

# Package ‘tidylearn’

February 6, 2026

**Title** A Unified Tidy Interface to R's Machine Learning Ecosystem

**Version** 0.1.0

**Description** Provides a unified tidyverse-compatible interface to R's machine learning packages. Wraps established implementations from 'glmnet', 'randomForest', 'xgboost', 'e1071', 'rpart', 'gbm', 'nnet', 'cluster', 'dbscan', and others - providing consistent function signatures, tidy tibble output, and unified 'ggplot2'-based visualization. The underlying algorithms are unchanged; 'tidylearn' simply makes them easier to use together. Access raw model objects via the \$fit slot for package-specific functionality. Methods include random forests Breiman (2001) <[doi:10.1023/A:1010933404324](https://doi.org/10.1023/A:1010933404324)>, LASSO regression Tibshirani (1996) <[doi:10.1111/j.2517-6161.1996.tb02080.x](https://doi.org/10.1111/j.2517-6161.1996.tb02080.x)>, elastic net Zou and Hastie (2005) <[doi:10.1111/j.1467-9868.2005.00503.x](https://doi.org/10.1111/j.1467-9868.2005.00503.x)>, support vector machines Cortes and Vapnik (1995) <[doi:10.1007/BF00994018](https://doi.org/10.1007/BF00994018)>, and gradient boosting Friedman (2001) <[doi:10.1214/aos/1013203451](https://doi.org/10.1214/aos/1013203451)>.

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**Encoding** UTF-8

**RoxygenNote** 7.3.2

**Depends** R (>= 3.6.0)

**Imports** dplyr (>= 1.0.0), ggplot2 (>= 3.3.0), tibble (>= 3.0.0), tidyr (>= 1.0.0), purrr (>= 0.3.0), rlang (>= 0.4.0), magrittr, stats, e1071, gbm, glmnet, nnet, randomForest, rpart, rsample, ROCR, yardstick, cluster (>= 2.1.0), dbscan (>= 1.1.0), MASS, smacof (>= 2.1.0)

**Suggests** arules, arulesViz, car, caret, DT, GGally, ggforce, gridExtra, keras, knitr, lmtest, mclust, moments, NeuralNetTools, onnx, parsnip, recipes, reticulate, rmarkdown, rpart.plot, scales, shiny, shinydashboard, tensorflow, testthat (>= 3.0.0), workflows, xgboost

**Config/testthat/edition** 3

**URL** <https://github.com/ces0491/tidylearn>

**BugReports** <https://github.com/ces0491/tidylearn/issues>

**VignetteBuilder** knitr

**Collate** 'utils.R' 'core.R' 'preprocessing.R'  
 'supervised-classification.R' 'supervised-regression.R'  
 'supervised-regularization.R' 'supervised-trees.R'  
 'supervised-svm.R' 'supervised-neural-networks.R'  
 'supervised-deep-learning.R' 'supervised-xgboost.R'  
 'unsupervised-distance.R' 'unsupervised-pca.R'  
 'unsupervised-mds.R' 'unsupervised-clustering.R'  
 'unsupervised-hclust.R' 'unsupervised-dbscan.R'  
 'unsupervised-market-basket.R' 'unsupervised-validation.R'  
 'integration.R' 'pipeline.R' 'model-selection.R' 'tuning.R'  
 'interactions.R' 'diagnostics.R' 'metrics.R' 'visualization.R'  
 'workflows.R'

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2026-02-06 13:50:02 UTC

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augment\_dbscan

*Augment Data with DBSCAN Cluster Assignments***Description**

Augment Data with DBSCAN Cluster Assignments

**Usage**

```
augment_dbscan(dbscan_obj, data)
```

**Arguments**

dbscan_obj	A tidy_dbscan object
data	Original data frame

**Value**

Original data with cluster information added

---

augment_hclust	<i>Augment Data with Hierarchical Cluster Assignments</i>
----------------	---

---

**Description**

Add cluster assignments to original data

**Usage**

```
augment_hclust(hclust_obj, data, k = NULL, h = NULL)
```

**Arguments**

hclust_obj	A tidy_hclust object
data	Original data frame
k	Number of clusters (optional)
h	Height at which to cut (optional)

**Value**

Original data with cluster column added

---

augment_kmeans	<i>Augment Data with K-Means Cluster Assignments</i>
----------------	--

---

**Description**

Augment Data with K-Means Cluster Assignments

**Usage**

```
augment_kmeans(kmeans_obj, data)
```

**Arguments**

kmeans_obj	A tidy_kmeans object
data	Original data frame

**Value**

Original data with cluster column added

---

augment_pam	<i>Augment Data with PAM Cluster Assignments</i>
-------------	--

---

**Description**

Augment Data with PAM Cluster Assignments

**Usage**

```
augment_pam(pam_obj, data)
```

**Arguments**

pam_obj	A tidy_pam object
data	Original data frame

**Value**

Original data with cluster column added

---

augment_pca	<i>Augment Original Data with PCA Scores</i>
-------------	--

---

**Description**

Add PC scores to the original dataset

**Usage**

```
augment_pca(pca_obj, data, n_components = NULL)
```

**Arguments**

pca_obj	A tidy_pca object
data	Original data frame
n_components	Number of PCs to add (default: all)

**Value**

Original data with PC scores added

---

calc_validation_metrics	<i>Calculate Cluster Validation Metrics</i>
-------------------------	---

---

**Description**

Comprehensive validation metrics for a clustering result

**Usage**

```
calc_validation_metrics(clusters, data = NULL, dist_mat = NULL)
```

**Arguments**

clusters	Vector of cluster assignments
data	Original data frame (for WSS calculation)
dist_mat	Distance matrix (for silhouette)

**Value**

A tibble with validation metrics



---

calc_wss	<i>Calculate Within-Cluster Sum of Squares for Different k</i>
----------	--

---

**Description**

Used for elbow method to determine optimal k

**Usage**

```
calc_wss(data, max_k = 10, nstart = 25)
```

**Arguments**

data	A data frame or tibble
max_k	Maximum number of clusters to test (default: 10)
nstart	Number of random starts for each k (default: 25)

**Value**

A tibble with k and corresponding total within-cluster SS

---

compare_clusterings	<i>Compare Multiple Clustering Results</i>
---------------------	--

---

**Description**

Compare Multiple Clustering Results

**Usage**

```
compare_clusterings(cluster_list, data, dist_mat = NULL)
```

**Arguments**

cluster_list	Named list of cluster assignment vectors
data	Original data
dist_mat	Distance matrix

**Value**

A tibble comparing all clustering results

---

compare_distances	<i>Compare Distance Methods</i>
-------------------	---------------------------------

---

**Description**

Compute distances using multiple methods for comparison

**Usage**

```
compare_distances(data, methods = c("euclidean", "manhattan", "maximum"))
```

**Arguments**

data	A data frame or tibble
methods	Character vector of methods to compare

**Value**

A list of dist objects named by method

---

create_cluster_dashboard	<i>Create Summary Dashboard</i>
--------------------------	---------------------------------

---

**Description**

Generate a multi-panel summary of clustering results

**Usage**

```
create_cluster_dashboard(  
  data,  
  cluster_col = "cluster",  
  validation_metrics = NULL  
)
```

**Arguments**

data	Data frame with cluster assignments
cluster_col	Cluster column name
validation_metrics	Optional tibble of validation metrics

**Value**

Combined plot grid

---

`explore_dbscan_params` *Explore DBSCAN Parameters*

---

**Description**

Test multiple eps and minPts combinations

**Usage**

```
explore_dbscan_params(data, eps_values, minPts_values)
```

**Arguments**

<code>data</code>	A data frame or matrix
<code>eps_values</code>	Vector of eps values to test
<code>minPts_values</code>	Vector of minPts values to test

**Value**

A tibble with parameter combinations and resulting cluster counts

---

`filter_rules_by_item` *Filter Rules by Item*

---

**Description**

Subset rules containing specific items

**Usage**

```
filter_rules_by_item(rules_obj, item, where = "both")
```

**Arguments**

<code>rules_obj</code>	A tidy_apriori object or tibble of rules
<code>item</code>	Character; item to filter by
<code>where</code>	Character; "lhs", "rhs", or "both" (default: "both")

**Value**

A tibble of filtered rules

---

find_related_items	<i>Find Related Items</i>
--------------------	---------------------------

---

**Description**

Find items frequently purchased with a given item

**Usage**

```
find_related_items(rules_obj, item, min_lift = 1.5, top_n = 10)
```

**Arguments**

rules_obj	A tidy_apriori object
item	Character; item to find associations for
min_lift	Minimum lift threshold (default: 1.5)
top_n	Number of top associations to return (default: 10)

**Value**

A tibble of related items with association metrics

---

get_pca_loadings	<i>Get PCA Loadings in Wide Format</i>
------------------	--

---

**Description**

Get PCA Loadings in Wide Format

**Usage**

```
get_pca_loadings(pca_obj, n_components = NULL)
```

**Arguments**

pca_obj	A tidy_pca object
n_components	Number of components to include (default: all)

**Value**

A tibble with loadings in wide format

---

get_pca_variance	<i>Get Variance Explained Summary</i>
------------------	---------------------------------------

---

**Description**

Get Variance Explained Summary

**Usage**

```
get_pca_variance(pca_obj)
```

**Arguments**

pca_obj	A tidy_pca object
---------	-------------------

**Value**

A tibble with variance statistics

---

inspect_rules	<i>Inspect Association Rules</i>
---------------	----------------------------------

---

**Description**

View rules sorted by various quality measures

**Usage**

```
inspect_rules(rules_obj, by = "lift", n = 10, decreasing = TRUE)
```

**Arguments**

rules_obj	A tidy_apriori object or rules object
by	Sort by: "support", "confidence", "lift" (default), "count"
n	Number of rules to display (default: 10)
decreasing	Sort in decreasing order? (default: TRUE)

**Value**

A tibble of top rules

---

optimal_clusters	<i>Find Optimal Number of Clusters</i>
------------------	--

---

**Description**

Use multiple methods to suggest optimal k

**Usage**

```
optimal_clusters(data, max_k = 10, methods = c("silhouette", "gap", "wss"))
```

**Arguments**

data	A data frame or tibble
max_k	Maximum k to test (default: 10)
methods	Vector of methods: "silhouette", "gap", "wss" (default: all)

**Value**

A list with results from each method

---

optimal_hclust_k	<i>Determine Optimal Number of Clusters for Hierarchical Clustering</i>
------------------	---

