Package ‘OmicNavigator’

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Type Package

Title Open-Source Software for 'Omic' Data Analysis and Visualization

Description A tool for interactive exploration of the results from 'omics' experiments to facilitate novel discoveries from high-throughput biology. The software includes R functions for the 'bioinformatician' to deposit study metadata and the outputs from statistical analyses (e.g. differential expression, enrichment). These results are then exported to an interactive JavaScript dashboard that can be interrogated on the user's local machine or deployed online to be explored by collaborators. The dashboard includes 'sortable' tables, interactive plots including network visualization, and fine-grained filtering based on statistical significance.

Version 1.13.13

URL https://github.com/abbvie-external/OmicNavigator

BugReports https://github.com/abbvie-external/OmicNavigator/issues

License MIT + file LICENSE

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License_is_FOSS yes

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Depends R (>= 3.2.0)

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Description

Package options to control package-wide behavior are described below.

Details

The default prefix for OmicNavigator study packages is "ONstudy". If you would prefer to use a different prefix, you can change the package option OmicNavigator.prefix. For example, to use the prefix "OmicNavigatorStudy", you could add the following line to your .Rprofile file.

```r
options(OmicNavigator.prefix = "OmicNavigatorStudy")
```

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Authors:

- Terrence Ernst (Web application)
- Paul Nordlund (Web application)
- Justin Moore (UpSet-related functions and web application)
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- Joe LoGrasso (Support for plotly)

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See Also

Useful links:

- [https://github.com/abbvie-external/OmicNavigator](https://github.com/abbvie-external/OmicNavigator)
- Report bugs at [https://github.com/abbvie-external/OmicNavigator/issues](https://github.com/abbvie-external/OmicNavigator/issues)
addAnnotations

Description
Add annotations

Usage
addAnnotations(study, annotations, reset = FALSE)

Arguments
- **study**: An OmicNavigator study created with `createStudy`
- **annotations**: The annotations used for the enrichment analyses. The input is a nested list. The top-level list contains one entry per annotation database, e.g. reactome. The names correspond to the name of each annotation database. Each of these elements should be a list that contains more information about each annotation database. Specifically the sublist should contain 1) `description`, a character vector that describes the resource, 2) `featureID`, the name of the column in the features table that was used for the enrichment analysis, and 3) `terms`, a list of annotation terms. The names of terms sublist correspond to the name of the annotation terms. Each of the annotation terms should be a character vector of featureIDs.
- **reset**: Reset the data prior to adding the new data (default: `FALSE`). The default is to add to or modify any previously added data (if it exists). Setting `reset = TRUE` enables you to remove existing data you no longer want to include in the study.

Value
Returns the original `onStudy` object passed to the argument `study`, but modified to include the newly added data

addAssays

Description
Add assays

Usage
addAssays(study, assays, reset = FALSE)
Arguments

study  An OmicNavigator study created with createStudy

assays  The assays from the study. The input object is a list of data frames (one per model). The row names should correspond to the featureIDs (addFeatures). The column names should correspond to the sampleIDs (addSamples). The data frame should only contain numeric values. To share a data frame across multiple models, use the modelID "default".

reset  Reset the data prior to adding the new data (default: FALSE). The default is to add to or modify any previously added data (if it exists). Setting reset = TRUE enables you to remove existing data you no longer want to include in the study.

Value

Returns the original onStudy object passed to the argument study, but modified to include the newly added data

addBarcodes Add barcode plot metadata

Description

The app can display a barcode plot of the enrichment results for a given annotation term. The metadata in ‘barcodes’ instructs the app how to create and label the barcode plot.

Usage

addBarcodes(study, barcodes, reset = FALSE)

Arguments

study  An OmicNavigator study created with createStudy

barcodes  The metadata variables that describe the barcode plot. The input object is a list of lists (one per model). Each sublist must contain the element statistic, which is the column name in the results table to use to construct the barcode plot. Each sublist may additionally contain any of the following optional elements: 1) absolute - Should the statistic be converted to its absolute value (default is TRUE). 2) logFoldChange - The column name in the results table that contains the log fold change values. 3) labelStat - The x-axis label to describe the statistic. 4) labelLow - The left-side label to describe low values of the statistic. 5) labelHigh - The right-side label to describe high values of the statistic. 6) featureDisplay - The feature variable to use to label the barcode plot on hover. To share metadata across multiple models, use the modelID "default".

reset  Reset the data prior to adding the new data (default: FALSE). The default is to add to or modify any previously added data (if it exists). Setting reset = TRUE enables you to remove existing data you no longer want to include in the study.
addEnrichments

Value

Returns the original onStudy object passed to the argument study, but modified to include the newly added data

Usage

addEnrichments(study, enrichments, reset = FALSE)

Arguments

study  An OmicNavigator study created with createStudy
enrichments  The enrichment results from each model. The input is a nested named list. The names of the list correspond to the model names. Each list element should be a list of the annotation databases tested (addAnnotations). The names of the list correspond to the annotation databases. Each list element should be another list of tests (addTests). The names correspond to the tests performed. Each of these elements should be a data frame with enrichment results. Each table must contain the following columns: "termID", "description", "nominal" (the nominal statistics), and "adjusted" (the statistics after adjusting for multiple testing). Any additional columns are ignored.
reset  Reset the data prior to adding the new data (default: FALSE). The default is to add to or modify any previously added data (if it exists). Setting reset = TRUE enables you to remove existing data you no longer want to include in the study.

Value

Returns the original onStudy object passed to the argument study, but modified to include the newly added data
**addEnrichmentsLinkouts**

*Add linkouts to external resources in the enrichments table*

**Description**

You can provide additional information on the annotation terms in your study by providing linkouts to external resources. These will be embedded directly in the enrichments table.

**Usage**

```r
addEnrichmentsLinkouts(study, enrichmentsLinkouts, reset = FALSE)
```

**Arguments**

- `study`: An OmicNavigator study created with `createStudy`
- `enrichmentsLinkouts`: The URL patterns that describe linkouts to external resources (see Details below). The input object is a named list. The names of the list correspond to the annotation names. Each element of the list is a character vector of linkouts for that annotationID.
- `reset`: Reset the data prior to adding the new data (default: `FALSE`). The default is to add to or modify any previously added data (if it exists). Setting `reset = TRUE` enables you to remove existing data you no longer want to include in the study.

**Details**

For each linkout, the URL pattern you provide will be concatenated with the value of the termID column. As an example, if you used the annotation database AmiGO 2 for your enrichments analysis, you can provide a linkout for each termID using the following pattern:

```r
go = "https://amigo.geneontology.org/amigo/term/
```

As another example, if you used the annotation database Reactome for your enrichments analysis, you can provide a linkout for each termID using the following pattern:

```r
reactome = "https://reactome.org/content/detail/
```

Note that you can provide more than one linkout per termID.

**Value**

Returns the original `onStudy` object passed to the argument `study`, but modified to include the newly added data

**See Also**

`addAnnotations`, `addEnrichments`


Examples

```r
study <- createStudy("example")
enrichmentsLinkouts <- list(
  gobp = c("https://amigo.geneontology.org/amigo/term/",
          "https://www.ebi.ac.uk/QuickGO/term/"),
  reactome = "https://reactome.org/content/detail/
)
study <- addEnrichmentsLinkouts(study, enrichmentsLinkouts)
```

---

### addFeatures

**Add feature metadata**

**Description**

Add feature metadata

**Usage**

```r
addFeatures(study, features, reset = FALSE)
```

**Arguments**

- **study** An OmicNavigator study created with `createStudy`
- **features** The metadata variables that describe the features in the study. The input object is a list of data frames (one per model). The first column of each data frame is used as the featureID, so it must contain unique values. To share a data frame across multiple models, use the modelID "default". All columns will be coerced to character strings.
- **reset** Reset the data prior to adding the new data (default: `FALSE`). The default is to add to or modify any previously added data (if it exists). Setting `reset = TRUE` enables you to remove existing data you no longer want to include in the study.

**Value**

Returns the original `onStudy` object passed to the argument `study`, but modified to include the newly added data.
addMapping

*Add mapping object*

**Description**

Add mapping object

**Usage**

```r
addMapping(study, mapping, reset = FALSE)
```

**Arguments**

- **study**: An OmicNavigator study created with `createStudy`
- **mapping**: Feature IDs from models. The input object is a list of named data frames. For each data frame, column names indicate model names while rows indicate feature IDs per model. Features with same index position across columns are treated as mapped across models. For each model, feature IDs must match feature IDs available in the results object of the respective model. 1:N relationships are allowed.

