CPH Seminar in Precision Medicine

"Bayesian modeling and integration for NGS data analysis"

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Next-generation sequencing techniques have been widely used in cancer research to uncover molecular mechanisms underlying the development and progression of cancers. Multiple ChIP-seq and RNA-seq profiles can now be readily used to infer functional regulatory networks (FRNs). In this talk, I will present two computational approaches, (1) ChIP-BIT and (2) CRNET, to help analyze and integrate ChIP-seq and RNA-seq data for FRN identification. ChIP-BIT is first developed to reliably detect transcription factor binding sites (TFBSs) and their target genes. As a unique feature of ChIP-BIT, a Gaussian mixture model is used to capture both binding and background signals in sample data; background signals are modeled by a local Gaussian distribution that is accurately estimated from the input data. CRNET is then developed to integrate large-scale ChIP-seq and RNA-seq profiles for FRN identification. A novel two-stage Gibbs sampler is used to iteratively estimate hidden transcription factor activities and the posterior probabilities of binding events. A statistic measure that takes into account both regulation strength and regression error enables the sampling process of CRNET to converge much quickly, thus making CRNET very efficient for large-scale FRN inference.

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