

# Project -proposal with Gregory

## **Aim 1:**

- We want to quantify how much the genetic background influences the essential genes on that background.

## **How are we going to accomplish our aim?**

- We are going to use the Satay dataset from Benoit to know the essential genes in the wild tpe background, and represent them in the genetic interaction network.
- We are going to compare that dataset with the “annotated” essential genes (synthetic lethals) of Bem1, Bem3 , Nrp1, and Bem2, to analyze the differences between them and the WT.
  - Venn diagram
  - GO terms relationships
- Based on the previous analysis , we want to visualize how the genetic networks changes across genetic backgrounds , looking at the essential/synthetic lethals genes.

## **Aim 2:**

- Use the mutants satay data , for the individual and double deleted to decipher the network reorganization when both deletions take place.
- Use this information to predict what happens with bem1bem3 double deletion,in terms of how the essential genes can change with respect individual backgrounds.

## **How are we going to achieve that goal?**

- By the application of machine learning on the existing datasets for satay, plus go terms.