  Mapping list elements are required to be named as 'default' or after a model name as provided in `addModels()`. If a single data frame is provided, this list element is recommended to be named 'default'. For multiple list elements, each with its own data frame, list elements should be named after model name(s) (a single element may still be named 'default'). In that case, when navigating in ON front-end (FE), mapping element related to the selected model in the FE will be used in multimodel plots. If a selected model in FE does not have a corresponding mapping list element, it may still use the mapping list element called 'default' if this is available.

  E.g., if in a study there are models "transcriptomics" and "proteomics" and the user wants to create a plot based on data from both, a mapping list should be provided with `addMapping()`. In this case, the mapping list element may be named 'default'. This should contain a data frame with column names 'transcriptomics' and 'proteomics', where feature IDs that map across models are found in the same row.

- **reset**: Reset the data prior to adding the new data (default: `FALSE`). The default is to add to or modify any previously added data (if it exists). Setting `reset = TRUE` enables you to remove existing data you no longer want to include in the study.

**Value**

Returns the original `onStudy` object passed to the argument `study`, but modified to include the newly added data

**See Also**

`getPlottingData`, `plotStudy`
addMetaFeatures

Add meta-feature metadata

Description

The meta-features table is useful anytime there are metadata variables that cannot be mapped 1:1 to your features. For example, a peptide may be associated with multiple proteins.

Usage

addMetaFeatures(study, metaFeatures, reset = FALSE)

Arguments

study An OmicNavigator study created with createStudy
metaFeatures The metadata variables that describe the meta-features in the study. The input object is a list of data frames (one per model). The first column of each data frame is used as the featureID, so it must contain the same IDs as the corresponding features data frame (addFeatures). To share a data frame across multiple models, use the modelID "default". All columns will be coerced to character strings.
reset Reset the data prior to adding the new data (default: FALSE). The default is to add to or modify any previously added data (if it exists). Setting reset = TRUE enables you to remove existing data you no longer want to include in the study.

Value

Returns the original onStudy object passed to the argument study, but modified to include the newly added data

addMetaFeaturesLinkouts

Add linkouts to external resources in the metaFeatures table

Description

You can provide additional information on the metaFeatures in your study by providing linkouts to external resources. These will be embedded directly in the metaFeatures table.

Usage

addMetaFeaturesLinkouts(study, metaFeaturesLinkouts, reset = FALSE)
**Arguments**

- **study**: An OmicNavigator study created with `createStudy`
- **metaFeaturesLinkouts**: The URL patterns that describe linkouts to external resources (see Details below). The input object is a nested named list. The names of the list correspond to the model names. Each element of the list is a named list of character vectors. The names of this nested list must correspond to the column names of the matching metaFeatures table (addMetaFeatures). To share linkouts across multiple models, use the modelID "default".
- **reset**: Reset the data prior to adding the new data (default: FALSE). The default is to add to or modify any previously added data (if it exists). Setting reset = TRUE enables you to remove existing data you no longer want to include in the study.

**Details**

For each linkout, the URL pattern you provide will be concatenated with the value of that column for each row. As an example, if your metaFeatures table included a column named "ensembl" that contained the Ensembl Gene ID for each feature, you could create a linkout to Ensembl using the following pattern:

```r
ensembl = "https://ensembl.org/Homo_sapiens/Gene/Summary?g="
```

As another example, if you had a column named "entrez" that contained the Entrez Gene ID for each feature, you could create a linkout to Entrez using the following pattern:

```r
```

Note that you can provide more than one linkout per column.

**Value**

Returns the original onStudy object passed to the argument study, but modified to include the newly added data.

**See Also**

- `addMetaFeatures`

**Examples**

```r
study <- createStudy("example")
metaFeaturesLinkouts <- list(
  default = list(
    ensembl = c("https://ensembl.org/Homo_sapiens/Gene/Summary?g=",
                "https://www.genome.ucsc.edu/cgi-bin/hgGene?hgGene=hg38"),
  )
)
study <- addMetaFeaturesLinkouts(study, metaFeaturesLinkouts)
```
**Description**

Add models

**Usage**

```r
addModels(study, models, reset = FALSE)
```

**Arguments**

- `study` An OmicNavigator study created with `createStudy`
- `models` The models analyzed in the study. The input is a named list. The names correspond to the names of the models. The elements correspond to the descriptions of the models. Alternatively, instead of a single character string, you can provide a list of metadata fields about each model. The field "description" will be used to derive the tooltip displayed in the app.
- `reset` Reset the data prior to adding the new data (default: `FALSE`). The default is to add to or modify any previously added data (if it exists). Setting `reset = TRUE` enables you to remove existing data you no longer want to include in the study.

**Value**

Returns the original `onStudy` object passed to the argument `study`, but modified to include the newly added data

**Examples**

```r
study <- createStudy("example")
models <- list(
    model_01 = "Name of first model",
    model_02 = "Name of second model"
)
study <- addModels(study, models)

# Alternative: provide additional metadata about each model
models <- list(
    model_01 = list(
        description = "Name of first model",
        data_type = "transcriptomics"
    ),
    model_02 = list(
        description = "Name of second model",
        data_type = "proteomics"
    )
)
```
addOverlaps

Add overlaps between annotation gene sets

Description

The app’s network view of the enrichments results requires pairwise overlap metrics between all the terms of each annotation in order to draw the edges between the nodes/terms. These overlaps are calculated automatically when installing or exporting an OmicNavigator study. If you’d like, you can manually calculate these pairwise overlaps by calling addOverlaps prior to installing or exporting your study.

Usage

addOverlaps(study, reset = FALSE)

Arguments

study An OmicNavigator study created with createStudy
reset Reset the data prior to adding the new data (default: FALSE). The default is to add to or modify any previously added data (if it exists). Setting reset = TRUE enables you to remove existing data you no longer want to include in the study.

Value

Returns the original onStudy object passed to the argument study, but modified to include the newly added data

addPlots

Add custom plotting functions

Description

Include custom plots that the app will display when a feature is selected by the user.

Usage

addPlots(study, plots, reset = FALSE)
Arguments

study  An OmicNavigator study created with `createStudy`
plots  Custom plotting functions for the study. The input object is a nested list. The first list corresponds to the modelID(s). The second list corresponds to the name(s) of the function(s) defined in the current R session. The third list provides metadata to describe each plot. The only required metadata element is `displayName`, which controls how the plot will be named in the app. You are encouraged to also specify the `plotType`, e.g. "singleFeature", "multiFeature", "multiTest", "multiModel". `plotType` accepts vector of entries, whenever applicable, e.g., `plotType = c("multiFeature", "multiTest")`. If you do not specify the `plotType`, the plot will be assumed to be "singleFeature" and "singleTest". Optionally, if the plotting function requires external packages, these can be defined in the element `packages`. To share plots across multiple models, use the modelID "default". To add a plotting function that returns an interactive plotly plot, add "plotly" to the `plotType` vector.
reset  Reset the data prior to adding the new data (default: FALSE). The default is to add to or modify any previously added data (if it exists). Setting `reset = TRUE` enables you to remove existing data you no longer want to include in the study.

Details

Custom plotting functions are passed a list of data frames: `assays` with the measurements, `features` with the feature data, `samples` with the sample data, and `results` with test results data. Note that `assays`, `features` and `results` only include data for the specified featureID(s) (and re-ordered so their rows match). Thus your custom plotting function must have at least one argument. It can have additional arguments if you wish, but these must be provided with default values, because `plotStudy` only passes the plotting data to the first argument.

Note that any ggplot2 plots will require extra care. This is because the plotting code will be inserted into a study package, and thus must follow the best practices for using ggplot2 within packages. Specifically, when you refer to columns of the data frame, e.g. `aes(x = group)`, you need to prefix it with `.data$`, so that it becomes `aes(x = .data$group)`. Fortunately this latter code will also run fine as you interactively develop the function.

Value

Returns the original `onStudy` object passed to the argument `study`, but modified to include the newly added data

See Also

`getPlottingData, plotStudy`
addReports  Add reports

Description

You can include reports of the analyses you performed to generate the results.