---

**Description**

Use silhouette or gap statistic to find optimal k

**Usage**

```
optimal_hclust_k(hclust_obj, method = "silhouette", max_k = 10)
```

**Arguments**

hclust_obj	A tidy_hclust object
method	Character; "silhouette" (default) or "gap"
max_k	Maximum number of clusters to test (default: 10)

**Value**

A list with optimal k and evaluation results

---

plot.tidylearn_eda	<i>Plot EDA results</i>
--------------------	-------------------------

---

**Description**

Plot EDA results

**Usage**

```
## S3 method for class 'tidylearn_eda'  
plot(x, ...)
```

**Arguments**

x	A tidylearn_eda object
...	Additional arguments (ignored)

**Value**

Invisibly returns the input object x, called for side effects (plotting)

---

plot.tidylearn_model	<i>Plot method for tidylearn models</i>
----------------------	---

---

**Description**

Plot method for tidylearn models

**Usage**

```
## S3 method for class 'tidylearn_model'  
plot(x, type = "auto", ...)
```

**Arguments**

x	A tidylearn model object
type	Plot type (default: "auto")
...	Additional arguments passed to plotting functions

**Value**

A ggplot2 object or NULL, called primarily for side effects

---

plot_clusters	<i>Plot Clusters in 2D Space</i>
---------------	----------------------------------

---

**Description**

Visualize clustering results using first two dimensions or specified dimensions

**Usage**

```
plot_clusters(  
  data,  
  cluster_col = "cluster",  
  x_col = NULL,  
  y_col = NULL,  
  centers = NULL,  
  title = "Cluster Plot",  
  color_noise_black = TRUE  
)
```

**Arguments**

- data                    A data frame with cluster assignments
- cluster\_col           Name of cluster column (default: "cluster")
- x\_col                  X-axis variable (if NULL, uses first numeric column)
- y\_col                  Y-axis variable (if NULL, uses second numeric column)
- centers                Optional data frame of cluster centers
- title                  Plot title
- color\_noise\_black      If TRUE, color noise points (cluster 0) black

**Value**

A ggplot object

---

plot_cluster_comparison	<i>Create Cluster Comparison Plot</i>
-------------------------	---------------------------------------

---

**Description**

Compare multiple clustering results side-by-side

**Usage**

```
plot_cluster_comparison(data, cluster_cols, x_col, y_col)
```



**Arguments**

data	Data frame with multiple cluster columns
cluster_cols	Vector of cluster column names
x_col	X-axis variable
y_col	Y-axis variable

**Value**

A grid of ggplot objects

---

plot_cluster_sizes	<i>Plot Cluster Size Distribution</i>
--------------------	---------------------------------------

---

**Description**

Create bar plot of cluster sizes

**Usage**

```
plot_cluster_sizes(clusters, title = "Cluster Size Distribution")
```

**Arguments**

clusters	Vector of cluster assignments
title	Plot title (default: "Cluster Size Distribution")

**Value**

A ggplot object

---

plot_dendrogram	<i>Plot Dendrogram with Cluster Highlights</i>
-----------------	--

---

**Description**

Enhanced dendrogram with colored cluster rectangles

**Usage**

```
plot_dendrogram(  
  hclust_obj,  
  k = NULL,  
  title = "Hierarchical Clustering Dendrogram"  
)
```

**Arguments**

hclust_obj	Hierarchical clustering object (hclust or tidy_hclust)
k	Number of clusters to highlight
title	Plot title

**Value**

Invisibly returns hclust object (plots as side effect)

---

plot\_distance\_heatmap *Create Distance Heatmap*

---

**Description**

Visualize distance matrix as heatmap

**Usage**

```
plot_distance_heatmap(  
  dist_mat,  
  cluster_order = NULL,  
  title = "Distance Heatmap"  
)
```

**Arguments**

dist_mat	Distance matrix (dist object)
cluster_order	Optional vector to reorder observations by cluster
title	Plot title

**Value**

A ggplot object

---

plot_elbow	Create Elbow Plot for K-Means
------------	-------------------------------

---

**Description**

Plot total within-cluster sum of squares vs number of clusters

**Usage**

```
plot_elbow(wss_data, add_line = FALSE, suggested_k = NULL)
```

**Arguments**

wss_data	A tibble with columns k and tot_withinss (from calc_wss)
add_line	Add vertical line at suggested optimal k? (default: FALSE)
suggested_k	If add_line=TRUE, which k to highlight

**Value**

A ggplot object

---

plot_gap_stat	Plot Gap Statistic
---------------	--------------------

---

**Description**

Plot Gap Statistic

**Usage**

```
plot_gap_stat(gap_obj, show_methods = FALSE)
```

**Arguments**

gap_obj	A tidy_gap object
show_methods	Logical; show all three k selection methods? (default: FALSE)

**Value**

A ggplot object

---

plot_knn_dist	<i>Plot k-NN Distance Plot</i>
---------------	--------------------------------

---

**Description**

Visualize k-NN distances to help choose eps

**Usage**

```
plot_knn_dist(data, k = 4, add_suggestion = TRUE, percentile = 0.95)
```

**Arguments**

data	A data frame or tidy_knn_dist result
k	If data is a data frame, k for k-NN (default: 4)
add_suggestion	Add suggested eps line? (default: TRUE)
percentile	Percentile for suggestion (default: 0.95)

**Value**

A ggplot object

---

plot_mds	<i>Plot MDS Configuration</i>
----------	-------------------------------

---

**Description**

Visualize MDS results

**Usage**

```
plot_mds(mds_obj, color_by = NULL, label_points = TRUE, dim_x = 1, dim_y = 2)
```

**Arguments**

mds_obj	A tidy_mds object
color_by	Optional variable to color points by
label_points	Logical; add point labels? (default: TRUE)
dim_x	Which dimension for x-axis (default: 1)
dim_y	Which dimension for y-axis (default: 2)

**Value**

A ggplot object

---

plot_silhouette	<i>Plot Silhouette Analysis</i>
-----------------	---------------------------------

---

**Description**

Plot Silhouette Analysis

**Usage**

```
plot_silhouette(sil_obj)
```

**Arguments**

sil\_obj            A tidy\_silhouette object or tibble from tidy\_silhouette\_analysis

**Value**

A ggplot object

---

plot_variance_explained	<i>Plot Variance Explained (PCA)</i>
-------------------------	--------------------------------------

---

**Description**

Create combined scree plot showing individual and cumulative variance

**Usage**

```
plot_variance_explained(variance_tbl, threshold = 0.8)
```

**Arguments**

variance\_tbl      Variance tibble from tidy\_pca  
threshold          Horizontal line for variance threshold (default: 0.8 for 80%)

**Value**

A ggplot object

---

predict.tidylearn\_model

*Predict using a tidylearn model*

---

### Description

Unified prediction interface for both supervised and unsupervised models

### Usage

```
## S3 method for class 'tidylearn_model'
predict(object, new_data = NULL, type = "response", ...)
```

### Arguments

object	A tidylearn model object
new_data	A data frame containing the new data. If NULL, uses training data.
type	Type of prediction. For supervised: "response" (default), "prob", "class". For unsupervised: "scores", "clusters", "transform" depending on method.
...	Additional arguments

### Value

Predictions as a tibble

---

predict.tidylearn\_stratified

*Predict from stratified models*

---

### Description

Predict from stratified models

### Usage

```
## S3 method for class 'tidylearn_stratified'
predict(object, new_data = NULL, ...)
```

### Arguments

object	A tidylearn_stratified model object
new_data	New data for predictions
...	Additional arguments

### Value

A tibble of predictions with cluster assignments

---

```
predict.tidylearn_transfer
```

*Predict with transfer learning model*

---

**Description**

Predict with transfer learning model

**Usage**

```
## S3 method for class 'tidylearn_transfer'  
predict(object, new_data, ...)
```

**Arguments**

object	A tidylearn_transfer model object
new_data	New data for predictions
...	Additional arguments

**Value**

A tibble of predictions

---

```
print.tidylearn_automl
```

*Print auto ML results*

---

**Description**

Print auto ML results

**Usage**

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

**Arguments**

x	A tidylearn_automl object
...	Additional arguments (ignored)

**Value**

Invisibly returns the input object x

---

`print.tidylearn_eda`    *Print EDA results*

---

**Description**

Print EDA results

**Usage**

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

**Arguments**

<code>x</code>	A tidylearn_eda object
<code>...</code>	Additional arguments (ignored)

**Value**

Invisibly returns the input object x

---

`print.tidylearn_model`    *Print method for tidylearn models*

---

**Description**

Print method for tidylearn models

**Usage**

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

**Arguments**

<code>x</code>	A tidylearn model object
<code>...</code>	Additional arguments (ignored)

**Value**

Invisibly returns the input object x



---

```
print.tidylearn_pipeline
```

*Print a tidylearn pipeline*

---

**Description**

Print a tidylearn pipeline

**Usage**

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

**Arguments**

x	A tidylearn pipeline object
...	Additional arguments (not used)

**Value**

Invisibly returns the pipeline

---

```
print.tidy_apriori
```

*Print Method for tidy\_apriori*

---

**Description**

Print Method for tidy\_apriori

**Usage**

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

**Arguments**

x	A tidy_apriori object
...	Additional arguments (ignored)

**Value**

Invisibly returns the input object x

---

print.tidy_dbscan	<i>Print Method for tidy_dbscan</i>
-------------------	-------------------------------------

---

**Description**

Print Method for tidy\_dbscan

**Usage**

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

**Arguments**

x	A tidy_dbscan object
...	Additional arguments (ignored)

**Value**

Invisibly returns the input object x

---

print.tidy_gap	<i>Print Method for tidy_gap</i>
----------------	----------------------------------

---

**Description**

Print Method for tidy\_gap

**Usage**

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

**Arguments**

x	A tidy_gap object
...	Additional arguments (ignored)

**Value**

Invisibly returns the input object x

---

print.tidy_hclust	<i>Print Method for tidy_hclust</i>
-------------------	-------------------------------------

---

**Description**

Print Method for tidy\_hclust

**Usage**

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

**Arguments**

x	A tidy_hclust object
...	Additional arguments (ignored)

**Value**

Invisibly returns the input object x

---

print.tidy_kmeans	<i>Print Method for tidy_kmeans</i>
-------------------	-------------------------------------

---

**Description**

Print Method for tidy\_kmeans

**Usage**

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

**Arguments**

x	A tidy_kmeans object
...	Additional arguments (ignored)

