

Opm An R Package For Analysing Omnilog Phenotype

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Opm An R Package For

The opm R package facilitates management, visualisation and statistical analysis of PM data and similar data such as growth curves. Raw measurements can easily be input into R, combined with relevant meta-information and accordingly analysed. The kinetics can be aggregated by estimating curve parameters using several methods. Some of them

opm: An R package for analysing phenotype microarray and ...

The opm package for R is a comprehensive software for analysing phenotype microarray and growth-curve data. For more information, see the opm R-Forge site or the main tutorial for opm. Installation. The package can be used on Windows, Mac and Linux/UNIX systems. As a prerequisite, one needs to obtain the statistical computing environment R.

OPM and its Helper Packages

General-purpose optimization wrapper function that calls other R tools for optimization, including the existing optim() function. Also tries to unify the calling sequence to allow a number of tools to use the same front-end.</p> <p>Note that optim() itself allows Nelder–Mead, quasi-Newton and conjugate-gradient algorithms as well as box-constrained optimization via L-BFGS-B.

opm function | R Documentation

Tools for analysing OmniLog(R) Phenotype Microarray (PM) data as produced by the device distributed by BIOLOG Inc. and similar kinds of data such as growth curves are available in the opm package. The package opmextra contains functions for special purposes and thus have not been placed in opm.

R-Forge: opm and opmdata: R Development Page

the terms object used. The function summary (i.e., summary.opm) can be used to obtain or print a summary of the results. The generic accessor functions coefficients, fitted.values , residuals, logLik, and df.residual can be used to extract various useful features of the value returned by opm.

opm function | R Documentation

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General-purpose optimization wrapper function that calls multiple other R tools for optimization, including the existing optim() function tools. Because SANN does not return a meaningful convergence code (conv), opm() does not call the SANN method, but it can be invoked in optimr() . There is a pseudo-method "ALL" that runs all available methods.

opm function | R Documentation

Summary:opm is an R package designed to analyse multidimensional OmniLog® phenotype microarray (PM) data. opm provides management, visualization and statistical analysis of PM data, including curve-parameter estimation and discretization, dedicated and customizable plots, metadata management, automated generation of textual and tabular reports, mapping of substrates to databases, batch conversion of files and export to phylogenetic software in the YAML markup language.

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[PDF] Opm An R Package

The opm R package facilitates management, visualization and statistical analysis of Phenotype Microarray data. Raw measurements can be easily input into R, combined with relevant meta-information and accordingly analysed. The kinetics can be aggregated by estimating curve parameters using two distinct methods.

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