Usage

addReports(study, reports, reset = FALSE)

Arguments

- study: An OmicNavigator study created with `createStudy`
- reports: The analysis report(s) that explain how the study results were generated. The input object is a list of character vectors (one per model). Each element should be either a URL or a path to a file on your computer. If it is a path to a file, this file will be included in the exported study package. To share a report across multiple models, use the modelID "default".
- reset: Reset the data prior to adding the new data (default: FALSE). The default is to add to or modify any previously added data (if it exists). Setting reset = TRUE enables you to remove existing data you no longer want to include in the study.

Value

Returns the original `onStudy` object passed to the argument study, but modified to include the newly added data

addResults  Add inference results

Description

Add inference results

Usage

addResults(study, results, reset = FALSE)
Arguments

study  An OmicNavigator study created with `createStudy`
results  The inference results from each model. The input is a nested named list. The names of the list correspond to the model names. Each element in the list should be a list of data frames with inference results, one for each test. In each data frame, the featureID must be in the first column, and all other columns must be numeric.
reset  Reset the data prior to adding the new data (default: FALSE). The default is to add to or modify any previously added data (if it exists). Setting reset = TRUE enables you to remove existing data you no longer want to include in the study.

Value

Returns the original `onStudy` object passed to the argument `study`, but modified to include the newly added data

### addResultsLinkouts

*Add linkouts to external resources in the results table*

**Description**

You can provide additional information on the features in your study by providing linkouts to external resources. These will be embedded directly in the results table.

**Usage**

`addResultsLinkouts(study, resultsLinkouts, reset = FALSE)`

**Arguments**

study  An OmicNavigator study created with `createStudy`
resultsLinkouts  The URL patterns that describe linkouts to external resources (see Details below). The input object is a nested named list. The names of the list correspond to the model names. Each element of the list is a named list of character vectors. The names of this nested list must correspond to the column names of the matching features table. To share linkouts across multiple models, use the modelID "default".
reset  Reset the data prior to adding the new data (default: FALSE). The default is to add to or modify any previously added data (if it exists). Setting reset = TRUE enables you to remove existing data you no longer want to include in the study.
Details
For each linkout, the URL pattern you provide will be concatenated with the value of that column for each row. As an example, if your features table included a column named "ensembl" that contained the Ensembl Gene ID for each feature, you could create a linkout to Ensembl using the following pattern:

ensmbl = "https://ensembl.org/Homo_sapiens/Gene/Summary?g="

As another example, if you had a column named "entrez" that contained the Entrez Gene ID for each feature, you could create a linkout to Entrez using the following pattern:


Note that you can provide more than one linkout per column.

Value
Returns the original onStudy object passed to the argument study, but modified to include the newly added data

See Also
addFeatures

Examples
study <- createStudy("example")
resultsLinkouts <- list(
default = list(
    ensembl = c("https://ensembl.org/Homo_sapiens/Gene/Summary?g=",
                 "https://www.genome.ucsc.edu/cgi-bin/hgGene?hgg_gene="),
  )
)
study <- addResultsLinkouts(study, resultsLinkouts)

---

addSamples  Add sample metadata

Description
Add sample metadata

Usage
addSamples(study, samples, reset = FALSE)
addTests

Arguments

study          An OmicNavigator study created with createStudy
samples       The metadata variables that describe the samples in the study. The input object
              is a named list of data frames (one per model). The first column of each data
              frame is used as the sampleID, so it must contain unique values. To share a data
              frame across multiple models, use the modelID "default".
reset          Reset the data prior to adding the new data (default: FALSE). The default is to
              add to or modify any previously added data (if it exists). Setting reset = TRUE
              enables you to remove existing data you no longer want to include in the study.

Value

Returns the original onStudy object passed to the argument study, but modified to include the
newly added data

Description

Add tests

Usage

addTests(study, tests, reset = FALSE)

Arguments

study          An OmicNavigator study created with createStudy
tests          The tests from the study. The input object is a list of lists. Each element of
              the top-level list is a model. The names should be the modelIDs. For each
              modelID, each element of the nested list is a test. The names should be the
              testIDs. The value should be a single character string describing the testID.
              To share tests across multiple models, use the modelID "default". Instead of a
              single character string, you can provide a list of metadata fields about each test.
              The field "description" will be used to derive the tooltip displayed in the app.
reset          Reset the data prior to adding the new data (default: FALSE). The default is to
              add to or modify any previously added data (if it exists). Setting reset = TRUE
              enables you to remove existing data you no longer want to include in the study.

Value

Returns the original onStudy object passed to the argument study, but modified to include the
newly added data
Examples

```r
study <- createStudy("example")
tests <- list(
    default = list(
        test_01 = "Name of first test",
        test_02 = "Name of second test"
    )
)
study <- addTests(study, tests)

# Alternative: provide additional metadata about each test
tests <- list(
    default = list(
        test_01 = list(
            description = "Name of first test",
            comparison_type = "treatment vs control",
            effect_size = "beta"
        ),
        test_02 = list(
            description = "Name of second test",
            comparison_type = "treatment vs control",
            effect_size = "logFC"
        )
    )
)
```

basal.vs.lp  

basal.vs.lp from Bioconductor workflow RNAseq123

Description

A subset of the object basal.vs.lp from Bioconductor workflow RNAseq123.

Usage

basal.vs.lp

Format

A data frame with 24 rows and 8 columns:

<table>
<thead>
<tr>
<th>ENTREZID</th>
<th>Entrez ID of mouse gene</th>
</tr>
</thead>
<tbody>
<tr>
<td>SYMBOL</td>
<td>Symbol of mouse gene</td>
</tr>
<tr>
<td>TXCHROM</td>
<td>Chromosome location of mouse gene</td>
</tr>
<tr>
<td>logFC</td>
<td>Log fold change</td>
</tr>
<tr>
<td>AveExpr</td>
<td>Average expression level of the gene across all samples</td>
</tr>
<tr>
<td>t</td>
<td>Moderated t-statistic</td>
</tr>
</tbody>
</table>
basal.vs.ml

**P.Value**  p-value  
**adj.P.Val**  Adjusted p-value

**Source**


**References**


**Examples**

```
head(basal.vs.lp)
str(basal.vs.lp)
```

---

basal.vs.ml  

*basal.vs.ml from Bioconductor workflow RNAseq123*

**Description**

A subset of the object `basal.vs.ml` from Bioconductor workflow RNAseq123.

**Usage**

`basal.vs.ml`

**Format**

A data frame with 24 rows and 8 columns:

- **ENTREZID**  Entrez ID of mouse gene
- **SYMBOL**  Symbol of mouse gene
- **TXCHROM**  Chromosome location of mouse gene
- **logFC**  Log fold change
- **AveExpr**  Average expression level of the gene across all samples
- **t**  Moderated t-statistic
- **P.Value**  p-value
- **adj.P.Val**  Adjusted p-value
cam.BasalvsLP

Source


References


Examples

head(basal.vs.ml)
str(basal.vs.ml)

cam.BasalvsLP

cam.BasalvsLP from Bioconductor workflow RNAseq123

Description

A subset of the object cam.BasalvsLP from Bioconductor workflow RNAseq123.

Usage

cam.BasalvsLP

Format

A data frame with 4 rows and 4 columns:

NGenes  Number of genes in each term
Direction  Direction of the enrichment
PValue  Nominal p-value
FDR  Multiple-testing adjusted p-value

Source

References


Examples

head(cam.BasalvsLP)
str(cam.BasalvsLP)

Description

A subset of the object cam.BasalvsML from Bioconductor workflow RNAseq123.

Usage

cam.BasalvsML

Format

A data frame with 4 rows and 4 columns:

NGenes Number of genes in each term
Direction Direction of the enrichment
PValue Nominal p-value
FDR Multiple-testing adjusted p-value

Source


References


combineStudies

Examples

```r
head(cam.BasalvsML)
str(cam.BasalvsML)
```

Description

Create a new OmicNavigator study by combining two or more existing study objects.

Usage

```r
combineStudies(...)
```

Arguments

... Two or more objects of class `onStudy`

Details

This is a convenience function to quickly and conveniently combine studies. However, it is naive, and you will likely need to edit the new study after combining. When there are conflicting elements (e.g. different study names or different maintainers), then the value for the latter study is kept. As a concrete example, if you combined 5 studies, the name of the combined study would be the name of the 5th study.

