Package ‘celldex’

August 1, 2024

Title  Index of Reference Cell Type Datasets
Version  1.14.0
Date  2024-04-25
Description  Provides a collection of reference expression datasets with curated cell
type labels, for use in procedures like automated annotation of single-cell
data or deconvolution of bulk RNA-seq.
License  GPL-3
Depends  SummarizedExperiment
Imports  utils, methods, Matrix, ExperimentHub, AnnotationHub,
         AnnotationDbi, S4Vectors, DelayedArray, DelayedMatrixStats,
gypsum, alabaster.base, alabaster.matrix, alabaster.se, DBI,
         RSQLite, jsonlite
Suggests  testthat, knitr, rmarkdown, BiocStyle, DT, jsonvalidate,
          BiocManager, ensembldb
biocViews  ExperimentHub, ExperimentData, ExpressionData,
          SequencingData, RNASeqData
VignetteBuilder  knitr
Encoding  UTF-8
URL  https://github.com/LTLA/celldex
BugReports  https://support.bioconductor.org/
RoxygenNote  7.3.1
git_url  https://git.bioconductor.org/packages/celldex
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Repository  Bioconductor 3.19
Date/Publication  2024-08-01
**BlueprintEncodeData**

**Description**

Obtain human bulk RNA-seq data from Blueprint and ENCODE.

**Usage**

```r
BlueprintEncodeData(
  rm.NA = c("rows", "cols", "both", "none"),
  ensembl = FALSE,
  cell.ont = c("all", "nonna", "none"),
  legacy = FALSE
)
```
Arguments

- **rm.NA**: String specifying how missing values should be handled. "rows" will remove genes with at least one missing value, "cols" will remove samples with at least one missing value, "both" will remove any gene or sample with at least one missing value, and "none" will not perform any removal.

- **ensembl**: Logical scalar indicating whether to convert row names to Ensembl IDs. Genes without a mapping to a non-duplicated Ensembl ID are discarded.

- **cell.ont**: String specifying whether Cell Ontology terms should be included in the colData. If "nonna", all samples without a valid term are discarded; if "all", all samples are returned with (possibly NA) terms; if "none", terms are not added.

- **legacy**: Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

This function provides normalized expression values for 259 bulk RNA-seq samples generated by Blueprint and ENCODE from pure populations of stroma and immune cells (Martens and Stunnenberg, 2013; The ENCODE Consortium, 2012). The samples were processed and normalized as described in Aran, Looney and Liu et al. (2019), i.e., the raw RNA-seq counts were downloaded from Blueprint and ENCODE in 2016 and normalized via edgeR (TPMs).

Blueprint Epigenomics contains 144 RNA-seq pure immune samples annotated to 28 cell types. ENCODE contains 115 RNA-seq pure stroma and immune samples annotated to 17 cell types. All together, this reference contains 259 samples with 43 cell types ("label.fine"), manually aggregated into 24 broad classes ("label.main"). The fine labels have also been mapped to the Cell Ontology ("label.ont", if cell.ont is not "none"), which can be used for further programmatic queries.

Value

A SummarizedExperiment object with a "logcounts" assay containing the log-normalized expression values, along with cell type labels in the colData.

Author(s)

Friederike Dündar

References


DatabaseImmuneCellExpressionData

Obtain human bulk RNA-seq data from DICE

Description

Download and cache the normalized expression values of 1561 bulk RNA-seq samples of sorted cell populations from the Database of Immune Cell Expression (DICE).

Usage

```r
DatabaseImmuneCellExpressionData(
  ensembl = FALSE,
  cell.ont = c("all", "nonna", "none"),
  legacy = FALSE
)
```

Arguments

- `ensembl` - Logical scalar indicating whether to convert row names to Ensembl IDs. Genes without a mapping to a non-duplicated Ensembl ID are discarded.
- `cell.ont` - String specifying whether Cell Ontology terms should be included in the `colData`. If "nonna", all samples without a valid term are discarded; if "all", all samples are returned with (possibly NA) terms; if "none", terms are not added.
- `legacy` - Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

This function provides normalized expression values of 1561 bulk RNA-seq samples generated by DICE from pure populations of human immune cells.

