

A WEB-BASED APPLICATION FOR EVALUATING PARAMETER IDENTIFIABILITY OF BIOCHEMICAL MODELS IN POLYNOMIAL FORM

Marcos Simoes *•

mabs@kdbio.inesc-id.pt

Susana Vinga *◦

svinga@kdbio.inesc-id.pt

- * INESC-ID: Instituto de Engenharia de Sistemas e Computadores - Investigação e Desenvolvimento, Portugal
 • Instituto Superior Técnico - Universidade Técnica de Lisboa, Portugal
 ◦ Faculdade de Ciências Médicas - Universidade Nova de Lisboa, Portugal

1 Abstract

State-space models are very often used for the quantitative modelling of biochemical systems. Together with parameter estimation, a necessary and early step in the building of such models is the assessment of identifiability properties: Whether the structure of the model and the available experimental data allow for the determination of a unique value for each of its parameters. The approach taken with structural identifiability attempts to determine the algebraic solvability of the model's parameters under the assumption of infinite-resolution and error-free data. A model is said to be:

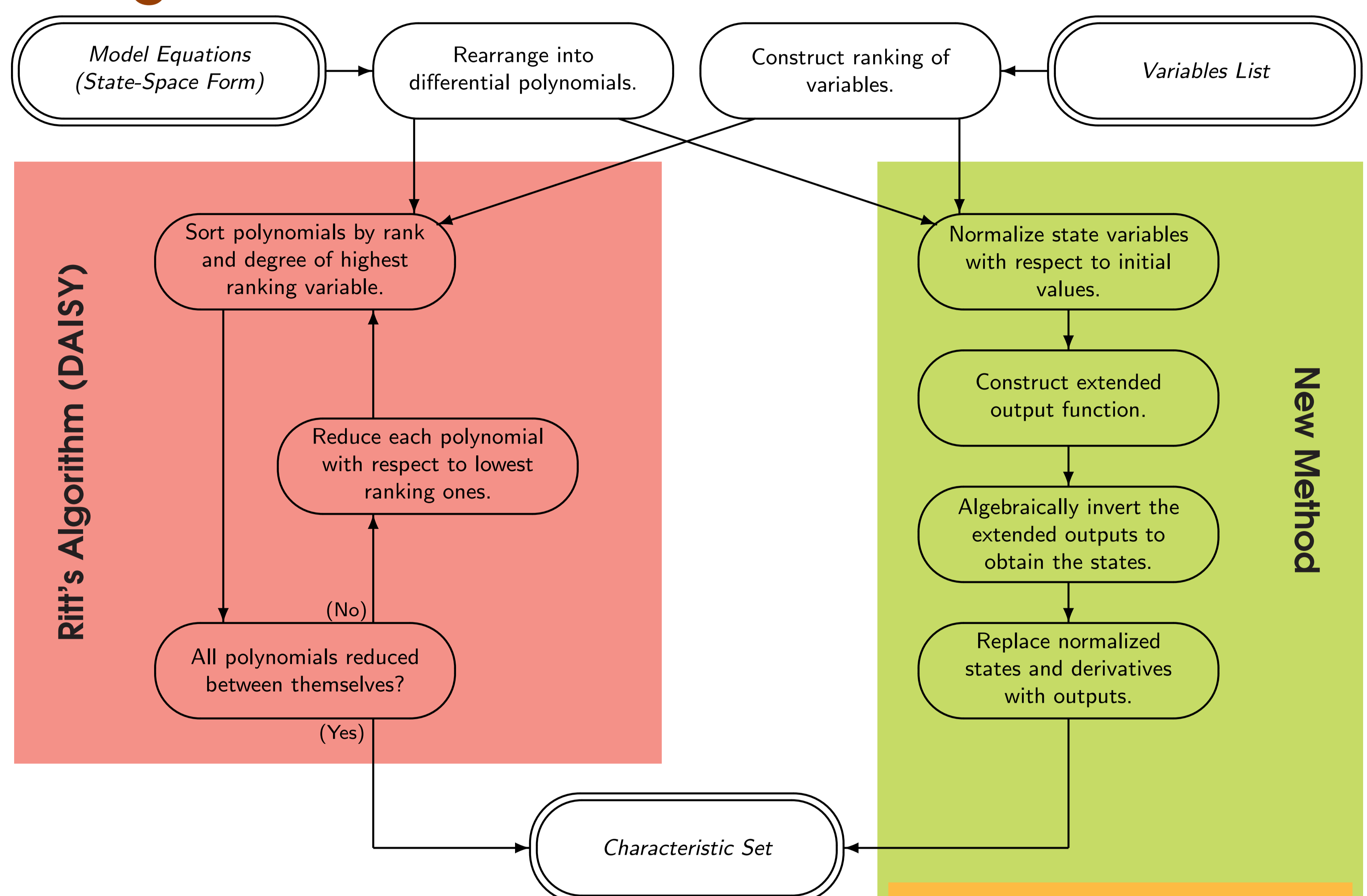
Globally identifiable when its algebraic structure allows for the determination of a single solution to all its parameters.

