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Deciphering the metazoan regulatory code

Pr. Bart Deplancke
Laboratory of Systems Biology and Genetics, Institute of Bio-engineering and School of Life Sciences, EPFL, Switzerland

Differential gene expression is central to most fundamental biological processes, but little is still known about the composition and dynamic properties of the corresponding gene regulatory networks that control the expression of these genes. The core members of these regulatory networks are transcription factors (TFs) which function by integrating extra- and intracellular cues through protein-protein or protein-ligand interactions and translating these cues into gene expression output by binding to gene regulatory elements. One of the main goals of my Lab is to develop and integrate novel resources and both experimental and computational tools to generate gene-centered regulatory network models in *Drosophila melanogaster.* During this talk, I will present our latest efforts to enable automated protein-DNA interaction screens with *Drosophila* regulatory elements. In addition, I will discuss our recent results in using naturally occurring genetic variation in fly lines belonging to the *Drosophila* genetic reference panel to demarcate the genome into high-resolution regions of regulatory activity. Collectively, our results have already revealed central gene regulatory principles which may be relevant in other organisms including humans.