Package 'snazzieR'

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Type Package

Title Chic and Sleek Functions for Beautiful Statisticians

Version 0.1.2

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Description Because your linear models deserve better than console output.
A sleek color palette and kable styling to make your regression results look sharper than they are.
Includes support for Partial Least Squares (PLS) regression via both the SVD and NIPALS algorithms,
along with a unified interface for model fitting and fabulous LaTeX and console output formatting.
See the package website at
<https://finitesample.space/snazzier>.

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Encoding UTF-8

LazyData true

ByteCompile true

Imports ggplot2, knitr, kableExtra, dplyr, stats

RoxygenNote 7.3.2

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Suggests rmarkdown, testthat (>= 3.0.0)

Config/testthat/edition 3

VignetteBuilder knitr

URL https://detectivefierce.github.io/snazzieR/

NeedsCompilation no

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Contents

`ANOVA.summary.table` *Generate a Summary Table for ANOVA Results*

Description

This function creates a summary table for ANOVA results, including degrees of freedom, sum of squares, mean squares, F-values, and p-values. The table can be output as either LaTeX (for PDF reports) or plain text (for console viewing).

Usage

```
ANOVA.summary.table(model, caption, latex = TRUE)
```

Arguments

`model`	A model object for which ANOVA results are computed (e.g., output from ‘lm()‘ or ‘aov()‘).
`caption`	A character string to be used as the caption for the table.
`latex`	Logical; if ‘TRUE‘, returns a LaTeX-formatted table using ‘kableExtra‘. If ‘FALSE‘, prints a plain-text version to the console.

Value

If ‘latex = TRUE‘, a LaTeX-formatted table object. If ‘latex = FALSE‘, prints the summary table and returns it (invisibly).

Examples

```
# Fit a linear model
model <- lm(mpg ~ wt + hp, data = mtcars)

# Generate a plain-text ANOVA summary table
ANOVA.summary.table(model, caption = "ANOVA Summary", latex = FALSE)
```

`color.ref` *Display a Color Reference Palette*

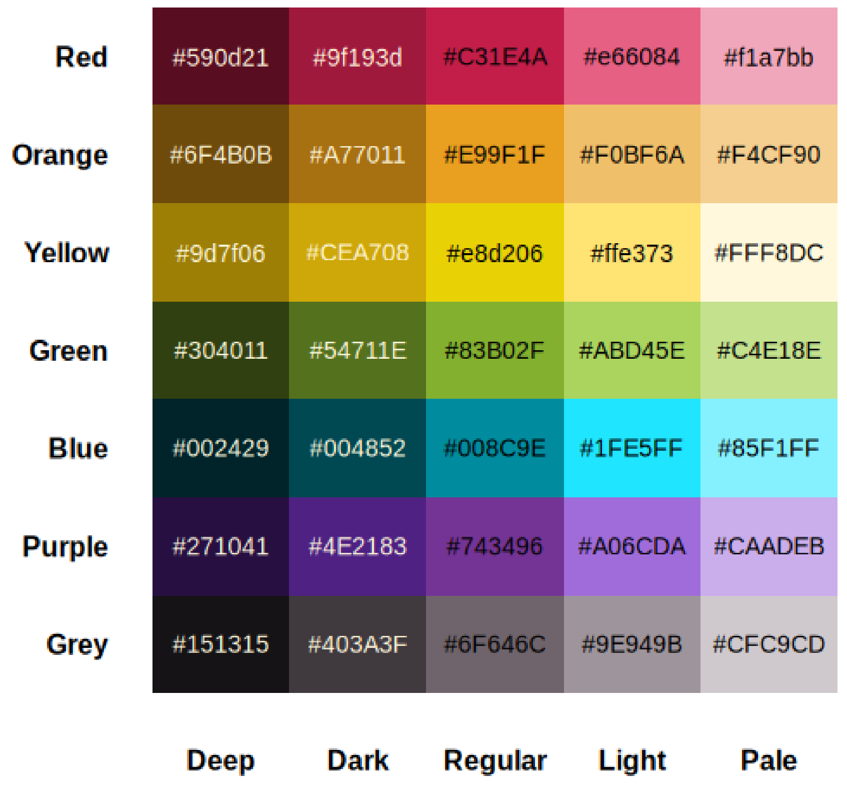
Description

This function generates a plot displaying a predefined color palette with color codes for easy reference. The palette includes shades of Red, Orange, Yellow, Green, Blue, Purple, and Grey.

