

exposomeShiny User's Guide

Escribà Montagut, Xavier; González, Juan R.

2021-02-19

Contents

1	Overview	5
2	Setup	7
2.1	R, RStudio and Packages Versions	7
2.2	Downloading the source files, installing the libraries and running the application	8
2.3	Pulling the official Docker image from DockerHub	10
3	Data sets	13
3.1	Exposome dataset	13
3.2	Plain datasets	15
3.3	Omics dataset	16
4	Bioconductor packages	17
4.1	rexosome	17
4.2	omicReposome	17
4.3	CTDquerier	17
5	Analysis flowcharts	19
5.1	Exposome health analysis	19
5.2	Exposome-Omic analysis	48
5.3	Exposome-Omic integration (e.g. crossomics)	74
6	General application functionalities	75
7	Methods	79
7.1	Missing data imputation	79
7.2	Normality	80
7.3	Principal component analysis (PCA)	80
7.4	Exposures correlation	80
7.5	Exposures clustering	80
7.6	Exposome Association Analysis	81
7.7	Exposome-Omic Association Analysis	81
7.8	Enrichment analysis	82

Chapter 1

Overview



exosomeShiny is a data analysis toolbox with the following features:

- Data handling: imputation, LOD, transformation, ...
- Exposome characterization
- Exposome-wide association analysis
- Multivariate association
- Omic data integration
- Post-omic data analysis: CTD database

To do so, exosomeShiny relies on previously existent Bioconductor packages (rexosome, omicReXosome and CTDquerier), it uses them in a seamless way so the final user of exosomeShiny can perform the same studies that would conduct using the Bioconductor packages but without writing a single line of code.

Chapter 2

Setup

2.1 R, RStudio and Packages Versions

If the user chooses to install and use exposomeShiny using RStudio instead of Docker, the list of package versions used for the development of the application is provided for stability purposes. When using the Docker version of the application, all of the following is bundled on the image so the user does not have to deal with the installation of any package.

Software:

R software	Version
R	4.0.2
RStudio	1.4.1103

R packages:

R Packages	Version
shiny	1.5.0
shinyBS	0.61
rexposome	1.12.2
omicRexposome	1.12.0
MultiDataSet	1.18.0
mice	3.11.0
DT	0.16
ggplot2	3.3.2
data.table	1.13.2
truncdist	1.0

R Packages	Version
shinyalert	2.0.0
shinydashboard	0.7.1
shinyjs	2.0.0
TxDb.Hsapiens.UCSC.hg19.knownGene	3.2.2
org.Hs.eg.db	3.12.0
GenomicRanges	1.42.0
CTDquerier	1.4.3
shinycssloaders	1.0.0
pastecs	1.3.21
shinyWidgets	0.5.4
clusterProfiler	3.18.1
enrichplot	1.10.2
ggupset	0.3.0
imputeLCMD	2.0

There are two different ways of setting up and using exposomeShiny

2.2 Downloading the source files, installing the libraries and running the application

The user can choose to download the source code of the shiny application and install all the required libraries on their local R installation. Make sure Rtools is installed to use this method.

```
# Set working directory
setwd(dir = "/some/path/")

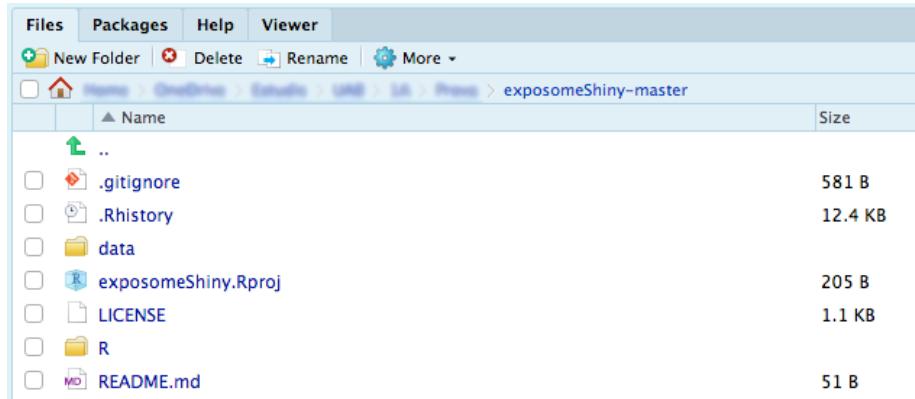
# Download zip
download.file(url = "https://github.com/isglobal-brge/exosomeShiny/archive/master.zip")

# Unzip the .zip to the working directory
unzip(zipfile = "master.zip")

# Set the working directory inside the downloaded folder
setwd(dir = "/some/path/exosomeShiny-master")
```

Now all the source files are downloaded to the location of chose and the working directory moved to the correct folder, to start the project, open the Rproj file by clicking it on the Files explorer of RStudio.

2.2. DOWNLOADING THE SOURCE FILES, INSTALLING THE LIBRARIES AND RUNNING THE APPLICATION



The screenshot shows the RStudio interface with the 'Files' tab selected. The sidebar shows the path: Home > Downloads > Desktop > User > Public > exposomeShiny-master. The main area displays a file list with the following contents:

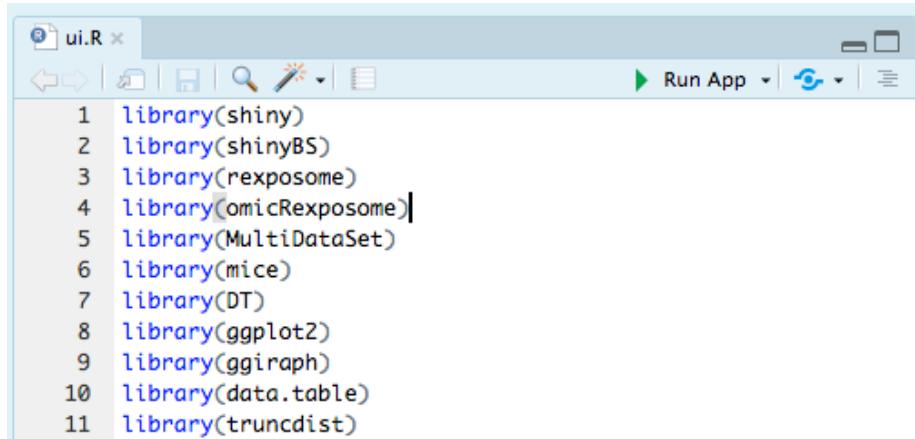
	Name	Size
..		
.	.gitignore	581 B
..	.Rhistory	12.4 KB
..	data	
..	exposomeShiny.Rproj	205 B
..	LICENSE	1.1 KB
..	R	
..	README.md	51 B

Once the project is loaded, the file found on the source folder called `installer.R` has to be sourced and run. This will install the newest versions of the packages required by Exposome Shiny on this R session. To do so, run the following code on the RStudio console.

```
source("installer.R")
```

This is only needed on the first run, once completed it doesn't need to be done prior to launching the application itself any other time.

Now everything is ready to launch the Shiny application. To do so there are two approaches, one is to open the `ui.R` or the `server.R` files that are inside the `R` folder and press `Run App`.



The screenshot shows the RStudio interface with the 'ui.R' file open. The code editor contains the following R code:

```
1 library(shiny)
2 library(shinyBS)
3 library(rexposome)
4 library(omicRexposome)
5 library(MultiDataSet)
6 library(mice)
7 library(DT)
8 library(ggplot2)
9 library(ggiraph)
10 library(data.table)
11 library(truncdist)
```

Or the other option is to input the following command on the console.

```
shiny::runApp('R')
```

2.3 Pulling the official Docker image from DockerHub

If there's any trouble downloading the required R packages to make exposomeShiny work, there's the option of using Docker. It has the disadvantage of being a little bit difficult to install on a Windows machine, however, it's extremely simple on a Mac OS X / Linux environment. For the Windows users refer to the following links for instructions on how to install Docker and setup your machine to run WSL2 and launch bash commands on Windows 1, 2, 3.

To download and launch exposomeShiny, execute the following command on a bash terminal(make sure Docker is running, if not search for the **Docker Desktop** app and launch it).

```
docker run --rm -p 80:80 brgelab/exosome-shiny
```

This command will download the Docker image of exposomeShiny (be aware it weights ~ 3 GB, so if your internet connection is slow it may take a while) and run a container with it. The container will be exposed on the local port 80 and it will render on that port the application itself, so to start using exposomeShiny open your web browser and go to the site

```
localhost:80
```

At the beginning it may take some time for the application to render, this is because all the needed R libraries are being loaded, to be sure the container is actually working, take a look at the terminal where you inputed the Docker command, there you will see all the R verbose stating the libraries are being loaded.

Once the user has finished using exposomeShiny, the container needs to be stopped to avoid wasting CPU resources, to do so, input the following command on a bash terminal (the command needs to be inputed on a new bash window):

```
docker container ls
```

This will prompt all the running containers, find the one with the NAMES **brgelab/exosome-shiny** and copy it's CONTAINER ID, then input the following bash command:

```
docker stop xxxxxxxxxxxx
```

Where **xxxxxxxxxxxx** is the CONTAINER ID.

To run the application again, just enter the first bash command (**docker run --rm -p 80:80 brgelab/exosome-shiny**), since it has already been down-

2.3. PULLING THE OFFICIAL DOCKER IMAGE FROM DOCKERHUB

11

loaded, the application is cached on the computer and it will launch straight away. If the user wants to remove the Docker image from the computer, input the following bash command:

```
docker image rm brgelab/exosome-shiny
```


Chapter 3

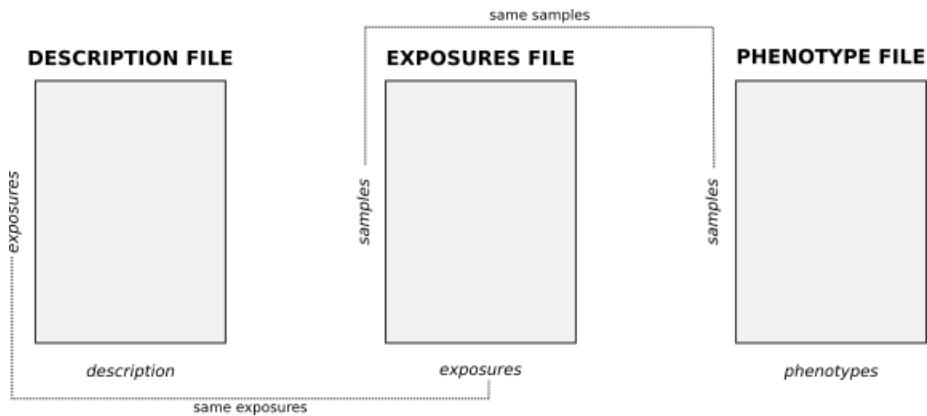
Data sets

3.1 Exposome dataset

The exposome is composed of three different files (in `*.csv` format). Those files are referred inside the Shiny as exposures, description and phenotypes. Their content is the following:

- The `exposures` file contains the measures of each exposure for all the individuals included on the analysis. It is a matrix-like file having a row per individual and a column per exposures. It must include a column with the subject's identifier.
- The `description` file contains a row for each exposure and, at last, defined the families of exposures. Usually, this file incorporates a description of the exposures, the matrix where it was obtained and the units of measurement among others.
- The `phenotypes` file contains the covariates to be included in the analysis as well as the health outcomes of interest. It contains a row per individual included in the analysis and a column for each covariate and outcome. Moreover, it must include a column with the individual's identifier.

A visual representation of the three matrices and how they correlate is the following.



Exposures data file example:

```

id      bde100  bde138  bde209  PFOA      ...
sub01   2.4665  0.7702  1.6866  2.0075 ...
sub02   0.7799  1.4147  1.2907  1.0153 ...
sub03   -1.6583 -0.9851 -0.8902 -0.0806 ...
sub04   -1.0812 -0.6639 -0.2988 -0.4268 ...
sub05   -0.2842 -0.1518 -1.5291 -0.7365 ...
...     ...     ...     ...     ...

```

Description data file example:

exposure	family	matrix	description
bde100	PBDEs	colostrum	BDE 100 - log10
bde138	PBDEs	colostrum	BDE 138 - log10
bde209	PBDEs	colostrum	BDE 209 - log10
PFOA	PFAS	cord blood	PFOA - log10
PFNA	PFAS	cord blood	PFNA - log10
PFOA	PFAS	maternal serum	PFOA - log10
PFNA	PFAS	maternal serum	PFNA - log10
hg	Metals	cord blood	hg - log 10
Co	Metals	urine	Co (creatinine) - log10
Zn	Metals	urine	Zn (creatinine) - log10
Pb	Metals	urine	Pb (creatinine) - log10
THM	Water	---	Average total THM uptake - log10
CHCL3	Water	---	Average Chloroform uptake - log10
BROM	Water	---	Average Brominated THM uptake - log10
NO2	Air	---	NO2 levels whole pregnancy- log10
Ben	Air	---	Benzene levels whole pregnancy- log10

Phenotypes data file example:

```

id      asthma    BMI      sex   age   ...
sub01  control   23.2539 boy    4     ...
sub02  asthma    24.4498 girl   5     ...

```

```

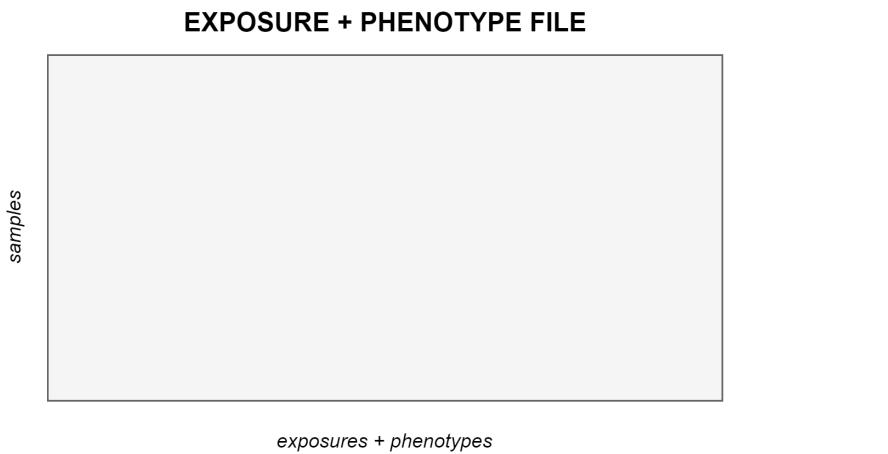
sub03 asthma 15.2356 boy 4 ...
sub04 control 25.1387 girl 4 ...
sub05 control 22.0477 boy 5 ...
...
...
...
...
...

```

3.2 Plain datasets

If the researcher has gathered all the data on a single file which contains both phenotype and exposure data, this file can be used too. The user interface has a selector for it, more information on the correspondent section.

A visual representation of a plain dataset is the following.



* the exposures and phenotypes columns can be mixed

* the Family infomation (Description file) can be manually set by the user when using the application

Plain dataset example (3 exposures + 2 phenotypes):

```

id   bde100  bde138  bde209  asthma  BMI    ...
sub01 2.4665  0.7702  1.6866  control 23.2539 ...
sub02 0.7799  1.4147  1.2907  asthma  24.4498 ...
sub03 -1.6583 -0.9851 -0.8902  asthma  15.2356 ...
sub04 -1.0812 -0.6639 -0.2988  control 25.1387 ...
sub05 -0.2842 -0.1518 -1.5291  control 22.0477 ...
...
...
...
...

```

3.3 Omics dataset

The omics data inputed to the Shiny must be provided as an `*.RData`. This file has to contain an `ExpressionSet`, which is an S4 object. This object is a data container of the Bioconductor toolset.

For further information on `ExpressionSet` and how to create and manipulate them, please visit the official documentation and this selected vignette.

Chapter 4

Bioconductor packages

This Shiny application is a front end support for other Bioconductor packages in order to provide a comfortable environment on to conduct different analysis with those packages. In concrete the packages are rexposome, omicRexosome and CTDquerier.

4.1 rexposome

Rexposome is a package that allows to explore the exposome and to perform association analyses between exposures and health outcomes.

4.2 omicRexosome

OmicRexosome is a package that systematizes the association evaluation between exposures and omic data, taking advantage of MultiDataSet for coordinated data management, rexposome for exposome data definition and limma for association testing. Also to perform data integration mixing exposome and omic data using multi co-inherent analysis (omicade4) and multi-canonical correlation analysis (PMA).

4.3 CTDquerier

CTDquerier is a package to retrieve and visualize data from the Comparative Toxicogenomics Database. The downloaded data is formated as DataFrames for further downstream analyses.

Chapter 5

Analysis flowcharts

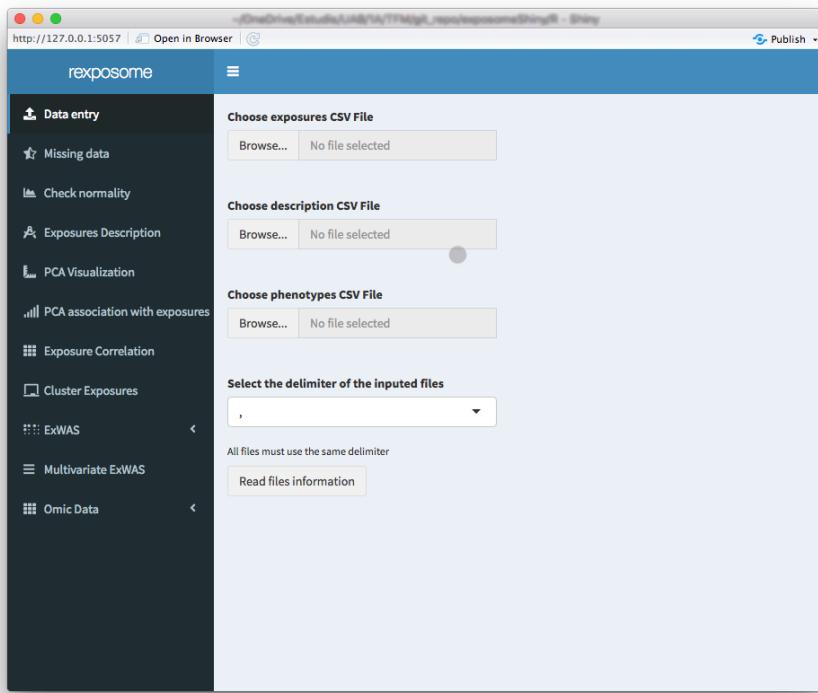
5.1 Exposome health analysis

As any user would need to do using the Bioconductor packages (rexosome, omicRexosome and CTDquerier) when performing an analysis using an R script, there is some kind of flow (or pipeline) to follow in order to get to the results, this is also true on exposomeShiny, even though it's a seamless and codeless integration of the packages there's still some need for a flowchart to get the desired results. All the required flowcharts will be detailed with a box flowchart as well as screenshots of exposomeShiny in order to provide extra guidance if needed.

5.1.1 Data entry

5.1.1.1 Exposome data

Input the exposures, description and phenotypes files and load them into the application. These files have to be provided as `csv` or `txt`, there is a selector on the UI to select the type of separation used, it can be either commas, semicolons or tabs/spaces. Excel files or R objects are not supported as inputs.



Once the tables are read two new main elements will appear, 1) the option to explore the inputted table, using a selector of the table and a button to trigger the visualization; and 2) six input fields will appear on the right side of the file browsers, they are to select the following parameters:

- Column name in the *description* file that contains the exposures
- Column name in the *description* file that contains the families
- Column name in the *exposures* file that contains the id's
- Column name in the *phenotypes* file that contains the id's
- The threshold of to select between continuous or factor exposures. More than this number of unique items will be considered as 'continuous'
- The encoding to search for limit of detection (LOD) missings. It can be either a number (example: -1) or a string (example: LOD).

