Thesis structure comments

Contents

- Title: "*Exploring evolution using Saturated Transposon Analyis In Yeast*"
  - Comments:
    - The title does not convey the right picture of what you did in the thesis.
    - You should focus more on the GI part to understand a particular adaptive evolutionary pathway, like the one from Δ bem1 .
    - An alternative could be: "*Genome-wise quantification of genetic context influence on gene deletions in budding yeast*" **The case of the bem1-bem3 pair in the context of adaptive evolution**.

1. Introduction
    1. The Δbem1 adaptive evolutionary trajectory
    2. Genetic interactions in yeast
    3. State of the art (**of what??**)
        - here you can also put , state of start approaches to measure GI in yeast.
    4. SATAY as an alternative technique to compute GI
        - Description of the technique
        - why could it be a good candidate to quantify GI in yeast in a high-throughput manner.
    5. Introduction to the research problem
        - Intro of what we still dont know
        - The relevance of tackling that question to gain understanding in how biological networks do change during evolution.
    6. Research questions
    7. Hypotheses
    8. Goals
        - Experimental goals
        - Modelling goals
2. Materials & Methods
    1. Yeast strain construction
        - Construction of a bem1 bem3 strain
    2. SATAY
        1. Library formation
        2. DNA extraction
        3. DNA sequencing
            - DNA Digestion
            - DNA ligation
            - PCR

3. Media
4. OD measurements
    - nanodrop machine
5. Population growth assays
    - Biotek protocols
6. Data analysis
    - Population growth assays
    - SATAY library complexity
    - Access to the software

3. Model

    1. Current knowledge
        - Interactors of bem1
        - Interactors of bem3
        - Interaction type between bem1 and bem3 , when bem3 is knocked down after a bem1 deletion.
            - Change in fitness from population growth data from Δbem1 genotype to Δbem3Δbem1.
        - Interaction type between bem1 and bem3 , when bem1 is knocked down after a bem3 deletion.
            - Change in fitness from population growth data from Δbem3 genotype to Δbem3Δbem1.
    2. What is predicted to change after bem1 deletion in WT and in Δbem3 background.
        - focus on the genetic interactors from bem1 in both backgrounds
    3. What is predicted to change after bem3 deletion in WT and in Δbem1 background.
        - focus on the genetic interactors from bem3 in both backgrounds
    4. Expanding on previous systems to know which lethal deletions of Δbem3Δbem1 are not lethal in Δbem3
        - From Wessel results using ML on trying to predict gene essentiality using a different set of genes
        - Look at common observables that can be extrapolated to our system , like common go terms, common interactors , or functional enrichment of predicted genes in relation with the gene of interest.

4. Results

    1. Experimental results
        - Complexity of the satay library
        - Sequencing results
    2. Modelling results
        1. Prediction on what is the effect of bem1 deletion on a network that do not have bem3 , based on what is known in WT.
        2. Prediction of which type of genes are more prone to be SL in dbem1dbem3 background that are not in the single knockouts backgrounds.

5. Conclusion & Discussion

    - What do we learn after doing this research?
    - Do we accomplish what we proposed to do at the beginning?
    - How our findings align with our initial hypotheses?
    - Implications of the results for our new understanding on how biological networks do change during evolution.

6. Future research
    - What is still left and yet relevant to do?
7. References
8. Appendix
    - A Protocols
    - B Primer sequences
    - C Strains
    - D Python code