

# Package ‘scClassifR’

October 14, 2021

**Type** Package

**Title** Pretrained learning models for cell type prediction on single cell RNA-sequencing data

**Version** 1.0.0

**Description** The package comprises a set of pretrained machine learning models to predict basic immune cell types. This enables all users to quickly get a first annotation of the cell types present in their dataset without requiring prior knowledge. scClassifR also allows users to train their own models to predict new cell types based on specific research needs.

**License** MIT + file LICENSE

**Encoding** UTF-8

**biocViews** SingleCell, Transcriptomics, GeneExpression, SupportVectorMachine, Classification, Software

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**Suggests** knitr, scRNAseq, testthat

**VignetteBuilder** knitr

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cell_type	<i>cell_type</i>
-----------	------------------

---

**Description**

Returns the cell type for the given classifier.

**Usage**

```
cell_type(classifier)
```

**Arguments**

classifier     `scClassifR` object

**Value**

cell type of object

`cell_type<-`

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### Examples

```
data("tirosh_mel80_example")
selected_features_B = c("CD19", "MS4A1", "CD79A")
set.seed(123)
clf_b <- train_classifier(train_obj = tirosh_mel80_example,
cell_type = "B cells", features = selected_features_B)
cell_type(clf_b)
```

---

`cell_type<-`                      *Setter for cell\_type Change cell type for a classifier*

---

### Description

Setter for cell\_type Change cell type for a classifier

### Usage

```
cell_type(classifier) <- value
```

### Arguments

`classifier`        scClassifR object. The object is returned from the `train_classifier` function.  
`value`             the new cell type

### Value

scClassifR object with the new cell type.

### Examples

```
data("tirosh_mel80_example")
selected_features_B = c("CD19", "MS4A1", "CD79A")
set.seed(123)
clf_b <- train_classifier(train_obj = tirosh_mel80_example,
features = selected_features_B, cell_type = "B cells")
cell_type(clf_b) <- "B cell"
```

---

checkObjectValidity    *Internal functions of scClassifR package*

---

### Description

Check if a scClassifR object is valid  
Filter cells from ambiguous chars and non applicable cells in a [Seurat](#) object  
Filter cells from ambiguous chars and non applicable cells in a [SingleCellExperiment](#) object  
Construct a uniform tag vector for all forms of labels in a [Seurat](#) object  
Construct a uniform tag vector for all forms of labels in a [SingleCellExperiment](#) object  
Process parent classifier in a [Seurat](#) object  
Process parent classifier in a [SingleCellExperiment](#) object

### Usage

```
checkObjectValidity(object)  
  
checkCellTypeValidity(cell_type)  
  
checkFeaturesValidity(features)  
  
checkParentValidity(parent)  
  
checkPThresValidity(p_thres)  
  
checkClassifierValidity(clf)  
  
parent(classifier) <- value  
  
clf(classifier) <- value  
  
features(classifier) <- value  
  
balance_dataset(mat, tag)  
  
train_func(mat, tag)  
  
transform_to_zscore(mat)  
  
load_models(path_to_models)  
  
select_features(mat, features)  
  
check_parent_child_coherence(  
  obj,
```

```
    pos_parent,  
    parent_cell,  
    cell_type,  
    target_cell_type,  
    ...  
)  
  
filter_cells(obj, tag_slot)  
  
## S4 method for signature 'Seurat'  
filter_cells(obj, tag_slot)  
  
## S4 method for signature 'SingleCellExperiment'  
filter_cells(obj, tag_slot)  
  
construct_tag_vect(obj, cell_type, ...)  
  
## S4 method for signature 'Seurat'  
construct_tag_vect(obj, cell_type, tag_slot)  
  
## S4 method for signature 'SingleCellExperiment'  
construct_tag_vect(obj, cell_type, tag_slot)  
  
process_parent_clf(  
  obj,  
  parent_tag_slot,  
  parent_cell_type,  
  parent_clf,  
  path_to_models,  
  zscore = TRUE,  
  ...  
)  
  
## S4 method for signature 'Seurat'  
process_parent_clf(  
  obj,  
  parent_tag_slot,  
  parent_cell_type,  
  parent_clf,  
  path_to_models,  
  zscore = TRUE,  
  seurat_assay,  
  seurat_slot,  
  ...  
)  
  
## S4 method for signature 'SingleCellExperiment'  
process_parent_clf(  
  obj,  
  parent_tag_slot,  
  parent_cell_type,  
  parent_clf,  
  path_to_models,  
  zscore = TRUE,  
  seurat_assay,  
  seurat_slot,  
  ...  
)
```

```

    obj,
    parent_tag_slot,
    parent_cell_type,
    parent_clf,
    path_to_models,
    zscore = TRUE,
    sce_assay,
    ...
)

make_prediction(mat, classifier, pred_cells, ignore_ambiguous_result = TRUE)

simplify_prediction(meta.data, mat, classifiers)

verify_parent(mat, classifier, meta.data)

test_performance(mat, classifier, tag)

