Package 'plsmod'

Title Model Wrappers for Projection Methods

Version 0.0.1

Description Bindings for additional regression models for use
with the 'parsnip' package, including ordinary and spare partial least
squares models for regression and classification (Rohart et al (2017)
<doi:10.1371/journal.pcbi.1005752>).

URL https://github.com/tidymodels/plsmod

BugReports https://github.com/tidymodels/plsmod/issues

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Encoding UTF-8

LazyData true

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biocViews mixOmics

Depends parsnip (>= 0.1.0)

Imports tibble, mixOmics, dplyr, tidyr, generics, magrittr, purrr,
rlang

Suggests modeldata, testthat, covr, spelling

Language en-US

NeedsCompilation no

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Repository CRAN

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R topics documented:

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multi_predict._mixo_pls

Model predictions across many sub-models

Description

Model predictions across many sub-models

Usage

```
## S3 method for class '`_mixo_pls`'
multi_predict(object, new_data, num_comp = NULL, type = NULL, ...)

## S3 method for class '`_mixo_spls`'
multi_predict(object, new_data, num_comp = NULL, type = NULL, ...)

## S3 method for class '`_mixo_plsda`'
multi_predict(object, new_data, num_comp = NULL, type = NULL, ...)

## S3 method for class '`_mixo_splsda`'
multi_predict(object, new_data, num_comp = NULL, type = NULL, ...)
```

Arguments

object	An object of class model_fit
new_data	A rectangular data object, such as a data frame.
num_comp	An integer vector for the number of PLS terms to retain.
type	A single character value or NULL. Possible values are "numeric", "class", or "prob". When NULL, predict() will choose an appropriate value based on the model's mode.
...	Not currently used.

Examples

```
data(meats, package = "modeldata")

mv_meats <-
  pls(num_comp = 20, num_terms = 10) %>%
  set_engine("mixOmics") %>%
  set_mode("regression") %>%
  fit_xy(x = meats[-(1:5), 1:100], y = meats[-(1:5), 101:103])

pred_vals <- multi_predict(mv_meats, meats[1:5, 1:100], num_comp = 1:10)
# Predictions over components nested within sample rows
pred_vals
```

```
# For first sample:
pred_vals$.pred[[1]]
```

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pls   *General Interface for Partial Least Squares (PLS)*

Description

`pls()` is a way to generate a *specification* of a model before fitting and allows the model to be created using R. The main arguments for the model are:

- `num_terms`: The number of predictors that are allowed to affect each PLS loading.
- `num_comp`: The number of PLS components to retain.

These arguments are converted to their specific names at the time that the model is fit. Other options and argument can be set using `set_engine()`. If left to their defaults here (NULL), the values are taken from the underlying model functions. If parameters need to be modified, `update()` can be used in lieu of recreating the object from scratch.

Usage

```
pls(mode = "unknown", num_terms = NULL, num_comp = NULL)

## S3 method for class 'pls'
update(
  object,
  parameters = NULL,
  num_terms = NULL,
  num_comp = NULL,
  fresh = FALSE,
  ...
)
```

Arguments

mode	A single character string for the type of model. Possible values for this model are "unknown", "regression", or "classification".
num_terms	The number of predictors that are allowed to affect each PLS loading. The default allows each predictor to have non-zero loadings for each PLS component.
num_comp	The number of PLS components to retain.
object	A PLS model specification.
parameters	A 1-row tibble or named list with *main* parameters to update. If the individual arguments are used, these will supersede the values in `parameters`. Also, using engine arguments in this object will result in an error.
fresh	A logical for whether the arguments should be modified in-place of or replaced wholesale.
...	Not used for `update()`.

Details

The model can be created using the `fit()` function using the following *engines*:

- **R**: `"mixOmics"` (the default)

Engine Details

Engines may have pre-set default arguments when executing the model fit call. The possible model calls are shown in the Examples section below.

Examples

```
pls(num_comp = 2, num_terms = 10) %>%
  set_engine("mixOmics") %>%
  set_mode("regression") %>%
  translate()

pls(num_comp = 2, num_terms = 10) %>%
  set_engine("mixOmics") %>%
  set_mode("classification") %>%
  translate()

pls(num_comp = 6) %>%
  set_engine("mixOmics") %>%
  set_mode("regression") %>%
  translate()

pls() %>%
  set_engine("mixOmics") %>%
  set_mode("classification") %>%
  translate()


model <- pls(num_terms = 10)
model
update(model, num_terms = 1)
update(model, num_terms = 1, fresh = TRUE)
```

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tidy.mixo_pls   *Tidy methods for pls and spls objects*

Description

Tidy methods for pls and spls objects

Usage

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

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

Arguments

x	An object with class `mixo_pls` or `mixo_spls`.
...	Not currently used.

Value

A tibble with columns `terms` (the predictor names), `value` (the loadings), `type` (either "predictors" or "outcomes"), and `component` (the component number).

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