Usage

```
color.ref()
```

Details



	Deep	Dark	Regular	Light	Pale
Red	#590d21	#9f193d	#C31E4A	#e66084	#f1a7bb
Orange	#6F4B0B	#A77011	#E99F1F	#F0BF6A	#F4CF90
Yellow	#9d7f06	#CEA708	#e8d206	#ffe373	#FFF8DC
Green	#304011	#54711E	#83B02F	#ABD45E	#C4E18E
Blue	#002429	#004852	#008C9E	#1FE5FF	#85F1FF
Purple	#271041	#4E2183	#743496	#A06CDA	#CAADEB
Grey	#151315	#403A3F	#6F646C	#9E949B	#CFC9CD

Value

A plot displaying the color palette.

Examples

```
color.ref()
```

`colors` *SnazzieR Color Palette*

Description

A collection of named hex colors grouped by hue and tone. Each color is available as an exported object (e.g., `Red`, `Dark.Red`).

Usage

```
color.list
```

Format

Each color is a character string representing a hex code.

An object of class `character` of length 1.

An object of class `list` of length 35.

Details

This palette consists of named hex colors. Each color's name (e.g., `Dark.Red`) is available as an exported object.

Swatch images are embedded below (not selectable):

Color	**Swatch**	**Color**	**Swatch**	**Color**	**Swatch**
Deep.Red	🟥	Deep.Green	🟩	Deep.Grey	⬛
Dark.Red	🟥	Dark.Green	🟩	Dark.Grey	⬛
Red	🟥	Green	🟩	Grey	⬛
Light.Red	🟥	Light.Green	🟩	Light.Grey	⬜
Pale.Red	🟥	Pale.Green	🟩	Pale.Grey	⬜
Deep.Orange	🟫	Deep.Blue	🟦		
Dark.Orange	🟧	Dark.Blue	🟦		
Orange	🟧	Blue	🟦		
Light.Orange	🟧	Light.Blue	🟦		
Pale.Orange	🟧	Pale.Blue	🟦		
Deep.Yellow	🟨	Deep.Purple	🟪		
Dark.Yellow	🟨	Dark.Purple	🟪		
Yellow	🟨	Purple	🟪		
Light.Yellow	🟨	Light.Purple	🟪		
Pale.Yellow	⬜	Pale.Purple	🟪		

For the full list and hex codes, use `names(color.list)` or see `?color.list`.

See Also

`color.ref`, `snazzieR.theme`

`create_kfold_splits` *Create K-Fold Cross Validation Splits*

Description

Create K-Fold Cross Validation Splits

Usage

```
create_kfold_splits(data, k = 5, seed = NULL)
```

Arguments

`data`	A data frame containing the dataset
`k`	Number of folds (default: 5)
`seed`	Random seed for reproducibility (optional)

Value

A list containing fold assignments for each observation

`cv.mse` *Compute Cross-Validated Mean Squared Error*

Description

Computes mean squared error via k-fold cross-validation for a fixed lambda value.

Usage

```
cv.mse(x, y, lambda, folds = 5, fold_indices = NULL)
```

Arguments

`x`	A standardized design matrix (n × p)
`y`	A centered response vector (n × 1)
`lambda`	A non-negative regularization scalar
`folds`	Number of cross-validation folds (default: 5)

Value

A numeric scalar representing the CV-MSE

`eigen.summary` *Summarize Eigenvalues and Eigenvectors of a Covariance Matrix*

Description

This function computes the eigenvalues and eigenvectors of a given covariance matrix, ensures sign consistency in the eigenvectors, and outputs either a LaTeX table or plaintext summary displaying the results.

Usage

```
eigen.summary(
  cov.matrix,
  caption = "Eigenvectors of Covariance Matrix",
  latex = TRUE
)
```

Arguments

`cov.matrix`	A square numeric matrix representing the covariance matrix.
`caption`	A character string specifying the table caption (default: "Eigenvectors of Covariance Matrix").
`latex`	A logical indicating whether to output LaTeX table (default: TRUE). If FALSE, prints as plain text.

Value

A LaTeX formatted table (if latex = TRUE) or plaintext console output (if latex = FALSE).