```

### Arguments

object	The request classifier to check.
cell_type	name of cell type
features	list of selected features
parent	Classifier parent to check.
p_thres	Classifier probability threshold to check.
clf	Classifier to check.
classifier	classifier
value	the new classifier
mat	expression matrix
tag	tag of data
path_to_models	path to databases, or by default
obj	object
pos_parent	a vector indicating parent clf prediction
parent_cell	name of parent cell type
target_cell_type	alternative cell types (in case of testing clf)
...	arguments passed to other methods
tag_slot	tag slot in <a href="#">SingleCellExperiment</a> object indicating cell type
parent_tag_slot	string, name of annotation tag slot in object indicating pre-assigned/predicted parent cell type
parent_cell_type	name of parent cell type

parent_clf	scClassifR object corresponding to classification model for the parent cell type
zscore	boolean indicating the transformation of gene expression in object to zscore or not
seurat_assay	name of assay to use in Seurat object
seurat_slot	type of expression data to use in Seurat object
sce_assay	name of assay to use in SingleCellExperiment object
pred_cells	a whole prediction for all cells
ignore_ambiguous_result	whether ignore ambiguous result
meta.data	object meta data
classifiers	classifiers

**Value**

TRUE if the classifier is valid or the reason why it is not  
 TRUE if the cell type is valid or the reason why it is not.  
 TRUE if the features is valid or the reason why it is not.  
 TRUE if the parent is valid or the reason why it is not.  
 TRUE if the p\_thres is valid or the reason why it is not.  
 TRUE if the classifier is valid or the reason why it is not.  
 scClassifR object with the new parent.  
 scClassifR object with the new trained classifier.  
 scClassifR object with the new features.  
 a list of balanced count matrix and corresponding tags of balanced count matrix  
 the classification model (caret object)  
 row wise center-scaled count matrix  
 list of classifiers  
 filtered matrix  
 list of adjusted object and adjusted tag slot  
 adjusted Seurat object  
 adjusted SingleCellExperiment object  
 a binary vector for cell tag  
 list of cells which are positive to parent clf  
 prediction  
 simplified prediction  
 applicable matrix  
 clf performance

---

check\_parent\_child\_coherence,Seurat-method  
*Internal functions of scClassifR package*

---

### Description

Check label coherence in parent and child cell type in a [Seurat](#) object.

Check label coherence in parent and child cell type in a [SingleCellExperiment](#) object

### Usage

```
## S4 method for signature 'Seurat'
check_parent_child_coherence(
  obj,
  pos_parent,
  parent_cell,
  cell_type,
  target_cell_type,
  tag_slot
)

## S4 method for signature 'SingleCellExperiment'
check_parent_child_coherence(
  obj,
  pos_parent,
  parent_cell,
  cell_type,
  target_cell_type,
  tag_slot
)
```

### Arguments

obj	object
pos_parent	a vector indicating parent clf prediction
parent_cell	name of parent cell type
cell_type	name of cell type
target_cell_type	alternative cell types (in case of testing clf)
tag_slot	tag slot in <a href="#">SingleCellExperiment</a> object indicating cell type

### Value

TRUE if the classifier is valid or the reason why it is not

TRUE if the cell type is valid or the reason why it is not.



