exp_addEntityName Add an entity type

Description

Adds an entity type of the given name with a plural human-readable label.

Usage

exp_addEntityName(ent_type, label = paste(ent_type, "s", sep=""))

Arguments

ent_type The unique identifier of the entity type
label The plural label used for the tab in the metadata notebook.

Details

When an entity type is added to exploRase, a new tab is added to the metadata notebook with the provided plural label. Data and metadata corresponding to the type may then be loaded into exploRase.

Author(s)

Michael Lawrence <mflawren@fhcrc.org>
exp_addFilterRule  *Add a filter rule*

**Description**

Adds a filter rule to the exploRase filter model for the given entity type

**Usage**

```
exp_addFilterRule(id, column, op, expr, active = T, ent_type = exp_entityType())
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>id</td>
<td>A unique identifier for the filter rule</td>
</tr>
<tr>
<td>column</td>
<td>The metadata column checked by the rule</td>
</tr>
<tr>
<td>op</td>
<td>The operator (&lt;, &gt;, ==, etc) used for checking the values</td>
</tr>
<tr>
<td>expr</td>
<td>The right hand expression against which the values are checked</td>
</tr>
<tr>
<td>active</td>
<td>Whether the rule should be immediately active</td>
</tr>
<tr>
<td>ent_type</td>
<td>The entity type of the metadata being filtered</td>
</tr>
</tbody>
</table>

**Author(s)**

Michael Lawrence <mflawren@fhcrc.org>

---

exp_calcAngleDist  *Calculate angle distance*

**Description**

Calculates angle distance between sample vectors $x$ and $y$

**Usage**

```
exp_calcAngleDist(x, y)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>x</td>
<td>normally a column from the experimental data matrix</td>
</tr>
<tr>
<td>y</td>
<td>normally a column from the experimental data matrix</td>
</tr>
</tbody>
</table>

**Author(s)**

Michael Lawrence <mflawren@fhcrc.org>
exp_calcCanberraDist

*Calculate Canberra distance*

**Description**

Calculates Canberra distance between `ent` and the other entities across the conditions the samples (columns) in the data frame `ent_data`.

**Usage**

```r
exp_calcCanberraDist(ent_data, ent)
```

**Arguments**

- `ent_data`: a data frame of experimental data, according to exploRase conventions.
- `ent`: the id of an entity that is compared to the entities in `ent_data`.

**Author(s)**

Michael Lawrence <mflawren@fhcrc.org>

---

exp_calcCorrelationDist

*Calculate correlation distance*

**Description**

Calculates correlation distance between `ent` and the other entities across the conditions the samples (columns) in the data frame `ent_data`.

**Usage**

```r
exp_calcCorrelationDist(ent_data, ent)
```

**Arguments**

- `ent_data`: a data frame of experimental data, according to exploRase conventions.
- `ent`: the id of an entity that is compared to the entities in `ent_data`.

**Author(s)**

Michael Lawrence <mflawren@fhcrc.org>
exp_calcDiff  Calculate difference

Description
Just calculates $y - x$. You’re probably better off just doing that.

Usage
exp_calcDiff(x, y)

Arguments
x  normally a column from the experimental data matrix
y  normally a column from the experimental data matrix

Author(s)
Michael Lawrence <mflawren@fhcrc.org>

exp_calcEuclideanDist  Calculate Euclidean distance

Description
Calculates Euclidean distance between ent and the other entities across the samples (columns) in the data frame ent_data.

Usage
exp_calcEuclideanDist(ent_data, ent)

Arguments
ent_data  a data frame of experimental data, according to exploRase conventions
ent  the id of an entity that is compared to the entities in ent_data

Author(s)
Michael Lawrence <mflawren@fhcrc.org>
exp_calcMahalanobisDist

*Calculate Mahalanobis distance*

**Description**

Calculates mahalanobis distance between the samples (columns) in the data frame `ent_data`.

**Usage**

```
exp_calcMahalanobisDist(ent_data)
```

**Arguments**

- `ent_data` - a data frame of experimental data, according to exploRase conventions.

