

# Package ‘SingleR’

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**Title** Reference-Based Single-Cell RNA-Seq Annotation

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**Description** Performs unbiased cell type recognition from single-cell RNA sequencing data, by leveraging reference transcriptomic datasets of pure cell types to infer the cell of origin of each single cell independently.

**License** GPL-3 + file LICENSE

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**Author** Dvir Aran [aut, cph],  
 Aaron Lun [ctb, cre],  
 Daniel Bunis [ctb],  
 Jared Andrews [ctb],  
 Friederike Dündar [ctb]

**Maintainer** Aaron Lun <infinite.monkeys.with.keyboards@gmail.com>

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---

.mockRefData	<i>Mock data for examples</i>
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---

### Description

Make up some test and reference data for the various examples in the **SingleR** package.

### Usage

```
.mockRefData(ngroups = 5, nreps = 4, ngenes = 1000, prop = 0.5)
.mockTestData(mock.ref, ncells = 100)
```

### Arguments

ngroups	Integer scalar specifying the number of groups.
nreps	Integer scalar specifying the number of replicates per group.
ngenes	Integer scalar specifying the number of genes in the dataset.
prop	Numeric scalar specifying the proportion of genes that are DE between groups.

mock.ref        A [SummarizedExperiment](#) object produced by `.mockRefData`.  
ncells         Integer scalar specifying the number of cells to simulate.

### Details

This functions are simply provided to simulate some data in the Examples of the documentation. The simulations are very simple and should not be used for performance comparisons.

### Value

Both functions return a [SummarizedExperiment](#) object containing simulated counts in the counts assay, with the group assignment of each sample in the "label" field of the `colData`.

### Author(s)

Aaron Lun

### Examples

```
ref <- .mockRefData()
test <- .mockTestData(ref)
```

---

aggregateReference     *Aggregate reference samples*

---

### Description

Aggregate reference samples for a given label by averaging their count profiles. This can be done with varying degrees of resolution to preserve the within-label heterogeneity.

### Usage

```
aggregateReference(  
  ref,  
  labels,  
  ncenters = NULL,  
  power = 0.5,  
  ntop = 1000,  
  assay.type = "logcounts",  
  rank = 20,  
  subset.row = NULL,  
  check.missing = TRUE,  
  BPPARAM = SerialParam(),  
  BSPARAM = bsparam()  
)
```

## Arguments

ref	A numeric matrix of reference expression values, usually containing log-expression values. Alternatively, a <a href="#">SummarizedExperiment</a> object containing such a matrix.
labels	A character vector or factor of known labels for all cells in ref.
ncenters	Integer scalar specifying the maximum number of aggregated profiles to produce for each label.
power	Numeric scalar between 0 and 1 indicating how much aggregation should be performed, see Details.
ntop	Integer scalar specifying the number of highly variable genes to use for the PCA step.
assay.type	An integer scalar or string specifying the assay of ref containing the relevant expression matrix, if ref is a <a href="#">SummarizedExperiment</a> object.
rank	Integer scalar specifying the number of principal components to use during clustering.
subset.row	Integer, character or logical vector indicating the rows of ref to use for k-means clustering.
check.missing	Logical scalar indicating whether rows should be checked for missing values (and if found, removed).
BPPARAM	A <a href="#">BiocParallelParam</a> object indicating how parallelization should be performed.
BSPARAM	A <a href="#">BiocSingularParam</a> object indicating which SVD algorithm should be used in <a href="#">runPCA</a> .

## Details

With single-cell reference datasets, it is often useful to aggregate individual cells into pseudo-bulk samples to serve as a reference. This improves speed in downstream assignment with [classifySingleR](#) or [SingleR](#). The most obvious aggregation is to simply average all counts for all cells in a label to obtain a single pseudo-bulk profile. However, this discards information about the within-label heterogeneity (e.g., the “shape” and spread of the population in expression space) that may be informative for assignment, especially for closely related labels.

The default approach in this function is to create a series of pseudo-bulk samples to represent each label. This is achieved by performing vector quantization via k-means clustering on all cells in a particular label. Cells in each cluster are subsequently averaged to create one pseudo-bulk sample that serves as a representative for that location in the expression space. This reduces the number of separate observations (for speed) while preserving some level of population heterogeneity (for fidelity).

The number of pseudo-bulk samples per label is controlled by `ncenters`. By default, we set the number of clusters to  $X^{\text{power}}$  where  $X$  is the number of cells for that label. This ensures that labels with more cells have more resolved representatives. If `ncenters` is greater than the number of samples for a label and/or `power=1`, no aggregation is performed. Setting `power=0` will aggregate all cells of a label into a single pseudo-bulk profile.

In practice, k-means clustering is actually performed on the first rank principal components as computed using [runPCA](#). The use of PCs compacts the data for more efficient operation of [kmeans](#); it

also removes some of the high-dimensional noise to highlight major factors of within-label heterogeneity. Note that the PCs are only used for clustering and the full expression profiles are still used for the final averaging. Users can disable the PCA step by setting `rank=Inf`.

By default, we speed things up by only using the top `ntop` genes with the largest variances in the PCA. More subsetting of the matrix prior to the PCA can be achieved by setting `subset.row` to an appropriate indexing vector. This option may be useful for clustering based on known genes of interest but retaining all genes in the aggregated results. (If both options are set, subsetting by `subset.row` is done first, and then the top `ntop` genes are selected.) In both cases, though, the aggregation is performed on the full expression profiles.

We use the average rather than the sum in order to be compatible with `trainSingleR`'s internal marker detection. Moreover, unlike counts, the sum of transformed and normalized expression values generally has little meaning. We do not use the median to avoid consistently obtaining zeros for lowly expressed genes.

### Value

A `SummarizedExperiment` object with a "logcounts" assay containing a matrix of aggregated expression values, and a label column metadata field specifying the label corresponding to each column.

### Author(s)

Aaron Lun

### Examples

```
library(scuttle)
sce <- mockSCE()
sce <- logNormCounts(sce)

# Making up some labels for demonstration purposes:
labels <- sample(LETTERS, ncol(sce), replace=TRUE)

# Aggregation at different resolutions:
(aggr <- aggregateReference(sce, labels, power=0.5))

(aggr <- aggregateReference(sce, labels, power=0))

# No aggregation:
(aggr <- aggregateReference(sce, labels, power=1))
```

---

classifySingleR

*Classify cells with SingleR*

---

### Description

Assign labels to each cell in a test dataset, using a pre-trained classifier combined with an iterative fine-tuning approach.

**Usage**

```

classifySingleR(
  test,
  trained,
  quantile = 0.8,
  fine.tune = TRUE,
  tune.thresh = 0.05,
  sd.thresh = NULL,
  prune = TRUE,
  assay.type = "logcounts",
  check.missing = TRUE,
  BPPARAM = SerialParam()
)

```

**Arguments**

<code>test</code>	A numeric matrix of single-cell expression values where rows are genes and columns are cells. Alternatively, a <a href="#">SummarizedExperiment</a> object containing such a matrix.
<code>trained</code>	A <a href="#">List</a> containing the output of the <a href="#">trainSingleR</a> function. Alternatively, a List of Lists produced by <a href="#">trainSingleR</a> for multiple references.
<code>quantile</code>	A numeric scalar specifying the quantile of the correlation distribution to use to compute the score for each label.
<code>fine.tune</code>	A logical scalar indicating whether fine-tuning should be performed.
<code>tune.thresh</code>	A numeric scalar specifying the maximum difference from the maximum correlation to use in fine-tuning.
<code>sd.thresh</code>	A numeric scalar specifying the threshold on the standard deviation, for use in gene selection during fine-tuning. This is only used if <code>genes="sd"</code> when constructing <code>trained</code> and defaults to the value used in <a href="#">trainSingleR</a> .
<code>prune</code>	A logical scalar indicating whether label pruning should be performed.
<code>assay.type</code>	Integer scalar or string specifying the matrix of expression values to use if <code>test</code> is a <a href="#">SummarizedExperiment</a> .
<code>check.missing</code>	Logical scalar indicating whether rows should be checked for missing values (and if found, removed).
<code>BPPARAM</code>	A <a href="#">BiocParallelParam</a> object specifying the parallelization scheme to use.

