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## **The power of theoretical and practical identifiability analysis for modeling (micro-) biological processes**

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When modeling biological systems, one major step of the modeling exercise is the confrontation between the theory (the model) and the reality (the data). Such a confrontation passes through the resolution of the parameter identification (model calibration) problem, which aims at finding a set of parameters that best fits the variables predicted by the model to the data. The parameter identification step is often addressed like a downstream process. Using this approach, once the data are collected, the modeler has a minimal degree of freedom to improve the accuracy of her model. Instead, the modeler can identify opportunities for improving model accuracy if the parameter identification problem is addressed like an upstream process. For instance, one of these opportunities is to determine for a given experimental setup (before the actual data collection), whether the optimization problem is well-posed (that it is, if the problem has unique solution). Knowing this information beforehand is useful to set up an experimental protocol that guarantees the uniqueness of the parameter estimates. This question of uniqueness is related to the notion of structural (theoretical) identifiability. The modeler might also be interested in knowing whether the available data that will result from the experimental protocol will be informative enough to identify the model parameters accurately. The question of parameter accuracy based on the quality of available data is related to the notion of practical identifiability. This work aims to present the theoretical basis of structural and practical identifiability analysis. By capitalizing on the use of dedicated software tools, we will illustrate further the power of structural and practical identifiability analysis in the modeling exercise using relevant examples for the modeling of microbiological processes such as the rumen microbial fermentation.