**Author(s)**

Michael Lawrence <mflawren@fhcrc.org>

---

exp_calcResiduals

*Calculate residuals*

**Description**

Calculates the residuals from a linear regression of sample \( y \) against sample \( x \).

**Usage**

```
exp_calcResiduals(x, y)
```

**Arguments**

- `x` - normally a column from the experimental data matrix.
- `y` - normally a column from the experimental data matrix.

**Author(s)**

Michael Lawrence <mflawren@fhcrc.org>
exp_calcZeroCorDist

*Calculate zero-correlation distance*

**Description**

Calculates zero (uncentered) correlation distance between `ent` and the other entities across the samples (columns) in the data frame `ent_data`.

**Usage**

```r
exp_calcZeroCorDist(ent_data, ent)
```

**Arguments**

- `ent_data`: a data frame of experimental data, according to exploRase conventions.
- `ent`: the id of an entity that is compared to the entities in `ent_data`.

**Author(s)**

Michael Lawrence <mflawren@fhcrc.org>

---

exp_close

*Close exploRase*

**Description**

Close (shutdown) exploRase

**Usage**

```r
exp_close()
```

**Author(s)**

Michael Lawrence
**exp_colorEntities**  

*Coloring entities*

**Description**  
Set the color for the specified entities of the current entity type in GGobi

**Usage**  

```r  
exp_colorEntities(entities = getEntityIds(), color)  
```

**Arguments**  

- **entities**: the entities to color  
- **color**: the color index (as interpreted by GGobi) for the entities

**Author(s)**  
Michael Lawrence <mflawren@fhcrc.org>

---

**exp_dataset**  

*Get experimental data*

**Description**  
Get experimental data of the specified type out of exploRase

**Usage**  

```r  
exp_dataset(ent_type = exp_entityType())  
exp_dataFrame(ent_type = exp_entityType())  
```

**Arguments**  

- **ent_type**: the entity type ("gene", "met", ...) of the data

**Details**  
The result of `exp_dataset` allows one to directly manipulate the GGobi dataset. If only a data.frame is required, `exp_dataFrame` is a more convenient path.

**Value**  
For `exp_dataset`, a GGobi dataset, see rggobi documentation. For `exp_dataFrame`, a data.frame coerced from the result of `exp_dataset`.

**Author(s)**  
Michael Lawrence <mflawren@fhcrc.org>
exp_designFactors  Get the exp. design factors

Description

Gets a vector of the names of the factors in the experimental design

Usage

exp_designFactors(ent_type = exp_entityType(), treatments_only = FALSE)

Arguments

ent_type  the entity type ("gene", "met", etc)
treatments_only
  if TRUE, only include treatments (eg genotype), leaving out eg ID and replicate.

Value

A vector of factor names

Author(s)

Michael Lawrence <mflawren@fhcrc.org>

exp_designFrame  Get the exp. design

Description

Gets a data frame containing the experimental design information for the given entity type.

Usage

exp_designFrame(ent_type = exp_entityType(), treatments_only = FALSE)

Arguments

ent_type  the entity type ("gene", "met", etc)
treatments_only
  if TRUE, only include treatment columns (eg genotype), leaving out eg ID and replicate.

Value

A data frame with conditions as rows and factors as columns.

Author(s)

Michael Lawrence <mflawren@fhcrc.org>
exp_designSelection

*Get selected conditions*

**Description**

Gets a vector of the names of the selected conditions in the condition list.

**Usage**

```r
exp_designSelection()
```

**Value**

A vector of condition names

**Author(s)**

Michael Lawrence <mflawren@fhcrc.org>

---

exp_entitiesInList

*Get the entities in a list*

**Description**

Gets the ID’s of the entities in a specified list and of the specified types.

