**Modelling Gene Expression and Attenuation in Bacteriophage PhiX-174**

\*completed, ~in progress, ^future

**AIM 1: Recapitulate Gene Expression patterns in wildtype PhiX-174**

1. \*Created script to parse genbank file, extract genomic coordinates, and linearize circular genome (parsing\_genbank)

1. \*Created script to run pinetree using linearized genomic coordinates; manually toggled parameter values (phiX174\_optimization)

c) \*Implement Hill Climbing algorithm to optimize 1 parameter (mini\_optimization)

d) ~repeat Hill Climbing to optimize each parameter individually

e) ^optimize multiple parameters w/ step idea

**AIM 2: Capture change in viral fitness after genomic modularization**

1. ~write script that calculates fitness from transcript levels using stoichiometric relationships (Leuven 2020)

1. ^linearize genome & remove overlapping features (Wright 2020) and find change in fitness.

**~~AIM 3: Capture change in viral fitness after whole codon deoptimization~~**

1. ~~^Extract amino acid sequences for each gene from genbank file~~
2. ~~^Play with transcription rates/weights applied to the genes to mimic deoptimized codon usage~~