The behavior is more complex for study elements that are nested lists of data frames (e.g. results). If the 5 studies included a results table for the same modelID/testID combination, then only the results from the 5th study would be retained. However, if they each defined a different modelID, then the results for all 5 modelIDs would be included in the combined study. Please note that you should be extra cautious in the situation where the studies have the same modelID/testID combination. Ideally they should all have the same column names. Since a data frame is technically a list, the workhorse function `modifyList` will retain any uniquely named columns from earlier studies along with the columns from the final study.

Note that as a shortcut you can also combine studies using the S3 method `c`.

If a study you would like to combine is already installed, you can convert it to a study object by importing it with `importStudy`.

Value

Returns a new combined OmicNavigator study object, which is a named nested list with class `onStudy`

See Also

`createStudy`, `importStudy`
createStudy

Examples

# Define three study objects
studyOne <- createStudy(name = "One",
                         description = "First study",
                         studyMeta = list(metafield1 = "metavalue1"))

studyTwo <- createStudy(name = "Two",
                         description = "Second study",
                         maintainer = "The Maintainer",
                         studyMeta = list(metafield2 = "metavalue2"))

studyThree <- createStudy(name = "Three",
                           description = "Third study",
                           studyMeta = list(metafield3 = "metavalue3"))

# Combine the three studies
combineStudies(studyOne, studyTwo, studyThree)

# Equivalently, can use c()
c(studyOne, studyTwo, studyThree)

createStudy Create a study

Description

Create a new OmicNavigator study.

Usage

createStudy(
  name,
  description = name,
  samples = list(),
  features = list(),
  models = list(),
  assays = list(),
  tests = list(),
  annotations = list(),
  results = list(),
  enrichments = list(),
  metaFeatures = list(),
  plots = list(),
  mapping = list(),
  barcodes = list(),
  reports = list(),
)
resultsLinkouts = list(),
enrichmentsLinkouts = list(),
metaFeaturesLinkouts = list(),
version = NULL,
maintainer = NULL,
maintainerEmail = NULL,
studyMeta = list()
)

Arguments

name Name of the study
description Description of the study
samples The metadata variables that describe the samples in the study. The input object is a named list of data frames (one per model). The first column of each data frame is used as the sampleID, so it must contain unique values. To share a data frame across multiple models, use the modelID "default".
features The metadata variables that describe the features in the study. The input object is a list of data frames (one per model). The first column of each data frame is used as the featureID, so it must contain unique values. To share a data frame across multiple models, use the modelID "default". All columns will be coerced to character strings.
models The models analyzed in the study. The input is a named list. The names correspond to the names of the models. The elements correspond to the descriptions of the models. Alternatively, instead of a single character string, you can provide a list of metadata fields about each model. The field "description" will be used to derive the tooltip displayed in the app.
assays The assays from the study. The input object is a list of data frames (one per model). The row names should correspond to the featureIDs (addFeatures). The column names should correspond to the sampleIDs (add Samples). The data frame should only contain numeric values. To share a data frame across multiple models, use the modelID "default".
tests The tests from the study. The input object is a list of lists. Each element of the top-level list is a model. The names should be the modelIDs. For each modelID, each element of the nested list is a test. The names should be the testIDs. The value should be a single character string describing the testID. To share tests across multiple models, use the modelID "default". Instead of a single character string, you can provide a list of metadata fields about each test. The field "description" will be used to derive the tooltip displayed in the app.
annotations The annotations used for the enrichment analyses. The input is a nested list. The top-level list contains one entry per annotation database, e.g. reactome. The names correspond to the name of each annotation database. Each of these elements should be a list that contains more information about each annotation database. Specifically the sublist should contain 1) description, a character vector that describes the resource, 2) featureID, the name of the column in the features table that was used for the enrichment analysis, and 3) terms, a list of annotation terms. The names of terms sublist correspond to the name of the
annotation terms. Each of the annotation terms should be a character vector of featureIDs.

**results**  
The inference results from each model. The input is a nested named list. The names of the list correspond to the model names. Each element in the list should be a list of data frames with inference results, one for each test. In each data frame, the featureID must be in the first column, and all other columns must be numeric.

**enrichments**  
The enrichment results from each model. The input is a nested named list. The names of the list correspond to the model names. Each list element should be a list of the annotation databases tested (addAnnotations). The names of the list correspond to the annotation databases. Each list element should be another list of tests (addTests). The names correspond to the tests performed. Each of these elements should be a data frame with enrichment results. Each table must contain the following columns: "termID", "description", "nominal" (the nominal statistics), and "adjusted" (the statistics after adjusting for multiple testing). Any additional columns are ignored.

**metaFeatures**  
The metadata variables that describe the meta-features in the study. The input object is a list of data frames (one per model). The first column of each data frame is used as the featureID, so it must contain the same IDs as the corresponding features data frame (addFeatures). To share a data frame across multiple models, use the modelID "default". All columns will be coerced to character strings.

**plots**  
Custom plotting functions for the study. The input object is a nested list. The first list corresponds to the modelID(s). The second list corresponds to the name(s) of the function(s) defined in the current R session. The third list provides metadata to describe each plot. The only required metadata element is displayName, which controls how the plot will be named in the app. You are encouraged to also specify the plotType, e.g. "singleFeature", "multiFeature", "multiTest", "multiModel". PlotType accepts vector of entries, whenever applicable, e.g., plotType = c("multiFeature", "multiTest"). If you do not specify the plotType, the plot will be assumed to be "singleFeature" and "singleTest". Optionally, if the plotting function requires external packages, these can be defined in the element packages. To share plots across multiple models, use the modelID "default". To add a plotting function that returns an interactive plotly plot, add "plotly" to the plotType vector.

**mapping**  
Feature IDs from models. The input object is a list of named data frames. For each data frame, column names indicate model names while rows indicate featureIDs per model. Features with same index position across columns are treated as mapped across models. For each model, feature IDs must match feature IDs available in the results object of the respective model. 1:N relationships are allowed.

Mapping list elements are required to be named as 'default' or after a model name as provided in addModels(). If a single data frame is provided, this list element is recommended to be named 'default'. For multiple list elements, each with its own data frame, list elements should be named after model name(s) (a single element may still be named 'default'). In that case, when navigating in ON front-end (FE), mapping element related to the selected model in the FE
will be used in multimodel plots. If a selected model in FE does not have a corresponding mapping list element, it may still use the mapping list element called 'default' if this is available.

E.g., if in a study there are models "transcriptomics" and "proteomics" and the user wants to create a plot based on data from both, a mapping list should be provided with addMapping(). In this case, the mapping list element may be named 'default'. This should contain a data frame with column names 'transcriptomics' and 'proteomics', where feature IDs that map across models are found in the same row.

**barcodes**
The metadata variables that describe the barcode plot. The input object is a list of lists (one per model). Each sublist must contain the element `statistic`, which is the column name in the results table to use to construct the barcode plot. Each sublist may additionally contain any of the following optional elements:

1) `absolute` - Should the statistic be converted to its absolute value (default is `TRUE`). 2) `logFoldChange` - The column name in the results table that contains the log fold change values. 3) `labelStat` - The x-axis label to describe the statistic. 4) `labelLow` - The left-side label to describe low values of the statistic. 5) `labelHigh` - The right-side label to describe high values of the statistic. 6) `featureDisplay` - The feature variable to use to label the barcode plot on hover.

To share metadata across multiple models, use the modelID "default".

**reports**
The analysis report(s) that explain how the study results were generated. The input object is a list of character vectors (one per model). Each element should be either a URL or a path to a file on your computer. If it is a path to a file, this file will be included in the exported study package. To share a report across multiple models, use the modelID "default".

**resultsLinkouts**
The URL patterns that describe linkouts to external resources (see Details below). The input object is a nested named list. The names of the list correspond to the model names. Each element of the list is a named list of character vectors. The names of this nested list must correspond to the column names of the matching features table. To share linkouts across multiple models, use the modelID "default".

**enrichmentsLinkouts**
The URL patterns that describe linkouts to external resources (see Details below). The input object is a named list. The names of the list correspond to the annotation names. Each element of the list is a character vector of linkouts for that annotationID.

**metaFeaturesLinkouts**
The URL patterns that describe linkouts to external resources (see Details below). The input object is a nested named list. The names of the list correspond to the model names. Each element of the list is a named list of character vectors. The names of this nested list must correspond to the column names of the matching metaFeatures table (addMetaFeatures). To share linkouts across multiple models, use the modelID "default".

