

Testing Biological Models for Non-linear Sensitivity with a Programmability Test

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1 Introduction

We address the question of what kind of test could be implemented to establish whether an artificial system is living or not with a computability and programmability test as advanced in [2]. We claim that necessary conditions for life are non-linear behavioural variability and sensitivity to external stimuli.

We advance an algorithmic information concept of programmability as a combination of behavioural change and external control similar to the one presented in [1] in the context of self-assembly and non-DNA spatial computation. We look into evaluating, classifying and discriminating biological models from the BioModels Database (<http://www.ebi.ac.uk/biomodels-main/>), a centralized database of curated quantitative models of biochemical interest whose dynamical space, time-evolution and model's reaction to their "environment" (sensitivity) is studied, leading to questions such as the robustness and param-

eter orthogonality.

Similarity metrics and information distances are applied and results are presented in the direction of characterisations of the behaviour of physical and natural systems, allowing the classification of qualitative properties and the assessment of simulation results in terms of algorithmic information content with special focus on transitions, clustering, variability and space parameter discovery and behavioural mapping.

The testing approach based on a system capability to react to external stimuli and transfer information as reflected in the proposed measures of programmability indicate the susceptibility of a system to be (efficiently) programmed where we can ask questions such as whether programmability differences originate from either (a) a structural difference in the modelling equations, or (b) differences in how much parameters are allowed to vary, and thereby having a greater/smaller flexibility to respond to external stimuli. Model understanding may be hindered by the assumed dataset and the estimated parameters on which models are often heavily dependent. The approach promises to provide some further insight on different types of biological models.

References

- [1] G. Terrazas, H. Zenil and N. Krasnogor, Exploring Programmable Self-Assembly in Non-DNA based Molecular Computing, submitted to *Natural Computing* (in 2nd. revision).
- [2] What is Nature-like Computation? A Behavioural Approach and a Notion of Programmability, *Philosophy & Technology*, 2013. <http://link.springer.com/article/10.1007/s13347-012-0095-2>