**Introduction:** Pharmacometrics workflow can be defined by a succession of well-defined tasks ranging from exploratory data analysis, modeling (execution, diagnostics, validation, simulation) and communication. Although each of these steps often require dedicated software and technologies, they share common needs (e.g. data visualization, reporting) which could take benefit from interactive analyses. The recent growth of data science related tools in R, in particular the web-application framework Shiny, brings new opportunities for the development of tools facilitating these activities.

**Methods:** A suite of interactive web-applications was developed to help NONMEM modelers within Sanofi in the processing of several stages of a pharmacometric analysis using R and the shiny package.

**PMXPLORE**
Interactive visualizations and summaries of dependent variables, dosing regimens and covariates (distributions, longitudinal evolution).

Provides dataset manipulation functionalities.

**PMXRUN**
Pilots the execution of NONMEM runs either on a local computer or within a PBS-based HPC infrastructure like the Sanofi Popkin cluster.

Generates control files for batch analysis (e.g. bootstrap, initial value search, sensitivity analysis), prior-based

**PMXPLOIT**
PMXPLOIT is an R package dedicated to NONMEM runs post-processing, willing to make the modeler's job easier when analyzing run results.

It provides helper functions for generating of diagnostic plots, computing statistics related to parameters and covariates, calculating numerical quality criteria or comparing multiple runs.

A shiny-based NONMEM Toolbox application has been developed alongside PMXPLOIT to bring interactivity with a dynamic front-end.

A user can rapidly obtain summaries of estimation results (e.g. convergence, parameters estimates, shrinkage), generate visualizations, detect outliers or compare runs on-the-fly, improving model diagnostics and data exploration.

Generated plots and tables can easily be integrated into reports as well as splitted and filtered for subgroups analyses (e.g. goodness-of-fit by compartment, parameter distribution per gender...).

**NonMEM post-processing analysis**
PMXPLORE is an R package dedicated to NONMEM runs post-processing, willing to make the modeler's job easier when analyzing run results.

**Exploratory Data Analysis** of NONMEM-like datasets

Fig. 1 - Dataset exploration with PMXplore

Fig. 2 - PMXrun list of running models

Fig. 3 - Parameter convergence monitoring

**NONMEM run management**

Fig. 4 - NONMEM Toolbox user interface

Fig. 5 - Interactive diagnostic plots

Fig. 6 - Visual Predictive Checks tab (using the vpc R package)

**Dynamic model-based simulations applications**

Interactive applications dedicated to specific projects or models.

Models developed either with NONMEM or Monolix are implemented using mrgsolve, RxODE or mlxR R packages.

User interfaces are adapted to each particular situation: comparison of dosing scenarios, computation of exposure parameters, comparison to literature, exploration of complex dynamical systems or visualizing inter-individual variability.

Facilitates communication of modeling results and fosters collaboration with non-modelers, increasing the visibility of pharmacometry and its contribution to decision-making.

**Conclusion**

A suite of web-applications dedicated to several steps of pharmacometrics workflow, from data exploration to simulation-based decision making, was developed. PopkinR shows the ability of interactive applications to improve the efficiency of pharmacometricians' work and the communication of modeling and simulation contribution to a wider audience to support drug development.

PMXPLORE package and PopkinR applications source code will be publicly available as soon as possible.

**References**

8. Presented at the 27th Population Approach Group in Europe meeting, Montreux, Switzerland, 29 May - 1 June, 2018