* Sync local computer and remote server
  + rsync -azv /Users/simontye/Documents/Research/Projects/Zygoptera/2020\_Zygoptera/ simontye@razor.uark.edu:/storage/simontye/2020\_Zygoptera
* Step 1: Obtain sequences (GenBank)
  + Downloaded all COI genes for Odonata from GenBank
    - Complete files (11,935 individuals)
      * odonata\_coi\_20200328.gff3
      * odonata\_coi\_20200328.fasta
    - Test files (10 individuals)
      * test\_coi\_20200328.gff3
      * test\_coi\_20200328.fasta
  + To do:
    - Write code that automatically downloads GenBank data so that the workflow will work for future updates
* Step 2: Align sequences (MUSCLE)
  + Python (Attempt 1)
    - Working draft using Bio methods
      * 2020\_Zygoptera.ipynb
  + Bash (Attempt 2; test files)
    - Local computer
      * Move 64-bit muscle and iqtree programs to ~/local/src/programs
      * Change PATH in .bash\_profile to include the new programs folder
        + PATH=$PATH:$HOME/local/src/programs
        + export PATH
      * Change file permissions
        + chmod +x ~/local/src/programs/muscle
        + chmod +x ~/local/src/programs/iqtree
      * Change directory to 2020\_Zygoptera
        + zygo
      * Run muscle
        + muscle -in test\_coi\_20200328.fasta -out test\_coi\_20200328.phy
      * Run iqtree
        + iqtree -s test\_coi\_20200328.phy
      * Open .phy.treefile in FigTree
  + Bash (Attempt 3; test files)
    - Razor cluster
      * Run muscle; no iqtree on razor
        + test\_coi.pbs
        + test\_coi.sh
  + Bash (Attempt 4; complete files)
    - Local computer
      * Run muscle (fastest interation settings)
        + muscle -in odonata\_coi\_20200328.fasta -out odonata\_coi\_20200328.phy -maxiters 1 -diags1 -sv -distance kbit20\_3
        + Running now
      * Run iqtree
        + Next up
* To do list
  + Wait and see which of coi, coi2, and coi3 finishes with the given wall times