

Testing structural identifiability by a simple scaling method

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Abstract-

Successful mathematical modeling of biological processes relies on the expertise of the modeler to capture the essential mechanisms in the process at hand and on the ability to extract useful information from empirical data. A model is said to be structurally unidentifiable, if different quantitative sets of parameters provide the same observable outcome. This is typical (but not exclusive) of partially observed problems in which only a few variables can be experimentally measured. Most of the available methods to test the structural identifiability of a model are either too complex mathematically for the general practitioner to be applied, or require involved calculations or numerical computation for complex non-linear models. In this work, we present a new analytical method to test structural identifiability of models based on ordinary differential equations, based on the invariance of the equations under the scaling transformation of its parameters. The method is based on rigorous mathematical results but it is easy and quick to apply, even to test the identifiability of sophisticated highly non-linear models. We illustrate our method by example and compare its performance with other existing methods in the literature.

Index Terms-

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Citation:

Castro, M.; de Boer, R. J. "Testing structural identifiability by a simple scaling method", Plos Computational Biology, vol.16, no.11, pp.e1008248-1-e1008248-15, November, 2020.