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**Genetic networks and the flow of positional information in embryonic development**

WILLIAM BIALEK, Princeton University

When we study a biological system, we make inferences about the underlying mechanisms and dynamics. But biological systems themselves must also solve inference problems, as when our brains draw conclusions about the world given (often quite limited) data from our eyes and ears. My colleagues and I have been exploring both of these inference problems as they play out in the first hours of development in the fruit fly embryo. In this system, the concentrations of particular molecules encode the position of each cell in the embryo, and these concentrations are the outputs of a genetic network. Putting ourselves in the place of the cells, we have been able to read the code, building a dictionary that maps gene expression levels back into estimates of position. If our dictionary really is the one used by the embryo, then mutants should build predictably distorted body plans, and preliminary results show quantitative agreement with these predictions. Independent of their role as carriers of information, we can also analyze the patterns of gene expression to draw inferences about the underlying network. Finally, it is possible that the network architecture and parameters have been chosen to optimize the flow of information, and we see signatures of this optimization. Joint work with CG Callan, JO Dubuis, T Gregor, D Krotov, M Petkova, TR Sokolowski, G Tkacik, AM Walczak, and EF Wieschaus.