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Effects of different discretisations of the Laplacian in stochastic simulations

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A deterministic model of biochemical reaction networks is not always appropriate. Gene expression, for example, often involves a small number of molecules which means that noise can significantly influence the dynamics. By discretising space into voxels and letting the molecule dynamics be governed by the reaction-diffusion master equation, it is possible to model the reaction and diffusion of individual molecules on an arbitrary domain. Following on from the work of Meinecke and Lötstedt we apply a variety of numerical methods to the Laplacian operator in order to derive the jump rates that simulate the diffusion of molecules. We discuss how pattern formation within a Turing model might be influenced by the geometry of the spatial discretisation and the numerical method.

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