

## Abstract of Presentation

Presentation Title:

Inferring transcriptional regulatory networks with deep sequencing data.

Abstract :

With the aid of new deep sequencing technologies it is now possible to not only identify transcription start sites (TSSs) genome-wide at single base pair resolution in mammals, but also to quantify the expression of each individual TSS. I will present a newly developed computational methodology that predicts transcription factor binding sites (TFBSs) for over 200 mammalian regulatory motifs in proximal promoters genome-wide and models the expression dynamics of all individual TSSs in terms of the predicted TFBSs. In particular, the methodology infers time- and tissue-dependent activities of all regulatory motifs. I will illustrate the power of motif activity analysis by showing examples in which it is used to infer the key transcription factors that are driving gene expression changes:

- 1) involved in particular cellular differentiation processes.
- 2) that differentiate between normal and tumor tissues.
- 3) that occur in response to particular treatments.
- 4) that differentiate related tissues.