Submitting an abstract for the PAGE meeting

Abstracts must be submitted online to the PAGE web site (www.page-meeting.org) by clicking on 'Register / submit abstract' under the heading for the upcoming meeting. You must register as a participant before you can submit an abstract and you can only register after you have created an account. When you click "Submit" you will immediately receive an email with your abstract attached. This e-mail will also be sent to the committee responsible for peer review in the selected category. ***Therefore, only click "Submit" when you are done editing.*** Abstracts will remain invisible until release of the final program. Each participant is only allowed to submit one abstract, but does not need to be the first author. Do not submit separate oral and poster abstracts: if your request for an oral presentation is not granted, you will be contacted to switch your abstract from an oral to a poster category. The abstracts are text-only: no figures are possible.

All abstracts are reviewed and abstracts that do not comply with the guidelines given here, may run the risk of not being accepted. If the abstract is not satisfactory after review, the abstract may be rejected and will not be published at the PAGE website. A minimum requirement concerning the contents of the abstract is that concrete results are included. Accordingly, **abstracts without results will be rejected**, i.e. statements such as "…will be shown…", "…will be available at the time of the conference…" are not acceptable. Furthermore, abstracts for an anonymous drug (drug X) will not be accepted unless the work clearly describes a new methodology/new disease model for a specific therapeutic area (or similar), i.e. is of value to the pharmacometric community without the identity of the drug. Accordingly, a 2-compartment population PK model for drug X will not be acceptable. **Please note the minimum and maximum abstract length, to allow a better assessment of the intended presentation.**

A structured abstract is required (Objectives/ Methods/ Results/ Conclusion/ References) with number of characters (including spaces) **not exceeding 4,500 but not less than 3,000** for the abstract itself (i.e. excluding Title/ Authors/ Affiliation and References). An example is provided below.

There are separate fields for entering your abstract title, the authors, the associated institution or affiliation and the type of abstract you wish to present (oral or poster category):

Title: The title of your abstract (DO **NOT** USE ALL CAPITALS)
Author: Author1 (1), Author2 (1), Author3 (2) (DO **NOT** USE ALL CAPITALS)
Institution: (1) Affiliation1, (2) Affiliation2
Type: Please choose the appropriate oral or poster category from the following categories, which will facilitate the review of abstracts and to help structure the poster sessions. Note that a new poster category was added this year: **Poster: Methodology – Artificial Intelligence/Machine learning**

Oral: Clinical Applications (see clarification below)
Oral: Drug/Disease Modelling (see clarification below)
Oral: Lewis Sheiner Student Session
Oral: Methodology - New Modelling Approaches
Oral: Methodology - New Tools
Oral: Other Topics
Poster: Clinical Applications (see clarification below)
Poster: Drug/Disease Modelling - Absorption & PBPK
Poster: Drug/Disease Modelling - CNS
Poster: Drug/Disease Modelling - Endocrine
Poster: Drug/Disease Modelling - Infection

Poster: Drug/Disease Modelling - Oncology
Poster: Drug/Disease Modelling - Other Topics
Poster: Drug/Disease Modelling - Paediatrics
Poster: Drug/Disease Modelling - Safety
Poster: Methodology – AI/Machine Learning
Poster: Methodology - Covariate/Variability Models
Poster: Methodology - Estimation Methods
Poster: Methodology - Model Evaluation
Poster: Methodology - New Modelling Approaches
Poster: Methodology - Other topics
Poster: Methodology - Study Design
Software Demonstration

Clinical Applications: these abstracts are expected to deal with applications of pharmacometrics whose aim is to improve individual patient treatment. They may include studies that have identified covariates that can be applied to calculate the dose, or even better, if the application was able to take patient response (concentration, biomarker) and further improve the individual dose. They can include simulation studies that explore how to improve patient treatment by dose individualization. The abstract must indicate an algorithm demonstrating how an individual patient dose is calculated.

Drug-Disease modelling: these abstracts are expected to be description of and applications of PK, PKPD, disease progression models for all type of data (continuous, categorical, TTE, count etc, preclinical/clinical/in silico). These may have suggestions for clinical practice application as a side-benefit (e.g. covariates) but if that is not the main focus then they do not belong in the Clinical Application category.

There are two editor windows, one for the core abstract and one for the references to allow counting the number characters. The core abstract text itself must have the following layout:

Introduction/Objectives: Text regarding objectives.

Methods: Text regarding methods.

Results: Text regarding results. Concrete results need to be included in the abstract. Statements such as "…will be shown…", "…will be available at the time of the conference…" are not acceptable. Abstracts for an anonymous drug (drug X) will not be accepted unless the work clearly describes a new methodology/new disease model for a specific therapeutic area (or similar), i.e. is of value to the pharmacometric community without the identity of the drug.

Conclusions: Text regarding conclusions.

The references in the separate references editor must have the following layout:

References:
[1] Text for reference 1.
[2] Text for reference 2, etc etc

Separate the different sections in the core abstract window with a simple <Enter> (hard return), but separate the different references with a <Shift><Enter> so you do not get extra white lines between the references

The "PDF poster/presentation" option below the editor window will allow you to add the pdf of your ultimate poster or presentation as a service to your audience, and is **not** intended for a pdf of your abstract, and is **not** required at the time of abstract submission.