**Value**

Invisibly returns the input object x

---

print.tidy_mds	<i>Print Method for tidy_mds</i>
----------------	----------------------------------

---

**Description**

Print Method for tidy\_mds

**Usage**

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

**Arguments**

x	A tidy_mds object
...	Additional arguments (ignored)

**Value**

Invisibly returns the input object x

---

print.tidy_pam	<i>Print Method for tidy_pam</i>
----------------	----------------------------------

---

**Description**

Print Method for tidy\_pam

**Usage**

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

**Arguments**

x	A tidy_pam object
...	Additional arguments (ignored)

**Value**

Invisibly returns the input object x

---

print.tidy_pca	<i>Print Method for tidy_pca</i>
----------------	----------------------------------

---

**Description**

Print Method for tidy\_pca

**Usage**

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

**Arguments**

x	A tidy_pca object
...	Additional arguments (ignored)

**Value**

Invisibly returns the input object x

---

print.tidy_silhouette	<i>Print Method for tidy_silhouette</i>
-----------------------	---

---

**Description**

Print Method for tidy\_silhouette

**Usage**

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

**Arguments**

x	A tidy_silhouette object
...	Additional arguments (ignored)

**Value**

Invisibly returns the input object x

---

recommend_products	<i>Generate Product Recommendations</i>
--------------------	---

---

**Description**

Get product recommendations based on basket contents

**Usage**

```
recommend_products(rules_obj, basket, top_n = 5, min_confidence = 0.5)
```

**Arguments**

rules_obj	A tidy_apriori object
basket	Character vector of items in current basket
top_n	Number of recommendations to return (default: 5)
min_confidence	Minimum confidence threshold (default: 0.5)

**Value**

A tibble with recommended items and metrics

---

standardize_data	<i>Standardize Data</i>
------------------	-------------------------

---

**Description**

Center and/or scale numeric variables

**Usage**

```
standardize_data(data, center = TRUE, scale = TRUE)
```

**Arguments**

data	A data frame or tibble
center	Logical; center variables? (default: TRUE)
scale	Logical; scale variables to unit variance? (default: TRUE)

**Value**

A tibble with standardized numeric variables

---

suggest_eps	<i>Suggest eps Parameter for DBSCAN</i>
-------------	---

---

**Description**

Use k-NN distance plot to suggest eps value

**Usage**

```
suggest_eps(data, minPts = 5, method = "percentile", percentile = 0.95)
```

**Arguments**

data	A data frame or matrix
minPts	Minimum points parameter (used as k for k-NN)
method	Method to suggest eps: "knee" (default), "percentile"
percentile	If method="percentile", which percentile to use (default: 0.95)

**Value**

A list containing:

- eps: suggested epsilon value
- knn\_distances: full tibble of k-NN distances
- method: method used

**Examples**

```
eps_info <- suggest_eps(iris, minPts = 5)
eps_info$eps
```

---

summarize_rules	<i>Summarize Association Rules</i>
-----------------	------------------------------------

---

**Description**

Get summary statistics about rules

**Usage**

```
summarize_rules(rules_obj)
```

**Arguments**

rules_obj	A tidy_apriori object or rules tibble
-----------	---------------------------------------

**Value**

A list with summary statistics

---

summary.tidylearn\_model

*Summary method for tidylearn models*

---

**Description**

Summary method for tidylearn models

**Usage**

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

**Arguments**

object	A tidylearn model object
...	Additional arguments (ignored)

**Value**

Invisibly returns the input object

---

summary.tidylearn\_pipeline

*Summarize a tidylearn pipeline*

---

**Description**

Summarize a tidylearn pipeline

**Usage**

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

**Arguments**

object	A tidylearn pipeline object
...	Additional arguments (not used)

**Value**

Invisibly returns the pipeline



---

`tidylearn-classification`*Classification Functions for tidylearn*

---

**Description**

Logistic regression and classification metrics functionality

---

`tidylearn-core`*tidylearn: A Unified Tidy Interface to R's Machine Learning Ecosystem*

---

**Description**

Core functionality for tidylearn. This package provides a unified tidyverse-compatible interface to established R machine learning packages including glmnet, randomForest, xgboost, e1071, rpart, gbm, nnet, cluster, and dbSCAN. The underlying algorithms are unchanged - tidylearn wraps them with consistent function signatures, tidy tibble output, and unified ggplot2-based visualization. Access raw model objects via model\$fit.

---

`tidylearn-deep-learning`*Deep Learning for tidylearn*

---

**Description**

Deep learning functionality using Keras/TensorFlow

---

`tidylearn-diagnostics` *Advanced Diagnostics Functions for tidylearn*

---

**Description**

Functions for advanced model diagnostics, assumption checking, and outlier detection

---

`tidylearn-interactions`*Interaction Analysis Functions for tidylearn*

---

**Description**

Functions for testing, visualizing, and analyzing interactions

---

`tidylearn-metrics`*Metrics Functionality for tidylearn*

---

**Description**

Functions for calculating model evaluation metrics

---

`tidylearn-model-selection`*Model Selection Functions for tidylearn*

---

**Description**

Functions for stepwise model selection, cross-validation, and hyperparameter tuning

---

`tidylearn-neural-networks`*Neural Networks for tidylearn*

---

**Description**

Neural network functionality for classification and regression

---

`tidylearn-pipeline`*Model Pipeline Functions for tidylearn*

---

**Description**

Functions for creating end-to-end model pipelines

---

tidylearn-regression	<i>Regression Functions for tidylearn</i>
----------------------	---

---

**Description**

Linear and polynomial regression functionality

---

tidylearn-regularization	<i>Regularization Functions for tidylearn</i>
--------------------------	---

---

**Description**

Ridge, Lasso, and Elastic Net regularization functionality

---

tidylearn-svm	<i>Support Vector Machines for tidylearn</i>
---------------	--

---

**Description**

SVM functionality for classification and regression

---

tidylearn-trees	<i>Tree-based Methods for tidylearn</i>
-----------------	---

---

**Description**

Decision trees, random forests, and boosting functionality

---

tidylearn-tuning	<i>Hyperparameter Tuning Functions for tidylearn</i>
------------------	--

---

**Description**

Functions for automatic hyperparameter tuning and selection

---

tidylearn-visualization

*Visualization Functions for tidylearn*


---

### Description

General visualization functions for tidylearn models

---

tidylearn-xgboost

*XGBoost Functions for tidylearn*


---

### Description

XGBoost-specific implementation for gradient boosting

---

tidy\_apriori

*Tidy Apriori Algorithm*


---

### Description

Mine association rules using the Apriori algorithm with tidy output

### Usage

```
tidy_apriori(
  transactions,
  support = 0.01,
  confidence = 0.5,
  minlen = 2,
  maxlen = 10,
  target = "rules"
)
```

### Arguments

transactions	A transactions object or data frame
support	Minimum support (default: 0.01)
confidence	Minimum confidence (default: 0.5)
minlen	Minimum rule length (default: 2)
maxlen	Maximum rule length (default: 10)
target	Type of association mined: "rules" (default), "frequent itemsets", "maximally frequent itemsets"

**Value**

A list of class "tidy\_rules" containing:

- rules\_tbl: tibble of rules with lhs, rhs, and quality measures
- rules: original rules object
- parameters: parameters used

**Examples**

```
data("Groceries", package = "arules")

# Basic apriori
rules <- tidy_apriori(Groceries, support = 0.001, confidence = 0.5)

# Access rules
rules$rules_tbl
```

---

tidy\_clara

*Tidy CLARA (Clustering Large Applications)*


---

**Description**

Performs CLARA clustering (scalable version of PAM)

**Usage**

```
tidy_clara(data, k, metric = "euclidean", samples = 50, sampsize = NULL)
```

**Arguments**

data	A data frame or tibble
k	Number of clusters
metric	Distance metric (default: "euclidean")
samples	Number of samples to draw (default: 50)
sampsize	Sample size (default: min(n, 40 + 2*k))

**Value**

A list of class "tidy\_clara" containing clustering results

**Examples**

```
# CLARA for large datasets
large_data <- iris[rep(1:nrow(iris), 10), 1:4]
clara_result <- tidy_clara(large_data, k = 3, samples = 50)
print(clara_result)
```

---

tidy_cutree	<i>Cut Hierarchical Clustering Tree</i>
-------------	---

---

**Description**

Cut dendrogram to obtain cluster assignments

**Usage**

```
tidy_cutree(hclust_obj, k = NULL, h = NULL)
```

**Arguments**

hclust_obj	A tidy_hclust object or hclust object
k	Number of clusters (optional)
h	Height at which to cut (optional)

**Value**

A tibble with observation IDs and cluster assignments

---

tidy_dbscan	<i>Tidy DBSCAN Clustering</i>
-------------	-------------------------------

---

**Description**

Performs density-based clustering with tidy output

**Usage**

```
tidy_dbscan(data, eps, minPts = 5, cols = NULL, distance = "euclidean")
```

**Arguments**

data	A data frame, tibble, or distance matrix
eps	Neighborhood radius (epsilon)
minPts	Minimum number of points to form a dense region (default: 5)
cols	Columns to include (tidy select). If NULL, uses all numeric columns.
distance	Distance metric if data is not a dist object (default: "euclidean")

**Value**

A list of class "tidy\_dbscan" containing:

- clusters: tibble with observation IDs and cluster assignments (0 = noise)
- core\_points: logical vector indicating core points
- n\_clusters: number of clusters (excluding noise)
- n\_noise: number of noise points
- model: original dbscan object

**Examples**

```
# Basic DBSCAN
db_result <- tidy_dbscan(iris, eps = 0.5, minPts = 5)

# With suggested eps from k-NN distance plot
eps_suggestion <- suggest_eps(iris, minPts = 5)
db_result <- tidy_dbscan(iris, eps = eps_suggestion$eps, minPts = 5)
```

---

tidy_dendrogram	<i>Plot Dendrogram</i>
-----------------	------------------------

---

**Description**

Create dendrogram visualization

**Usage**

```
tidy_dendrogram(hclust_obj, k = NULL, hang = 0.01, cex = 0.7)
```

**Arguments**

hclust_obj	A tidy_hclust object or hclust object
k	Optional; number of clusters to highlight with rectangles
hang	Fraction of plot height to hang labels (default: 0.01)
cex	Label size (default: 0.7)

**Value**

Invisibly returns the hclust object (plots as side effect)