TPM normalized values for each cell type were downloaded from https://dice-database.org/downloads. Genes with no reads across samples were removed, and values were log2 normalized after a pseudocount of 1 was added.

The dataset contains 1561 human RNA-seq samples annotated to 5 main cell types ("label.main"): B cells, Monocytes, NK cells, T cells, CD8+, T cells, CD4+.
Samples were additionally annotated to 15 fine cell types ("label.fine"):

- B cells, naive
- Monocytes, CD14+
- Monocytes, CD16+
- NK cells
- T cells, memory TREG
- T cells, CD4+, naive
- T cells, CD4+, naive, stimulated
- T cells, CD4+, naive Treg
- T cells, CD4+, Th1
- T cells, CD4+, Th1_17
- T cells, CD4+, Th2
- T cells, CD8+, naïve
- T cells, CD8+, naïve, stimulated
- T cells, CD4+, TFH
- T cells, CD4+, Th17

The subtypes have also been mapped to the Cell Ontology ("label.ont", if cell.ont is not "none"), which can be used for further programmatic queries.

**Value**

A `SummarizedExperiment` object with a "logcounts" assay containing the log-normalized expression values, along with cell type labels in the `colData`.

**Author(s)**

Jared Andrews

**References**


**Examples**

```r
ref.se <- DatabaseImmuneCellExpressionData()
```
fetchReference

Fetch a reference dataset

Description

Fetch a reference dataset (or its metadata) from the gypsum backend.

Usage

fetchReference(
  name,
  version,
  path = NA,
  package = "celldex",
  cache = cacheDirectory(),
  overwrite = FALSE,
  realize.assays = FALSE,
  ...
)

fetchMetadata(
  name,
  version,
  path = NA,
  package = "celldex",
  cache = cacheDirectory(),
  overwrite = FALSE
)

Arguments

name           String containing the name of the reference dataset.
version        String containing the version of the dataset.
path           String containing the path to a subdataset, if name contains multiple reference datasets. Defaults to NA if no subdatasets are present.
package        String containing the name of the package.
cache, overwrite Arguments to pass to saveVersion or saveFile.
realize.assays Logical scalar indicating whether to realize assays into memory. Dense and sparse ReloadedArray objects are converted into ordinary arrays and dgCMatrix objects, respectively.
...            Further arguments to pass to readObject.
Value

fetchReference returns the dataset as a `SummarizedExperiment`. This is guaranteed to have a "logcounts" assay with log-normalized expression values, along with at least one character vector of labels in the column data.

fetchMetadata returns a named list of metadata for the specified dataset.

Author(s)

Aaron Lun

See Also

https://github.com/ArtifactDB/bioconductor-metadata-index, on the expected schema for the metadata.

`saveReference` and `uploadDirectory`, to save and upload a dataset.

`listReferences` and `listVersions`, to get possible values for name and version.

Examples

fetchReference("immgen", "2024-02-26")
str(fetchMetadata("immgen", "2024-02-26"))

HumanPrimaryCellAtlasData

Obtain the HPCA data

Description

Download and cache the normalized expression values of the data stored in the Human Primary Cell Atlas. The data will be downloaded from ExperimentHub, returning a `SummarizedExperiment` object for further use.

