MULTIPLE EMITTER FITTING USING REVERSIBLE JUMP MARKOV CHAIN MONTE CARLO

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In single molecule based super-resolution imaging, high labeling density or the desire for greater data collection speed can lead to clusters of overlapping PSFs in the raw super-resolution image data. Multi-emitter fitting algorithms can identify and localize the particles in those dense regions of the data. In this work, we improve upon the state-of-the art in multi-emitter fitting by employing Reversible Jump Markov Chain Monte Carlo (RJMCMC) [1]. Markov Chain Monte Carlo (MCMC) can be used to find the posterior distribution of a set of parameters, which in the multi-emitter fitting problem consists of the particle positions and intensities and a local background. RJMCMC takes this concept further and allows jumps between parameter spaces, in this case allowing the addition or subtraction of emitters in the model. We allow four mechanisms to make jumps between spaces of various models, called birth, death, merge and split. Birth (death) allows the addition (deletion) of an emitter anywhere in the sample. Split allows the possibility that an existing particle can be actually two or more neighboring particles. Merge allows the chance of two adjacent particles to join into a single particle. RJMCMC averages over the possible models, weighting them by their probabilities. This Bayesian approach also allows prior knowledge on intensity, background and particle density to be easily input in a principled manner. Although demonstrated here in 2D, the approach can be easily extended to analysis of 3D data with arbitrary PSFs.

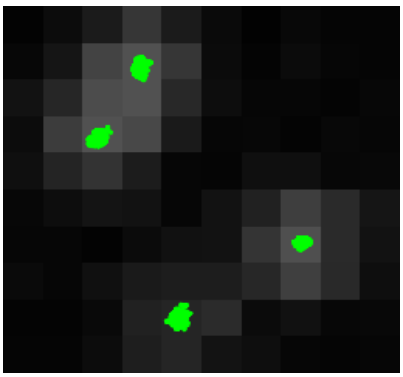

Fig. 1: Synthetic data analyzed with the RJMCMC method. Green shows the posterior position density generated by the Markov Chain

We describe the mathematical formalism for the RJMCMC model and compare the results under a range of conditions to other existing multi-emitter fitting approaches using synthetic and experimental data. Figure 1 shows the result of the RJMCMC analysis for a small region of simulated data.

[1] P. Green, *Biometrika,* 82, 711-732, 1995.