This short course will provide an overview of a few of the current knowledge-based pathway analysis approaches widely used in genomic research. It covers basic information on frequently used databases (i.e. gene ontology categories), as well as curated knowledge bases from scientific literature and the public domain. It also focuses on two commonly used statistical approaches (Hypergeometric/Fisher exact test and Kolmogorov Smirnov) in pathway analysis with a hint of theoretical illustration. In this course, we will introduce a few (publicly available/free access and license-based) applications which implement either of the two statistical approaches. In the end, we will touch on some questions about the pros and cons in the pathway analysis package(s) and explore ways to deal with such concerns. The goal is to provide the scientists at the institute with a solid understanding of the fundamental concepts behind commonly used analytical tools for pathway analysis in order to empower them to maximize the analysis of their data and enhance interpretation of their results.