COMPUTATIONAL BIOLOGY WEBINAR @ IMSc

COMPUTATIONAL TACKLING OF BIOLOGICAL SYSTEMS: CIRCADIAN CLOCK AND HUMAN MICROBIOME

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A primary challenge in biology is to explain how complex phenotypes arise from individual molecules encoded in genes. Molecular interaction networks offer a key to understand how genotypes are translated into phenotypes. For example, sleep/wake cycles in animals are generated by molecular circuits of interacting genes and gene products, called circadian clocks. Circadian clocks are important for both animal and plant life as well. I will discuss how the molecular interactions for rhythmic protein turnover are related to a presumable driving force of the circadian clock machinery—the biosynthetic cost reduction. However, considering only genes in a given organism and its own molecular interactions may not be enough to understand the holistic picture of the organism's phenotypes. For example, our resident gut microbial community, or gut microbiome, provides us with a variety of biochemical capabilities not encoded in our genes. This human gut microbiome is linked not only to our health, but also to various disorders such as obesity, cancer, and diabetes. We constructed the literature-curated global interaction network of the human gut microbiome mediated by various chemicals. Our network framework shows promise for investigating complex microbe-microbe and host-microbe chemical cross-talk, and identifying disease-associated features.

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