Usage

HumanPrimaryCellAtlasData(
    ensembl = FALSE,
    cell.ont = c("all", "nonna", "none"),
    legacy = FALSE
)
Arguments

- `ensembl` Logical scalar indicating whether to convert row names to Ensembl IDs. Genes without a mapping to a non-duplicated Ensembl ID are discarded.
- `cell.ont` String specifying whether Cell Ontology terms should be included in the `colData`. If "nonna", all samples without a valid term are discarded; if "all", all samples are returned with (possibly NA) terms; if "none", terms are not added.
- `legacy` Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

This function provides normalized expression values for 713 microarray samples from the Human Primary Cell Atlas (HPCA) (Mabbott et al., 2013). These 713 samples were processed and normalized as described in Aran, Looney and Liu et al. (2019).

Each sample has been assigned to one of 37 main cell types ("label.main") and 157 subtypes ("label.fine"). The subtypes have also been mapped to the Cell Ontology ("label.ont", if `cell.ont` is not "none"), which can be used for further programmatic queries.

Value

A `SummarizedExperiment` object with a "logcounts" assay containing the log-normalized expression values, along with cell type labels in the `colData`.

Author(s)

Friederike Dündar

References


Examples

```r
ref.se <- HumanPrimaryCellAtlasData()
```
Description

Download and cache the normalized expression values of 830 microarray samples of pure mouse immune cells, generated by the Immunologic Genome Project (ImmGen).

Usage

```r
ImmGenData(
  ensembl = FALSE,
  cell.ont = c("all", "nonna", "none"),
  legacy = FALSE
)
```

Arguments

- **ensembl**
  Logical scalar indicating whether to convert row names to Ensembl IDs. Genes without a mapping to a non-duplicated Ensembl ID are discarded.

- **cell.ont**
  String specifying whether Cell Ontology terms should be included in the `colData`. If "nonna", all samples without a valid term are discarded; if "all", all samples are returned with (possibly NA) terms; if "none", terms are not added.

- **legacy**
  Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

This function provides normalized expression values of 830 microarray samples generated by ImmGen from pure populations of murine immune cells (<http://www.immgen.org/>). The samples were processed and normalized as described in Aran, Looney and Liu et al. (2019), i.e., CEL files from the Gene Expression Omnibus (GEO; GSE15907 and GSE37448), were downloaded, processed, and normalized using the robust multi-array average (RMA) procedure on probe-level data.

This dataset consists of 20 broad cell types ("label.main") and 253 finely resolved cell subtypes ("label.fine"). The subtypes have also been mapped to the Cell Ontology ("label.ont", if `cell.ont` is not "none"), which can be used for further programmatic queries.

Value

A `SummarizedExperiment` object with a "logcounts" assay containing the log-normalized expression values, along with cell type labels in the `colData`.

Author(s)

Friederike Dündar
References


Examples

```r
ref.se <- ImmGenData()
```

---

**listReferences**

*List available references*

**Description**

List the available reference datasets and the associated versions in `celldex`.

**Usage**

```r
listReferences()
listVersions(name)
fetchLatestVersion(name)
```

**Arguments**

- `name` : String containing the name of the reference dataset.

**Value**

- For `listReferences`, a character vector containing the names of the available references.
- For `listVersions`, a character vector containing the names of the available versions of the name reference.
- For `fetchLatestVersion`, a string containing the name of the latest version.

**Author(s)**

Aaron Lun

**Examples**

```r
listReferences()
listVersions("immgen")
fetchLatestVersion("immgen")
```
Obtain bulk RNA-seq data of sorted human immune cells

**Description**

Download and cache the normalized expression values of 114 bulk RNA-seq samples of sorted immune cell populations that can be found in GSE107011.

