Poster

[P27-9] P27-9: Pharmacokinetics and PK/PD

Chair: Kosuke Doki, Japan
Wed. Sep 27, 2017 12:30 PM - 1:30 PM Annex Hall (1F)

(Wed. Sep 27, 2017 12:30 PM - 1:30 PM Annex Hall)

[P27-9-3] KinPop++ enables clinicians to easily develop new PK/PD population models for use in the MwPharm++ therapeutic drug management (TDM) software using an iterative two-stage bayesian (ITSB) technique

Jiri Potucek[1], Nieko Punt[2], Jiri Dousa[3] (1.MEDIWARE A.S., 2.Medimatics, 3.First Faculty of Medicine, Charles University in Prague)

Keywords: PK/PD population modeling, therapeutic drug monitoring, dose calculation, software, simulation and optimization

Background

PK/PD population modeling is a complex process involving software tools having a steep learning curve. Also the collection of patient data is often an elaborate process because data must be exchanged between different software packages. The DOS version of MwPharm TDM software features an integrated KinPop module which has direct access to the MwPharm patient database. We recently created an equivalent software plugin called KinPop++ for the MwPharm++ model designer application Edsim++.

Methods

Edsim++ and MwPharm++ are the main applications in the next generation pharmacokinetic software suite developed by Mediware. Edsim++ is a drag-and-drop / point-and-click visual modeling tool, which employs the concept of object oriented modeling (OOM). Models developed in Edsim++ can be imported into the MwPharm++ pharmacokinetic database (SQLite, SQL Server or MySQL) in order to use them in routine therapeutic drug management. The new KinPop++ plugin for Edsim++ can perform population analysis of an extracted subset of MwPharm++ patients using an iterative two-stage Bayesian technique (ITSB).

Results

The windows KinPop++ plugin yielded comparable population analysis results as the DOS KinPop module using a number of different test datasets. Also the results of several diagnostic methods (Monte Carlo simulations, bootstrap analysis and covariate analysis) were similar. All observed (small) differences could be explained by differences in the single precision (KinPop) and double precision (KinPop++) mathematics libraries. Results (tables and plots) can be exported to an Excel spreadsheet which allows the optimization of the presentation layout or post-processing of data using other software tools.

Conclusions

We demonstrated the new population analysis plugin KinPop++ yields similar results as the existing DOS KinPop module. KinPop++ completes the pharmacokinetic software suite from Mediware so that migration from the DOS to the windows version is now feasible. Proost and Eleveld (Pharmaceutical Research, Vol. 23, No. 12, December 2006) showed that for rich data sets the ITSB technique performs better than non-linear Mixed Effect Modeling (MEM) and is superior to the Standard Two-Stage (STS) analysis. We are currently in the process of repeating the same experiment for sparse data sets.