**Details**

Consider each cell in the test set `test` and each label in the training set. We compute Spearman's rank correlations between the test cell and all cells in the training set with the given label, based on the expression profiles of the genes selected by `trained`. The score is defined as the quantile of the distribution of correlations, as specified by `quantile`. (Technically, we avoid explicitly computing all correlations by using a nearest neighbor search, but the resulting score is the same.) After repeating this across all labels, the label with the highest score is used as the prediction for that cell. If `fine.tune=TRUE`, an additional fine-tuning step is performed for each cell to improve resolution. We identify all labels with scores that are no more than `tune.thresh` below the maximum score.

These labels are used to identify a fresh set of marker genes, and the calculation of the score is repeated using only these genes. The aim is to refine the choice of markers and reduce noise when distinguishing between closely related labels. The best and next-best scores are reported in the output for use in diagnostics, e.g., [pruneScores](#).

The default `assay.type` is set to "logcounts" simply for consistency with [trainSingleR](#). In practice, the raw counts (for UMI data) or the transcript counts (for read count data) can also be used without normalization and log-transformation. Any monotonic transformation will have no effect the calculation of the correlation values other than for some minor differences due to numerical precision.

If `prune=TRUE`, label pruning is performed as described in [pruneScores](#) with default arguments. This aims to remove low-quality labels that are ambiguous or correspond to misassigned cells. However, the default settings can be somewhat aggressive and discard otherwise useful labels in some cases - see [?pruneScores](#) for details.

If `trained` was generated from multiple references, the per-reference statistics are combined into a single `DataFrame` of results. This is done using [combineRecomputedResults](#) if `recompute=TRUE` in [trainSingleR](#), otherwise it is done using [combineCommonResults](#).

## Value

A `DataFrame` where each row corresponds to a cell in `test`. In the case of a single reference, this contains:

- `scores`, a numeric matrix of correlations at the specified quantile for each label (column) in each cell (row). This will contain NAs if multiple references were supplied to [trainSingleR](#) with `recompute=TRUE`.
- `first.labels`, a character vector containing the predicted label *before* fine-tuning. Only added if `fine.tune=TRUE`.
- `tuned.scores`, a `DataFrame` containing `first` and `second`. These are numeric vectors containing the best and next-best scores at the final round of fine-tuning for each cell. Only added if `fine.tune=TRUE`.
- `labels`, a character vector containing the predicted label based on the maximum entry in `scores`.
- `pruned.labels`, a character vector containing the pruned labels where "low-quality". `els` are replaced with NAs. Only added if `prune=TRUE`.

The `metadata` of the `DataFrame` contains:

- `common.genes`, a character vector of genes used to compute the correlations prior to fine-tuning.
- `de.genes`, a list of list of genes used to distinguish between each pair of labels. Only returned if `genes="de"` when constructing `trained`, see [?trainSingleR](#) for more details.

In the case of multiple references, the output of [combineCommonResults](#) or [combineRecomputedResults](#) is returned, depending on whether `recompute=TRUE` when constructing `trained`. This is a `DataFrame` containing:

- `scores`, a numeric matrix of scores for each cell (row) across all labels in all references (columns). This will contain NAs if recomputation is performed.

- `labels`, `first.labels` (if `fine.tune=TRUE`) and `pruned.labels` (if `prune=TRUE`), containing the consolidated labels of varying flavors as described above.
- `orig.results`, a `DataFrame` of `DataFrame`s containing the results of running `classifySingleR` against each individual reference. Each nested `DataFrame` has the same format as described above.

See `?combineCommonResults` and `?combineRecomputedResults` for more details.

### Author(s)

Aaron Lun, based on the original `SingleR` code by Dvir Aran.

### See Also

`trainSingleR`, to prepare the training set for classification.

`pruneScores`, to remove low-quality labels based on the scores.

`combineCommonResults`, to combine results from multiple references.

### Examples

```
# Mocking up data with log-normalized expression values:
ref <- .mockRefData()
test <- .mockTestData(ref)

ref <- scuttle::logNormCounts(ref)
test <- scuttle::logNormCounts(test)

# Setting up the training:
trained <- trainSingleR(ref, label=ref$label)

# Performing the classification:
pred <- classifySingleR(test, trained)
table(predicted=pred$labels, truth=test$label)
```

---

`combineCommonResults` *Combine SingleR results with common genes*

---

### Description

Combine results from multiple runs of `classifySingleR` (usually against different references) into a single `DataFrame`. This assumes that each run of `classifySingleR` was performed using a common set of marker genes.

### Usage

```
combineCommonResults(results)
```



## Arguments

`results` A list of [DataFrame](#) prediction results as returned by [classifySingleR](#) when run on each reference separately.

## Details

Here, the strategy is to performed classification separately within each reference, then collating the results to choose the label with the highest score across references. For each cell, we identify the reference with the highest score across all of its labels. The “combined label” is then defined as the label assigned to that cell in the highest-scoring reference. (The same logic is also applied to the first and pruned labels, if those are available.)

Each result should be generated from training sets that use a common set of genes during classification, i.e., `common.genes` should be the same in the `trained` argument to each [classifySingleR](#) call. This is because the scores are not comparable across results if they were generated from different sets of genes. It is also for this reason that we use the highest score prior to fine-tuning, even if it does not correspond to the score of the fine-tuned label.

It is highly unlikely that this function will be called directly by the end-user. Users are advised to use the multi-reference mode of [SingleR](#) and related functions, which will take care of the use of a common set of genes before calling this function to combine results across references.

## Value

A [DataFrame](#) is returned containing the annotation statistics for each cell or cluster (row). This mimics the output of [classifySingleR](#) and contains the following fields:

- `scores`, a numeric matrix of correlations formed by combining the equivalent matrices from `results`.
- `labels`, a character vector containing the per-cell combined label across references.
- `references`, an integer vector specifying the reference from which the combined label was derived.
- `orig.results`, a [DataFrame](#) containing `results`.

It may also contain `first.labels` and `pruned.labels` if these were also present in `results`.

The `metadata` contains `common.genes`, a character vector of the common genes that were used across all references in `results`; and `label.origin`, a [DataFrame](#) specifying the reference of origin for each label in `scores`.

## Author(s)

Jared Andrews, Aaron Lun

## See Also

[SingleR](#) and [classifySingleR](#), for generating predictions to use in `results`.  
[combineRecomputedResults](#), for another approach to combining predictions.

**Examples**

```

# Making up data (using one reference to seed another).
ref <- .mockRefData(nreps=8)
ref1 <- ref[,1:2%%2==0]
ref2 <- ref[,1:2%%2==1]
ref2$label <- tolower(ref2$label)

test <- .mockTestData(ref1)

# Applying classification with SingleR's multi-reference mode.
ref1 <- scuttle::logNormCounts(ref1)
ref2 <- scuttle::logNormCounts(ref2)
test <- scuttle::logNormCounts(test)

pred <- SingleR(test, list(ref1, ref2), labels=list(ref1$label, ref2$label))
pred[,1:5] # Only viewing the first 5 columns for visibility.

```

---

combineRecomputedResults

*Combine SingleR results with recomputation*

---

**Description**

Combine results from multiple runs of [classifySingleR](#) (usually against different references) into a single [DataFrame](#). The label from the results with the highest score for each cell is retained. Unlike [combineCommonResults](#), this does not assume that each run of [classifySingleR](#) was performed using the same set of common genes, instead recomputing the scores for comparison across references.