**Usage**

```r
MonacoImmuneData( 
  ensembl = FALSE, 
  cell.ont = c("all", "nonna", "none"), 
  legacy = FALSE 
)
```

**Arguments**

- `ensembl`: Logical scalar indicating whether to convert row names to Ensembl IDs. Genes without a mapping to a non-duplicated Ensembl ID are discarded.
- `cell.ont`: String specifying whether Cell Ontology terms should be included in the `colData`. If "nonna", all samples without a valid term are discarded; if "all", all samples are returned with (possibly NA) terms; if "none", terms are not added.
- `legacy`: Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

**Details**

The dataset contains 114 human RNA-seq samples annotated to 10 main cell types ("label.main"):

- CD8+ T cells
- T cells
- CD4+ T cells
- Progenitors
- B cells
- Monocytes
- NK cells
- Dendritic cells
- Neutrophils
- Basophils

Samples were additionally annotated to 29 fine cell types ("label.fine"):

- Naive CD8 T cells
• Central memory CD8 T cells
• Effector memory CD8 T cells
• Terminal effector CD8 T cells
• MAIT cells
• Vd2 gd T cells
• Non-Vd2 gd T cells
• Follicular helper T cells
• T regulatory cells
• Th1 cells
• Th1/Th17 cells
• Th17 cells
• Th2 cells
• Naive CD4 T cells
• Terminal effector CD4 T cells
• Progenitor cells
• Naive B cells
• Non-switched memory B cells
• Exhausted B cells
• Switched memory B cells
• Plasmablasts
• Classical monocytes
• Intermediate monocytes
• Non classical monocytes
• Natural killer cells
• Plasmacytoid dendritic cells
• Myeloid dendritic cells
• Low-density neutrophils
• Low-density basophils

The subtypes have also been mapped to the Cell Ontology ("label.ont", if cell.ont is not "none"), which can be used for further programmatic queries.

Value

A SummarizedExperiment object with a "logcounts" assay containing the log-normalized expression values, along with cell type labels in the colData.

Author(s)

Jared Andrews
MouseRNAseqData

References


Examples

ref.se <- MonacoImmuneData()

---

MouseRNAseqData Obtain mouse bulk expression data of sorted cell populations (RNA-seq)

Description

Download and cache the normalized expression values of 358 bulk RNA-seq samples of sorted cell populations that can be found at GEO.

Usage

MouseRNAseqData(
  ensembl = FALSE,
  cell.ont = c("all", "nonna", "none"),
  legacy = FALSE
)

Arguments

ensembl Logical scalar indicating whether to convert row names to Ensembl IDs. Genes without a mapping to a non-duplicated Ensembl ID are discarded.

cell.ont String specifying whether Cell Ontology terms should be included in the colData. If "nonna", all samples without a valid term are discarded; if "all", all samples are returned with (possibly NA) terms; if "none", terms are not added.

legacy Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

This dataset was contributed by the Benayoun Lab that identified, downloaded and processed data sets on GEO that corresponded to sorted cell types (Benayoun et al., 2019).

The dataset contains 358 mouse RNA-seq samples annotated to 18 main cell types ("label.main"):

- Adipocytes
- Astrocytes
- B cells
- Cardiomyocytes
MouseRNAseqData

- Dendritic cells
- Endothelial cells
- Epithelial cells
- Erythrocytes
- Fibroblasts
- Granulocytes
- Hepatocytes
- Macrophages
- Microglia
- Monocytes
- Neurons
- NK cells
- Oligodendrocytes
- T cells

These are split further into 28 subtypes ("label.fine"). The subtypes have also been mapped to the Cell Ontology ("label.ont", if cell.ont is not "none"), which can be used for further programmatic queries.

Value

A SummarizedExperiment object with a "logcounts" assay containing the log-normalized expression values, along with cell type labels in the colData.

Author(s)

Friederike Dündar

References


Code at https://github.com/BenayounLaboratory/Mouse_Aging_Epigenomics_2018/tree/master/FigureS7_CIBERSORT/RNAseq_datasets_for_Deconvolution/2017-01-18

Examples

ref.se <- MouseRNAseqData()
Obtain bulk microarray expression for sorted hematopoietic cells

Description

Download and cache the normalized expression values of 211 bulk human microarray samples of sorted hematopoietic cell populations that can be found in GSE24759.

