explorase
November 11, 2009

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exp_addEntityType  Add an entity type

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

Usage
exp_addEntityType(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
id A unique identifier for the filter rule
column The metadata column checked by the rule
op The operator (<, >, ==, etc) used for checking the values
expr The right hand expression against which the values are checked
active Whether the rule should be immediately active
ent_type The entity type of the metadata being filtered
bioc_integration  ExpressionSet Integration

Description

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

Usage

\[
\text{exp_loadExpressionSet}(\text{exprset}, \text{type} = \text{exp_entityType}()) \\
\text{exp_phenoData}(\text{type} = \text{exp_entityType}()) \\
\text{exp_featureData}(\text{type} = \text{exp_entityType}()) \\
\text{exp_expressionSet}(\text{type} = \text{exp_entityType}())
\]

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.

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.
exp_calcAngleDist  

*Calculate angle distance*

**Description**

Calculates angle distance between sample vectors \( x \) and \( y \)

**Usage**

```r
exp_calcAngleDist(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_calcCanberraDist  

*Calculate Canberra distance*

**Description**

Calculates Canberra distance between \( \text{ent} \) and the other entities across the conditions the samples (columns) in the data frame \( \text{ent_data} \)

**Usage**

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

**Arguments**

- \( \text{ent_data} \) a data frame of experimental data, according to exploRase conventions
- \( \text{ent} \) the id of an entity that is compared to the entities in \( \text{ent_data} \)

**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**

```
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**

```r
def 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
def 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
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
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
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
exp_designFrame

*Get the exp. design*

**Description**

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

**Usage**

```r
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**

```r
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**

```r
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

*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

Get all entity types

Description

Retrieves the identifiers for all entity types in exploRase.

Usage

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 ncol(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  Get the GGobi session

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

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)
exp_loadDesign  

**Load experimental design**

**Description**

Loads a matrix describing the experimental conditions

**Usage**

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

**Arguments**

- `design_info` a data frame with conditions for rows and factors for cols
- `ent_type` the type of entity to which this design applies. This links this design to the experimental data and entity information.

**Author(s)**

Michael Lawrence <mflawren@fhcrc.org>

---

exp_loadFiles  

**Load files**

**Description**

Loads a set of files into explorase

**Usage**

```r
exp_loadFiles(filenames, data_type = NULL, entity_type = "gene", ignoreUnknown = TRUE)
```

**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.
- `ignoreUnknown` If FALSE, throw an error if the data/entity type cannot be determined for a file; otherwise, the file is ignored.
exp_loadInfo

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)

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**

```r
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**

```r
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>
exporase

Start exploRase

Description

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

Usage

exporase(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 exporase is exited

Author(s)

Michael Lawrence

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
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>
Description

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

Usage

exp_toggleFilterRules(rules, active = T, ent_type = 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>
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