

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/aurisiber/DRomics>;

and an extended web page

<https://aurisiber.github.io/DRomics/>

➤ Vignette and cheat sheet:

- https://aurisiber.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/aurisiber/DRomics/issues>