Questions for Simon

* Best way to say we are essentially ignoring the time between observations (~30 days), as it’s so short? For modelling M and M section
* Figure 3 - Error bars represent the 95% confidence interval?
* Do I need to use the p-values from the emmeans contrast so they’re adjusted for multiple comparisons?
* For evaluation of interaction term and also main effects- Wald or F test?
  + *For a categorical predictor with more than 2 categories, we will first want to know if the predictor (IMI status) is significantly associated with the dependent variable (SCS) (i.e. F test). If this is the case, we will then want to compare the levels with each other (i.e. T tests). Two problems then arise:*
    - *1) Multiple comparison problem; we will want to adjust our P values ​​or our 95% CIs depending on the number of comparisons carried out.*
    - *2) The table with the regression coefficients reports the T test for each coefficient when compared to the reference level, but not between them.*
* ~~How to present 3-degree polynomial DIM term in model output table~~

1. In the a) SCS LSM estimates as function of bacterial species and DIM figures and the b) estimated SCS by IMI status at 91 DIM table (from which the figures are made), do the error bars (figure) and the upper and lower CL (table) represent the upper and lower 95% confidence interval? Sorry if I missed this, I tried to double check by combing through the code but it didn’t jump out at me.
2. Does the spatial exponential correlation structure you used (based off DIM) in the model account for both the correlation between milk samples collected on the same quarter, and for the variation of this correlation with the varying amount of time between sample collections? Just so I can be detailed enough describing it in the M and M :)
3. In order to determine if the interaction terms are significant in the model, we do an F-test (with significance set at p<=0.05); in order to determine if each staph. spp. group was different from the “no growth” group, we look at the t-test p-value, which is in the model output. Do I have this right? Tried to check myself by going through our notes from when you met with John and I, and the Epi module you sent a few years back but just wanted to make sure I’m saying the right thing for the manuscript…
4. If I wanted to present the output of the model in a table (below), the most appropriate value to put in the “p-value” column is the uncorrected p-value from the t-test and the model output, as we’re asking if each staph spp. group was different from the reference/no growth group. If I’m not making comparisons between staph. species groups, I don’t need to adjust the p-value for multiple comparisons with a Tukey test or anything, correct?