**Usage**

```

combineRecomputedResults(
  results,
  test,
  trained,
  quantile = 0.8,
  assay.type.test = "logcounts",
  check.missing = TRUE,
  allow.lost = FALSE,
  warn.lost = TRUE,
  BNPARAM = KmknParam(),
  BPPARAM = SerialParam()
)

```

**Arguments**

results	A list of <a href="#">DataFrame</a> prediction results as returned by <a href="#">classifySingleR</a> when run on each reference separately.
test	A numeric matrix of single-cell expression values where rows are genes and columns are cells. Alternatively, a <a href="#">SummarizedExperiment</a> object containing such a matrix.
trained	A list of <a href="#">Lists</a> containing the trained outputs of multiple references, equivalent to either (i) the output of <a href="#">trainSingleR</a> on multiple references with <code>recompute=TRUE</code> , or (ii) running <a href="#">trainSingleR</a> on each reference separately and manually making a list of the trained outputs.
quantile	Further arguments to pass to <a href="#">classifySingleR</a> .
assay.type.test	An integer scalar or string specifying the assay of test containing the relevant expression matrix, if test is a <a href="#">SummarizedExperiment</a> object.
check.missing	Logical scalar indicating whether rows should be checked for missing values (and if found, removed).
allow.lost	Logical scalar indicating whether to use lost markers in references where they are available.
warn.lost	Logical scalar indicating whether to emit a warning if markers from one reference in trained are “lost” in other references.
BNPARAM	A <a href="#">BiocNeighborParam</a> object specifying the algorithm to use for building nearest neighbor indices.
BPPARAM	A <a href="#">BiocParallelParam</a> object specifying how parallelization should be performed, if any.

**Details**

Here, the strategy is to perform classification separately within each reference, then collate the results to choose the label with the highest score across references. For a given cell in test, we extract its assigned label from results for each reference. We also retrieve the marker genes associated with that label and take the union of markers across all references. This defines a common feature space in which the score for each reference’s assigned label is recomputed using ref; the label from the reference with the top recomputed score is then reported as the combined annotation for that cell.

Unlike [combineCommonResults](#), the union of markers is not used for the within-reference calls. This avoids the inclusion of noise from irrelevant genes in the within-reference assignments. Obviously, [combineRecomputedResults](#) is slower as it does require recomputation of the scores, but the within-reference calls are faster as there are fewer genes in the union of markers for assigned labels (compared to the union of markers across all labels, as required by [combineCommonResults](#)), so it is likely that the net compute time should be lower.

**Value**

A [DataFrame](#) is returned containing the annotation statistics for each cell or cluster (row). This mimics the output of [classifySingleR](#) and contains the following fields:

- `scores`, a numeric matrix of correlations containing the *recomputed* scores. For any given cell, entries of this matrix are only non-NA for the assigned label in each reference; scores are not recomputed for the other labels.
- `labels`, a character vector containing the per-cell combined label across references.
- `references`, an integer vector specifying the reference from which the combined label was derived.
- `orig.results`, a `DataFrame` containing results.

It may also contain `first.labels` and `pruned.labels` if these were also present in results.

The `metadata` contains `label.origin`, a `DataFrame` specifying the reference of origin for each label in `scores`. Note that, unlike `combineCommonResults`, no `common.genes` is reported as this function does not use a common set of genes across all references.

### Dealing with mismatching gene availabilities

It is strongly recommended that the universe of genes be the same across all references in trained. If this is not the case, the intersection of genes across all trained will be used in the recomputation. This at least provides a common feature space for comparing correlations, though differences in the availability of markers between references may have unpredictable effects on the results (and so a warning will be emitted by default, when when `warn.lost=TRUE`).

That said, the intersection may be too string when dealing with many references with diverse feature annotations. In such cases, we can set `allow.lost=TRUE` so that the recomputation for each reference will use all available markers in that reference. The idea here is to avoid penalizing all references by removing an informative marker when it is only absent in a single reference. We hope that the recomputed scores are still roughly comparable if the number of lost markers is relatively low, coupled with the use of ranks in the calculation of the Spearman-based scores to reduce the influence of individual markers. This is perhaps as reliable as one might imagine, so setting `allow.lost=TRUE` should be considered a last resort.

### Author(s)

Aaron Lun

### References

Lun A, Bunis D, Andrews J (2020). Thoughts on a more scalable algorithm for multiple references. <https://github.com/LTLA/SingleR/issues/94>

### See Also

`SingleR` and `classifySingleR`, for generating predictions to use in results.  
`combineCommonResults`, for another approach to combining predictions.

### Examples

```
# Making up data.
ref <- .mockRefData(nreps=8)
ref1 <- ref[,1:2%%2==0]
```

```
ref2 <- ref[,1:2%%2==1]
ref2$label <- tolower(ref2$label)

test <- .mockTestData(ref)

# Performing classification within each reference.
test <- scuttle::logNormCounts(test)

ref1 <- scuttle::logNormCounts(ref1)
train1 <- trainSingleR(ref1, labels=ref1$label)
pred1 <- classifySingleR(test, train1)

ref2 <- scuttle::logNormCounts(ref2)
train2 <- trainSingleR(ref2, labels=ref2$label)
pred2 <- classifySingleR(test, train2)

# Combining results with recomputation of scores.
combined <- combineRecomputedResults(
  results=list(pred1, pred2),
  test=test,
  trained=list(train1, train2))

combined[,1:5]
```

---

datasets

*Reference dataset extractors*

---

## Description

These dataset getter functions are deprecated as they have been migrated to the **celldex** package for more general use throughout the Bioconductor package ecosystem.

## Usage

HumanPrimaryCellAtlasData(...)

BlueprintEncodeData(...)

ImmGenData(...)

MouseRNAseqData(...)

DatabaseImmuneCellExpressionData(...)

NovershternHematopoieticData(...)

MonacoImmuneData(...)

**Arguments**

... Further arguments to pass to the **celldex** function of the same name.

**Value**

A [SummarizedExperiment](#) object containing the reference dataset.

**Author(s)**

Aaron Lun

---

getClassicMarkers      *Get classic markers*

---

**Description**

Find markers between pairs of labels using the “classic” approach, i.e., based on the log-fold change between the medians of labels.

**Usage**

```
getClassicMarkers(
  ref,
  labels,
  assay.type = "logcounts",
  check.missing = TRUE,
  de.n = NULL,
  BPPARAM = SerialParam()
)
```

**Arguments**

ref	A numeric matrix of expression values where rows are genes and columns are reference samples (individual cells or bulk samples). Each row should be named with the gene name. In general, the expression values are expected to be log-transformed, see <a href="#">Details</a> . Alternatively, a <a href="#">SummarizedExperiment</a> object containing such a matrix. Alternatively, a list or <a href="#">List</a> of <a href="#">SummarizedExperiment</a> objects or numeric matrices containing multiple references, in which case the row names are expected to be the same across all objects.
labels	A character vector or factor of known labels for all samples in ref. Alternatively, if ref is a list, labels should be a list of the same length. Each element should contain a character vector or factor specifying the label for the corresponding entry of ref.
assay.type	An integer scalar or string specifying the assay of ref containing the relevant expression matrix, if ref is a <a href="#">SummarizedExperiment</a> object (or is a list that contains one or more such objects).

check.missing	Logical scalar indicating whether rows should be checked for missing values (and if found, removed).
de.n	An integer scalar specifying the number of DE genes to use. Defaults to $500 * (2/3) ^ \log_2(N)$ where N is the number of unique labels.
BPPARAM	A <a href="#">BiocParallelParam</a> object specifying how parallelization should be performed.

## Details

This function implements the classic mode of marker detection in **SingleR**, based only on the magnitude of the log-fold change between labels. In many respects, this approach may be suboptimal as it does not consider the variance within each label and has limited precision when the expression values are highly discrete. Nonetheless, it is often the only possible approach when dealing with reference datasets that lack replication and thus cannot be used with more advanced marker detection methods.

If multiple references are supplied, ranking is performed based on the average of the log-fold changes within each reference. This avoids comparison of expression values across references that can be distorted by batch effects. If a pair of labels does not co-occur in at least one reference, no attempt is made to perform the comparison and the corresponding character vector is left empty in the output.

The character vector corresponding to the comparison of a label to itself is always empty.

## Value

A list of lists of character vectors, where both the outer and inner lists have names equal to the unique levels of labels. The character vector contains the names of the top `de.n` genes with the largest positive log-fold changes in one label (entry of the outer list) against another label (entry of the inner list).