This is illustrated on the following figure.

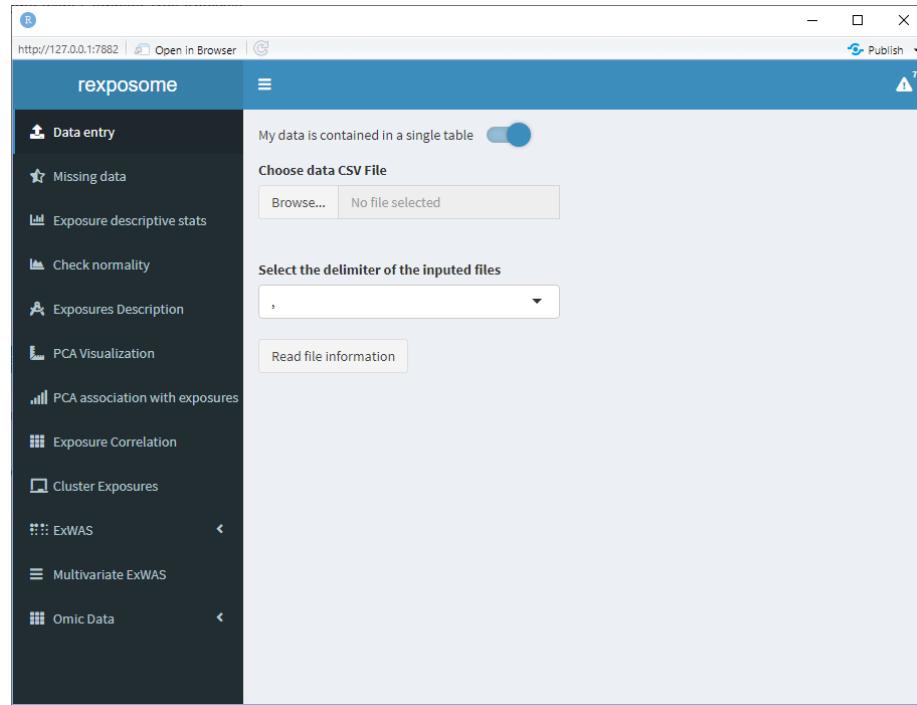
The screenshot shows the 'exposome' web application interface. On the left, a sidebar menu lists various analysis options: Data entry, Missing data, Check normality, Exposures Description, PCA Visualization, PCA association with exposures, Exposure Correlation, Cluster Exposures, ExWAS, Multivariate ExWAS, and Omic Data. The main panel is titled 'Data entry' and contains several configuration fields:

- Choose exposures CSV File:** A file selector set to 'exposures_lod_test.csv' with the status 'Upload complete'.
- Select column of 'exposures' that contains the id's:** A dropdown set to 'idnum'.
- Choose description CSV File:** A file selector set to 'description.csv' with the status 'Upload complete'.
- Select column of 'phenotypes' that contains the id's:** A dropdown set to 'idnum'.
- Choose phenotypes CSV File:** A file selector set to 'phenotypes.csv' with the status 'Upload complete'.
- Select column of 'description' that contains the exposures:** A dropdown set to 'Family'.
- Select column of 'description' that contains the families:** A dropdown set to 'Family'.
- Select the delimiter of the inputted files:** A dropdown set to ','.
- All files must use the same delimiter:** A checkbox labeled 'Read files information'.
- Table to explore:** A dropdown set to 'exposures'.
- The exposures with more than this number of unique items will be considered as 'continuous':** An input field set to '5'.
- Select LOD encoding to search:** An input field set to '-1'.
- Explore selected table:** A button.
- Validate selections:** A button.

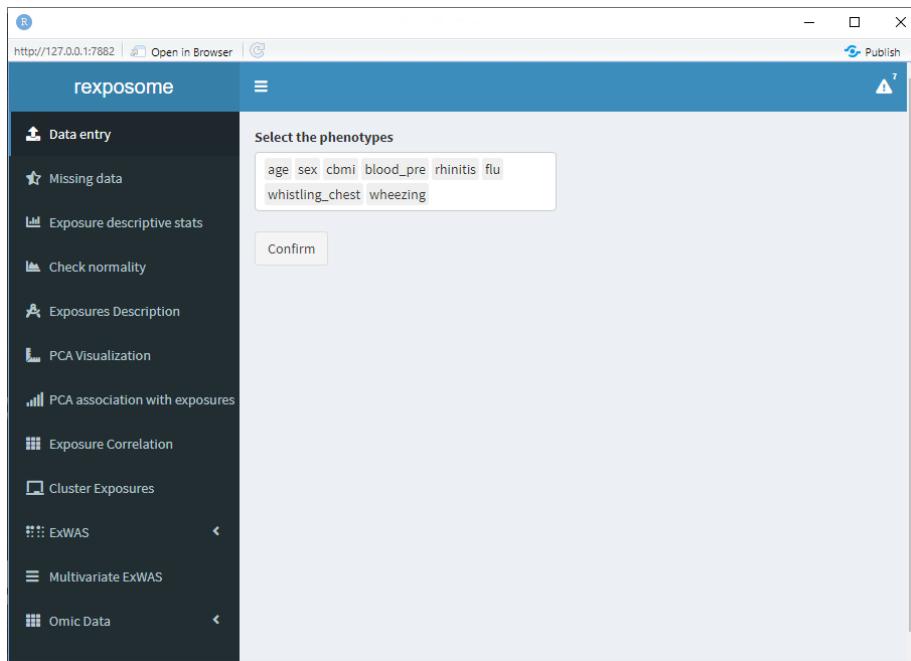
Once the fields are completed, please press the *Validate selections* button in order to check if all the parameters allow for a successful load of the exposome dataset, if not, a pop-up will be prompted to the user. In the case that everything is correct, the UI will be updated and a button that reads *Load selected data to analyze it* will appear, by clicking this button the dataset will be loaded and the analysis can begin. The input fields are still visible past this point for the case that the user wants to load a new dataset into the application without restarting it.

5.1.1.2 Plain data

When dealing with a single file that contains the exposures and phenotype data, press the “My data is contained in a single table” toggle. This will change the interface to only show one file selector.



Select a file and press “Read file information”. This will change the interface to show a multiple selector input, all the available columns will be listed, select the ones which correspond to phenotypes.



When all the phenotypes are selected, press “Confirm”. Now the researcher can group the exposures into families, to do so, select them on the table, input the family name on the field “Family of selected exposures” and press “Assign”. All the exposures that have empty “Family” fields will be treated as they are their own family.

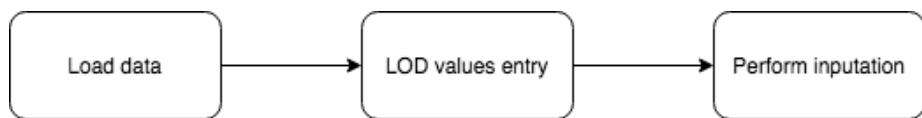
The screenshot shows the exposomeShiny web application interface. On the left is a sidebar with various analysis options: Data entry, Missing data, Exposure descriptive stats, Check normality, Exposures Description, PCA Visualization, PCA association with exposures, Exposure Correlation, Cluster Exposures, ExWAS, Multivariate ExWAS, and Omic Data. The main panel displays a table titled "Exposures" with columns "Exposures" and "Family". The table lists entries such as PMcoarse, AbsPM25, Dens, Conn, Green (Family: Noises), Noise_d (Family: Noises), Noise_n (Family: Noises), and Temp. Above the table, there is a dropdown menu "Show 10 entries". To the right of the table, there are two configuration fields: "The exposures with more than this number of unique items will be considered as 'continuous'" with a value of "5", and "Select LOD encoding to search" with a value of "-1". Below these fields is a button "Assign". At the bottom of the main panel, it says "Showing 81 to 88 of 88 entries" with a navigation bar showing pages 1 through 9, with page 9 highlighted.

Finally, there are two configuration fields:

- The threshold of to select between continuous or factor exposures. More than this number of unique items will be considered as ‘continuous’
- The encoding to search for limit of detection (LOD) missings. It can be either a number (example: -1) or a string (example: LOD).

Be sure to revise them before pressing “Load data”.

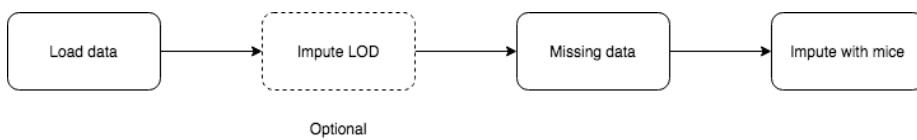
5.1.2 LOD imputation



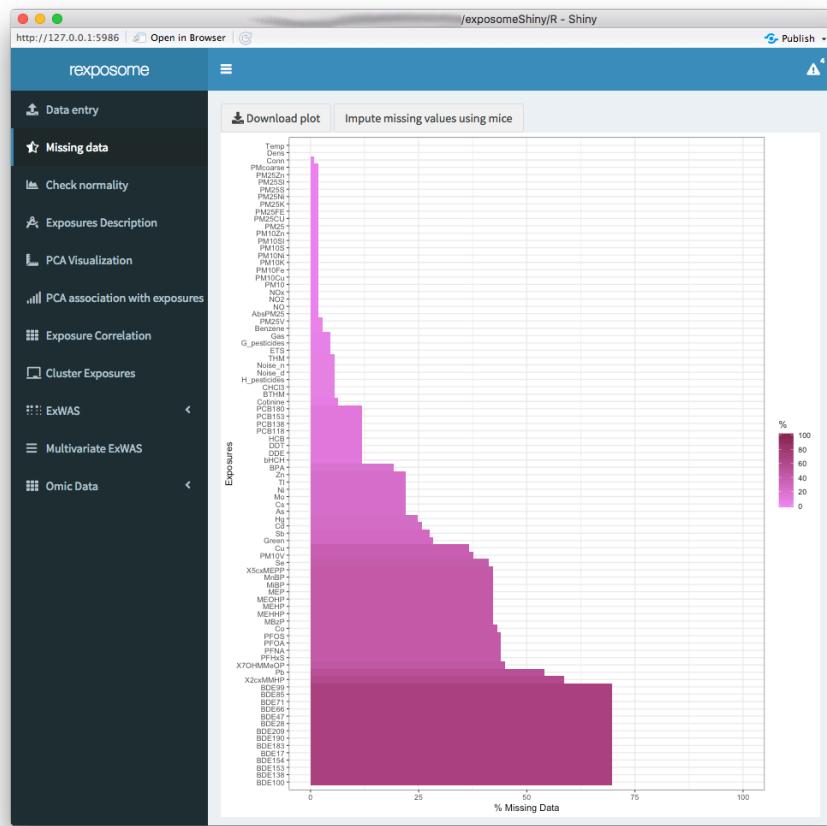
If exposomeShiny detects LODs (limit of detection) on the exposures file, it will prompt the table with the exposures with LOD and double clicking on

the desired cell will enable edit mode to input the instrument LOD. There's also the option of selecting "Random imputation" on the imputation method in order to impute with random values (truncated log distribution) instead of LOD/sqrt(2). If the user imputes the LOD missings, the dataset will be imputed and the user will not need to reimport it, the loaded dataset will be updated to have the LOD missings imputed, this can be checked by clicking on the ! symbol at the top bar of the application.

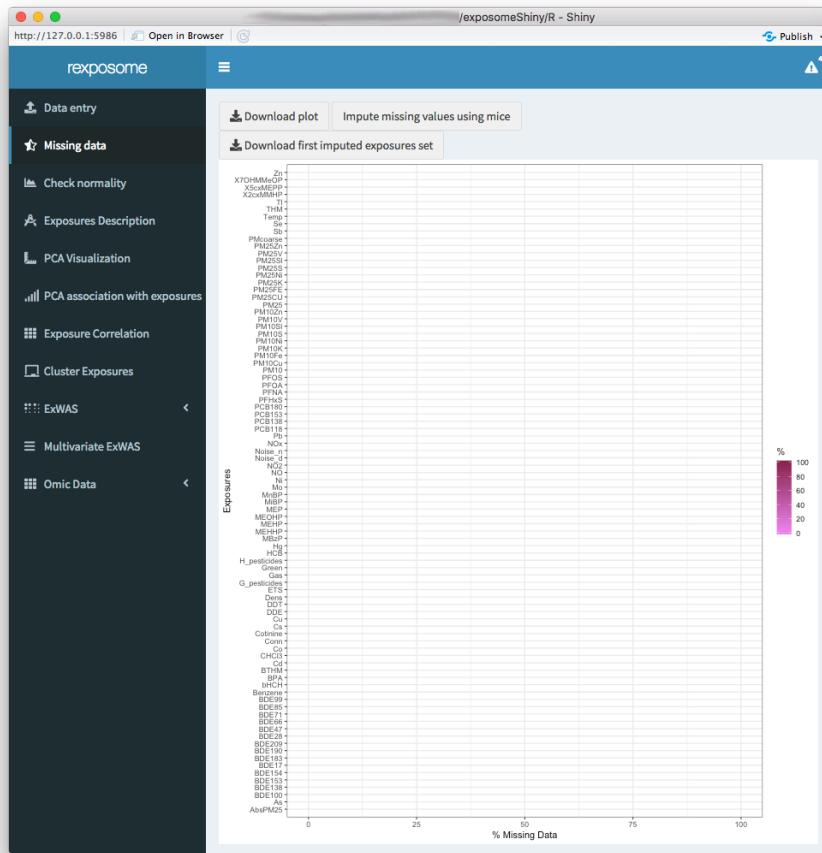
5.1.3 Missing imputation



Once the dataset is loaded into the Shiny, look at the "Missing Data" tab to check the percentages of missing data for each exposure present.



To impute the missing values select “Impute missing values using mice” (Multiple Imputation by Chained Equations), no other method of imputation is available in the software at the moment. After the process finishes, the expect output should be a new missing data graph where there’s no missing of any exposure.



The new imputed exposures set can be downloaded as a *.csv file, please note that the downloaded file just assigns numbers to the `idnum` column, if the data you are using has different `idnum` format it's needed to format it properly so that it matches the `idnum` on the phenotypes input file when inputting it to the Shiny.

5.1.4 Exposures description

There's the option of visualizing the main descriptive stats of the exposures dataset, available for quantitative exposure variables. The descriptive stats (per exposure) included on the table are:

- Number of values
 - Number of NULLs
 - Number of NAs
 - Minimum

- Maximum
- Range of values
- Sum of values
- Median
- Mean
- Standard Error of mean
- 0.95 confidence interval of the mean
- Variance
- Standard deviation
- Variance coefficient

This table will have the descriptive stats of the loaded dataset, this means that if the user has imputed the missings (remember that after imputing the missings, the imputed dataset becomes active) it will be reflected on the table as it will show 0 NAs.

~/OneDrive/Estudis/UAB/IAA/TFM/git_repo/exposomeShiny/R - Shiny
http://127.0.0.1:5237 | Open in Browser | ⚙️ Publish ▾

rexosome

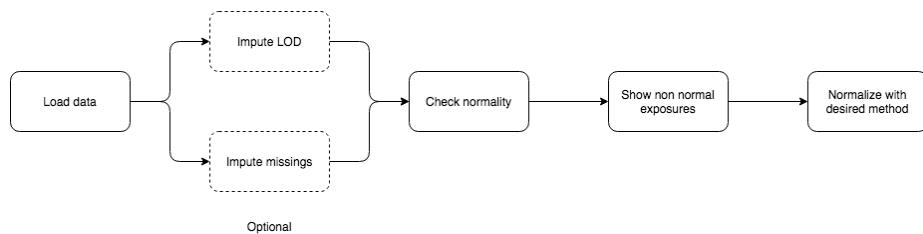
Show 14 entries								Search: <input type="text"/>
Stat	AbsPM25	As	BDE100	BDE138	BDE153	BDE154	BDE17	
nbr.val	107	85	33	33	33	33	3	
nbr.null	0	0	0	0	0	0	0	
nbr.na	2	24	76	76	76	76	7	
min	0.2	0.775	-1.415	-2.119	-0.76	-1.153	-2.30	
max	0.556	2.613	0.504	-0.909	0.428	0.203	-0.17	
range	0.356	1.838	1.919	1.21	1.188	1.356	2.12	
sum	37.951	129.504	-18.092	-55.046	-3.518	-14.069	-60.61	
median	0.354	1.506	-0.554	-1.688	-0.087	-0.446	-1.87	
mean	0.355	1.524	-0.548	-1.668	-0.107	-0.426	-1.83	
SE.mean	0.007	0.042	0.07	0.04	0.058	0.044	0.06	
CI.mean.0.95	0.014	0.083	0.142	0.081	0.118	0.089	0.12	
var	0.005	0.148	0.161	0.053	0.111	0.063	0.12	
std.dev	0.074	0.385	0.401	0.229	0.334	0.251	0.35	
coef.var	0.209	0.253	-0.731	-0.137	-3.13	-0.589	-0.19	

Showing 1 to 14 of 14 entries

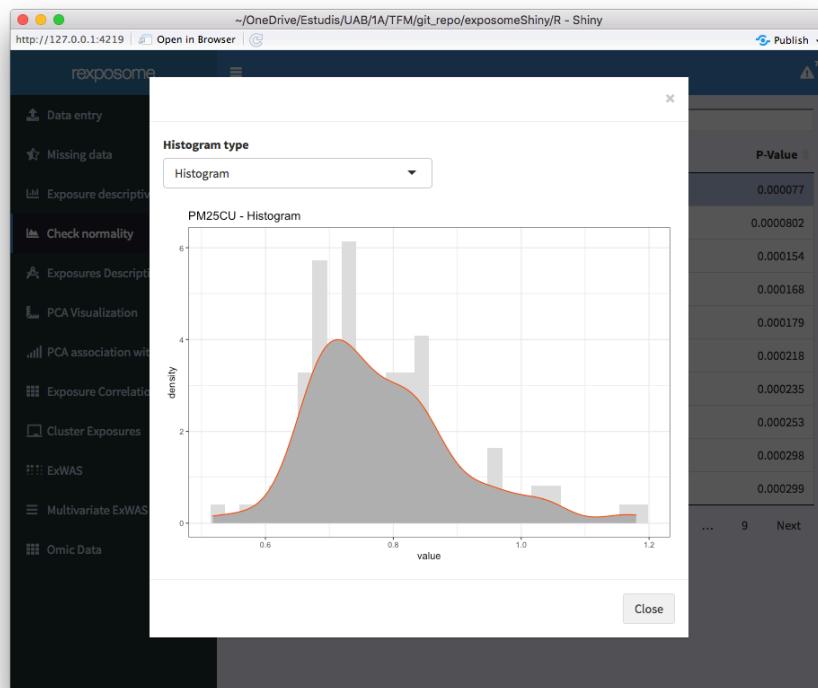
Previous 1 Next

[Download table](#)