---

tidy_dist	<i>Tidy Distance Matrix Computation</i>
-----------	---

---

**Description**

Compute distance matrices with tidy output

**Usage**

```
tidy_dist(data, method = "euclidean", cols = NULL, ...)
```

**Arguments**

data	A data frame or tibble
method	Character; distance method (default: "euclidean"). Options: "euclidean", "manhattan", "maximum", "gower"
cols	Columns to include (tidy select). If NULL, uses all numeric columns.
...	Additional arguments passed to distance functions

**Value**

A dist object with tidy attributes

---

tidy_gap_stat	<i>Tidy Gap Statistic</i>
---------------	---------------------------

---

**Description**

Compute gap statistic for determining optimal number of clusters

**Usage**

```
tidy_gap_stat(data, FUN_cluster = NULL, max_k = 10, B = 50, nstart = 25)
```

**Arguments**

data	A data frame or tibble
FUN_cluster	Clustering function (default: uses kmeans internally)
max_k	Maximum number of clusters (default: 10)
B	Number of bootstrap samples (default: 50)
nstart	If using kmeans, number of random starts (default: 25)

**Value**

A list of class "tidy\_gap" containing gap statistics



---

tidy\_gower

---

*Gower Distance Calculation***Description**

Computes Gower distance for mixed data types (numeric, factor, ordered)

**Usage**

```
tidy_gower(data, weights = NULL)
```

**Arguments**

data	A data frame or tibble
weights	Optional named vector of variable weights (default: equal weights)

**Details**

Gower distance handles mixed data types:

- Numeric: range-normalized Manhattan distance
- Factor/Character: 0 if same, 1 if different
- Ordered: treated as numeric ranks

Formula:  $d_{ij} = \text{sum}(w_k * d_{ijk}) / \text{sum}(w_k)$  where  $d_{ijk}$  is the dissimilarity for variable  $k$  between obs  $i$  and  $j$

**Value**

A dist object containing Gower distances

**Examples**

```
# Create example data with mixed types
car_data <- data.frame(
  horsepower = c(130, 250, 180),
  weight = c(1200, 1650, 1420),
  color = factor(c("red", "black", "blue"))
)

# Compute Gower distance
gower_dist <- tidy_gower(car_data)
```

---

tidy_hclust	<i>Tidy Hierarchical Clustering</i>
-------------	-------------------------------------

---

**Description**

Performs hierarchical clustering with tidy output

**Usage**

```
tidy_hclust(data, method = "average", distance = "euclidean", cols = NULL)
```

**Arguments**

data	A data frame, tibble, or dist object
method	Agglomeration method: "ward.D2", "single", "complete", "average" (default), "mcquitty", "median", "centroid"
distance	Distance metric if data is not a dist object (default: "euclidean")
cols	Columns to include (tidy select). If NULL, uses all numeric columns.

**Value**

A list of class "tidy\_hclust" containing:

- model: hclust object
- dist: distance matrix used
- method: linkage method used
- data: original data (for plotting)

**Examples**

```
# Basic hierarchical clustering
hc_result <- tidy_hclust(USArrests, method = "average")

# With specific distance
hc_result <- tidy_hclust(mtcars, method = "complete", distance = "manhattan")
```

---

tidy_kmeans	<i>Tidy K-Means Clustering</i>
-------------	--------------------------------

---

**Description**

Performs k-means clustering with tidy output

**Usage**

```
tidy_kmeans(  
  data,  
  k,  
  cols = NULL,  
  nstart = 25,  
  iter_max = 100,  
  algorithm = "Hartigan-Wong"  
)
```

**Arguments**

data	A data frame or tibble
k	Number of clusters
cols	Columns to include (tidy select). If NULL, uses all numeric columns.
nstart	Number of random starts (default: 25)
iter_max	Maximum number of iterations (default: 100)
algorithm	K-means algorithm: "Hartigan-Wong" (default), "Lloyd", "Forgy", "MacQueen"

**Value**

A list of class "tidy\_kmeans" containing:

- clusters: tibble with observation IDs and cluster assignments
- centers: tibble of cluster centers
- metrics: tibble with clustering quality metrics
- model: original kmeans object

**Examples**

```
# Basic k-means  
km_result <- tidy_kmeans(iris, k = 3)
```

---

tidy_knn_dist	<i>Compute k-NN Distances</i>
---------------	-------------------------------

---

**Description**

Calculate distances to k-th nearest neighbor for each point

**Usage**

```
tidy_knn_dist(data, k = 4, cols = NULL)
```

**Arguments**

data	A data frame or matrix
k	Number of nearest neighbors (default: 4)
cols	Columns to include (tidy select). If NULL, uses all numeric columns.

**Value**

A tibble with observation IDs and k-NN distances

---

tidy_mds	<i>Tidy Multidimensional Scaling</i>
----------	--------------------------------------

---

**Description**

Unified interface for MDS methods with tidy output

**Usage**

```
tidy_mds(data, method = "classical", ndim = 2, distance = "euclidean", ...)
```

**Arguments**

data	A data frame, tibble, or distance matrix
method	Character; "classical" (default), "metric", "nonmetric", "sammon", or "kruskal"
ndim	Number of dimensions for output (default: 2)
distance	Character; distance metric if data is not already a dist object (default: "euclidean")
...	Additional arguments passed to specific MDS functions

**Value**

A list of class "tidy\_mds" containing:

- config: tibble of MDS configuration (coordinates)
- stress: goodness-of-fit measure (if applicable)
- method: character string of method used
- model: original model object

**Examples**

```
# Classical MDS
mds_result <- tidy_mds(eurodist, method = "classical")
print(mds_result)
```

---

tidy_mds_classical	<i>Classical (Metric) MDS</i>
--------------------	-------------------------------

---

**Description**

Performs classical multidimensional scaling using cmdscale()

**Usage**

```
tidy_mds_classical(dist_mat, ndim = 2, add_rownames = TRUE)
```

**Arguments**

dist_mat	A distance matrix (dist object)
ndim	Number of dimensions (default: 2)
add_rownames	Preserve row names from distance matrix (default: TRUE)

**Value**

A tidy\_mds object

---

tidy_mds_kruskal	<i>Kruskal's Non-metric MDS</i>
------------------	---------------------------------

---

**Description**

Performs Kruskal's isoMDS

**Usage**

```
tidy_mds_kruskal(dist_mat, ndim = 2, ...)
```

**Arguments**

dist_mat	A distance matrix (dist object)
ndim	Number of dimensions (default: 2)
...	Additional arguments passed to MASS::isoMDS()

**Value**

A tidy\_mds object

---

tidy_mds_sammon	<i>Sammon Mapping</i>
-----------------	-----------------------

---

**Description**

Performs Sammon's non-linear mapping

**Usage**

```
tidy_mds_sammon(dist_mat, ndim = 2, ...)
```

**Arguments**

dist_mat	A distance matrix (dist object)
ndim	Number of dimensions (default: 2)
...	Additional arguments passed to MASS::sammon()

**Value**

A tidy\_mds object

---

tidy_mds_smacof	<i>SMACOF MDS (Metric or Non-metric)</i>
-----------------	--

---

**Description**

Performs MDS using SMACOF algorithm from the smacof package

**Usage**

```
tidy_mds_smacof(dist_mat, ndim = 2, type = "ratio", ...)
```

**Arguments**

dist_mat	A distance matrix (dist object)
ndim	Number of dimensions (default: 2)
type	Character; "ratio" for metric, "ordinal" for non-metric (default: "ratio")
...	Additional arguments passed to smacof::mds()

**Value**

A tidy\_mds object

---

tidy_pam	<i>Tidy PAM (Partitioning Around Medoids)</i>
----------	---

---

**Description**

Performs PAM clustering with tidy output

**Usage**

```
tidy_pam(data, k, metric = "euclidean", cols = NULL)
```

**Arguments**

data	A data frame, tibble, or dist object
k	Number of clusters
metric	Distance metric (default: "euclidean"). Use "gower" for mixed data types.
cols	Columns to include (tidy select). If NULL, uses all columns.

**Value**

A list of class "tidy\_pam" containing:

- clusters: tibble with observation IDs and cluster assignments
- medoids: tibble of medoid indices and values
- silhouette: average silhouette width
- model: original pam object

**Examples**

```
# PAM with Euclidean distance
pam_result <- tidy_pam(iris, k = 3)

# PAM with Gower distance for mixed data
pam_result <- tidy_pam(mtcars, k = 3, metric = "gower")
```

---

tidy\_pca

*Tidy Principal Component Analysis*


---

**Description**

Performs PCA on a dataset using tidyverse principles. Returns a tidy list containing scores, loadings, variance explained, and the original model.

**Usage**

```
tidy_pca(data, cols = NULL, scale = TRUE, center = TRUE, method = "prcomp")
```

**Arguments**

data	A data frame or tibble
cols	Columns to include in PCA (tidy select syntax). If NULL, uses all numeric columns.
scale	Logical; should variables be scaled to unit variance? Default TRUE.
center	Logical; should variables be centered? Default TRUE.
method	Character; "prcomp" (default, recommended) or "princomp"

**Value**

A list of class "tidy\_pca" containing:

- scores: tibble of PC scores with observation identifiers
- loadings: tibble of variable loadings in long format
- variance: tibble of variance explained by each PC
- model: the original prcomp/princomp object
- settings: list of scale, center, method used



**Examples**

```
# Basic PCA
pca_result <- tidy_pca(USArrests)

# Access components
pca_result$scores
pca_result$loadings
pca_result$variance
```

---

tidy_pca_biplot	Create PCA Biplot
-----------------	-------------------

---

**Description**

Visualize both observations and variables in PC space

**Usage**

```
tidy_pca_biplot(
  pca_obj,
  pc_x = 1,
  pc_y = 2,
  color_by = NULL,
  arrow_scale = 1,
  label_obs = FALSE,
  label_vars = TRUE
)
```

**Arguments**

pca_obj	A tidy_pca object
pc_x	Principal component for x-axis (default: 1)
pc_y	Principal component for y-axis (default: 2)
color_by	Optional column name to color points by
arrow_scale	Scaling factor for variable arrows (default: 1)
label_obs	Logical; label observations? (default: FALSE)
label_vars	Logical; label variables? (default: TRUE)

**Value**

A ggplot object

---

tidy_pca_screepLOT	Create PCA Scree Plot
--------------------	-----------------------