## Author(s)

Aaron Lun, based on the original `SingleR` code by Dvir Aran.

## See Also

[trainSingleR](#) and [SingleR](#), where this function is used when `genes="de"` and `de.method="classic"`.

## Examples

```
ref <- .mockRefData()
ref <- scuttle::logNormCounts(ref)
out <- getClassicMarkers(ref, labels=ref$label)
str(out)

# Works with multiple references:
ref2 <- .mockRefData()
ref2 <- scuttle::logNormCounts(ref2)
out2 <- getClassicMarkers(list(ref, ref2), labels=list(ref$label, ref2$label))
str(out2)
```

---

getDeltaFromMedian      *Compute the difference from median*

---

### Description

Compute the delta value for each cell, defined as the difference between the score for the assigned label and the and median score across all labels.

### Usage

```
getDeltaFromMedian(results)
```

### Arguments

results      A [DataFrame](#) containing the output generated by [SingleR](#) or [classifySingleR](#).

### Details

This function computes the same delta value that is used in [pruneScores](#), for users who want to apply more custom filters or visualizations.

### Value

A numeric vector containing delta values for each cell in results.

### Author(s)

Aaron Lun

### See Also

[pruneScores](#), where the delta values are used.

### Examples

```
# Running the SingleR() example.
example(SingleR, echo=FALSE)

summary(getDeltaFromMedian(pred))
```



---

matchReferences	<i>Match labels from two references</i>
-----------------	---

---

### Description

Match labels from a pair of references, corresponding to the same underlying cell type or state but with differences in nomenclature.

### Usage

```
matchReferences(ref1, ref2, labels1, labels2, ...)
```

### Arguments

ref1, ref2	Numeric matrices of single-cell (usually log-transformed) expression values where rows are genes and columns are cells. Alternatively, <a href="#">SummarizedExperiment</a> objects containing such matrices.
labels1, labels2	A character vector or factor of known labels for all cells in ref1 and ref2, respectively.
...	Further arguments to pass to <a href="#">SingleR</a> .

### Details

It is often the case that two references contain the same cell types for the same biological system, but the two sets of labels differ in their nomenclature. This makes it difficult to compare results from different references. It also interferes with attempts to combine multiple datasets to create a larger, more comprehensive reference.

The `matchReferences` function attempts to facilitate matching of labels across two reference datasets. It does so by using one of the references (say, `ref1`) to assign its labels to the other (`ref2`). For each label `X` in `labels2`, we compute the probability of assigning a sample of `X` to each label `Y` in `labels1`. We also use `ref2` to assign labels to `ref1`, to obtain the probability of assigning a sample of `Y` to label `X`.

We then consider the probability of mutual assignment, i.e., assigning a sample of `X` to `Y` *and* a sample of `Y` to `X`. This is computed by simply taking the product of the two probabilities mentioned earlier. The output matrix contains mutual assignment probabilities for all pairs of `X` (rows) and `Y` (columns).

The mutual assignment probabilities are only high if there is a 1:1 mapping between labels. A perfect mapping manifests as probabilities of 1 in the relevant entries of the output matrix. Lower values are expected for ambiguous mappings and near-zero values for labels that are specific to one reference.

### Value

A numeric matrix containing a probability table of mutual assignment. Values close to 1 represent a 1:1 mapping between labels across the two references.

**Author(s)**

Aaron Lun

**See Also**[SingleR](#), to do the actual cross-assignment.**Examples**

```
example(SingleR, echo=FALSE)
test$label <- paste0(test$label, "_X") # modifying the labels.
matchReferences(test, ref, labels1=test$label, labels2=ref$label)
```

---

plotDeltaDistribution *Plot delta distributions*

---

**Description**

Plot the distribution of deltas (i.e., the gap between the assignment score for the assigned label and those of the remaining labels) across cells assigned to each reference label.

**Usage**

```
plotDeltaDistribution(
  results,
  show = c("delta.med", "delta.next"),
  labels.use = colnames(results$scores),
  references = NULL,
  chosen.only = TRUE,
  size = 2,
  ncol = 5,
  dots.on.top = TRUE,
  this.color = "#000000",
  pruned.color = "#E69F00",
  grid.vars = list()
)
```

**Arguments**

results	A <a href="#">DataFrame</a> containing the output from <a href="#">SingleR</a> , <a href="#">classifySingleR</a> , <a href="#">combineCommonResults</a> , or <a href="#">combineRecomputedResults</a> .
show	String specifying whether to show the difference from the median ("delta.med") or the difference from the next-best score ("delta.next").
labels.use	Character vector specifying the labels to show in the plot facets. Defaults to all labels in results.
references	Integer scalar or vector specifying the references to visualize. This is only relevant for combined results, see Details.

<code>chosen.only</code>	Logical scalar indicating whether to only show deltas for individual labels that were chosen as the final label in a combined result.
<code>size</code>	Numeric scalar to set the size of the dots.
<code>ncol</code>	Integer scalar to set the number of labels to display per row.
<code>dots.on.top</code>	Logical scalar specifying whether cell dots should be plotted on top of the violin plots.
<code>this.color</code>	String specifying the color for cells that were assigned to the label.
<code>pruned.color</code>	String specifying the color for cells that were assigned to the label but pruned.
<code>grid.vars</code>	Named list of extra variables to pass to <code>grid.arrange</code> , used to arrange the multiple plots generated when <code>references</code> is of length greater than 1.

### Details

This function creates jitter and violin plots showing the deltas for all cells across one or more labels. The idea is to provide a visual diagnostic for the confidence of assignment of each cell to its label. The `show` argument determines what values to show on the y-axis:

- `"delta.med"`, the difference between the score of the assigned label and the median of all scores for each cell.
- `"delta.next"`, the difference between best and second-best scores of each cell at the last round of fine-tuning.

If any fine-tuning was performed, the highest scoring label for an individual cell may not be its final label. This may manifest as negative values when `show="delta.med"`. `show="delta.next"` is guaranteed to be positive but may be overly stringent for references involving very similar labels.

Pruned calls are identified as NAs in the `pruned.labels` field in `results`. Points corresponding to cells with pruned calls are colored by `pruned.color`; this can be disabled by setting `pruned.color=NA`.

For combined results (see [?combineRecomputedResults](#)), this function will show the deltas faceted by the assigned label within each individual reference. The references to show in this manner can be specified using the `references` argument, entries of which refer to columns of `results$orig.results`.

By default, a separate plot is created for each individual reference in a combined `results`. Deltas are only shown in each plot if the label in the corresponding reference was chosen as the overall best label in the combined results. However, this can be changed to show all deltas for an individual reference by setting `chosen.only=FALSE`.

### Value

If `references` specifies a single set of deltas, a `ggplot` object is returned showing the deltas in violin plots.

If `references` specifies multiple deltas for a combined result, multiple `ggplot` objects are generated in a grid on the current graphics device.

If `delta.use` specifies multiple deltas and `grid.vars` is set to `NULL`, a list is returned containing the `ggplot` objects for manual display.

### Author(s)

Daniel Bunis and Aaron Lun

**See Also**

[pruneScores](#), to remove low-quality labels based on the scores.

[plotScoreDistribution](#) and [plotScoreHeatmap](#), for alternative diagnostic plots.

**Examples**

```
example(SingleR, echo=FALSE)

# Showing the delta to the median:
plotDeltaDistribution(pred)

# Showing the delta to the next-highest score:
plotDeltaDistribution(pred, show = "delta.next")

# Multi-reference compatibility:
example(combineRecomputedResults, echo = FALSE)

plotDeltaDistribution(results = combined)

plotDeltaDistribution(results = combined, chosen.only=FALSE)

# Tweaking the grid controls:
plotDeltaDistribution(combined, grid.vars = list(ncol = 2))
```

---

plotScoreDistribution *Plot score distributions*

---

**Description**

Plot the distribution of assignment scores across all cells assigned to each reference label.