**Usage**

```r
exp_entitiesInList(list, types = exp_entityTypes())
```

**Arguments**

- `list` The name of the entity list
- `types` The types of entities to return

**Value**

The entity ID’s of the specified types belonging to the list

**Author(s)**

Michael Lawrence <mflawren@fhcrc.org>
exp_entityFrame  

Get entity metadata

Description
Retrieves the entity metadata table for the given type as a data frame

Usage
exp_entityFrame(ent_type = exp_entityType())

Arguments
ent_type  
the entity type for which the metadata is retrieved

Author(s)
Michael Lawrence <mflawren@fhcrc.org>

exp_entitySelection
Get selected entities

Description

Gets the ID’s of the entities selected in the metadata table of the given type.

Usage
exp_entitySelection(ent_type = exp_entityType())

Arguments
ent_type  
The entity type for which the selected is retrieved

Value
The entity ID’s

Author(s)
Michael Lawrence <mflawren@fhcrc.org>
**exp_entityType**

---

### exp_entityType

**Get the current entity type**

#### Description

Retrieves the entity type with its tab selected in the metadata notebook.

#### Usage

```r
exp_entityType()
```

#### Value

Name of the current entity type

#### Author(s)

Michael Lawrence <mflawren@fhcrc.org>

---

**exp_entityTypes**

---

### exp_entityTypes

**Get all entity types**

#### Description

Retrieves the identifiers for all entity types in exploRase.

#### Usage

```r
exp_entityTypes()
```

#### Value

Vector of entity type names

#### Author(s)

Michael Lawrence <mflawren@fhcrc.org>
exp_filterRules  Get filter rules

Description

Gets the filter rules for the metadata of the given type

Usage

exp_filterRules(ent_type = exp_entityType())

Arguments

ent_type  the entity type of the metadata being filtered by the rules

Author(s)

Michael Lawrence <mflawren@fhcrc.org>

exp_findPatterns  Find Patterns

Description

Finds patterns in data. Transitions within range of ’fraction’ (centered on median) are considered flat (unchanging). Those below are falling and those above are rising.

Usage

exp_findPatterns(data, flat_fraction)

Arguments

data  A data frame of experimental data according to exploRase conventions.

flat_fraction  The fraction of transitions considered unchanged, centered on median.

Value

A data frame, with a row for each gene. The first column is the sum of $x^i$ over all $i$ from 1 to $n\text{col}(data)-1$, where $x$ is 1, 2, or 3, depending on whether the pattern is up, same, or down, respectively, for transition $i$. The second column contains the magnitude of the pattern.

Author(s)

Michael Lawrence <mflawren@fhcrc.org>
exp_ggobi

Description

Gets the GGobi session being used by exploRase. Will restart GGobi if it died

Usage

exp_ggobi()

Value

The GGobi session

Author(s)

Michael Lawrence <mflawren@fhcrc.org>

exp_isRunning

Check whether exploRase is running

Description

Currently a hack that checks if the main window exists

Usage

exp_isRunning()

Value

whether exploRase is currently running

Author(s)

Michael Lawrence <mflawren@fhcrc.org>
exp_listFrame  Get entity lists

Description

Gets the entity lists loaded in exploRase

Usage

exp_listFrame()

Value

A data frame with a single column "name" holding the names of the lists

Author(s)

Michael Lawrence <mflawren@fhcrc.org>

exp_listSelection  Get selected lists

Description

Gets the names of the lists selected in the exploRase GUI.

Usage

exp_listSelection()

Value

The names of the selected lists

Author(s)

Michael Lawrence <mflawren@fhcrc.org>
**exp_loadData**  
*Load experimental data*

**Description**

Load experimental data of a specified type into exploRase (and GGobi).

**Usage**

```r
exp_loadData(exp_data, data_name = "expression", ent_type = "gene", sync = FALSE, add_to_design = !nrow(exp_designFrame(ent_type)))
```

**Arguments**

- **exp_data**: a data frame containing experimental data, with observations as rows and conditions as columns.
- **data_name**: name of the dataset in GGobi
- **ent_type**: the entity type ("gene", "met", ...) of the data
- **sync**: whether to synchronize the other data models with the experimental data. If `sync` is TRUE, the entity information and experimental design tables will be limited to the observations and conditions, respectively, in the experimental data. This is experimental.
- **add_to_design**: whether to add the columns in the dataset as conditions in the experimental design, if they are not there already

