[19sp]:

* (hanap): simplest\_greatest\_ape\_tree test instructions say “it is easy to write test cases for the new version” — and then we provide 2 tests for them. can we make it clear that we don’t expect them to write further tests?
* (Placeholder for todos added from Slack)

[18fa]:

* Make sure rubric items don’t overlap with provided tests
  + first acids\_of\_helix test fulfills “No end codon, run out of triplets”
  + first helix\_of\_tree and unlabel\_tree tests fulfill multi-level
  + DH: Rubrics needs to remove multi-level from the
* ~~Instructions for “acids\_of\_helix” confusing, rephrase “in the latter case”~~
  + ~~“Stop decoding when either (a) we run out of triplets or (b) we encounter one of the triplets encoding the END acid ([A; T; T], [A; C; T], or [A; T; C]).~~ **~~In the latter case, the END marker should NOT be included in the output acid list~~**~~.”~~
    - ~~Makes it seem like if we run out of triplets (the former case), the END marker~~ *~~should~~* ~~be inserted in the output~~
* Improve tests for unlabel\_tree
  + nick corona: “for hw02 one of my recitation students wrote unlabel\_tree such that when it handles a leaf it only unlabels it if it has a helix of length 1 (she handles nodes just fine and made a wildcard case for leaves with longer helices, in which case it returns Leaf [ ]). She still passed all of the submission tests, so perhaps the tests don't have any helices of length > 1 in their leaves?”

From Fall 2017:

~~[BD]: uncommenting print lines —> prints answers HIGHER UP in terminal but it gets cut off by the tests running below - if this assignment is used in Codio again, add a clarifying comment in the code itself: see https://piazza.com/class/j6dr9a61zsv5vx?cid=163~~

--- various ---

**HW02 -**

* ~~JC: Clarify why printing out in dna.exe the greater apes will look different than what is visually displayed on the website and that lesser apes should be coded based on the website picture.~~
* ~~JC: We always get a question on height vs depth for a tree~~ (Note: height and depth is not mentioned in the directions)
* ~~PP: (add\_ancestor\_labels and simplest\_tree) Behavior of these functions need to be better defined when the outputted tree is a complete inversion of the desired tree (and other similar cases). Also, I think we should reconsider whether it should be a requirement that simplest\_tree returns the first tree encountered in the case where multiple trees have the same complexity.~~
  + Fixed on the grading server. After discussing with Stephanie, it was decided that the added complexity of explaining why we need to perform a special kind of equality here is not worth the benefit of fixing the bug in the hw stub (since no one has come across it in the wild as far as we know).
* ~~JC: Clarify that decreasing\_similarity should be strictly decreasing~~
* ~~JC: Clarify that you must hard-code the list for question\_most\_like\_human, either by including the words “hard-code” in the description or by making it of type helix list instead of () -> helix list~~
* ~~JC: Explicitly mention that you can run a failing test with run\_failing\_test, as currently there is only an example of this, and there have been a lot of questions about it~~
* ~~JC: acids\_of\_helix: add test for add test for end codon before start codon (should start anyway)~~
* ~~JC: test for all 3 end codons in acid\_of\_list~~
* LM: The thing about grading on the "Multi-Element, True  
  (not question\_most\_like\_human ())" test is that the unit tests are technically logically complete without the student including that test. So, there are students who are writing really good tests but not including that one (since they see a logically equivalent one is already there) and I’m docking points. Chill, not chill?