



COMPUTATIONAL BIOLOGY WEBINAR @ IMSc

ROADMAPS OF INTERACTION BETWEEN THE CODING AND THE NONCODING RNA WORLD: ORCHESTRATING DISEASE BIOLOGY

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The causal factor that makes cancer easy to recur and metastasize is still an enigma to the scientific community. A subpopulation of cells named as cancer stem cells, within a tumor possess the capacity to self-renew and produce heterogeneous lineages of cancer cells that comprise the tumor. We are primarily interested in unearthing the molecular mechanisms and find the main players that deliver the stem cell its oncogenic potential. In our search for regulators, we came across non coding RNAs, which, once considered as mere junk have emerged to be one of the key players in maintaining both healthy and diseased condition of our system. Comprising of more than 98% of the human genome, they can be categorized into two types viz. small non coding RNAs like microRNAs (miRNAs), piwi interacting RNAs (piRNAs) and long non coding RNAs (lncRNAs). Their versatile regulatory role motivated us to delve deeper into their disposition and action, and all detailed information of our findings and analysis are now maintained in the form of two dedicated databases, LncRBase and piRNAQuest. Our interest also lies in their interacting coding RNA partners, the culmination of which is our noncoding RNA target prediction tools-miRTPred and LncRTPred, and we are working forward to bring about similar solutions for piRNAs in the future. Placing together all these information and connecting the dots, we hope to unravel some of the hidden roadmaps of interaction between the coding and the noncoding RNA world.

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