**AGRO-932 Homework 2** (100 points)

Due Tuesday, March 11, 2025

Format: submit online via Canvas by providing your GitHub link

1. Use the GitHub repository from Homework 1 (*hw1*) to host Homework 2 (*hw2*). If you no longer have access to your *hw1* repository, it is acceptable to create a new repository for *hw2*. However, the repository should remain lightweight and should not be nested within another repository. Address my suggestions/comments from *hw1* in your updated repository—this includes enhancing your README, creating a proper directory structure if you haven't done so, reorganizing *hw1* into a separate subfolder, or adopting a numerical naming system, etc. *(30 pts)*

2. Follow the process outlined in “*profiling/3.lab6”* to manually compute Fst for the two populations you downloaded in *hw1*. Document the process step by step. If mapping is too time-consuming, consider using only a portion of a chromosome for the analysis. Note that you must use your real-world downloaded data—simulated data is not acceptable for this homework. *(30 pts)*

3. Provide your Slurm script in the “*slurm-script/*” folder. Use “.gitignore” to exclude Slurm log files and files in “largedata/” folder from being tracked in the repository. Provide the path, but I wouldn’t visit these files. *(20 pts)*

4. Finally, output your final results in a git tracked folder, i.e., “cache/”, visualize your Fst results using a histogram to show the distribution and a chromosome-wide view to display signals across chromosomes. Or other creative ways to visualize the results. Again, this needs to be fully documented. *(20 pts)*