(\)](#), [getArgumentExclusions\(\)](#), [lcMethod-class](#), [lcMethodAkmedoids](#), [lcMethodCrimCV](#), [lcMethodCustom](#), [lcMethodFeature](#), [lcMethodFunFEM](#), [lcMethodGCKM](#), [lcMethodKML](#), [lcMethodLMKM](#), [lcMethodLcmmGBTM](#), [lcMethodLcmmGMM](#), [lcMethodLongclust](#), [lcMethodMclustLLPA](#), [lcMethodMixAK\\_GLMM](#), [lcMethodMixtoolsGMM](#), [lcMethodMixtoolsNPRM](#), [lcMethodRandom](#), [lcMethodStratify](#)

### Examples

```
library(dtwclust)  
data(latrendData)  
method <- lcMethodDtwclust("Y", id = "Id", time = "Time", nClusters = 3)  
model <- latrend(method, latrendData)
```

---

lcMethodFeature      *Feature-based clustering*

---

### Description

Feature-based clustering.

### Usage

```
lcMethodFeature(
  response,
  representationStep,
  clusterStep,
  standardize = scale,
  center = meanNA,
  time = getOption("latrend.time"),
  id = getOption("latrend.id"),
  ...
)
```

### Arguments

response	The name of the response variable.
representationStep	A function with signature <code>function(method, data)</code> that computes the representation per strata, returned as a matrix. Alternatively, <code>representationStep</code> is a pre-computed representation matrix.
clusterStep	A function with signature <code>function(repdata)</code> that outputs a <code>lcModel</code> .
standardize	A function to standardize the output matrix of the representation step. By default, the output is shifted and rescaled to ensure zero mean and unit variance.
center	Optional function for computing the longitudinal cluster centers, with signature <code>(x)</code> .
time	The name of the time variable.
id	The name of the trajectory identification variable.
...	Additional arguments.

### Linear regression & k-means example

In this example we define a feature-based approach where each trajectory is represented using a linear regression model. The coefficients of the trajectories are then clustered using k-means.

Note that this method is already implemented as `lcMethodLMKM()`.

Representation step:

```

repStep <- function(method, data, verbose) {
  library(data.table)
  library(magrittr)
  xdata = as.data.table(data)
  coefdata <- xdata[,
    lm(method$formula, .SD)
    keyby = c(method$id)
  ]
  # exclude the id column
  coefmat <- subset(coefdata, select = -1)
  rownames(coefmat) <- coefdata[[method$id]]
  return(coefmat)
}

```

Cluster step:

```

clusStep <- function(method, data, repMat, envir, verbose) {
  km <- kmeans(repMat, centers = method$nClusters)

  lcModelCustom(
    response = method$response,
    method = method,
    data = data,
    trajectoryAssignments = km$cluster,
    clusterTrajectories = method$center,
    model = km
  )
}

```

Now specify the method and fit the model:

```

data(latrendData)
method <- lcMethodFeature(
  formula = Y ~ Time,
  response = "Y",
  id = "Id",
  time = "Time",
  representationStep = repStep,
  clusterStep = clusStep

model <- latrend(method, data = latrendData)
)

```

### See Also

Other lcMethod implementations: [getArgumentDefaults\(\)](#), [getArgumentExclusions\(\)](#), [lcMethod-class](#), [lcMethodAkmedoids](#), [lcMethodCrimCV](#), [lcMethodCustom](#), [lcMethodDtwclust](#), [lcMethodFunFEM](#), [lcMethodGCKM](#), [lcMethodKML](#), [lcMethodLMKM](#), [lcMethodLcmmGBTM](#), [lcMethodLcmmGMM](#), [lcMethodLongclust](#), [lcMethodMclustLLPA](#), [lcMethodMixAK\\_GLMM](#), [lcMethodMixtoolsGMM](#), [lcMethodMixtoolsNPRM](#), [lcMethodRandom](#), [lcMethodStratify](#)

---

lcMethodFlexmix      *Method interface to flexmix()*

---

### Description

Wrapper to the flexmix() method from the flexmix package.

### Usage

```
lcMethodFlexmix(
  formula,
  formula.mb = ~1,
  time = getOption("latrend.time"),
  id = getOption("latrend.id"),
  nClusters = 2,
  ...
)
```

### Arguments

formula	A formula specifying the model.
formula.mb	A formula specifying the class membership model. By default, an intercept-only model is used.
time	The name of the time variable.
id	The name of the trajectory identifier variable.
nClusters	The number of clusters to estimate.
...	Arguments passed to <code>flexmix::flexmix</code> . The following arguments are ignored: data, concomitant, k.

### References

Grün B, Leisch F (2008). "FlexMix Version 2: Finite Mixtures with Concomitant Variables and Varying and Constant Parameters." *Journal of Statistical Software*, **28**(4), 1–35. doi: [10.18637/jss.v028.i04](https://doi.org/10.18637/jss.v028.i04).

### See Also

Other lcMethod package interfaces: [lcMethodFlexmixGBTM](#)

### Examples

```
library(flexmix)
data(latrendData)
method <- lcMethodFlexmix(Y ~ Time, id = "Id", time = "Time", nClusters = 3)
model <- latrend(method, latrendData)
```



---

 lcMethodFlexmixGBTM *Group-based trajectory modeling using flexmix*


---

## Description

Fits a GBTM based on the `flexmix::FLXMRglm` driver.

## Usage

```
lcMethodFlexmixGBTM(
  formula,
  formula.mb = ~1,
  time = getOption("latrend.time"),
  id = getOption("latrend.id"),
  nClusters = 2,
  ...
)
```

## Arguments

<code>formula</code>	A formula specifying the model.
<code>formula.mb</code>	A formula specifying the class membership model. By default, an intercept-only model is used.
<code>time</code>	The name of the time variable.
<code>id</code>	The name of the trajectory identifier variable.
<code>nClusters</code>	The number of clusters to estimate.
<code>...</code>	Arguments passed to <code>flexmix::flexmix</code> or <code>flexmix::FLXMRglm</code> . The following arguments are ignored: <code>data</code> , <code>k</code> , <code>trace</code> .

## References

Grün B, Leisch F (2008). "FlexMix Version 2: Finite Mixtures with Concomitant Variables and Varying and Constant Parameters." *Journal of Statistical Software*, **28**(4), 1–35. doi: [10.18637/jss.v028.i04](https://doi.org/10.18637/jss.v028.i04).

## See Also

Other lcMethod package interfaces: `lcMethodFlexmix`

## Examples

```
library(flexmix)
data(latrendData)
method <- lcMethodFlexmixGBTM(Y ~ Time, id = "Id", time = "Time", nClusters = 3)
model <- latrend(method, latrendData)
```

---

lcMethodFunFEM	<i>Specify a FunFEM method</i>
----------------	--------------------------------

---

### Description

Specify a FunFEM method

### Usage

```
lcMethodFunFEM(
  response,
  time = getOption("latrend.time"),
  id = getOption("latrend.id"),
  nClusters = 2,
  basis = function(time) fda::create.bspline.basis(time, nbasis = 10, norder = 4),
  ...
)
```

### Arguments

response	The name of the response variable.
time	The name of the time variable.
id	The name of the trajectory identifier variable.
nClusters	The number of clusters to estimate.
basis	The basis function. By default, a 3rd-order B-spline with 10 breaks is used.
...	Arguments passed to <code>funFEM::funFEM</code> . The following external arguments are ignored: <code>fd</code> , <code>K</code> , <code>disp</code> , <code>graph</code> .

### References

Bouveyron C (2015). *funFEM: Clustering in the Discriminative Functional Subspace*. R package version 1.1, <https://CRAN.R-project.org/package=funFEM>.

### See Also

Other lcMethod implementations: `getArgumentDefaults()`, `getArgumentExclusions()`, `lcMethod-class`, `lcMethodAkmedoids`, `lcMethodCrimCV`, `lcMethodCustom`, `lcMethodDtwclust`, `lcMethodFeature`, `lcMethodGCKM`, `lcMethodKML`, `lcMethodLMKM`, `lcMethodLcmmGBTM`, `lcMethodLcmmGMM`, `lcMethodLongclust`, `lcMethodMclustLLPA`, `lcMethodMixAK_GLMM`, `lcMethodMixtoolsGMM`, `lcMethodMixtoolsNPRM`, `lcMethodRandom`, `lcMethodStratify`

**Examples**

```

library(funFEM)
library(fda)
data(latrendData)
method <- lcMethodFunFEM("Y", id = "Id", time = "Time", nClusters = 3)
model <- latrend(method, latrendData)

method <- lcMethodFunFEM("Y",
  basis = function(time) {
    create.bspline.basis(time,
      nbasis = 10, norder = 4)
  })

```

---

lcMethodGCKM	<i>Two-step clustering through latent growth curve modeling and k-means</i>
--------------	---

---

**Description**

Two-step clustering through latent growth curve modeling and k-means.

**Usage**

```

lcMethodGCKM(
  formula,
  time = getOption("latrend.time"),
  id = getOption("latrend.id"),
  nClusters = 2,
  center = meanNA,
  standardize = scale,
  ...
)

```

**Arguments**

formula	Formula, including a random effects component for the trajectory. See <a href="#">lme4::lmer</a> formula syntax.
time	The name of the time variable..
id	The name of the trajectory identifier variable.
nClusters	The number of clusters.
center	A function that computes the cluster center based on the original trajectories associated with the respective cluster. By default, the mean is computed.
standardize	A function to standardize the output matrix of the representation step. By default, the output is shifted and rescaled to ensure zero mean and unit variance.
...	Arguments passed to <a href="#">lme4::lmer</a> . The following external arguments are ignored: data, centers, trace.

**See Also**

Other lcMethod implementations: [getArgumentDefaults\(\)](#), [getArgumentExclusions\(\)](#), [lcMethod-class](#), [lcMethodAkmedoids](#), [lcMethodCrimCV](#), [lcMethodCustom](#), [lcMethodDtwclust](#), [lcMethodFeature](#), [lcMethodFunFEM](#), [lcMethodKML](#), [lcMethodLMKM](#), [lcMethodLcmmGBTM](#), [lcMethodLcmmGMM](#), [lcMethodLongclust](#), [lcMethodMclustLLPA](#), [lcMethodMixAK\\_GLMM](#), [lcMethodMixtoolsGMM](#), [lcMethodMixtoolsNPRM](#), [lcMethodRandom](#), [lcMethodStratify](#)

**Examples**

```
library(lme4)
data(latrendData)
method <- lcMethodGCKM(Y ~ (Time | Id), id = "Id", time = "Time", nClusters = 3)
model <- latrend(method, latrendData)
```

---

lcMethodKML

*Specify a longitudinal k-means (KML) method*


---

**Description**

Specify a longitudinal k-means (KML) method

**Usage**

```
lcMethodKML(
  response,
  time = getOption("latrend.time"),
  id = getOption("latrend.id"),
  nClusters = 2,
  ...
)
```

**Arguments**

response	The name of the response variable.
time	The name of the time variable.
id	The name of the trajectory identifier variable.
nClusters	The number of clusters to estimate.
...	Arguments passed to <a href="#">kml::parALGO</a> and <a href="#">kml::kml</a> .

The following external arguments are ignored: object, nbClusters, parAlgo, toPlot, saveFreq

**References**

Genolini C, Alacoque X, Sentenac M, Arnaud C (2015). “kml and kml3d: R Packages to Cluster Longitudinal Data.” *Journal of Statistical Software*, **65**(4), 1–34. doi: [10.18637/jss.v065.i04](https://doi.org/10.18637/jss.v065.i04).

**See Also**

Other lcMethod implementations: [getArgumentDefaults\(\)](#), [getArgumentExclusions\(\)](#), [lcMethod-class](#), [lcMethodAkmedoids](#), [lcMethodCrimCV](#), [lcMethodCustom](#), [lcMethodDtwclust](#), [lcMethodFeature](#), [lcMethodFunFEM](#), [lcMethodGCKM](#), [lcMethodLMKM](#), [lcMethodLcmmGBTM](#), [lcMethodLcmmGMM](#), [lcMethodLongclust](#), [lcMethodMclustLLPA](#), [lcMethodMixAK\\_GLMM](#), [lcMethodMixtoolsGMM](#), [lcMethodMixtoolsNPRM](#), [lcMethodRandom](#), [lcMethodStratify](#)

**Examples**

```
library(kml)
data(latrendData)
method <- lcMethodKML("Y", id = "Id", time = "Time", nClusters = 3)
model <- latrend(method, latrendData)
```

---

lcMethodLcmmGBTM	<i>Specify GBTM method</i>
------------------	----------------------------

---

**Description**

Group-based trajectory modeling through fixed-effects modeling.

**Usage**

```
lcMethodLcmmGBTM(
  fixed,
  mixture = ~1,
  classmb = ~1,
  time = getOption("latrend.time"),
  id = getOption("latrend.id"),
  nClusters = 2,
  init = "default",
  ...
)
```

**Arguments**

fixed	The fixed effects formula.
mixture	The mixture-specific effects formula. See <a href="#">lcmm::hlme</a> for details.
classmb	The cluster membership formula for the multinomial logistic model. See <a href="#">lcmm::hlme</a> for details.
time	The name of the time variable.
id	The name of the trajectory identifier variable. This replaces the subject argument of <a href="#">lcmm::hlme</a> .
nClusters	The number of clusters to fit. This replaces the ng argument of <a href="#">lcmm::hlme</a> .

`init` Alternative for the B argument of `lcmm::hlme`, for initializing the hlme fitting procedure. If `"lme.random"` (default): random initialization through a standard linear mixed model. Assigns a fitted standard linear mixed model enclosed in a call to `random()` to the B argument. If `"lme"`, fits a standard linear mixed model and passes this to the B argument. If `NULL` or `"default"`, the default `lcmm::hlme` input for B is used.

The argument is ignored if the B argument is specified, or `nClusters = 1`.

`...` Arguments passed to `lcmm::hlme`. The following arguments are ignored: `data`, `fixed`, `random`, `mixture`, `subject`, `classmb`, `returndata`, `ng`, `verbose`, `subset`.

## References

Proust-Lima C, Philipps V, Lique B (2017). "Estimation of Extended Mixed Models Using Latent Classes and Latent Processes: The R Package `lcmm`." *Journal of Statistical Software*, **78**(2), 1–56. doi: [10.18637/jss.v078.i02](https://doi.org/10.18637/jss.v078.i02).

