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Contribution ID: **3166** Type: **Oral Competition (Graduate Student) / Compétition orale (Étudiant(e) du 2e ou 3e cycle)**

(G*) Inferring gene regulation from static snapshots of gene expression variability

Tuesday 7 June 2022 10:00 (15 minutes)

A key challenge of systems biology is to translate cell heterogeneity data obtained from single-cell sequencing or flow cytometry experiments into causal and dynamic interactions. We show how static population snapshots of gene expression reporters can be used to infer causal and dynamic properties of gene regulatory networks without using perturbations. For instance, we derive correlation conditions that detect causal interactions and closed-loop feedback regulation in gene regulatory networks from snapshots of transcript-levels. Furthermore, we show how oscillating transcription rates can be identified from the variability of co-regulated fluorescent proteins with unequal maturation times. Our approach exploits the fact that unequal fluorescent reporters effectively probe their upstream dynamics on separate time-scales such that their correlations implicitly encode information about the temporal dynamics of their upstream regulation. Synthetic genetic circuits provide exciting opportunities to verify these co-variability conditions with well characterized engineered systems. Lastly we report on ongoing experiments where we quantitatively test our theory with variants of a synthetic oscillator, the Repressilator, in single-cells using time-lapse microscopy and microfluidics.

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