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Major focus of Sugano Lab is the integrated transcriptome analysis using various methods based on the next generation sequencers (NGS). These include RNA-sequence, genome-sequence, determination of the binding sites of a transcription factors, determination of genome wide histone modifications patterns (ChIP-seq), DNA methylation patterns, transcriptional start sites (TSS-seq), miRNA sequence and the determination of RNA half-life. Thus, Sugano Lab has huge stocks of NGS data that await in depth analysis. In this internship, we offer an opportunity to analyze NGS data, starting from ABC like finding copy number variation or 1 or 2 base mutations from genome-sequence or constructing expression profile from RNA-seq data. Eventually, more complex analysis, like finding fusion transcripts in cancer cells, can be done according to your research interest. Some experience in programming using a script language like, perl, python or ruby is preferred.