
Gene network inference using single-cell data: from mechanistic modelling to statistics

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Abstract

Inferring regulatory networks from gene expression data is a longstanding question in systems biology. So far, most studies have been based on population-averaged data: now that we can observe mRNA levels in individual cells, a revolution in terms of precision, the network reconstruction problem paradoxically remains more challenging than ever. I will present a bottom-up approach to tackle this problem, going from a mechanistic model of gene expression to a promising statistical model where stochasticity is not just noise but also contains information.

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