**Usage**

```
plotScoreDistribution(
  results,
  show = NULL,
  labels.use = colnames(results$scores),
  references = NULL,
  scores.use = NULL,
  calls.use = 0,
  pruned.use = NULL,
  size = 0.5,
  ncol = 5,
  dots.on.top = TRUE,
  this.color = "#F0E442",
  pruned.color = "#E69F00",
  other.color = "gray60",
```

```

    show.nmads = 3,
    show.min.diff = NULL,
    grid.vars = list()
  )

```

### Arguments

results	A <a href="#">DataFrame</a> containing the output from <a href="#">SingleR</a> , <a href="#">classifySingleR</a> , <a href="#">combineCommonResults</a> , or <a href="#">combineRecomputedResults</a> .
show	Deprecated, use <a href="#">plotDeltaDistribution</a> instead for show!="scores".
labels.use	Character vector specifying the labels to show in the plot facets. Defaults to all labels in results.
references	Integer scalar or vector specifying the references to visualize. This is only relevant for combined results, see Details.
scores.use	Deprecated, see references.
calls.use	Deprecated and ignored.
pruned.use	Deprecated and ignored.
size	Numeric scalar to set the size of the dots.
ncol	Integer scalar to set the number of labels to display per row.
dots.on.top	Logical scalar specifying whether cell dots should be plotted on top of the violin plots.
this.color	String specifying the color for cells that were assigned to the label.
pruned.color	String specifying the color for cells that were assigned to the label but pruned.
other.color	String specifying the color for other cells not assigned to the label.
show.nmads, show.min.diff	Deprecated, use <a href="#">plotDeltaDistribution</a> instead.
grid.vars	Named list of extra variables to pass to <a href="#">grid.arrange</a> , used to arrange the multiple plots generated when references is of length greater than 1.

### Details

This function creates jitter and violin plots showing assignment scores for all cells across one or more labels. Each facet represents a label in `labels.use` and contains three violin plots:

- “Assigned”, containing scores for all cells assigned to that label. Colored according to `this.color`.
- “Pruned”, containing scores for all cells assigned to that label but pruned out, e.g., by [pruneScores](#). Colored according to `pruned.color`, and can be omitted by setting `pruned.color=NA`.
- “Other”, containing the scores for all cells assigned to other labels. Colored according to `other.color`.

The expectation is that the former is higher than the latter, though the deltas generated by [plotDeltaDistribution](#) are often more informative in this regard.

For combined results (see [?combineRecomputedResults](#)), this function can show both the combined and individual scores. This is done using the `references` argument, entries of which refer to columns of `results$orig.results` if positive or to the combined results if zero. For example:

- If we set references=2, we will plot the scores from the second individual reference.
- If we set references=1:2, we will plot the scores from first and second references (in separate plots) faceted by their corresponding labels.
- By default, the function will create a separate plot for the combined scores and each individual reference, equivalent to references=0:N for N individual references.

### Value

If references specifies a single set of scores, a [ggplot](#) object is returned showing the scores in violin plots.

If references specifies multiple scores for a combined result, multiple ggplot objects are generated in a grid on the current graphics device.

If references specifies multiple scores and grid.vars=NULL, a list is returned containing the ggplot objects for manual display.

### Author(s)

Daniel Bunis and Aaron Lun

### See Also

[pruneScores](#), to remove low-quality labels based on the scores.

[plotDeltaDistribution](#) and [plotScoreHeatmap](#), for alternative diagnostic plots.

### Examples

```
example(SingleR, echo=FALSE)

# To show the distribution of scores grouped by label:
plotScoreDistribution(results = pred)

# We can display a particular label using the label
plotScoreDistribution(results = pred,
  labels.use = "B")

# For multiple references, default output will contain separate plots for
# each original reference as well as for the the combined scores.
example(combineRecomputedResults, echo = FALSE)
plotScoreDistribution(results = combined)

# 'references' specifies which original results to plot distributions for.
plotScoreDistribution(results = combined, references = 0)
plotScoreDistribution(results = combined, references = 1:2)

# Tweaking the grid arrangement:
plotScoreDistribution(combined, grid.vars = list(ncol = 2))
```

---

plotScoreHeatmap      *Plot a score heatmap*

---

## Description

Create a heatmap of the [SingleR](#) assignment scores across all cell-label combinations.

## Usage

```
plotScoreHeatmap(  
  results,  
  cells.use = NULL,  
  labels.use = NULL,  
  clusters = NULL,  
  show.labels = TRUE,  
  show.pruned = FALSE,  
  max.labels = 40,  
  normalize = TRUE,  
  cells.order = NULL,  
  order.by = c("labels", "clusters"),  
  rows.order = NULL,  
  scores.use = NULL,  
  calls.use = 0,  
  na.color = "gray30",  
  cluster_cols = FALSE,  
  annotation_col = NULL,  
  show_colnames = FALSE,  
  color = (grDevices::colorRampPalette(c("#D1147E", "white", "#00A44B")))(100),  
  silent = FALSE,  
  ...,  
  grid.vars = list()  
)
```

## Arguments

results	A <a href="#">DataFrame</a> containing the output from <a href="#">SingleR</a> , <a href="#">classifySingleR</a> , <a href="#">combineCommonResults</a> , or <a href="#">combineRecomputedResults</a> .
cells.use	Integer or string vector specifying the single cells (i.e., rows of results) to show. If NULL, all cells are shown.
labels.use	Character vector specifying the labels to show in the heatmap rows. Defaults to all labels in results.
clusters	String vector or factor containing cell cluster assignments, to be shown as an annotation bar in the heatmap.
show.labels	Logical indicating whether the assigned labels should be shown as an annotation bar.

<code>show.pruned</code>	Logical indicating whether the pruning status of the cell labels, as defined by <code>pruneScores</code> , should be shown as an annotation bar.
<code>max.labels</code>	Integer scalar specifying the maximum number of labels to show.
<code>normalize</code>	Logical specifying whether correlations should be normalized to lie in [0, 1].
<code>cells.order</code>	Integer or String vector specifying how to order the cells/columns of the heatmap. Regardless of <code>cells.use</code> , this input should be the same length as the total number of cells. Ignored if <code>cluster_cols</code> is set.
<code>order.by</code>	String providing the annotation to be used for cells/columns ordering. Can be "labels" (default) or "clusters" (when provided). Ignored if <code>cells.order</code> or <code>cluster_cols</code> are specified.
<code>rows.order</code>	String vector specifying how to order rows of the heatmap. Contents should be the reference-labels in the order you would like them to appear, from top-to-bottom. For combined results, include labels for all plots in a single vector and labels relevant to each plot will be extracted.
<code>scores.use</code>	Integer scalar or vector specifying the individual annotation result from which to take scores. This is only relevant for combined results, see Details.
<code>calls.use</code>	Integer scalar or vector specifying the individual annotation result from which to take labels, for use in the annotation bar when <code>show.labels=TRUE</code> . This is only relevant for combined results, see Details.
<code>na.color</code>	String specifying the color for non-calculated scores of combined results.
<code>annotation_col</code> , <code>cluster_cols</code> , <code>show_colnames</code> , <code>color</code> , <code>silent</code> , ...	Additional parameters for heatmap control passed to <code>pheatmap</code> .
<code>grid.vars</code>	A named list of extra variables to pass to <code>grid.arrange</code> , used to arrange the multiple plots generated when <code>scores.use</code> is of length greater than 1.

## Details

This function creates a heatmap containing the `SingleR` initial assignment scores for each cell (columns) to each reference label (rows). Users can then easily identify the high-scoring labels associated with each cell and/or cluster of cells.

If `show.labels=TRUE`, an annotation bar will be added to the heatmap showing the label assigned to each cell. This is also used to order the columns for a more organized visualization when `order.by="label"`. Note that scores shown in the heatmap are initial scores prior to the fine-tuning step, so the reported labels may not match up to the visual maximum for each cell in the heatmap.

If `max.labels` is less than the total number of unique labels, only the top labels are shown in the plot. Labels that were called most frequently are prioritized. The remaining labels are then selected based on:

- Labels with max z-scores after per-cell centering and scaling of the scores matrix, if `results` does not contain combined scores.
- Labels which were suggested most frequently by individual references, if `results` contains combined scores.