Examples

```
cov_matrix <- matrix(c(4, 2, 2, 3), nrow = 2)
eigen.summary(cov_matrix, caption = "Eigenvalues and Eigenvectors", latex = FALSE)
```

`fit.ridge` *Fit Ridge Regression with Closed-Form Solution*

Description

Computes ridge regression coefficients and standard errors using the closed-form solution: $\hat{\beta} = (X^T X + \lambda I)^{-1} X^T y$

Usage

```
fit.ridge(x, y, lambda)
```

Arguments

`x`	A standardized design matrix (n × p)
`y`	A centered response vector (n × 1)
`lambda`	A non-negative regularization scalar

Value

A list containing:

coefficients Ridge regression coefficients (length p)

std_errors Standard errors of the coefficients (length p)

`format.pls` *Format PLS Model Output as LaTeX or Console Tables*

Description

Formats and displays Partial Least Squares (PLS) model output from `pls.regression()` as either LaTeX tables (for PDF rendering) or console-friendly output.

Usage

```
## S3 method for class 'pls'
format(x, ..., include.scores = TRUE, latex = FALSE)
```

Arguments

`x`	A list returned by `pls.regression()` (class `"pls"`) containing PLS model components.
`...`	Further arguments passed to or from methods (unused).
`include.scores`	Logical. Whether to include score matrices (T and U). Default is `TRUE`.
`latex`	Logical. If `TRUE`, produces LaTeX output (for PDF rendering). If `FALSE`, prints to console. Default is `FALSE`.

Value

When `latex = TRUE`, returns a `knitr::asis_output` object (LaTeX code). When `FALSE`, prints formatted tables to console.

`kfold_cross_validation`
Perform K-Fold Cross Validation

Description

Perform K-Fold Cross Validation

Usage

```
kfold_cross_validation(
  data,
  formula,
  model_function,
  predict_function = predict,
  metric_function = NULL,
  k = 5,
  seed = NULL,
  ...
)
```

Arguments

`data`	A data frame containing the dataset
`formula`	A formula specifying the model (e.g., y ~ x1 + x2)
`model_function`	Function to fit the model (e.g., lm, glm)
`predict_function`	Function to make predictions (default: predict)
`metric_function`	Function to calculate performance metric
`k`	Number of folds (default: 5)
`seed`	Random seed for reproducibility (optional)
`...`	Additional arguments passed to model_function

Value

A list containing fold results and summary statistics

`model.equation` *Generate a Model Equation from a Linear Model*

Description

This function extracts and formats the equation from a linear model object. It includes an option to return the equation as a LaTeX-formatted string or print it to the console.

Usage

```
model.equation(model, latex = TRUE)
```

Arguments

`model`	A linear model object (e.g., output from ‘lm()‘).
`latex`	A logical value indicating whether to return a LaTeX-formatted equation (default: TRUE). If FALSE, the equation is printed to the console.

Value

If ‘latex‘ is TRUE, the equation is returned as LaTeX code using ‘knitr::asis_output()‘. If FALSE, the equation is printed to the console.

Examples

```
# Fit a linear model
model <- lm(mpg ~ wt + hp, data = mtcars)

# Get LaTeX equation
model.equation(model)

# Print equation to console
model.equation(model, latex = FALSE)
```

---

model.summary.table   *Generate a Summary Table for a Linear Model*

Description

This function creates a summary table for a linear model, including estimated coefficients, standard errors, p-values with significance codes, and model statistics such as MSE and R-squared. The table can be output as either LaTeX (for PDF reports) or plain text (for console viewing).

Usage

```
model.summary.table(model, caption, latex = TRUE)
```

Arguments

`model`	A linear model object (typically the result of ‘lm()‘).
`caption`	A character string to be used as the caption for the table.
`latex`	Logical; if ‘TRUE‘ (default), returns a LaTeX-formatted table using ‘kableExtra‘. If ‘FALSE‘, prints plain-text summary tables to the console.

Value

If ‘latex = TRUE‘, returns a LaTeX-formatted ‘kableExtra‘ table object. If ‘latex = FALSE‘, prints formatted summary tables to the console and returns the underlying data frame.

Examples

```
# Fit a linear model
model <- lm(mpg ~ wt + hp, data = mtcars)

# Print a plain-text version to the console
model.summary.table(model, caption = "Linear Model Summary", latex = FALSE)
```

`NIPALS.pls` *Partial Least Squares Regression via NIPALS (Internal)*

Description

This function is called internally by `pls.regression` and is not intended to be used directly. Use `pls.regression(..., calc.method = "NIPALS")` instead.

