Abstract: The next-generation sequencing technology revolutionizes the genomic research by providing the capability of generating overwhelmingly large amount of data in a short period of time. However, the analysis of this type of data is in dire need of computational power, mathematics, statistics, and bioinformatics expertise. In this talk, I will first give a brief introduction to a maximization (or optimization) problem that I derived from our sequencing data analysis. Next, I will introduce the basic terminology of sequencing and discuss the underlying statistical method of the software SOAP (Li. et al. 2008) that we are using. Finally, I will present some preliminary results of our chrX exon sequencing data analysis and the maximization problem that was introduced at the beginning.