TRUE if the features is valid or the reason why it is not.  
 TRUE if the parent is valid or the reason why it is not.  
 TRUE if the p\_thres is valid or the reason why it is not.  
 TRUE if the classifier is valid or the reason why it is not.  
 scClassifR object with the new parent.  
 scClassifR object with the new trained classifier.  
 scClassifR object with the new features.  
 a list of balanced count matrix and corresponding tags of balanced count matrix  
 the classification model (caret object)  
 row wise center-scaled count matrix  
 list of classifiers  
 filtered matrix  
 list of adjusted object and adjusted tag slot  
 adjusted [Seurat](#) object  
 adjusted [SingleCellExperiment](#) object  
 a binary vector for cell tag  
 list of cells which are positive to parent clf  
 prediction  
 simplified prediction  
 applicable matrix  
 clf performance

---

 classify\_cells

*Classify cells from multiple models*


---

### Description

Classify cells from multiple models

### Usage

```

classify_cells(
  classify_obj,
  classifiers = NULL,
  cell_types = "all",
  path_to_models = c("default", "."),
  ignore_ambiguous_result = FALSE,
  ...
)
  
```

```

## S4 method for signature 'Seurat'
classify_cells(
  classify_obj,
  classifiers = NULL,
  cell_types = "all",
  path_to_models = c("default", "."),
  ignore_ambiguous_result = FALSE,
  seurat_assay = "RNA",
  seurat_slot = "counts",
  ...
)

## S4 method for signature 'SingleCellExperiment'
classify_cells(
  classify_obj,
  classifiers = NULL,
  cell_types = "all",
  path_to_models = c("default", "."),
  ignore_ambiguous_result = FALSE,
  sce_assay = "logcounts",
  ...
)

```

### Arguments

<code>classify_obj</code>	the object containing cells to be classified
<code>classifiers</code>	list of classification models. The model is obtained from <code>train_classifier</code> function or available in current working space. Users may test the model using <code>test_classifier</code> before using this function. If classifiers contain classifiers for sub cell types, classifiers for parent cell type must be indicated first in order to be applied before children classifiers. If classifiers is NULL, the method will use all classifiers in database.
<code>cell_types</code>	list of cell types containing models to be used for classification, only applicable if the models have been saved to package.
<code>path_to_models</code>	path to the folder containing the list of models. As default value, the pretrained models in the package will be used. If user has trained new models, indicate the folder containing the <code>new_models.rda</code> file.
<code>ignore_ambiguous_result</code>	return all ambiguous predictions (multiple cell types) to empty. When this parameter turns to TRUE, most probably predicted cell types will be ignored.
<code>...</code>	arguments passed to other methods
<code>seurat_assay</code>	name of assay to use in <code>Seurat</code> object, defaults to 'RNA' assay.
<code>seurat_slot</code>	type of expression data to use in <code>Seurat</code> object. Some available types are: "counts", "data" and "scale.data". Default to "counts", which is unnormalized data.
<code>sce_assay</code>	name of assay to use in <code>SingleCellExperiment</code> object, defaults to 'logcounts' assay.

**Value**

the input object with new slots in cells meta data New slots are: predicted\_cell\_type, most\_probable\_cell\_type, slots in form of [cell\_type]\_p and [cell\_type]\_class

**Examples**

```
# load small example dataset
data("tirosh_mel80_example")

# train one classifier for one cell type, for ex, B cell
# define genes to use to classify this cell type
selected_features_B = c("CD19", "MS4A1", "CD79A")

# train the classifier
set.seed(123)
clf_b <- train_classifier(train_obj = tirosh_mel80_example,
  features = selected_features_B, cell_type = "B cells")

# do the same thing with other cell types, for example, T cells
selected_features_T = c("CD4", "CD8A", "CD8B")
set.seed(123)
clf_t <- train_classifier(train_obj = tirosh_mel80_example,
  features = selected_features_T, cell_type = "T cells")

# create a list of classifiers
classifier_ls <- list(clf_b, clf_t)

# classify cells with list of classifiers
seurat.obj <- classify_cells(classify_obj = tirosh_mel80_example,
  classifiers = classifier_ls)
```

---

clf

*clf*


---

**Description**

Returns the classifier of the [scClassifR](#) object

**Usage**

```
clf(classifier)
```

**Arguments**

classifier      [scClassifR](#) object

**Value**

Classifier is the object returned by caret SVM learning process. More information about the caret package: <https://topepo.github.io/caret/>

**Examples**

```
data("tirosh_mel80_example")
selected_features_B = c("CD19", "MS4A1", "CD79A")
set.seed(123)
clf_b <- train_classifier(train_obj = tirosh_mel80_example,
  features = selected_features_B, cell_type = "B cells")
clf(clf_b)
```

---

default_models	<i>Pretrained classifiers for human cells</i>
----------------	---

---

**Description**

Pretrained classifier obtained by training Sade-Feldman dataset and testing on Jerby-Arnon dataset.

