Analysis of ChIP-Seq data

Abstract: The next-gen sequencing revolution has arrived. Nowhere is this more apparent than with human genome-wide ChIP studies, for example, to identify transcription factor binding sites, find regions of RNA Pol II activity, or to map histone modifications. From day 1, this was better and cheaper by next-gen sequencing than by the corresponding microarray assays (ChIP-chip). Naturally there is a need for novel analyses. In this talk, I will describe some existing solutions, work in progress and some of the challenges I see ahead in analyzing ChIP-Seq data.