## Value

If `scores.use` specifies a single set of scores, the output of `pheatmap` is returned showing the heatmap on the current graphics device.

If `scores.use` specifies multiple scores for a combined result, multiple heatmaps are generated in a grid on the current graphics device.

If `scores.use` specifies multiple scores and `grid.vars` is set to `NULL`, a list is returned containing the `pheatmap` globs for manual display.

## Working with combined results

For combined results (see `?combineRecomputedResults`), this function can show both the combined and individual scores or labels. This is done using the `scores.use` and `calls.use` arguments, entries of which refer to columns of `results$orig.results` if positive or to the combined results if zero. For example:

- If we set `scores.use=2` and `calls.use=1`, we will plot the scores from the second individual reference with the annotation bar containing label assignments from the first reference.
- If we set `scores.use=1:2` and `calls.use=1:2`, we will plot the scores from first and second references (in separate plots) with the annotation bar in each plot containing the corresponding label assignments.
- By default, the function will create a separate plot the combined scores and each individual reference. In each plot, the annotation bar contains the combined labels; this is equivalent to `scores.use=0:N` and `calls.use=0` for `N` individual references.

## Tweaking the output

Additional arguments can be passed to `pheatmap` for further tweaking of the heatmap. Particularly useful parameters are `show_colnames`, which can be used to display cell/cluster names; `treeheight_row`, which sets the width of the clustering tree; and `annotation_col`, which can be used to add extra annotation layers. Clustering, pruning and label annotations are automatically generated and appended to `annotation_col` when available.

## Normalization of colors

If `normalize=TRUE`, scores will be linearly adjusted for each cell so that the smallest score is 0 and the largest score is 1. This is followed by cubing of the adjusted scores to improve dynamic range near 1. Visually, the color scheme is changed to a blue-green-yellow scale.

The adjustment is intended to inflate differences between scores within a given cell for easier visualization. This is because the scores are often systematically shifted between cells, making the raw values difficult to directly compare. However, it may be somewhat misleading; fine-tuning may appear to assign a cell to a label with much lower score whereas the actual scores are much closer. It is for this reason that the color bar values are not shown as the absolute values of the score have little meaning.

Note that this transformation is not dependent on the choice of the top `max.labels` labels. Altering `max.labels` will not change the normalized values, only the labels that are shown. However, the transformation will respond to `labels.use`.

**Author(s)**

Daniel Bunis, based on code by Dvir Aran.

**See Also**

[SingleR](#), to generate scores.

[pruneScores](#), to remove low-quality labels based on the scores.

[pheatmap](#), for additional tweaks to the heatmap.

[grid.arrange](#), for tweaks to the how heatmaps are arranged when multiple are output together.

**Examples**

```
# Running the SingleR() example.
example(SingleR, echo=FALSE)

# Grab the original identities of the cells as mock clusters
clusts <- test$label

# Creating a heatmap with just the labels.
plotScoreHeatmap(pred)

# Creating a heatmap with clusters also displayed.
plotScoreHeatmap(pred,
  clusters=clusts)

# Creating a heatmap with whether cells were pruned displayed.
plotScoreHeatmap(pred,
  show.pruned = TRUE)

# We can also turn off the normalization with Normalize = FALSE
plotScoreHeatmap(pred, clusters=clusts,
  normalize = FALSE)

# To only show certain labels, you can use labels.use or max.labels
plotScoreHeatmap(pred, clusters=clusts,
  labels.use = c("A","B","D"))
plotScoreHeatmap(pred, clusters=clusts,
  max.labels = 4)

# We can pass extra tweaks the heatmap as well
plotScoreHeatmap(pred, clusters=clusts,
  fontsize_row = 20)
plotScoreHeatmap(pred, clusters=clusts,
  treeheight_row = 15)
plotScoreHeatmap(pred, clusters=clusts, cluster_col = TRUE,
  cutree_cols = 5)

### Multi-Reference Compatibility ###

example(combineRecomputedResults, echo = FALSE)
plotScoreHeatmap(combined)
```

```

# 'scores.use' sets which particular run's scores to show, and can be multiple
plotScoreHeatmap(combined,
  scores.use = 1)
plotScoreHeatmap(combined,
  scores.use = c(0,2))

# 'calls.use' adjusts which run's labels and pruning calls to display.
plotScoreHeatmap(combined,
  calls.use = 1)

# To have plots output in a grid rather than as separate pages, provide,
# a list of inputs for gridExtra::grid.arrange() to 'grids.vars'.
plotScoreHeatmap(combined,
  grids.vars = list(ncol = 1))

# An empty list will use grid.arrange default
plotScoreHeatmap(combined,
  grids.vars = list())

```

---

pruneScores

*Prune out low-quality assignments*


---

### Description

Remove low-quality assignments based on the cell-label score matrix returned by [classifySingleR](#).

### Usage

```

pruneScores(
  results,
  nmads = 3,
  min.diff.med = -Inf,
  min.diff.next = 0,
  get.thresholds = FALSE
)

```

### Arguments

results	A <a href="#">DataFrame</a> containing the output generated by <a href="#">SingleR</a> or <a href="#">classifySingleR</a> .
nmads	Numeric scalar specifying the number of MADs to use for defining low outliers in the per-label distribution of delta values (i.e., difference from median).
min.diff.med	Numeric scalar specifying the minimum acceptable delta for each cell.
min.diff.next	Numeric scalar specifying the minimum difference between the best score and the next best score in fine-tuning.
get.thresholds	Logical scalar indicating whether the per-label thresholds on the deltas should be returned.

## Details

By itself, the SingleR algorithm will always assign a label to every cell. This occurs even if the cell's true label is not represented in the reference set of labels, resulting in assignment of an incorrect label to that cell. The `pruneScores` function aims to mitigate this effect by removing poor-quality assignments with "low" scores.

We compute a "delta" value for each cell, defined as the difference between the score for the assigned label and the median score across all labels. If the delta is small, this indicates that the cell matches all labels with the same confidence such that the assigned label is not particularly meaningful. The aim is to discard low delta values caused by (i) ambiguous assignments with closely related reference labels and (ii) incorrect assignments that match poorly to all reference labels.

We use an outlier-based approach to obtain a minimum threshold for filtering "low" delta values. For each (pre-fine-tuning) label, we obtain a distribution of deltas across all assigned cells. Cells that are more than `nmads` below the median score for each label are ignored. This assumes that most cells are correctly assigned to their true label and that cells of the same label have a unimodal distribution of delta values.

Filtering on outliers is useful as it adapts to the spread and scale of delta values. For example, references with many closely related cell types will naturally yield lower deltas. By comparison, references with more distinct cell types would yield large deltas, even for cells that have no representative type in the reference and are incorrectly assigned to the next-most-related label. The outlier definition procedure adjusts naturally to these situations.

The default `nmads` is motivated by the fact that, for a normal distribution, 99% of observations lie within 3 standard deviations from the mean. Smaller values for `nmads` will increase the stringency of the pruning.

## Value

A logical vector is returned by default, specifying which assignments in results should be ignored.

If `get.thresholds=TRUE`, a numeric vector is returned containing the per-label thresholds on the deltas, as defined using the outlier-based approach with `nmads`.

## Applying a hard filter on the deltas

If `min.diff.med` is specified, cells with deltas below this threshold are discarded. This is provided as an alternative filtering approach if the assumptions of outlier detection are violated. For example, if one label is consistently missassigned, the incorrect assignments would not be pruned. In such cases, one could set a threshold with `min.diff.med` to forcibly remove low-scoring cells.

It is possible for the per-label delta distribution to be multimodal yet still correct, e.g., due to cells belonging to subtypes nested within a main type label. This violates the unimodal assumption mentioned above for the outlier detection. In such cases, it may be better to set `nmads=Inf` and rely on `min.diff.med` for filtering instead.

Note that the deltas do not consider the effects of fine-tuning as scores are not comparable across different fine-tuning steps. In situations involving a majority of labels with only subtle distinctions, it is possible for the scores to be relatively similar but for the labels to be correctly assigned after fine-tuning. While outlier detection will automatically adapt to smaller scores, this effect should be considered if a threshold needs to be manually chosen for use in `min.diff.med`.