---

**Description**

Visualize variance explained by each principal component

**Usage**

```
tidy_pca_screepLOT(pca_obj, type = "proportion", add_line = TRUE)
```

**Arguments**

pca_obj	A tidy_pca object
type	Character; "variance" or "proportion" (default)
add_line	Logical; add horizontal line at eigenvalue = 1? (for Kaiser criterion)

**Value**

A ggplot object

---

tidy_rules	Convert Association Rules to Tidy Tibble
------------	--

---

**Description**

Convert Association Rules to Tidy Tibble

**Usage**

```
tidy_rules(rules)
```

**Arguments**

rules	A rules object from arules
-------	----------------------------

**Value**

A tibble with one row per rule

---

tidy_silhouette	<i>Tidy Silhouette Analysis</i>
-----------------	---------------------------------

---

**Description**

Compute silhouette statistics for cluster validation

**Usage**

```
tidy_silhouette(clusters, dist_mat)
```

**Arguments**

clusters	Vector of cluster assignments
dist_mat	Distance matrix (dist object)

**Value**

A list of class "tidy\_silhouette" containing:

- silhouette\_data: tibble with silhouette values for each observation
- avg\_width: average silhouette width
- cluster\_avg: average silhouette width by cluster

---

tidy_silhouette_analysis	<i>Silhouette Analysis Across Multiple k Values</i>
--------------------------	---

---

**Description**

Silhouette Analysis Across Multiple k Values

**Usage**

```
tidy_silhouette_analysis(  
  data,  
  max_k = 10,  
  method = "kmeans",  
  nstart = 25,  
  dist_method = "euclidean",  
  linkage_method = "average"  
)
```

**Arguments**

data	A data frame or tibble
max_k	Maximum number of clusters to test (default: 10)
method	Clustering method: "kmeans" (default) or "hclust"
nstart	If kmeans, number of random starts (default: 25)
dist_method	Distance metric (default: "euclidean")
linkage_method	If hclust, linkage method (default: "average")

**Value**

A tibble with k and average silhouette widths

---

tl\_add\_cluster\_features

*Cluster-Based Features*

---

**Description**

Add cluster assignments as features for supervised learning. This semi-supervised approach can capture non-linear patterns.

**Usage**

```
tl_add_cluster_features(data, response = NULL, method = "kmeans", ...)
```

**Arguments**

data	A data frame
response	Response variable name (will be excluded from clustering)
method	Clustering method: "kmeans", "pam", "hclust", "dbscan"
...	Additional arguments for clustering

**Value**

Original data with cluster assignment column(s) added

**Examples**

```
# Add cluster features before supervised learning
data_with_clusters <- tl_add_cluster_features(iris, response = "Species",
                                              method = "kmeans", k = 3)
model <- tl_model(data_with_clusters, Species ~ ., method = "forest")
```

---

tl_anomaly_aware	<i>Anomaly-Aware Supervised Learning</i>
------------------	--

---

**Description**

Detect outliers using DBSCAN or other methods, then optionally remove them or down-weight them before supervised learning.

**Usage**

```
tl_anomaly_aware(  
  data,  
  formula,  
  response,  
  anomaly_method = "dbscan",  
  action = "flag",  
  supervised_method = "logistic",  
  ...  
)
```

**Arguments**

data	A data frame
formula	Model formula
response	Response variable name
anomaly_method	Method for anomaly detection: "dbscan", "isolation_forest"
action	Action to take: "remove", "flag", "downweight"
supervised_method	Supervised learning method
...	Additional arguments

**Value**

A tidylearn model or list with model and anomaly info

**Examples**

```
model <- tl_anomaly_aware(iris, Species ~ ., response = "Species",  
                          anomaly_method = "dbscan", action = "flag")
```

---

tl_auto_interactions	<i>Find important interactions automatically</i>
----------------------	--

---

### Description

Find important interactions automatically

### Usage

```
tl_auto_interactions(
  data,
  formula,
  top_n = 3,
  min_r2_change = 0.01,
  max_p_value = 0.05,
  exclude_vars = NULL
)
```

### Arguments

data	A data frame containing the data
formula	A formula specifying the base model without interactions
top_n	Number of top interactions to return
min_r2_change	Minimum change in R-squared to consider
max_p_value	Maximum p-value for significance
exclude_vars	Character vector of variables to exclude from interaction testing

### Value

A tidylearn model with important interactions

---

tl_auto_ml	<i>High-Level Workflows for Common Machine Learning Patterns</i>
------------	--

---

### Description

These functions provide end-to-end workflows that showcase tidylearn's ability to seamlessly combine multiple learning paradigms Auto ML: Automated Machine Learning Workflow

**Usage**

```
tl_auto_ml(  
  data,  
  formula,  
  task = "auto",  
  use_reduction = TRUE,  
  use_clustering = TRUE,  
  time_budget = 300,  
  cv_folds = 5,  
  metric = NULL  
)
```

**Arguments**

data	A data frame
formula	Model formula (for supervised learning)
task	Task type: "classification", "regression", or "auto" (default)
use_reduction	Whether to try dimensionality reduction (default: TRUE)
use_clustering	Whether to add cluster features (default: TRUE)
time_budget	Time budget in seconds (default: 300)
cv_folds	Number of cross-validation folds (default: 5)
metric	Evaluation metric (default: auto-selected based on task)

**Details**

Automatically explores multiple modeling approaches including dimensionality reduction, clustering, and various supervised methods. Returns the best performing model based on cross-validation.

**Value**

Best model with performance comparison

**Examples**

```
# Automated modeling  
result <- tl_auto_ml(iris, Species ~ .)  
best_model <- result$best_model  
result$leaderboard
```

---

```
tl_calc_classification_metrics
```

*Calculate classification metrics*

---

### Description

Calculate classification metrics

### Usage

```
tl_calc_classification_metrics(
  actuals,
  predicted,
  predicted_probs = NULL,
  metrics = c("accuracy", "precision", "recall", "f1", "auc"),
  thresholds = NULL,
  ...
)
```

### Arguments

actuals	Actual values (ground truth)
predicted	Predicted class values
predicted_probs	Predicted probabilities (for metrics like AUC)
metrics	Character vector of metrics to compute
thresholds	Optional vector of thresholds to evaluate for threshold-dependent metrics
...	Additional arguments

### Value

A tibble of evaluation metrics

---

```
tl_check_assumptions
```

*Check model assumptions*

---

### Description

Check model assumptions

### Usage

```
tl_check_assumptions(model, test = TRUE, verbose = TRUE)
```



**Arguments**

model	A tidylearn model object
test	Logical; whether to perform statistical tests
verbose	Logical; whether to print test results and explanations

**Value**

A list with assumption check results

---

tl_compare_cv	<i>Compare models using cross-validation</i>
---------------	--

---

**Description**

Compare models using cross-validation

**Usage**

```
tl_compare_cv(data, models, folds = 5, metrics = NULL, ...)
```

**Arguments**

data	A data frame containing the training data
models	A list of tidylearn model objects
folds	Number of cross-validation folds
metrics	Character vector of metrics to compute
...	Additional arguments

**Value**

A tibble with cross-validation results for all models

---

tl_compare_pipeline_models	<i>Compare models from a pipeline</i>
----------------------------	---------------------------------------

---

**Description**

Compare models from a pipeline

**Usage**

```
tl_compare_pipeline_models(pipeline, metrics = NULL)
```

**Arguments**

pipeline	A tidylearn pipeline object with results
metrics	Character vector of metrics to compare (if NULL, uses all available)

**Value**

A comparison plot of model performance

---

tl_cv	<i>Cross-validation for tidylearn models</i>
-------	--

---

**Description**

Cross-validation for tidylearn models

**Usage**

```
tl_cv(data, formula, method, folds = 5, ...)
```

**Arguments**

data	Data frame
formula	Model formula
method	Modeling method
folds	Number of cross-validation folds
...	Additional arguments

**Value**

Cross-validation results

---

tl_dashboard	Create interactive visualization dashboard for a model
--------------	--

---

**Description**

Create interactive visualization dashboard for a model

**Usage**

```
tl_dashboard(model, new_data = NULL, ...)
```

**Arguments**

model	A tidylearn model object
new_data	Optional data frame for evaluation (if NULL, uses training data)
...	Additional arguments

**Value**

A Shiny app object

---

tl_default_param_grid	Create pre-defined parameter grids for common models
-----------------------	--

---

**Description**

Create pre-defined parameter grids for common models

**Usage**

```
tl_default_param_grid(method, size = "medium", is_classification = TRUE)
```

**Arguments**

method	Model method ("tree", "forest", "boost", "svm", etc.)
size	Grid size: "small", "medium", "large"
is_classification	Whether the task is classification or regression

**Value**

A named list of parameter values to tune

---

tl_detect_outliers	<i>Detect outliers in the data</i>
--------------------	------------------------------------

---

**Description**

Detect outliers in the data

**Usage**

```
tl_detect_outliers(
  data,
  variables = NULL,
  method = "iqr",
  threshold = NULL,
  plot = TRUE
)
```

**Arguments**

data	A data frame containing the data
variables	Character vector of variables to check for outliers
method	Method for outlier detection: "boxplot", "z-score", "cook", "iqr", "mahalanobis"
threshold	Threshold for outlier detection
plot	Logical; whether to create a plot of outliers

**Value**

A list with outlier detection results

---

tl_diagnostic_dashboard	<i>Create a comprehensive diagnostic dashboard</i>
-------------------------	--

---

**Description**

Create a comprehensive diagnostic dashboard

**Usage**

```
tl_diagnostic_dashboard(
  model,
  include_influence = TRUE,
  include_assumptions = TRUE,
  include_performance = TRUE,
  arrange_plots = "grid"
)
```

**Arguments**

model	A tidylearn model object
include_influence	Logical; whether to include influence diagnostics
include_assumptions	Logical; whether to include assumption checks
include_performance	Logical; whether to include performance metrics
arrange_plots	Layout arrangement (e.g., "grid", "row", "column")

**Value**

A plot grid with diagnostic plots

---

tl_evaluate	<i>Evaluate a tidylearn model</i>
-------------	-----------------------------------

---

**Description**

Evaluate a tidylearn model

**Usage**

```
tl_evaluate(object, new_data = NULL, ...)
```

**Arguments**

object	A tidylearn model object
new_data	Optional new data for evaluation (if NULL, uses training data)
...	Additional arguments