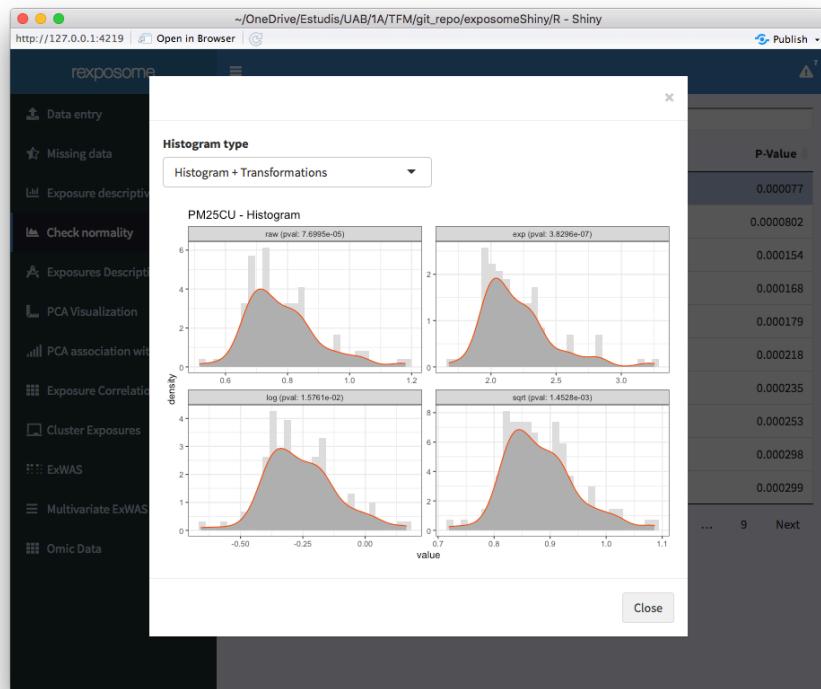
5.1.5 Normality correction



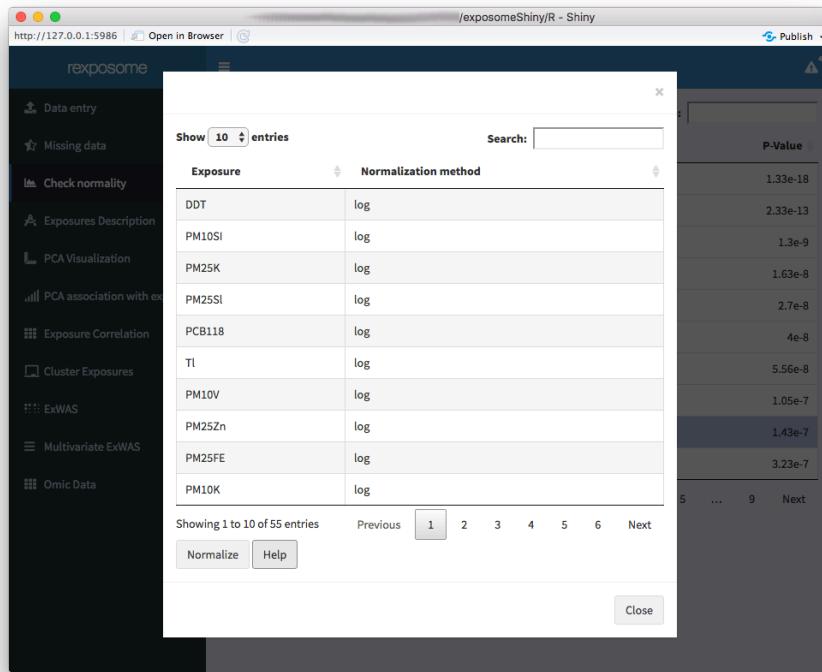
Once the dataset is loaded into the Shiny, look at the “Check Normality” tab to check which exposures are not normal (Normality = false), this are the results of Shapiro–Wilk testing. By selecting from the table the desired exposure and clicking the “Plot histogram of selected exposure”, as the label of the button implies, a histogram of the selected exposure from the table can be seen.



There is also the option of visualizing the histogram for the implemented transformations along the normality test p-value for said transformations.

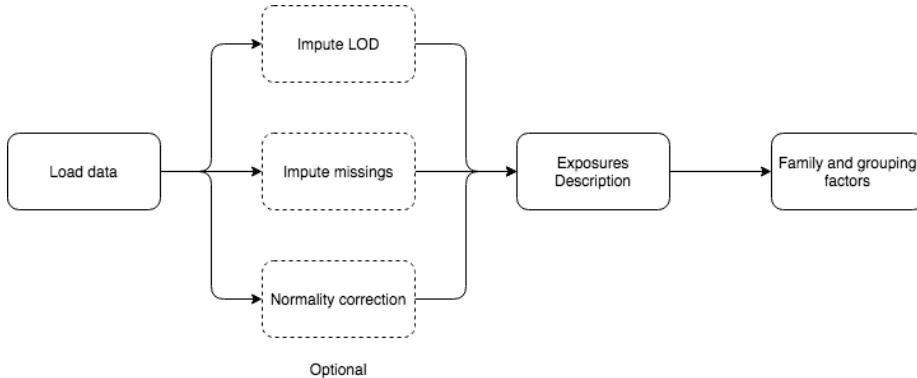


By clicking the “Show false” button, all the non normal exposures are listed with the method that will be applied to normalize, this table can be edited (the “Normalization method” column) by double clicking on the desired row. There are three possible methods to use, “log” (default, natural logarithm), “ $^{1/3}$ ” and “sqrt”. If no method is desired to be applied to an exposure (keep the original variable) input “none”. The normalization method refers to applying X function to a column of the exposures tables, to transform it.



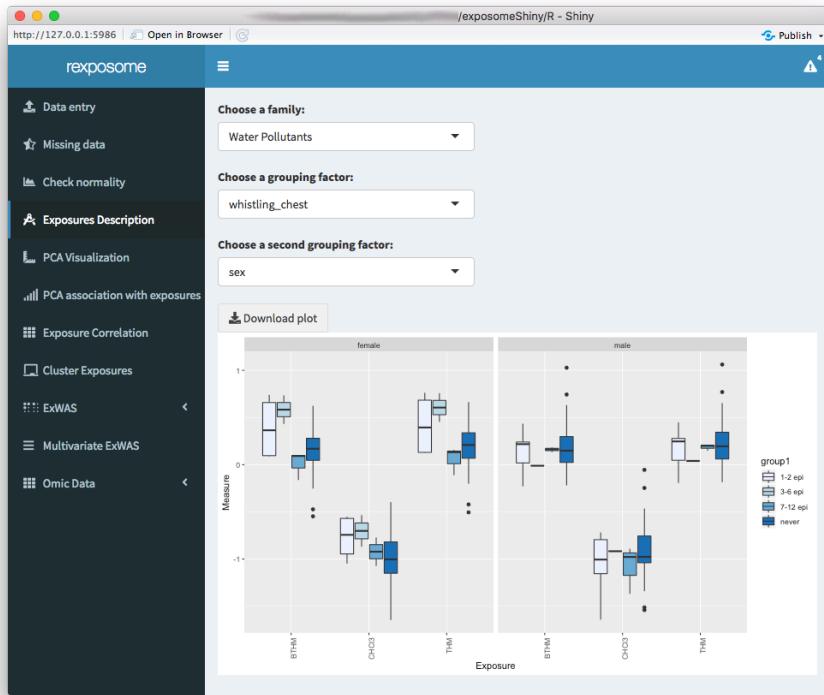
Click “Normalize” and the normalization method selected will be applied, the table on the “Check Normality” tab will be updated with the results of the normalization.

5.1.6 Exposures description

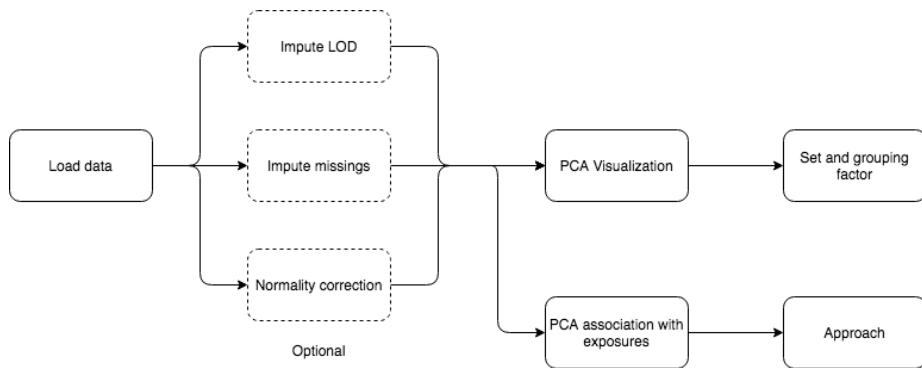


To see all the insights of the exposures dataset loaded into the Shiny, once

loaded it check the exposures description tab, there are three options to dig into the dataset, the family (family of the exposure) to visualize and two grouping factors (phenotypes).

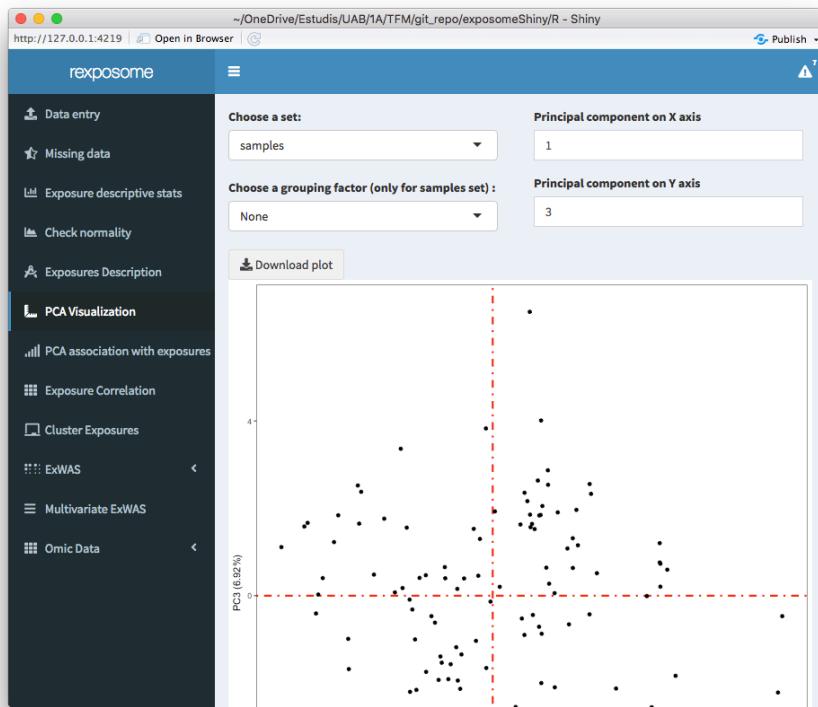


5.1.7 PCA Analysis

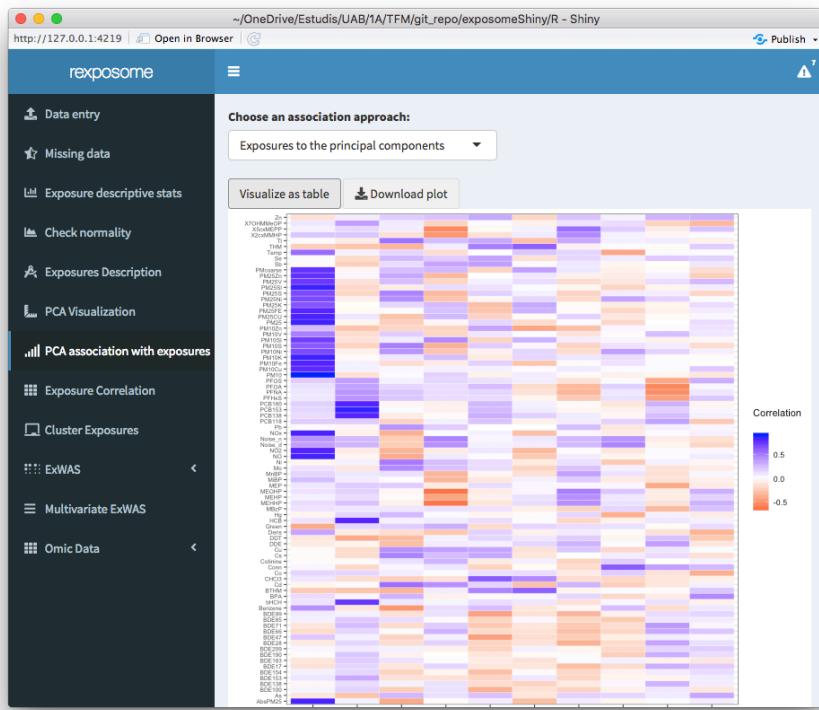


To see the results of a PCA (principal component analysis) study, load the

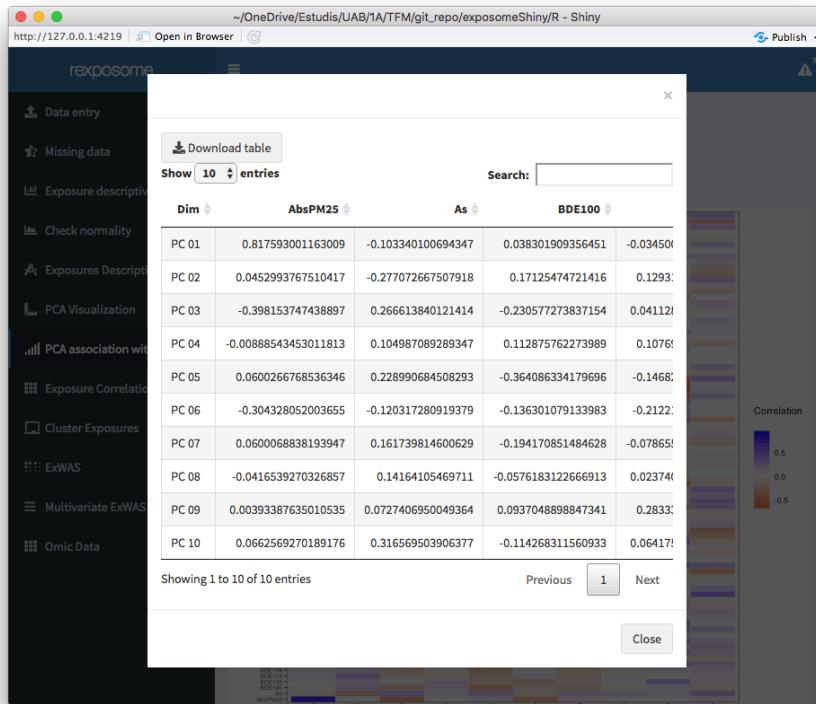
data and check the PCA Visualization tab, there a set and grouping factor can be choose, it's important noting (as it's already stated on the Shiny) that the grouping parameter only works when the set is selected to "samples". There are also selectors to choose which principal component to visualize on each axis, 10 principal components are computed.



If the association of the PCA analysis with the exposures is desired to visualize, check the "PCA association with exposures" tab, there are two grouping methods to visualize, the phenotypes to principal components and the exposures to principal components.



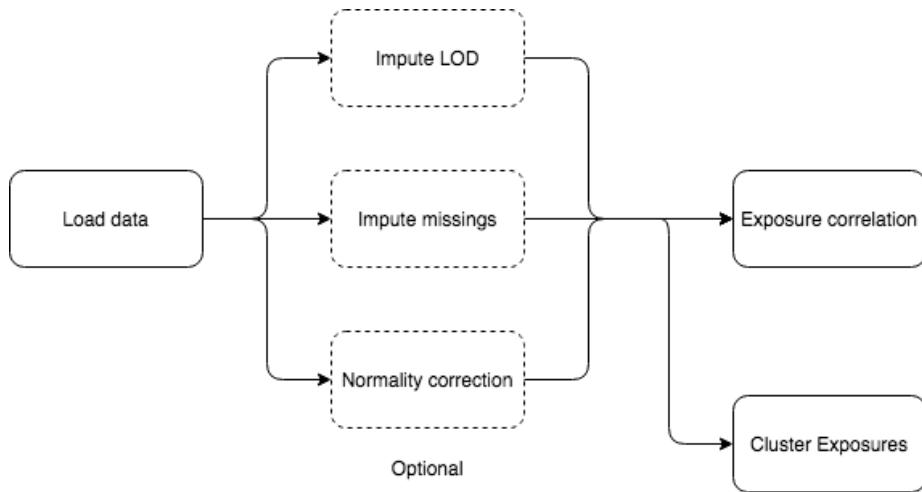
By clicking on “Visualize as table”, the table corresponding to the selected association will be prompted on a pop-up window, this table can be downloaded as a csv.



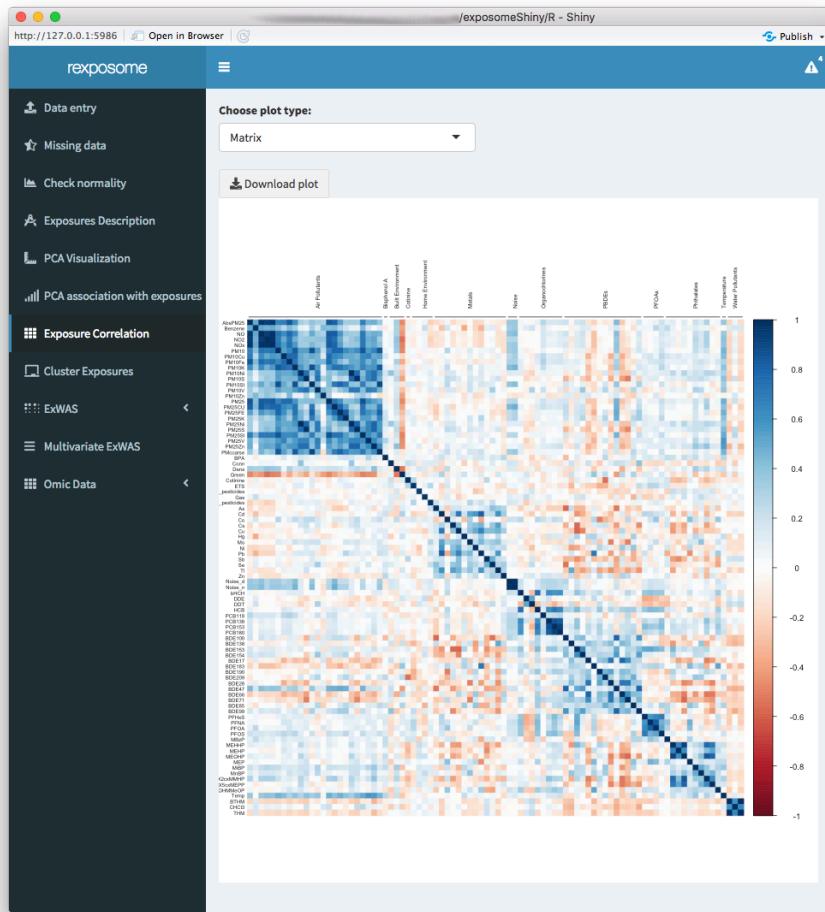
5.1.8 Clusterization and correlation of exposures

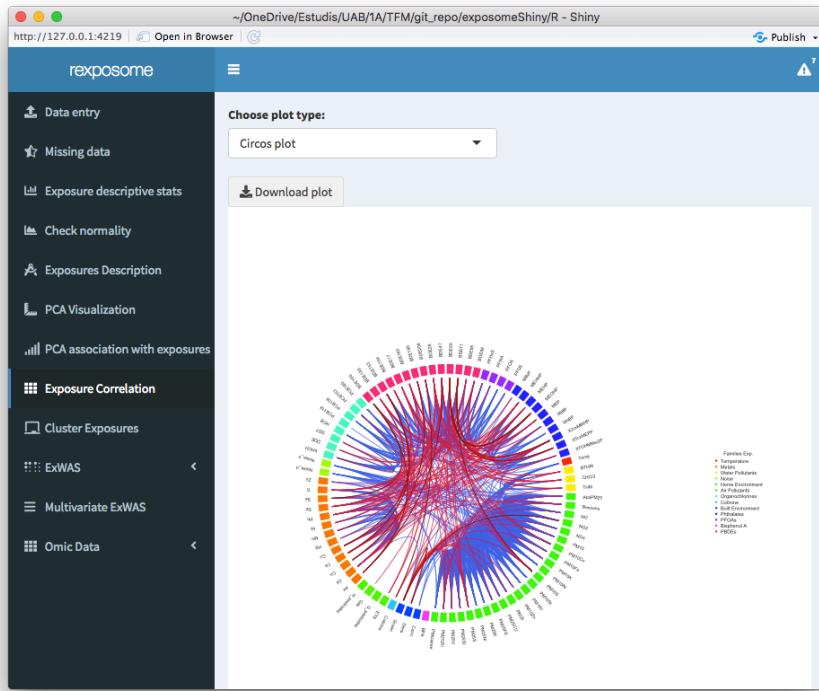
Displaying the correlation of the exposures can help to visualize intra and inter family relations between the exposures, for that reason there are two different visualization options, the circos and the matrix.

