Week of May 11

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1 Goals for the Week

1. Install LaTeX for these notes
2. Get access to the repository and Gauley
3. Read through all of Logan's previous notes
4. Brush up on R by looking through the user manual
5. Begin looking through the code on the repository
6. Create a repository for these notes

2 Progress/Notes

2.1 Install LaTeX for these notes

1. LaTeXhas been installed and tested

2.2 Get access to the repository and Gauley

1. With Dr. Gilchrist, I was able to get access to both repositories (the one with Logan's notes and the one containing CUBfits). I also was granted an account on Gauley and Newton.

2.3 Read through all of Logan's previous notes

1. I should check out his script repository later, when I need to begin testing this. He says it's located at https://github.com/ozway/cubmisc

2. After reading through all the notes, it appears that his code is close to completion. There are a few things that he mentioned wanting to do, and I'm not sure if he got around to those.

3. He mentions moving the code to C from R, but he feels that it would be more work than it is worth.

4. He also mentions debugging his genome creation process by using a genome that is totally dominated by mutation bias, and see if the genome is correctly created across all phi values.

5. He also mentions changing some divisions to subtractions using logarithm rules, since that would be quicker.

6. Just some terminology that I need to remember:

   (a) CBU – codon usage bias

   (b) η – cost-benefit ratio of protein synthesis

   (c) ϕ – protein synthesis rate

   (d) N_e ??

   (e) ROC – ribosome overhead costs

   (f) NSE ??

(g) ORFs – Open Reading Frames

(h) q – proportional decline in fitness per ATP wasted per unit time

(i) ΔM – mutation bias

(j) $E(\phi)$ – expected protein synthesis rate, should be 1 if time units are defined correctly

2.4 Read the R Manual

1. Read the first 3 chapters

2.5 Create a repository for these notes

1. Repository has been created at `https://github.com/jeremyrogers/EEB`