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>.

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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