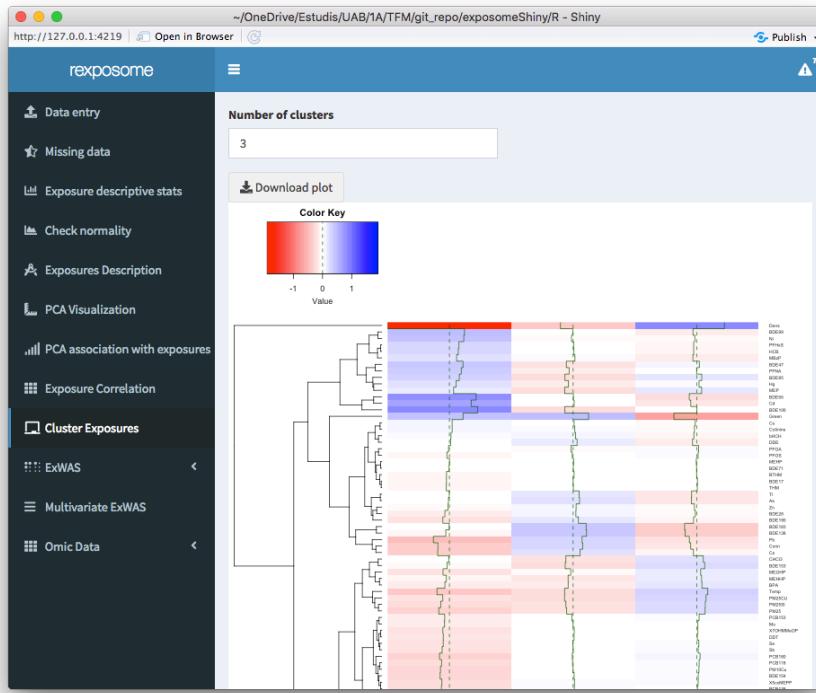
The clusterization of exposures uses a hierarchical clustering algorithm to classify the individuals profiles of exposures in k groups, where k can be selected by the user. The plot shows the profile for each group of individuals.



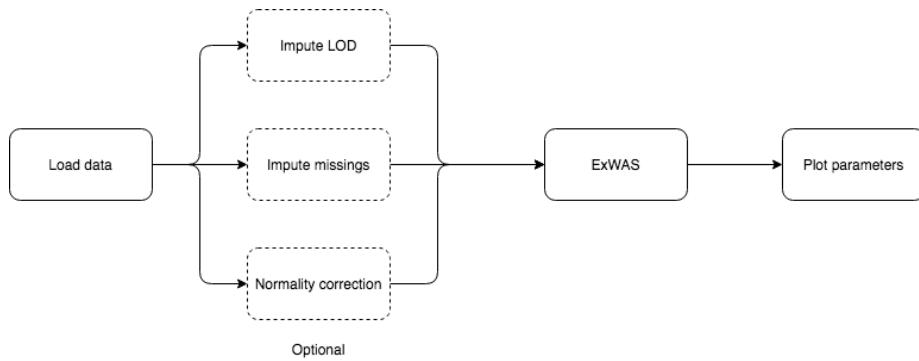
To see the results of the exposure correlation and clustering, select the corresponding tab to each analysis. For the exposure correlation analysis there are two visualizations, the matrix representation and the circos. The correlation uses Pearson method for numerical-to-numerical correlation, Cramer's V for categorical-to-categorical correlation and linear models for categorical-to-numerical.







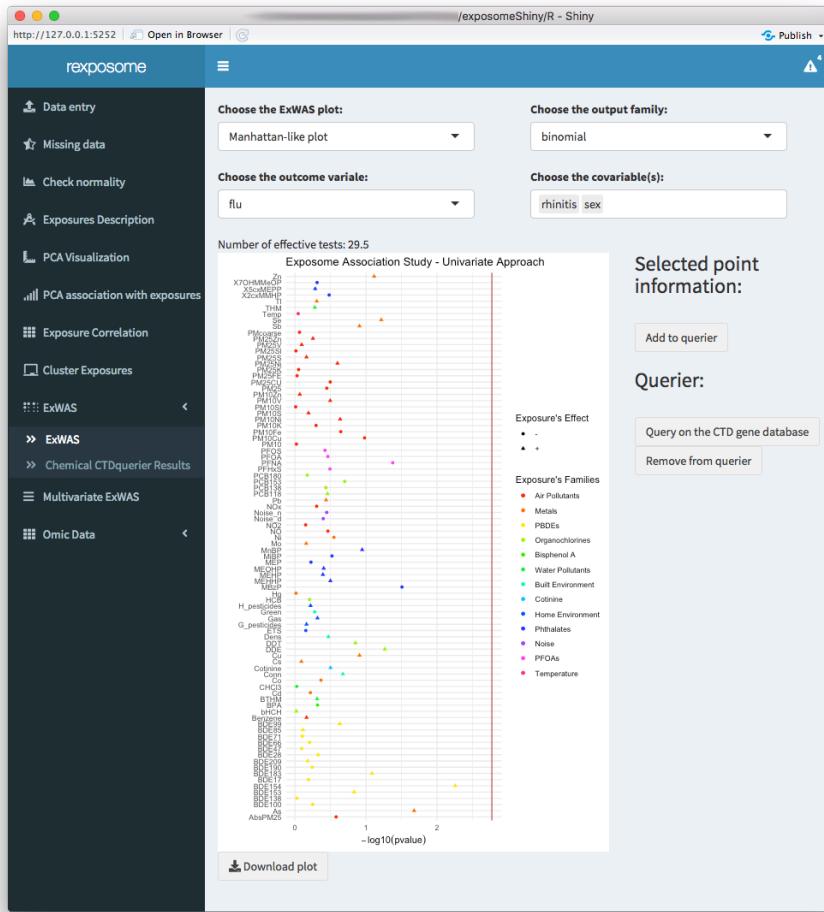
5.1.9 ExWAS



5.1.9.1 Regular

To perform an ExWAS (exposome-wide association, univariate test of the association between exposures and health outcomes using generalized linear mod-

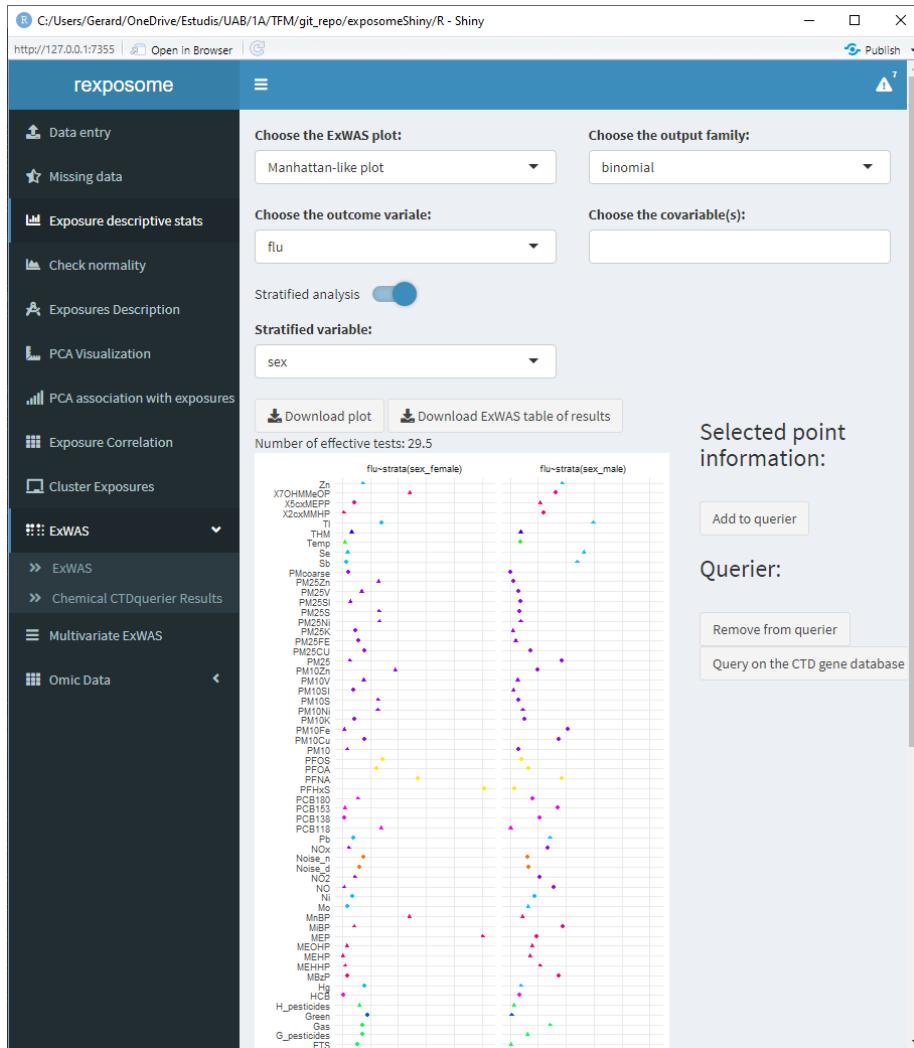
els) study, check the ExWAS tab and select the addequate parameters for the ExWAS plot, there are two different plot representations, the output variable to choose (phenotype), the output family and as many covariables (phenotypes) as the user wants. There are internal checks to advise the user on which parameters to select depending if the selected outcome is numerical or bionomial.



5.1.9.2 Stratified

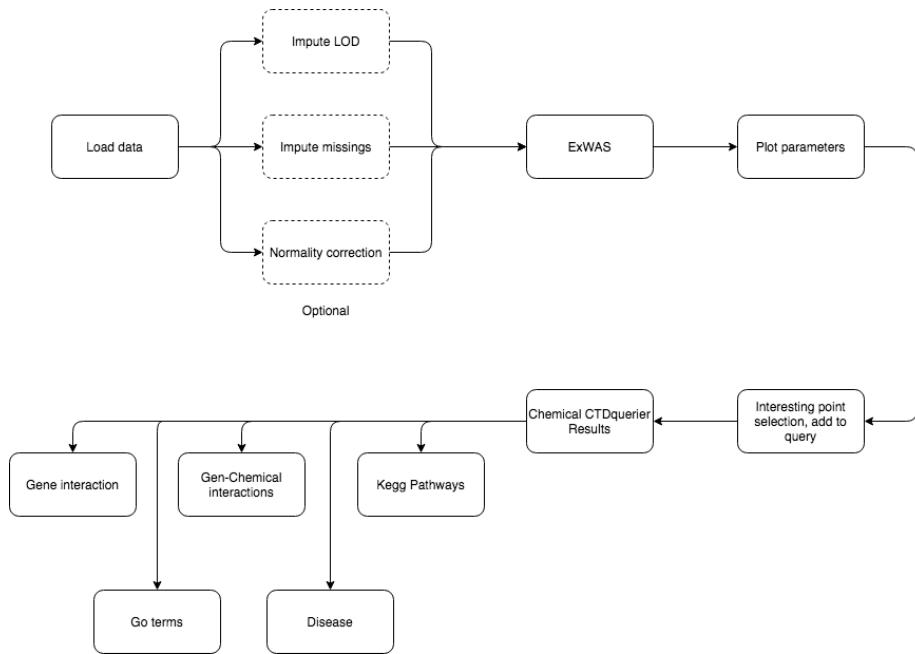
There is an option to perform a stratified ExWAS, to do so, check the toggle “Stratified analysis”, this will display a new input field to select a categorical phenotype to stratify by. This analysis will yield as many ExWAS plots as levels has the category selected, when downloading the table of results for a stratified analysis, a .zip file will be downloaded with a table corresponding to

each plot. The naming of the tables corresponds to the stratifying variable with the category name attached (`sex_female.csv` / `sex_male.csv` in the presented case).

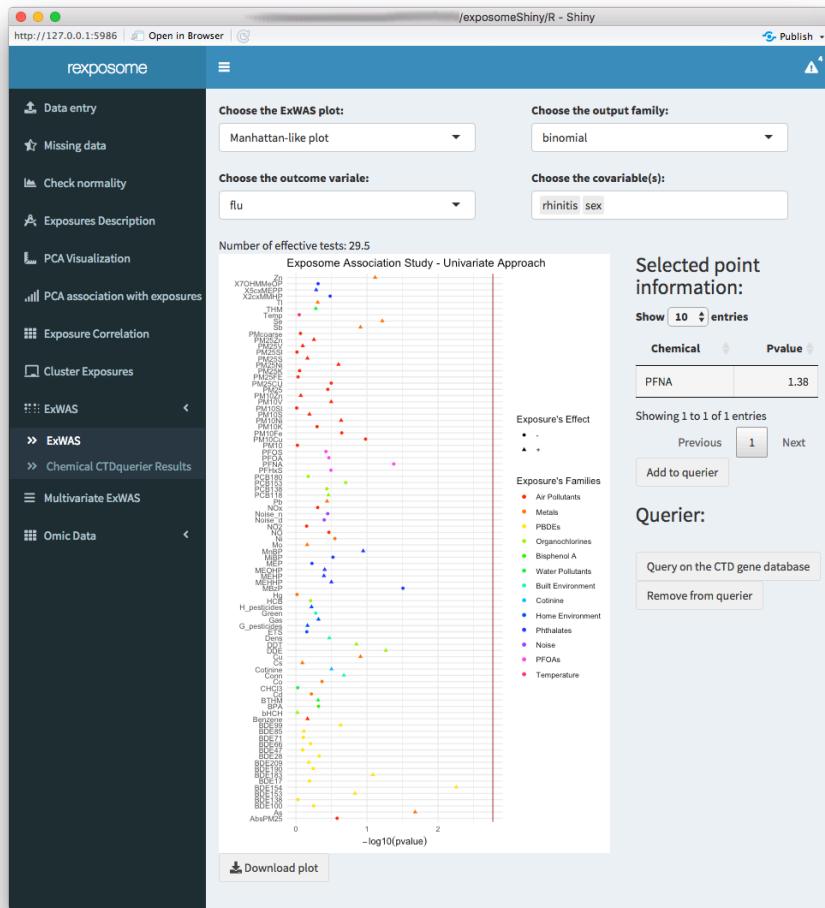


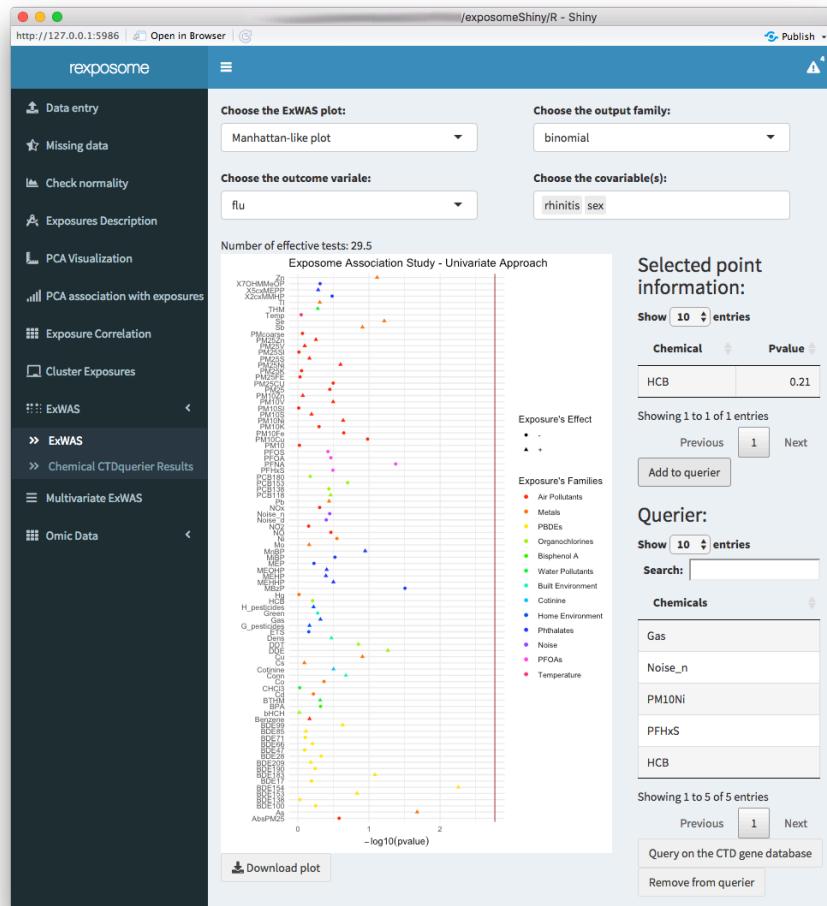
5.1.10 ExWAS - CTDquerier

The ExWAS tab also is able to perform a CTD query of the desired chemicals.

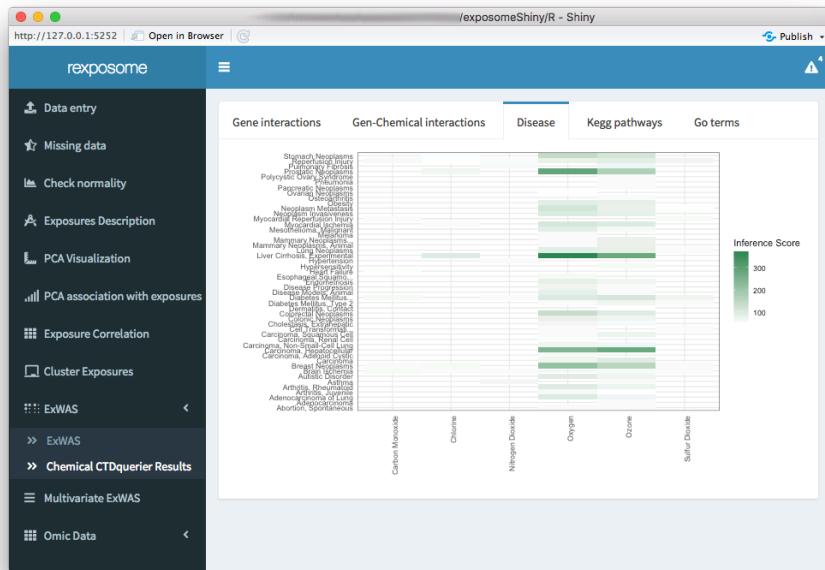


To perform a CTDquerier of chemicals with the results of the ExWAS, click on the desired exposure to preload it into the query, when clicked, a chemical name with its associated P-Value will appear on the table on the right, if that's the desired chemical to add to the query list click "Add to querier". In the case of adding an unwanted chemical to the query list, select it (or them) by clicking on the Querier list and click on "Remove from querier".



