**Workflow of the second Shiny app.**

**Name : DRomics\_multilevels**

**Examples :**

* Scenedesmus, triclosan (cf. triclosanSVcontigres.txt, triclosanSVcontigannot.txt, triclosanSVmetabres.txt, triclosanSVmetabannot.txt – faire un essai en ajoutant des lignes avec des id non annotés)
* Nicolas Creusot data ? PB because it was not aimed to do metabolomics
* PICT study when it will be published
* Another data with metabolomics time (Mechthild)
* IRSN data zebra fish at different times (sujet de M1 avril-mai 2022)

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First input : the number of experimental levels e.g. different molecular levels (transcriptomics, metabolomis, …) , different experimental time points or different biological models (different species, different experimental settings), …

**The name of the column that gives the id in annotation file is asked for only for the first level : the name of the other column is stored and a message printed to say that the column used for the annotation at the other levels should always have this name.**

Step to repeat (+ button or numerical input with the number of results ):

Merge for each results data frame form the workflow, corresponding to a condition (PICT or not), a molecular level (metabolo or transcripto), a time, … -> identified by an **experimental level**

**We can consider that ten levels is a big max !**

Input :

* the name of the experimental level (string)
* the results data frame from the DRomics workflow (DRomics\_output ) : .txt
* the annotation data frame that may be longer (one item with more than one **annotation**) or shorter (items without any annotation) than DRomics\_output with only two columns (only one annotation) : .txt (check in defensive programming that there is no duplicated lines and remove duplicate lines with a warning in case)

Action :

* merge on id + add of a column named “**experimental\_level**” -> **extendedres\_ith**
* At the end -> rbind of all the extendedres\_ith -> extendedres

The app. must check that the the different data to rbind have the same columns and that there is at least one BMD ‘BMD.zSD of BMD.xfold. **Is it necessary to define a function in the package to do those steps ? To think… Possibility also to make enrichment test in case of annotated organisms ?**

If one BMD is missing, the corresponding button must be inactive in the following

**Page 2**

Numerical input : minimal number of items (default 3, from 1 to 10 ) to keep the item for one factor level

Do we keep the item in the other factor levels if it appears more than min\_nb\_of\_items in another factor level ? YES or give the choice. For the moment we calculate the max nb of items per pathway per experimental level

METTRE UNE FONCTION dans le package pour cela ?

Faire une fonction plus générale qui peut être basée sur nb items min par niveau ou dans au moins un des niveaux, et/ou sur niveaux les plus sensibles (basés sur BMD median or BMD25%) en faisant rentrer une BMDmax … ou liste d’annotations… en indiquant bien la chronologie des filtres.

Pour le moment j’ai mis dans le share une fonction selectgroups qui fait le job, séparément par niveau expérimental. L’amélioration qu’on pourrait faire à mon avis serait de pouvoir mettre une vecteur dans nitemsmin, pour pouvoir sélectionner sur un nb différent en multi-omiques, par exemple si on a beaucoup plus d’items qui sortent en transcripto qu’en métabolo.

Aurélie je te laisse regarder avant d’inclure cela dans le package

selection2plot()

PB with quantiles – write a message to say that quantiles on low number of items are not reliable

Radio- button : Ordering of the annotations : **alphabetic order** (must be ordered within Shiny before calling sensitivityplot and use ECDF\_plot = FALSE), or order of apparition (chosen by the user – NOT POSSIBLE FROM a.txt File) in the input, **ordered by total number of items in all the experimental levels (or if only one experimental level : ordered by number of items**) (must be ordered within Shiny before calling sensitivityplot and use ECDF\_plot = FALSE), **and if only one experimental level : ordered by BMD summary value** (call to sensitivityplot with ECDF\_plot = TRUE)

Action :

* Filtering of annotations to plot
* Trendplot and sensitivity

trendplot()

* (extendedres)
* (group = annotation)
* (facetby = label)
* add.color = TRUE

sensitivityplot()

* (extendedres)
* BMD type = (“zSD”, “xfold”)
* BMD summary = c(“first.quartile”, “median”, “median.and.IQR”)
* (group = annotation)
* colorby = label or nothing
* if no colorby ECDF\_plot = TRUE
* BMD\_log\_transfo = FALSE

Each with possible exportation of the plot

**Page 3**

Put again the input of page 2 with the last value proposed by the user as the default value

Optional focus on some annotations : mark the chosen annotations (by default none are marked) with a button to mark all

**Common arguments (in bold)** so only one question for both functions, except add.CI and colorby

bmdplot()

* **(Extendedres)**
* **BMD type = (“zSD”, “xfold”)**
* add.CI = FALSE
* **facetby (for columns) = annotation or label or none**
* **facetby2 (for rows) = label or annotation or none (conditioned by facetby)**
* colorby (select input in the columns of extendedres)
* **shapeby** (select input in the columns of extendedres) (not proposed if add.label = TRUE)
* **BMD\_log\_transfo = FALSE**
* **add.label = FALSE**

bmdplotwithgradient()

* **(extendedres)**
* **BMD type = (“zSD”, “xfold”)**
* **facetby (for columns) = annotation or label or none**
* **facetby2 (for rows) = label or annotation or none (conditioned by facetby)**
* **BMD\_log\_transfo = FALSE**
* **add.label = FALSE**
* **shapeby** (select input in the columns of extendedres) (not proposed if add.label = TRUE)

**Page 4**

Put again the input of page 3 with the last value proposed by the user as the default value

Optional focus on some annotations : mark the chosen annotations (by default the ones marked on page 3) with a button to mark all

curvesplot()

* (extendedres)
* Min and max doses to define the range for DR curves
* facetby (for columns) = annotation or label or none (by default the one in page 3)
* facetby2 (for rows) = label or annotation or none (conditioned by facetby) (by default the one in page 3)
* colorby (select input in the columns of extendedres)
* dose\_log\_transfo = (by default the one in page 3 for BMD\_log\_transfo)

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The script