Brief Summary of Gerstein Lab Research on ChIP-Seq and RNA-Seq as of Dec. 2015:

*Analytical tools for ChIP-Seq.* ChIP-Seq is a mainstream experimental method for genome-wide identification of transcription factor (TF) binding and chromatin modification sites and will be fundamental to characterizing the interactions of nuclear bodies with chromatin. The Gerstein lab developed PeakSeq (70)\cite{19122651}, a versatile tool for identification of TF binding sites and a standard peak calling program used by the ENCODE and modENCODE consortia for ChIP-Seq datasets (78)\cite{19122651}. More recently, we developed MUSIC, a peak caller that performs multiscale decomposition of ChIP signals to enable simultaneous and accurate detection of enrichment at a range of narrow and broad peak breadths (70, 80) \cite{22955619}. This tool is particularly applicable to studies of histone modifications and previously uncharacterized transcription factors, both of which may display both broad and punctate regions of enrichment.

*Analytical tools for RNA-Seq.* For RNA-Seq analysis, we have developed a range of tools that handle challenges in read quantification: RSEQtools, enabling expression quantification of annotated RNAs \cite{21134889}; tools that detect, store and query unannotated transcripts \cite{22251872, 21765801, 22955620, 18451266, 15539566, 20565764, 17567993}; and methods (e.g. incRNA) that predict and analyze novel ncRNAs, which may be discovered in the course of this project \cite{21177971}. We have used many of these tools to conduct large-scale analyses, particularly for the ENCODE and modENCODE consortia \cite{25164755, 21177976}.