Abstract:

Chromatin immunoprecipitation is used to enrich DNA sequences that are associated with a protein of interest, and is used to map those sequences to the genomic regions. Studying these DNA-protein binding regions provides an understanding of gene regulation and chromatin remodeling. However, some signals in fact represent no binding event and are known as false positives. This thesis discusses the main sources of false-positive signals that commonly arise during ChIP-seq analysis, and offers possible solutions on how to minimize or filter them.

Keywords: ChIP-seq, chromatin imunoprecipitation, quality control, data filtration