COMPUTATIONAL BIOLOGY WEBINAR @ IMSc

HOW IS INFORMATION PROCESSED IN DEVELOPING SPINAL CORD?

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TUESDAY, 20 OCTOBER 2020, 3 PM IST

The development of multicellular organisms is a dynamic process in which cells divide, rearrange, and interpret molecular signals to adopt specific cell fates. Despite the intrinsic stochasticity of cellular events, the cells identify their position within the tissue with striking precision of one cell diameter in the fruit fly or three cell diameters in the vertebrate spinal cord. How do cells acquire this positional information? How is this information encoded and how do cells decode it to achieve the observed level of cell fate reproducibility? These are fundamental questions in biology that are still poorly understood. In this talk, I will combine both information theory methods and mechanistic models to address these questions in the context of spinal cord development. I will consider the two opposing morphogen signals that are integrated to specify the arrayed pattern of neural progenitor domains that later on give raise to different type of neurons. Based on the maximum likelihood estimation rule I will define decoding map that provides predictions for shifts in the target gene domains in mutants. The predictions will be validated using experimental data obtained from naïve chick neural plate explants and from embryos with altered ventral morphogen signaling. I will present a simple model of a gene regulatory network that integrates the two morphogen signals and is sufficient to recapitulate the observed shifts in the target domains. I will investigate to what extent the level of noise in the input signals affects precision of the resulting gene expression pattern. In the long-term, the contribution from the proposed basic research might be utilized in designing neuroregenerative therapies.

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