FOR IMMEDIATE RELEASE

PharmML: a flexible format for model exchange

Leiden, The Netherlands, 3rd of June 2015 – ***PharmML, a flexible format for exchanging computational models in pharmaceutical R&D, opens new opportunities for drug discovery and clinical research.***

- PharmML is a key component of DDMoRe's platform for interoperability between computational models in pharmacometric and quantitative systems pharmacology;
- PharmML encoded models can be deposited in the DDMoRe model repository, helping researchers collaborate on models to improve the design of cost effective, reliable clinical trials of new and repurposed drugs;
- A paper published in the journal *CPT:PSP* highlights features that facilitate smooth, error-free transmission of models between tools, and that make reporting and bug tracking easier. For predictive medicine to become a practical reality, scientists must be able to build, share and access accurate, efficient models of disease and drug action. Pharmacometric modelling is essential for designing cost–effective, reliable clinical trials to test new or repurposed medicines, but until now it has been difficult for researchers to pool their knowledge and develop these models collaboratively between organisations.

PharmML, developed at EMBL-EBI, is helping researchers collaborate on computational models of disease and drug action. An article published in the journal *Clinical Pharmacology & Therapeutics: Pharmacometrics and Systems Pharmacology* (*CPT:PSP*) introduces PharmML as a key component of a software platform that improves computational tools for drug discovery, built by the Drug Disease Model Resources consortium (DDMoRe).

"PharmML is an exchange format for pharmacometric and systems-pharmacology models," explains Lutz Harnisch, Coordinator of the DDMoRe consortium. "The public repository built on PharmML lets researchers in systems biology, quantitative systems pharmacology and pharmacometrics carefully scrutinise a broad range of published models. It provides easy access to models in their context of use, and helps authors enhance their credibility based on the use and reusability of their approaches. These are all vital to improving transparency in scientific communication."

PharmML is being developed to facilitate smooth, error-free transmission of models between tools, and to make reporting and bug tracking easier. It provides support for the implementation of non-linear, mixed-effect models for the analysis of longitudinal population data from clinical trials in a 'tool agnostic' manner. PharmML also makes it easier to navigate complex workflows and improves interactions with regulatory agencies regarding modelling and simulation.

"As a biostatistician involved in pharmacometrics for several decades, I am very pleased to see such a well constructed and clever language that encompasses all the statistical features needed in this area of computational modelling. It will also be a very valuable tool for teaching Masters-level and PhD students," says France Mentré, Professor of Biostatistics at Université Paris Diderot and director of an INSERM research team.

"The pharmaceutical industry and regulatory agencies have a long track record of adopting standards because this makes it much easier to achieve real advances in quality, quantity and efficiency," says Peter Milligan, Head of Pharmacometrics at Pfizer and EFPIA group participant for DDMoRe. "I see the potential for PharmML to be the standard that makes it possible to use a burgeoning variety of quantitative approaches in this sector. Until now, this has been inconceivable simply because of the inherent incompatibility of current modelling tools."

"The development of PharmML is a brilliant example of what can be achieved when public bioscience research joins forces with pharmaceutical research, and I have no doubt that it will have a significant impact on pharmacometrics," says Nicolas le Novère, EMBL-EBI alumni and Senior Group Leader at the Babraham Institute. "Standards for pharmacometric modelling developed by the DDMoRe project improve sharing and reproducibility of quantitative studies in drug development. One can use the same mathematical model with different tools and pass the model through different stages of the drug development pipeline – from preclinical to clinical. The result is that these models can be accessible to everyone by way of public model repositories."

"Designing PharmML has been a fascinating challenge, and not just a technical one," says Maciej Swat, lead developer of PharmML at EMBL-EBI. "It requires an intimate understanding of both statistical methods used in pharmacometrics, and the needs of the modellers. We've been lucky to have so many top European pharmacometric groups and experts in the DDMoRe consortium, sharing their invaluable experience and know-how."

Source article

Swat MJ, et al. (2015) Pharmacometrics Markup Language (PharmML): Opening new perspectives for model exchange in drug development. CPT: Pharmacometrics & Systems Pharmacology (in press). Published online 29 May; DOI:

About DDMoRe

The DDMoRe consortium (www.ddmore.eu) is a five-year project of the Innovative Medicines Initiative (IMI, www.imi.europa.eu), involving 27 partners from the pharmaceutical industry, small and medium-sized enterprises and academic research organisations. DDMoRe was formed in 2011 to address the lack of common tools, languages and standards for informed decision making throughout the drug-discovery pipeline. DDMoRe aims to facilitate modelling and simulation by establishing standards for encoding models and workflows, and for storage and transfer of models and their associated metadata; by developing a fully searchable, public drug and disease model repository encompassing model descriptions, algorithms, code, data, metadata, assumptions, Bayesian priors, and links to references; by developing an open-source interoperability framework to facilitate access to modelling

tools; and by developing the Modelling Description Language (MDL). As of October 2014 DDMoRe has released MDL, MDL-IDE, PharmML (www.ddmore.eu/pharmml) and a set of encoded published models for the study of diabetes, oncology, central nervous system disorders, infectious diseases and inflammatory diseases, provided from a public model repository.

For more information,

Lutz Harnisch	*Mats Karlsson*	*Wendy Aartsen*
Coordinator	Scientific Coordinator	Project Communication

E-mail: info@ddmore.eu

Support

The research leading to these results has received support from the Innovative Medicines Initiative Joint Undertaking under grant agreement n° 115156, resources of which are composed of financial contributions from the European Union's Seventh Framework Programme (FP7/2007-2013) and EFPIA companies' in kind contribution. The DDMoRe project is also financially supported by contributions from Academic and SME partners.

About the Babraham Institute

The Babraham Institute, which is strategically funded by the Biotechnology and Biological Sciences Research Council (BBSRC), undertakes international quality life sciences research to generate new knowledge of biological mechanisms underpinning ageing, development and the maintenance of health. The Institute's research provides greater understanding of the biological events that underlie the normal functions of cells and the implication of failure or abnormalities in these processes. Research focuses on signalling and genome regulation, particularly the interplay between the two and how epigenetic signals can influence important physiological adaptations during the lifespan of an organism. By determining how the body reacts to dietary and environmental stimuli and manages microbial and viral interactions, we aim to improve wellbeing and healthier ageing.

About EMBL-EBI

The European Bioinformatics Institute is part of EMBL, and is a global leader in the storage, analysis and dissemination of large biological datasets. EMBL-EBI helps scientists realise the potential of 'big data' by enhancing their ability to exploit complex information to make discoveries that benefit mankind. We are a non-profit, intergovernmental organisation funded by EMBL's 21 member states and two associate member states. Our 570 staff hail from 57 countries, and we welcome a regular stream of visiting scientists throughout the year. We are located on the Wellcome Genome Campus in Hinxton, Cambridge in the United Kingdom. www.ebi.ac.uk