Proust-Lima C, Philipps V, Diakite A, Lique B (2019). *lcmm: Extended Mixed Models Using Latent Classes and Latent Processes*. R package version: 1.8.1, <https://cran.r-project.org/package=lcmm>.

## See Also

Other `lcMethod` implementations: `getArgumentDefaults()`, `getArgumentExclusions()`, `lcMethod-class`, `lcMethodAkmedoids`, `lcMethodCrimCV`, `lcMethodCustom`, `lcMethodDtwclust`, `lcMethodFeature`, `lcMethodFunFEM`, `lcMethodGCKM`, `lcMethodKML`, `lcMethodLMKM`, `lcMethodLcmmGMM`, `lcMethodLongclust`, `lcMethodMclustLLPA`, `lcMethodMixAK_GLMM`, `lcMethodMixtoolsGMM`, `lcMethodMixtoolsNPRM`, `lcMethodRandom`, `lcMethodStratify`

## Examples

```
data(latrendData)
method <- lcMethodLcmmGBTM(fixed = Y ~ Time, mixture = ~ 1,
  id = "Id", time = "Time", nClusters = 3)
gbtm <- latrend(method, data = latrendData)
summary(gbtm)

method <- lcMethodLcmmGBTM(fixed = Y ~ Time, mixture = ~ Time,
  id = "Id", time = "Time", nClusters = 3)
```

---

lcMethodLcmmGMM

*Specify GMM method using lcmm*

---

## Description

Growth mixture modeling through latent-class linear mixed modeling.

**Usage**

```
lcMethodLcmmGMM(
  fixed,
  mixture = ~1,
  random = ~1,
  classmb = ~1,
  time = getOption("latrend.time"),
  id = getOption("latrend.id"),
  init = "default",
  nClusters = 2,
  ...
)
```

**Arguments**

<code>fixed</code>	The fixed effects formula.
<code>mixture</code>	The mixture-specific effects formula. See <a href="#">lcmm::hlme</a> for details.
<code>random</code>	The random effects formula. See <a href="#">lcmm::hlme</a> for details.
<code>classmb</code>	The cluster membership formula for the multinomial logistic model. See <a href="#">lcmm::hlme</a> for details.
<code>time</code>	The name of the time variable.
<code>id</code>	The name of the trajectory identifier variable. This replaces the subject argument of <a href="#">lcmm::hlme</a> .
<code>init</code>	Alternative for the B argument of <a href="#">lcmm::hlme</a> , for initializing the hlme fitting procedure. If "lme.random" (default): random initialization through a standard linear mixed model. Assigns a fitted standard linear mixed model enclosed in a call to <code>random()</code> to the B argument. If "lme", fits a standard linear mixed model and passes this to the B argument. If NULL or "default", the default <a href="#">lcmm::hlme</a> input for B is used. The argument is ignored if the B argument is specified, or <code>nClusters = 1</code> .
<code>nClusters</code>	The number of clusters to fit. This replaces the <code>ng</code> argument of <a href="#">lcmm::hlme</a> .
<code>...</code>	Arguments passed to <a href="#">lcmm::hlme</a> . The following arguments are ignored: <code>data</code> , <code>fixed</code> , <code>random</code> , <code>mixture</code> , <code>subject</code> , <code>classmb</code> , <code>returndata</code> , <code>ng</code> , <code>verbose</code> , <code>subset</code> .

**References**

Proust-Lima C, Philipps V, Lique B (2017). "Estimation of Extended Mixed Models Using Latent Classes and Latent Processes: The R Package lcmm." *Journal of Statistical Software*, **78**(2), 1–56. doi: [10.18637/jss.v078.i02](https://doi.org/10.18637/jss.v078.i02).

Proust-Lima C, Philipps V, Diakite A, Lique B (2019). *lcmm: Extended Mixed Models Using Latent Classes and Latent Processes*. R package version: 1.8.1, <https://cran.r-project.org/package=lcmm>.

**See Also**

Other lcMethod implementations: `getArgumentDefaults()`, `getArgumentExclusions()`, `lcMethod-class`, `lcMethodAkmedoids`, `lcMethodCrimCV`, `lcMethodCustom`, `lcMethodDtwclust`, `lcMethodFeature`, `lcMethodFunFEM`, `lcMethodGCKM`, `lcMethodKML`, `lcMethodLMKM`, `lcMethodLcmmGBTM`, `lcMethodLongclust`, `lcMethodMclustLLPA`, `lcMethodMixAK_GLMM`, `lcMethodMixtoolsGMM`, `lcMethodMixtoolsNPRM`, `lcMethodRandom`, `lcMethodStratify`

**Examples**

```
data(latrendData)
method <- lcMethodLcmmGMM(fixed = Y ~ Time,
  mixture = ~ Time, random = ~ 1,
  id = "Id", time = "Time", , nClusters = 3)
gmm <- latrend(method, data = latrendData)
summary(gmm)

method <- lcMethodLcmmGMM(fixed = Y ~ Time,
  mixture = ~ Time, random = ~ Time,
  id = "Id", time = "Time", nClusters = 3)
```

---

 lcMethodLMKM

*Two-step clustering through linear regression modeling and k-means*


---

**Description**

Two-step clustering through linear regression modeling and k-means

**Usage**

```
lcMethodLMKM(
  formula,
  time = getOption("latrend.time"),
  id = getOption("latrend.id"),
  nClusters = 2,
  center = meanNA,
  standardize = scale,
  ...
)
```

**Arguments**

<code>formula</code>	A formula specifying the linear trajectory model.
<code>time</code>	The name of the time variable.
<code>id</code>	The name of the trajectory identification variable.
<code>nClusters</code>	The number of clusters to estimate.
<code>center</code>	A function that computes the cluster center based on the original trajectories associated with the respective cluster. By default, the mean is computed.



standardize     A function to standardize the output matrix of the representation step. By default, the output is shifted and rescaled to ensure zero mean and unit variance.

...                Arguments passed to `stats::lm`. The following external arguments are ignored: `x`, `data`, `control`, `centers`, `trace`.

### See Also

Other lcMethod implementations: `getArgumentDefaults()`, `getArgumentExclusions()`, `lcMethod-class`, `lcMethodAkmedoids`, `lcMethodCrimCV`, `lcMethodCustom`, `lcMethodDtwclust`, `lcMethodFeature`, `lcMethodFunFEM`, `lcMethodGCKM`, `lcMethodKML`, `lcMethodLcmmGBTM`, `lcMethodLcmmGMM`, `lcMethodLongclust`, `lcMethodMclustLLPA`, `lcMethodMixAK_GLMM`, `lcMethodMixtoolsGMM`, `lcMethodMixtoolsNPRM`, `lcMethodRandom`, `lcMethodStratify`

### Examples

```
data(latrendData)
method <- lcMethodLMKM(Y ~ Time, id = "Id", time = "Time", nClusters = 3)
model <- latrend(method, latrendData)
```

---

lcMethodLongclust     *Specify Longclust method*

---

### Description

Specify Longclust method

### Usage

```
lcMethodLongclust(
  response,
  time = getOption("latrend.time"),
  id = getOption("latrend.id"),
  nClusters = 2,
  ...
)
```

### Arguments

`response`        The name of the response variable.

`time`             The name of the time variable.

`id`                The name of the trajectory identifier variable.

`nClusters`        The number of clusters to estimate.

...                Arguments passed to `longclust::longclustEM`. The following external arguments are ignored: `data`, `x`, `Gmin`, `Gmax`, `userseed`.

## References

McNicholas PD, Jampani KR, Subedi S (2019). *longclust: Model-Based Clustering and Classification for Longitudinal Data*. R package version 1.2.3, <https://CRAN.R-project.org/package=longclust>.

## See Also

Other lcMethod implementations: [getArgumentDefaults\(\)](#), [getArgumentExclusions\(\)](#), [lcMethod-class](#), [lcMethodAkmedoids](#), [lcMethodCrimCV](#), [lcMethodCustom](#), [lcMethodDtwclust](#), [lcMethodFeature](#), [lcMethodFunFEM](#), [lcMethodGCKM](#), [lcMethodKML](#), [lcMethodLMKM](#), [lcMethodLcmmGBTM](#), [lcMethodLcmmGMM](#), [lcMethodMclustLLPA](#), [lcMethodMixAK\\_GLMM](#), [lcMethodMixtoolsGMM](#), [lcMethodMixtoolsNPRM](#), [lcMethodRandom](#), [lcMethodStratify](#)

## Examples

```
library(longclust)
data(latrendData)
method <- lcMethodLongclust("Y", id = "Id", time = "Time", nClusters = 3)
model <- latrend(method, latrendData)
```

---

lcMethodMclustLLPA      *Longitudinal latent profile analysis*

---

## Description

Latent profile analysis or finite Gaussian mixture modeling.

## Usage

```
lcMethodMclustLLPA(
  response,
  time = getOption("latrend.time"),
  id = getOption("latrend.id"),
  nClusters = 2,
  ...
)
```

## Arguments

response	The name of the response variable.
time	The name of the time variable.
id	The name of the trajectory identifier variable.
nClusters	The number of clusters to estimate.
...	Arguments passed to <a href="#">mclust::Mclust</a> . The following external arguments are ignored: data, G, verbose.

## References

Scrucca L, Fop M, Murphy TB, Raftery AE (2016). “mclust 5: clustering, classification and density estimation using Gaussian finite mixture models.” *The R Journal*, **8**(1), 205–233.

## See Also

Other lcMethod implementations: [getArgumentDefaults\(\)](#), [getArgumentExclusions\(\)](#), [lcMethod-class](#), [lcMethodAkmedoids](#), [lcMethodCrimCV](#), [lcMethodCustom](#), [lcMethodDtwclust](#), [lcMethodFeature](#), [lcMethodFunFEM](#), [lcMethodGCKM](#), [lcMethodKML](#), [lcMethodLMKM](#), [lcMethodLcmmGBTM](#), [lcMethodLcmmGMM](#), [lcMethodLongclust](#), [lcMethodMixAK\\_GLMM](#), [lcMethodMixtoolsGMM](#), [lcMethodMixtoolsNPRM](#), [lcMethodRandom](#), [lcMethodStratify](#)

## Examples

```
library(mclust)
data(latrendData)
method <- lcMethodMclustLLPA("Y", id = "Id", time = "Time", nClusters = 3)
model <- latrend(method, latrendData)
```

---

lcMethodMixAK\_GLMM      *Specify a GLMM iwht a normal mixture in the random effects*

---

## Description

Specify a GLMM iwht a normal mixture in the random effects

## Usage

```
lcMethodMixAK_GLMM(
  fixed,
  random,
  time = getOption("latrend.time"),
  id = getOption("latrend.id"),
  nClusters = 2,
  ...
)
```

## Arguments

fixed	A formula specifying the fixed effects of the model, including the response. Creates the y and x arguments for the call to <a href="#">mixAK::GLMM_MCMC</a> .
random	A formula specifying the random effects of the model, including the random intercept. Creates the z and random.intercept arguments for the call to <a href="#">mixAK::GLMM_MCMC</a> .
time	The name of the time variable.
id	The name of the trajectory identifier variable. This is used to generate the id vector argument for the call to <a href="#">mixAK::GLMM_MCMC</a> .

nClusters      The number of clusters.  
 ...            Arguments passed to `mixAK::GLMM_MCMC`. The following external arguments are ignored: `y`, `x`, `z`, `random.intercept`, `silent`.

## References

Komárek A (2009). “A New R Package for Bayesian Estimation of Multivariate Normal Mixtures Allowing for Selection of the Number of Components and Interval-Censored Data.” *Computational Statistics & Data Analysis*, **53**(12), 3932–3947. doi: [10.1016/j.csda.2009.05.006](https://doi.org/10.1016/j.csda.2009.05.006).

## See Also

Other lcMethod implementations: `getArgumentDefaults()`, `getArgumentExclusions()`, `lcMethod-class`, `lcMethodAkmedoids`, `lcMethodCrimCV`, `lcMethodCustom`, `lcMethodDtwclust`, `lcMethodFeature`, `lcMethodFunFEM`, `lcMethodGCKM`, `lcMethodKML`, `lcMethodLMKM`, `lcMethodLcmmGBTM`, `lcMethodLcmmGMM`, `lcMethodLongclust`, `lcMethodMclustLLPA`, `lcMethodMixtoolsGMM`, `lcMethodMixtoolsNPRM`, `lcMethodRandom`, `lcMethodStratify`

## Examples

```
data(latrendData)
# this example only runs when the mixAK package is installed
try({
  method <- lcMethodMixAK_GLMM(fixed = Y ~ 1, random = ~ Time,
    id = "Id", time = "Time", nClusters = 3)
  model <- latrend(method, latrendData)
  summary(model)
})
```

---

lcMethodMixtoolsGMM      *Specify mixed mixture regression model using mixtools*

---

## Description

Specify mixed mixture regression model using mixtools

## Usage

```
lcMethodMixtoolsGMM(
  formula,
  time = getOption("latrend.time"),
  id = getOption("latrend.id"),
  nClusters = 2,
  ...
)
```

**Arguments**

formula	Formula, including a random effects component for the trajectory. See <a href="#">lme4::lmer</a> formula syntax.
time	The name of the time variable..
id	The name of the trajectory identifier variable.
nClusters	The number of clusters.
...	Arguments passed to <a href="#">mixtools::regmixEM.mixed</a> . The following arguments are ignored: data, y, x, w, k, addintercept.fixed, verb.

**References**

Benaglia T, Chauveau D, Hunter DR, Young D (2009). “mixtools: An R Package for Analyzing Finite Mixture Models.” *Journal of Statistical Software*, **32**(6), 1–29. doi: [10.18637/jss.v032.i06](https://doi.org/10.18637/jss.v032.i06).

