This short course will provide an overview on current knowledge based pathway analysis widely used in genomic research. It covers the basic information on the available databases, i.e. gene ontology categories as well as well-curated knowledge base from the current scientific publication. It also focuses on two common statistical approaches (Hypergeometric/FET and Kolmogorov Smirnov) in pathway analysis with comfortable theoretical illustration. In the course, we will introduce a few commonly used (publicly free access and license based) applications, which implement either of the two statistical approaches. In the end, we will touch on some questions and concerns about the pros and cons in the pathway analysis package(s) and research proceedings to deal with such problems. Our goal is to facilitate the scientists at the institute with solid understanding of the concept behind commonly available analytical tools for the pathway analysis, so that our scientists will be able to choose the right knowledge base and approaches, and be able to interpret the analysis results.