

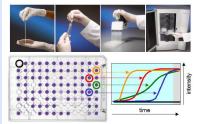
Software Development in the DSMZ

'OPM' – an R package for analysing OmniLog Phenotype MicroArray (PM) data

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www.dsmz.de

You have
numerous OmniLog Phenotype MicroArray data



- of closely related organisms or cell lines?
- of numerous well-defined mutants?
- obtained under diverse physiological test conditions?

and you want to explore them
full-fledged and quantitatively
into diverse directions of analysis frameworks?

opm
offers the solution you need:

opm is an R software package, designed for graphical and statistical analysis of your OmniLog PM data.

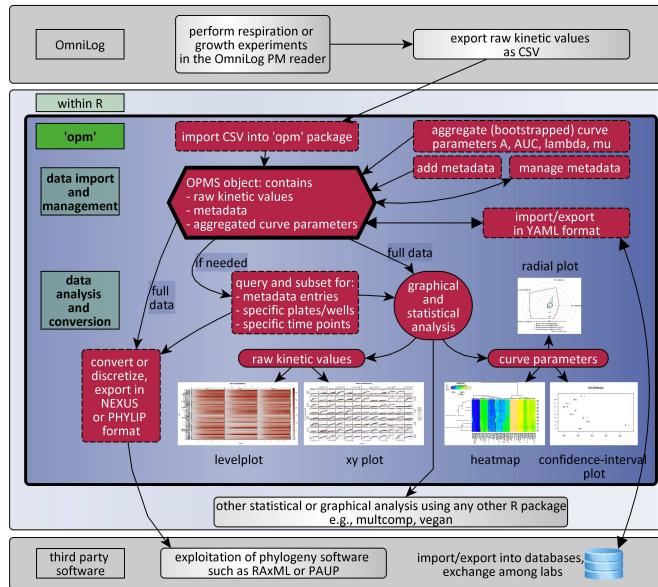
R is a free software environment for statistical computing and graphics. It compiles and runs on a wide variety of UNIX platforms, Windows and MacOS.

<http://www.r-project.org/>

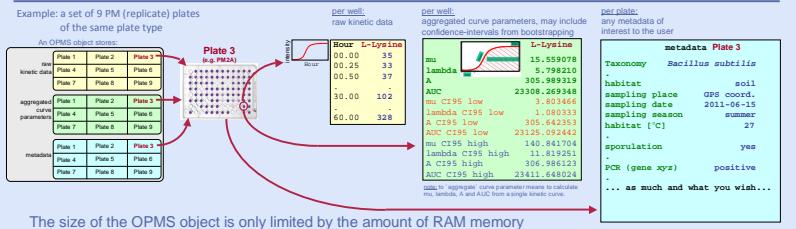
opm
enables you :

- ✓ to organize your PM data, curve parameters and metadata
- ✓ to subset and query your data
- ✓ graphical display of raw kinetics or aggregated curve parameters
- ✓ exploit the full statistics implemented in R
- ✓ export to third-party software using YAML

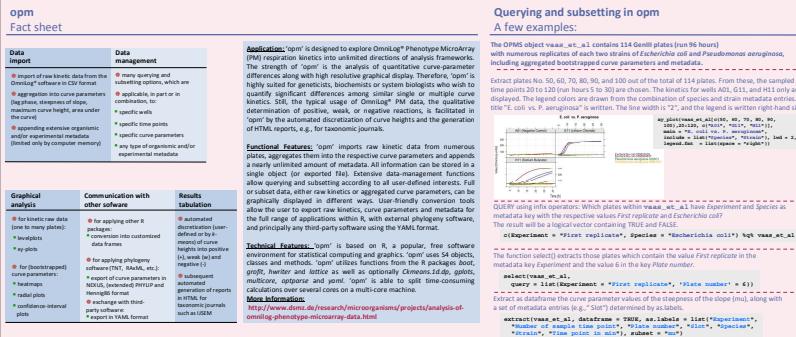
General workflow chart of analysing Phenotype MicroArray data using the R package 'opm'



opm
organizes your PM data as OPMS objects:

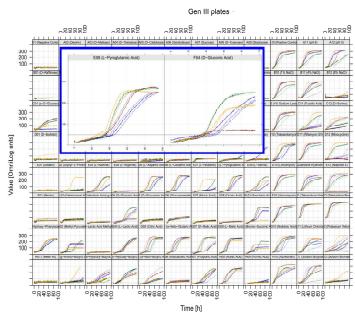


The size of the OPMS object is only limited by the amount of RAM memory

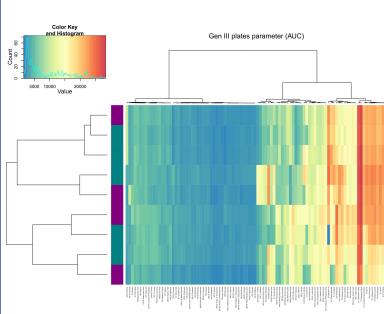


opm graphical analyses

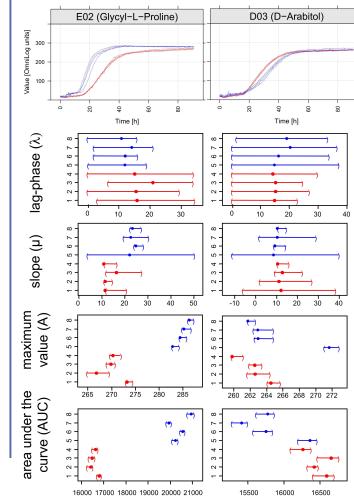
➤ e.g., xy plots of kinetic data



➤ e.g., heatmaps of curve parameters



➤ e.g., confidence-interval plots of bootstrapped curve parameters



opm flyer

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