**See Also**

Other lcMethod implementations: [getArgumentDefaults\(\)](#), [getArgumentExclusions\(\)](#), [lcMethod-class](#), [lcMethodAkmedoids](#), [lcMethodCrimCV](#), [lcMethodCustom](#), [lcMethodDtwclust](#), [lcMethodFeature](#), [lcMethodFunFEM](#), [lcMethodGCKM](#), [lcMethodKML](#), [lcMethodLMKM](#), [lcMethodLcmmGBTM](#), [lcMethodLcmmGMM](#), [lcMethodLongclust](#), [lcMethodMclustLLPA](#), [lcMethodMixAK\\_GLMM](#), [lcMethodMixtoolsNPRM](#), [lcMethodRandom](#), [lcMethodStratify](#)

**Examples**

```
library(mixtools)
data(latrendData)
method <- lcMethodMixtoolsGMM(
  formula = Y ~ Time + (1 | Id),
  id = "Id", time = "Time",
  nClusters = 3,
  arb.R = FALSE)
```

---

lcMethodMixtoolsNPRM *Specify non-parametric estimation for independent repeated measures*

---

**Description**

Specify non-parametric estimation for independent repeated measures

**Usage**

```
lcMethodMixtoolsNPRM(
  response,
  time = getOption("latrend.time"),
  id = getOption("latrend.id"),
  nClusters = 2,
  blockid = NULL,
  bw = NULL,
  h = NULL,
  ...
)
```

**Arguments**

response	The name of the response variable.
time	The name of the time variable.
id	The name of the trajectory identifier variable.
nClusters	The number of clusters to estimate.
blockid	See <a href="#">mixtools::npEM</a> .
bw	See <a href="#">mixtools::npEM</a> .
h	See <a href="#">mixtools::npEM</a> .
...	Arguments passed to <a href="#">mixtools::npEM</a> . The following optional arguments are ignored: data, x, mu0, verb.

**References**

Benaglia T, Chauveau D, Hunter DR, Young D (2009). "mixtools: An R Package for Analyzing Finite Mixture Models." *Journal of Statistical Software*, **32**(6), 1–29. doi: [10.18637/jss.v032.i06](https://doi.org/10.18637/jss.v032.i06).

**See Also**

Other lcMethod implementations: [getArgumentDefaults\(\)](#), [getArgumentExclusions\(\)](#), [lcMethod-class](#), [lcMethodAkmedoids](#), [lcMethodCrimCV](#), [lcMethodCustom](#), [lcMethodDtwclust](#), [lcMethodFeature](#), [lcMethodFunFEM](#), [lcMethodGCKM](#), [lcMethodKML](#), [lcMethodLMKM](#), [lcMethodLcmmGBTM](#), [lcMethodLcmmGMM](#), [lcMethodLongclust](#), [lcMethodMclustLLPA](#), [lcMethodMixAK\\_GLMM](#), [lcMethodMixtoolsGMM](#), [lcMethodRandom](#), [lcMethodStratify](#)

**Examples**

```
library(mixtools)
data(latrendData)
method <- lcMethodMixtoolsNPRM("Y", id = "Id", time = "Time", nClusters = 3)
model <- latrend(method, latrendData)
```

---

lcMethodMixTVEM	<i>Specify a MixTVEM</i>
-----------------	--------------------------

---

**Description**

Specify a MixTVEM

**Usage**

```
lcMethodMixTVEM(
  formula,
  formula.mb = ~1,
  time = getOption("latrend.time"),
  id = getOption("latrend.id"),
  nClusters = 2,
  ...
)
```

**Arguments**

formula	A formula excluding the time component. Time-invariant covariates are detected automatically as these are a special case in MixTVEM.
formula.mb	A formula for cluster-membership prediction. Covariates must be time-invariant. Furthermore, the formula must contain an intercept.
time	The name of the time variable.
id	The name of the trajectory identifier variable.
nClusters	The number of clusters. This replaces the numClasses argument of the TVEMMixNormal function call.
...	Arguments passed to the TVEMMixNormal() function. The following optional arguments are ignored: doPlot, getSEs, numClasses.

**Note**

In order to use this method, you must download and source MixTVEM.R. See the reference below.

**References**

<https://github.com/dziakjl/MixTVEM>

Dziak JJ, Li R, Tan X, Shiffman S, Shiyko MP (2015). "Modeling intensive longitudinal data with mixtures of nonparametric trajectories and time-varying effects." *Psychological Methods*, **20**(4), 444–469. ISSN 1939-1463, doi: [10.1037/met0000048](https://doi.org/10.1037/met0000048).

## Examples

```
# this example only runs if you download and place MixTVEM.R in your wd
try({
  source('MixTVEM.R')
  method = lcMethodMixTVEM(Value ~ time(1) - 1,
                           time='Assessment',
                           id='Id', nClusters=3)
})
```

---

lcMethodRandom	<i>Specify a random-partitioning method</i>
----------------	---

---

## Description

Creates a model with random cluster assignments according to the random cluster proportions drawn from a Dirichlet distribution.

## Usage

```
lcMethodRandom(
  response,
  alpha = 10,
  center = meanNA,
  time = getOption("latrend.time"),
  id = getOption("latrend.id"),
  nClusters = 2,
  name = "random",
  ...
)
```

## Arguments

response	The name of the response variable.
alpha	The Dirichlet parameters. Either scalar or of length nClusters. The higher alpha, the more uniform the clusters will be.
center	Optional function for computing the longitudinal cluster centers, with signature (x).
time	The name of the time variable.
id	The name of the trajectory identification variable.
nClusters	The number of clusters.
name	The name of the method.
...	Additional arguments, such as the seed.



## References

Frigyik BA, Kapila A, Gupta MR (2010). "Introduction to the Dirichlet distribution and related processes." Technical Report UWEETR-2010-0006, Department of Electrical Engineering, University of Washington.

## See Also

Other lcMethod implementations: [getArgumentDefaults\(\)](#), [getArgumentExclusions\(\)](#), [lcMethod-class](#), [lcMethodAkmedoids](#), [lcMethodCrimCV](#), [lcMethodCustom](#), [lcMethodDtwclust](#), [lcMethodFeature](#), [lcMethodFunFEM](#), [lcMethodGCKM](#), [lcMethodKML](#), [lcMethodLMKM](#), [lcMethodLcmmGBTM](#), [lcMethodLcmmGMM](#), [lcMethodLongclust](#), [lcMethodMclustLLPA](#), [lcMethodMixAK\\_GLMM](#), [lcMethodMixtoolsGMM](#), [lcMethodMixtoolsNPRM](#), [lcMethodStratify](#)

## Examples

```
data(latrendData)
method <- lcMethodRandom(response = "Y", id = "Id", time = "Time")
model <- latrend(method, latrendData)

# uniform clusters
method <- lcMethodRandom(alpha = 1e3, nClusters = 3, response = "Y", id = "Id", time = "Time")

# single large cluster
method <- lcMethodRandom(alpha = c(100, 1, 1, 1), nClusters = 4,
  response = "Y", id = "Id", time = "Time")
```

---

 lcMethods

*Generate a list of lcMethod objects*


---

## Description

Generates a list of lcMethod objects for all combinations of the provided argument values.

## Usage

```
lcMethods(method, ..., envir = NULL)
```

## Arguments

method	The lcMethod to use as the template, which will be updated for each of the other arguments.
...	Any other arguments to update the lcMethod definition with. Values must be scalar, vector, list, or encapsulated in a <code>.()</code> call. Arguments wrapped in <code>.()</code> are passed as-is to the model call, ensuring a readable method. Arguments comprising a single symbol (e.g. a variable name) are interpreted as a constant. To force evaluation, specify <code>arg=(var)</code> or <code>arg=force(var)</code> . Arguments of type vector or list are split across a series of method fit calls. Arguments of type scalar are constant across the method fits. If a list is intended to be passed

as a constant argument, then specifying `arg=(listObject)` results in it being treated as such.

`envir` The environment in which to evaluate the method arguments.

### Value

A list of `lcMethod` objects.

### Examples

```
data(latrendData)
baseMethod <- lcMethodKML("Y", id = "Id", time = "Time")
methods <- lcMethods(baseMethod, nClusters = 1:6)

nclus <- 1:6
methods <- lcMethods(baseMethod, nClusters = nclus)

methods <- lcMethods(baseMethod, nClusters = 3, center = .(mean, mean, median))
length(methods) # 3

methods <- lcMethods(baseMethod, nClusters = 1:3, center = .(mean, mean, median))
length(methods) # 9
```

---

<code>lcMethodStratify</code>	<i>Specify a stratification method</i>
-------------------------------	--

---

### Description

Specify a stratification method

### Usage

```
lcMethodStratify(
  response,
  stratify,
  center = meanNA,
  nClusters = NaN,
  clusterNames = NULL,
  time = getOption("latrend.time"),
  id = getOption("latrend.id"),
  name = "stratify"
)
```

### Arguments

`response` The name of the response variable.

`stratify` An expression returning a number or factor value per trajectory, representing the cluster assignment. Alternatively, a function can be provided that takes separate trajectory data.frame as input.

center	The function for computing the longitudinal cluster centers, used for representing the cluster trajectories.
nClusters	The number of clusters. This is optional, as this can be derived from the largest assignment number by default, or the number of factor levels.
clusterNames	The names of the clusters. If a factor assignment is returned, the levels are used as the cluster names.
time	The name of the time variable.
id	The name of the trajectory identification variable.
name	The name of the method.

**See Also**

Other lcMethod implementations: [getArgumentDefaults\(\)](#), [getArgumentExclusions\(\)](#), [lcMethod-class](#), [lcMethodAkmedoids](#), [lcMethodCrimCV](#), [lcMethodCustom](#), [lcMethodDtwclust](#), [lcMethodFeature](#), [lcMethodFunFEM](#), [lcMethodGCKM](#), [lcMethodKML](#), [lcMethodLMKM](#), [lcMethodLcmmGBTM](#), [lcMethodLcmmGMM](#), [lcMethodLongclust](#), [lcMethodMclustLLPA](#), [lcMethodMixAK\\_GLMM](#), [lcMethodMixtoolsGMM](#), [lcMethodMixtoolsNPRM](#), [lcMethodRandom](#)

**Examples**

```
data(latrendData)
# Stratification based on the mean response level
method <- lcMethodStratify("Y", mean(Y) > 0,
  clusterNames = c("Low", "High"), id = "Id", time = "Time")
model <- latrend(method, latrendData)
summary(model)

# Stratification function
stratfun <- function(trajdata) {
  trajmean <- mean(trajdata$Y)
  factor(trajmean > 1.7,
    levels = c(FALSE, TRUE),
    labels = c("Low", "High"))
}
method <- lcMethodStratify("Y", stratfun, id = "Id", time = "Time")

# Multiple clusters
stratfun3 <- function(trajdata) {
  trajmean <- mean(trajdata$Y)
  cut(trajmean,
    c(-Inf, .5, 2, Inf),
    labels = c("Low", "Medium", "High"))
}
method <- lcMethodStratify("Y", stratfun3, id = "Id", time = "Time")
```

---

<code>lcModel-class</code>	<i>lcModel class</i>
----------------------------	----------------------

---

### Description

Abstract class for defining estimated longitudinal cluster models.

### Arguments

<code>object</code>	The <code>lcModel</code> object.
<code>...</code>	Any additional arguments.

### Details

An extending class must implement the following methods to ensure basic functionality:

- `predict.lcModelExt`: Used to obtain the fitted cluster trajectories and trajectories.
- `postprob(lcModelExt)`: The posterior probability matrix is used to determine the cluster assignments of the trajectories.

For predicting the posterior probability for unseen data, the `predictPostprob()` should be implemented.

### Slots

<code>method</code>	The <a href="#">lcMethod-class</a> object specifying the arguments under which the model was fitted.
<code>call</code>	The call that was used to create this <code>lcModel</code> object. Typically, this is the call to <code>latrend()</code> or any of the other fitting functions.
<code>model</code>	An arbitrary underlying model representation.
<code>data</code>	A <code>data.frame</code> object, or an expression to resolves to the <code>data.frame</code> object.
<code>date</code>	The date-time when the model estimation was initiated.
<code>id</code>	The name of the trajectory identifier column.
<code>time</code>	The name of the time variable.
<code>response</code>	The name of the response variable.
<code>label</code>	The label assigned to this model.
<code>ids</code>	The trajectory identifier values the model was fitted on.
<code>times</code>	The exact times on which the model has been trained
<code>clusterNames</code>	The names of the clusters.
<code>estimationTime</code>	The time, in seconds, that it took to fit the model.
<code>tag</code>	An arbitrary user-specified data structure. This slot may be accessed and updated directly.

**See Also**

Other model-specific methods: [clusterTrajectories\(\)](#), [coef.lcModel\(\)](#), [converged\(\)](#), [deviance.lcModel\(\)](#), [df.residual.lcModel\(\)](#), [fitted.lcModel\(\)](#), [fittedTrajectories\(\)](#), [logLik.lcModel\(\)](#), [model.frame.lcModel\(\)](#), [nobs.lcModel\(\)](#), [postprob\(\)](#), [predict.lcModel\(\)](#), [predictAssignments\(\)](#), [predictForCluster\(\)](#), [predictPostprob\(\)](#), [residuals.lcModel\(\)](#), [sigma.lcModel\(\)](#), [time.lcModel\(\)](#)

---

lcModelCustom	<i>Specify a model based on a pre-computed result.</i>
---------------	--

---

**Description**

Specify a model based on a pre-computed result.

**Usage**

```
lcModelCustom(
  data,
  response,
  trajectoryAssignments = NULL,
  clusterTrajectories = mean,
  trajectories = data,
  time = getOption("latrend.time"),
  id = getOption("latrend.id"),
  clusterNames = NULL,
  converged = TRUE,
  postprob = NULL,
  model = NULL,
  name = "custom",
  predict = NULL,
  predictPostprob = NULL,
  method = new("lcMethod")
)
```

**Arguments**

<code>data</code>	The data on which the cluster result is based, a <code>data.frame</code> .
<code>response</code>	The response variable.
<code>trajectoryAssignments</code>	A vector indicating cluster membership per strata. Either a numeric vector with range <code>1:numClus</code> , or a factor.
<code>clusterTrajectories</code>	The cluster trajectories as a <code>data.frame</code> , or a function computing the center trajectory based on the strata of the respective cluster.
<code>trajectories</code>	The fitted trajectories.
<code>time</code>	The time variable.

id	The id variable.
clusterNames	The names of the clusters. Optional.
converged	Convergence state of the model. TRUE by default.
postprob	Optional posterior probability matrix.
model	An optional object representing the internal model.
name	The name of the model.
predict	Predict function for the response.
predictPostprob	Predict function for the posterior probability.
method	The method used to create this lcModelCustom instance. Optional.

---

lcModelPartition	<i>Create a lcModel with pre-defined partitioning</i>
------------------	---

---

### Description

Represents an arbitrary partitioning of a set of trajectories. As such, this model has no predictive capabilities. The cluster trajectories are represented by the specified center function (mean by default).

