DRomics

DRomics is a freely available tool for dose-response (or concentration-response) characterization from omics data. It is especially dedicated to omics data obtained using a typical dose-response design, favoring a great number of tested doses (or concentrations) rather than a great number of replicates (no need of replicates to use DRomics).

> The CRAN package:

https://cran.r-project.org/web/packages/DRomics/ ↗

> The development version on GitHub:

https://github.com/aursiber/DRomics; ↗

and an extended web page

https://aursiber.github.io/DRomics/ ↗

> Vignette and cheat sheet:

- https://aursiber.github.io/DRomics/articles/DRomics_vignette.html ↗

- https://lbbe.univ-lyon1.fr/sites/default/files/media/downloads/dromics.pdf

> The two shiny apps:

- https://lbbe-shiny.univ-lyon1.fr/DRomics/inst/DRomics-shiny/ ↗

- https://lbbe-shiny.univ-lyon1.fr/DRomics/inst/DRomicsInterpreter-shiny/ ↗

> Contact and issues:

- dromics@univ-lyon1.fr

- https://github.com/aursiber/DRomics/issues ↗