Locally identifiable when a single global solution cannot be guaranteed but there exist a multitude of solutions which, however, lie isolated in parameter space.

Unidentifiable when at least a single continuous range of solutions is possible.

We present an **online application** that computes these properties for polynomial models in a completely automated manner.

2 Algorithms



3 Implementation

<http://kdbio.inesc-id.pt/~mabs/DynaMo> ✓

State variables:
x1, x2, x3

Output variables:
y

Input variables:
u, g

Model state functions (ODE's):
 $x1' = -(k_p + (F01/V1)/g + k21) * x1 + k12 * x2$
 $x2' = k21 * x1 - (k02 + x3 + k12) * x2$
 $x3' = -k_b * x3 + k_a * u$

Output functions:
y = x1 / V

... The model's evolution functions here...
 ... And the outputs.

Method to use: Standard DAISY Improved Method

Clear Everything
Revert Changes

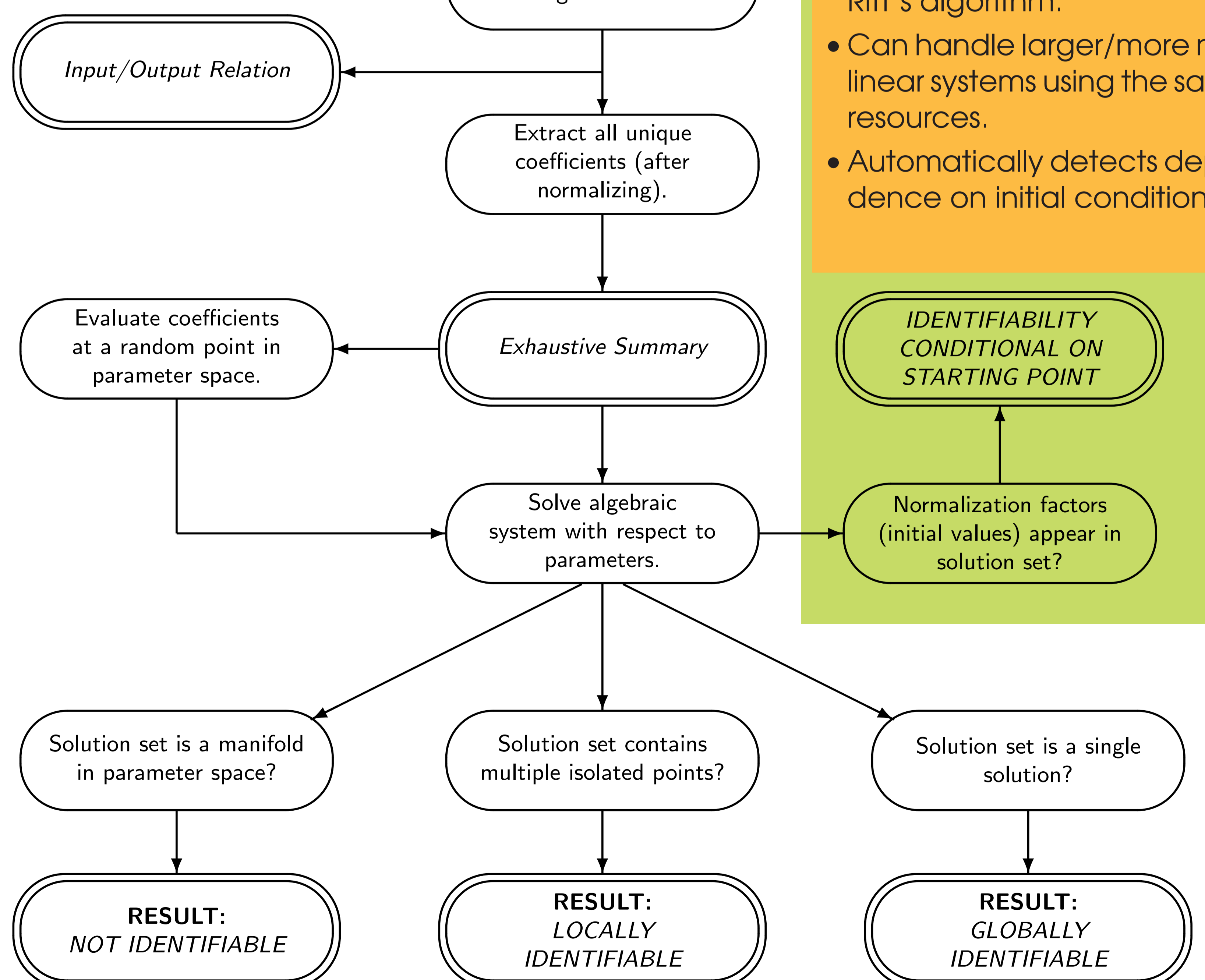
Evaluate Model

RESULT: Not Identifiable

This means that there is no set of input/output experiments that can provide a unique solution for all model parameters, not even locally (that is, at least one parameter has always a continuum of possible solutions). In this case, identifiability may only be attained by restructuring the model.

4 Conclusions

- New method usually faster than Rit's algorithm.
- Can handle larger/more non-linear systems using the same resources.
- Automatically detects dependence on initial conditions.



References:

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