### Usage

```
lcModelPartition(
  data,
  response,
  trajectoryAssignments,
  nClusters = NA,
  clusterNames = NULL,
  time = getOption("latrend.time"),
  id = getOption("latrend.id"),
  name = "part",
  center = meanNA,
  envir = parent.frame()
)
```

### Arguments

data	A data.frame representing the trajectory data.
response	The name of the response variable.
trajectoryAssignments	A vector of cluster membership per trajectory, a data.frame with an id column and "Cluster" column, or the name of the cluster membership column in the data argument.. For vector input, the type must be factor, character, or integer (1 to nClusters). The order of the trajectory, and thus the respective assignments, is determined by the id column of the data. Provide a factor id column for the input data to ensure that the ordering is as you expect.

nClusters	The number of clusters. Should be NA for trajectory assignments of type factor.
clusterNames	The names of the clusters, or a function with input n outputting a character vector of names. If unspecified, the names are determined from the trajectoryAssignments argument.
time	The name of the time variable.
id	The name of the trajectory identification variable.
name	The name of the method.
center	The function for computing the longitudinal cluster centers, used for representing the cluster trajectories.
envir	The environment associated with the model. Used for evaluating the assigned data object by <a href="#">model.data.lcModel</a> .

### Examples

```
# comparing a model to the ground truth using the adjusted Rand index
data(latrendData)
model <- latrend(lcMethodKML(), data = latrendData, response = "Y")
# extract the reference class from the Class column
trajLabels <- aggregate(Class ~ Id, head, 1, data = latrendData)
trajLabels$Cluster <- trajLabels$Class
refModel <- lcModelPartition(latrendData, response = "Y", trajectoryAssignments = trajLabels)
externalMetric(model, refModel, 'adjustedRand') # 0.76
```

---

lcModels	<i>Construct a flat (named) list of lcModel objects</i>
----------	---

---

### Description

The `lcModels` S3 class represents a list of `lcModel` objects. This makes it easier to work with a set of models in a more structured manner.

The `lcModels()` function takes the inputs and generates a named `lcModels` object containing a list of the input models. Duplicates are preserved.

### Usage

```
lcModels(...)
```

### Arguments

... `lcModel`, `lcModels`, or a recursive list of `lcModel` objects. Arguments may be named.

### Value

A `lcModels` object containing all specified `lcModel` objects.

**See Also**

Other lcModel list functions: [as.lcModels\(\)](#), [print.lcModels\(\)](#), [subset.lcModels\(\)](#)

**Examples**

```
data(latrendData)
kml <- latrend(lcMethodKML("Y", id = "Id", time = "Time"), latrendData)
gmm <- latrend(lcMethodLcmmGMM(fixed = Y ~ Time, mixture = ~ Time,
  id = "Id", time = "Time"), latrendData)
lcModels(kml, gmm)

lcModels(defaults = c(kml, gmm))
```

---

lcModelWeightedPartition

*Create a lcModel with pre-defined weighted partitioning*

---

**Description**

Create a lcModel with pre-defined weighted partitioning

**Usage**

```
lcModelWeightedPartition(
  data,
  response,
  weights,
  clusterNames = colnames(weights),
  time = getOption("latrend.time"),
  id = getOption("latrend.id"),
  name = "wpart"
)
```

**Arguments**

data	The data on which the cluster result is based, a data.frame.
response	The name of the response variable.
weights	A numIds x numClusters matrix of partition probabilities.
clusterNames	The names of the clusters, or a function with input n outputting a character vector of names.
time	The name of the time variable.
id	The name of the trajectory identification variable.
name	The name of the method.



---

logLik.lcModel	<i>Extract the log-likelihood of a lcModel</i>
----------------	--

---

### Description

Extract the log-likelihood of a lcModel

### Usage

```
## S3 method for class 'lcModel'  
logLik(object, ...)
```

### Arguments

object	The lcModel object.
...	Additional arguments.

### Details

The default implementation checks for the existence of the logLik() function for the internal model, and returns the output, if available.

### Value

A numeric with the computed log-likelihood. If unavailable, NA is returned.

### See Also

[stats::logLik](#) metric

Other model-specific methods: [clusterTrajectories\(\)](#), [coef.lcModel\(\)](#), [converged\(\)](#), [deviance.lcModel\(\)](#), [df.residual.lcModel\(\)](#), [fitted.lcModel\(\)](#), [fittedTrajectories\(\)](#), [lcModel-class](#), [model.frame.lcModel\(\)](#), [nobs.lcModel\(\)](#), [postprob\(\)](#), [predict.lcModel\(\)](#), [predictAssignments\(\)](#), [predictForCluster\(\)](#), [predictPostprob\(\)](#), [residuals.lcModel\(\)](#), [sigma.lcModel\(\)](#), [time.lcModel\(\)](#)

### Examples

```
data(latrendData)  
method <- lcMethodLcmmGBTM(fixed = Y ~ Time, mixture = ~ 1,  
  id = "Id", time = "Time", nClusters = 3)  
gbtm <- latrend(method, data = latrendData)  
logLik(gbtm)
```

---

max.lcModels	<i>Select the lcModel with the highest metric value</i>
--------------	---

---

**Description**

Select the lcModel with the highest metric value

**Usage**

```
## S3 method for class 'lcModels'
max(x, name, ...)
```

**Arguments**

x	The lcModels object.
name	The name of the internal metric.
...	Additional arguments.

**Value**

The lcModel with the highest metric value

**See Also**

[min.lcModels externalMetric](#)

**Examples**

```
data(latrendData)
baseMethod <- lcMethodKML(response = "Y", id = "Id", time = "Time")
km11 <- latrend(baseMethod, nClusters = 1, latrendData)
km12 <- latrend(baseMethod, nClusters = 2, latrendData)
km13 <- latrend(baseMethod, nClusters = 3, latrendData)
models <- lcModels(km11, km12, km13)
max(models, 'WRSS')
```

---

meltRepeatedMeasures	<i>Convert a repeated measures data matrix to a data.frame</i>
----------------------	--

---

**Description**

Convert a repeated measures data matrix to a data.frame

**Usage**

```
meltRepeatedMeasures(
  data,
  response,
  id = getOption("latrend.id"),
  time = getOption("latrend.time"),
  ids = rownames(data),
  times = colnames(data),
  as.data.table = FALSE
)
```

**Arguments**

<code>data</code>	The matrix containing a trajectory on each row.
<code>response</code>	The response column name.
<code>id</code>	The id column name.
<code>time</code>	The time column name.
<code>ids</code>	A vector specifying the id names. Should match the number of rows of data.
<code>times</code>	A numeric vector specifying the times of the measurements. Should match the number of columns of data.
<code>as.data.table</code>	Whether to return the result as a <code>data.table</code> , or a <code>data.frame</code> otherwise.

**Value**

A `data.table` or `data.frame` containing the repeated measures.

---

<code>metric</code>	<i>Compute internal model metric(s)</i>
---------------------	---

---

**Description**

Compute one or more internal metrics for the given `lcModel` object.

Note that there are many metrics available, and there exists no metric that works best in all scenarios. It is recommended to carefully consider which metric is most appropriate for your use case.

Recommended overview papers:

- van der Nest et al. (2020) provide an overview of metrics for mixture models (GBTM, GMM); primarily likelihood-based or posterior probability-based metrics.
- Henson et al. (2007) provide an overview of likelihood-based metrics for mixture models.

Call `getInternalMetricNames()` to retrieve the names of the defined internal metrics.

See the *Details* section below for a list of supported metrics.

**Usage**

```
## S4 method for signature 'lcModel'
metric(object, name = getOption("latrend.metric", c("WRSS", "APPA.mean")), ...)

## S4 method for signature 'list'
metric(object, name, drop = TRUE)

## S4 method for signature 'lcModels'
metric(object, name, drop = TRUE)
```

**Arguments**

object	The lcModel, lcModels, or list of lcModel objects to compute the metrics for.
name	The name(s) of the metric(s) to compute. If no names are given, the names specified in the latrend.metric option (WRSS, APPA, AIC, BIC) are used.
...	Additional arguments.
drop	Whether to return a numeric vector instead of a data.frame in case of a single metric.

**Details**

List of currently supported metrics:

<b>Metric name</b>	<b>Description</b>
AIC	<b>Akaike information criterion</b>
APPA.mean	Mean of the average posterior probability of assignment (APPA) across clusters
APPA.min	Lowest APPA among the clusters
BIC	<b>Bayesian information criterion</b>
CAIC	Consistent Akaike information criterion
CLC	Classification likelihood criterion
converged	Whether the model converged during estimation
deviance	The model <b>deviance</b>
entropy	Entropy of the posterior probabilities
estimationTime	The time needed for fitting the model
ED	<b>Euclidean distance</b> between the cluster trajectories and the assigned observed trajectories
ED.fit	Euclidean distance between the cluster trajectories and the assigned fitted trajectories
ICL.BIC	Integrated classification likelihood (ICL) approximated using the BIC
logLik	Model log-likelihood
MAE	<b>Mean absolute error</b> of the fitted trajectories (assigned to the most likely respective cluster) to the observed trajectories
Mahalanobis	<b>Mahalanobis distance</b> between the cluster trajectories and the assigned observed trajectories
MSE	<b>Mean squared error</b> of the fitted trajectories (assigned to the most likely respective cluster) to the observed trajectories
relativeEntropy, RE	The normalized version of entropy, scaled between [0, 1].
RSS	<b>Residual sum of squares</b> under most likely cluster allocation
scaledEntropy	See relativeEntropy
sigma	The residual standard deviation
ssBIC	Sample-size adjusted BIC
SED	Standardized Euclidean distance between the cluster trajectories and the assigned observed trajectories

SED.fit	The cluster-weighted standardized Euclidean distance between the cluster trajectories and the assignment probabilities
WMAE	MAE weighted by cluster-assignment probability
WMSE	MSE weighted by cluster-assignment probability
WRSS	RSS weighted by cluster-assignment probability

### Value

For `metric(lcModel)`: A named numeric vector with the computed model metrics.

For `metric(list)`: A `data.frame` with a metric per column.

For `metric(lcModels)`: A `data.frame` with a metric per column.

### Implementation

See the documentation of the `defineInternalMetric()` function for details on how to define your own metrics.

### References

Akaike H (1974). "A new look at the statistical model identification." *IEEE Transactions on Automatic Control*, **19**(6), 716-723. doi: [10.1109/TAC.1974.1100705](https://doi.org/10.1109/TAC.1974.1100705).

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Bozdogan H (1987). "Model Selection and Akaike's Information Criterion (AIC): The General Theory and Its Analytical Extensions." *Psychometrika*, **52**, 345-370. doi: [10.1007/BF02294361](https://doi.org/10.1007/BF02294361).

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Muthén B (2004). "Latent variable analysis: Growth mixture modeling and related techniques for longitudinal data." In *The SAGE Handbook of Quantitative Methodology for the Social Sciences*, 346-369. SAGE Publications, Inc. doi: [10.4135/9781412986311.n19](https://doi.org/10.4135/9781412986311.n19).

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Slove SL (1987). “Application of model-selection criteria to some problems in multivariate analysis.” *Psychometrika*, **52**(3), 333–343. doi: [10.1007/BF02294360](https://doi.org/10.1007/BF02294360).

van der Nest G, Lima Passos V, Candel MJ, van Breukelen GJ (2020). “An overview of mixture modelling for latent evolutions in longitudinal data: Modelling approaches, fit statistics and software.” *Advances in Life Course Research*, **43**, 100323. ISSN 1040-2608, doi: [10.1016/j.alcr.2019.100323](https://doi.org/10.1016/j.alcr.2019.100323).

### See Also

[externalMetric](#) [min.lcModels](#) [max.lcModels](#)

Other metric functions: [defineExternalMetric\(\)](#), [defineInternalMetric\(\)](#), [externalMetric](#), [lcModel](#), [lcModel-metric](#), [getExternalMetricDefinition\(\)](#), [getExternalMetricNames\(\)](#), [getInternalMetricDefinition\(\)](#), [getInternalMetricNames\(\)](#)

### Examples

```
data(latrendData)
model <- latrend(lcMethodLcmmGMM(fixed = Y ~ Time, mixture = ~ Time,
  id = "Id", time = "Time"), latrendData)
bic <- metric(model, "BIC")

ic <- metric(model, c("AIC", "BIC"))
```

---

min.lcModels

*Select the lcModel with the lowest metric value*

---

### Description

Select the lcModel with the lowest metric value

### Usage

```
## S3 method for class 'lcModels'
min(x, name, ...)
```

### Arguments

x	The lcModels object
name	The name of the internal metric.
...	Additional arguments.

**Value**

The lcModel with the lowest metric value

**See Also**

[max.lcModels externalMetric](#)

**Examples**

```
data(latrendData)
baseMethod <- lcMethodKML(response = "Y", id = "Id", time = "Time")
km11 <- latrend(baseMethod, nClusters = 1, latrendData)
km12 <- latrend(baseMethod, nClusters = 2, latrendData)
km13 <- latrend(baseMethod, nClusters = 3, latrendData)
models <- lcModels(km11, km12, km13)
min(models, 'WRSS')
```

---

`model.data.lcModel`      *Extract the model data that was used for fitting*

---

**Description**

Evaluates the data call in the environment that the model was trained in.

**Usage**

```
## S3 method for class 'lcModel'
model.data(object, ...)
```

**Arguments**

`object`            The lcModel object.  
`...`              Additional arguments.

**Value**

The full data.frame that was used for fitting the lcModel.

**See Also**

[model.frame.lcModel time.lcModel](#)

**Examples**

```
data(latrendData)
method <- lcMethodKML("Y", id = "Id", time = "Time", nClusters = 3)
km1 <- latrend(method, latrendData)
model.data(km1)
```

---

```
model.frame.lcModel Extract model training data
```

---

### Description

See [stats::model.frame\(\)](#) for more details.

### Usage

```
## S3 method for class 'lcModel'
model.frame(formula, ...)
```

### Arguments

formula	The lcModel object.
...	Additional arguments.

### Value

A data.frame containing the variables used by the model.

### See Also

[stats::model.frame](#) [model.data.lcModel](#)

Other model-specific methods: [clusterTrajectories\(\)](#), [coef.lcModel\(\)](#), [converged\(\)](#), [deviance.lcModel\(\)](#), [df.residual.lcModel\(\)](#), [fitted.lcModel\(\)](#), [fittedTrajectories\(\)](#), [lcModel-class](#), [logLik.lcModel\(\)](#), [nobs.lcModel\(\)](#), [postprob\(\)](#), [predict.lcModel\(\)](#), [predictAssignments\(\)](#), [predictForCluster\(\)](#), [predictPostprob\(\)](#), [residuals.lcModel\(\)](#), [sigma.lcModel\(\)](#), [time.lcModel\(\)](#)

### Examples

```
data(latrendData)
method <- lcMethodLMKM(Y ~ Time, id = "Id", time = "Time", nClusters = 3)
lmkm <- latrend(method, data = latrendData)
model.frame(lmkm)
```

---

```
names,lcMethod-method lcMethod argument names
```

---

### Description

Extract the argument names or number of arguments from an lcMethod object.



