Written by the authors of the Dromics package (see https://lbbe.univ-lyon1.fr/fr/dromics) - updated in July 2021

DRomics Cheat Sheet

Workflow for analysis of raw data

Functions with their main arguments (see help pages for a complete description)

Step 1: import, check and pretreatment

```
microarraydata(file,
   norm.method = c("cyclicloess", "quantile", "scale", "none"))
RNAseqdata(file, transfo.method = c("rlog", "vst"))
continuousomicdata(file)
continuousanchoringdata(file)
```

Step 2: selection of significantly responsive items

```
itemselect(omicdata,
   select.method = c("quadratic", "linear", "ANOVA"), FDR)
```

Step 3: dose-response modelling for responsive items

```
drcfit(itemselect, information.criterion = c("AICc", "BIC", "AIC"))
```

Step 4: Computation of benchmark doses

```
bmdcalc(f, z = 1, x = 10, minBMD)
```

Step 5: Bootstrap to compute BMD confidence intervals

```
bmdboot(r, niter = 1000, conf.level = 0.95)
```

Format of data in input

Data can be imported from a .txt file (e.g. "mydata.txt") containing one row per item after a first row giving the doses or concentrations for each sample , with the first column corresponding to the identifier of each item. Alternatively an R object of class data.frame can be directly given in input, corresponding to the output of read.table(file, header = FALSE) on a file described as above.

Identifiers of items (contigs, probes, metabolites, …)

Tested doses or conc.

Signal (counts or reads, continuous signal in log2, …)

RefSeq	0	0	0.22	0.22	0.
NM_144958	2072	2506	2519	2116	21
NR_102758	0	0	0	0	
NM_172405	198	265	250	245	2
NM_029777	18	29	25	19	
NM_0011301	0	0	0	0	
NM_0011623	3	1	2	0	
NM_008117	0	0	0	0	
NM_0011682	61	65	79	85	
NM_010910	7	10	9	3	
NR_002862	139	172	165	159	1
NR_033520	318	407	425	437	3

Typical script for the workflow

```
o <- RNAseq(datafilename)
s <- itemselect(o)
f <- drcfit(s)
r <- bmdcalc(f)
b <- bmdboot(r)
b$res
```

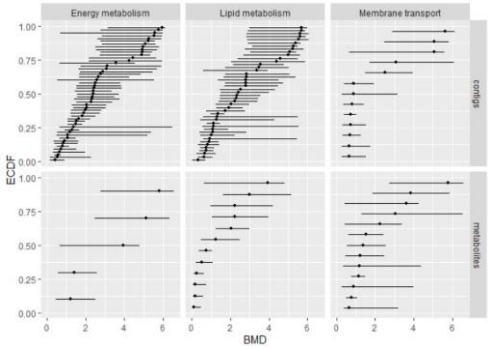
Each function of this workflow returns a S3 class object that can printed and plotted.

Other functions to help the interpretation of results winthin a multi-omics approach using a same biological annotation

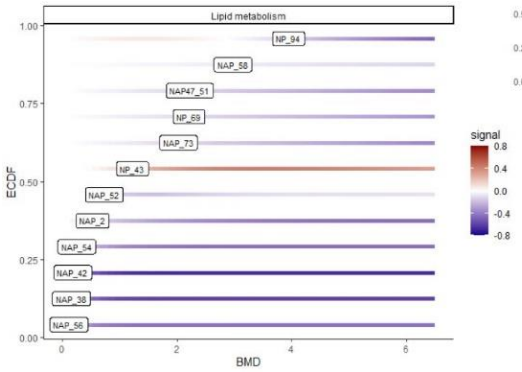
Functions taking as a first argument extendedres, a dataframe with the main workflow results, extended with additional columns coding for example for a biological of items. Some lines of the workflow results can be replicated for items having more than one annotation. Results obtained on different molecular (see help pages for a complete description of argument of those functions)

BMD plot

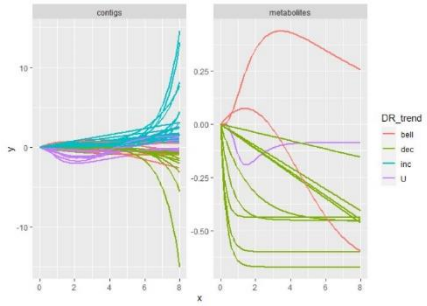
```
bmdplot(extendedres, add.CI,
facetby, facetby2, shapeby, colorby,
add.label, BMD_log_transfo)
```



BMD plot with gradient




```
bmdplotwithgradient(extendedres,
xmin, xmax, facetby, facetby2,
shapeby, add.label,
BMD_log_transfo)
```

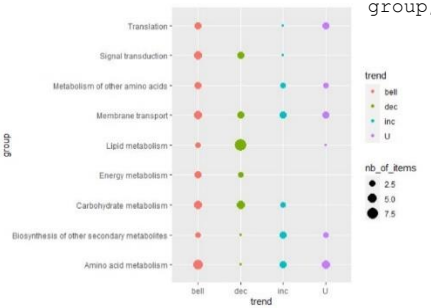


Dose-response curves plot

```
curvesplot(extendedres, xmin, xmax,
facetby, facetby2, colorby,
dose_log_transfo = FALSE)
```

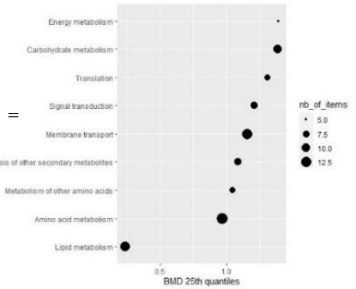
Trend plot

```
trendplot(extendedres,
group, facetby)
```



Sensitivity plot

```
sensitivityplot(
extendedres, group,
colorby, BMDsummary =
c("first.quartile",
"median" ,
"median.and.IQR"),
BMD_log_transfo)
```



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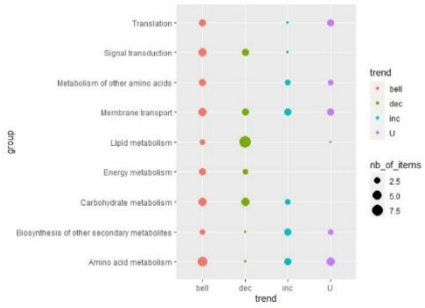

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