**Value**

A tibble of evaluation metrics

---

tl_explore	<i>Exploratory Data Analysis Workflow</i>
------------	---

---

**Description**

Comprehensive EDA combining unsupervised learning techniques to understand data structure before modeling

**Usage**

```
tl_explore(data, response = NULL, max_components = 5, k_range = 2:6)
```

**Arguments**

data	A data frame
response	Optional response variable for colored visualizations
max_components	Maximum PCA components to compute (default: 5)
k_range	Range of k values for clustering (default: 2:6)

**Value**

An EDA object with multiple analyses

**Examples**

```
eda <- tl_explore(iris, response = "Species")
plot(eda)
```

---

tl_get_best_model	<i>Get the best model from a pipeline</i>
-------------------	---

---

**Description**

Get the best model from a pipeline

**Usage**

```
tl_get_best_model(pipeline)
```

**Arguments**

pipeline	A tidylearn pipeline object with results
----------	--

**Value**

The best tidylearn model

---

`tl_influence_measures` *Calculate influence measures for a linear model*

---

**Description**

Calculate influence measures for a linear model

**Usage**

```
tl_influence_measures(  
  model,  
  threshold_cook = NULL,  
  threshold_leverage = NULL,  
  threshold_dffits = NULL  
)
```

**Arguments**

<code>model</code>	A tidylearn model object
<code>threshold_cook</code>	Cook's distance threshold (default: 4/n)
<code>threshold_leverage</code>	Leverage threshold (default: 2*(p+1)/n)
<code>threshold_dffits</code>	DFFITS threshold (default: 2*sqrt((p+1)/n))

**Value**

A data frame with influence measures

---

`tl_interaction_effects`  
*Calculate partial effects based on a model with interactions*

---

**Description**

Calculate partial effects based on a model with interactions

**Usage**

```
tl_interaction_effects(model, var, by_var, at_values = NULL, intervals = TRUE)
```

**Arguments**

model	A tidylearn model object
var	Variable to calculate effects for
by_var	Variable to calculate effects by (interaction variable)
at_values	Named list of values at which to hold other variables
intervals	Logical; whether to include confidence intervals

**Value**

A data frame with marginal effects

---

tl_load_pipeline	<i>Load a pipeline from disk</i>
------------------	----------------------------------

---

**Description**

Load a pipeline from disk

**Usage**

```
tl_load_pipeline(file)
```

**Arguments**

file	Path to the pipeline file
------	---------------------------

**Value**

A tidylearn pipeline object

---

tl_model	<i>Create a tidylearn model</i>
----------	---------------------------------

---

**Description**

Unified interface for creating machine learning models by wrapping established R packages. This function dispatches to the appropriate underlying package based on the method specified.

**Usage**

```
tl_model(data, formula = NULL, method = "linear", ...)
```



**Arguments**

data	A data frame containing the training data
formula	A formula specifying the model. For unsupervised methods, use <code>~ vars</code> or <code>NULL</code> .
method	The modeling method. Supervised: "linear" (stats::lm), "logistic" (stats::glm), "tree" (rpart), "forest" (randomForest), "boost" (gbm), "ridge"/"lasso"/"elastic_net" (glmnet), "svm" (e1071), "nn" (nnet), "deep" (keras), "xgboost" (xgboost). Unsupervised: "pca" (stats::prcomp), "mds" (stats/MASS/smacof), "kmeans" (stats::kmeans), "pam"/"clara" (cluster), "hclust" (stats::hclust), "dbscan" (dbscan).
...	Additional arguments passed to the underlying model function

**Details**

The wrapped packages include: stats (lm, glm, prcomp, kmeans, hclust), glmnet, randomForest, xgboost, gbm, e1071, nnet, rpart, cluster, and dbscan. The underlying algorithms are unchanged - this function provides a consistent interface and returns tidy output.

Access the raw model object from the underlying package via `model$fit`.

**Value**

A tidylearn model object containing the fitted model (`$fit`), specification, and training data

**Examples**

```
# Classification -> wraps randomForest::randomForest()
model <- tl_model(iris, Species ~ ., method = "forest")
model$fit # Access the raw randomForest object

# Regression -> wraps stats::lm()
model <- tl_model(mtcars, mpg ~ wt + hp, method = "linear")
model$fit # Access the raw lm object

# PCA -> wraps stats::prcomp()
model <- tl_model(iris, ~ ., method = "pca")
model$fit # Access the raw prcomp object

# Clustering -> wraps stats::kmeans()
model <- tl_model(iris, method = "kmeans", k = 3)
model$fit # Access the raw kmeans object
```

---

tl\_pipeline

---

*Create a modeling pipeline*


---

**Description**

Create a modeling pipeline

**Usage**

```
tl_pipeline(  
  data,  
  formula,  
  preprocessing = NULL,  
  models = NULL,  
  evaluation = NULL,  
  ...  
)
```

**Arguments**

data	A data frame containing the data
formula	A formula specifying the model
preprocessing	A list of preprocessing steps
models	A list of models to train
evaluation	A list of evaluation criteria
...	Additional arguments

**Value**

A tidylearn pipeline object

---

tl\_plot\_cv\_comparison *Plot comparison of cross-validation results*

---

**Description**

Plot comparison of cross-validation results

**Usage**

```
tl_plot_cv_comparison(cv_results, metrics = NULL)
```

**Arguments**

cv_results	Results from tl_compare_cv function
metrics	Character vector of metrics to plot (if NULL, plots all metrics)

**Value**

A ggplot object

---

tl_plot_cv_results	<i>Plot cross-validation results</i>
--------------------	--------------------------------------

---

**Description**

Plot cross-validation results

**Usage**

```
tl_plot_cv_results(cv_results, metrics = NULL)
```

**Arguments**

cv_results	Cross-validation results from tl_cv function
metrics	Character vector of metrics to plot (if NULL, plots all metrics)

**Value**

A ggplot object with cross-validation results

---

tl_plot_deep_architecture	<i>Plot deep learning model architecture</i>
---------------------------	--

---

**Description**

Plot deep learning model architecture

**Usage**

```
tl_plot_deep_architecture(model, ...)
```

**Arguments**

model	A tidylearn deep learning model object
...	Additional arguments

**Value**

A plot of the deep learning model architecture

---

tl_plot_deep_history	<i>Plot deep learning model training history</i>
----------------------	--

---

**Description**

Plot deep learning model training history

**Usage**

```
tl_plot_deep_history(model, metrics = c("loss", "val_loss"), ...)
```

**Arguments**

model	A tidylearn deep learning model object
metrics	Which metrics to plot (default: c("loss", "val_loss"))
...	Additional arguments

**Value**

A ggplot object with training history

---

tl_plot_gain	<i>Plot gain chart for a classification model</i>
--------------	---

---

**Description**

Plot gain chart for a classification model

**Usage**

```
tl_plot_gain(model, new_data = NULL, bins = 10, ...)
```

**Arguments**

model	A tidylearn classification model object
new_data	Optional data frame for evaluation (if NULL, uses training data)
bins	Number of bins for grouping predictions (default: 10)
...	Additional arguments

**Value**

A ggplot object with gain chart

---

`tl_plot_importance_comparison`*Plot feature importance across multiple models*

---

**Description**

Plot feature importance across multiple models

**Usage**

```
tl_plot_importance_comparison(..., top_n = 10, names = NULL)
```

**Arguments**

<code>...</code>	tidylearn model objects to compare
<code>top_n</code>	Number of top features to display (default: 10)
<code>names</code>	Optional character vector of model names

**Value**

A ggplot object with feature importance comparison

---

`tl_plot_importance_regularized`*Plot variable importance for a regularized regression model*

---

**Description**

Plot variable importance for a regularized regression model

**Usage**

```
tl_plot_importance_regularized(model, lambda = "1se", top_n = 20, ...)
```

**Arguments**

<code>model</code>	A tidylearn regularized model object
<code>lambda</code>	Which lambda to use ("1se" or "min", default: "1se")
<code>top_n</code>	Number of top features to display (default: 20)
<code>...</code>	Additional arguments

**Value**

A ggplot object

---

tl_plot_influence	<i>Plot influence diagnostics</i>
-------------------	-----------------------------------

---

**Description**

Plot influence diagnostics

**Usage**

```
tl_plot_influence(  
  model,  
  plot_type = "cook",  
  threshold_cook = NULL,  
  threshold_leverage = NULL,  
  threshold_dffits = NULL,  
  n_labels = 3,  
  label_size = 3  
)
```

**Arguments**

model	A tidylearn model object
plot_type	Type of influence plot: "cook", "leverage", "index"
threshold_cook	Cook's distance threshold (default: 4/n)
threshold_leverage	Leverage threshold (default: 2*(p+1)/n)
threshold_dffits	DFFITS threshold (default: 2*sqrt((p+1)/n))
n_labels	Number of points to label (default: 3)
label_size	Text size for labels (default: 3)

**Value**

A ggplot object

---

tl_plot_interaction	<i>Plot interaction effects</i>
---------------------	---------------------------------

---

**Description**

Plot interaction effects

**Usage**

```
tl_plot_interaction(
  model,
  var1,
  var2,
  n_points = 100,
  fixed_values = NULL,
  confidence = TRUE,
  ...
)
```

**Arguments**

model	A tidylearn model object
var1	First variable in the interaction
var2	Second variable in the interaction
n_points	Number of points to use for continuous variables
fixed_values	Named list of values for other variables in the model
confidence	Logical; whether to show confidence intervals
...	Additional arguments to pass to predict()

**Value**

A ggplot object

---

tl_plot_intervals	<i>Create confidence and prediction interval plots</i>
-------------------	--

---

**Description**

Create confidence and prediction interval plots

**Usage**

```
tl_plot_intervals(model, new_data = NULL, level = 0.95, ...)
```

**Arguments**

model	A tidylearn regression model object
new_data	Optional data frame for prediction (if NULL, uses training data)
level	Confidence level (default: 0.95)
...	Additional arguments

**Value**

A ggplot object

---

tl_plot_lift	<i>Plot lift chart for a classification model</i>
--------------	---

---

**Description**

Plot lift chart for a classification model

**Usage**

```
tl_plot_lift(model, new_data = NULL, bins = 10, ...)
```

**Arguments**

model	A tidylearn classification model object
new_data	Optional data frame for evaluation (if NULL, uses training data)
bins	Number of bins for grouping predictions (default: 10)
...	Additional arguments

**Value**

A ggplot object with lift chart

---

tl_plot_model_comparison	<i>Plot model comparison</i>
--------------------------	------------------------------

