

Modelling transcription activation using microarray data

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Abstract

Gene transcription is a process activated by its associated transcription factor, possibly modified by other proteins, which may inhibit or facilitate this transcription. Although gene transcription is a stochastic process, when viewed on the level of single molecules, typically microarray data averages out such stochasticity, making the combination of statistical error, technical variation and the average transcription activation process the largest components of variation in such circumstances. Our aim is to model gene activation and activation modifications using a modified set of Michaelis-Menten kinetics and a random effects model. Several examples will be provided throughout.