Commentary on 'Addressing the Malaise in Neoclassical Economics: A Call for Partial Models'

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The article by Ron Wallace 'proposes the deployment of partial modelling, utilising Boolean networks (BNs), as an inductive discovery procedure for the development of economic theory'. The central argument in favour of partial models is well-made, and while I agree with this aspect of the paper, and the conclusion that models should serve as 'cognitive instruments in a regime of exploration,' I have a number of comments about the proposed strategy and the example of BNs.

The paper states that a theory 'should be tested for its ability to predict an actual economy,' and notes that BNs have been applied to areas including systems biology, 'frequently yielding results with high predictive power'. The implication is that a technique which is predictive in systems biology may also be useful for predicting the economy. However (speaking as someone who works in the area), in systems biology the word 'predict' tends to be used rather loosely. It often just means that a result which is already known and/or non-surprising can be reproduced, which is not the same as the usual meaning (e.g. predicting a financial crisis). A typical usage for example is the title of the paper 'Boolean Network Model Predicts Cell Cycle Sequence of Fission Yeast'. And when researchers refer to 'testing against empirical data to assess predictive power' (as in the response to a comment from Steve Keen on the *Economic Thought* Open Peer Discussion forum), this usually means calibration, unless it is done in a blind-tested fashion, which is extremely rare. This is an important distinction for this paper, because a sufficiently complicated model is very flexible and can be made to match known data, but may be poor at making non-trivial predictions (examples are given below). The article notes that 'BNs are remarkably flexible', which is not necessarily a good thing.

The article describes a method whereby BNs can be combined together to form a larger model; however this relies on 'simplification of the partial models to avoid an intractable result when they are combined', such as 'excluding node values that will produce multiple steady states. In addition, feedback loops are excluded because they can frequently yield oscillations.' An advantage of the strategy is 'the ability of BNs to include system components (e.g. cultural or religious variables) for which quantitative data are minimal or lacking, without significant loss of predictive power'. Furthermore 'it is possible to convert a BN into a continuous dynamical system configured as ordinary differential equations (ODEs)'.

The idea is therefore to patch together simple models to create a larger and more sophisticated model, while pruning features which create problems, and adding new nodes for missing information. However it should be noted that, if models are viewed as patches, it need not follow that combining the patches will give a better result, or that simply adding a node to a network is enough to account for missing information or dynamics.

To give a few examples from different contexts: in a model of gene regulation in yeast (Ramsey et al., 2006), it turned out that the main (experimentally verified) prediction concerned stochastic effects that were invisible to *any* ODE model, no matter how many equations or parameters were added. Predictive (and blind-tested) models used by drug companies to optimise cancer treatments rely on the careful modelling of dynamical cell

population effects of the sort that cannot be captured by either BNs or ODEs, so instead a combined ODE/agent-based approach is used (https://www.physiomics-plc.com/technology/), which nonetheless limits parameters to things that can be measured or estimated experimentally. A simple model, based on just a few parameters, outperformed large-scale biophysical 'gold standard' cardiac models, containing hundreds of parameters, at predicting the cardiac toxicity of drug compounds (Mistry, 2018). In cognitive science, quantum decision theory shows that decisions are inconsistent with classical probability: interference effects need not more detail, but a different kind of probability (Yukalov and Sornette, 2015). In economics, as Bezemer (2012) notes, the money system 'is alien to the (DS)GE models structure and trying to introduce it undermines key model properties'. It isn't therefore enough to add a 'finance node' to a model (general equilibrium or other). In all these cases, the proposed strategy would fail, because extending the model doesn't address the problem, which is not model size or complexity (in fact small is often better), but model structure (which is never perfect because a complex system doesn't reduce to equations) and the difficulty of identifying parameter values.

More generally, as these examples also illustrate, the strategy does not address the main practical limitations of modelling complex living systems, from a cell to an economy. The first is that as further detail is added to a model (e.g. extra nodes or equations), the number of unknown parameters increases, as does uncertainty about model structure, resulting in 'sloppy parameters' which cannot be determined from data (Gutenkunst et al., 2007). Second, such systems are also characterised by opposing positive and negative feedback loops (which the paper notes are sometimes omitted during model integration because they are destabilising). These are extremely hard to tease out from data because they are usually hidden (being often in a state of tension, they seem to cancel out), and also lead to complex unstable behaviour. Instability is of course not a problem in itself, since natural systems also exploit dynamic instability in order to produce rapid change, but in a model it means that a small change in parameters can give a very different result (Orrell, 2007, p. 266), and attempts to dampen the instability may just make the model less realistic.

What the cited paper (Schlatter et al., 2012) calls 'the final goal of a comprehensive dynamic model' may therefore remain elusive in systems biology as in other fields, despite its enduring popularity. (General equilibrium models were born out of neoclassical economists' intention to build such a 'comprehensive dynamic model' of the economy, though the dynamics were of the equilibrium sort.) However the problem is not the size or scope of the system being modelled, but its complexity – modelling a single cell is as hard as modelling the climate system.

One result of these limitations is that, paradoxically, simple models usually give the best predictive results (Makridakis and Hibon, 2000), but at the same time never give a complete picture. I therefore agree completely that models should be viewed as partial approximations and I found the discussion of this very interesting. It is also certainly the case that economics can learn much from systems biology, which uses a variety of models including ODEs, stochastic models, agent-based models, machine learning, BNs, and so on. However the argument of the paper points towards the goal of a comprehensive model (even if it is only for a segment of the economy such as HFT), patched together using semi-automatic techniques; and it isn't clear how this strategy (joining and extending models while pruning features) can address the main problems with economics models, which is that: (a) all the difficult features – such as feedback loops, human behaviour, money, and so on – have already been pruned out to avoid conflicts or an 'intractable result'; and (b) there are already too many 'sloppy parameters' that can't be determined from data (Romer, 2016).

In light of the structural and predictive limitations of models, I have argued for a different dashboard approach, which uses a range of model types (as in systems biology), but keeps them mostly separate, on the understanding that none are correct but each captures some complementary aspect of the underlying reality (see Orrell, 2018, p. 254; Orrell, 2017, p. 21-22). Model size should be limited in order to avoid the above-mentioned problems associated with dimensionality. So instead of seeing a BN (or other) as a partial model on which to add another model in order to form a larger (and less partial?) model, one treats any model as a partial model to be *complemented* by different models or approaches.

Finally, one should consider the role of incentives. In an area such as systems biology, which is relatively unconstrained by the need to make blind-tested predictions, there is a tendency to build ever-larger models of the sort critiqued in Mistry (2018). For something like 'theoretical controversies related to high-frequency trading' on the other hand, where, unlike in systems biology the debate over regulation is a matter of considerable interest to the financial sector, there are extremely powerful incentives at work which shape both underlying assumptions and the kinds of questions which are asked (Wilmott and Orrell, 2017, p. 194). I think a first step before combining models would be to investigate influences such as the source of funds for the various modelling approaches.

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