### Filtering on fine-tuning scores

If fine-tuning was performed to generate results, we ignore any cell for which the fine-tuning score is not more than `min.diff.next` greater than the next best score. This aims to only retain labels for which there is no ambiguity in assignment, especially when some labels have similar scores because they are closely related (and thus easily confused).

Typical values of `min.diff.next` would lie between `[0, 0.1]`. That said, the `min.diff.next` cutoff can be harmful in some applications involving highly related labels. From a user perspective, any confusion between these labels may not be a problem as the assignment is broadly correct; however, the best and next best scores will be very close and cause the labels to be unnecessarily discarded.

### Author(s)

Aaron Lun and Daniel Bunis

### See Also

[classifySingleR](#), to generate results.

[getDeltaFromMedian](#), to compute the per-cell deltas.

### Examples

```
# Running the SingleR() example.
example(SingleR, echo=FALSE)

summary(pruneScores(pred))
pruneScores(pred, get.thresholds=TRUE)

# Less stringent:
summary(pruneScores(pred, min.diff.med=0))
summary(pruneScores(pred, nmads=5))

# More stringent:
summary(pruneScores(pred, min.diff.med=0.1))
summary(pruneScores(pred, nmads=2))
summary(pruneScores(pred, min.diff.next=0.1))
```

---

SingleR

*Annotate scRNA-seq data*

---

### Description

Returns the best annotation for each cell in a test dataset, given a labelled reference dataset in the same feature space.

**Usage**

```

SingleR(
  test,
  ref,
  labels,
  method = NULL,
  clusters = NULL,
  genes = "de",
  sd.thresh = 1,
  de.method = "classic",
  de.n = NULL,
  de.args = list(),
  aggr.ref = FALSE,
  aggr.args = list(),
  recompute = TRUE,
  restrict = NULL,
  quantile = 0.8,
  fine.tune = TRUE,
  tune.thresh = 0.05,
  prune = TRUE,
  assay.type.test = "logcounts",
  assay.type.ref = "logcounts",
  check.missing = TRUE,
  BNPARAM = KmknnParam(),
  BPPARAM = SerialParam()
)

```

**Arguments**

test	A numeric matrix of single-cell expression values where rows are genes and columns are cells. Alternatively, a <a href="#">SummarizedExperiment</a> object containing such a matrix.
ref	A numeric matrix of (usually log-transformed) expression values from a reference dataset, or a <a href="#">SummarizedExperiment</a> object containing such a matrix; see <a href="#">trainSingleR</a> for details. Alternatively, a list or <a href="#">List</a> of <a href="#">SummarizedExperiment</a> objects or numeric matrices containing multiple references. Row names may be different across entries but only the intersection will be used, see <a href="#">Details</a> .
labels	A character vector or factor of known labels for all samples in ref. Alternatively, if ref is a list, labels should be a list of the same length. Each element should contain a character vector or factor specifying the label for the corresponding entry of ref.
method	Deprecated.
clusters	A character vector or factor of cluster identities for each cell in test. If set, annotation is performed on the aggregated cluster profiles, otherwise it defaults to per-cell annotation.

genes, sd.thresh, de.method, de.n, de.args	Arguments controlling the choice of marker genes used for annotation, see <a href="#">trainSingleR</a> .
aggr.ref, aggr.args	Arguments controlling the aggregation of the references prior to annotation, see <a href="#">trainSingleR</a> .
recompute	Logical scalar indicating whether to set up indices for later recomputation of scores, when ref contains multiple references from which the individual results are to be combined. (See the difference between <a href="#">combineCommonResults</a> and <a href="#">combineRecomputedResults</a> .)
restrict	A character vector of gene names to use for marker selection. By default, all genes in ref are used.
quantile, fine.tune, tune.thresh, prune	Further arguments to pass to <a href="#">classifySingleR</a> .
assay.type.test	An integer scalar or string specifying the assay of test containing the relevant expression matrix, if test is a <a href="#">SummarizedExperiment</a> object.
assay.type.ref	An integer scalar or string specifying the assay of ref containing the relevant expression matrix, if ref is a <a href="#">SummarizedExperiment</a> object (or is a list that contains one or more such objects).
check.missing	Logical scalar indicating whether rows should be checked for missing values (and if found, removed).
BNPARAM	A <a href="#">BiocNeighborParam</a> object specifying the algorithm to use for building nearest neighbor indices.
BPPARAM	A <a href="#">BiocParallelParam</a> object specifying how parallelization should be performed, if any.

## Details

This function is just a convenient wrapper around [trainSingleR](#) and [classifySingleR](#). The function will automatically restrict the analysis to the intersection of the genes in both ref and test. If this intersection is empty (e.g., because the two datasets use different gene annotations), an error will be raised.

If clusters is specified, per-cell profiles are summed to obtain per-cluster profiles. Annotation is then performed by running [classifySingleR](#) on these profiles. This yields a `DataFrame` with one row per level of clusters.

The default settings of this function are based on the assumption that ref contains or bulk data. If it contains single-cell data, this usually requires a different de.method choice. Read the Note in [?trainSingleR](#) for more details.

## Value

A `DataFrame` is returned containing the annotation statistics for each cell (one cell per row). This is identical to the output of [classifySingleR](#).

## Author(s)

Aaron Lun, based on code by Dvir Aran.

## References

Aran D, Looney AP, Liu L et al. (2019). Reference-based analysis of lung single-cell sequencing reveals a transitional profibrotic macrophage. *Nat. Immunology* 20, 163–172.

## Examples

```
# Mocking up data with log-normalized expression values:
ref <- .mockRefData()
test <- .mockTestData(ref)

ref <- scuttle::logNormCounts(ref)
test <- scuttle::logNormCounts(test)

# Running the classification with different options:
pred <- SingleR(test, ref, labels=ref$label)
table(predicted=pred$labels, truth=test$label)

k.out<- kmeans(t(assay(test, "logcounts")), center=5) # mock up a clustering
pred2 <- SingleR(test, ref, labels=ref$label, clusters=k.out$cluster)
table(predicted=pred2$labels, cluster=rownames(pred2))
```

---

trainSingleR

*Train the SingleR classifier*


---

## Description

Train the SingleR classifier on one or more reference datasets with known labels.

## Usage

```
trainSingleR(
  ref,
  labels,
  genes = "de",
  sd.thresh = 1,
  de.method = c("classic", "wilcox", "t"),
  de.n = NULL,
  de.args = list(),
  aggr.ref = FALSE,
  aggr.args = list(),
  recompute = TRUE,
  restrict = NULL,
  assay.type = "logcounts",
  check.missing = TRUE,
  BNPARAM = KmknnParam(),
  BPPARAM = SerialParam()
)
```



