Lipids are essential components of biological membranes and are regarded as an important form of storage energy. There is a convincing evidence that fatty acyl chains exert the maintenance of properly biological function. Understanding of fatty acid and lipid metabolisms expands the benefit to human applications. With the explosion of sequence information available to public domains, the field of bioinformatics is playing an increasingly considerable role in the study of both fundamental and applied biological processes. In the present work, we focus on the metabolic pathway of lipid biosynthesis using *Saccharomyces cerevisiae* as a model. Based on the available information of the complete genome sequences of *S. cerevisiae*, and knowledge of metabolic pathways, its lipid biosynthesis pathway was mapped.

In this work, the ORFs were collected from several databases such as SGD [http://genome-www.stanford.edu/Saccharomyces], MIPS [http://www.mips.biochem.mpg.de], GenBank [http://www.ncbi.nlm.nih.gov] for generating a catalog of the biochemical reactions of the lipid biosynthesis and related pathways. Metabolic pathways in KEGG were used as templates towards the metabolic network construction. Then the metabolic components are systemically connected. This information can be integrated to form the lipid biosynthesis pathway of *S. cerevisiae*.

A prototype derived will provide the possibility for making similar progress in other biochemical processes of other microorganisms and plants. Moreover, the systematic analysis of the reconstructed pathway of lipid biosynthesis will lead to the goal of strain improvement for production of desired compound.