Bayesian detection of embryonic gene expression onset in *C. elegans*

PhD candidate: Jie Hu
Supervisor: Professor Xiaodan Fan

Department of Statistics, The Chinese University of Hong Kong

Abstract

One fundamental question in biology is how a zygote develops into an embryo with different tissues. To approach this goal, large-scale 4D confocal movies of *C.elegans* embryos have been produced by experimental biologists. However, the lack of principled statistical methods for the highly noisy data has hindered the comprehensive analysis of these data sets. We introduced a probabilistic change point model on the cell lineage tree to estimate the embryonic gene expression onset time. A Bayesian approach is used to fit the 4D confocal movies data to the model. Subsequent classification methods are used to decide a model selection threshold and further refine the expression onset time from the branch level to the specific cell time level. Extensive simulations have shown the high accuracy of our method. Its application on real data yielded both previously known results and new findings.