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

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

Tested doses or conc.

Signal (counts of 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
```

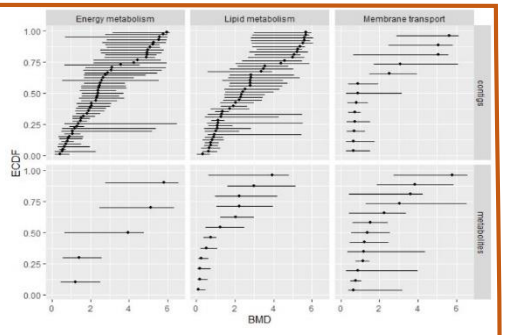
Each function of this workflow returns a S3 class object that can be printed and plotted.

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

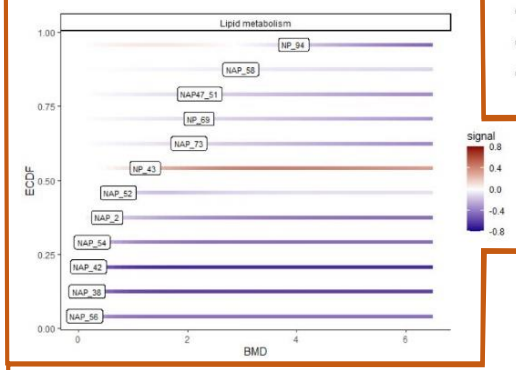
Functions taking as a first argument extendedres, a dataframe with the main workflow results (optionally gathering results obtained at different modelcular levels) extended with additional columns coding for example for the biological annotation of items (and for the molecular level if needed). Some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

BMD plot

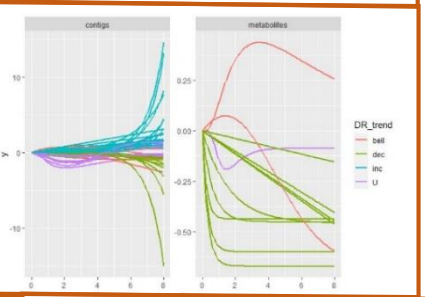
```
bmdplot(extendedres, add.CI,
facetby, facetby2, shapeby, colorby,
add.label, BMD_log_transfo)
```



BMD plot with gradient




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

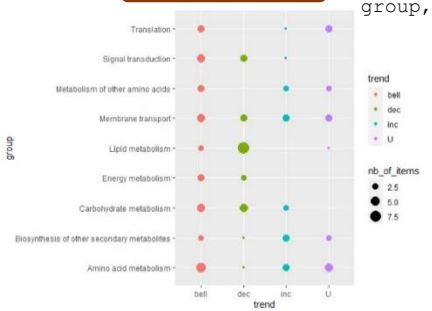


Dose-response curves plot

```
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)
```