**version**
(Optional) Include a version number to track the updates to your study package. If you export the study to a package, the version is used as the package version.

**maintainer**
(Optional) Include the name of the study package’s maintainer
exportStudy

maintainerEmail
  (Optional) Include the email of the study package’s maintainer

studyMeta    (Optional) Define metadata about your study. The input is a list of key:value pairs. See below for more details.

Details

You can add metadata to describe your study by passing a named list to to the argument studyMeta. The names of the list cannot contain spaces or colons, and they can’t start with # or -. The values of each list should be a single value. Also, your metadata fields cannot use any of the reserved fields for R’s DESCRIPTION file.

Value

Returns a new OmicNavigator study object, which is a named nested list with class onStudy

See Also

addSamples, addFeatures, addModels, addAssays, addTests, addAnnotations, addResults, addEnrichments, addMetaFeatures, addPlots, addMapping, addBarcodes, addReports, addResultsLinkouts, addEnrichmentsLinkouts, addMetaFeaturesLinkouts, exportStudy, installStudy

Examples

study <- createStudy(name = "ABC",
  description = "An analysis of ABC")

# Define a version and study metadata
study <- createStudy(name = "ABC",
  description = "An analysis of ABC",
  version = "0.1.0",
  maintainer = "My Name",
  maintainerEmail = "me@email.com",
  studyMeta = list(department = "immunology",
                    organism = "Mus musculus"))

---

Export a study

Description

Export a study
getAnnotations

Usage

```r
exportStudy(
    study,
    type = c("tarball", "package"),
    path = NULL,
    requireValid = TRUE
)
```

Arguments

- **study**: An OmicNavigator study
- **type**: Export study as a package tarball ("tarball") or as a package directory ("package")
- **path**: Optional file path to save the object
- **requireValid**: Require that study is valid before exporting

Value

Invisibly returns the name of the tarball file ("tarball") or the path to the package directory ("package")

See Also

validateStudy

getAnnotations

Get annotations from a study

Description

Get annotations from a study

Usage

```r
getAnnotations(study, annotationID = NULL, quiet = FALSE, libraries = NULL)
```

Arguments

- **study**: An OmicNavigator study. Either an object of class `onStudy`, or the name of an installed study package.
- **annotationID**: Filter by annotationID
- **quiet**: Suppress messages (default: FALSE)
- **libraries**: The directories to search for installed study packages. If left as NULL (default), then `installed.packages` will use the result of `.libPaths`. 
Value

The object returned depends on the data available and any filters (e.g. the argument modelID):
If no filters are specified, then the object returned is a nested list, similar to the original input object.
If one or more filters are applied, then only a subset of the original nested list is returned. Techni-
cally, each filter applied is used to subset the original nested list using [[
If no data is available, an empty list is returned (list()).

---

**getAssays**

*Get assays from a study*

**Description**

Get assays from a study

**Usage**

```
getAssays(study, modelID = NULL, quiet = FALSE, libraries = NULL)
```

**Arguments**

- **study**: An OmicNavigator study. Either an object of class onStudy, or the name of an
  installed study package.
- **modelID**: Filter by modelID
- **quiet**: Suppress messages (default: FALSE)
- **libraries**: The directories to search for installed study packages. If left as NULL (the de-
  fault), then `installed.packages` will use the result of `.libPaths`.

**Value**

The object returned depends on the data available and any filters (e.g. the argument modelID):
If no filters are specified, then the object returned is a nested list, similar to the original input object.
If one or more filters are applied, then only a subset of the original nested list is returned. Techni-
cally, each filter applied is used to subset the original nested list using [[
If no data is available, an empty list is returned (list()).
getBarcodeData  

Get data for barcode and violin plots

Description

Get data for barcode and violin plots

Usage

getBarcodeData(study, modelID, testID, annotationID, termID)

Arguments

- study: An OmicNavigator study. Either an object of class onStudy, or the name of an installed study package.
- modelID: Filter by modelID
- testID: Filter by testID
- annotationID: Filter by annotationID
- termID: Filter by termID

Value

A list with the following components:

- data: Data frame with the differential statistics to plot
- highest: (numeric) The largest differential statistic, rounded up to the next integer
- labelStat: (character) The x-axis label to describe the differential statistic
- labelLow: (character) The vertical axis label on the left to describe smaller values (default is "Low")
- labelHigh: (character) The vertical axis label on the right to describe larger values (default is "High")

See Also

addBarcodes, getBarcodes
**getBarcodes**

*Get barcodes from a study*

**Description**

Get barcodes from a study

**Usage**

```r
getBarcodes(study, modelID = NULL, quiet = FALSE, libraries = NULL)
```

**Arguments**

- **study**: An OmicNavigator study. Either an object of class `onStudy`, or the name of an installed study package.
- **modelID**: Filter by modelID
- **quiet**: Suppress messages (default: `FALSE`)
- **libraries**: The directories to search for installed study packages. If left as `NULL` (the default), then `installed.packages` will use the result of `.libPaths`.

**Value**

The object returned depends on the data available and any filters (e.g. the argument `modelID`):
- If no filters are specified, then the object returned is a nested list, similar to the original input object.
- If one or more filters are applied, then only a subset of the original nested list is returned. Technically, each filter applied is used to subset the original nested list using `[[]].
- If no data is available, an empty list is returned (`list()`).

**getEnrichments**

*Get enrichments from a study*

**Description**

Get enrichments from a study

**Usage**

```r
getEnrichments(
  study,
  modelID = NULL,
  annotationID = NULL,
  testID = NULL,
  quiet = FALSE,
  libraries = NULL
)
```
getEnrichmentsIntersection

Arguments

study         An OmicNavigator study. Either an object of class onStudy, or the name of an installed study package.
modelID      Filter by modelID
annotationID Filter by annotationID
testID        Filter by testID
quiet         Suppress messages (default: FALSE)
libraries     The directories to search for installed study packages. If left as NULL (the default), then installed.packages will use the result of .libPaths.

Value

The object returned depends on the data available and any filters (e.g. the argument modelID):

If no filters are specified, then the object returned is a nested list, similar to the original input object.

If one or more filters are applied, then only a subset of the original nested list is returned. Technically, each filter applied is used to subset the original nested list using \[
\]

If no data is available, an empty list is returned (list()).

getEnrichmentsIntersection

Description

getEnrichmentsIntersection

Usage

getEnrichmentsIntersection(
    study, modelID, annotationID, mustTests, notTests, sigValue, operator, type
)
Get enrichments table linkouts from a study

Description

Get enrichments table linkouts from a study

Usage

getEnrichmentsLinkouts(
  study,
  annotationID = NULL,
  quiet = FALSE,
  libraries = NULL
)
getEnrichmentsNetwork

Arguments

study  An OmicNavigator study. Either an object of class onStudy, or the name of an installed study package.

annotationID Filter by annotationID

quiet Suppress messages (default: FALSE)

libraries The directories to search for installed study packages. If left as NULL (the default), then installed.packages will use the result of .libPaths.

Value

The object returned depends on the data available and any filters (e.g. the argument modelID):

- If no filters are specified, then the object returned is a nested list, similar to the original input object.
- If one or more filters are applied, then only a subset of the original nested list is returned. Technically, each filter applied is used to subset the original nested list using [[]].
- If no data is available, an empty list is returned (list()).

Description

Get enrichments network from a study

Usage

getEnrichmentsNetwork(study, modelID, annotationID, libraries = NULL)

Arguments

study  An OmicNavigator study. Either an object of class onStudy, or the name of an installed study package.

modelID Filter by modelID

annotationID Filter by annotationID

libraries The directories to search for installed study packages. If left as NULL (the default), then installed.packages will use the result of .libPaths.

Value

Returns a list with the following components:

tests (character) Vector of testIDs

nodes (data frame) The description of each annotation term (i.e. node). The nominal and adjusted p-values are in list-columns.

links (list) The statistics for each pairwise overlap between the annotation terms (i.e. nodes)
**getEnrichmentsTable**  
Get enrichments table from a study

**Description**
Get enrichments table from a study

**Usage**

```r
getEnrichmentsTable(
    study,  
    modelID,  
    annotationID,  
    type = "nominal",  
    libraries = NULL
)
```

**Arguments**

- **study**: An OmicNavigator study. Either an object of class `onStudy`, or the name of an installed study package.
- **modelID**: Filter by modelID
- **annotationID**: Filter by annotationID
- **type**: Type of p-value: ("nominal" or "adjusted")
- **libraries**: The directories to search for installed study packages. If left as `NULL` (the default), then `installed.packages` will use the result of `.libPaths`.