Usage

NovershternHematopoieticData(
  ensembl = FALSE,
  cell.ont = c("all", "nonna", "none"),
  legacy = FALSE
)

Arguments

ensemb1 Logical scalar indicating whether to convert row names to Ensembl IDs. Genes without a mapping to a non-duplicated Ensembl ID are discarded.

cell.ont String specifying whether Cell Ontology terms should be included in the colData. If "nonna", all samples without a valid term are discarded; if "all", all samples are returned with (possibly NA) terms; if "none", terms are not added.

legacy Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

The dataset contains 211 human microarray samples annotated to 16 main cell types ("label.main"):  
- Basophils  
- B cells  
- CMPs  
- Dendritic cells  
- Eosinophils  
- Erythroid cells  
- GMPS  
- Granulocytes  
- HSCs  
- Megakaryocytes  
- MEPs  
- Monocytes
• NK cells  
• NK T cells  
• CD8+ T cells  
• CD4+ T cells

Samples were additionally annotated to 38 fine cell types ("label.fine"):  
• Basophils  
• Naive B cells  
• Mature B cells class able to switch  
• Mature B cells  
• Mature B cells class switched  
• Common myeloid progenitors  
• Plasmacytoid Dendritic Cells  
• Myeloid Dendritic Cells  
• Eosinophils  
• Erythroid_CD34+ CD71+ GlyA-  
• Erythroid_CD34- CD71+ GlyA-  
• Erythroid_CD34- CD71+ GlyA+  
• Erythroid_CD34- CD71lo GlyA+  
• Erythroid_CD34- CD71- GlyA+  
• Granulocyte/monocyte progenitors  
• Colony Forming Unit-Granulocytes  
• Granulocyte (Neutrophilic Metamyelocytes)  
• Granulocyte (Neutrophils)  
• Hematopoietic stem cells_CD133+ CD34dim  
• Hematopoietic stem cell_CD38- CD34+  
• Colony Forming Unit-Megakaryocytic  
• Megakaryocytes  
• Megakaryocyte/erythroid progenitors  
• Colony Forming Unit-Monocytes  
• Monocytes  
• Mature NK cells_CD56- CD16+ CD3-  
• Mature NK cells_CD56+ CD16+ CD3-  
• Mature NK cells_CD56- CD16- CD3-  
• NK T cells  
• Early B cells  
• Pro B cells  
• CD8+ Effector Memory RA
- Naive CD8+ T cells
- CD8+ Effector Memory
- CD8+ Central Memory
- Naive CD4+ T cells
- CD4+ Effector Memory
- CD4+ Central Memory

The subtypes have also been mapped to the Cell Ontology ("label.ont", if cell.ont is not "none"), which can be used for further programmatic queries.

**Value**

A `SummarizedExperiment` object with a "logcounts" assay containing the log-normalized expression values, along with cell type labels in the `colData`.

**Author(s)**

Jared Andrews

**References**


**Examples**

```r
ref.se <- NovershternHematopoieticData()
```

**Description**

These objects are imported from other packages. Follow the links below to see their documentation.

`gypsum` defineTextQuery
saveReference  

Save a reference dataset

Description

Save a reference dataset to disk, usually in preparation for upload via uploadDirectory.

Usage

saveReference(x, labels, path, metadata)

Arguments

x  
Matrix of log-normalized expression values. This may be sparse or dense, but should be non-integer and have no missing values. Row names should be present and unique for all rows.

labels  
DataFrame of labels. Each row of labels corresponds to a column of x and contains the label(s) for that column. Each column of labels represents a different label type; typically, the column name has a label. prefix to distinguish between, e.g., label.fine, label.broad and so on. At least one column should be present.

path  
String containing the path to a directory in which to save x.

metadata  
Named list containing metadata for this reference dataset, see the schema returned by fetchMetadataSchema(). Note that the applications.takane property will be automatically added by this function and does not have to be supplied.

