This short course will provide an overview of several 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. This course will focus on two commonly used statistical approaches (Hypergeometric/Fisher exact test and Kolmogorov Smirnov) in pathway analysis with a hint of theoretical illustration. We will demonstrate the pathway analysis strategies with a few (publicly available/free access and license-based) applications; we will also touch on some questions about the pros and cons in the pathway analysis package(s) and explore ways to deal with such concerns. For the first time, the course will be offered in our computer training where attendees will be given the opportunity to have hands on practice on GSEA and IPA. , . 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.