Performs Partial Least Squares (PLS) regression using the NIPALS (Nonlinear Iterative Partial Least Squares) algorithm. This method estimates the latent components (scores, loadings, weights) by iteratively updating the X and Y score directions until convergence. It is suitable for cases where the number of predictors is large or predictors are highly collinear.

Usage

```
NIPALS.pls(x, y, n.components = NULL)
```

Arguments

`x`	A numeric matrix or data frame of predictors (X). Should have dimensions n × p.
`y`	A numeric matrix or data frame of response variables (Y). Should have dimensions n × q.
`n.components`	Integer specifying the number of PLS components to extract. If NULL, it defaults to `qr(x)$rank`.

Details

The algorithm standardizes both `x` and `y` using z-score normalization. It then performs the following for each of the `n.components` latent variables:

1. Initializes a random response score vector u.
2. Iteratively:
   - Updates the X weight vector $w = E^\top u$, normalized.
   - Computes the X score $t = Ew$, normalized.
   - Updates the Y loading $q = F^\top t$, normalized.
   - Updates the response score $u = Fq$.
   - Repeats until t converges below a tolerance threshold.
3. Computes scalar regression coefficient $b = t^\top u$.
4. Deflates residual matrices E and F to remove current component contribution.

After component extraction, the final regression coefficient matrix $B_{original}$ is computed and rescaled to the original data units. Explained variance is also computed component-wise and cumulatively.

Value

A list with the following elements:

model.type Character string indicating the model type ("PLS Regression").

T Matrix of X scores (n × H).

U Matrix of Y scores (n × H).

W Matrix of X weights (p × H).

C Matrix of normalized Y weights (q × H).

P_loadings Matrix of X loadings (p × H).

Q_loadings Matrix of Y loadings (q × H).

B_vector Vector of regression scalars (length H), one for each component.

coefficients Matrix of regression coefficients in original data scale (p × q).

intercept Vector of intercepts (length q). Always zero here due to centering.

X_explained Percent of total X variance explained by each component.

Y_explained Percent of total Y variance explained by each component.

X_cum_explained Cumulative X variance explained.

Y_cum_explained Cumulative Y variance explained.

References

Wold, H., & Lyttkens, E. (1969). Nonlinear iterative partial least squares (NIPALS) estimation procedures. *Bulletin of the International Statistical Institute*, 43, 29–51.

Examples

```
## Not run:
X <- matrix(rnorm(100 * 10), 100, 10)
Y <- matrix(rnorm(100 * 2), 100, 2)
model <- pls.regression(X, Y, n.components = 3, calc.method = "NIPALS")
model$coefficients

## End(Not run)
```

optimize.cv.lambda *Optimize Lambda Using Cross-Validation*

Description

Searches the lambda range to minimize CV-MSE using Brent's method via 'optimize()'.

Usage

```
optimize.cv.lambda(x, y, lambda.range, folds)
```

Arguments

`x`	A standardized design matrix (n × p)
`y`	A centered response vector (n × 1)
`lambda.range`	A numeric vector of length 2 specifying the search interval
`folds`	Number of cross-validation folds

Value

A list containing:

minimum Optimal lambda value

objective Minimum CV-MSE achieved

trace Data frame with lambda and CV-MSE pairs

`pls.regression` *Partial Least Squares (PLS) Regression Interface*

Description

Performs Partial Least Squares (PLS) regression using either the NIPALS or SVD algorithm for component extraction. This is the main user-facing function for computing PLS models. Internally, it delegates to either `NIPALS.pls()` or `SVD.pls()`.

Usage

```
pls.regression(x, y, n.components = NULL, calc.method = c("SVD", "NIPALS"))
```

Arguments

`x`	A numeric matrix or data frame of predictor variables (X), with dimensions n × p.
`y`	A numeric matrix or data frame of response variables (Y), with dimensions n × q.
`n.components`	Integer specifying the number of latent components (H) to extract. If NULL, defaults to the rank of `x`.
`calc.method`	Character string indicating the algorithm to use. Must be either `"SVD"` (default) or `"NIPALS"`.

