Deriving the Drosophila gap gene system ab initio by optimizing information flow

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Spatio-temporal protein patterns are crucial for communicating information within and between cells. However, their ability to convey signals robustly is hampered by noise in gene regulation and biochemical transport. It remains largely unclear how nature orchestrates different biochemical noise control strategies to maximize information flow, especially in spatial scenarios. Here we take the approach of theoretically predicting the best gene-regulatory design of a developmental patterning system that optimizes transmission of relevant information, starting only from biophysical principles and without any fitting involved. To this end, we construct a generic spatial-stochastic model which allows for rigorous quantification of information flow in an ensemble of gene-regulatory units encoding a spatially distributed input signal in multiple downstream target outputs [1,2]. By optimizing information capacity over all relevant model parameters, we obtain predictions for the gene-regulatory architectures that maximize encoding of positional information in the output patterns [1,3]. We exemplify our approach by applying it to a paradigmatic developmental system, the gap gene patterns in the early development of the *Drosophila* fly [6]. The theoretically predicted optimal patterns are compared to high-quality experimental measurements of means and covariances of the gap gene products [4,5], using the same model framework for inference.

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