**Details**

Organizes experimental data, loads it into GGobi and synchronizes it with other data (design and entity info)

**Author(s)**

Michael Lawrence <mflawren@fhcrc.org>

---

**exp_loadDesign**  
*Load experimental design*

**Description**

Loads a matrix describing the experimental conditions

**Usage**

```r
exp_loadDesign(design_info, ent_type = exp_entityType())
```
exp_loadFiles  

Load files

Description
Loads a set of files into exploRase

Usage
exp_loadFiles(filenames, data_type, entity_type = "gene")

Arguments
filenames  filenames The paths to the files to load
data_type  The data type ("data", "design", "info", "list")
entity_type  The entity type (by default: "gene", "met", "prot"), only used if data_type is provided.

Details
If the data_type is specified, it is assumed that all the files are of the given data_type and entity_type. Otherwise, the types are autodetected based on file extensions.

Author(s)
Michael Lawrence <mflawren@fhcrc.org>

exp_loadInfo  

Load entity metadata

Description
Loads a data frame of entity metadata into the metadata table of the given type(s).

Usage
exp_loadInfo(ent_info, ent_types = "gene", append_col = TRUE, keywords = NULL, update_view = TRUE, sync = FALSE)
exp_loadLists

Arguments

ent_info the data frame of entity information
ent_types a single type identifier (applies to all rows) or a
append_col whether the column should be appended or inserted after ID
keywords a vector of identifiers that describe the added metadata
update_view whether the metadata view should be updated
sync whether metadata rows should be filtered out if they don't

Details

The loaded entity metadata is merged with any existing data and the view is optionally updated to reflect the change. The new set of columns may be appended to the end or inserted just after the "ID" column.

Metadata for multiple entity types may be added simultaneously, if ent_types is a vector with the same number of elements as the number of rows in ent_info and specifies the type of the entity described by each row.

Author(s)

Michael Lawrence <mflawren@fhcrc.org>

exp_loadLists Load entity lists

Description

Loads a list of entity lists (matrices) into exploRase

Usage

exp_loadLists(ent_lists)

Arguments

ent_lists a list of entity lists (1 or 2 column matrices)

Details

An entity list matrix may have one or two columns. The last column specifies the entity ID’s and its name is the name of the entity list. If there are two columns, the first specifies the type of each entity, allowing entity lists holding entities of different types.

Author(s)

Michael Lawrence <mflawren@fhcrc.org>
exp_loadProject  
Load a project

Description
Loads a project (a file system directory) into exploRase

Usage
exp_loadProject(project)

Arguments
project The path to the directory holding the project

Details
Loads all of the files in a specified directory, using their file extensions to determine their purpose.

Author(s)
Michael Lawrence <mflawren@fhcrc.org>

exp_newList  
Create an entity list

Description
Forms the actual entity list matrix from the name, ents, and types

Usage
exp_newList(name, ents, types)

Arguments
name The name of the entity list
ents The ID’s of the entities in the list
types The types of the entities in the list

Value
A matrix conforming to the structure for entity lists

Author(s)
Michael Lawrence <mflawren@fhcrc.org>
exp_removeFilterRules

Remove filter rules

Description

Removes the filter rules with the given identifiers for the given type

Usage

exp_removeFilterRules(rules, ent_type = exp_entityType())

Arguments

rules the identifiers of the rules to remove
ent_type the entity type of the metadata being filtered

Author(s)

Michael Lawrence <mflawren@fhcrc.org>

exp_showClustering Show a hierarchical clustering

Description

 Shows a hierarchical clustering using the “GGobi” dendrogram viewer.