Details

This function provides a unified interface for Partial Least Squares regression. Based on the value of `calc.method`, it computes latent variables using either:

- `"SVD"` — A direct method using the singular value decomposition of the cross-covariance matrix ($X^\top Y$).
- `"NIPALS"` — An iterative method that alternately estimates predictor and response scores until convergence.

The outputs from both methods include scores, weights, loadings, regression coefficients, and explained variance.

Value

A list (from either `SVD.pls()` or `NIPALS.pls()`) containing:

model.type Character string ("PLS Regression").

T, U Score matrices for X and Y.

W, C Weight matrices for X and Y.

P_loadings, Q_loadings Loading matrices.

B_vector Component-wise regression weights.

coefficients Final regression coefficient matrix (rescaled).

intercept Intercept vector (typically zero due to centering).

X_explained, Y_explained Variance explained by each component.

X_cum_explained, Y_cum_explained Cumulative variance explained.

References

Abdi, H., & Williams, L. J. (2013). Partial least squares methods: Partial least squares correlation and partial least square regression. *Methods in Molecular Biology (Clifton, N.J.)*, 930, 549–579. doi:10.1007/9781627030595_23

de Jong, S. (1993). SIMPLS: An alternative approach to partial least squares regression. *Chemometrics and Intelligent Laboratory Systems*, 18(3), 251–263. doi:10.1016/01697439(93)85002X

See Also

`SVD.pls`, `NIPALS.pls`

Examples

```
## Not run:
X <- matrix(rnorm(100 * 10), 100, 10)
Y <- matrix(rnorm(100 * 2), 100, 2)

# Using SVD (default)
model1 <- pls.regression(X, Y, n.components = 3)

# Using NIPALS
model2 <- pls.regression(X, Y, n.components = 3, calc.method = "NIPALS")

## End(Not run)
```

`pls.summary` *Format PLS Model Output as LaTeX Tables*

Description

Formats and displays Partial Least Squares (PLS) model output from `pls.regression()` as LaTeX tables for PDF rendering.

Usage

```
pls.summary(x, ..., include.scores = TRUE)
```

Arguments

`x`	A list returned by `pls.regression()` (class `"pls"`) containing PLS model components.
`...`	Further arguments passed to or from methods (unused).
`include.scores`	Logical. Whether to include score matrices (T and U). Default is `TRUE`.

Value

Returns a `knitr::asis_output` object (LaTeX code) for PDF rendering.

Examples

```
# Load example data
data(mtcars)

# Prepare data for PLS regression
X <- mtcars[, c("wt", "hp", "disp")]
Y <- mtcars[, "mpg", drop = FALSE]

# Fit PLS model with 2 components
pls.fit <- pls.regression(X, Y, n.components = 2)

# Print a LaTeX-formatted summary
pls.summary(pls.fit, include.scores = FALSE)
```

`predict.ridge.model` *Predict Method for Ridge Model Objects*

Description

Predicts response values for new data using a fitted ridge model.

Usage

```
## S3 method for class 'ridge.model'
predict(object, newdata = NULL, ...)
```

Arguments

`object`	A ‘ridge.model‘ object
`newdata`	A data frame or matrix containing new predictor values
`...`	Additional arguments (not used)

Value

A numeric vector of predicted values

`print.ridge.model` *Print Method for Ridge Model Objects*

Description

Prints a summary of the ridge model fit.

Usage

```
## S3 method for class 'ridge.model'
print(x, ...)
```

Arguments

`x`	A ‘ridge.model‘ object
`...`	Additional arguments (not used)

`ridge.regression` *Ridge Regression with Automatic Lambda Selection*

Description

Performs ridge regression with automatic selection of the optimal regularization parameter ‘lambda‘ by minimizing k-fold cross-validated mean squared error (CV-MSE) using Brent’s method. Supports both formula and matrix interfaces.

Usage

```
ridge.regression(
  formula = NULL,
  data = NULL,
  x = NULL,
  y = NULL,
  lambda.range = c(1e-04, 100),
  folds = 5,
  ...
)
```

Arguments

`formula`	A model formula like ‘y ~ x1 + x2‘. Mutually exclusive with ‘x‘/‘y‘.
`data`	A data frame containing all variables used in the formula.
`x`	A numeric matrix of predictor variables (n × p). Used when formula is not provided.
`y`	A numeric vector of response variables (n × 1). Used when formula is not provided.
`lambda.range`	A numeric vector of length 2 specifying the interval for lambda optimization. Default: ‘c(1e-4, 100)‘.
`folds`	An integer specifying the number of cross-validation folds. Default: ‘5‘.
`...`	Additional arguments passed to internal methods.