**Arguments**

ref	<p>A numeric matrix of expression values where rows are genes and columns are reference samples (individual cells or bulk samples). Each row should be named with the gene name. In general, the expression values are expected to be log-transformed, see Details.</p> <p>Alternatively, a <a href="#">SummarizedExperiment</a> object containing such a matrix.</p> <p>Alternatively, a list or <a href="#">List</a> of SummarizedExperiment objects or numeric matrices containing multiple references, in which case the row names are expected to be the same across all objects.</p>
labels	<p>A character vector or factor of known labels for all samples in ref.</p> <p>Alternatively, if ref is a list, labels should be a list of the same length. Each element should contain a character vector or factor specifying the label for the corresponding entry of ref.</p>
genes	<p>A string specifying the feature selection method to be used, see Details.</p> <p>Alternatively, if ref is <i>not</i> a list, genes can be either:</p> <ul style="list-style-type: none"> <li>• A list of lists of character vectors containing DE genes between pairs of labels.</li> <li>• A list of character vectors containing marker genes for each label.</li> </ul> <p>If ref <i>is</i> a list, genes can be a list of length equal to ref. Each element of the list should be one of the two above choices described for non-list ref, containing markers for labels in the corresponding entry of ref.</p>
sd.thresh	<p>A numeric scalar specifying the minimum threshold on the standard deviation per gene. Only used when genes="sd".</p>
de.method	<p>String specifying how DE genes should be detected between pairs of labels. Defaults to "classic", which sorts genes by the log-fold changes and takes the top de.n. Setting to "wilcox" or "t" will use Wilcoxon ranked sum test or Welch t-test between labels, respectively, and take the top de.n upregulated genes per comparison.</p>
de.n	<p>An integer scalar specifying the number of DE genes to use when genes="de". If de.method="classic", defaults to <math>500 * (2/3) ^ \log_2(N)</math> where N is the number of unique labels. Otherwise, defaults to 10.</p>
de.args	<p>Named list of additional arguments to pass to <a href="#">pairwiseTTests</a> or <a href="#">pairwiseWilcox</a> when de.method="wilcox" or "t".</p>
aggr.ref	<p>Logical scalar indicating whether references should be aggregated to pseudo-bulk samples for speed, see <a href="#">aggregateReference</a>.</p>
aggr.args	<p>Further arguments to pass to <a href="#">aggregateReference</a> when aggr.ref=TRUE.</p>
recompute	<p>Logical scalar indicating whether to set up indices for later recomputation of scores, when ref contains multiple references from which the individual results are to be combined. (See the difference between <a href="#">combineCommonResults</a> and <a href="#">combineRecomputedResults</a>.)</p>
restrict	<p>A character vector of gene names to use for marker selection. By default, all genes in ref are used.</p>

assay.type	An integer scalar or string specifying the assay of ref containing the relevant expression matrix, if ref is a <a href="#">SummarizedExperiment</a> object (or is a list that contains one or more such objects).
check.missing	Logical scalar indicating whether rows should be checked for missing values (and if found, removed).
BNPARAM	A <a href="#">BiocNeighborParam</a> object specifying the algorithm to use for building nearest neighbor indices.
BPPARAM	A <a href="#">BiocParallelParam</a> object specifying how parallelization should be performed.

## Details

This function uses a training data set to select interesting features and construct nearest neighbor indices in rank space. The resulting objects can be re-used across multiple classification steps with different test data sets via [classifySingleR](#). This improves efficiency by avoiding unnecessary repetition of steps during the downstream analysis.

Several options are available for feature selection:

- `genes="de"` identifies genes that are differentially expressed between labels. This is done by identifying the median expression within each label, and computing differences between medians for each pair of labels. For each label, the top `de.n` genes with the largest differences compared to another label are chosen as markers to distinguish the two labels. The set of all features is defined as the union of markers from all pairwise comparisons.
- `genes="sd"` identifies genes that are highly variable across labels. This is done by identifying the median expression within each label, and computing the standard deviation in the medians across all labels. The set of all features is defined as those genes with standard deviations above `sd.thresh`.
- `genes="all"` will not perform any feature selection.

If `genes="de"` or `"sd"`, the expression values are expected to be log-transformed and normalized.

If `restrict` is specified, `ref` is subsetting to only include the rows with names that are in `restrict`. Marker selection and all subsequent classification will be performed using this restrictive subset of genes. This can be convenient for ensuring that only appropriate genes are used (e.g., not pseudo-genes or predicted genes).

## Value

For a single reference, a [List](#) is returned containing:

`common.genes`: A character vector of all genes that were chosen by the designated feature selection method.

`nn.indices`: A List of [BiocNeighborIndex](#) objects containing pre-constructed neighbor search indices.

`original.exprs`: A List of numeric matrices where each matrix contains all cells for a particular label.

`search`: A List of additional information on the feature selection, for use by [classifySingleR](#). This includes `mode`, a string containing the selection method; `args`, method-specific arguments that can be re-used during classification; and `extras`, method-specific structures that can be re-used during classification.

For multiple references, a List of Lists is returned where each internal List corresponds to a reference in `ref` and has the same structure as described above.

### Custom feature specification

Rather than relying on the in-built feature selection, users can pass in their own features of interest to genes. The function expects a named list of named lists of character vectors, with each vector containing the DE genes between a pair of labels. For example:

```
genes <- list(
  A = list(A = character(0), B = "GENE_1", C = c("GENE_2", "GENE_3")),
  B = list(A = "GENE_100", B = character(0), C = "GENE_200"),
  C = list(A = c("GENE_4", "GENE_5"), B = "GENE_5", C = character(0))
)
```

If we consider the entry `genes$A$B`, this contains marker genes for label "A" against label "B". That is, these genes are upregulated in "A" compared to "B". The outer list should have one list per label, and each inner list should have one character vector per label. (Obviously, a label cannot have markers against itself, so this is just set to `character(0)`.)

Alternatively, `genes` can be a named list of character vectors containing per-label markers. For example:

```
genes <- list(
  A = c("GENE_1", "GENE_2", "GENE_3"),
  B = c("GENE_100", "GENE_200"),
  C = c("GENE_4", "GENE_5")
)
```

The entry `genes$A` represent the genes that are upregulated in A compared to some or all other labels. This allows the function to handle pre-defined marker lists for specific cell populations. However, it obviously captures less information than marker sets for the pairwise comparisons.

If `genes` is manually passed, `ref` can be the raw counts or any monotonic transformation thereof. There is no need to supply (log-)normalized expression values for the benefit of the automatic marker detection. Similarly, for manual `genes`, `de.n` and `sd.thresh` have no effect.

### Dealing with multiple references

The default **SingleR** policy for dealing with multiple references is to perform the classification for each reference separately and combine the results (see [?combineRecomputedResults](#) for an explanation). To this end, if `ref` is a list with multiple references, marker genes are identified separately within each reference when `genes="de"` or `"sd"`. Rank calculation and index construction is then performed within each reference separately.

Alternatively, `genes` can still be used to explicitly specify marker genes for each label in each of multiple references. This is achieved by passing a list of lists to `genes`, where each inner list corresponds to a reference in `ref` and can be of any format described in "Custom feature specification". Thus, it is possible for `genes` to be - wait for it - a list (per reference) of lists (per label) of lists (per label) of character vectors.

If `recompute=TRUE`, the output is exactly equivalent to running `trainSingleR` on each reference separately. If `recompute=FALSE`, `trainSingleR` is also run each reference but the difference is that the final common set of genes consists of the union of common genes across all references. This is necessary to ensure that correlations are computed from the same set of genes across reference and are thus reasonably comparable in `combineCommonResults`.

### Note on single-cell references

The default marker selection is based on log-fold changes between the per-label medians and is very much designed with bulk references in mind. It may not be effective for single-cell reference data where it is not uncommon to have more than 50% zero counts for a given gene such that the median is also zero for each group. Users are recommended to either set `de.method` to another DE ranking method, or detect markers externally and pass a list of markers to `genes` (see Examples).

In addition, it is generally unnecessary to have single-cell resolution on the reference profiles. We can instead set `aggr.ref=TRUE` to aggregate per-cell references into a set of pseudo-bulk profiles using `aggregateReference`. This improves classification speed while using vector quantization to preserve within-label heterogeneity and mitigate the loss of information. Note that any aggregation is done *after* marker gene detection; this ensures that the relevant tests can appropriately penalize within-label variation. Users should also be sure to set the seed as the aggregation involves randomization.

### Author(s)

Aaron Lun, based on the original SingleR code by Dvir Aran.

### See Also

`classifySingleR`, where the output of this function gets used.

`combineCommonResults` and `combineRecomputedResults`, to combine results from multiple references.

### Examples

```
# Making up some data for a quick demonstration.
ref <- .mockRefData()

# Normalizing and log-transforming for automated marker detection.
ref <- scuttle::logNormCounts(ref)

trained <- trainSingleR(ref, ref$label)
trained
trained$nn.indices
length(trained$common.genes)

# Alternatively, computing and supplying a set of label-specific markers.
by.t <- scan::pairwiseTTests(assay(ref, 2), ref$label, direction="up")
markers <- scan::getTopMarkers(by.t[[1]], by.t[[2]], n=10)
trained <- trainSingleR(ref, ref$label, genes=markers)
length(trained$common.genes)
```

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