Usage

exp_showClustering(ids, data, clustering)

Arguments

ids The ids of the entities that were clustered
data The experimental data that was clustered
clustering the clustering, as returned by hclust()

Author(s)

Michael Lawrence <mflawren@fhcrc.org>
exp_showPatterns  Show patterns

Description
Show the calculated patterns in the GUI

Usage
exp_showPatterns(patterns, desc, samples = exp_designSelection())

Arguments
patterns  a data frame, with a row for each gene and the first column being the pattern codes and the second the magnitude of the pattern (as returned by `exp_findPatterns`).
desc  a description of the patterns, for labeling them in the GUI
samples  the samples involved in the calculation, for labeling

Author(s)
Michael Lawrence <mflawren@fhcrc.org>

exp_showResults  Show analysis results

Description
Add a column of analysis results to the exploRase table and the GGobi dataset.

Usage
exp_showResults(results, label, sublabels = "", types = exp_entityType(), keyword = NULL, explorase = T, ggobi = T)

Arguments
results  the data frame of results. To include results for multiple entity types at once, the result for each type should be concatenated in the same order as the `types` parameter.
label  a root label for the result (like the type of analysis)
sublabels  other labels concatenated to the root (such as the conditions involved)
types  the entity type(s) of the data from which this result was derived.
keyword  a keyword identifying this result, for use in context-sensitive help
explorase  whether to show the result in the explorase table
ggobi  whether to add the result to the GGobi dataset

Author(s)
Michael Lawrence <mflawren@fhcrc.org>
exp_toggleFilterRules

Toggle filter rules

Description

Toggles (activates or deactivates) the specified rules for the specified type.

Usage

\[ \text{exp\_toggleFilterRules}(\text{rules}, \text{active} = T, \text{ent\_type} = \text{exp\_entityType}()) \]

Arguments

- **rules**: The identifiers of the rules to toggle
- **active**: Whether to activate or deactivate the rules
- **ent\_type**: The entity type of the metadata being filtered by the rules

Author(s)

Michael Lawrence <mflawren@fhcrc.org>

bioc_integration ExpressionSet Integration

Description

Functions loading and retrieving Bioconductor ExpressionSet objects to and from exploRase.

Usage

\[
\begin{align*}
\text{exp\_loadExpressionSet} & (\text{exprset}, \text{type} = \text{exp\_entityType}()) \\
\text{exp\_phenoData} & (\text{type} = \text{exp\_entityType}()) \\
\text{exp\_featureData} & (\text{type} = \text{exp\_entityType}()) \\
\text{exp\_expressionSet} & (\text{type} = \text{exp\_entityType}())
\end{align*}
\]

Arguments

- **exprset**: The ExpressionSet to load.
- **type**: The type of the biological entity (e.g. gene).

Details

To load a ExpressionSet instance into exploRase, call **exp\_loadExpressionSet**.

The function **exp\_expressionSet** retrieves the ExpressionSet representing the data stored in exploRase for the given entity type. **exp\_phenoData** and **exp\_featureData** retrieve only the phenoData and featureData components, respectively.
explorase

Value

For `exp_expressionSet`, an `ExpressionSet`. For `exp_phenoData`, an `AnnotatedDataFrame` representing the phenotype data (i.e. experimental design, see `exp_designFrame`). For `exp_featureData`, an `AnnotatedDataFrame` representing the feature annotations (i.e. the entity info, see `exp_entityFrame`).

Author(s)

Michael Lawrence

See Also

`explorase` for loading data and starting exploRase in one call. `exp_designFrame`, `exp_entityFrame`, `exp_dataset`, etc for retrieving data from exploRase.

explorase  Start exploRase

Description

The main function of exploRase, normally invoked without arguments, unless one already has data/metadata in the R session to load.

Usage

```r
explorase(exp_data = NULL, entity_info = NULL, design_info = NULL, type = "gene", network = NULL, entity_lists = NULL, gobi = ggobi_get(), quit_on_exit = F)
```

Arguments

- **exp_data**: Experimental data to load
- **entity_info**: Entity metadata to load
- **design_info**: Experimental design information to load
- **type**: The entity type of the data being loaded
- **network**: A Bioconductor "graph" to load (not yet implemented)
- **entity_lists**: A list of entity lists to load
- **gobi**: The GGobi session to use
- **quit_on_exit**: Whether R should quit when exploRase is exited

Author(s)

Michael Lawrence
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