Package 'atlasapprox'

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Title Cell Atlas Approximations

Version 0.1.0

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Description Provides an interface in R to cell atlas approximations. See the vignette under ``Getting started" for instructions. You can also explore the reference documentation for specific functions. Additional interfaces and resources are available at <https://atlasapprox.readthedocs.io>.

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URL https://atlasapprox.readthedocs.io/en/latest/R/index.html, https://github.com/fabilab/cell_atlas_approximations_API

BugReports https://github.com/fabilab/cell_atlas_approximations_API/issues

Imports httr

Suggests testthat (>= 3.0.0), knitr, rmarkdown

Config/testthat/edition 3

Encoding UTF-8

RoxygenNote 7.3.2

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

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Contents

`api_version` *api_version*

Description

api_version

Usage

```
api_version
```

Format

An object of class `character` of length 1.

`GetAverage` *GetAverage*

Description

Get the average gene expression for specified features across cell types in a given organism and organ.

Usage

```
GetAverage(organism, organ, features)
```

Arguments

`organism`	The organism you would like to query
`organ`	The organ you would like to query
`features`	The features (genes) you would like to query

Value

A data.frame of average gene expression by cell type in that organism and organ

Examples

```
GetAverage("h_sapiens", "Lung", c("COL1A1", "PTPRC"))
```

GetCelltypeLocation *GetCelltypeLocation*

Description

Get the organs where a specified cell type is found in a given organism.

Usage

```
GetCelltypeLocation(organism, cell_type)
```

Arguments

organism	The organism you would like to query
cell_type	The cell type you would like to query

Value

An array of organs in which that cell type is found

Examples

```
GetCelltypeLocation("h_sapiens", "fibroblast")
```

GetCelltypes *GetCelltypes*

Description

Get all available cell types for a specified organism and organ.

Usage

```
GetCelltypes(organism, organ)
```

Arguments

organism	The organism you would like to query
organ	The organ you would like to query

Value

An array of available cell types from that organism and organ

Examples

```
GetCelltypes("h_sapiens", "Lung")
```

`GetDataSources` *GetDataSources*

Description

Get information about the cell atlases used as data sources for the approximations.

Usage

```
GetDataSources()
```

Value

A list containing information about the cell atlases used as data sources

Examples

```
GetDataSources()
```

`GetFeatures` *GetFeatures*

Description

Get a list of available features (typically genes) for a specified organism.

Usage

```
GetFeatures(organism)
```

Arguments

`organism`	The organism you would like to query

Value

An array of available features (genes) from that organism

Examples

```
GetFeatures("h_sapiens")
```

GetFractionDetected *GetFractionDetected*

Description

Get the fraction of cells expressing specified features across cell types in a given organism and organ.

Usage

```
GetFractionDetected(organism, organ, features)
```

Arguments

organism	The organism you would like to query
organ	The organ you would like to query
features	The features (genes) you would like to query

Value

A data.frame of fraction of expressing cells by cell type in that organism and organ

Examples

```
GetFractionDetected("h_sapiens", "Lung", c("COL1A1", "PTPRC"))
```

GetHighestMeasurement *GetHighestMeasurement*

Description

Get the cell types with the highest expression of a specified feature in a given organism.

Usage

```
GetHighestMeasurement(organism, feature, number)
```

Arguments

organism	The organism you would like to query
feature	The feature you would like to query
number	The number of highest expressors you would like to get

Value

A dataframe of cell types, organs, and averages for the cell types with the highest measurement for that feature

Examples

```
GetHighestMeasurement("h_sapiens", "PTPRC", 5)
```

`GetMarkers` *GetMarkers*

Description

Get marker genes for a specified cell type in a given organism and organ.

Usage

```
GetMarkers(organism, organ, cell_type, number)
```

Arguments

`organism`	The organism you would like to query
`organ`	The organ you would like to query
`cell_type`	The cell type you would like to query
`number`	The number of markers you would like to get

Value

An array of markers for that cell type in that organism and organ

Examples

```
GetMarkers("h_sapiens", "Lung", "fibroblast", 5)
```

GetOrganisms *GetOrganisms*

Description

Get a list of organisms available for querying in the atlasapprox api.

Usage

```
GetOrganisms()
```

Value

An array of available organisms

Examples

```
GetOrganisms()
```

GetOrgans *GetOrgans*

Description

Get all available organs for an organism

Usage

```
GetOrgans(organism)
```

Arguments

organism	The organism you would like to query

Value

An array of available organs from that organism

Examples

```
GetOrgans("h_sapiens")
```

GetSimilarFeatures *GetSimilarFeatures*

Description

Get features with similar expression patterns to a specified feature in a given organism and organ.

Usage

```
GetSimilarFeatures(organism, organ, feature, number, method)
```

Arguments

organism	The organism you would like to query
organ	The organ you would like to query
feature	The feature to find similarities for
number	The number of similar features you would like to get.
method	The method used to compute similarity between features. The following methods are available: - correlation (default): Pearson correlation of the fraction_detected - cosine: Cosine similarity/distance of the fraction_detected - euclidean: Euclidean distance of average measurement (e.g. expression) - manhattan: Taxicab/Manhattan/L1 distance of average measurement - log-euclidean: Log the average measurement with a pseudocount of 0.001, then compute euclidean distance. This tends to highlight sparsely measured features

Value

A dataframe of similar features and their distances from the focal feature according to the method chosen

Examples

```
GetSimilarFeatures("h_sapiens", "lung", "PTPRC", 5, "correlation")
```

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