**Value**
A data frame of enrichments with the following columns:

- **termID**: The unique ID for the annotation term
- **description**: The description of the annotation term
- ... One column for each of the enrichments
getEnrichmentsUpset  getEnrichmentsUpset

Description

getEnrichmentsUpset

Usage

getEnrichmentsUpset(
  study,
  modelID,
  annotationID,
  sigValue,
  operator,
  type,
  tests = NULL
)

Arguments

study  An OmicNavigator study. Either an object of class onStudy, or the name of an installed study package.
modelID  Filter by modelID
annotationID  Filter by annotationID
sigValue  The numeric significance value to use as a cutoff for each column
operator  The comparison operators for each column, e.g. "<"
type  Type of p-value: ("nominal" or "adjusted")
tests  Restrict UpSet plot to only include these tests

Value

No return value. This function is called for the side effect of creating an UpSet plot.

getFavicons  Get favicon URLs for table linkouts

Description

To enhance the display of the linkouts in the app’s tables, it can fetch the favicon URL for each website.
getFeatures

Usage

getFavicons(linkouts)

Arguments

linkouts Character vector or (potentially nested) list of character vectors containing the
URLs for the table linkouts.

Value

The URLs to the favicons for each linkout. The output returned will always be the same class and
structure as the input.

See Also

getResultsLinkouts, getEnrichmentsLinkouts

---

getFeatures Get features from a study

Description

Get features from a study

Usage

getFeatures(study, modelID = NULL, quiet = FALSE, libraries = NULL)

Arguments

study An OmicNavigator study. Either an object of class onStudy, or the name of an
installed study package.

modelID Filter by modelID

quiet Suppress messages (default: FALSE)

libraries The directories to search for installed study packages. If left as NULL (the de-
fault), then installed.packages will use the result of .libPaths.

Value

A data frame (if modelID is specified) or a list of data frames. All the columns will be character
strings, even if the values appear numeric.
getInstalledStudies  Get installed OmicNavigator studies

Description
Get installed OmicNavigator studies

Usage
getInstalledStudies(libraries = NULL)

Arguments
libraries  Character vector of library directories to search for study packages. If NULL, uses .libPaths.

Value
Returns a character vector of the installed OmicNavigator study packages

getLinkFeatures  Get the shared features in a network link

Description
Get the shared features in a network link

Usage
getLinkFeatures(study, annotationID, termID1, termID2)

Arguments
study  An OmicNavigator study. Only accepts name of installed study package.
annotationID  Filter by annotationID
termID1, termID2  Linked terms to find overlapping features

Value
Returns a character vector with the features included in both termIDs (i.e. the intersection)

See Also
getNodeFeatures
getMapping

Get mapping object from a study

Description
Get mapping object from a study

Usage
getMapping(study, modelID = NULL, quiet = FALSE, libraries = NULL)

Arguments
- **study**: An OmicNavigator study. Either an object of class `onStudy`, or the name of an installed study package.
- **modelID**: Filter by modelID
- **quiet**: Suppress messages (default: FALSE)
- **libraries**: The directories to search for installed study packages. If left as NULL (the default), then `installed.packages` will use the result of `.libPaths`.

Value
The object returned depends on the data available and any filters (e.g. the argument `modelID`):
- If no filters are specified, then the object returned is a nested list, similar to the original input object.
- If one or more filters are applied, then only a subset of the original nested list is returned. Technically, each filter applied is used to subset the original nested list using `[[].
- If no data is available, an empty list is returned (list()).

getMetaFeatures

Get metaFeatures from a study

Description
Get metaFeatures from a study

Usage
getMetaFeatures(study, modelID = NULL, quiet = FALSE, libraries = NULL)
**getMetaFeaturesLinkouts**

*Description*

Get metaFeatures table linkouts from a study

*Usage*

`getMetaFeaturesLinkouts(study, modelID = NULL, quiet = FALSE, libraries = NULL)`

**Arguments**

- **study**: An OmicNavigator study. Either an object of class onStudy, or the name of an installed study package.
- **modelID**: Filter by modelID
- **quiet**: Suppress messages (default: FALSE)
- **libraries**: The directories to search for installed study packages. If left as NULL (the default), then `installed.packages` will use the result of `.libPaths`.

**Value**

The object returned depends on the data available and any filters (e.g. the argument `modelID`):

- If no filters are specified, then the object returned is a nested list, similar to the original input object.
- If one or more filters are applied, then only a subset of the original nested list is returned. Technically, each filter applied is used to subset the original nested list using `[[]]`.
- If no data is available, an empty list is returned (`list()`).
getMetaFeaturesTable  
*Get metaFeatures for a given feature*

**Description**
Get metaFeatures for a given feature

**Usage**
```
getMetaFeaturesTable(study, modelID, featureID)
```

**Arguments**
- **study**: An OmicNavigator study. Either an object of class `onStudy`, or the name of an installed study package.
- **modelID**: Filter by modelID
- **featureID**: Filter by featureID

**Value**
Returns a data frame with the metaFeatures for the provided featureID. If the featureID is not found in the metaFeatures table, the data frame will have zero rows.

**See Also**
- `addMetaFeatures`, `getMetaFeatures`

getModels  
*Get models from a study*

**Description**
Get models from a study

**Usage**
```
getModels(study, modelID = NULL, quiet = FALSE, libraries = NULL)
```

**Arguments**
- **study**: An OmicNavigator study. Either an object of class `onStudy`, or the name of an installed study package.
- **modelID**: Filter by modelID
- **quiet**: Suppress messages (default: `FALSE`)
- **libraries**: The directories to search for installed study packages. If left as `NULL` (the default), then `installed.packages` will use the result of `.libPaths`. 
**getNodeFeatures**

**Value**

The object returned depends on the data available and any filters (e.g. the argument modelID):

If no filters are specified, then the object returned is a nested list, similar to the original input object.

If one or more filters are applied, then only a subset of the original nested list is returned. Technically, each filter applied is used to subset the original nested list using `[[`. If no data is available, an empty list is returned (`list()`).

---

### getNodeFeatures

*Get the features in a network node*

**Description**

Get the features in a network node

**Usage**

```
getNodeFeatures(study, annotationID, termID, libraries = NULL)
```

**Arguments**

- **study** An OmicNavigator study. Only accepts name of installed study package.
- **annotationID** Filter by annotationID
- **termID** Filter by termID
- **libraries** The directories to search for installed study packages. If left as `NULL` (the default), then `installed.packages` will use the result of `.libPaths`.

**Value**

Returns a character vector with the features in the termID

**See Also**

`getLinkFeatures`
getOverlaps

Get overlaps from a study

Description

Get overlaps from a study

Usage

getOverlaps(study, annotationID = NULL, quiet = FALSE, libraries = NULL)

Arguments

study An OmicNavigator study. Either an object of class onStudy, or the name of an installed study package.
annotationID Filter by annotationID
quiet Suppress messages (default: FALSE)
libraries The directories to search for installed study packages. If left as NULL (the default), then installed.packages will use the result of .libPaths.

Value

The object returned depends on the data available and any filters (e.g. the argument modelID):
If no filters are specified, then the object returned is a nested list, similar to the original input object. If one or more filters are applied, then only a subset of the original nested list is returned. Technically, each filter applied is used to subset the original nested list using [[]. If no data is available, an empty list is returned (list()).

getPackageVersion

Get version of OmicNavigator package

Description

This is a convenience function for the app. It is easier to always call the OmicNavigator package functions via OpenCPU than to call the utils package for this one endpoint.

Usage

getPackageVersion()

Value

Returns a one-element character vector with the version of the currently installed OmicNavigator R package
getPlots

**Get plots from a study**

**Description**

Get plots from a study

**Usage**

getPlots(study, modelID = NULL, quiet = FALSE, libraries = NULL)

**Arguments**

- **study**: An OmicNavigator study. Either an object of class `onStudy`, or the name of an installed study package.
- **modelID**: Filter by modelID
- **quiet**: Suppress messages (default: FALSE)
- **libraries**: The directories to search for installed study packages. If left as NULL (the default), then `installed.packages` will use the result of `.libPaths`.

