

A method for sensitivity analysis and parameter estimation applied to a large reaction-diffusion model of cell polarization

Parameter sensitivity analysis and parameter estimation is challenging in many biological systems due to large parameter counts. Too many parameters can make sampling of the parameter space computationally implausible, especially for partial differential equation models that are expensive to solve. In this work, we propose a method for parameter sensitivity analysis and parameter estimation that can be significantly less costly for large problems. The key step in this method is the construction of a polynomial surrogate model. The method is applied to a large reaction-diffusion model of yeast cell polarization containing 35 parameters.