---

**Description**

Plot model comparison

**Usage**

```
tl_plot_model_comparison(..., new_data = NULL, metrics = NULL, names = NULL)
```

**Arguments**

...	tidylearn model objects to compare
new_data	Optional data frame for evaluation (if NULL, uses training data)
metrics	Character vector of metrics to compute
names	Optional character vector of model names

**Value**

A ggplot object with model comparison



---

tl_plot_nn_architecture	<i>Plot neural network architecture</i>
-------------------------	---

---

**Description**

Plot neural network architecture

**Usage**

```
tl_plot_nn_architecture(model, ...)
```

**Arguments**

model	A tidylearn neural network model object
...	Additional arguments

**Value**

A ggplot object with neural network architecture

---

tl_plot_nn_tuning	<i>Plot neural network training history</i>
-------------------	---

---

**Description**

Plot neural network training history

**Usage**

```
tl_plot_nn_tuning(model, ...)
```

**Arguments**

model	A tidylearn neural network model object
...	Additional arguments

**Value**

A ggplot object with training history

---

`tl_plot_partial_dependence`*Plot partial dependence for tree-based models*

---

**Description**

Plot partial dependence for tree-based models

**Usage**

```
tl_plot_partial_dependence(model, var, n.pts = 20, ...)
```

**Arguments**

<code>model</code>	A tidylearn tree-based model object
<code>var</code>	Variable name to plot
<code>n.pts</code>	Number of points for continuous variables (default: 20)
<code>...</code>	Additional arguments

**Value**

A ggplot object

---

`tl_plot_regularization_cv`*Plot cross-validation results for a regularized regression model*

---

**Description**

Shows the cross-validation error as a function of lambda for ridge, lasso, or elastic net models fitted with `cv.glmnet`.

**Usage**

```
tl_plot_regularization_cv(model, ...)
```

**Arguments**

<code>model</code>	A tidylearn regularized model object (ridge, lasso, or <code>elastic_net</code> )
<code>...</code>	Additional arguments (currently unused)

**Value**

A ggplot object showing CV error vs lambda

---

`tl_plot_regularization_path`*Plot regularization path for a regularized regression model*

---

**Description**

Plot regularization path for a regularized regression model

**Usage**

```
tl_plot_regularization_path(model, label_n = 5, ...)
```

**Arguments**

<code>model</code>	A tidylearn regularized model object
<code>label_n</code>	Number of top features to label (default: 5)
<code>...</code>	Additional arguments

**Value**

A ggplot object

---

`tl_plot_svm_boundary` *Plot SVM decision boundary*

---

**Description**

Plot SVM decision boundary

**Usage**

```
tl_plot_svm_boundary(model, x_var = NULL, y_var = NULL, grid_size = 100, ...)
```

**Arguments**

<code>model</code>	A tidylearn SVM model object
<code>x_var</code>	Name of the x-axis variable
<code>y_var</code>	Name of the y-axis variable
<code>grid_size</code>	Number of points in each dimension for the grid (default: 100)
<code>...</code>	Additional arguments

**Value**

A ggplot object with decision boundary

---

tl_plot_svm_tuning	<i>Plot SVM tuning results</i>
--------------------	--------------------------------

---

**Description**

Plot SVM tuning results

**Usage**

```
tl_plot_svm_tuning(model, ...)
```

**Arguments**

model	A tidylearn SVM model object
...	Additional arguments

**Value**

A ggplot object with tuning results

---

tl_plot_tree	<i>Plot a decision tree</i>
--------------	-----------------------------

---

**Description**

Plot a decision tree

**Usage**

```
tl_plot_tree(model, ...)
```

**Arguments**

model	A tidylearn tree model object
...	Additional arguments to pass to rpart.plot()

**Value**

A plot of the decision tree

---

`tl_plot_tuning_results`*Plot hyperparameter tuning results*

---

**Description**

Plot hyperparameter tuning results

**Usage**

```
tl_plot_tuning_results(  
  model,  
  top_n = 5,  
  param1 = NULL,  
  param2 = NULL,  
  plot_type = "scatter"  
)
```

**Arguments**

<code>model</code>	A tidylearn model object with tuning results
<code>top_n</code>	Number of top parameter sets to highlight
<code>param1</code>	First parameter to plot (for 2D grid or scatter plots)
<code>param2</code>	Second parameter to plot (for 2D grid or scatter plots)
<code>plot_type</code>	Type of plot: "scatter", "grid", "parallel", "importance"

**Value**

A ggplot object

---

`tl_plot_xgboost_importance`*Plot feature importance for an XGBoost model*

---

**Description**

Plot feature importance for an XGBoost model

**Usage**

```
tl_plot_xgboost_importance(model, top_n = 10, importance_type = "gain", ...)
```

**Arguments**

model	A tidylearn XGBoost model object
top_n	Number of top features to display (default: 10)
importance_type	Type of importance: "gain", "cover", "frequency"
...	Additional arguments

**Value**

A ggplot object

---

tl_plot_xgboost_shap_dependence	<i>Plot SHAP dependence for a specific feature</i>
---------------------------------	--

---

**Description**

Plot SHAP dependence for a specific feature

**Usage**

```
tl_plot_xgboost_shap_dependence(
  model,
  feature,
  interaction_feature = NULL,
  data = NULL,
  n_samples = 100
)
```

**Arguments**

model	A tidylearn XGBoost model object
feature	Feature name to plot
interaction_feature	Feature to use for coloring (default: NULL)
data	Data for SHAP value calculation (default: NULL, uses training data)
n_samples	Number of samples to use (default: 100, NULL for all)

**Value**

A ggplot object with SHAP dependence plot

---

`tl_plot_xgboost_shap_summary`*Plot SHAP summary for XGBoost model*

---

**Description**

Plot SHAP summary for XGBoost model

**Usage**

```
tl_plot_xgboost_shap_summary(model, data = NULL, top_n = 10, n_samples = 100)
```

**Arguments**

<code>model</code>	A tidylearn XGBoost model object
<code>data</code>	Data for SHAP value calculation (default: NULL, uses training data)
<code>top_n</code>	Number of top features to display (default: 10)
<code>n_samples</code>	Number of samples to use (default: 100, NULL for all)

**Value**

A ggplot object with SHAP summary

---

`tl_plot_xgboost_tree` *Plot XGBoost tree visualization*

---

**Description**

Plot XGBoost tree visualization

**Usage**

```
tl_plot_xgboost_tree(model, tree_index = 0, ...)
```

**Arguments**

<code>model</code>	A tidylearn XGBoost model object
<code>tree_index</code>	Index of the tree to plot (default: 0, first tree)
<code>...</code>	Additional arguments

**Value**

Tree visualization

---

tl_predict_pipeline	<i>Make predictions using a pipeline</i>
---------------------	--

---

**Description**

Make predictions using a pipeline

**Usage**

```
tl_predict_pipeline(  
  pipeline,  
  new_data,  
  type = "response",  
  model_name = NULL,  
  ...  
)
```

**Arguments**

pipeline	A tidylearn pipeline object with results
new_data	A data frame containing the new data
type	Type of prediction (default: "response")
model_name	Name of model to use (if NULL, uses the best model)
...	Additional arguments passed to predict

**Value**

Predictions

---

tl_prepare_data	<i>Data Preprocessing for tidylearn</i>
-----------------	---

---

**Description**

Unified preprocessing functions that work with both supervised and unsupervised workflows Prepare Data for Machine Learning



**Usage**

```
tl_prepare_data(  
  data,  
  formula = NULL,  
  impute_method = "mean",  
  scale_method = "standardize",  
  encode_categorical = TRUE,  
  remove_zero_variance = TRUE,  
  remove_correlated = FALSE,  
  correlation_cutoff = 0.95  
)
```

**Arguments**

data	A data frame
formula	Optional formula (for supervised learning)
impute_method	Method for missing value imputation: "mean", "median", "mode", "knn"
scale_method	Scaling method: "standardize", "normalize", "robust", "none"
encode_categorical	Whether to encode categorical variables (default: TRUE)
remove_zero_variance	Remove zero-variance features (default: TRUE)
remove_correlated	Remove highly correlated features (default: FALSE)
correlation_cutoff	Correlation threshold for removal (default: 0.95)

**Details**

Comprehensive preprocessing pipeline including imputation, scaling, encoding, and feature engineering

**Value**

A list containing processed data and preprocessing metadata

**Examples**

```
processed <- tl_prepare_data(iris, Species ~ ., scale_method = "standardize")  
model <- tl_model(processed$data, Species ~ ., method = "logistic")
```

---

tl_reduce_dimensions	<i>Integration Functions: Combining Supervised and Unsupervised Learning</i>
----------------------	--

---

### Description

These functions demonstrate the power of tidylearn's unified approach by seamlessly integrating supervised and unsupervised learning techniques. Feature Engineering via Dimensionality Reduction

### Usage

```
tl_reduce_dimensions(  
  data,  
  response = NULL,  
  method = "pca",  
  n_components = NULL,  
  ...  
)
```

### Arguments

data	A data frame
response	Response variable name (will be preserved)
method	Dimensionality reduction method: "pca", "mds"
n_components	Number of components to retain
...	Additional arguments for the dimensionality reduction method

### Details

Use PCA, MDS, or other dimensionality reduction as a preprocessing step for supervised learning. This can improve model performance and interpretability.

### Value

A list containing the transformed data and the reduction model

### Examples

```
# Reduce dimensions before classification  
reduced <- tl_reduce_dimensions(iris, response = "Species", method = "pca", n_components = 3)  
model <- tl_model(reduced$data, Species ~ ., method = "logistic")
```

---

tl_run_pipeline	<i>Run a tidylearn pipeline</i>
-----------------	---------------------------------

---

**Description**

Run a tidylearn pipeline

**Usage**

```
tl_run_pipeline(pipeline, verbose = TRUE)
```

**Arguments**

pipeline	A tidylearn pipeline object
verbose	Logical; whether to print progress

**Value**

A tidylearn pipeline with results

---

tl_save_pipeline	<i>Save a pipeline to disk</i>
------------------	--------------------------------

---

**Description**

Save a pipeline to disk

**Usage**

```
tl_save_pipeline(pipeline, file)
```

**Arguments**

pipeline	A tidylearn pipeline object
file	Path to save the pipeline

**Value**

Invisible NULL

---

tl_semisupervised	<i>Semi-Supervised Learning via Clustering</i>
-------------------	--

---

## Description

Train a supervised model with limited labels by first clustering the data and propagating labels within clusters.