Details

The SummarizedExperiment saved to path is guaranteed to have the "logcounts" assay and at least one column in labels. This mirrors the expectation for reference datasets obtained via fetchReference.

Value

x and labels are used to create a SummarizedExperiment that is saved into path. NULL is invisibly returned.

Author(s)

Aaron Lun

See Also

uploadDirectory, to upload the saved dataset to the gypsum backend.

fetchReference, to download an existing dataset into the current session.
Examples

# Mocking up some data to be saved.
x <- matrix(rnorm(1000), ncol=10)
rownames(x) <- sprintf("GENE_%i", seq_len(nrow(x)))
labels <- DataFrame(
    labels.broad = sample(c("B", "T", "NK"), ncol(x), replace=TRUE),
    labels.fine = sample(c("PC", "pre-B", "pro-B", "Th2", "CD4+T", "NK"),
        ncol(x), replace=TRUE)
)

# Making up some metadata as well.
meta <- list(
    title="New reference dataset",
    description="This is a new reference dataset, generated from blah blah.",
    genome="GRCm38",
    taxonomy_id="10090",
    sources=list(
        list(provider="GEO", id="GSE123456"),
        list(provider="PubMed", id="123456"),
        list(provider="URL", id="https://reference.data.com", version="2024-02-26")
    ),
    maintainer_name="Chihaya Kisaragi",
    maintainer_email="kisaragi.chihaya@765.com"
)

# Actually saving it.
tmp <- tempfile()
saveReference(x, labels, tmp, meta)

# Reloading it to make sure it looks good.
alabaster.base::readObject(tmp)
str(jsonlite::fromJSON(file.path(tmp, "_bioconductor.json")))

searchReferences Search reference metadata

Description

Search for reference datasets of interest based on matching text in the associated metadata.

Usage

searchReferences(
    query,
    cache = cacheDirectory(),
    overwrite = FALSE,
    latest = TRUE
)
surveyReferences

Arguments

query       String or a gypsum.search.object, see Examples.
cache, overwrite
Arguments to pass to fetchMetadataDatabase.
latest       Whether to only consider the latest version of each dataset.

Details

The returned DataFrame contains the usual suspects like the title and description for each dataset, the number of rows and columns, the organisms and genome builds involved, whether the dataset has any pre-computed reduced dimensions, and so on. More details can be found in the Bioconductor metadata schema at https://github.com/ArtifactDB/bioconductor-metadata-index.

Value

A DataFrame where each row corresponds to a dataset, containing various columns of metadata. Some columns may be lists to capture 1:many mappings.

Author(s)

Aaron Lun

See Also

surveyReferences, to easily obtain a listing of all available datasets.

Examples

searchReferences(defineTextQuery("immun%", partial=TRUE))[,c("name", "title")]
searchReferences(defineTextQuery("10090", field="taxonomy_id"))[,c("name", "title")]
searchReferences(
  defineTextQuery("10090", field="taxonomy_id") &
  defineTextQuery("immun%", partial=TRUE)
)[,c("name", "title")]

surveyReferences        Survey reference metadata

Description

Metadata survey for all available reference datasets in the celldex package.

Usage

surveyReferences(cache = cacheDirectory(), overwrite = FALSE, latest = TRUE)
Arguments

- cache, overwrite
  Arguments to pass to `fetchMetadataDatabase`.
- latest
  Whether to only consider the latest version of each dataset.

Details

The returned DataFrame contains the usual suspects like the title and description for each dataset, the number of samples and types of labels, the organisms and genome builds involved, and so on. More details can be found in the Bioconductor metadata schema at https://github.com/ArtifactDB/bioconductor-metadata-index.

Value

A DataFrame where each row corresponds to a dataset, containing various columns of metadata. Some columns may be lists to capture 1:many mappings.

Author(s)

Aaron Lun

See Also

- `searchReferences`, to search on the metadata for specific datasets.

Examples

```r
surveyReferences()
```
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