Details

This function implements ridge regression with automatic hyperparameter tuning. The algorithm:

- Standardizes predictor variables (centers and scales)
- Centers the response variable
- Uses k-fold cross-validation to find the optimal lambda
- Fits the final model with the optimal lambda
- Returns a structured object for prediction and analysis

The ridge regression solution is computed using the closed-form formula: $\hat{\beta} = (X^T X + \lambda I)^{-1} X^T y$

Value

A ‘ridge.model‘ object containing:

coefficients Final ridge coefficients (no intercept)

std_errors Standard errors of the coefficients

intercept Intercept term (from y centering)

optimal.lambda Best lambda minimizing CV-MSE

cv.ms Minimum CV-MSE achieved

cv.results Data frame with lambda and CV-MSE pairs

x.scale Standardization info: mean and sd for each predictor

y.center Centering constant for y

fitted.values Final model predictions on training data

residuals Training residuals (y - fitted)

call Matched call (for debugging)

method Always "ridge"

folds Number of CV folds used

formula Stored if formula interface used

terms Stored if formula interface used

References

Hoerl, A. E., & Kennard, R. W. (1970). Ridge regression: Biased estimation for nonorthogonal problems. *Technometrics*, 12(1), 55-67.

See Also

`predict.ridge.model`

Examples

```
## Not run:
# Formula interface
model1 <- ridge.regression(mpg ~ wt + hp + disp, data = mtcars)

# Matrix interface
X <- as.matrix(mtcars[, c("wt", "hp", "disp")])
y <- mtcars$mpg
```

```
model2 <- ridge.regression(x = X, y = y)

# Custom lambda range and folds
model3 <- ridge.regression(mpg ~ .,
    data = mtcars,
    lambda.range = c(0.1, 10), folds = 10
)

## End(Not run)
```

`ridge.summary` *Format Ridge Model Output as LaTeX Tables*

Description

Formats and displays ridge regression model output from `ridge.regression()` as LaTeX tables for PDF rendering or plain text for console viewing.

Usage

```
ridge.summary(x, ..., include.cv.trace = TRUE, latex = TRUE)
```

Arguments

`x`	A ridge model object returned by `ridge.regression()` (class `"ridge.model"`).
`...`	Further arguments passed to or from methods (unused).
`include.cv.trace`	Logical. Whether to include cross-validation trace information. Default is `TRUE`.
`latex`	Logical; if `TRUE` (default), returns LaTeX-formatted tables using `kableExtra`. If `FALSE`, prints plain-text summary tables to the console.

Value

If `latex` = `TRUE`, returns a `knitr::asis_output` object (LaTeX code) for PDF rendering. If `latex` = `FALSE`, prints formatted summary tables to the console and returns the underlying data frames.

Examples

```
# Load example data
data(mtcars)

# Fit ridge regression model
ridge.fit <- ridge.regression(mpg ~ wt + hp + disp, data = mtcars)

# Print a LaTeX-formatted summary
ridge.summary(ridge.fit, include.cv.trace = FALSE)

# Print a plain-text summary
ridge.summary(ridge.fit, include.cv.trace = FALSE, latex = FALSE)
```

`snazzieR.theme` *A Custom ggplot2 Theme for Publication-Ready Plots*

Description

This theme provides a clean, polished look for ggplot2 plots, with a focus on readability and aesthetics. It includes a custom color palette and formatting for titles, axes, and legends.

Usage

```
snazzieR.theme()
```

Value

A ggplot2 theme object.

