Y. lipolytica, typically known as a non-conventional yeast, is a eukaryotic unicellular organism. With a genome of 7357 genes and 6472 coded proteins, this organism is classified in the hemiascomycetes class and dipodascaceae family. It has 6 chromosomes named Yali A to Yali F and their sizes vary between 2.3 to 4.2 Mb.

To completely understand this organism, it is necessary to isolate and make experiments for each gene either with known or unknown function. Unfortunately, *in vitro* experimentation could take too much time and resources to be carried out. It is in this context that an *in silico* model with the capacity to imitate the behavior of each enzymatic reaction is proposed.

We need to generate a new methodology based on the knowledge of stoichiometry and the metabolic requirements of the organism. This is to represent and analyze correctly each one of the enzymatic reactions of the optimal growth of the cell under specific conditions, its metabolic consumption, and the metabolic fluxes. However, it is necessary to make a more complex simulation to observe the changes produced in their enzymatic pathway by defined genetic modifications.

To be able to achieve this, the flux balance analysis (FBA) needs to be extended toward a more dynamic analysis that can optimize each individual reaction on the stoichiometric matrix during a specific period. Changing the stoichiometric equation to a differential reaction can give us the metabolic flux profile and the concentration of each metabolite in each second, hour, or day depending on the specification of the model .

This project focuses on developing a better GEM model on the *Yarrowia lipolytica*, one of the organisms that is proving to be one of the best models for developing and producing highly valuable industrial compounds. The focus on odd chain fatty acids and the propionate pathway is the key to produce compounds with medical, industrial, and fuel potential. The development of an industrial process using the *Yarrowia lipolytica* has the potential to be cleaner and highly efficient. The potential of this model to pinpoint which gene overexpression or deletion needs to be done to improve the production of the desired odd chain fatty acids can help a lot in improving the time necessary to develop an improved industrial-ready strain.

As it is possible to see in the results part, the propionate pathway was correctly included into the *Yarrowia lipolytica* model. Including also the stoichiometric equations for the production of margaric and Pentadecanoic acid, both which are our main objectives.