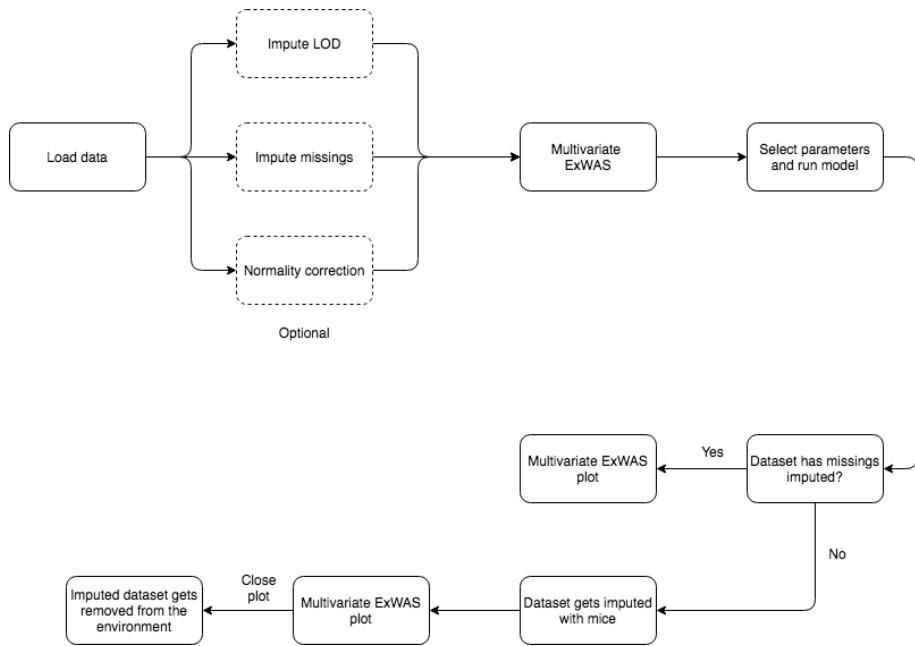


To do the query of the chemicals to de CTD database click on “Query on the CTD gene database” and see the results on the “Chemical CTDquerier Results” subtab. It’s important noting that on the “Kegg pathways” and “Go terms” the input field corresponds to the negative exponent of the filter.

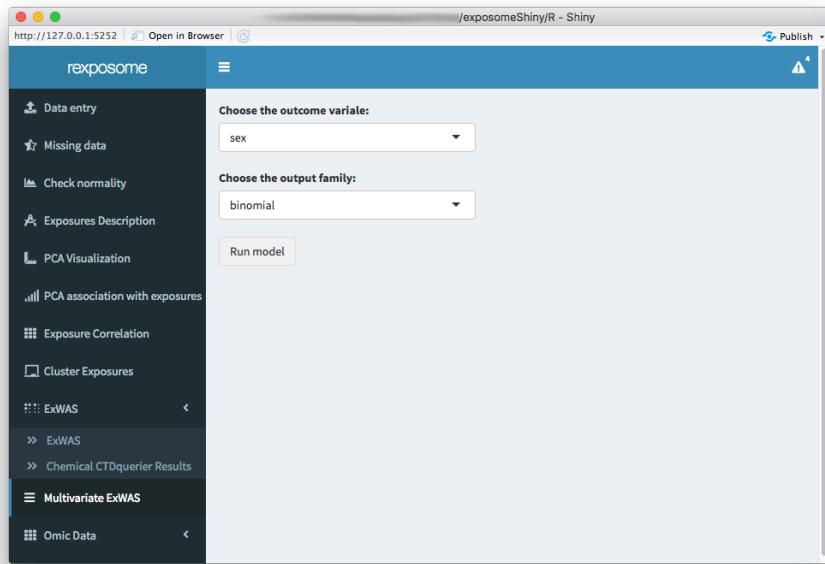


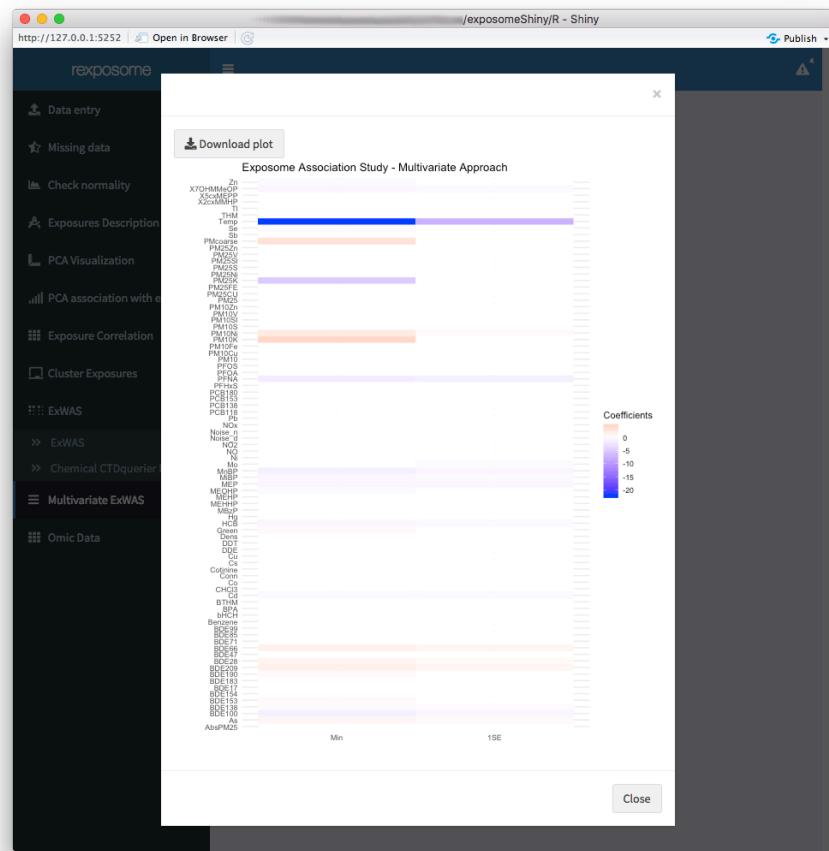
5.1.11 Multivariate ExWAS

Multivariate analysis using Elastic Net (LASSO regression). Multivariate ExWAS applies elastic net to the exposures given a health outcome of interest. The heat map is coloured with the coefficient of each exposure in relation with the health outcome, so the ones in white are not interesting. The two columns of the heat map correspond to the minimum lambda (Min) and to the lambda which gives the most regularised model such that error is within one standard error of the minimum (1SE).



To perform a multivariate ExWAS study, check the Multivariate ExWAS tab and select the desired output parameter, click on run model to generate the plot. As on the ExWAS plot options there's implemented an internal check to advise the user on which parameters to select depending if the selected outcome is numerical or bionomial, as the diagrams states if the dataset has not been imputed the missings, it will automatically do it to perform the Multivariate ExWAS, however when closing the plot the imputed dataset will be removed from the environment, so all the other studies performed afterwards will not be altered.



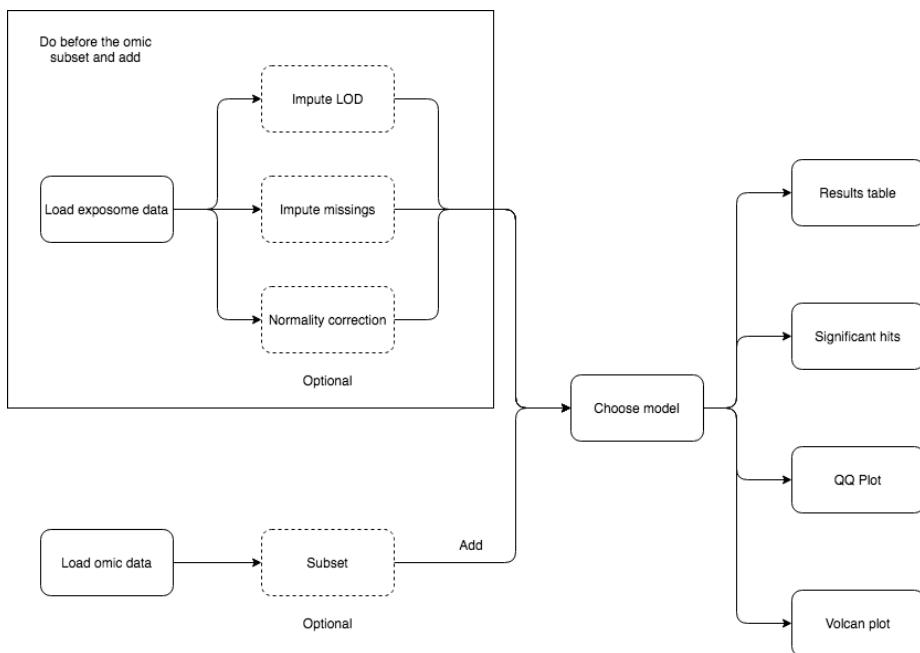


5.2 Exposome-Omic analysis

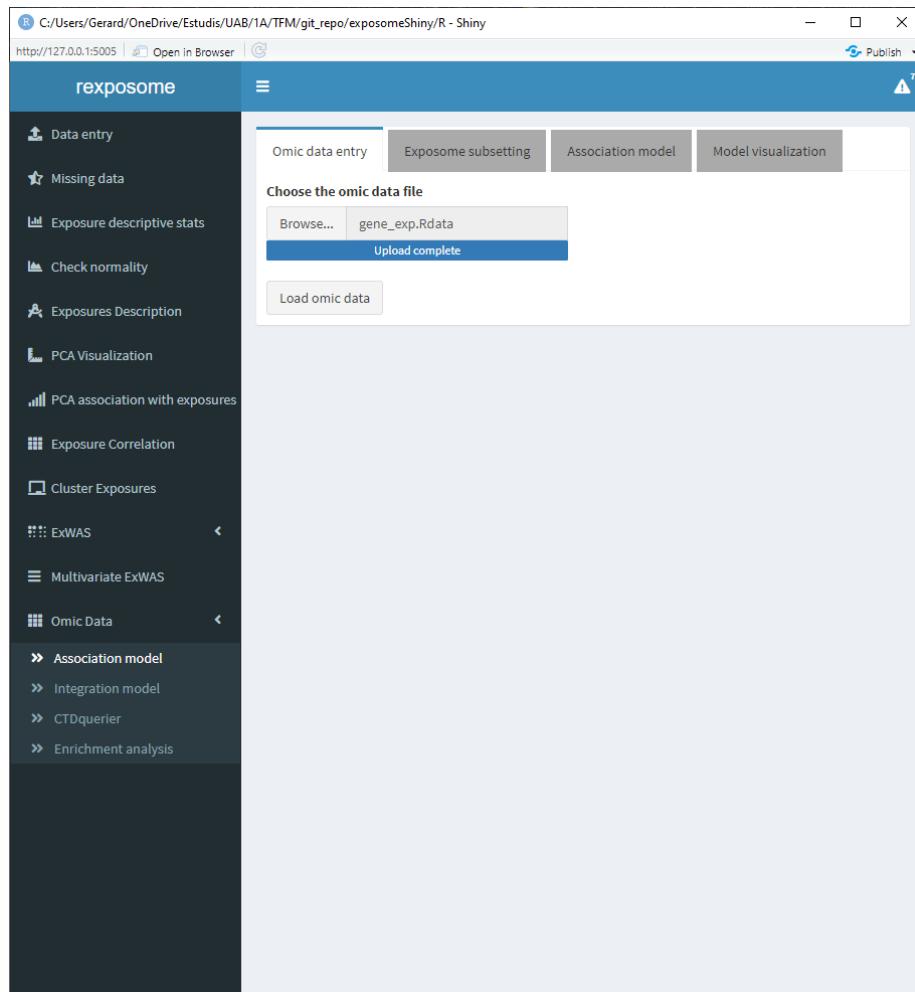
It's important noting that the maximum size of the omics data is 30 MB, if the omics file to be analyzed is bigger, change the line number 2 of the `server.R` file.

```
# the "30" refers to 30MB, change as needed  
options(shiny.maxRequestSize=30*1024^2)
```

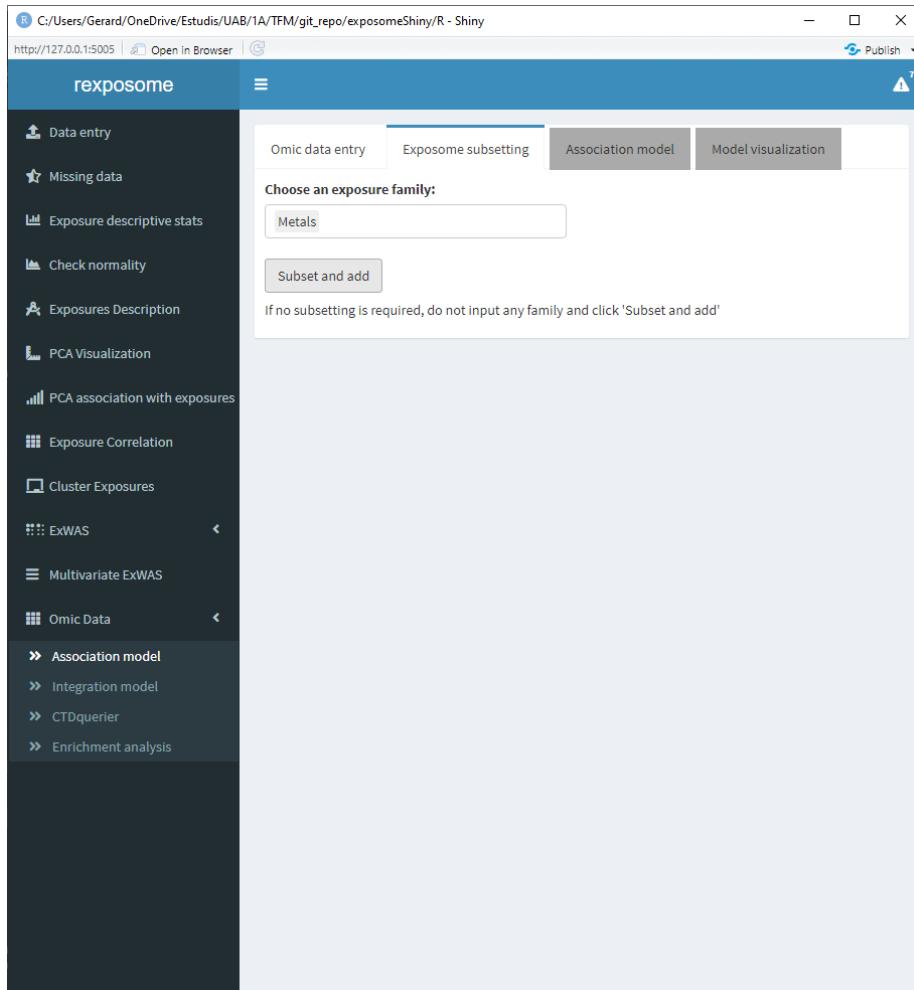
5.2.1 Association analysis



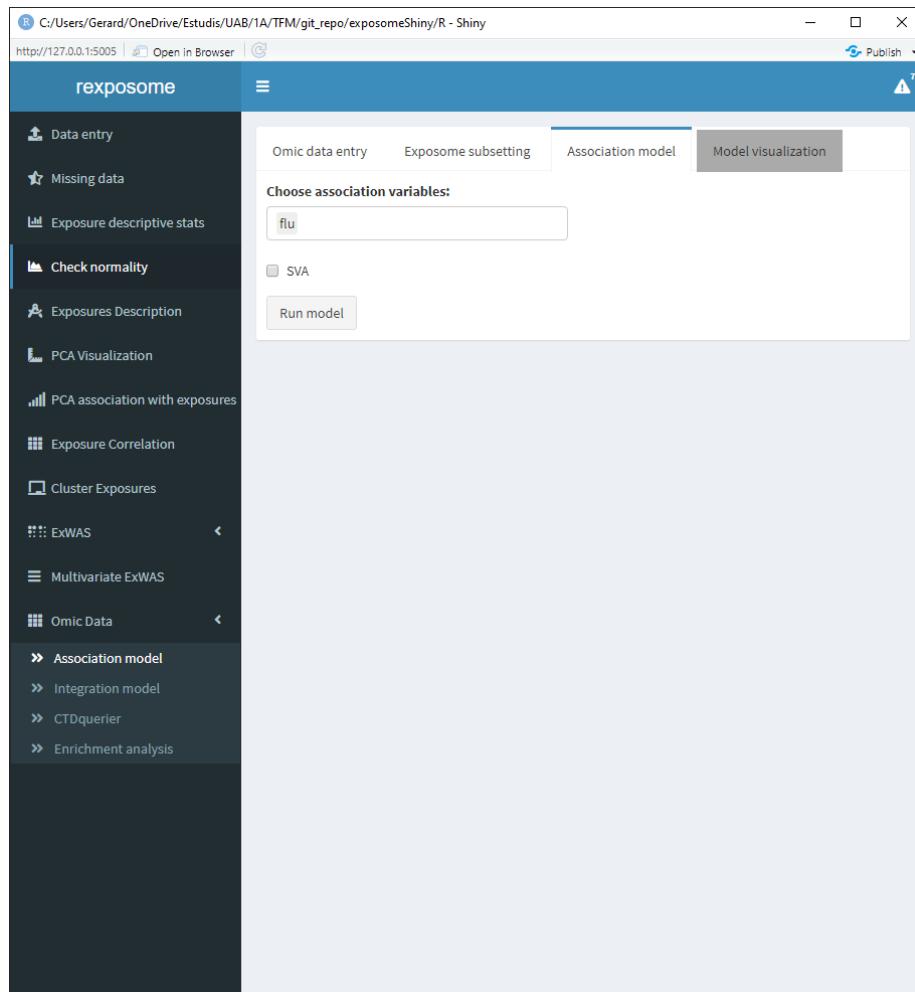
Do first the proceeding of exposome data load and corresponding treatment if desired, then proceed to load the omic dataset on the “Data Entry” subtab. The omic data should be provided as a ***.RData** file.



The exposome dataset can be subseted by families for this analysis, on the “Exposome subsetting” subtab select the families that are desired to be included in this new set to study, if all the families are desired just don’t input any and proceed to click the “Subset and add”, which will trigger the action to combine the subsetted (or not) exposome dataset with the provided omic dataset.



Select the variables for the association analysis (linear models) and if SVA (surrogate variable analysis) is wanted on the “Association model” subtab.



There are tabs to visualize the results of running the association model, all of the are on the “Model visualization” subtab. The “Results table” shows the gene, log of the fold change, p-value and adjusted p-value.