**Usage**

```
default_models
```

**Format**

a list of `scClassifR` objects

**Author(s)**

Vy Nguyen, November 2020

---

delete_model	<i>Delete model/branch from package</i>
--------------	---

---

**Description**

Delete model/branch from package

**Usage**

```
delete_model(cell_type, path.to.models = ".")
```

**Arguments**

`cell_type` string indicating the cell type of which the model will be removed from package  
Attention: deletion of a parent model will also delete all of child model.

`path.to.models` path to the folder containing the list of models in which the to-be-deleted model is.

**Value**

no return value, but the model is deleted from database

**Examples**

```
# load small example dataset
data("tirosh_mel80_example")

# train a classifier
set.seed(123)
selected_features_T = c("CD4", "CD8A", "CD8B")
clf_t <- train_classifier(train_obj = tirosh_mel80_example,
  features = selected_features_T, cell_type = "t cells")

# save a classifier to system
save_new_model(new_model = clf_t)

# delete classifier from system
delete_model("t cells")
```

---

features	<i>features</i>
----------	-----------------

---

**Description**

Returns the set of features for the given classifier.

**Usage**

```
features(classifier)
```

**Arguments**

`classifier` scClassifR object

**Value**

Applied features of object

### Examples

```
data("tirosh_mel80_example")
selected_features_B = c("CD19", "MS4A1", "CD79A")
set.seed(123)
clf_b <- train_classifier(train_obj = tirosh_mel80_example,
  features = selected_features_B, cell_type = "B cells")
features(clf_b)
```

---

parent

*parent*

---

### Description

Returns the parent of the cell type corresponding to the given classifier.

### Usage

```
parent(classifier)
```

### Arguments

classifier      scClassifR object

### Value

Parent model of object

### Examples

```
data("tirosh_mel80_example")
selected_features_B = c("CD19", "MS4A1", "CD79A")
set.seed(123)
clf_b <- train_classifier(train_obj = tirosh_mel80_example,
  features = selected_features_B, cell_type = "B cells")
parent(clf_b)
```

---

plant_tree	<i>Plant tree from list of models</i>
------------	---------------------------------------

---

**Description**

Plant tree from list of models

**Usage**

```
plant_tree(models.file.path = c("default", "."))
```

**Arguments**

models.file.path  
list of models. If not provided, list of default pretrained models in the package will be used.

**Value**

tree structure and plot of tree

**Examples**

```
# to create the tree of classifiers  
# (in this example, based on default classifiers)  
plant_tree()
```

---

plot_roc_curve	<i>Plot roc curve</i>
----------------	-----------------------

---

**Description**

Plot roc curve

**Usage**

```
plot_roc_curve(test_result)
```

**Arguments**

test\_result     result of test\_classifier function

**Value**

ggplot2 roc curve

**Examples**

```
# load small example dataset
data("tirosh_mel80_example")

# train a classifier, for ex: B cell
selected_features_B = c("CD19", "MS4A1", "CD79A")
set.seed(123)
clf_b <- train_classifier(train_obj = tirosh_mel80_example,
  features = selected_features_B, cell_type = "B cells")

clf_b_test <- test_classifier(test_obj = tirosh_mel80_example,
  classifier = clf_b)

# run plot curve on the test result
roc_curve <- plot_roc_curve(test_result = clf_b_test)
```

---

*p\_thres*

*p\_thres*

---

**Description**

Returns the probability threshold for the given classifier.

**Usage**

```
p_thres(classifier)
```

**Arguments**

*classifier*      scClassifR object

**Value**

Predicting probability threshold of object

**Examples**

```
data("tirosh_mel80_example")
selected_features_B = c("CD19", "MS4A1", "CD79A")
set.seed(123)
clf_b <- train_classifier(train_obj = tirosh_mel80_example,
  features = selected_features_B, cell_type = "B cells")
p_thres(clf_b)
```



---

p\_thres<-                      *Setter for predicting probability threshold*

---

**Description**

Setter for predicting probability threshold

**Usage**

```
p_thres(classifier) <- value
```

**Arguments**

`classifier`      scClassifR object. The object is returned from the `train_classifier` function.  
`value`            the new threshold

**Value**

scClassifR object with the new threshold.

