

# comoRbidity: molecular comorbidities functionalities

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# 1 Installation

```
> library( "devtools" )
> install_bitbucket( "ibi_group/comoRbidity" )
> library( "comoRbidity" )
```

# 2 Molecular comorbidity study

For the molecular comorbidity analysis, a file containing two columns, identifier and name, is required.

```
> filePth <- system.file("extdata", package="comoRbidity")
> codesEx <- read.delim( paste0(filePth, "/exampleInput.txt"), header = TRUE, sep = "\t" )
> head(codesEx)
```

	identifier	name
1	C0001539	Depressive disorders
2	C0001548	Depressive disorders
3	C0001723	Depressive disorders
4	C0001726	Depressive disorders
5	C0001940	Alcohol use disorders
6	C0001950	Alcohol use disorders

Applying the `quermolecular` function, we will extract all the genes associated to our diseases of interest, based on DisGeNET data. The database in which the query is done, as well as the score cut-off can be selected.

```
> diseaseCodes <- paste0(filePth, "/exampleInput.txt")
> mc <- quermolecular ( filePth = diseaseCodes,
+                       unify = TRUE,
+                       database = "CURATED",
+                       score = c(">", 0))
```

As a result, a `molecularComorbidity` object will be obtained. This object will show us some interesting data such as:

- Aggregate the disease codes: the name column will be used for the comorbidity analysis
- N. Input Diseases: number of diseases that the user gives as input
- N. Index Diseases Present: number of diseases that present associated genes in DisGeNET.
- N. Genes: number of genes associated to the diseases.

Object of class 'molecularComorbidity'

```
. Search: list
. Aggregate the disease codes: TRUE
. N. Input Diseases: 7
. N. Index Diseases Present: 7
. N. Genes : 558
```

We can extract the `molecularComorbidity` data using the `extract` function as follows:

```
> head(comoRbidity::extract(mc))
```

	geneId	geneSymbol	diseaseId	diseaseName
1	6095	RORA	umls:C0011570	Depressive disorders
2	6532	SLC6A4	umls:C0011581	Depressive disorders
3	627	BDNF	umls:C0011581	Depressive disorders
4	2908	NR3C1	umls:C0011581	Depressive disorders
5	1392	CRH	umls:C0011581	Depressive disorders
6	3569	IL6	umls:C0011581	Depressive disorders

```
> mcAnalysis <- comorbidityAnalysisMolecular(input = mc,
+                                           pValue = TRUE,
+                                           nboot = 1000)
```

As a result, a molecularAnalysis object will be obtained. This object will show us some interesting data such as:

- Overlap Min: minimum value of the gene overlap for the disease comorbidities.
- Overlap Max: maximum value of the gene overlap for the disease comorbidities.
- Jaccard Min: minimum value of the jaccard for the disease comorbidities.
- Jaccard Max: maximum value of the jaccard for the disease comorbidities.
- P-value: it is TRUE is the p-value has been estimated.
- Number of comorbidities: show the number of comorbidities with gene overlap.

Object of class 'molecularAnalysis'

```
. Overlap Min : 1
. Overlap Max : 30
. Jaccard Min : 0.01
. Jaccard Max : 0.175
. P-value      : TRUE
. Number of comorbidities: 13
```

We can extract the molecularAnalysis data using the extract function as follows:

```
> head(comorbidity::extract(mcAnalysis))
```

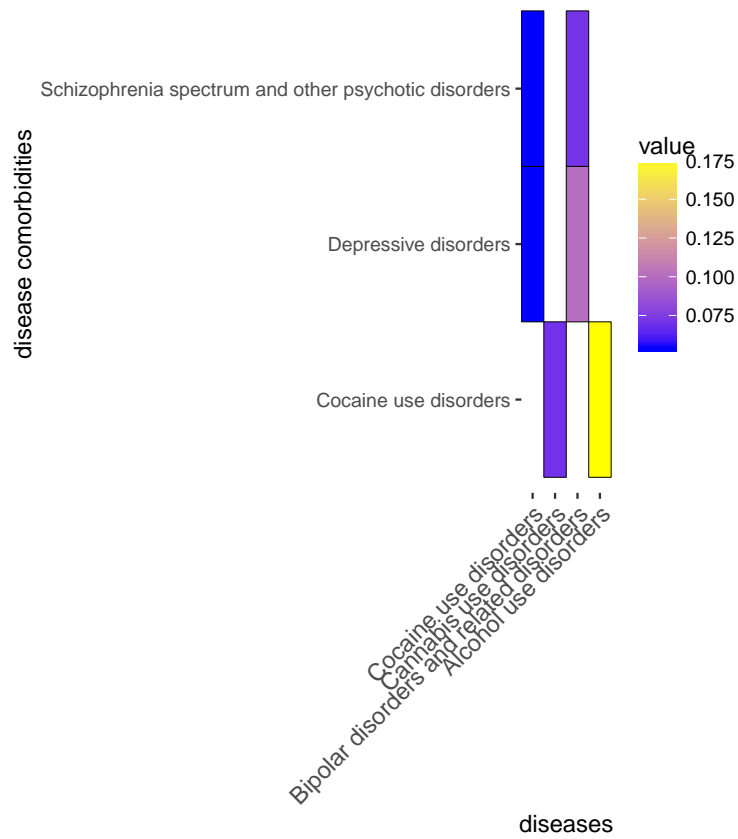
	V1		V2	geneV1	geneV2	overlap
1	Alcohol use disorders					
2	Alcohol use disorders					
3	Alcohol use disorders					
4	Alcohol use disorders					
6	Alcohol use disorders					
8	Bipolar disorders and related disorders					
1	Bipolar disorders and related disorders		91	72		7
2	Cannabis use disorders		91	11		1
3	Cocaine use disorders		91	110		30
4	Depressive disorders		91	81		8
6	Schizophrenia spectrum and other psychotic disorders		91	313		12
8	Cocaine use disorders		72	110		8
	jaccard	pval				
1	0.045	0.01199				
2	0.010	0.18581				
3	0.175	0.00000				
4	0.049	0.00500				
6	0.031	0.21878				
8	0.046	0.01099				

## 2.1 Molecular comorbidity visualization

Heatmap

```
> mcHeatmap <- heatmapPlot( input = mcAnalysis ,
+                           selectValue = "jaccard",
+                           cutOff = 0.05,
+                           interactive = FALSE,
+                           lowColor = "#0000FF",
+                           highColor = "yellow" )
> mcHeatmap
```

## Molecular comorbidity between diseases



## Network

```
> mcNetwork <- network( input = mcAnalysis ,
+                         layout = "layout.circle",
+                         selectValue = "jaccard",
+                         title = "Molecular comorbidity network",
+                         cutOff = 0.05,
+                         prop    = 0.2,
+                         diseaseColor = "olivedrab1",
+                         interactive = FALSE,
+ )
```

## Molecular comorbidity network