**Value**

The object returned depends on the data available and any filters (e.g. the argument modelID):
- If no filters are specified, then the object returned is a nested list, similar to the original input object.
- If one or more filters are applied, then only a subset of the original nested list is returned. Technically, each filter applied is used to subset the original nested list using `[[]].`
- If no data is available, an empty list is returned (`list()`).

getPlottingData

**Get plotting data**

**Description**

This function creates the input data that `plotStudy` passes to custom plotting functions added with `addPlots`. You can use it directly when you are interactively creating your custom plotting functions. Note that for multiModel plots `testID` is required to be a named vector, with each `testID` named after the related `modelID`.

**Usage**

getPlottingData(study, modelID, featureID, testID = NULL, libraries = NULL)
getPlottingData

Arguments

study
An OmicNavigator study. Either an object of class onStudy, or the name of an installed study package.

modelID
Filter by modelID

featureID
Filter by featureID

testID
Filter by testID

libraries
The directories to search for installed study packages. If left as NULL (the default), then installed.packages will use the result of .libPaths.

Value

Returns a list of 4 data frames:

assays
A data frame that contains the assay measurements, filtered to only include the row(s) corresponding to the input featureID(s) (see getAssays). If multiple featureIDs are requested, the rows are reordered to match the order of this input. The column order is unchanged.

samples
A data frame that contains the sample metadata for the given modelID (see getSamples). The rows are reordered to match the columns of the assays data frame.

features
A data frame that contains the feature metadata, filtered to only include the row(s) corresponding to the input featureID(s) (see getFeatures). If multiple featureIDs are requested, the rows are reordered to match the order of this input (and thus match the order of the assays data frame).

results
A data frame that contains the test results, filtered to only include the row(s) corresponding to the input featureID(s). If multiple featureIDs are requested, the rows are reordered to match the order of this input. The column order is unchanged. If multiple testIDs are provided, they are stored in a list object.

The data frame results is only returned if you pass a testID. By default the app will always pass the currently selected testID. To make results a list of data frames (one for each testID for the currently selected modelID), set the plotType to be "multiTest" when adding the plot with addPlots. For "multiModel" plots, testID and modelID should be vectors of same length, where the index position indicate which test in testID relate to which model in modelID.

See Also

addPlots, plotStudy
getReportLink  \hspace{1em} \textit{Get link to report}

\textbf{Description}

Get link to report

\textbf{Usage}

\begin{verbatim}
getReportLink(study, modelID)
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{study} \hspace{2em} An OmicNavigator study. Either an object of class \texttt{onStudy}, or the name of an installed study package.
  \item \texttt{modelID} \hspace{2em} Filter by modelID
\end{itemize}

\textbf{Value}

Returns a one-element character vector with either a path to a report file or a URL to a report web page. If no report is available for the modelID, an empty character vector is returned.

generateReports  \hspace{1em} \textit{Get reports from a study}

\textbf{Description}

Get reports from a study

\textbf{Usage}

\begin{verbatim}
getReports(study, modelID = NULL, quiet = FALSE, libraries = NULL)
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{study} \hspace{2em} An OmicNavigator study. Either an object of class \texttt{onStudy}, or the name of an installed study package.
  \item \texttt{modelID} \hspace{2em} Filter by modelID
  \item \texttt{quiet} \hspace{2em} Suppress messages (default: \texttt{FALSE})
  \item \texttt{libraries} \hspace{2em} The directories to search for installed study packages. If left as \texttt{NULL} (the default), then \texttt{installed.packages} will use the result of \texttt{.libPaths}.
\end{itemize}
Value
The object returned depends on the data available and any filters (e.g. the argument `modelID`):

If no filters are specified, then the object returned is a nested list, similar to the original input object.
If one or more filters are applied, then only a subset of the original nested list is returned. Techni-
cally, each filter applied is used to subset the original nested list using `[[`.
If no data is available, an empty list is returned (`list()`).

---

**getResults**  
*Get results from a study*

**Description**
Get results from a study

**Usage**
```r
getResults(
  study,
  modelID = NULL,
  testID = NULL,
  quiet = FALSE,
  libraries = NULL
)
```

**Arguments**
- `study` An OmicNavigator study. Either an object of class `onStudy`, or the name of an installed study package.
- `modelID` Filter by modelID
- `testID` Filter by testID
- `quiet` Suppress messages (default: `FALSE`)
- `libraries` The directories to search for installed study packages. If left as `NULL` (the de-
  fault), then `installed.packages` will use the result of `.libPaths`.

**Value**
The object returned depends on the data available and any filters (e.g. the argument `modelID`):

If no filters are specified, then the object returned is a nested list, similar to the original input object.
If one or more filters are applied, then only a subset of the original nested list is returned. Techni-
cally, each filter applied is used to subset the original nested list using `[[`.
If no data is available, an empty list is returned (`list()`).
getResultsIntersection

Description

getResultsIntersection

Usage

getResultsIntersection(
  study,
  modelID,
  anchor,
  mustTests,
  notTests,
  sigValue,
  operator,
  column
)

Arguments

study An OmicNavigator study. Either an object of class onStudy, or the name of an installed study package.
modelID Filter by modelID
anchor The primary testID to filter the results
mustTests The testIDs for which a featureID (or termID for enrichment) must pass the filters
notTests The testIDs for which a featureID (or termID for enrichment) must not pass the filters. In other words, if a featureID passes the filter for a testID specified in notTests, that featureID is removed from the output
sigValue The numeric significance value to use as a cutoff for each column
operator The comparison operators for each column, e.g. "<"
column The columns to apply the filters

Value

Returns a data frame with the results, similar to getResultsTable. Only rows that pass all the filters are included. The new column Set_Membership is a comma-separated field that includes the testIDs in which the featureID passed the filters.

See Also

getResultsTable
getResultsLinkouts

Get results table linkouts from a study

Description
Get results table linkouts from a study

Usage
getResultsLinkouts(study, modelID = NULL, quiet = FALSE, libraries = NULL)

Arguments
- study: An OmicNavigator study. Either an object of class onStudy, or the name of an installed study package.
- modelID: Filter by modelID
- quiet: Suppress messages (default: FALSE)
- libraries: The directories to search for installed study packages. If left as NULL (the default), then installed.packages will use the result of .libPaths.

Value
The object returned depends on the data available and any filters (e.g. the argument modelID):
- If no filters are specified, then the object returned is a nested list, similar to the original input object.
- If one or more filters are applied, then only a subset of the original nested list is returned. Technically, each filter applied is used to subset the original nested list using [.
- If no data is available, an empty list is returned (list()).

getResultsTable

Get results table from a study

Description
Get results table from a study

Usage
getResultsTable(
  study,
  modelID,
  testID,
  annotationID = NULL,
  termID = NULL,
  libraries = NULL
)

getResultsUpset

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>An OmicNavigator study. Either an object of class onStudy, or the name of an installed study package.</td>
</tr>
<tr>
<td>modelID</td>
<td>Filter by modelID</td>
</tr>
<tr>
<td>testID</td>
<td>Filter by testID</td>
</tr>
<tr>
<td>annotationID</td>
<td>Filter by annotationID</td>
</tr>
<tr>
<td>termID</td>
<td>Filter by termID</td>
</tr>
<tr>
<td>libraries</td>
<td>The directories to search for installed study packages. If left as NULL (the default), then installed.packages will use the result of .libPaths.</td>
</tr>
</tbody>
</table>

Value

A data frame which includes the columns from the features table followed by the columns from the results table. All the columns from the features table will be character strings, even if the values appear numeric.

If the optional arguments annotationID and termID are provided, the table will be filtered to only include features in that annotation term.

getResultsUpset

getResultsUpset

Description

getResultsUpset

Usage

getResultsUpset(study, modelID, sigValue, operator, column, legacy = FALSE)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>An OmicNavigator study. Either an object of class onStudy, or the name of an installed study package.</td>
</tr>
<tr>
<td>modelID</td>
<td>Filter by modelID</td>
</tr>
<tr>
<td>sigValue</td>
<td>The numeric significance value to use as a cutoff for each column</td>
</tr>
<tr>
<td>operator</td>
<td>The comparison operators for each column, e.g. &quot;&lt;&quot;</td>
</tr>
<tr>
<td>column</td>
<td>The columns to apply the filters</td>
</tr>
<tr>
<td>legacy</td>
<td>Use legacy code (for testing purposes only)</td>
</tr>
</tbody>
</table>

Value

Invisibly returns the output from upset
**getSamples**

Get samples from a study

**Description**

Get samples from a study

**Usage**

```r
getSamples(study, modelID = NULL, quiet = FALSE, libraries = NULL)
```

**Arguments**

- **study**: An OmicNavigator study. Either an object of class `onStudy`, or the name of an installed study package.
- **modelID**: Filter by modelID
- **quiet**: Suppress messages (default: `FALSE`)
- **libraries**: The directories to search for installed study packages. If left as `NULL` (the default), then `installed.packages` will use the result of `.libPaths`.