The screenshot shows the rexposome Shiny application interface. The left sidebar contains a navigation menu with various options: Data entry, Missing data, Exposure descriptive stats, Check normality, Exposures Description, PCA Visualization, PCA association with exposures, Exposure Correlation, Cluster Exposures, ExWAS, Multivariate ExWAS, Omic Data, Association model (which is selected), Integration model, CTDquerier, and Enrichment analysis. The main panel has tabs for Omic data entry, Exposome subsetting, Association model, and Model visualization. The Model visualization tab is active, showing four sub-tabs: Results table, Significant hits (which is selected), QQ Plot, and Volcano plot. The Results table sub-tab displays a table of 10 entries from 20,000. The columns are logFC, PValue, and adj.PVal. The table data is as follows:

	logFC	PValue	adj.PVal
TC02001791.hg.1	-0.18	0	1
TC02003390.hg.1	-0.21	0	1
TC01004554.hg.1	-0.16	0	1
TC01004476.hg.1	-0.13	0	1
TC05001945.hg.1	-0.12	0	1
TC03001844.hg.1	-0.23	0	1
TC03003225.hg.1	0.15	0	1
TC05001428.hg.1	-0.21	0	1
TC02000545.hg.1	-0.2	0	1
TC02000374.hg.1	0.1	0	1

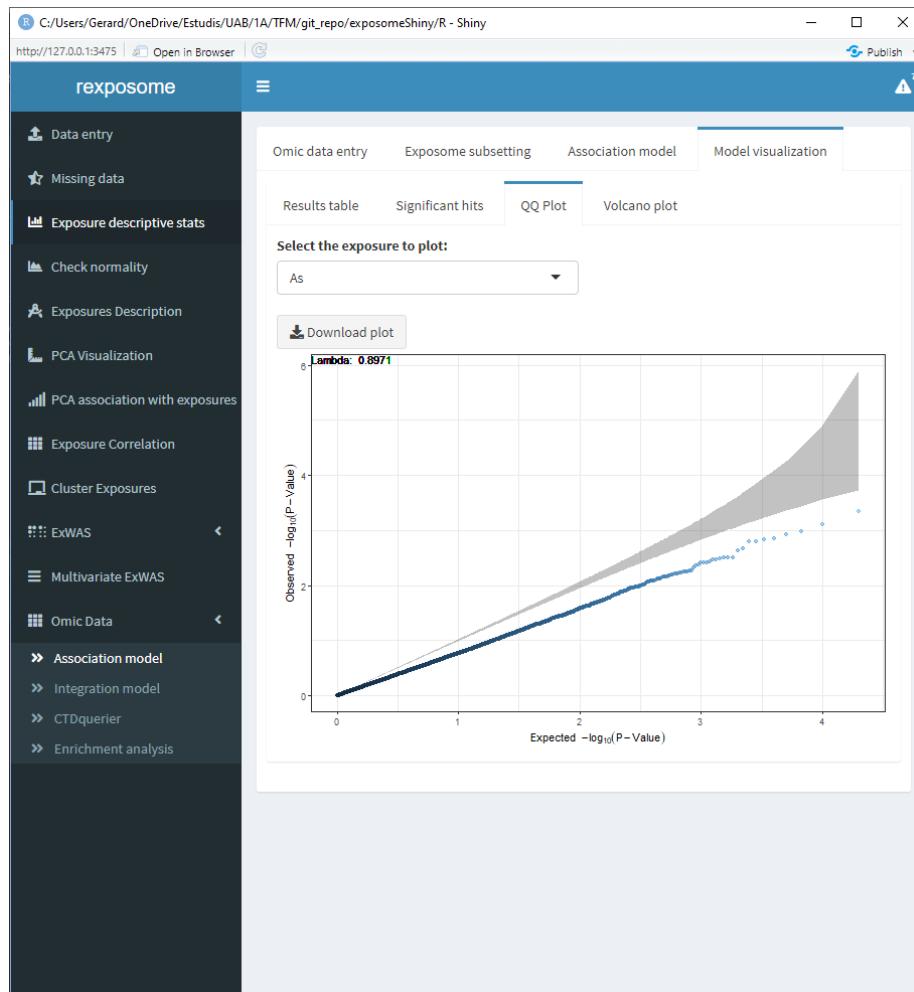
Below the table, it says "Showing 1 to 10 of 20,000 entries" and has a navigation bar with buttons for Previous, 1, 2, 3, 4, 5, ..., 2000, and Next.

The “Significant hits” shows the exposure, hits and lambda.

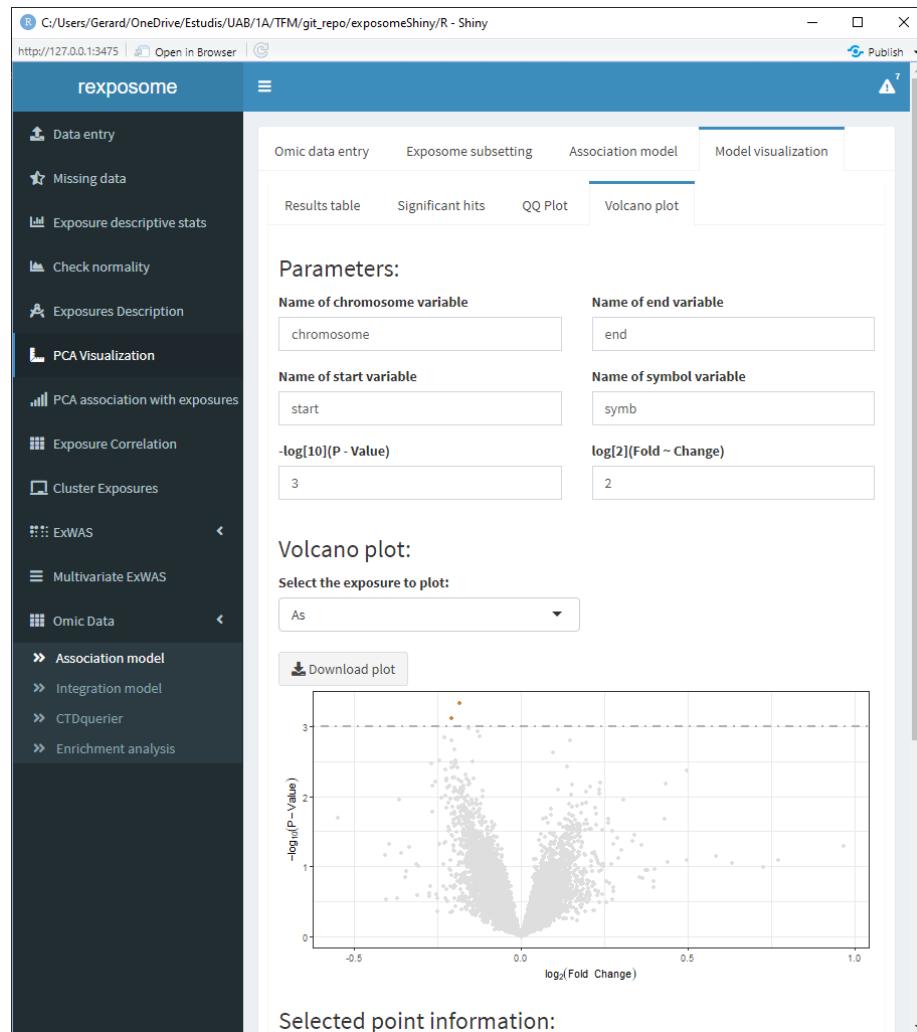
The screenshot shows a Shiny application window titled "reXposome". The left sidebar contains a menu with various options: Data entry, Missing data, Exposure descriptive stats, Check normality, Exposures Description, PCA Visualization, PCA association with exposures, Exposure Correlation, Cluster Exposures, ExWAS, Multivariate ExWAS, Omic Data, Association model, Integration model, CTDquerier, and Enrichment analysis. The main panel has tabs for Omic data entry, Exposome subsetting, Association model, and Model visualization. The "Significant hits" tab is selected. A table displays exposure data with columns for Exposure, Hits, and Lambda. The table shows 10 entries out of 13, with the first 10 highlighted in light blue. The table includes a search bar and navigation buttons for previous and next pages.

Exposure	Hits	Lambda
As	2	0.9
Cd	28	1.01
Co	5	0.84
Cs	17	0.99
Cu	18	0.94
Hg	4	0.9
Mo	5	0.93
Ni	56	1.82
Pb	9	0.95
Sb	5	0.83

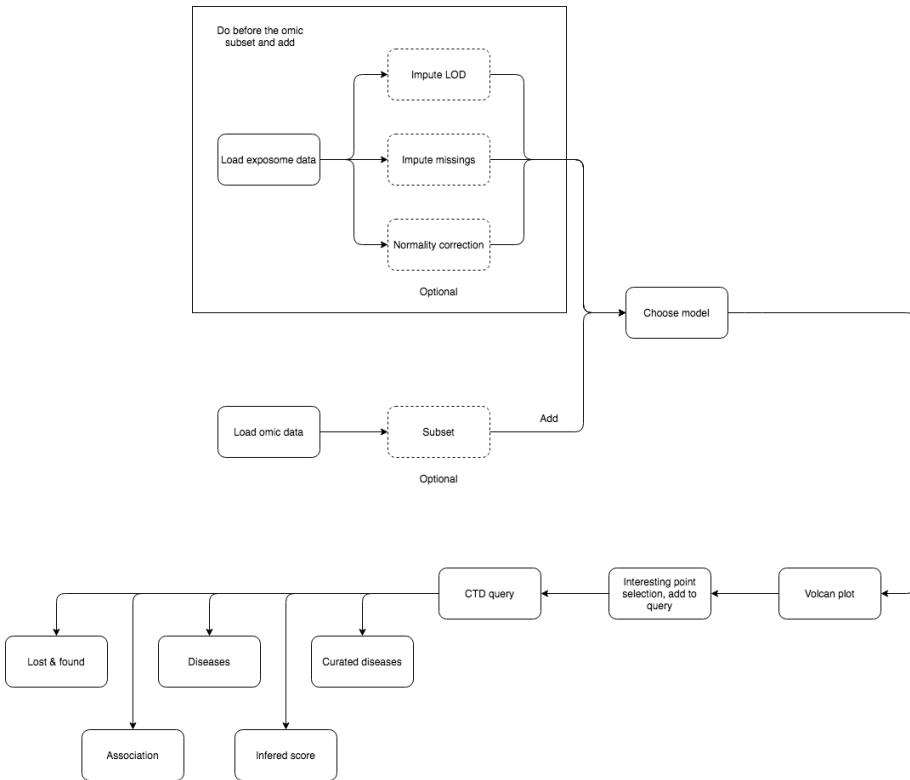
The QQ Plot shows a QQ plot (expected vs. observed -lo10(p-value)) for the selected exposure.



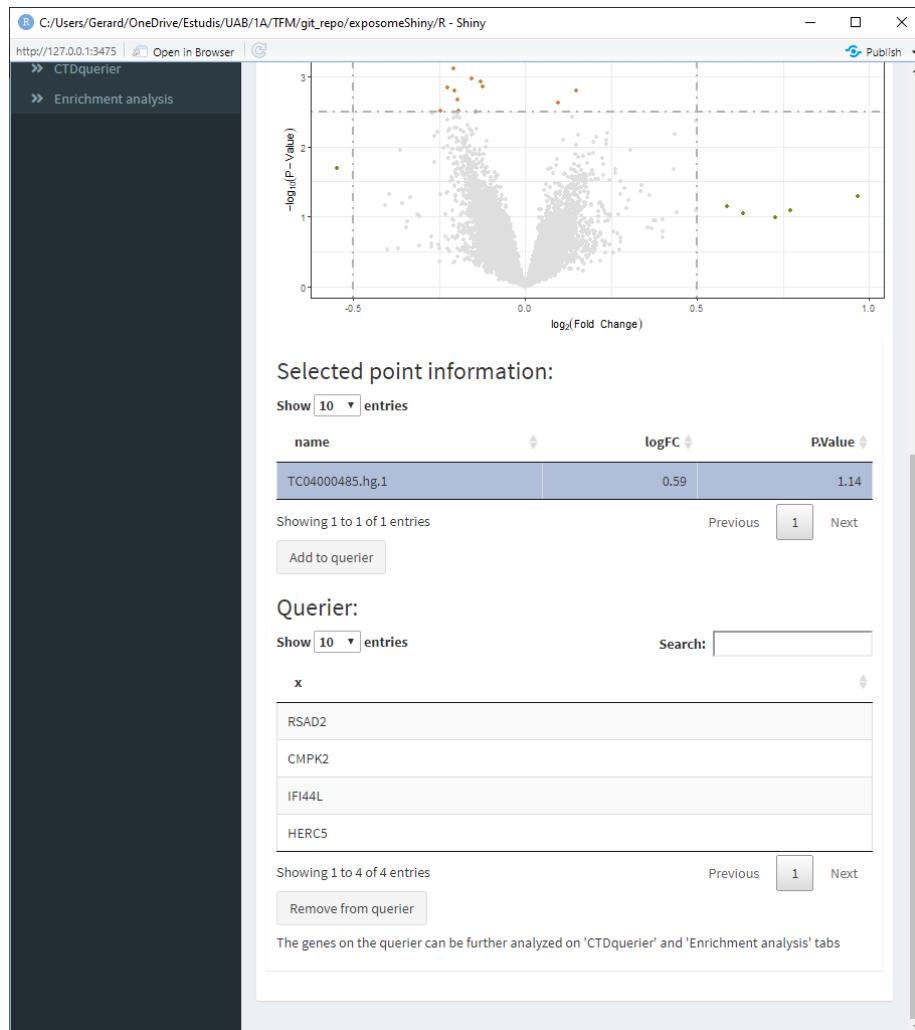
The Volcan plot shows a volcano plot ($\log_2(\text{fold change})$ vs $-\log_{10}(\text{p-value})$). For this plot there are two input cells to adjust the horizontal and vertical limit lines to filter out the results.



5.2.2 CTD querier



To perform a CTD querier study of the exposome-omic association analysis, as before, load both datasets and run the desired model with them, check the Volcano plot and click on the desired point on the Volcano plot, the information of the selected plot will appear on the table below the plot (sometimes there are many points close so more than one rows can appear on the table), select from the table the desired point to add to the query and click “Add to querier”. It’s important noting that when trying to add to the querier the Shiny will find on the fields of the omic dataset that the user specifies on top of the plot. If the search does not return any symbol a prompt will appear, however if it’s found it will be added to the lower table corresponding to the genes to query.



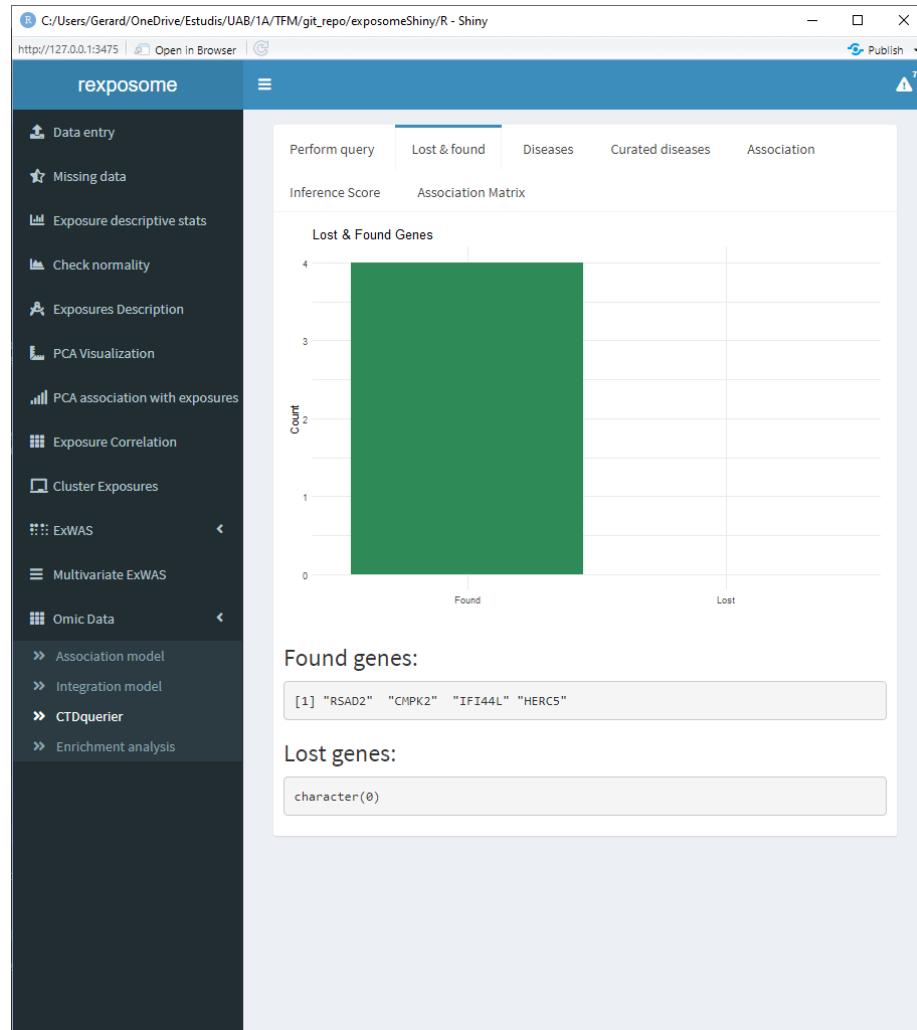
If by mistake some gene (or genes) were introduced to the querier, select them by clicking on the table row and click “Remove from querier”. Go to the CTDquerier tab to perform the query with the selected genes.

The screenshot shows the rexosome shiny web application interface. The left sidebar contains a vertical list of analysis tools:

- Data entry
- Missing data
- Exposure descriptive stats
- Check normality
- Exposures Description
- PCA Visualization
- PCA association with exposures
- Exposure Correlation
- Cluster Exposures
- ExWAS
- Multivariate ExWAS
- Omic Data
 - Association model
 - Integration model
 - CTDquerier
 - Enrichment analysis

The main content area has a top navigation bar with tabs: Perform query, Lost & found, Diseases, Curated diseases, Association, Inference Score, and Association Matrix. The "Perform query" tab is selected. Below this is a search bar labeled "Querier:" with a dropdown showing "Show 10 entries" and a search input field. A table lists four genes: RSAD2, CMPK2, IFI44L, and HERC5. At the bottom of the table are buttons for "Previous", "1", and "Next". A button labeled "Query genes on the CTD gene database" is also present.

There are six tabs showing different results interpretations. First there's the “Lost & found” tab which a plot to see the amount of genes found on the CTD database and the ones that were not found them, ther's also two lists stating the names of them.



The diseases tab shows a table of all the associated diseases found on the CTD database.

The screenshot shows the rexposome shiny application interface. The left sidebar contains a navigation menu with various options like Data entry, Missing data, Exposure descriptive stats, Check normality, Exposures Description, PCA Visualization, PCA association with exposures, Exposure Correlation, Cluster Exposures, ExWAS, Multivariate ExWAS, Omic Data (selected), Association model, Integration model, CTDquerier, and Enrichment analysis. The main content area has tabs at the top: Perform query, Lost & found, Diseases (selected), Curated diseases, and Association. Below the tabs are sections for Inference Score and Association Matrix. A search bar allows users to Show 10 entries or more. The main table displays 10 entries with columns for Disease.Name, Disease.ID, Direct.Evidence, Inference.Score, and Reference. The data is as follows:

	Disease.Name	Disease.ID	Direct.Evidence	Inference.Score	Reference
1	Myocardial Ischemia	MESH:D017202	marker/mechanism	16.99	
2	Influenza, Human	MESH:D007251	marker/mechanism	4.75	
3	Necrosis	MESH:D009336		228.75	
4	Chemical and Drug Induced Liver Injury	MESH:D056486		221.51	
5	Prenatal Exposure Delayed Effects	MESH:D011297		200.96	
6	Weight Loss	MESH:D015431		200.8	
7	Hyperplasia	MESH:D006965		192.75	
8	Inflammation	MESH:D007249		187.53	
9	Hepatomegaly	MESH:D006529		181.99	
10	Poisoning	MESH:D011041		164.68	

Showing 1 to 10 of 6,168 entries

Previous 1 2 3 4 5 ... 617 Next

The curated diseases tab shows the table of associated diseases but only shows the ones with direct evidence.

The screenshot shows the rexosome Shiny application interface. The left sidebar contains a navigation menu with various options: Data entry, Missing data, Exposure descriptive stats, Check normality, Exposures Description, PCA Visualization, PCA association with exposures, Exposure Correlation, Cluster Exposures, ExWAS, Multivariate ExWAS, Omic Data (with sub-options: Association model, Integration model, CTDquerier, Enrichment analysis), and a general section for Lost & found, Diseases, Curated diseases, and Association.