How to produce such an abstract

In contrast to previous years, abstracts can be prepared in your favourite text editor and simply pasted in the online abstract text window using <Ctrl><v>. This should remove almost all formatting except the allowed minimum (like bold). If you run into issues, contact rs@page-meeting.org.

Example abstract:

Title: nlmixr: an open-source package for pharmacometric modelling in R

Author: Rik Schoemaker (1,6), Matt Fidler (2,6), Justin Wilkins (1,6), Teun Post (3,6), Richard Hooijmakers (3,6), Mirjam Trame (2,6) , Yuan Xiong (4,6), Christian Laveille (5), Wenping Wang (2,6)

Institution: (1) Occams, The Netherlands, (2) Novartis Pharmaceuticals, USA, (3) LAP&P Consultants, The Netherlands, (4) Certara Strategic Consulting, USA, (5) Calvagone, France, (6) The nlmixr team

Editor window:

Introduction: ***nlmixr*** (www.nlmixr.org) is an open-source R package, freely available on CRAN[1] and GitHub[2]. It builds on RxODE[3], an R package for simulation of nonlinear mixed effect models using ordinary differential equations (ODEs), providing an efficient and versatile way to specify pharmacometric models and dosing scenarios, with rapid execution due to compilation in C. By combining the simulation core with population-type estimation routines, a versatile pharmacometric eco-system entirely contained within R becomes feasible. Currently, estimation routines comprise the nlme[4] package in R, a custom-built SAEM[5] implementation, and a proof-of-concept FOCE-I implementation, as well as adaptive Gaussian quadrature for 'odd-type' data. Both closed-form and ODE model definitions are included in ***nlmixr***.
nlmixr is under active development, and exciting new additions are:

- a unified user interface (UUI) that provides a common language for model definition for the different estimation routines,
- an interface[6] to the new xpose package[7] for graphical model diagnostics, and
- a ShinyMixR interface[8] for ***nlmixr*** project management that can be used to define and run ***nlmixr*** models in a friendly interface, and structure and examine ***nlmixr*** output.

In addition, parallel implementation of simulation and parameter estimation is at the horizon.

Objectives:

- Examine the estimation properties of the nlme and SAEM routines implemented in ***nlmixr*** for both rich data models and for a sparse sampling example

- Compare the results from the nlme and SAEM routines implemented in ***nlmixr*** with NONMEM FOCE-I

Methods: Richly sampled profiles were simulated for 4 different dose levels (10, 30, 60 and 120 mg) of 30 subjects each as single dose (over 72h), multiple dose (4 daily doses), single and multiple dose combined, and steady state dosing, for a range of test models: 1- and 2-compartment disposition, with and without 1st order absorption, with either linear or Michaelis-Menten (MM) clearance (MM without steady state dosing). This provided a total of 42 test cases. All inter-individual variabilities (IIVs) were set at 30%, residual error at 20% and overlapping PK parameters were the same for all models. A similar set of models was previously used to compare NONMEM and Monolix[9]. Additionally, a sparse data estimation situation was investigated where 500 datasets of 600 subjects each (150 per dose) were generated consisting of 4 random time point samples in 24 hours per subject, using a first-order absorption, 1-compartment disposition, linear elimination model. NONMEM®[10] with FOCE-I was used as a comparator to test the various ***nlmixr*** estimation routines for both closed-form and ODE implementations.

Results: Theta parameter estimates were comparable across estimation methods. The SAEM routine in ***nlmixr*** was particularly stable compared to the nlme routine, and consistently provided accurate results. For nlme, IIV estimates were regularly estimated close to 0% in ***nlmixr***, whereas both NONMEM, and SAEM in ***nlmixr***, provided estimates close to the original simulation values, for rich and sparse sampling alike.

Conclusion: These findings suggest that ***nlmixr*** provides a viable open-source parameter estimation package for nonlinear mixed effects pharmacometric models within the R environment. With a stable release on CRAN, and encouraging developments regarding new estimation routines (like FOCE-I) on their way, the ***nlmixr*** project is moving from prototype to mature application, ready for input from and adoption by the pharmacometric community.

References window:

References:

[1] https://cran.r-project.org/web/packages/nlmixr/index.html
[2] https://github.com/nlmixrdevelopment/nlmixr
[3] Wang W et al. CPT:PSP (2016) 5, 3–10.
[4] Pinheiro J et al. (2016). nlme: Linear and Nonlinear Mixed Effects Models.
[5] Kuhn E and Lavielle M. M. Comput Stat Data An, 49:1020–1038, 2005.
[6] https://github.com/nlmixrdevelopment/xpose.nlmixr
[7] https://CRAN.R-project.org/package=xpose
[8] https://github.com/nlmixrdevelopment/ShinyMixR
[9] Laveille C et al PAGE 17 (2008) Abstr 1356 [www.page-meeting.org/?abstract=1356]
[10] Beal SL et al. 1989-2011. NONMEM Users Guides. Icon Development Solutions, Ellicott City, Maryland, USA.