See Also

`color.list`, `color.ref`

Examples

```
library(ggplot2)
set.seed(123)
chains.df <- data.frame(
  Iteration = 1:500,
  alpha.1 = cumsum(rnorm(500, mean = 0.01, sd = 0.2)) + rnorm(1, 5, 0.2),
  alpha.2 = cumsum(rnorm(500, mean = 0.005, sd = 0.2)) + rnorm(1, 5, 0.2),
  alpha.3 = cumsum(rnorm(500, mean = 0.000, sd = 0.2)) + rnorm(1, 5, 0.2),
  alpha.4 = cumsum(rnorm(500, mean = -0.005, sd = 0.2)) + rnorm(1, 5, 0.2),
  alpha.5 = cumsum(rnorm(500, mean = -0.01, sd = 0.2)) + rnorm(1, 5, 0.2)
)
chain.colors <- c("Chain 1" = Red, "Chain 2" = Orange, "Chain 3" = Yellow,
                  "Chain 4" = Green, "Chain 5" = Blue)
ggplot(chains.df, aes(x = Iteration)) +
  geom_line(aes(y = alpha.1, color = "Chain 1"), linewidth = 1.2) +
  geom_line(aes(y = alpha.2, color = "Chain 2"), linewidth = 1.2) +
  geom_line(aes(y = alpha.3, color = "Chain 3"), linewidth = 1.2) +
  geom_line(aes(y = alpha.4, color = "Chain 4"), linewidth = 1.2) +
  geom_line(aes(y = alpha.5, color = "Chain 5"), linewidth = 1.2) +
  labs(x = "Iteration", y = expression(alpha),
       title = expression("Traceplot for " ~ alpha)) +
  scale_color_manual(values = chain.colors, name = "Chains") +
  snazzieR.theme()
```

`SVD.pls` *Partial Least Squares Regression via SVD (Internal)*

Description

This function is called internally by `pls.regression` and is not intended to be used directly. Use `pls.regression(..., calc.method = "SVD")` instead.

Performs Partial Least Squares (PLS) regression using the Singular Value Decomposition (SVD) of the cross-covariance matrix. This method estimates the latent components by identifying directions in the predictor and response spaces that maximize their covariance, using the leading singular vectors of the matrix $R = X^\top Y$.

Usage

```
SVD.pls(x, y, n.components = NULL)
```

Arguments

`x`	A numeric matrix or data frame of predictors (X). Should have dimensions n × p.
`y`	A numeric matrix or data frame of response variables (Y). Should have dimensions n × q.
`n.components`	Integer specifying the number of PLS components to extract. If NULL, defaults to `qr(x)$rank`.

Details

The algorithm begins by z-scoring both `x` and `y` (centering and scaling to unit variance). The initial residual matrices are set to the scaled values: `E = X_scaled`, `F = Y_scaled`.

For each component h = 1, ..., H:

1. Compute the cross-covariance matrix $R = E^\top F$.
2. Perform SVD on $R = UDV^\top$.
3. Extract the first singular vectors: $w = U[, 1]$, $q = V[, 1]$.
4. Compute scores: $t = Ew$ (normalized), $u = Fq$.
5. Compute loadings: $p = E^\top t$, regression scalar $b = t^\top u$.
6. Deflate residuals: $E \leftarrow E - tp^\top$, $F \leftarrow F - btq^\top$.

After all components are extracted, a post-processing step removes components with zero regression weight. The scaled regression coefficients are computed using the Moore–Penrose pseudoinverse of the loading matrix P, and then rescaled to the original variable units.

Value

A list containing:

model.type Character string indicating the model type ("PLS Regression").

T Matrix of predictor scores (n × H).

U Matrix of response scores (n × H).

W Matrix of predictor weights (p × H).

C Matrix of normalized response weights (q × H).

P_loadings Matrix of predictor loadings (p × H).

Q_loadings Matrix of response loadings (q × H).

B_vector Vector of scalar regression weights (length H).

coefficients Matrix of final regression coefficients in the original scale (p × q).

intercept Vector of intercepts (length q). All zeros due to centering.

X_explained Percent of total X variance explained by each component.

Y_explained Percent of total Y variance explained by each component.

X_cum_explained Cumulative X variance explained.

Y_cum_explained Cumulative Y variance explained.

References

Abdi, H., & Williams, L. J. (2013). Partial least squares methods: Partial least squares correlation and partial least square regression. *Methods in Molecular Biology (Clifton, N.J.)*, 930, 549–579. doi:10.1007/9781627030595_23

de Jong, S. (1993). SIMPLS: An alternative approach to partial least squares regression. *Chemometrics and Intelligent Laboratory Systems*, 18(3), 251–263. doi:10.1016/01697439(93)85002X

Examples

```
## Not run:
X <- matrix(rnorm(100 * 10), 100, 10)
Y <- matrix(rnorm(100 * 2), 100, 2)
model <- pls.regression(X, Y, n.components = 3, calc.method = "SVD")
model$coefficients

## End(Not run)
```

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