

# explorase

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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

**Author(s)**

Michael Lawrence <mflawren@fhcrc.org>

---

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**

<code>exprset</code>	The ExpressionSet to load.
<code>type</code>	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 *Caclulate angle distance*

---

**Description**

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

**Usage**

```
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 `ent` and the other entities across the conditions the samples (columns) in the data frame `ent_data`

**Usage**

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

**Arguments**

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

**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**

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

**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**

<code>x</code>	normally a column from the experimental data matrix
<code>y</code>	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**

```
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	<i>Get experimental data</i>
-------------	------------------------------

---

**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	<i>Get the exp. design factors</i>
-------------------	------------------------------------

---

**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**

```
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**

```
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

*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**

```
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  $\text{ncol}(\text{data}) - 1$ , 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)



**Author(s)**

Michael Lawrence <mflawren@fhcrc.org>

---

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 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(filenamees, data_type = NULL, entity_type = "gene",
              ignoreUnknown = TRUE)
```

**Arguments**

`filenamees`      filenamees 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.

**Author(s)**

Michael Lawrence <mflawren@fhcrc.org>

---

exp_loadInfo	<i>Load entity metadata</i>
--------------	-----------------------------

---

**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, u
```

**Arguments**

<code>ent_info</code>	the data frame of entity information
<code>ent_types</code>	a single type identifier (applies to all rows) or a
<code>append_col</code>	whether the column should be appended or inserted after ID
<code>keywords</code>	a vector of identifiers that describe the added metadata
<code>update_view</code>	whether the metadata view should be updated
<code>sync</code>	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	<i>Load entity lists</i>
---------------	--------------------------

---

**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	<i>Load a project</i>
-----------------	-----------------------

---

**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>

---

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

```
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\_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 <code>exp_findPatterns</code> ).
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 expIorase table and the GGobi dataset.

### Usage

```
exp_showResults(results, label, sublabels = "", types = exp_entityType(), keyword
```

### 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 <code>types</code> 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>

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