

Stochastically perturbed gene regulatory networks

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An analytic stochastic modeling approach is proposed, which incorporates intrinsic noise effects directly into a well established continuous and deterministic formalism for studying gene regulatory networks characterized by steep gene regulatory functions. The stochastic effects are described by white noises whose diffusion coefficients solely depend on the steepness parameters of the smooth regulatory functions. The basic technical tool consists in linking the systems with smooth regulatory functions with those containing step regulatory functions. The dynamics of the underlying smooth and piecewise smooth systems can be compared explicitly between and, which is more difficult, in the thresholds. The singularities arising around the discontinuities are studied with the help of the uniform version of the stochastic Tikhonov theorem in singular perturbation analysis going back to Yu. Kabanov and Yu. Pergamentshchikov.

References

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