Package ‘explorase’

January 30, 2017

Title GUI for exploratory data analysis of systems biology data
Version 1.38.0
Author Michael Lawrence, Eun-kyung Lee, Dianne Cook, Jihong Kim, Hogeun An, and Dongshin Kim
Depends R (>= 2.6.2)
Imports limma, rggobi, RGtk2
Suggests cairoDevice
Description explore and analyze *omics data with R and GGobi
Maintainer Michael Lawrence <michafla@gene.com>
License GPL-2
URL http://www.metnetdb.org/MetNet_exploRase.htm
biocViews Visualization,Microarray,GUI
NeedsCompilation no

R topics documented:

  bioc_integration .............................................................. 2
  explorase ................................................................. 3
  exp_addEntityTye ......................................................... 4
  exp_addFilterRule ....................................................... 4
  exp_calcAngleDist ....................................................... 5
  exp_calcCanberraDist ................................................... 5
  exp_calcCorrelationDist ................................................ 6
  exp_calcDiff ............................................................ 6
  exp_calcEuclideanDist .................................................. 6
  exp_calcMahalanobisDist ................................................. 7
  exp_calcResiduals ....................................................... 7
  exp_calcZeroCorDist .................................................... 8
  exp_close ............................................................... 8
  exp_colorEntities ...................................................... 9
  exp_dataset ............................................................ 9
  exp_designFactors ..................................................... 10
  exp_designFrame ........................................................ 10
  exp_designSelection .................................................... 11
  exp_entitiesInList ..................................................... 11
  exp_entityFrame ........................................................ 12
bioc_integration

ExpressionSet Integration

Description

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

Usage

exp_loadExpressionSet(exprset, type = exp_entityType())
exp_phenoData(type = exp_entityType())
exp_featureData(type = exp_entityType())
exp_expressionSet(type = 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.
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
exp_addEntitytype  

**Add an entity type**

**Description**

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

**Usage**

```r
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**

```r
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

**Author(s)**

Michael Lawrence <mflawren@fhcrc.org>
**exp_calcAngleDist**

_Calculate angle distance_

**Description**

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

**Usage**

\[
\text{exp_calcAngleDist}(x, y)
\]

**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**

\[
\text{exp_calcCanberraDist}(\text{ent\_data, ent})
\]

**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**
```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**
```r
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

```r
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

```r
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

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

Description
Close (shutdown) exploRase

Usage
exp_close()

Author(s)
Michael Lawrence

exp_colorEntities

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**

```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**

```r
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**

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

---

**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_entityFrame

---

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

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

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**

```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**

```r
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**

```r
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**

```r
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

```r
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)
exp_loadDesign  

**Load experimental design**

**Description**

Loads a matrix describing the experimental conditions

**Usage**

```
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 the 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**

```
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.

**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.
exp_loadInfo

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**  
```
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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>name</td>
<td>The name of the entity list</td>
</tr>
<tr>
<td>ents</td>
<td>The ID’s of the entities in the list</td>
</tr>
<tr>
<td>types</td>
<td>The types of the entities in the list</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>rules</td>
<td>the identifiers of the rules to remove</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_showClustering  
*Show a hierarchical clustering*

**Description**
Shows a hierarchical clustering using the "GGobi" dendrogram viewer.

**Usage**
```r
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**
```r
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

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>
Index

*Topic IO
  exp_loadFiles, 18
  exp_loadProject, 20

*Topic arith
  exp_calcAngleDist, 5
  exp_calcCanberraDist, 5
  exp_calcCorrelationDist, 6
  exp_calcDiff, 6
  exp_calcEuclideanDist, 7
  exp_calcMahalanobisDist, 7
  exp_calcZeroCorDist, 8
  exp_findPatterns, 15

*Topic dynamic
  exp_close, 9
  exp_colorEntities, 9
  exp_ggobi, 15
  exp_showClustering, 22
  exp_showPatterns, 22
  exp_showResults, 23
  explorase, 3

*Topic manip
  bioc_integration, 2
  exp_addEntityType, 4
  exp_addFilterRule, 4
  exp_dataset, 10
  exp_designFactors, 10
  exp_designFrame, 11
  exp_designSelection, 11
  exp_entitiesInList, 12
  exp_expressionSet, 12
  exp_expressionSelection, 13
  exp_expressionType, 13
  exp_expressionTypes, 14
  exp_filterRules, 14
  exp_listFrame, 16
  exp_listSelection, 17
  exp_loadData, 17
  exp_loadDesign, 18
  exp_loadInfo, 19
  exp_loadLists, 20
  exp_newList, 21
  exp_removeFilterRules, 21
  exp_showResults, 23
  exp_toggleFilterRules, 23

*Topic misc
  exp_isRunning, 16

*Topic regression
  exp_calcResiduals, 8
  bioc_integration, 2
  exp_addEntityType, 4
  exp_addFilterRule, 4
  exp_calcAngleDist, 5
  exp_calcCanberraDist, 5
  exp_calcCorrelationDist, 6
  exp_calcDiff, 6
  exp_calcEuclideanDist, 7
  exp_calcMahalanobisDist, 7
  exp_calcResiduals, 8
  exp_calcZeroCorDist, 8
  exp_close, 9
  exp_colorEntities, 9
  exp_dataFrame, 10
  exp_dataset, 10
  exp_designFactors, 10
  exp_designFrame, 11
  exp_designSelection, 11
  exp_entitiesInList, 12
  exp_expressionFrame, 12
  exp_expressionSelection, 13
  exp_expressionType, 13
  exp_expressionTypes, 14
  exp_expressionSet, 14
  exp_findPatterns, 15
  exp_ggobi, 15
  exp_isRunning, 16
  exp_listFrame, 16
  exp_listSelection, 17
  exp_loadData, 17
  exp_loadDesign, 18
  exp_loadInfo, 19
  exp_loadExpressionSet, 18
  exp_loadFiles, 18
  exp_loadInfo, 19
exp_loadLists, 20
exp_loadProject, 20
exp_newList, 21
exp_phenoData (biocIntegration), 2
exp_removeFilterRules, 21
exp_showClustering, 22
exp_showPatterns, 22
exp_showResults, 23
exp_toggleFilterRules, 23
explorase, 3, 3