**Usage**

```
## S4 method for signature 'lcMethod'
length(x)

## S4 method for signature 'lcMethod'
names(x)
```

**Arguments**

x                    The lcMethod object.

**Value**

The number of arguments, as integer.  
A character vector of argument names.

**See Also**

Other lcMethod functions: [\[\[,lcMethod-method](#), [as.data.frame.lcMethods\(\)](#), [as.data.frame.lcMethod\(\)](#), [as.lcMethods\(\)](#), [as.list.lcMethod\(\)](#), [evaluate.lcMethod\(\)](#), [formula.lcMethod\(\)](#), [lcMethod-class](#), [update.lcMethod\(\)](#)

**Examples**

```
m = lcMethodKML()
names(m)
length(m)
```

---

nClusters	<i>Number of clusters</i>
-----------	---------------------------

---

**Description**

Get the number of clusters estimated by the given lcModel object.

**Usage**

```
nClusters(object)
```

**Arguments**

object                The lcModel object.

**Value**

An integer with the number of clusters identified by the lcModel.

**See Also**[nIds nobs](#)**Examples**

```
data(latrendData)
method <- lcMethodKML("Y", id = "Id", time = "Time", nClusters = 3)
kml <- latrend(method, latrendData)
nClusters(kml)
```

---

**nIds***Number of trajectories*

---

**Description**

Get the number of trajectories (strata) that were used for fitting the given `lcModel` object. The number of trajectories is determined from the number of unique identifiers in the training data. In case the trajectory ids were supplied using a factor column, the number of trajectories is determined by the number of levels instead.

**Usage**

```
nIds(object)
```

**Arguments**

`object`            The `lcModel` object.

**Value**

An integer with the number of trajectories on which the `lcModel` was fitted.

**See Also**[nobs nClusters](#)**Examples**

```
data(latrendData)
method <- lcMethodKML("Y", id = "Id", time = "Time", nClusters = 3)
kml <- latrend(method, latrendData)
nIds(kml)
```

---

nobs.lcModel	<i>Extract the number of observations from a lcModel</i>
--------------	--

---

**Description**

Extract the number of observations from a lcModel

**Usage**

```
## S3 method for class 'lcModel'
nobs(object, ...)
```

**Arguments**

object	The lcModel object.
...	Additional arguments.

**See Also**

[nIds](#) [nClusters](#)

Other model-specific methods: [clusterTrajectories\(\)](#), [coef.lcModel\(\)](#), [converged\(\)](#), [deviance.lcModel\(\)](#), [df.residual.lcModel\(\)](#), [fitted.lcModel\(\)](#), [fittedTrajectories\(\)](#), [lcModel-class](#), [logLik.lcModel\(\)](#), [model.frame.lcModel\(\)](#), [postprob\(\)](#), [predict.lcModel\(\)](#), [predictAssignments\(\)](#), [predictForCluster\(\)](#), [predictPostprob\(\)](#), [residuals.lcModel\(\)](#), [sigma.lcModel\(\)](#), [time.lcModel\(\)](#)

**Examples**

```
data(latrendData)
method <- lcMethodKML("Y", id = "Id", time = "Time", nClusters = 3)
kml <- latrend(method, latrendData)
nobs(kml)
```

---

OCC	<i>Odds of correct classification (OCC)</i>
-----	---

---

**Description**

Computes the odds of correct classification (OCC) for each cluster.

**Usage**

```
OCC(object)
```

**Arguments**

object	The model, of type lcModel.
--------	-----------------------------

**Details**

An OCC of 1 indicates that the cluster assignment is no better than by random chance.

**Value**

The OCC per cluster, as a numeric vector of length `nClusters(object)`. Empty clusters will output NA.

**References**

Nagin DS (2005). *Group-based modeling of development*. Harvard University Press. ISBN 9780674041318, doi: [10.4159/9780674041318](https://doi.org/10.4159/9780674041318). Klijn SL, Weijenberg MP, Lemmens P, van den Brandt PA, Passos VL (2017). “Introducing the fit-criteria assessment plot - A visualisation tool to assist class enumeration in group-based trajectory modelling.” *Statistical Methods in Medical Research*, **26**(5), 2424-2436. doi: [10.1177/0962280215598665](https://doi.org/10.1177/0962280215598665). van der Nest G, Lima Passos V, Candel MJ, van Breukelen GJ (2020). “An overview of mixture modelling for latent evolutions in longitudinal data: Modelling approaches, fit statistics and software.” *Advances in Life Course Research*, **43**, 100323. ISSN 1040-2608, doi: [10.1016/j.alcr.2019.100323](https://doi.org/10.1016/j.alcr.2019.100323).

**See Also**

[confusionMatrix APPA](#)

---

OSA.adherence

*Biweekly Mean Treatment Adherence of OSA Patients over 1 Year*

---

**Description**

A simulated longitudinal dataset comprising 500 patients with obstructive sleep apnea (OSA) during their first year on CPAP therapy. The dataset contains the patient usage hours, averaged over 2-week periods.

The daily usage data underlying the downsampled dataset was simulated based on 7 different adherence patterns. The defined adherence patterns were inspired by the adherence patterns identified by Aloia et al. (2008), with slight adjustments

**Usage**

OSA.adherence

**Format**

A data.frame comprising longitudinal data of 500 patients, each having 26 observations over a period of 1 year. Each row represents a patient observation interval (two weeks), with columns:

**Patient** factor: The patient identifier, where each level represents a simulated patient.

**Biweek** integer: Two-week interval index. Starts from 1.

**MaxDay** integer: The last day used for the aggregation of the respective interval, integer

**UsageHours** numeric: The mean hours of usage in the respective week. Greater than or equal to zero, and typically around 4-6 hours.

**Group** factor: The reference group (i.e., adherence pattern) from which this patient was generated.

### Note

This dataset is only intended for demonstration purposes. While the data format will remain the same, the data content is subject to change in future versions.

### Source

This dataset was generated based on the cluster-specific descriptive statistics table provided in Aloia et al. (2008), with some adjustments made in order to improve cluster separation for demonstration purposes.

Aloia MS, Goodwin MS, Velicer WF, Arnedt JT, Zimmerman M, Skrekas J, Harris S, Millman RP (2008). "Time series analysis of treatment adherence patterns in individuals with obstructive sleep apnea." *Annals of Behavioral Medicine*, **36**(1), 44–53. ISSN 0883-6612, doi: [10.1007/s12160008-90529](https://doi.org/10.1007/s12160008-90529).

### Examples

```
library(latrend)
data(OSA.adherence)
plotTrajectories(OSA.adherence, id = "Patient", time = "Biweek", response = "UsageHours")

# plot according to cluster ground truth
plotTrajectories(OSA.adherence, id = "Patient", time = "Biweek", response = "UsageHours",
  cluster = "Group")
```

---

plot-lcModel-method    *Plot a lcModel*

---

### Description

Plot a `lcModel` object. By default, this plots the cluster trajectories of the model, along with the training data.

### Usage

```
## S4 method for signature 'lcModel'
plot(x, y, ...)
```

### Arguments

<code>x</code>	The <code>lcModel</code> object.
<code>y</code>	Not used.
<code>...</code>	Arguments passed on to <code>plotClusterTrajectories</code> object The (cluster) trajectory data.

**Value**

A ggplot object.

**See Also**

[plotClusterTrajectories](#) [plotFittedTrajectories](#) [plotTrajectories](#) [ggplot2::ggplot](#)

**Examples**

```
data(latrendData)
model <- latrend(method = lcMethodKML("Y", id = "Id", time = "Time"), latrendData)
plot(model)
```

---

plot-lcModels-method    *Grid plot for a list of models*

---

**Description**

Grid plot for a list of models

**Usage**

```
## S4 method for signature 'lcModels'
plot(x, y, ..., subset, gridArgs = list())
```

**Arguments**

x	The lcModels object.
y	Not used.
...	Additional parameters passed to the plot() call for each lcModel object.
subset	Logical expression based on the lcModel method arguments, indicating which lcModel objects to keep.
gridArgs	Named list of parameters passed to <a href="#">gridExtra::arrangeGrob</a> .

---

```
plotClusterTrajectories
      Plot cluster trajectories
```

---

### Description

Plot cluster trajectories

Plot the cluster trajectories of a lcModel

### Usage

```
## S4 method for signature 'data.frame'
plotClusterTrajectories(
  object,
  response,
  cluster = "Cluster",
  time = getOption("latrend.time"),
  center = meanNA,
  trajectories = c(FALSE, "sd", "se", "80pct", "90pct", "95pct", "range"),
  facet = !isFALSE(as.logical(trajectories[1])),
  id = getOption("latrend.id"),
  ...
)

## S4 method for signature 'lcModel'
plotClusterTrajectories(
  object,
  what = "mu",
  at = time(object),
  clusterLabels = NULL,
  trajectories = FALSE,
  facet = !isFALSE(as.logical(trajectories[1])),
  trajAssignments = trajectoryAssignments(object),
  ...
)
```

### Arguments

object	The (cluster) trajectory data.
response	The response variable name.
cluster	The cluster assignment column
time	The time variable name.
center	A function for aggregating multiple points at the same point in time

trajectories	Whether to additionally plot the original trajectories (TRUE), or to show the expected interval (standard deviation, standard error, range, or percentile range) of the observations at the respective moment in time. Note that visualizing the expected intervals is currently only supported for time-aligned trajectories, as the interval is computed at each unique moment in time. By default (FALSE), no information on the underlying trajectories is shown.
facet	Whether to facet by cluster. This is done by default when trajectories is enabled.
id	Id column. Only needed when trajectories = TRUE.
...	Arguments passed to <code>clusterTrajectories()</code> , or <code>ggplot2::geom_line()</code> for plotting the cluster trajectory lines.
what	The distributional parameter to predict. By default, the mean response 'mu' is predicted. The cluster membership predictions can be obtained by specifying <code>what = 'mb'</code> .
at	An optional vector of the times at which to compute the cluster trajectory predictions.
clusterLabels	Cluster display names. By default it's the cluster name with its proportion enclosed in parentheses.
trajAssignments	The cluster assignments for the fitted trajectories. Only used when trajectories = TRUE and facet = TRUE. See <a href="#">trajectoryAssignments</a> .

**Value**

A ggplot object.

**See Also**

[clusterTrajectories](#) [plotFittedTrajectories](#) [plotTrajectories](#) [plot](#)

**Examples**

```
data(latrendData)
model <- latrend(method = lcMethodKML("Y", id = "Id", time = "Time"), latrendData)
plotClusterTrajectories(model)

# show assigned trajectories
plotClusterTrajectories(model, trajectories = TRUE)

# show 95th percentile observation interval
plotClusterTrajectories(model, trajectories = "95pct")

# show observation standard deviation
plotClusterTrajectories(model, trajectories = "sd")

# show observation standard error
plotClusterTrajectories(model, trajectories = "se")
```



```
# show observation range
plotClusterTrajectories(model, trajectories = "range")
```

---

```
plotFittedTrajectories
```

*Plot fitted trajectories of a lcModel*

---

### Description

Plot fitted trajectories of a lcModel

### Usage

```
## S4 method for signature 'lcModel'
plotFittedTrajectories(object, ...)
```

### Arguments

object	The lcModel object.
...	Arguments passed on to <a href="#">trajectories</a>

### See Also

[fittedTrajectories](#) [plotClusterTrajectories](#) [plotTrajectories](#) [plot](#)

### Examples

```
data(latrendData)
model <- latrend(method = lcMethodKML("Y", id = "Id", time = "Time"), latrendData)
plotFittedTrajectories(model)
```

---

```
plotMetric
```

*Plot one or more internal metrics for all lcModels*

---

### Description

Plot one or more internal metrics for all lcModels

### Usage

```
plotMetric(models, name, by = "nClusters", subset, group = character())
```

**Arguments**

models	A lcModels or list of lcModel objects to compute and plot the metrics of.
name	The name(s) of the metric(s) to compute. If no names are given, the names specified in the <code>latrend.metric</code> option (WRSS, APPA, AIC, BIC) are used.
by	The argument name along which methods are plotted.
subset	Logical expression based on the lcModel method arguments, indicating which lcModel objects to keep.
group	The argument names to use for determining groups of different models. By default, all arguments are included. Specifying <code>group = character()</code> disables grouping. Specifying a single argument for grouping uses that specific column as the grouping column. In all other cases, groupings are represented by a number.

**Value**

ggplot2 object.

**Examples**

```
data(latrendData)
baseMethod <- lcMethodKML(response = "Y", id = "Id", time = "Time")
methods <- lcMethods(baseMethod, nClusters = 1:3)
models <- latrendBatch(methods, latrendData)
plotMetric(models, c("BIC", "WRSS"))
```

---

plotTrajectories      *Plot the data trajectories*

---

**Description**

Plots the output of [trajectories](#) for the given object.

**Usage**

```
plotTrajectories(object, ...)

## S4 method for signature 'data.frame'
plotTrajectories(
  object,
  response,
  time = getOption("latrend.time"),
  id = getOption("latrend.id"),
  cluster = NULL,
  facet = TRUE,
  ...
)
```

```
## S4 method for signature 'ANY'
plotTrajectories(object, ...)

## S4 method for signature 'lcModel'
plotTrajectories(object, ...)
```

### Arguments

object	The data or model or extract the trajectories from.
...	Arguments passed on to <a href="#">trajectories</a>
response	Response variable character name or a call.
time	The time variable name.
id	The identifier variable name.
cluster	Cluster variable name. If unspecified, trajectories are not grouped. Alternatively, cluster is a vector indicating cluster membership per id.
facet	Whether to facet by cluster.