The main content area is titled "Association". It features a table with the following data:

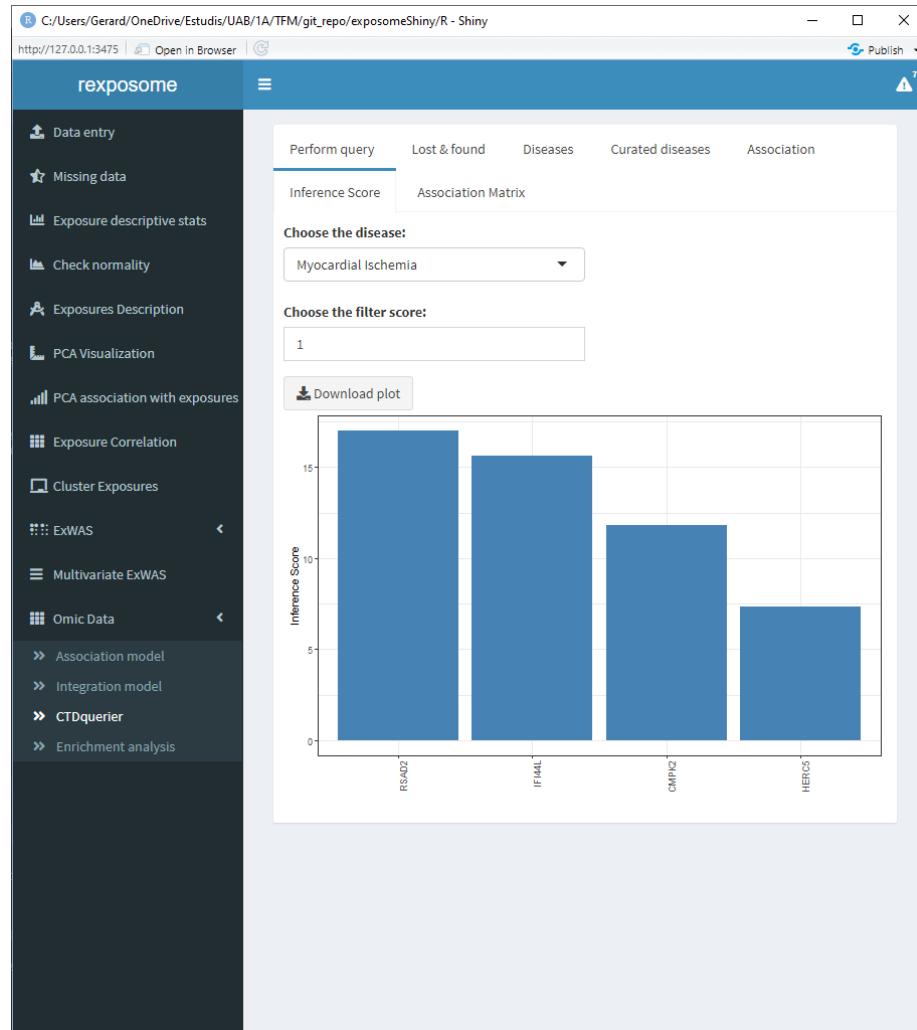
	Disease.Name	Disease.ID	Inference.Score	Reference.Count	Genes
1	Myocardial Ischemia	MESH:D017202	16.99	20	RSAD2
2	Influenza, Human	MESH:D007251	4.75	2	RSAD2
3	Depressive Disorder, Major	MESH:D003865	11.64	7	IFI44L
4	Influenza, Human	MESH:D007251		1	IFI44L
5	Carcinoma, Hepatocellular	MESH:D006528	40.21	90	HERC5
6	Endometriosis	MESH:D004715	4.08	8	HERC5
7	Influenza, Human	MESH:D007251		1	HERC5

Below the table, a message says "Showing 1 to 7 of 7 entries". Navigation buttons include "Previous", a page number "1", and "Next".

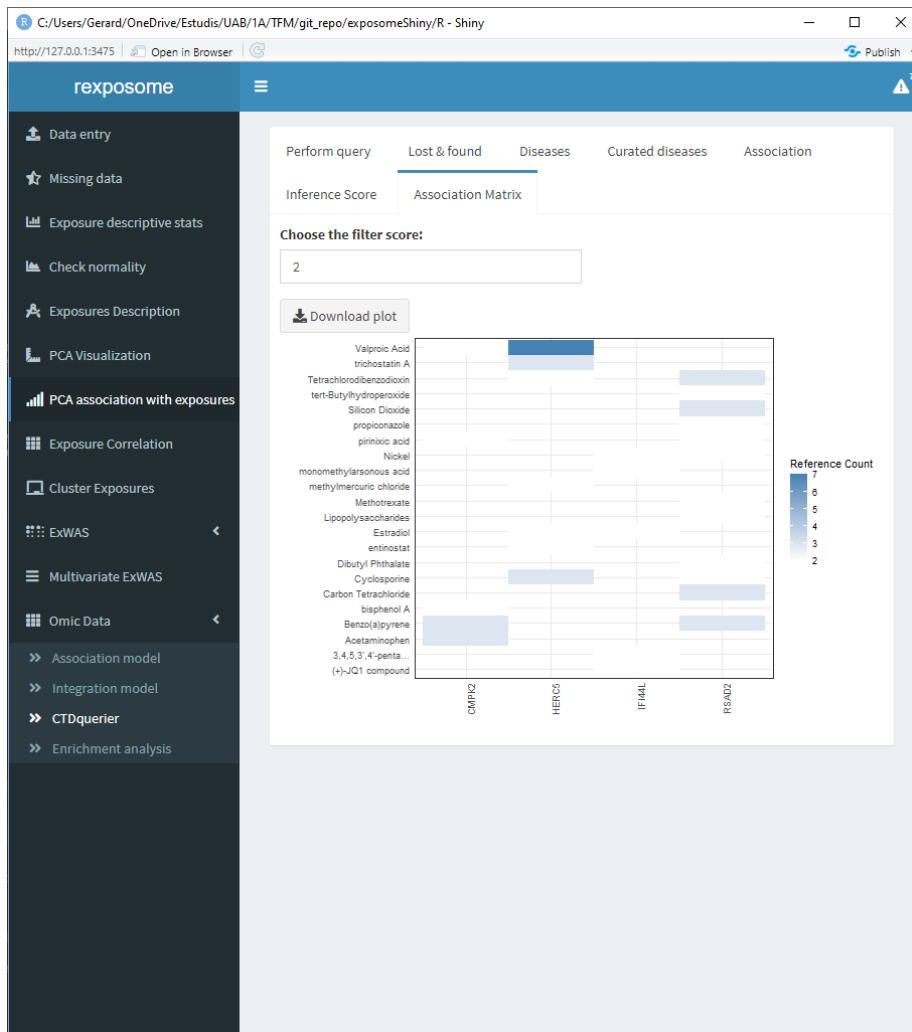
The association tab shows information about all the direct evidence associated diseases. Select the disease of interest to see the score and reference count of it.

The screenshot shows the rexposome Shiny application interface. The left sidebar contains a navigation menu with various analysis tools: Data entry, Missing data, Exposure descriptive stats, Check normality, Exposures Description, PCA Visualization, PCA association with exposures, Exposure Correlation, Cluster Exposures, ExWAS, Multivariate ExWAS, Omic Data, Association model, Integration model, CTDquerier, and Enrichment analysis. The main panel is titled 'Association' and includes tabs for 'Perform query', 'Lost & found', 'Diseases', 'Curated diseases', and 'Association'. Under the 'Association' tab, there are sections for 'Inference Score' and 'Association Matrix'. A dropdown menu labeled 'Choose the disease:' is set to 'Myocardial Ischemia'. Below it, 'Disease score:' is listed as '[1] 14.09158' and 'Reference count:' is listed as '[1] 10929'.

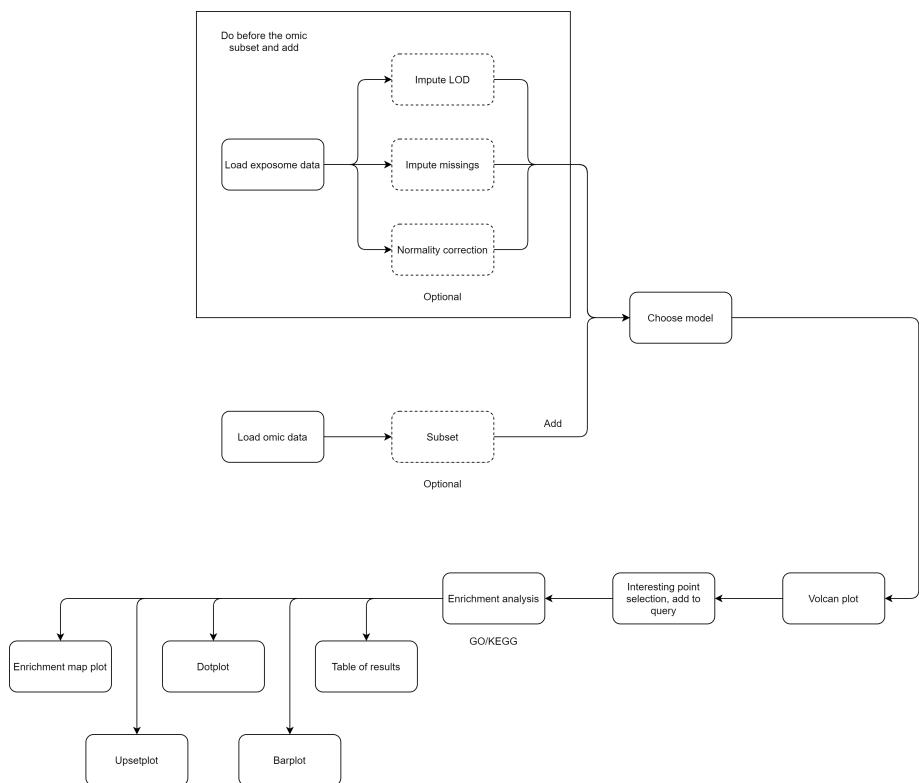
The inference score tab shows the inference score for each gene for a selected disease, the filter parameters puts out the genes with an inference score lower than the selected filter.



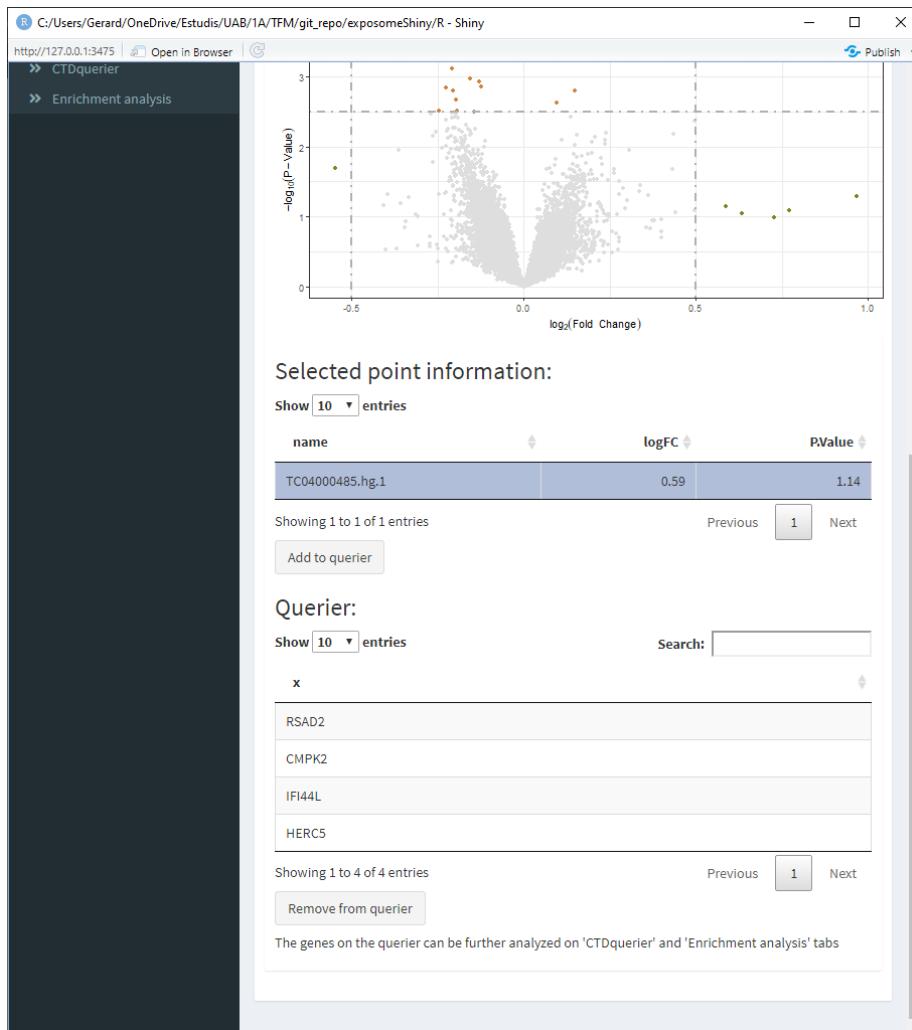
The association matrix tab shows a matrix of genes vs. chemicals with a heatmap representing the existing papers (references) providing evidence about the association between chemicals and genes.



5.2.3 Enrichment analysis



To perform an enrichment analysis, the genes of interest have to be selected as with the CTDquerier, using the volcano plot from the association analysis.



After selecting them, go to the “Enrichment analysis” tab, on it there is a selector to choose between GO and KEGG databases and a threshold selector for the cutoff pvalue of the enrichment analysis.

The screenshot shows the 'reXposome' Shiny application interface. On the left, a sidebar menu lists various analysis options: Data entry, Missing data, Exposure descriptive stats (selected), Check normality, Exposures Description, PCA Visualization, PCA association with exposures, Exposure Correlation, Cluster Exposures, ExWAS, Multivariate ExWAS, Omic Data (selected), Association model, Integration model, CTDquerier, and Enrichment analysis. The main panel has tabs for Database selection, Table of results (selected), Barplot, Dotplot, and Upsetplot. Under 'Database selection', 'GO' is selected. The 'Enrichment cutoff pvalue' is set to 0,05. The 'Querier' section displays a table of four entries: RSAD2, CMPK2, IFI44L, and HERC5. Below the table, it says 'Showing 1 to 4 of 4 entries'. A 'Perform enrichment analysis' button is at the bottom of the querier section.

When the enrichment analysis is performed, there are multiple visualization tabs for the results, the first one is a table with the plain results, which can be downloaded.

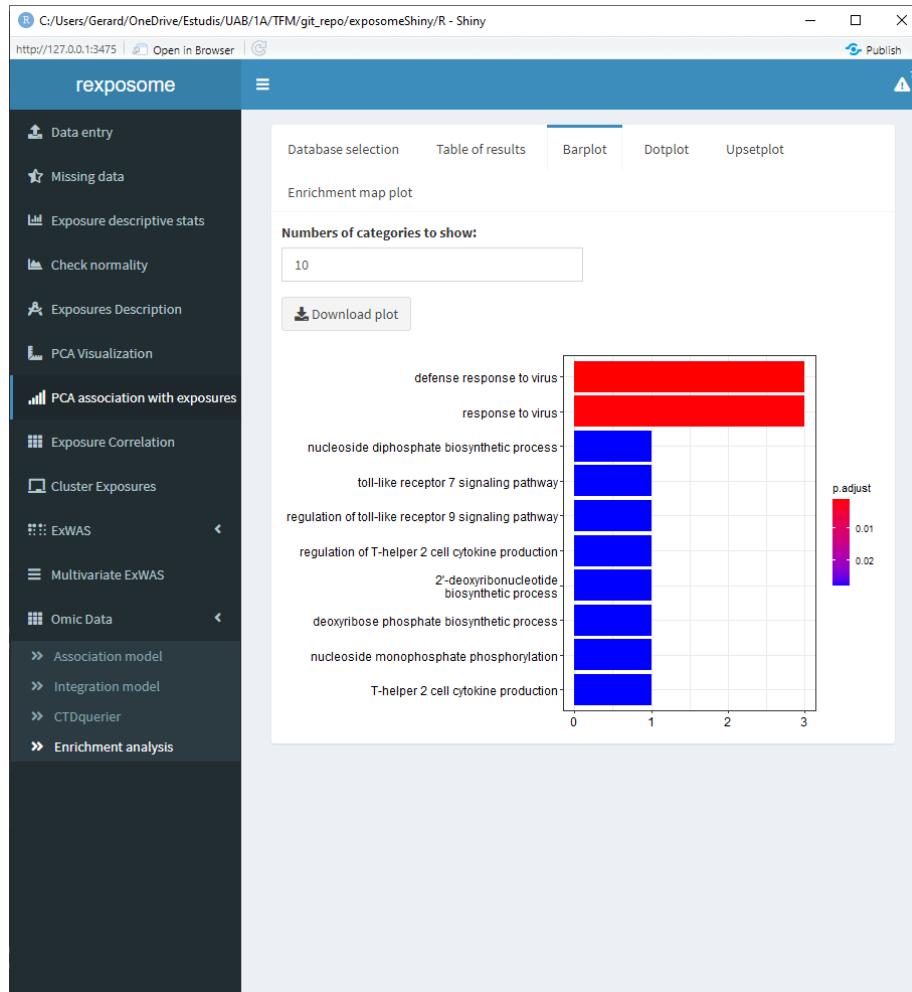
The screenshot shows the rexposome Shiny application interface. The left sidebar contains a navigation menu with the following items:

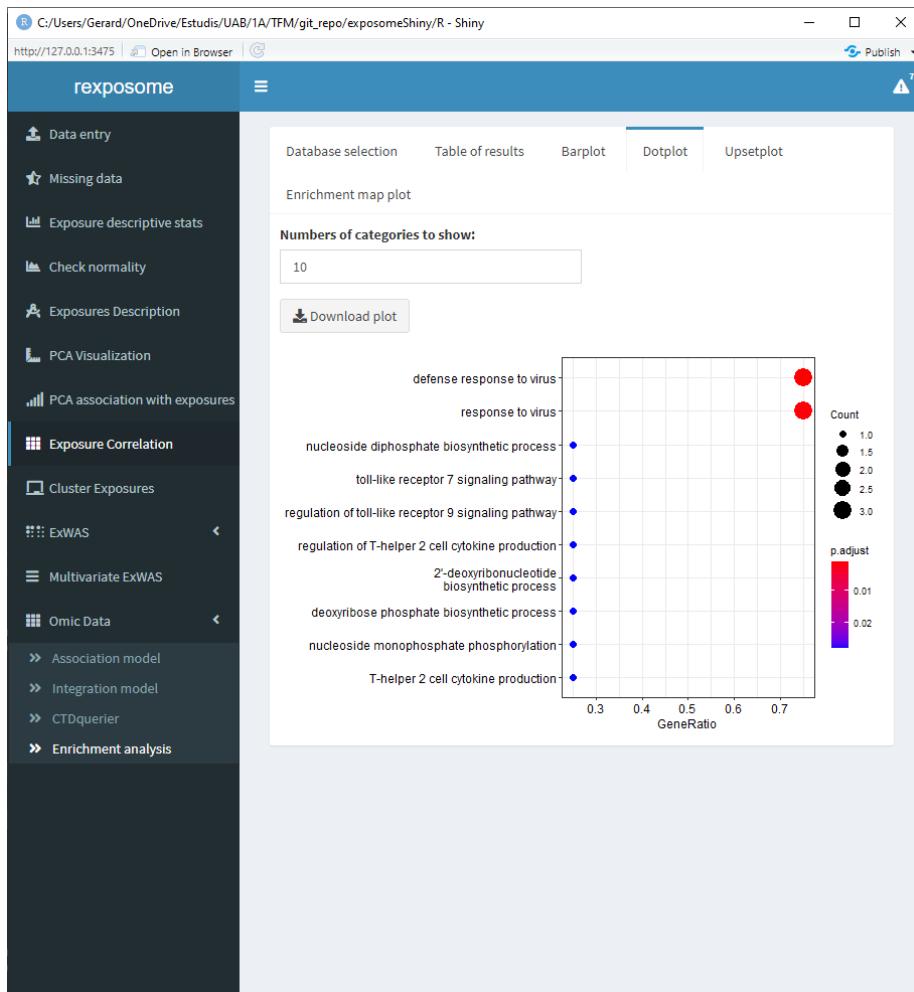
- Data entry
- Missing data
- Exposure descriptive stats
- Check normality
- Exposures Description
- PCA Visualization
- PCA association with exposures
- Exposure Correlation
- Cluster Exposures
- ExWAS
- Multivariate ExWAS
- Omic Data
 - Association model
 - Integration model
 - CTDquerier
 - Enrichment analysis

