

Summer Bridge Program/Research Experience for Undergraduates  
STEM FYE program & Laboratory of Marine Genomics (RSMAS)  
Fifth Homework assignment

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1. Using bioinformatics tools (Mega X) create a phylogenetic tree showing the relationship between and among populations. Edit this tree and create a caption so it can be used in your poster and paper. **REMEMBER:** the point of this activity is not to increase the complexity of your figure, on the contrary, it is to make the figure understandable to the audience that will visit your poster or read your manuscript. If possible, decide on one tree for the entire group.
2. Do the identification information provided by nBlast and BOLD match? Are their confidence levels similar? If they are not similar, provide an explanation as of why. How confident are you about these identifications?
3. Using your Fst values (and other parameters, e.g.  $\Pi$ ) determine whether or not your **group** hypothesis was correct. *Explain your answers:* Remember, there are not necessarily right or wrong answers. The point of this question is for you to identify how does the factual findings correlate with the theoretical expectations of your **group**.
4. As a group, produce a write up for all the result obtained during the bioinformatics analysis of your data. This “results” paragraph must be included in your paper and your poster. The results section must include:
  - a. Identification confidence levels from nBlast and BOLD.
    - i. Include a chromatograph of sequencing as an example
  - b. Fst values
  - c.  $\Pi$  values
  - d. The tree produced in question 1.

**Do not make analysis in this section. Analysis are done in “discussion”**

5. As a group, use your answers for questions 2 and 3 and craft a draft “Discussion” Paragraph (minimum 250 words). This paragraph will be used for the paper and the poster (which is due next week). The discussion paragraph must include the following information:
  - a. What does your findings (Fst,  $\Pi$ ) say about your **group** hypothesys (Question 2)
  - b. What is your analysis of the coefficient of confidence for your identification using bold and nBlast, how sure are you that those sequences belong to your organisms?
  - c. End the paragraph by stating what would be the next step in the research.
    - i. What other things would need to be investigated
    - ii. What questions remained unanswered
    - iii. What new questions arose
    - iv. What is the future of this line of research (mention ecosystem management, for instance).