**Examples**

```
data("tirosh_mel80_example")
selected_features_B = c("CD19", "MS4A1", "CD79A")
set.seed(123)
clf_b <- train_classifier(train_obj = tirosh_mel80_example,
  features = selected_features_B, cell_type = "B cells")
clf_b_test <- test_classifier(test_obj = tirosh_mel80_example,
  classifier = clf_b)
# assign a new threshold probability for prediction
p_thres(clf_b) <- 0.4
```

---

save\_new\_model                      *Save a model to the package*

---

**Description**

Save a model to the package

**Usage**

```
save_new_model(new_model, include.default = TRUE, path.to.models = ".")
```

**Arguments**

`new_model` new model to be added into the classification tree

`include.default` whether include the default models of the package in the list of new trained models or not. If users further want to classify cells, they can only use default pretrained model list or their new model list. Including default models in new trained models helps users using both of them once. In addition, default pretrained models of the package cannot be changed or removed. This can be done with the new trained model list.

`path.to.models` path to the folder containing the list of new models.

**Value**

no return value, but the model is now saved to database

**Examples**

```
# load small example dataset
data("tirosh_mel80_example")

# train classifier
selected_features_T = c("CD4", "CD8A", "CD8B")
set.seed(123)
clf_t <- train_classifier(train_obj = tirosh_mel80_example,
  features = selected_features_T, cell_type = "t cells")

# save the trained classifier to system
# (test classifier can be used before this step)
save_new_model(new_model = clf_t, path.to.models = ".")

# verify if new model has been saved
print(names(load("./new_models.rda")))
delete_model("t cells")
```

---

scClassifR

*scClassifR class.*

---

**Description**

This class is returned by the `train_classifier` function. Generally, scClassifR objects are never created directly.

**Usage**

```
scClassifR(cell_type, clf, features, p_thres, parent)
```

```
scClassifR(cell_type, clf, features, p_thres, parent)
```

**Arguments**

cell_type	character. Name of the cell type.
clf	list. Trained model returned by caret train function.
features	vector/character containing features used for the training.
p_thres	numeric. Probability threshold for the cell type to be assigned for a cell.
parent	character. Parent cell type.

**Value**

A scClassifR object.

**Slots**

cell_type	character. Name of the cell type.
clf	list. Trained model returned by caret train function.
features	vector/character containing features used for the training.
p_thres	numeric. Probability threshold for the cell type to be assigned for a cell.
parent	character. Parent cell type.

**Examples**

```
# load small example dataset
data("tirosh_mel180_example")

# train a classifier, for ex: B cell
selected_features_B = c("CD19", "MS4A1", "CD79A")
set.seed(123)
clf_b <- train_classifier(train_obj = tirosh_mel180_example,
                          features = selected_features_B, cell_type = "B cells")

clf_b
```

---

show,scClassifR-method

*Show object*

---

**Description**

Show object

**Usage**

```
## S4 method for signature 'scClassifR'
show(object)
```

**Arguments**

object            scClassifR object

**Value**

print to console information about the object

**Examples**

```
data("tirosh_mel180_example")
selected_features_B = c("CD19", "MS4A1", "CD79A")
set.seed(123)
clf_b <- train_classifier(train_obj = tirosh_mel180_example,
  features = selected_features_B, cell_type = "B cells")
clf_b
```

---

test_classifier	<i>Testing process.</i>
-----------------	-------------------------

---

**Description**

Testing process.

**Usage**

```
test_classifier(
  test_obj,
  classifier,
  target_cell_type = NULL,
  parent_clf = NULL,
  path_to_models = c("default", "."),
  zscore = TRUE,
  ...
)

## S4 method for signature 'Seurat,scClassifR'
test_classifier(
  test_obj,
  classifier,
  target_cell_type = NULL,
  parent_clf = NULL,
  path_to_models = c("default", "."),
  zscore = TRUE,
  seurat_tag_slot = "active.ident",
  seurat_parent_tag_slot = "predicted_cell_type",
  seurat_assay = "RNA",
```

```

    seurat_slot = "counts",
    ...
)

## S4 method for signature 'SingleCellExperiment,scClassifR'
test_classifier(
  test_obj,
  classifier,
  target_cell_type = NULL,
  parent_clf = NULL,
  path_to_models = c("default", "."),
  zscore = TRUE,
  sce_tag_slot = "ident",
  sce_parent_tag_slot = "predicted_cell_type",
  sce_assay = "logcounts",
  ...
)

