

Open source software from the Uppsala University Pharmacometrics group

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PsN (Perl speaks NONMEM)

Toolbox for population PK/PD model building using NONMEM. Functionality ranges from results extraction to advanced statistical methods. PsN simplifies the organization of NONMEM output files, helps with starting jobs on different types of clusters (i.e. slurm, torque, sge and lsf) and can perform a cornucopia of statistical and computational task. [1]

Example tools

<https://uupharmacometrics.github.io/PsN>

- **bootstrap** – assessing uncertainty of parameter estimates
- **frem** – full random effects modelling
- **linearize** – generation of model approximation using linearization and second order approximation for likelihood models
- **parallel_retries** – estimate the same model multiple times with different initial parameter estimates
- **qa** – fast and automatic assumption assessment and quality assurance of models
- **scm** – stepwise covariate model
- **simeval** – simulation evaluation diagnostics of outliers
- **sir** – sampling importance resampling for parameter uncertainty assessment
- **sse** – stochastic simulation and estimation
- **vpc** – visual predictive check

assemblerr

Tool for construction of pharmacometric models from scratch by combining pre-defined model components. It is intended to simplify the specification of pharmacometric models way. Models are specified using R code which assemblerr can render into a NONMEM control stream.

Features

<https://uupharmacometrics.github.io/assemblerr>
Available on CRAN

- Flexible assembly of models from predefined components: parameter model, observation model, compartment, flow, algebraic relationship
- Support for high-level components of PK models e.g. absorption
- Automatic recognition and optimized code generation for linear ODEs and ODEs with an analytic solution.
- Simple model task specification for output variable selection
Option to use mu-referencing for models

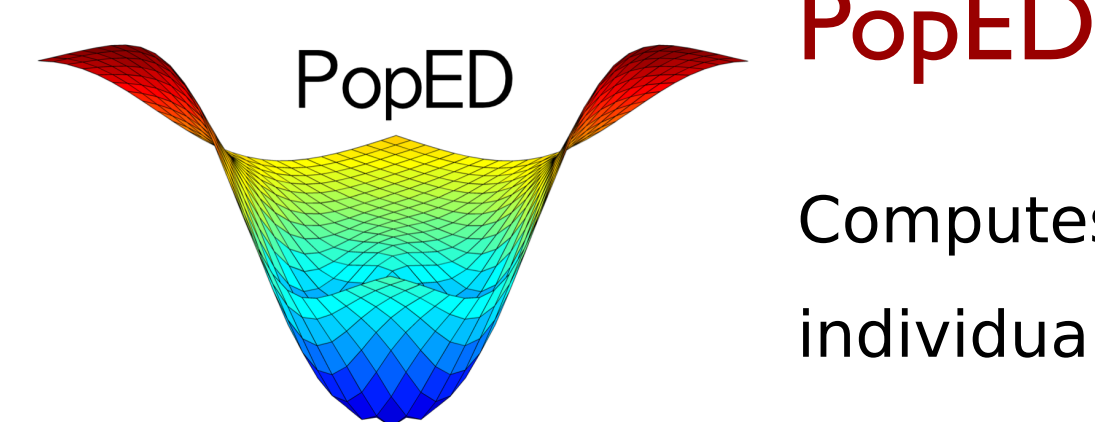
piraid

Aids the development of pharmacometric IRT and composite score models. It provides assistance for the creation of the models as well as for the generation of diagnostic plots.

Features

<https://github.com/UUPharmacometrics/piraid>
Available on CRAN

- Generation of NONMEM IRT models for binary and ordered categorical type items
- Estimation of item parameters and calculation of information curves
- Generation of bounded integer and continuous variable total score models as well as support for IRT-informed total score models



PopED

Computes optimal experimental designs for population or individual studies based on nonlinear mixed-effects models. [3]

Features

<https://andrewhooker.github.io/PopED>
Available on CRAN

- Flexible and robust model description, which can be done using various R-packages including mrgsolve, RxODE, PKPDsim, deSolve, and Rcpp
- Flexible and robust tools for design evaluation, design visualization and clinical trial simulation
- Flexible and robust design optimization handling complex designs and optimizing of a wide variety of design variables



xpose/xpose4

Model building aids for nonlinear mixed-effects model analysis using NONMEM, facilitating data set checkout, exploration and visualization, model diagnostics, candidate covariate identification and model comparison. [2]

Features

<https://uupharmacometrics.github.io/xpose>
<https://uupharmacometrics.github.io/xpose4>
Available on CRAN

- Tools for data visualization and data checkout
- Basic goodness-of-fit plots
- Structural and residual model diagnostics
- Parameter distribution diagnostics
- Visual predictive checks
- **Model evaluation tools** – plots and tables created to evaluate all aspects of a pharmacometric model
- **Model comparison tools** – graphs for comparing various aspects of two models fit to the same data
- **Model development tools** – used to help the modeler decide what to do next with the model. Most of these functions focus on aspects of covariate inclusion

ncappc

Flexible tool in R to:

- Perform non-compartmental analysis (NCA)
- Perform simulation-based posterior predictive checks (PPC) for population models using NCA metrics

<https://github.com/UUPharmacometrics/ncappc>
Available on CRAN

bemod

Facilitates model-integrated bioequivalence (BE) analysis. The tool can perform BE analyses with either a single model or a set of models used in model-averaged BE analysis. These methods have been shown to have a higher power while maintaining type 1 error in a number of clinically relevant situations.



Library and toolkit for pharmacometrics. See separate PAGE poster. [4]

List of references

- [1] Karlsson MO and Nordgren R et al. Psn: An open source toolkit for non-linear mixed effects modelling, 2004-. <https://uupharmacometrics.github.io/PsN/> [Online; accessed 2021-08-17], 2021.
- [2] Jonsson EN and Karlsson MO. Xpose – an s-plus based population pharmacokinetic/pharmacodynamic model building aid for nonmem. Computer Methods and Programs in Biomedicine 58(1):51-64, 1999.
- [3] Nyberg J, Ueckert S, Stroemberg EA, Hennig S, Karlsson MO, and Hooker AC. Poped: An extended, parallelized, nonlinear mixed effects models optimal design tool. Computer Methods and Programs in Biomedicine, 108, 2012.
- [4] Rikard Nordgren, Stella Belin, Zhe Huang, Aurelien Ooms, Simon J. Carter, Xiaomei Chen, Osama Qutishat, Alzahrá Hamdan, Shijun Wang, Tianwu Yang, Piyanan Assawasuwannakit, Simon Buatois, João A. Abrantes, Andrew C. Hooker, Mats O. Karlsson, PharmPy: a versatile open-source library for pharmacometrics, PAGE 2022