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

# DRomics Cheat Sheet

## Format of data

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 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 |

## Workflow for analysis of 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)
```

## Typical script for the workflow

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

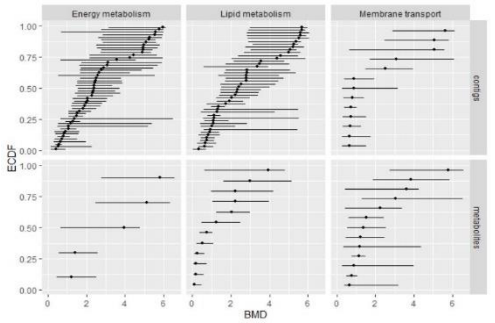
Each function of this workflow returns a S3 class object that can be printed and plotted.

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

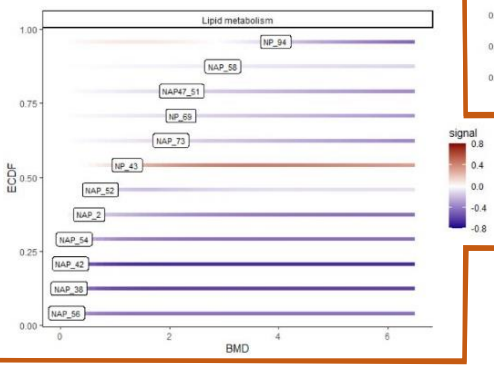
Functions taking as a first argument extendedres, a dataframe with the main workflow results (optionally gathering results obtained at different modelcular levels) extended with additional columns coding for example for the biological annotation of items (and for the molecular level if needed). Some 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

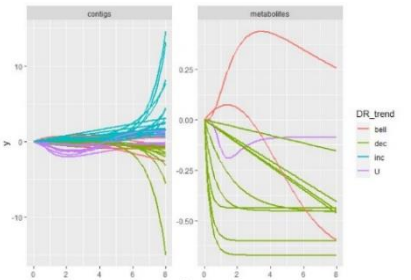
```
bmdplot(extendedres, add.CI,
facetby, facetby2, shapeby, colorby,
add.label, BMD_log_transfo)
```




### BMD plot with gradient




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

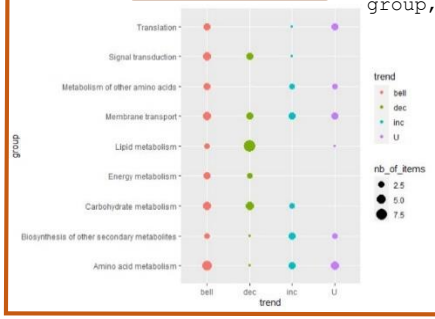



### Dose-response curves plot

```
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)
```