

Abstract Submitted  
for the MAR16 Meeting of  
The American Physical Society

**A generic spatial-stochastic framework for quantifying noisy information flow in multicellular systems** THOMAS SOKOLOWSKI<sup>1</sup>, GAŠPER TKAČIK<sup>2</sup>, IST Austria — Spatio-temporal protein signals play a crucial role in communicating information within and between cells. However, their ability to convey signals robustly is hampered by noise in gene regulation and biochemical transport, occurring at low copy numbers. While we increasingly understand distinct strategies of biochemical noise control, it remains unclear how nature orchestrates them to maximize information flow. Our recent work extends our information-theoretic framework for gene regulation to an explicitly spatial setting. We constructed a stochastic model enabling fast calculation of local means and variances in a spatially coupled gene regulatory system, which we use for rigorous quantification of information flow in an ensemble of units sensing a spatially distributed input and exchanging information via diffusion. By applying our framework to the paradigmatic Bcd-Hbk system in early fly development, we demonstrate that diffusive coupling can be of substantial benefit in encoding positional information, and uncover a novel optimal regulatory strategy relying on spatial coupling. Thanks to the generic methodology employed, our framework is universally applicable for realistic predictive modeling and data-driven inference of multicellular systems engaging in noisy communication.

<sup>1</sup>Institute of Science and Technology Austria, Am Campus 1, A-3400 Klosterneuburg, Austria

<sup>2</sup>Institute of Science and Technology Austria, Am Campus 1, A-3400 Klosterneuburg, Austria

Thomas Sokolowski  
IST Austria, Am Campus 1, A-3400 Klosterneuburg, Austria

Date submitted: 05 Nov 2015

Electronic form version 1.4