### See Also

[trajectories](#) [plotFittedTrajectories](#) [plotClusterTrajectories](#)

### Examples

```
data(latrendData)
plotTrajectories(latrendData, response = "Y", id = "Id", time = "Time")

plotTrajectories(latrendData, response = quote(exp(Y)), id = "Id", time = "Time")

plotTrajectories(latrendData, response = "Y", id = "Id", time = "Time", cluster = "Class")

# compute cluster membership based on the mean being below 0
assignments = aggregate(Y ~ Id, latrendData, mean)$Y < 0
plotTrajectories(latrendData,
  response = "Y", id = "Id", time = "Time", cluster = assignments)
data(latrendData)
model <- latrend(method = lcMethodKML("Y", id = "Id", time = "Time"), latrendData)
plotTrajectories(model)
```

---

 postFit

*lcMethod fit process: logic for post-processing the fitted lcModel*


---

## Description

Note: this function should not be called directly, as it is part of the `lcMethod` fitting process. For fitting an `lcMethod` object to a dataset, see `latrend()`.

The `postFit()` function of the `lcMethod` object defines how the `lcModel` object returned by `fit()` should be post-processed. This can be used, for example, to:

- Resolve label switching.
- Clean up the internal model representation.
- Correct estimation errors.
- Compute additional metrics.

By default, this method does not do anything. It merely returns the original `lcModel` object.

This is the last step in the `lcMethod` fitting procedure. The `postFit` method may be called again on fitted `lcModel` objects, allowing post-processing to be updated for existing models.

## Usage

```
## S4 method for signature 'lcMethod'
postFit(method, data, model, envir, verbose)
```

## Arguments

<code>method</code>	An object inheriting from <code>lcMethod</code> with all its arguments having been evaluated and finalized.
<code>data</code>	A <code>data.frame</code> representing the transformed training data.
<code>model</code>	The <code>lcModel</code> object returned by <code>fit()</code> .
<code>envir</code>	The environment containing variables generated by <code>prepareData()</code> and <code>preFit()</code> .
<code>verbose</code>	A <code>R.utils::Verbose</code> object indicating the level of verbosity.

## Value

The updated `lcModel` object.

## Implementation

The method is intended to be able to be called on previously fitted `lcModel` objects as well, allowing for potential bugfixes or additions to previously fitted models. Therefore, when implementing this method, ensure that you do not discard information from the model which would prevent the method from being run a second time on the object.

In this example, the `lcModelExample` class is assumed to be defined with a slot named "centers":

```

setMethod("postFit", "lcMethodExample", function(method, data, model, envir, verbose) {
  # compute and store the cluster centers
  model@centers <- INTENSIVE_COMPUTATION
  return(model)
})

```

### Fitting procedure

Each `lcMethod` subclass defines a type of methods in terms of a series of steps for estimating the method. These steps, as part of the fitting procedure, are executed by `latrend()` in the following order:

1. `compose()`: Evaluate and finalize the method argument values.
2. `validate()`: Check the validity of the method argument values in relation to the dataset.
3. `prepareData()`: Process the training data for fitting.
4. `preFit()`: Prepare environment for estimation, independent of training data.
5. `fit()`: Estimate the specified method on the training data, outputting an object inheriting from `lcModel`.
6. `postFit()`: Post-process the outputted `lcModel` object.

The result of the fitting procedure is an `lcModel` object that inherits from the `lcModel` class.

---

postprob

*Posterior probability per fitted trajectory*

---

### Description

Get the posterior probability matrix with element  $(i, j)$  indicating the probability of trajectory  $i$  belonging to cluster  $j$ .

### Usage

```

## S4 method for signature 'lcModel'
postprob(object, ...)

```

### Arguments

object	The <code>lcModel</code> .
...	Additional arguments.

### Details

This method should be extended by `lcModel` implementations. The default implementation returns uniform probabilities for all observations.

**Value**

A I-by-K matrix with  $I = nIds(object)$  and  $K = nClusters(object)$ .

**Implementation**

Classes extending `lcModel` should override this method.

```
setMethod("postprob", "lcModelExt", function(object, ...) {
  # return trajectory-specific posterior probability matrix
})
```

**See Also**

[trajectoryAssignments](#) [predictPostprob](#) [predictAssignments](#)

Other model-specific methods: [clusterTrajectories\(\)](#), [coef.lcModel\(\)](#), [converged\(\)](#), [deviance.lcModel\(\)](#), [df.residual.lcModel\(\)](#), [fitted.lcModel\(\)](#), [fittedTrajectories\(\)](#), [lcModel-class](#), [logLik.lcModel\(\)](#), [model.frame.lcModel\(\)](#), [nobs.lcModel\(\)](#), [predict.lcModel\(\)](#), [predictAssignments\(\)](#), [predictForCluster\(\)](#), [predictPostprob\(\)](#), [residuals.lcModel\(\)](#), [sigma.lcModel\(\)](#), [time.lcModel\(\)](#)

**Examples**

```
data(latrendData)
model <- latrend(lcMethodLcmmGMM(fixed = Y ~ Time, mixture = ~ Time,
  id = "Id", time = "Time"), data = latrendData)
postprob(model)
```

---

`postprobFromAssignments`

*Create a posterior probability matrix from a vector of cluster assignments.*

---

**Description**

For each trajectory, the probability of the assigned cluster is 1.

**Usage**

```
postprobFromAssignments(assignments, k)
```

**Arguments**

<code>assignments</code>	Integer vector indicating cluster assignment per trajectory
<code>k</code>	The number of clusters.

---

predict.lcModel	<i>lcModel predictions</i>
-----------------	----------------------------

---

### Description

Predicts the expected trajectory observations at the given time for each cluster.

### Usage

```
## S3 method for class 'lcModel'
predict(object, newdata = NULL, what = "mu", ...)
```

### Arguments

object	The lcModel object.
newdata	Optional data.frame for which to compute the model predictions. If omitted, the model training data is used. Cluster trajectory predictions are made when ids are not specified.
what	The distributional parameter to predict. By default, the mean response 'mu' is predicted. The cluster membership predictions can be obtained by specifying what = 'mb'.
...	Additional arguments.

### Value

If newdata specifies the cluster membership; a data.frame of cluster-specific predictions. Otherwise, a list of data.frame of cluster-specific predictions is returned.

### Implementation

Note: Subclasses of lcModel should preferably implement [predictForCluster\(\)](#) instead of overriding predict.lcModel as that function is designed to be easier to implement because it is single-purpose.

The predict.lcModelExt function should be able to handle the case where newdata = NULL by returning the fitted values. After post-processing the non-NULL newdata input, the observation- and cluster-specific predictions can be computed. Lastly, the output logic is handled by the [transformPredict\(\)](#) function. It converts the computed predictions (e.g., matrix or data.frame) to the appropriate output format.

```
predict.lcModelExt <- function(object, newdata = NULL, what = "mu", ...) {
  if (is.null(newdata)) {
    newdata = model.data(object)
    if (hasName(newdata, 'Cluster')) {
      # allowing the Cluster column to remain would break the fitted() output.
      newdata[['Cluster']] = NULL
    }
  }
}
```

```

}

# compute cluster-specific predictions for the given newdata
pred <- NEWDATA_COMPUTATIONS_HERE
transformPredict(pred = pred, model = object, newdata = newdata)
})

```

### See Also

[predictForCluster](#) [stats::predict.fitted.lcModel](#) [clusterTrajectories](#) [trajectories](#) [predictPostprob](#) [predictAssignments](#)

Other model-specific methods: [clusterTrajectories\(\)](#), [coef.lcModel\(\)](#), [converged\(\)](#), [deviance.lcModel\(\)](#), [df.residual.lcModel\(\)](#), [fitted.lcModel\(\)](#), [fittedTrajectories\(\)](#), [lcModel-class](#), [logLik.lcModel\(\)](#), [model.frame.lcModel\(\)](#), [nobs.lcModel\(\)](#), [postprob\(\)](#), [predictAssignments\(\)](#), [predictForCluster\(\)](#), [predictPostprob\(\)](#), [residuals.lcModel\(\)](#), [sigma.lcModel\(\)](#), [time.lcModel\(\)](#)

### Examples

```

data(latrendData)
model <- latrend(lcMethodLcmmGMM(
  fixed = Y ~ Time, mixture = ~ Time,
  id = "Id", time = "Time"), latrendData)
predFitted <- predict(model) # same result as fitted(model)

# Cluster trajectory of cluster A
predCluster <- predict(model, newdata = data.frame(Cluster = "A", Time = time(model)))

# Prediction for id S1 given cluster A membership
predId <- predict(model, newdata = data.frame(Cluster = "A", Id = "S1", Time = time(model)))

# Prediction matrix for id S1 for all clusters
predIdAll <- predict(model, newdata = data.frame(Id = "S1", Time = time(model)))

```

---

`predictAssignments`      *Predict the cluster assignments for new trajectories*

---

### Description

Computes the posterior probability based on the provided (observed) data.

### Usage

```

## S4 method for signature 'lcModel'
predictAssignments(object, newdata = NULL, strategy = which.max, ...)

```



**Arguments**

object	The lcModel object.
newdata	Optional data.frame for which to compute the model predictions. If omitted, the model training data is used. Cluster trajectory predictions are made when ids are not specified.
strategy	A function returning the cluster index based on the given vector of membership probabilities. By default (strategy = which.max), trajectories are assigned to the most likely cluster.
...	Additional arguments.

**Details**

The default implementation uses [predictPostprob](#) to determine the cluster membership.

**Value**

A factor of length nrow(newdata) that indicates the assigned cluster per trajectory per observation.

**See Also**

[predictPostprob](#) [predict.lcModel](#)

Other model-specific methods: [clusterTrajectories\(\)](#), [coef.lcModel\(\)](#), [converged\(\)](#), [deviance.lcModel\(\)](#), [df.residual.lcModel\(\)](#), [fitted.lcModel\(\)](#), [fittedTrajectories\(\)](#), [lcModel-class](#), [logLik.lcModel\(\)](#), [model.frame.lcModel\(\)](#), [nobs.lcModel\(\)](#), [postprob\(\)](#), [predict.lcModel\(\)](#), [predictForCluster\(\)](#), [predictPostprob\(\)](#), [residuals.lcModel\(\)](#), [sigma.lcModel\(\)](#), [time.lcModel\(\)](#)

**Examples**

```
## Not run:
data(latrendData)
model <- latrend(method = lcMethodKML("Y", id = "Id", time = "Time"), latrendData)
predictAssignments(model, newdata = data.frame(Id = 999, Y = 0, Time = 0))

## End(Not run)
```

---

predictForCluster      *lcModel prediction conditional on a cluster*

---

**Description**

Predicts the expected trajectory observations at the given time under the assumption that the trajectory belongs to the specified cluster.

The same result can be obtained by calling [predict\(\)](#) with the newdata data.frame having a "Cluster" assignment column. The main purpose of this function is to make it easier to implement the prediction computations for custom lcModel classes.

**Usage**

```
## S4 method for signature 'lcModel'
predictForCluster(object, newdata = NULL, cluster, ..., what = "mu")
```

**Arguments**

<code>object</code>	The <code>lcModel</code> object.
<code>newdata</code>	Optional <code>data.frame</code> for which to compute the model predictions. If omitted, the model training data is used. Cluster trajectory predictions are made when <code>ids</code> are not specified.
<code>cluster</code>	The cluster name (as character) to predict for.
<code>...</code>	Additional arguments.
<code>what</code>	The distributional parameter to predict. By default, the mean response 'mu' is predicted. The cluster membership predictions can be obtained by specifying <code>what = 'mb'</code> .

**Details**

The default `predictForCluster()` method makes use of `predict.lcModel()`, and vice versa. For this to work, any extending `lcModel` classes, e.g., `lcModelExample`, should implement either `predictForCluster(lcModelExample)` or `predict.lcModelExample()`. When implementing new models, it is advisable to implement `predictForCluster` as the cluster-specific computation generally results in shorter and simpler code.

**Value**

A vector with the predictions per `newdata` observation, or a `data.frame` with the predictions and `newdata` alongside.

**Implementation**

Classes extending `lcModel` should override this method, unless `predict.lcModel()` is preferred.

```
setMethod("predictForCluster", "lcModelExt",
  function(object, newdata = NULL, cluster, ..., what = "mu") {
    # return model predictions for the given data under the
    # assumption of the data belonging to the given cluster
  })
```

**See Also**

[predict.lcModel](#)

Other model-specific methods: [clusterTrajectories\(\)](#), [coef.lcModel\(\)](#), [converged\(\)](#), [deviance.lcModel\(\)](#), [df.residual.lcModel\(\)](#), [fitted.lcModel\(\)](#), [fittedTrajectories\(\)](#), [lcModel-class](#), [logLik.lcModel\(\)](#), [model.frame.lcModel\(\)](#), [nobs.lcModel\(\)](#), [postprob\(\)](#), [predict.lcModel\(\)](#), [predictAssignments\(\)](#), [predictPostprob\(\)](#), [residuals.lcModel\(\)](#), [sigma.lcModel\(\)](#), [time.lcModel\(\)](#)

**Examples**

```

data(latrendData)
method <- lcMethodKML("Y", id = "Id", time = "Time", nClusters = 3)
model <- latrend(method, latrendData)

predictForCluster(model,
  newdata = data.frame(Time = c(0, 1)),
  cluster = "B")

# all fitted values under cluster B
predictForCluster(model, cluster = "B")

```

---

predictPostprob	<i>lcModel posterior probability prediction</i>
-----------------	---

---

**Description**

Returns the observation-specific posterior probabilities for the given data. The default implementation returns a uniform probability matrix.

**Usage**

```

## S4 method for signature 'lcModel'
predictPostprob(object, newdata = NULL, ...)

```

**Arguments**

object	The lcModel to predict the posterior probabilities with.
newdata	Optional data frame for which to compute the posterior probability. If omitted, the model training data is used.
...	Additional arguments.

**Value**

A N-by-K matrix indicating the posterior probability per trajectory per measurement on each row, for each cluster (the columns). Here, N = nrow(newdata) and K = nClusters(object).

**Implementation**

Classes extending lcModel should override this method to enable posterior probability predictions for new data.

```

setMethod("predictPostprob", "lcModelExt", function(object, newdata = NULL, ...) {
  # return observation-specific posterior probability matrix
})

```

**See Also**

Other model-specific methods: `clusterTrajectories()`, `coef.lcModel()`, `converged()`, `deviance.lcModel()`, `df.residual.lcModel()`, `fitted.lcModel()`, `fittedTrajectories()`, `lcModel-class`, `logLik.lcModel()`, `model.frame.lcModel()`, `nobs.lcModel()`, `postprob()`, `predict.lcModel()`, `predictAssignments()`, `predictForCluster()`, `residuals.lcModel()`, `sigma.lcModel()`, `time.lcModel()`

preFit

*lcMethod fit process: method preparation logic***Description**

Note: this function should not be called directly, as it is part of the `lcMethod` fitting process. For fitting an `lcMethod` object to a dataset, see `latrend()`.