```

### Arguments

test_obj	xxobject that can be used for testing
classifier	classification model
target_cell_type	vector indicating other cell types than cell labels that can be considered as the main cell type in classifier, for example, c("plasma cell", "b cell", "b cells", "activating b cell"). Default as NULL.
parent_clf	<a href="#">scClassifR</a> object corresponding to classification model for the parent cell type
path_to_models	path to the folder containing the list of models. As default, the pretrained models in the package will be used. If user has trained new models, indicate the folder containing the new_models.rda file.
zscore	boolean, whether gene expression is transformed to zscore
...	arguments passed to other methods
seurat_tag_slot	string, name of annotation slot indicating cell tag/label in the testing object. Strings indicating cell types are expected in this slot. For <a href="#">Seurat</a> object, default value is "active.ident". Expected values is string or binary/logical, 0/"no"/F/FALSE: not being new cell type, 1/"yes"/T/TRUE: being new cell type.
seurat_parent_tag_slot	string, name of tag slot in cell meta data indicating pre-assigned/predicted parent cell type. Default field is "predicted_cell_type". The slot must contain only string values.
seurat_assay	name of assay to use in <a href="#">Seurat</a> object, defaults to 'RNA' assay.
seurat_slot	type of expression data to use in <a href="#">Seurat</a> object. Some available types are: "counts", "data" and "scale.data". Default to "counts", which contains unnormalized data.

sce_tag_slot	string, name of annotation slot indicating cell tag/label in the testing object. Strings indicating cell types are expected in this slot. Default value is "ident". Expected values are string or binary/logical, 0/"no"/F/FALSE: not being new cell type, 1/"yes"/T/TRUE: being new cell type.
sce_parent_tag_slot	string, name of tag slot in cell meta data indicating pre-assigned/predicted parent cell type. Default is "predicted_cell_type". The slot must contain only string values.
sce_assay	name of assay to use in <a href="#">SingleCellExperiment</a> object, defaults to 'logcounts' assay.

**Value**

result of testing process in form of a list, including predicted values, prediction accuracy at a probability threshold, and roc curve information.

**Note**

Only one cell type is expected for each cell. Ambiguous cell type, such as: "T cells/NK cells/ILC", will be ignored. Subtypes used in testing model for parent cell types can be indicated as parent cell type, or can be indicated in target\_cell\_type. For example, when testing for B cells, plasma cells can be annotated as B cells, or target\_cell\_type is set c("plasma cells").

**Examples**

```
# load small example dataset
data("tirosh_mel80_example")

# train the classifier
selected_features_B = c("CD19", "MS4A1", "CD79A")
set.seed(123)
clf_b <- train_classifier(train_obj = tirosh_mel80_example,
  features = selected_features_B, cell_type = "B cells")

# test the classifier, target cell type can be in other formats or
# alternative cell type that can be considered as the classified cell type
clf_b_test <- test_classifier(test_obj = tirosh_mel80_example,
  classifier = clf_b, target_cell_type = c("B cell"))
clf_b_test
```

---

tirosh\_mel80\_example *A Seurat Object Sample*

---

**Description**

A Seurat object sample was made from the dataset GSE72056, samples corresponding to patient CY80.

**Usage**

```
tirosh_mel180_example
```

**Format**

a [Seurat](#) object

**Author(s)**

Itay Tirosh, 2016-04-05

**Source**

WEIZMANN INSTITUTE OF SCIENCE

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train_classifier	<i>Train cell type classifier</i>
------------------	-----------------------------------

---

**Description**

Train a classifier for a new cell type. If cell type has a parent, only available for [scClassifR](#) object as parent cell classifying model.

**Usage**

```
train_classifier(  
  train_obj,  
  cell_type,  
  features,  
  parent_cell = NA_character_,  
  parent_clf = NULL,  
  path_to_models = c("default", "."),  
  zscore = TRUE,  
  balance = TRUE,  
  ...  
)  
  
## S4 method for signature 'Seurat'  
train_classifier(  
  train_obj,  
  cell_type,  
  features,  
  parent_cell = NA_character_,  
  parent_clf = NULL,  
  path_to_models = c("default", "."),  
  zscore = TRUE,  
  balance = TRUE,
```

```

seurat_tag_slot = "active.ident",
seurat_parent_tag_slot = "predicted_cell_type",
seurat_assay = "RNA",
seurat_slot = "counts",
...
)

## S4 method for signature 'SingleCellExperiment'
train_classifier(
  train_obj,
  cell_type,
  features,
  parent_cell = NA_character_,
  parent_clf = NULL,
  path_to_models = c("default", "."),
  zscore = TRUE,
  balance = TRUE,
  sce_tag_slot = "ident",
  sce_parent_tag_slot = "predicted_cell_type",
  sce_assay = "logcounts",
  ...
)

