

# Feedback on Miniproject preliminary drafts

December 23, 2020

- **Firstly**, make sure that you have carefully read the report [guidelines](#); some of the drafts suggest that (those some) of you have not.
  - For example, some of you are planning to write a Methods section that is too *Literal* (e.g., a script-by-script account, or explaining that you plotted using ggplot, etc. ) - avoid doing this.
  - Another example is that many of you have not stated the question(s) that you want to address in at the end of the Introduction.
  - *If any of the points in the guidelines are not clear, please do ask questions about them in the teams Miniproject channel (or me directly).*
- Some of you are finding that Linear models fit better. This indicates that some more optimization of the NLLS fitting is needed. Linear models will fit well, but will not outperform nonlinear models (at least not substantially) across the board.
  - If sampling results in more convergence and fewer errors (like **singular gradient matrix** error), but poorer fits, then you are doing something wrong with the sampling (maybe bounding the parameters too much).
  - Maybe have a look at the [revised NLLS fitting Chapter](#) of TheMulQuaBio for further insights and explanations (look at the new Michaelis-Menten example).
- Not all of you outlined 3-4 figures and/or tables that you plan to show. Even if you do not have all the actual Figures/Tables, you should visualize/anticipate what you would like to show, and put in placeholders.
  - For example, a figure placeholder could be an empty plot with a [notional](#) caption and description of what that figure would explain).
- **Avoid two-column format for the report!**
- As I have mentioned before, you can get high (70+) marks either by:
  - Fitting lots of models (including multiple nonlinear ones) and making it a sophisticated model comparison exercise, OR,
  - Delving into/ Exploring the “nitty-gritties” of model fitting methodology (e.g., comparing NLLS fitting algorithms / methods, exploring the effect of sampling, comparing AIC vs BIC as metrics, etc), OR,
  - Doing a more limited model fitting exercise, but extracting biological meaning from the data using.
  - If you manage to do all three of these, amazing, but don’t overreach!
  - **BUT a lot of the “devil” will be in the writing. Irrespective of whether you fitted lots of models, explored fitting methodology, or extracted biological meaning, an aesthetically-pleasing, succinct, and coherent report (50% of the mark) will be necessary.**

Overall, I am really happy with the progress you all made! The outlines/drafts largely meet my expectations. **GOOD LUCK WITH FINISHING UP!**