Using spatial point process models to describe cellular protein interactions

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We have initiated the development of spatial point process models for the distribution of proteins throughout living cells. Further, we have developed a model for the generation of Fluorescence Resonance Energy Transfer (FRET) pixel intensity data, given a protein configuration. By combining the two models a complete stochastic model for the generation of FRET pixel intensity data is obtained and it enables us to define a likelihood function for FRET data. .

Based on the combined model we are developing Markov chain Monte Carlo algorithms for Bayesian inference regarding parameters in the spatial point process model. This will allow us to draw quantitative statements concerning the protein arrangement at an inner pixel level.

We will discuss prior distributions and implementation of the MCMC algorithm for simulation of the posterior distribution. The performance of the proposed methodology is assessed for synthetic data sets generated by Poisson and hardcore-Strauss point processes.

References:

Corry, B., Jayatilaka, D. & Rigby, P. (2005): A flexible approach to the calculation of resonance energy transfer efficiency between multiple donors and acceptors in complex geometries. *Biophys. J.* **89**, 3822-3836.