The `preFit()` function of the `lcMethod` object performs preparatory work that is needed for fitting the method but should not be counted towards the method estimation time. The work is added to the provided environment, allowing the `fit()` function to make use of the prepared work.

**Usage**

```
## S4 method for signature 'lcMethod'
preFit(method, data, envir, verbose)
```

**Arguments**

method	An object inheriting from <code>lcMethod</code> with all its arguments having been evaluated and finalized.
data	A <code>data.frame</code> representing the transformed training data.
envir	The environment containing additional data variables returned by <code>prepareData()</code> .
verbose	A <code>R.utils::Verbose</code> object indicating the level of verbosity.

**Value**

The updated environment that will be passed to `fit()`.

**Implementation**

```
setMethod("preFit", "lcMethodExample", function(method, data, envir, verbose) {
  # update envir with additional computed work
  envir$x <- INTENSIVE_OPERATION
  return(envir)
})
```

### Fitting procedure

Each `lcMethod` subclass defines a type of methods in terms of a series of steps for estimating the method. These steps, as part of the fitting procedure, are executed by `latrend()` in the following order:

1. `compose()`: Evaluate and finalize the method argument values.
2. `validate()`: Check the validity of the method argument values in relation to the dataset.
3. `prepareData()`: Process the training data for fitting.
4. `preFit()`: Prepare environment for estimation, independent of training data.
5. `fit()`: Estimate the specified method on the training data, outputting an object inheriting from `lcModel`.
6. `postFit()`: Post-process the outputted `lcModel` object.

The result of the fitting procedure is an `lcModel` object that inherits from the `lcModel` class.

---

```
prepareData
```

```
lcMethod fit process: logic for preparing the training data
```

---

### Description

Note: this function should not be called directly, as it is part of the `lcMethod` fitting process. For fitting an `lcMethod` object to a dataset, see `latrend()`.

The `prepareData()` function of the `lcMethod` object processes the training data prior to fitting the method. Example uses:

- Transforming the data to another format, e.g., a matrix.
- Truncating the response variable.
- Computing derived covariates.
- Creating additional data objects.

The computed variables are stored in an environment which is passed to the `preFit()` function for further processing.

By default, this method does not do anything.

### Usage

```
## S4 method for signature 'lcMethod'
prepareData(method, data, verbose)
```

### Arguments

<code>method</code>	An object inheriting from <code>lcMethod</code> with all its arguments having been evaluated and finalized.
<code>data</code>	A <code>data.frame</code> representing the transformed training data.
<code>verbose</code>	A <code>R.utils::Verbose</code> object indicating the level of verbosity.

**Value**

An environment with the prepared data variable(s) that will be passed to `preFit()`.

**Implementation**

A common use case for this method is when the internal method fitting procedure expects the data in a different format. In this example, the method converts the training data `data.frame` to a matrix of repeated and aligned trajectory measurements.

```
setMethod("prepareData", "lcMethodExample", function(method, data, verbose) {
  envir = new.env()
  # transform the data to matrix
  envir$dataMat = dcastRepeatedMeasures(data,
    id = idColumn, time = timeColumn, response = valueColumn)
  return(envir)
})
```

**Fitting procedure**

Each `lcMethod` subclass defines a type of methods in terms of a series of steps for estimating the method. These steps, as part of the fitting procedure, are executed by `latrend()` in the following order:

1. `compose()`: Evaluate and finalize the method argument values.
2. `validate()`: Check the validity of the method argument values in relation to the dataset.
3. `prepareData()`: Process the training data for fitting.
4. `preFit()`: Prepare environment for estimation, independent of training data.
5. `fit()`: Estimate the specified method on the training data, outputting an object inheriting from `lcModel`.
6. `postFit()`: Post-process the outputted `lcModel` object.

The result of the fitting procedure is an `lcModel` object that inherits from the `lcModel` class.

---

```
print.lcMethod
```

*Print the arguments of an lcMethod object*

---

**Description**

Print the arguments of an `lcMethod` object

**Usage**

```
## S3 method for class 'lcMethod'
print(x, ..., eval = FALSE, width = 40, envir = NULL)
```

**Arguments**

x	The lcMethod object.
...	Not used.
eval	Whether to print the evaluated argument values.
width	Maximum number of characters per argument.
envir	The environment in which to evaluate the arguments when eval = TRUE.

---

print.lcModels	<i>Print lcModels list concisely</i>
----------------	--------------------------------------

---

**Description**

Print lcModels list concisely

**Usage**

```
## S3 method for class 'lcModels'
print(
  x,
  ...,
  summary = FALSE,
  excludeShared = !getOption("latrend.printSharedModelArgs")
)
```

**Arguments**

x	The lcModels object.
...	Not used.
summary	Whether to print the complete summary per model. This may be slow for long lists!
excludeShared	Whether to exclude model arguments which are identical across all models.

**See Also**

Other lcModel list functions: [as.lcModels\(\)](#), [lcModels](#), [subset.lcModels\(\)](#)

---

qqPlot	<i>Quantile-quantile plot</i>
--------	-------------------------------

---

### Description

Plot the quantile-quantile (Q-Q) plot for the fitted `lcModel` object. This function is based on the **qqplotr** package.

### Usage

```
## S4 method for signature 'lcModel'
qqPlot(object, byCluster = FALSE, ...)
```

### Arguments

<code>object</code>	The <code>lcModel</code> object.
<code>byCluster</code>	Whether to plot the Q-Q line per cluster
<code>...</code>	Additional arguments passed to <code>qqplotr::geom_qq_band()</code> , <code>qqplotr::stat_qq_line()</code> , and <code>qqplotr::stat_qq_point()</code> .

### Value

A ggplot object.

### See Also

[residuals.lcModel](#) [metric](#) [plotClusterTrajectories](#)

### Examples

```
data(latrendData)
model <- latrend(lcMethodLcmmGMM(fixed = Y ~ Time, mixture = ~ Time,
  id = "Id", time = "Time"), data = latrendData)
qqPlot(model)
```

---

<code>residuals.lcModel</code>	<i>Extract lcModel residuals</i>
--------------------------------	----------------------------------

---

### Description

Extract the residuals for a fitted `lcModel` object. By default, residuals are computed under the most likely cluster assignment for each trajectory.

### Usage

```
## S3 method for class 'lcModel'
residuals(object, ..., clusters = trajectoryAssignments(object))
```



**Arguments**

object	The lcModel object.
...	Additional arguments.
clusters	Optional cluster assignments per id. If unspecified, a matrix is returned containing the cluster-specific predictions per column.

**Value**

A numeric vector of residuals for the cluster assignments specified by clusters. If the clusters argument is unspecified, a matrix of cluster-specific residuals per observations is returned.

**See Also**

[fitted.lcModel](#) [trajectories](#) `data(latrendData) model <- latrend(lcMethodLcmmGMM(fixed = Y ~ Time, mixture = ~ Time, id = "Id", time = "Time"), data = latrendData) summary(residuals(model))`

Other model-specific methods: [clusterTrajectories\(\)](#), [coef.lcModel\(\)](#), [converged\(\)](#), [deviance.lcModel\(\)](#), [df.residual.lcModel\(\)](#), [fitted.lcModel\(\)](#), [fittedTrajectories\(\)](#), [lcModel-class](#), [logLik.lcModel\(\)](#), [model.frame.lcModel\(\)](#), [nobs.lcModel\(\)](#), [postprob\(\)](#), [predict.lcModel\(\)](#), [predictAssignments\(\)](#), [predictForCluster\(\)](#), [predictPostprob\(\)](#), [sigma.lcModel\(\)](#), [time.lcModel\(\)](#)

---

responseVariable	<i>Extract the response variable</i>
------------------	--------------------------------------

---

**Description**

Extracts the response variable from the given object.

**Usage**

```
## S4 method for signature 'lcMethod'
responseVariable(object, ...)
```

```
## S4 method for signature 'lcModel'
responseVariable(object, ...)
```

**Arguments**

object	The object to extract the response variable from.
...	Additional arguments.

**Details**

If the lcMethod object specifies a formula argument, then the response is extracted from the response term of the formula.

**Value**

The response variable name as a character.

**See Also**

Other lcModel variables: [idVariable\(\)](#), [timeVariable\(\)](#)

**Examples**

```
method <- lcMethodKML("Value")
responseVariable(method) # "Value"

method <- lcMethodLcmmGBTM(fixed = Value ~ Time, mixture = ~ Time)
responseVariable(method) # "Value"

data(latrendData)
model <- latrend(lcMethodKML("Y", id = "Id", time = "Time"), latrendData)
responseVariable(model) # "Value"
```

---

sigma.lcModel

*Extract residual standard deviation from a lcModel*


---

**Description**

Extracts or estimates the residual standard deviation. If [sigma\(\)](#) is not defined for a model, it is estimated from the residual error vector.

**Usage**

```
## S3 method for class 'lcModel'
sigma(object, ...)
```

**Arguments**

`object`            The lcModel object.  
`...`              Additional arguments.

**Value**

A numeric indicating the residual standard deviation.

**See Also**

[coef.lcModel](#) [metric](#)

Other model-specific methods: [clusterTrajectories\(\)](#), [coef.lcModel\(\)](#), [converged\(\)](#), [deviance.lcModel\(\)](#), [df.residual.lcModel\(\)](#), [fitted.lcModel\(\)](#), [fittedTrajectories\(\)](#), [lcModel-class](#), [logLik.lcModel\(\)](#), [model.frame.lcModel\(\)](#), [nobs.lcModel\(\)](#), [postprob\(\)](#), [predict.lcModel\(\)](#), [predictAssignments\(\)](#), [predictForCluster\(\)](#), [predictPostprob\(\)](#), [residuals.lcModel\(\)](#), [time.lcModel\(\)](#)

**Examples**

```
data(latrendData)
model <- latrend(lcMethodLcmmGMM(fixed = Y ~ Time, mixture = ~ Time,
  id = "Id", time = "Time"), data = latrendData)
sigma(model)
```

strip

*Reduce the lcModel memory footprint for serialization***Description**

Strip a `lcModel` of non-essential variables and environments in order to reduce the model size for serialization.

**Usage**

```
## S4 method for signature 'lcMethod'
strip(object, ..., classes = "formula")

## S4 method for signature 'ANY'
strip(object, ..., classes = "formula")

## S4 method for signature 'lcModel'
strip(object, ..., classes = "formula")
```

**Arguments**

<code>object</code>	The <code>lcModel</code> object.
<code>...</code>	Additional arguments.
<code>classes</code>	The object classes for which to remove their assigned environment. By default, only environments from formula are removed.

**Value**

An `lcModel` object of the same type as the `object` argument.

**Implementation**

Classes extending `lcModel` can override this method to remove additional non-essentials.

```
setMethod("strip", "lcModelExt", function(object, ..., classes = "formula") {
  object <- callNextMethod()
  # further process the object
  return(object)
})
```

**Examples**

```
data(latrendData)
model <- latrend(lcMethodLcmmGMM(fixed = Y ~ Time, mixture = ~ Time,
  id = "Id", time = "Time"), data = latrendData)
strip(model)
```

---

subset.lcModels	<i>Subsetting a lcModels list based on method arguments</i>
-----------------	---

---

**Description**

Subsetting a lcModels list based on method arguments

**Usage**

```
## S3 method for class 'lcModels'
subset(x, subset, drop = FALSE, ...)
```

**Arguments**

x	The lcModels or list of lcModel to be subsetted.
subset	Logical expression based on the lcModel method arguments, indicating which lcModel objects to keep.
drop	Whether to return a lcModel object if the result is length 1.
...	Not used.

**Value**

A lcModels list with the subset of lcModel objects.

**See Also**

Other lcModel list functions: [as.lcModels\(\)](#), [lcModels](#), [print.lcModels\(\)](#)

**Examples**

```
data(latrendData)
mKML <- lcMethodKML(response = "Y", id = "Id", time = "Time")
kml1 <- latrend(mKML, nClusters = 1, latrendData)
kml2 <- latrend(mKML, nClusters = 2, latrendData)
kml3 <- latrend(mKML, nClusters = 3, latrendData)
gmm <- latrend(lcMethodLcmmGMM(fixed = Y ~ Time, mixture = ~ Time,
  id = "Id", time = "Time"), latrendData)
models <- lcModels(kml1, kml2, kml3, gmm)

subset(models, nClusters > 1 & .method == 'kml')
```

---

summary.lcModel	<i>Summarize a lcModel</i>
-----------------	----------------------------

---

**Description**

Extracts all relevant information from the underlying model into a list

**Usage**

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

**Arguments**

object	The lcModel object.
...	Additional arguments.

---

time.lcModel	<i>Sampling times of a lcModel</i>
--------------	------------------------------------

---

**Description**

Extract the sampling times on which the lcModel was fitted.

**Usage**

```
## S3 method for class 'lcModel'
time(x, ...)
```

**Arguments**

x	The lcModel object.
...	Not used.

**Value**

A numeric vector of the unique times at which observations occur, in increasing order.

**See Also**

[timeVariable model.data](#)

Other model-specific methods: [clusterTrajectories\(\)](#), [coef.lcModel\(\)](#), [converged\(\)](#), [deviance.lcModel\(\)](#), [df.residual.lcModel\(\)](#), [fitted.lcModel\(\)](#), [fittedTrajectories\(\)](#), [lcModel-class](#), [logLik.lcModel\(\)](#), [model.frame.lcModel\(\)](#), [nobs.lcModel\(\)](#), [postprob\(\)](#), [predict.lcModel\(\)](#), [predictAssignments\(\)](#), [predictForCluster\(\)](#), [predictPostprob\(\)](#), [residuals.lcModel\(\)](#), [sigma.lcModel\(\)](#)

---

timeVariable	<i>Extract the time variable</i>
--------------	----------------------------------

---

### Description

Extracts the time variable (i.e., column name) from the given object.

### Usage

```
## S4 method for signature 'lcMethod'  
timeVariable(object, ...)
```

```
## S4 method for signature 'lcModel'  
timeVariable(object)
```

### Arguments

object	The object to extract the variable from.
...	Additional arguments.

### Value

The time variable name, as character.

