

Thomas Philipp, Stochastic gene expression in lineage trees

May 24 @ 4:00 pm - 5:00 pm KST

ZOOM ID: 997 8258 4700 (Biomedical Mathematics Online Colloquium), (pw: 1234) + Google Map https://www.ibs.re.kr/bimag/event/stochastic-gene-expression-in-lineage-trees/



SPEAKER

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Abstract: Stochasticity in gene expression is an important source of cell-to-cell variability (or noise) in clonal cell populations. So far, this phenomenon has been studied using the Gillespie Algorithm, or the Chemical Master Equation, which implicitly assumes that cells are independent and do neither grow nor divide. This talk will discuss recent developments in modelling populations of growing and dividing cells through agent-based approaches. I will show how the lineage structure affects gene expression noise over time, which leads to a straightforward interpretation of cell-to-cell variability in population snapshots. I will also illustrate how cell cycle variability shapes extrinsic noise across lineage trees. Finally, I outline how to construct effective chemical master equation models based on dilution reactions and extrinsic variability that provide surprisingly accurate approximations of the noise statistics across growing populations. The results highlight that it is crucial to consider cell growth and division when quantifying cellular noise.

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