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Christian Maass is a physicist and computational biologist with over ten years of academic and industrial international experience. He received his Master in Medical Physics from the University College London in 2012 and PhD from the University of Heidelberg in 2015, and worked as a postdoctoral researcher at the Massachusetts Institute of Technology (MIT), Cambridge, MA, USA until 2018. He specializes in method development for micro-physiological systems and Organs-on-Chips (OoC) in safety pharmacology and is passionate about the integration of computational modeling and biological experiments for translational pharmacology applications. As a senior scientist in industry, Dr. Maass works on applications in various therapeutic areas, e.g. neurodegenerative, inflammatory, and metabolic diseases (Alzheimer, rheumatoid arthritis, NASH/NAFLD). Among others, he developed individualized PBK models for molecular radiotherapy (leukemia), automated workflows for big data (*omics), network-based analysis of inflammation diseases, and mechanistic modeling of OoC data. He is leading projects to further develop strategies on how to best integrate OoC and computational modeling for translational pharmacology applications.

Abstract

Humanizing the Drug Development Process merging Organ-on-Chips and Computational Modelling

Organ-on-chips (OoC) have the potential to represent human physiology *in vitro* more appropriately than animals and hold great promise to humanize the drug development process. Their biggest impact is sought to improve efficacy and identify hazards in drug discovery and non-clinical studies. Yet, the technology is not regularly used in drug development, because its advantage over animal and other *in vitro* models related to predictivity of and translatability to human *in vivo* outcomes remains to be established. To do so, I propose a novel workflow that embeds OoC data in a computational modelling framework. First, analyzing OoC data using computational models can improve our mechanistic understanding of underlying biological principles, which are needed to optimize experimental designs for drug mechanism of action studies. Second, by combining OoC data from pharmacokinetics and toxicology studies with human computational models, it is possible to predict clinical outcomes (safety, efficacy) of novel drugs before testing in humans. In this keynote lecture, I will highlight the need, impact, and added value of such an integrated workflow by presenting literature-based examples and future prospects.