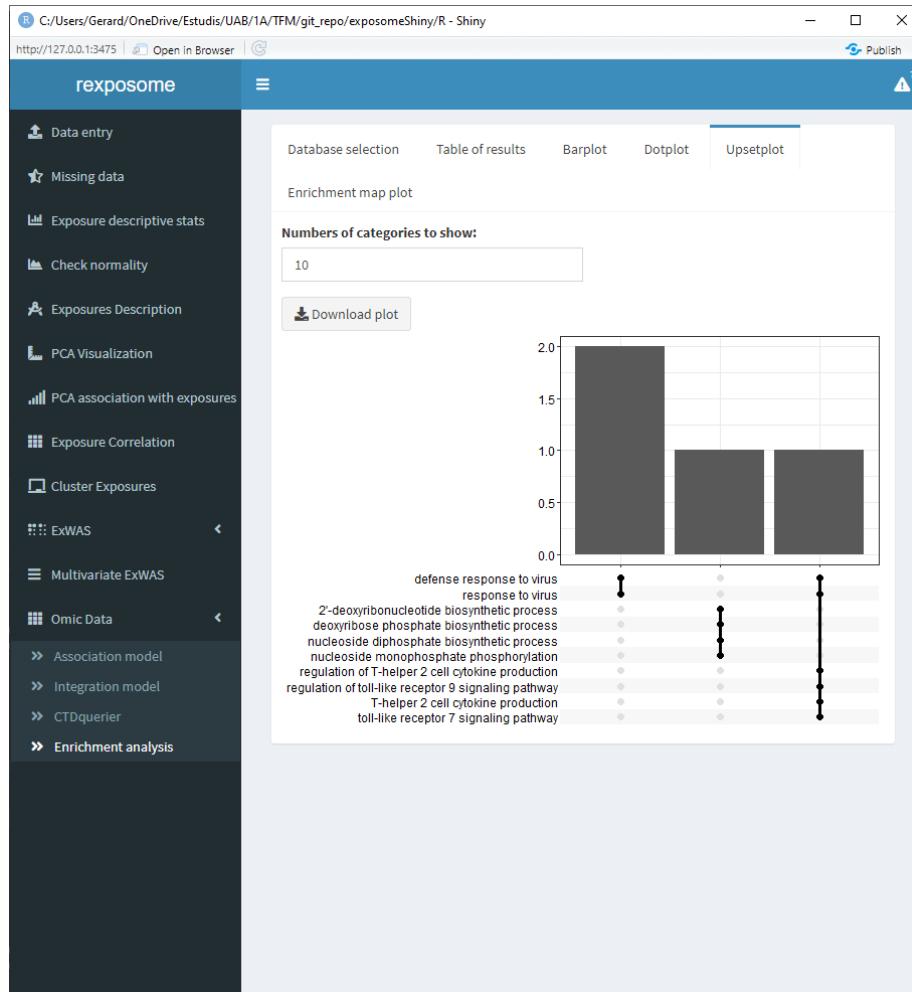
The main area displays an "Enrichment map plot" with a "Download table" button. Below it is a table with the following columns: ID, Description, GeneRatio, and BgRatio. The table lists various biological processes and their associated GO IDs and ratios.

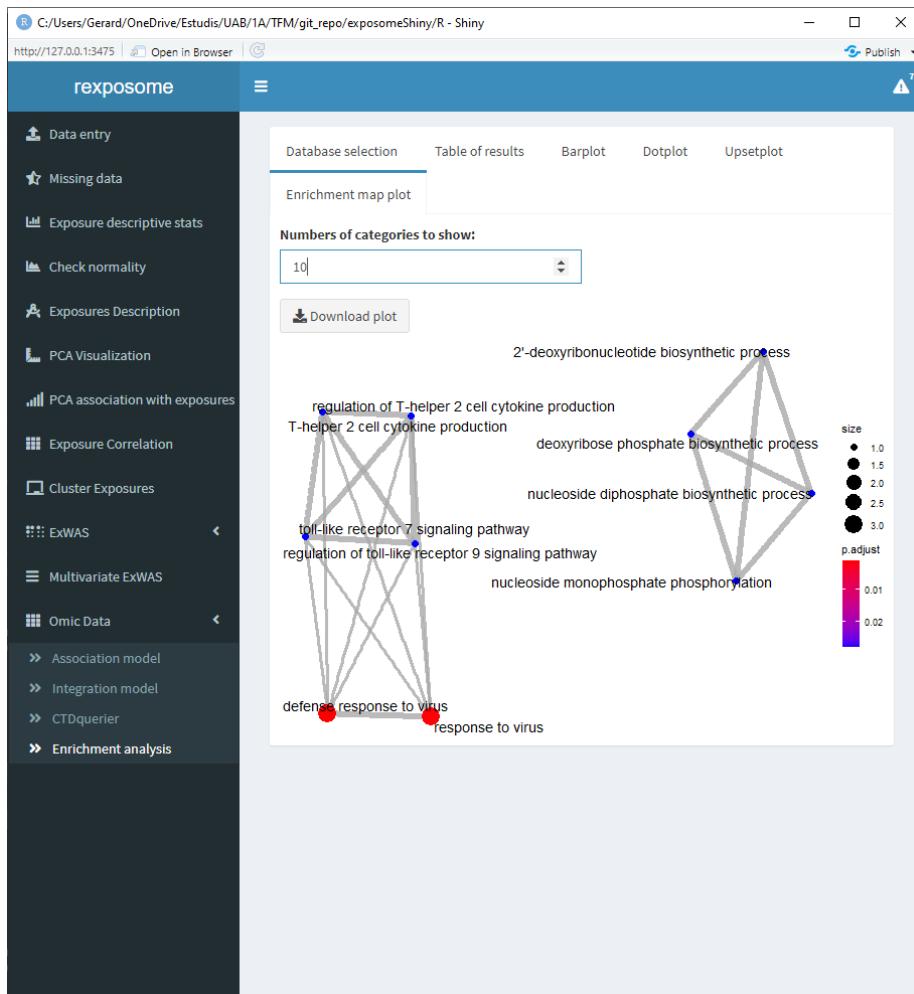
ID	Description	GeneRatio	BgRatio
GO:0051607	defense response to virus	3/4	258/18866 0.00001001
GO:0009615	response to virus	3/4	349/18866 0.00002476
GO:0009133	nucleoside diphosphate biosynthetic process	1/4	10/18866 0.00211
GO:0034154	toll-like receptor 7 signaling pathway	1/4	10/18866 0.00211
GO:0034163	regulation of toll-like receptor 9 signaling pathway	1/4	10/18866 0.00211
GO:2000551	regulation of T-helper 2 cell cytokine production	1/4	11/18866 0.002330
GO:0009265	2'-deoxyribonucleotide biosynthetic process	1/4	13/18866 0.002753
GO:0046385	deoxyribose phosphate biosynthetic process	1/4	13/18866 0.002753
GO:0046940	nucleoside monophosphate phosphorylation	1/4	14/18866 0.002965
GO:0035745	T-helper 2 cell cytokine production	1/4	15/18866 0.003176

The following four tabs correspond to different visualization options for the results. All of them can be downloaded.

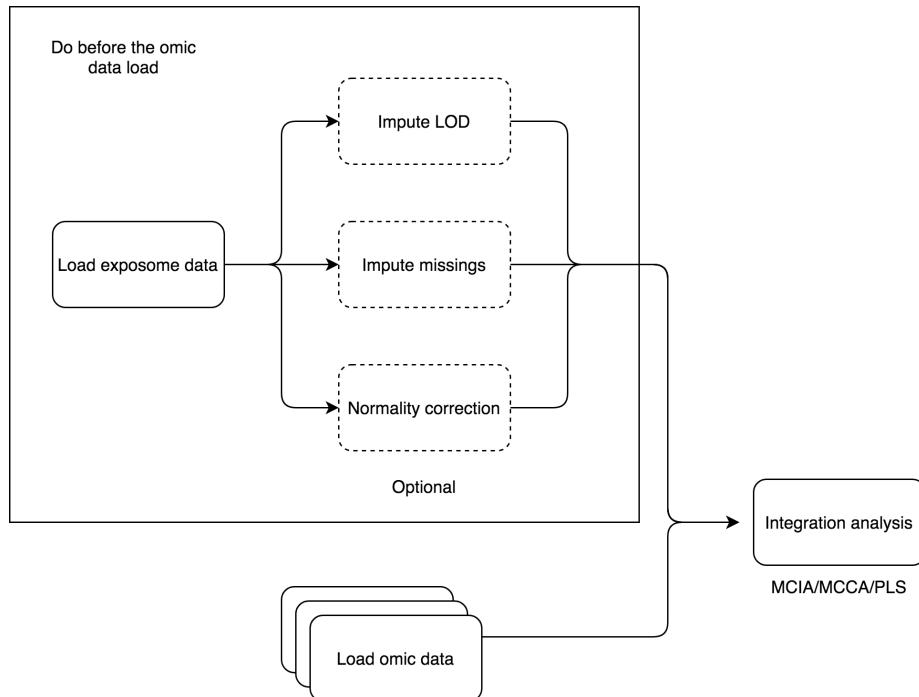








5.3 Exposome-Omic integration (e.g. crossomics)



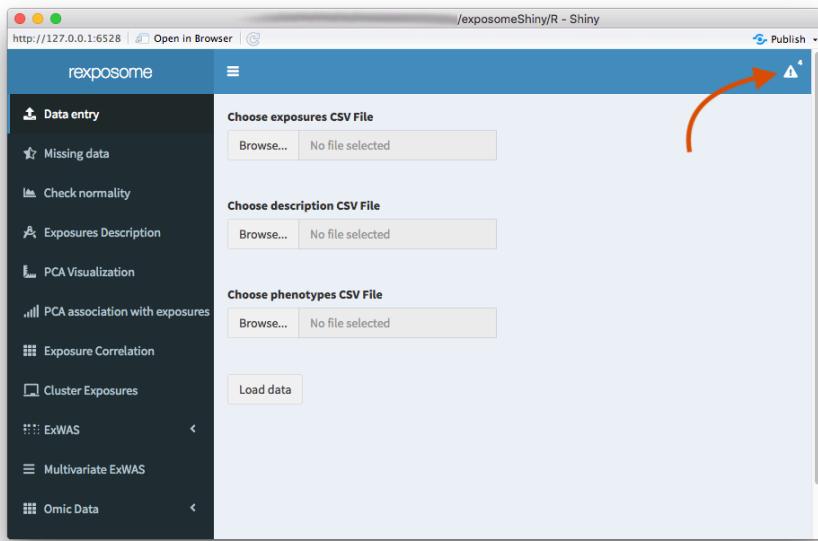
The relation between exposures and omic-features can be studied from another perspective, different from the association analyses. The integration analysis can be done, using multi canonical correlation analysis ,multiple co-inertia analysis or partial least squares (this method only is supported with one omics dataset). The first methods is implemented in R package PMA (CRAN) and the second in omicade4 R package (Bioconductor).

The differences between association and crossomics are that the first method test association between two complete data-sets, by removing the samples having missing values in any of the involved data-sets, and the second try to find latent relationships between two or more sets.

Chapter 6

General application functionalities

This whole Shiny application serves the purpose to perform a various number of exposome and omic analysis with an input set of data. To perform this analysis some operations can be performed on the inputted dataset prior to the analysis and so in order to follow track of what exactly has been done or what is loaded on the current session, there's implemented some sort of state tracker inside the Shiny application. In order to access it, press the icon on the top right of the application



When clicking it a dropdown menu appears, inside there are seven different notifications:

- Exposome dataset: Turns to 100% when an exposome dataset is loaded in the environment. Here's a graphical example.

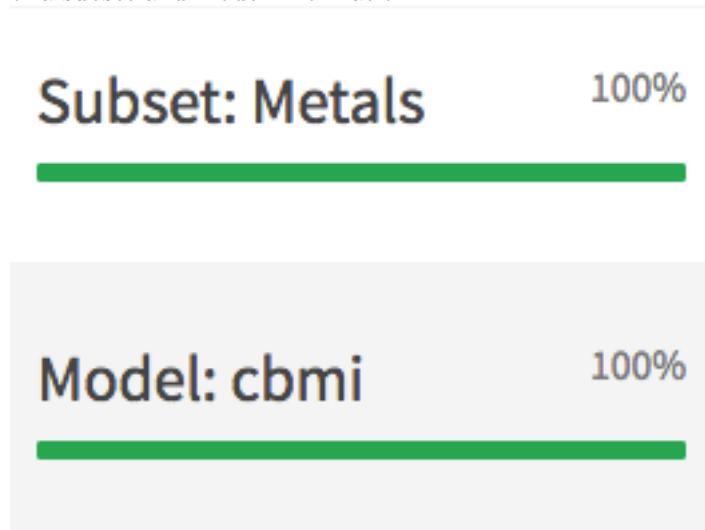
Exposome dataset 0%

Exposome dataset 100%

- LOD imputed: Turns to 100% if the exposome dataset is LOD imputed.
- Missing imputed: Turns to 100% if the exposome dataset has the missings imputed.
- Normality corrected: Turns to 100% if the exposome dataset is normality

corredted.

- Omics dataset: Turns to 100% when an omics dataset is loaded in the environment.
- Subset: Turns to 100% (and displays the subset family(ies)) when the exposome dataset is subseted.
- Model: Turns to 100% (and displays the association variable(s)) when a model is performed for an omics association analysis. Here's an example of a subset and model information.



Chapter 7

Methods

7.1 Missing data imputation

LOD missings are discovered through a encoding provided by the user, there is no method implemented to separate missing values between missing at random at LOD, meaning that all NA values are considered missing at random.

7.1.1 Limit of detection (LOD) missing

LOD missings can be imputed using two methodologies:

- LOD value / $\sqrt{2}$: Use a LOD value provided by the user (one value per exposures) divided by the square root of two. Richardson and Ciampi (2003)
- QRILC: a quantile regression approach for the imputation of left-censored missing data Lazar (2015).

7.1.2 Missing at random

Multiple imputation chained equations (MICE) is used to impute missing at random data. The *mice* package is used to do so. A brief explanation on the algorithm:

1. Imputation of the variable (exposure) x_n with the mean of all it's values.
2. Perform 1 for all the variables.
3. Set the mean imputed values from one variable back to missing.
4. Perform a regression model and fill those missings.
5. Repeat 3 and 4 for all the variables.
6. Repeat 3, 4 and 5 until the imputed values obtained are stabilized.

7.2 Normality

7.2.1 Normality testing

To test the normality of a variable, a Shapiro-Wilks test is used. The Shapiro-Wilks test, tests the null hypothesis of a sample (variable of the dataset) is normally distributed, to perform the test it calculates the W statistic.

$$W = \frac{\left(\sum_{i=1}^n a_i x_{(i)}\right)^2}{\sum_{i=1}^n (x_i - \bar{x})^2}$$

To perform this test exposome uses the *shapiro.test* function from the *base* package of R.

7.2.2 Normalization

A user selected function can be applied to exposures (selected by the user) to normalize them. The available functions are: *log*, *sqrt* and *^1/3*.

7.3 Principal component analysis (PCA)

Reposome contains two PCA methodologies

- Regular PCA Jolliffe and Cadima (2016) (only numerical exposures)
- FAMD Chavent et al. (2014) (numerical and categorical)

exosomeShiny uses regular PCA from the *FactoMineR* package. A toggle to select between the two may be added in future releases.

7.4 Exposures correlation

The correlation method takes into account the nature of each pair of exposures: continuous vs. continuous uses *cor* function from R *base*, categorical vs. categorical uses *cramerV* function from *lsr* R package and categorical vs. continuous exposures correlation is calculated as the square root of the adjusted r-square obtained from fitting a lineal model with the categorical exposures as dependent variable and the continuous exposure as independent variable.

7.5 Exposures clustering

Clustering analysis on samples can be performed to cluster individuals having similar exposure profiles. This is done using hierarchical clustering using the

function *hclust* from the *stats* R package. The results this analysis yields are the exposure profiles of a selected number of groups.

7.6 Exposome Association Analysis

7.6.1 Single Association Analysis

Exposome-Wide Association Study (ExWAS) is equivalent to a Genome-Wide Association Study (GWAS) in genomics or to Epigenetic-Wide Association Study (EWAS) in epigenomics. The ExWAS was first described by Patel et al. Patel et al. (2010) . ExWAS are based on generalized linear models using any formula describing the model that should be adjusted for (following standard formula options in R). That is, continuous or factor variables can be incorporated in the design, as well as interaction or splines using standard R functions and formulas. Multiple comparisons in the ExWAS analysis is addressed by computing the number of effective (Neff) tests as described by Li and Ju Li and Ji (2005) . The method estimates Neff by using the exposure correlation matrix that is corrected when it is not positive definite by using *nearPD* R function. The significant threshold is computed as $1-(1-0.05)M_{eff}$. This threshold is added to the Manhattan plots. When using imputed data, analysis is done for each imputed set and P-Values are pooled to obtain a global association score.

7.6.2 Multivariate Association Analysis

There are some authors that proposed to perform association analysis in a multivariate fashion, just to take into account the correlation across exposures Agier et al. (2016) . A Lasso regression is implemented using Elastic-Net regularized generalized linear models implemented in *glmnet* R package.

7.7 Exposome-Omic Association Analysis

Perform association analyses between exposures and omic data by fitting linear models as described in the *limma* R package Ritchie et al. (2015) . The pipeline implemented in association allows performing surrogate variable analysis in order to correct for unwanted variability. This adjustment is provided by *SVA* R package.

7.8 Enrichment analysis

Functional profiles of selected genes are obtained using the Bioconductor package `clusterProfiler` Yu et al. (2012) . The available enrichment databases are GO and KEGG.

Chapter 8

References

Bibliography

- Agier, L., Portengen, L., Chadeau-Hyam, M., Basagaña, X., Giorgis-Allemand, L., Siroux, V., Robinson, O., Vlaanderen, J., González, J. R., Nieuwenhuijsen, M. J., et al. (2016). A systematic comparison of linear regression–based statistical methods to assess exposome-health associations. *Environmental health perspectives*, 124(12):1848–1856.
- Chavent, M., Kuentz-Simonet, V., Labenne, A., and Saracco, J. (2014). Multivariate analysis of mixed data: The r package pcamixdata. *arXiv preprint arXiv:1411.4911*.
- Jolliffe, I. T. and Cadima, J. (2016). Principal component analysis: a review and recent developments. *Philosophical Transactions of the Royal Society A: Mathematical, Physical and Engineering Sciences*, 374(2065):20150202.
- Lazar, C. (2015). CRAN - Package imputeLCMD.
- Li, J. and Ji, L. (2005). Adjusting multiple testing in multilocus analyses using the eigenvalues of a correlation matrix. *Heredity*, 95(3):221–227.
- Patel, C. J., Bhattacharya, J., and Butte, A. J. (2010). An environment-wide association study (ewas) on type 2 diabetes mellitus. *PloS one*, 5(5):e10746.
- Richardson, D. B. and Ciampi, A. (2003). Effects of exposure measurement error when an exposure variable is constrained by a lower limit. *American Journal of Epidemiology*, 157(4):355–363.
- Ritchie, M. E., Phipson, B., Wu, D., Hu, Y., Law, C. W., Shi, W., and Smyth, G. K. (2015). limma powers differential expression analyses for rna-sequencing and microarray studies. *Nucleic acids research*, 43(7):e47–e47.
- Yu, G., Wang, L.-G., Han, Y., and He, Q.-Y. (2012). clusterProfiler: an r package for comparing biological themes among gene clusters. *OMICS: A Journal of Integrative Biology*, 16(5):284–287. PMID: 22455463.