### See Also

Other lcModel variables: [idVariable\(\)](#), [responseVariable\(\)](#)

### Examples

```
method <- lcMethodKML(time = "Assessment")  
timeVariable(method) # "Assessment"  
  
data(latrendData)  
model <- latrend(lcMethodKML("Y", id = "Id", time = "Time"), latrendData)  
idVariable(model) # "Id"
```

---

trajectories	<i>Extract the trajectories</i>
--------------	---------------------------------

---

### Description

Transform or extract the trajectories from the given object to a standardized format.

The standardized data format is for method estimation by [latrend](#), and for plotting functions.

**Usage**

```
trajectories(object, ...)

## S4 method for signature 'data.frame'
trajectories(object, id, time, response, ...)

## S4 method for signature 'matrix'
trajectories(object, id, time, response, ...)

## S4 method for signature 'call'
trajectories(object, ..., envir)

## S4 method for signature 'lcModel'
trajectories(object, ...)
```

**Arguments**

object	The data or model or extract the trajectories from.
...	Additional arguments.
id	The identifier variable name.
time	The time variable name.
response	The response variable name.
envir	The environment used to evaluate the data object in (e.g., in case object is of type call).

**Value**

A data.frame with columns matching the id, time, and response name arguments.

**See Also**

[plotTrajectories latrend](#)

---

trajectoryAssignments *Get the cluster membership of each trajectory*

---

**Description**

Classify the fitted trajectories based on the posterior probabilities computed by [postprob\(\)](#), according to a given classification strategy.

By default, trajectories are assigned based on the highest posterior probability using [which.max\(\)](#). In cases where identical probabilities are expected between clusters, it is preferable to use [which.is.max](#) instead, as this function breaks ties at random. Another strategy to consider is the function [which.weight\(\)](#), which enables weighted sampling of cluster assignments based on the trajectory-specific probabilities.

**Usage**

```
## S4 method for signature 'matrix'
trajectoryAssignments(
  object,
  strategy = which.max,
  clusterNames = colnames(object),
  ...
)

## S4 method for signature 'lcModel'
trajectoryAssignments(object, strategy = which.max, ...)
```

**Arguments**

object	The object to obtain the cluster assignments from.
strategy	A function returning the cluster index based on the given vector of membership probabilities. By default, ids are assigned to the cluster with the highest probability.
clusterNames	Optional character vector with the cluster names. If clusterNames = NULL, <a href="#">make.clusterNames()</a> is used.
...	Any additional arguments passed to the strategy function.

**Details**

In case object is a matrix: the posterior probability matrix, with the  $k$ th column containing the observation- or trajectory-specific probability for cluster  $k$ .

**Value**

A factor indicating the cluster membership for each trajectory.

**See Also**

[postprob](#) [clusterSizes](#) [predictAssignments](#)

**Examples**

```
data(latrendData)
model <- latrend(method = lcMethodKML("Y", id = "Id", time = "Time"), latrendData)
trajectoryAssignments(model)

# assign trajectories at random using weighted sampling
trajectoryAssignments(model, strategy = which.weight)
```



---

transformFitted	<i>Helper function for custom lcModel classes implementing fitted.lcModel()</i>
-----------------	---

---

## Description

A helper function for implementing the `fitted.lcModel()` method as part of your own `lcModel` class, ensuring the correct output type and format (see the Value section). Note that this function has no use outside of implementing `fitted.lcModel()`.

The function makes it easier to implement `fitted.lcModel` based on existing implementations that may output their results in different data formats. Furthermore, the function checks whether the input data is valid.

The prediction ordering depends on the ordering of the data observations that was used for fitting the `lcModel`.

By default, `transformFitted()` accepts one of the following inputs:

`data.frame` A `data.frame` in long format providing a cluster-specific prediction for each observation per row, with column names "Fit" and "Cluster". This `data.frame` therefore has `nobs(object) * nClusters(object)` rows.

`matrix` An N-by-K matrix where each row provides the cluster-specific predictions for the respective observation. Here, `N = nobs(object)` and `K = nClusters(object)`.

`list` A list of cluster-specific prediction vectors. Each prediction vector should be of length `nobs(object)`. The overall (named) list of cluster-specific prediction vectors is of length `nClusters(object)`.

Users can implement support for other prediction formats by defining the `transformFitted` method with other signatures.

## Usage

```
transformFitted(pred, model, clusters)

## S4 method for signature '`NULL`,lcModel'
transformFitted(pred, model, clusters = NULL)

## S4 method for signature 'matrix,lcModel'
transformFitted(pred, model, clusters = NULL)

## S4 method for signature 'list,lcModel'
transformFitted(pred, model, clusters = NULL)

## S4 method for signature 'data.frame,lcModel'
transformFitted(pred, model, clusters = NULL)
```

**Arguments**

pred	The cluster-specific predictions for each observation
model	The lcModel by which the prediction was made.
clusters	The trajectory cluster assignment per observation. Optional.

**Value**

If the `clusters` argument was specified, a vector of fitted values conditional on the given cluster assignment. Else, a matrix with the fitted values per cluster per column.

**Example implementation**

A typical implementation of `fitted.lcModel()` for your own `lcModel` class would have the following format:

```
fitted.lcModelExample <- function(object,
  clusters = trajectoryAssignments(object)) {
  # computations of the fitted values per cluster here
  predictionMatrix <- CODE_HERE
  transformFitted(pred = predictionMatrix, model = object, clusters = clusters)
}
```

For a complete and runnable example, see the custom models vignette accessible via `vignette("custom", package = "latrend")`.

---

transformPredict	<i>Helper function for custom lcModel classes implementing predict.lcModel()</i>
------------------	--

---

**Description**

A helper function for implementing the `predict.lcModel()` method as part of your own `lcModel` class, ensuring the correct output type and format (see the Value section). Note that this function has no use outside of ensuring valid output for `predict.lcModel`. For implementing `lcModel` predictions from scratch, it is advisable to implement `predictForCluster` instead of `predict.lcModel`. The prediction ordering corresponds to the observation ordering of the `newdata` argument.

By default, `transformPredict()` accepts one of the following inputs:

`data.frame` A `data.frame` in long format providing a cluster-specific prediction for each observation per row, with column names "Fit" and "Cluster". This `data.frame` therefore has `nobs(object) * nClusters(object)` rows.

`matrix` An N-by-K matrix where each row provides the cluster-specific predictions for the respective observations in `newdata`. Here,  $N = nrow(newdata)$  and  $K = nClusters(object)$ .

`vector` A vector of length `nrow(newdata)` with predictions corresponding to the rows of `newdata`.

Users can implement support for other prediction formats by defining the `transformPredict()` method with other signatures.

**Usage**

```

transformPredict(pred, model, newdata)

## S4 method for signature '`NULL`,lcModel'
transformPredict(pred, model, newdata)

## S4 method for signature 'vector,lcModel'
transformPredict(pred, model, newdata)

## S4 method for signature 'matrix,lcModel'
transformPredict(pred, model, newdata)

## S4 method for signature 'data.frame,lcModel'
transformPredict(pred, model, newdata)

```

**Arguments**

pred	The (per-cluster) predictions for newdata.
model	The lcModel for which the prediction was made.
newdata	A data.frame containing the input data to predict for.

**Value**

A data.frame with the predictions, or a list of cluster-specific prediction data.frames.

**Example implementation**

In case we have a custom lcModel class based on an existing internal model representation with a predict() function, we can use transformPredict() to easily transform the internal model predictions to the right format. A common output is a matrix with the cluster-specific predictions.

```

predict.lcModelExample <- function(object, newdata) {
  predictionMatrix <- predict(object@model, newdata)
  transformPredict(
    pred = predictionMatrix,
    model = object,
    newdata = newdata
  )
}

```

However, for ease of implementation it is generally advisable to implement [predictForCluster](#) instead of [predict.lcModel](#).

For a complete and runnable example, see the custom models vignette accessible via `vignette("custom", package = "latrend")`.

**See Also**

[predictForCluster](#), [predict.lcModel](#)

---

update.lcMethod	<i>Update a method specification</i>
-----------------	--------------------------------------

---

### Description

Update a method specification

### Usage

```
## S3 method for class 'lcMethod'
update(object, ..., .eval = FALSE, .remove = character(), envir = NULL)
```

### Arguments

object	The lcMethod object.
...	The new or updated method argument values.
.eval	Whether to assign the evaluated argument values to the method. By default (FALSE), the argument expression is preserved.
.remove	Names of arguments that should be removed.
envir	The environment in which to evaluate the arguments. If NULL, the environment associated with the object is used. If not available, the parent .frame() is used.

### Details

Updates or adds arguments to a lcMethod object. The inputs are evaluated in order to determine the presence of formula objects, which are updated accordingly.

### Value

The new lcMethod object with the additional or updated arguments.

### See Also

Other lcMethod functions: [\[\[,lcMethod-method](#), [as.data.frame.lcMethods\(\)](#), [as.data.frame.lcMethod\(\)](#), [as.lcMethods\(\)](#), [as.list.lcMethod\(\)](#), [evaluate.lcMethod\(\)](#), [formula.lcMethod\(\)](#), [lcMethod-class](#), [names,lcMethod-method](#)

### Examples

```
m <- lcMethodMixtoolsGMM(Value ~ 1)
m2 <- update(m, formula = ~ . + Time)

m3 <- update(m2, nClusters = 3)

k <- 2
m4 <- update(m, nClusters = k) # nClusters: k
```

```
m5 <- update(m, nClusters = k, .eval = TRUE) # nClusters: 2
```

---

update.lcModel	<i>Update a lcModel</i>
----------------	-------------------------

---

## Description

Fit a new model with modified arguments from the current model.

## Usage

```
## S3 method for class 'lcModel'
update(object, ...)
```

## Arguments

object	The lcModel object.
...	Arguments passed on to <a href="#">latrend</a>
method	An lcMethod object specifying the longitudinal cluster method to apply, or the name (as character) of an lcMethod subclass. See <a href="#">lcMethod</a> for details.
data	The data.frame to which to apply the method. Inputs supported by <a href="#">trajectories()</a> can also be used.
envir	The environment in which to evaluate the method arguments (by <a href="#">compose()</a> ). This environment is also used to evaluate the data argument if it is of type call.
verbose	The level of verbosity. Either an object of class Verbose (see <a href="#">R.utils::Verbose</a> for details), a logical indicating whether to show basic computation information, a numeric indicating the verbosity level (see <a href="#">Verbose</a> ), or one of <code>c('info', 'fine', 'finest')</code> .

## Value

The refitted lcModel object, of the same type as the object argument.

## See Also

[latrend](#) [getCall](#)

## Examples

```
data(latrendData)
m <- lcMethodKML("Y", id = "Id", time = "Time", nClusters = 3)
model <- latrend(method = m, data = latrendData)
# fit for a different number of clusters
update(model, nClusters = 2)
```

---

 validate

*lcMethod fit process: method argument validation logic*


---

### Description

Note: this function should not be called directly, as it is part of the `lcMethod` fitting process. For fitting an `lcMethod` object to a dataset, see `latrend()`.

The `validate()` function of the `lcMethod` object validates the method with respect to the training data. This enables a method to verify, for example:

- whether the formula covariates are present.
- whether the argument combination settings are valid.
- whether the data is suitable for training.

By default, the `validate()` function checks whether the `id`, `time`, and response variables are present as columns in the training data.

### Usage

```
## S4 method for signature 'lcMethod'
validate(method, data, envir = NULL, ...)
```

### Arguments

<code>method</code>	An object inheriting from <code>lcMethod</code> with all its arguments having been evaluated and finalized.
<code>data</code>	A <code>data.frame</code> representing the transformed training data.
<code>envir</code>	The environment in which the <code>lcMethod</code> should be evaluated
<code>...</code>	Not used.

### Value

Either `TRUE` if all validation checks passed, or a character containing a description of the failed validation checks.

### Implementation

An example implementation checking for the existence of specific arguments and type:

```
library(assertthat)
setMethod("validate", "lcMethodExample", function(method, data, envir = NULL, ...) {
  validate_that(
    hasName(method, "myArgument"),
    hasName(method, "anotherArgument"),
    is.numeric(method$myArgument)
  )
})
```

### Fitting procedure

Each `lcMethod` subclass defines a type of methods in terms of a series of steps for estimating the method. These steps, as part of the fitting procedure, are executed by `latrend()` in the following order:

1. `compose()`: Evaluate and finalize the method argument values.
2. `validate()`: Check the validity of the method argument values in relation to the dataset.
3. `prepareData()`: Process the training data for fitting.
4. `preFit()`: Prepare environment for estimation, independent of training data.
5. `fit()`: Estimate the specified method on the training data, outputting an object inheriting from `lcModel`.
6. `postFit()`: Post-process the outputted `lcModel` object.

The result of the fitting procedure is an `lcModel` object that inherits from the `lcModel` class.

### See Also

[assertthat::validate\\_that](#)

---

which.weight

*Sample an index of a vector weighted by the elements*

---

### Description

Returns a random index, weighted by the element magnitudes. This function is intended to be used as an optional strategy for [trajectoryAssignments](#), resulting in randomly sampled cluster membership.

### Usage

```
which.weight(x)
```

### Arguments

`x` A positive numeric vector.

### Value

An integer giving the index of the sampled element.

### Examples

```
x = c(.01, .69, .3)
which.weight(x) #1, 2, or 3
```

---

[[,lcMethod-method      *Retrieve and evaluate a lcMethod argument by name*

---

### Description

Retrieve and evaluate a lcMethod argument by name

### Usage

```
## S4 method for signature 'lcMethod'
x$name

## S4 method for signature 'lcMethod'
x[[i, eval = TRUE, envir = NULL]]
```

### Arguments

x	The lcMethod object.
name	The argument name, as character.
i	Name or index of the argument to retrieve.
eval	Whether to evaluate the call argument (enabled by default).
envir	The environment in which to evaluate the argument. This argument is only applicable when eval = TRUE.

### Value

The argument call or evaluation result.

### See Also

Other lcMethod functions: [as.data.frame.lcMethods\(\)](#), [as.data.frame.lcMethod\(\)](#), [as.lcMethods\(\)](#), [as.list.lcMethod\(\)](#), [evaluate.lcMethod\(\)](#), [formula.lcMethod\(\)](#), [lcMethod-class](#), [names.lcMethod-method](#), [update.lcMethod\(\)](#)

### Examples

```
m <- lcMethodKML(nClusters = 3)
m$nClusters # 3
m = lcMethodKML(nClusters = 5)
m[["nClusters"]] # 5

k = 2
m = lcMethodKML(nClusters = k)
m[["nClusters", eval=FALSE]] # k
```



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