```

### Arguments

train_obj	object that can be used for training the new model. <a href="#">Seurat</a> object or <a href="#">SingleCellExperiment</a> object is expected. If the training model has parent, parent_tag_slot may have been indicated. This field would have been filled out automatically if user precedently run classify_cells function. If no (predicted) cell type annotation provided, the function can be run if 1- parent_cell or 2- parent_clf is provided.
cell_type	string indicating the name of the subtype This must exactly match cell tag/label if cell tag/label is a string.
features	list of features used for the new training model
parent_cell	string indicated the name of the parent cell type, if parent cell type classifier has already been saved in model database. Adjust path_to_models for exact database.
parent_clf	classification model for the parent cell type
path_to_models	path to the folder containing the model database. As default, the pretrained models in the package will be used. If user has trained new models, indicate the folder containing the new_models.rda file.
zscore	whether gene expression in train_obj is transformed to zscore
balance	whether applying balancing on training set before training
...	arguments passed to other methods
seurat_tag_slot	string, name of slot in cell meta data indicating cell tag/label in the training object. Strings indicating cell types are expected in this slot. For <a href="#">Seurat</a> ob-



	ject, default value is "active.ident". Expected values are string or binary/logical, 0/"no"/F/FALSE: not being new cell type, 1/"yes"/T/TRUE: being new cell type.
seurat_parent_tag_slot	string, name of a slot in cell meta data indicating assigned/predicted cell type. Default is "predicted_cell_type". This slot would have been filled automatically if user have called <code>classify_cells</code> function. The slot must contain only string values.
seurat_assay	name of assay to use in training object. Default to 'RNA' assay.
seurat_slot	type of expression data to use in training object. For <code>Seurat</code> object, available types are: "counts", "data" and "scale.data". Default to "counts", which contains unnormalized data.
sce_tag_slot	string, name of annotation slot indicating cell tag/label in the training object. For <code>SingleCellExperiment</code> object, default value is "ident". Expected values are string or binary/logical, 0/"no"/F/FALSE: not being new cell type, 1/"yes"/T/TRUE: being new cell type.
sce_parent_tag_slot	string, name of a slot in cell meta data indicating pre-assigned/predicted cell type. Default field is "predicted_cell_type". This field would have been filled automatically when user called <code>classify_cells</code> function. The slot must contain only string values.
sce_assay	name of assay to use in training object. Default to 'logcounts' assay.

**Value**

`scClassifR` object

**Note**

Only one cell type is expected for each cell in object. Ambiguous cell type, such as: "T cells/NK cells/ILC", will be ignored from training. Subtypes used in training model for parent cell types must be indicated as parent cell type. For example, when training for B cells, plasma cells must be annotated as B cells in order to be used.

**Examples**

```
# load small example dataset
data("tirosh_mel180_example")

# this dataset already contains pre-defined cell labels
table(Seurat::Idents(tirosh_mel180_example))

# define genes to use to classify this cell type (B cells in this example)
selected_features_B = c("CD19", "MS4A1", "CD79A")

# train the classifier, the "cell_type" argument must match
# the cell labels in the data, except upper/lower case
set.seed(123)
clf_b <- train_classifier(train_obj = tirosh_mel180_example,
features = selected_features_B, cell_type = "b cells")
```

```
# classify cell types using B cell classifier,
# a test classifier process may be used before applying the classifier
tirosh_mel80_example <- classify_cells(classify_obj = tirosh_mel80_example,
classifiers = c(clf_b))

# tag all cells that are plasma cells (random example here)
tirosh_mel80_example[['plasma_cell_tag']] <- c(rep(1, 80), rep(0, 400))

# set new features for the subtype
p_features = c("SDC1", "CD19", "CD79A")

# train the classifier, the "B cell" classifier is used as parent.
# This means, only cells already classified as "B cells" will be evaluated.
# the "tag_slot" parameter tells the classifier to use this cell meta data
# for the training process.
set.seed(123)
plasma_clf <- train_classifier(train_obj = tirosh_mel80_example,
cell_type = "Plasma cell", features = p_features, parent_clf = clf_b,
seurat_tag_slot = 'plasma_cell_tag')
```

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