**Value**

The object returned depends on the data available and any filters (e.g. the argument `modelID`):

- If no filters are specified, then the object returned is a nested list, similar to the original input object.
- If one or more filters are applied, then only a subset of the original nested list is returned. Technically, each filter applied is used to subset the original nested list using `[[]`.
- If no data is available, an empty list is returned (`list()`).

**getTests**

Get tests from a study

**Description**

Get tests from a study

**Usage**

```r
getTests(study, modelID = NULL, testID = NULL, quiet = FALSE, libraries = NULL)
```
getUpsetCols

Arguments

study An OmicNavigator study. Either an object of class onStudy, or the name of an installed study package.

modelID Filter by modelID

testID Filter by testID

quiet Suppress messages (default: FALSE)

libraries The directories to search for installed study packages. If left as NULL (the default), then installed.packages will use the result of .libPaths.

Value

The object returned depends on the data available and any filters (e.g. the argument modelID):

- If no filters are specified, then the object returned is a nested list, similar to the original input object.
- If one or more filters are applied, then only a subset of the original nested list is returned. Technically, each filter applied is used to subset the original nested list using [[].
- If no data is available, an empty list is returned (list()).

Description

Determine the common columns across all tests of a model that are available for filtering with UpSet.

Usage

getUpsetCols(study, modelID)

Arguments

study An OmicNavigator study. Either an object of class onStudy, or the name of an installed study package.

modelID Filter by modelID

Value

Returns a character vector with the names of the common columns
### Description
A subset of the object `group` from Bioconductor workflow RNAseq123.

### Usage
```
group
```

### Format
A factor with 3 levels:
- **Basal** Basal cells
- **LP** Luminal progenitor cells
- **ML** Mature luminal cells

### Source

### References

### Examples
```
table(group)
str(group)
```
importStudy  
**Import a study package**

**Description**

Create an onStudy object by importing an installed study package

**Usage**

importStudy(study, libraries = NULL)

**Arguments**

- **study**
  Named of an installed OmicNavigator study
- **libraries**
  The directories to search for installed study packages. If left as NULL (the default), then `installed.packages` will use the result of `.libPaths`.

**Value**

Returns the onStudy object imported from the OmicNavigator study package

installApp  
**Install the OmicNavigator web app**

**Description**

In order to run the OmicNavigator web app on your local machine, the app must be installed in the www/ subdirectory of the R package. If you installed the release tarball from the GitHub Releases page, then you already have the app installed. If you installed directly from GitHub with `install_github`, or if you want to use a different version of the app, you can manually download and install the app.

**Usage**

installApp(version = NULL, overwrite = FALSE, lib.loc = NULL, ...)

**Arguments**

- **version**
  Version of the web app to install, e.g. "1.0.0"
- **overwrite**
  Should an existing installation of the app be overwritten?
- **lib.loc**
  a character vector with path names of R libraries. See ‘Details’ for the meaning of the default value of NULL.
- **...**
  Passed to `download.file`. If the download fails, you may need to adjust the download settings for your operating system. For example, to download with `wget`, pass the argument `method = "wget"`. 
installStudy

Value
A one-element character vector with the absolute path to the directory in which the app files were installed

installStudy

Install a study as an R package

Description
Install a study as an R package

Usage
installStudy(study, library = .libPaths()[1])

Arguments
study An OmicNavigator study to install (class onStudy)
library Directory to install package. Defaults to first directory returned by .libPaths.

Value
Invisibly returns the original onStudy object that was passed to the argument study

lane

lane from Bioconductor workflow RNAseq123

Description
A subset of the object lane from Bioconductor workflow RNAseq123.

Usage
lane

Format
A factor with 3 levels:

  L004  Sample sequenced on lane 4
  L006  Sample sequenced on lane 6
  L008  Sample sequenced on lane 8
lcpm

Source


References


Examples

```
teable(lane)
str(lane)
```

lcpm

A subset of the object lcpm from Bioconductor workflow RNAseq123.

Usage

```
lcpm
```

Format

A matrix with 24 rows and 9 columns

Source


References


listStudies

Examples

head(lcpm)
str(lcpm)

listStudies
List available studies and their metadata

Description
List available studies and their metadata

Usage

listStudies(libraries = NULL)

Arguments

libraries The directories to search for installed study packages. If left as NULL (the default), then installed.packages will use the result of .libPaths.

Value
Returns a nested list with one element per installed OmicNavigator study package. Each study package entry has the following sublist components:

 name (character) Name of the study
 package (list) The fields from DESCRIPTION
 results (nested list) The testIDs available for each modelID
 enrichments (nested list) The annotationIDs available for each modelID
 plots (nested list) The plotIDs available for each modelID

Mm.c2
Mm.c2 from Bioconductor workflow RNAseq123

Description
A subset of the object Mm.c2 from Bioconductor workflow RNAseq123.

Usage

Mm.c2
Format

A list of 4 character vectors

Source


References


Examples

```r
Mm.c2[[1]]
str(Mm.c2)
```

---

```r
plotStudy
  Plot a feature using a custom plotting function
```

Description

Plot a feature using a custom plotting function

Usage

```r
plotStudy(study, modelID, featureID, plotID, testID = NULL, libraries = NULL)
```

Arguments

- `study`: An OmicNavigator study. Either an object of class onStudy, or the name of an installed study package.
- `modelID`: Filter by modelID
- `featureID`: Filter by featureID
- `plotID`: Filter by plotID
- `testID`: Filter by testID
- `libraries`: The directories to search for installed study packages. If left as NULL (the default), then `installed.packages` will use the result of `.libPaths`. 
Details

The arguments study, modelID, featureID, and testID are passed to the function `getPlottingData`, and the nested list returned by this function is passed as the first argument to your custom plotting function.

Value

This function is called for the side effect of creating a plot. It invisibly returns the result from the custom plotting function specified by plotID. Previously it invisibly returned the study object. It's unlikely you relied on this behavior. For a ggplot2 plot, the return value will be the plotting object with class "ggplot".

See Also

`addPlots, getPlottingData`

---

**removeStudy**

Remove an installed study R package

**Description**

Remove an installed study R package

**Usage**

`removeStudy(study, library = .libPaths()[1])`

**Arguments**

study
The name of the study or an onStudy object. Do **not** include the prefix of the installed package, e.g. ONstudy.

library
Directory where the study package is installed. Defaults to first directory returned by `.libPaths`.

**Value**

Invisibly returns the path of the removed study package
Description

A subset of the object `samplenames` from Bioconductor workflow RNAseq123.

Usage

```
samplenames
```

Format

A character vector containing the unique sample identifiers

Source


References


Examples

```
head(samplenames)
str(samplenames)
```

Description

After you have installed at least one OmicNavigator study package with `installStudy`, you can explore the results in the app. The function `startApp` starts a local instance of the app running on your current machine. It will automatically open the app in your default browser. For the best experience, use Google Chrome. From the dropdown menu, you will be able to select from any of the studies you have installed on your machine. When you are finished, you can stop the web server by returning to the R console and pressing the Esc key (Windows) or Ctrl-C (Linux, macOS).
Usage

startApp(...)  

Arguments

... extra parameters passed to ocpu_start_server

Details

Note that the app can’t be run from within RStudio Server.

The app requires some additional R packages to run. If you receive an error about a missing package, please install it with install.packages. To ensure you have all the extra packages installed, you can run the command below:

install.packages(c("faviconPlease", "opencpu", "UpSetR"))

Value

No return value. This function is only called for the side effect of running a local instance of the app.
validateStudy

Validate a study

Description
Validate a study

Usage
validateStudy(study)

Arguments
study An OmicNavigator study object

Value
For a valid study object, the logical value TRUE is invisibly returned. For an invalid study object, there is no return value because an error is thrown.
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