In neuroscience, simulations have been and continue to be instrumental for modelling the activities of nervous systems, as it can be noted with the recent launch of the Human Brain Project. Traditional in vivo and in vitro experimental methods are increasingly complemented by so-called in silico experiments. As digital electronic computers do not seem to be among objects usually studied by biologists, the term deserves some attention. In this paper, I will explore the conditions under which simulations can be understood as experiments, the knowledge obtained by executing them, the hypotheses necessary for establishing inferences about the target systems and their justification.

To begin the analysis, the second relatum of the relation ,x is a simulation of y', usually referred to as target system, has to be specified. It can either be an individual dynamical system, a class of systems or a theory. If the relata are identical, it is straightforward to acknowledge that observations of computer simulations count as experiments, although some authors would call them computer simulation studies. However, biologists do not run computer simulations in order to learn about computers. In neuroscience as in biology in general, it is not always clear what the target of a simulation is. In case of the simulations performed in the Human Brain Project, one could suggest that the simulated system is a particular cortical column that was digitised. However, the simulation in question is far from a simple digitalisation of a particular system. Moreover, inferences made on the basis of the simulation do not concern any particular system. Therefore, the target of the simulation could be considered as a class of dynamical systems. But which one?

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One could opt for a narrow class of columns of "hind-limb somatosensory cortex of 2-week-old Wistar (Han) rat" or for a larger class of "neocortical microcircuitry". In both cases, in order to speak about an experiment, one could make the following counterfactual assumption – if the simulated system were real, it would be in one of the previously mentioned classes. However, the simulation itself is running on a real computer that is not considered to be a member of those classes. A more promising option would be to define a broad class including the computer running the simulation and the dynamical systems of the target class. If we assume that the generative and transition rules used in simulation also cover the target system for a given range of initial conditions, it is possible to treat the simulation as a genuine experiment.

Another important aspect is the stochastic nature of the generative and transition rules on the one hand and the variability of the biological structures on the other. In simulations where the target is a particular dynamical system the lack of correspondence with the spatial relations might be considered as a major defect. This is not the case for simulations of neuronal circuitry as some degree of variability is already present in classes as defined by biologists. Therefore, what needs to be justified is either the assumption that the simulation is a ,representative' member of the broad class or that the statistical distribution of parameters in various instances of the simulations corresponds to the statistical distribution of the parameters found in the target class.

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