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Specification and generation of structured neuronal network models with the NEST Topology Module

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Large, spatially structured computational models of the brain are an increasingly popular tool in the study of brain function, in particular the visual system [1,2]. Communicating the structure and connection patterns of these models in scientific papers is a challenge [3], as is their correct and efficient implementation in simulators for the purpose of independent validation and further scientific exploration. The NEST Topology Module facilitates the concise specification and efficient generation of large, spatially structured neuronal network models. The module is publicly available as part of the NEST 2 simulator package [4]. The Topology module organizes neuronal networks in two-dimensional sheets, reflecting the predominant architecture of the visual and other sensory pathways. A sheet can be composed of individual neurons or of compounds, such as microcolumns. Elements are assigned spatial coordinates (receptive field centers), either on a Cartesian grid or at arbitrary locations. The notion of sheets in the Topology module differs from cortical layers. Since most models of sensory pathways describe brain areas as composed of columns with specific receptive field properties, we consider it logical to describe spatial ordering at the column level. Model neurons can be labeled to facilitate connections to specific neuron types. Connections between sheets are represented using probability kernels and masks, which specify the probability for two neurons to be connected as a function of their distance (in stimulus space). Kernels can be divergent (choosing targets for each presynaptic neuron) or convergent (choosing senders for each postsynaptic neuron). At present, uniform and Gaussian kernels and rectangular, circular and doughnut masks are implemented. Connections between specific neuron types in sheets are requested by referring to the labels assigned to neurons. Generating network connections from probabilistic kernels by performing a Bernoulli trial on each potential target within the cut-off mask is inefficient when most connection probabilities are small. The Topology module first determines the number of connections to be made from a binomial distribution and then distributes connections within the mask according to relative probability. For non-uniform kernels this is implemented using Walker's alias method [5] or logarithmic classes [6], resulting in a tenfold speedup in realistic situations. The binomial approach is justified by Lyapunov's central limit theorem in this case.

The NEST Topology Module is a first step towards shared tools for the representation and generation of large, spatially structured brain models. Future developments will include three-dimensional sheets (volumes) and a callback scheme to allow flexible specification of element constructors, kernels and masks.

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