MLDM-L2: An introduction to mechanistic mathematical modeling approach in biology and medicine

Person in charge and Representative	Michael Meyer-Hermann
Contact person	Sahamoddin Khailaie (khailaie@theoretical-biology.de)
Semester	Possible at any time
Topic cluster	Machine Learning and Data Mining
Duration/Credit	8 lectures of 1.5 hours
Time	Lectures can be given in a compact 2-days block or one lecture per week. This can be decided based on the availability of lecturers and students.
Place	The lectures can be given using online platforms.
Prerequisite for the lecture/course	None.
Aim of the lecture/course	The aim of this lecture series is to introduce a mechanistic mathematical modeling approach for exploring time-resolved biological and medical data. This approach is proven useful for hypothesis testing, extracting biophysical parameters, predicting dynamical behavior under various conditions, optimizing therapeutic strategies and extracting novel ones. Common techniques will be presented along with their application to real data. This lecture presents the following steps in mechanistic mathematical modeling with examples:
	 Extracting basic principles underlying the kinetic data and formulating working or competing hypotheses Developing ordinary differential equations-based and agent-based models to analyze the working or competing hypotheses Fitting the mechanistic models to the time-resolved data, estimating the associated parameters, and investigating the quality of fit for model selection Design predictive or exploratory simulations from validated models Analyze and optimize existing therapeutic strategies, or extract novel ones This lecture will provide students with the basics to understand scientific materials containing mechanistic mathematical models, or tools to employ in their own data and research questions.