## Usage

```
tl_semisupervised(  
  data,  
  formula,  
  labeled_indices,  
  cluster_method = "kmeans",  
  supervised_method = "logistic",  
  ...  
)
```

## Arguments

data	A data frame
formula	Model formula
labeled_indices	Indices of labeled observations
cluster_method	Clustering method for label propagation
supervised_method	Supervised learning method for final model
...	Additional arguments

## Value

A tidylearn model trained on pseudo-labeled data

## Examples

```
# Use only 10% of labels  
labeled_idx <- sample(nrow(iris), size = 15)  
model <- tl_semisupervised(iris, Species ~ ., labeled_indices = labeled_idx,  
                           cluster_method = "kmeans", supervised_method = "logistic")
```

---

tl_split	<i>Split data into train and test sets</i>
----------	--

---

**Description**

Split data into train and test sets

**Usage**

```
tl_split(data, prop = 0.8, stratify = NULL, seed = NULL)
```

**Arguments**

data	A data frame
prop	Proportion for training set (default: 0.8)
stratify	Column name for stratified splitting
seed	Random seed for reproducibility

**Value**

A list with train and test data frames

**Examples**

```
split_data <- tl_split(iris, prop = 0.7, stratify = "Species")
train <- split_data$train
test <- split_data$test
```

---

tl_step_selection	<i>Perform stepwise selection on a linear model</i>
-------------------	---

---

**Description**

Perform stepwise selection on a linear model

**Usage**

```
tl_step_selection(  
  data,  
  formula,  
  direction = "backward",  
  criterion = "AIC",  
  trace = FALSE,  
  steps = 1000,  
  ...  
)
```

**Arguments**

data	A data frame containing the training data
formula	A formula specifying the initial model
direction	Direction of stepwise selection: "forward", "backward", or "both"
criterion	Criterion for selection: "AIC" or "BIC"
trace	Logical; whether to print progress
steps	Maximum number of steps to take
...	Additional arguments to pass to step()

**Value**

A selected model

---

tl\_stratified\_models    *Stratified Features via Clustering*

---

**Description**

Create cluster-specific supervised models for heterogeneous data

**Usage**

```
tl_stratified_models(
  data,
  formula,
  cluster_method = "kmeans",
  k = 3,
  supervised_method = "linear",
  ...
)
```

**Arguments**

data	A data frame
formula	Model formula
cluster_method	Clustering method
k	Number of clusters
supervised_method	Supervised learning method
...	Additional arguments

**Value**

A list of models (one per cluster) plus cluster assignments

**Examples**

```
models <- tl_stratified_models(mtcars, mpg ~ ., cluster_method = "kmeans",
                              k = 3, supervised_method = "linear")
```

---

tl_test_interactions	<i>Test for significant interactions between variables</i>
----------------------	--

---

**Description**

Test for significant interactions between variables

**Usage**

```
tl_test_interactions(
  data,
  formula,
  var1 = NULL,
  var2 = NULL,
  all_pairs = FALSE,
  categorical_only = FALSE,
  numeric_only = FALSE,
  mixed_only = FALSE,
  alpha = 0.05
)
```

**Arguments**

data	A data frame containing the data
formula	A formula specifying the base model without interactions
var1	First variable to test for interactions
var2	Second variable to test for interactions (if NULL, tests var1 with all others)
all_pairs	Logical; whether to test all variable pairs
categorical_only	Logical; whether to only test categorical variables
numeric_only	Logical; whether to only test numeric variables
mixed_only	Logical; whether to only test numeric-categorical pairs
alpha	Significance level for interaction tests

**Value**

A data frame with interaction test results

---

`tl_test_model_difference`
*Perform statistical comparison of models using cross-validation*


---

### Description

Perform statistical comparison of models using cross-validation

### Usage

```
tl_test_model_difference(
  cv_results,
  baseline_model = NULL,
  test = "t.test",
  metric = NULL
)
```

### Arguments

<code>cv_results</code>	Results from <code>tl_compare_cv</code> function
<code>baseline_model</code>	Name of the model to use as baseline for comparison
<code>test</code>	Type of statistical test: "t.test" or "wilcox"
<code>metric</code>	Name of the metric to compare

### Value

A data frame with statistical test results

---

`tl_transfer_learning`    *Transfer Learning Workflow*


---

### Description

Use unsupervised pre-training (e.g., autoencoder features) before supervised learning

### Usage

```
tl_transfer_learning(
  data,
  formula,
  pretrain_method = "pca",
  supervised_method = "logistic",
  ...
)
```



**Arguments**

data	Training data
formula	Model formula
pretrain_method	Pre-training method: "pca", "autoencoder"
supervised_method	Supervised learning method
...	Additional arguments

**Value**

A transfer learning model

**Examples**

```
model <- tl_transfer_learning(iris, Species ~ ., pretrain_method = "pca")
```

---

tl_tune_deep	<i>Tune a deep learning model</i>
--------------	-----------------------------------

---

**Description**

Tune a deep learning model

**Usage**

```
tl_tune_deep(
  data,
  formula,
  is_classification = FALSE,
  hidden_layers_options = list(c(32), c(64, 32), c(128, 64, 32)),
  learning_rates = c(0.01, 0.001, 1e-04),
  batch_sizes = c(16, 32, 64),
  epochs = 30,
  validation_split = 0.2,
  ...
)
```

**Arguments**

data	A data frame containing the training data
formula	A formula specifying the model
is_classification	Logical indicating if this is a classification problem

hidden_layers_options	List of vectors defining hidden layer configurations to try
learning_rates	Learning rates to try (default: c(0.01, 0.001, 0.0001))
batch_sizes	Batch sizes to try (default: c(16, 32, 64))
epochs	Number of training epochs (default: 30)
validation_split	Proportion of data for validation (default: 0.2)
...	Additional arguments

**Value**

A list with the best model and tuning results

---

tl_tune_grid	<i>Tune hyperparameters for a model using grid search</i>
--------------	---

---

**Description**

Tune hyperparameters for a model using grid search

**Usage**

```
tl_tune_grid(
  data,
  formula,
  method,
  param_grid,
  folds = 5,
  metric = NULL,
  maximize = NULL,
  verbose = TRUE,
  ...
)
```

**Arguments**

data	A data frame containing the training data
formula	A formula specifying the model
method	The modeling method to tune
param_grid	A named list of parameter values to tune
folds	Number of cross-validation folds
metric	Metric to optimize
maximize	Logical; whether to maximize (TRUE) or minimize (FALSE) the metric
verbose	Logical; whether to print progress
...	Additional arguments passed to tl_model

**Value**

A list with the best model and tuning results

---

tl\_tune\_nn

*Tune a neural network model*

---

**Description**

Tune a neural network model

**Usage**

```
tl_tune_nn(  
  data,  
  formula,  
  is_classification = FALSE,  
  sizes = c(1, 2, 5, 10),  
  decays = c(0, 0.001, 0.01, 0.1),  
  folds = 5,  
  ...  
)
```

**Arguments**

data	A data frame containing the training data
formula	A formula specifying the model
is_classification	Logical indicating if this is a classification problem
sizes	Vector of hidden layer sizes to try
decays	Vector of weight decay parameters to try
folds	Number of cross-validation folds (default: 5)
...	Additional arguments to pass to nnet()

**Value**

A list with the best model and tuning results

---

tl_tune_random	<i>Tune hyperparameters for a model using random search</i>
----------------	---

---

**Description**

Tune hyperparameters for a model using random search

**Usage**

```
tl_tune_random(  
  data,  
  formula,  
  method,  
  param_space,  
  n_iter = 10,  
  folds = 5,  
  metric = NULL,  
  maximize = NULL,  
  verbose = TRUE,  
  seed = NULL,  
  ...  
)
```

**Arguments**

data	A data frame containing the training data
formula	A formula specifying the model
method	The modeling method to tune
param_space	A named list of parameter spaces to sample from
n_iter	Number of random parameter combinations to try
folds	Number of cross-validation folds
metric	Metric to optimize
maximize	Logical; whether to maximize (TRUE) or minimize (FALSE) the metric
verbose	Logical; whether to print progress
seed	Random seed for reproducibility
...	Additional arguments passed to tl_model

**Value**

A list with the best model and tuning results

---

tl_tune_xgboost	<i>Tune XGBoost hyperparameters</i>
-----------------	-------------------------------------

---

## Description

Tune XGBoost hyperparameters

## Usage

```
tl_tune_xgboost(  
  data,  
  formula,  
  is_classification = FALSE,  
  param_grid = NULL,  
  cv_folds = 5,  
  early_stopping_rounds = 10,  
  verbose = TRUE,  
  ...  
)
```

## Arguments

data	A data frame containing the training data
formula	A formula specifying the model
is_classification	Logical indicating if this is a classification problem
param_grid	Named list of parameter values to try
cv_folds	Number of cross-validation folds (default: 5)
early_stopping_rounds	Early stopping rounds (default: 10)
verbose	Logical indicating whether to print progress (default: TRUE)
...	Additional arguments

## Value

A list with the best model and tuning results

---

tl_version	<i>Get tidylearn version information</i>
------------	--

---

**Description**

Get tidylearn version information

**Usage**

```
tl_version()
```

**Value**

A package\_version object containing the version number

---

tl_xgboost_shap	<i>Generate SHAP values for XGBoost model interpretation</i>
-----------------	--

---

**Description**

Generate SHAP values for XGBoost model interpretation

**Usage**

```
tl_xgboost_shap(model, data = NULL, n_samples = 100, trees_idx = NULL)
```

**Arguments**

model	A tidylearn XGBoost model object
data	Data for SHAP value calculation (default: NULL, uses training data)
n_samples	Number of samples to use (default: 100, NULL for all)
trees_idx	Trees to include (default: NULL, uses all trees)

**Value**

A data frame with SHAP values

---

visualize_rules	<i>Visualize Association Rules</i>
-----------------	------------------------------------

---

**Description**

Create visualizations of association rules

**Usage**

```
visualize_rules(rules_obj, method = "scatter", top_n = 50, ...)
```

**Arguments**

rules_obj	A tidy_apriori object, rules object, or rules tibble
method	Visualization method: "scatter" (default), "graph", "grouped", "paracoord"
top_n	Number of top rules to visualize (default: 50)
...	Additional arguments passed to plot() for rules visualization

**Value**

Visualization (side effect) or ggplot object

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