* PCR\_TI.py and TC\_TI.py can be used to find the tolerance interval for PCR and TC thermal runs respectively.
  + Both scripts are dependent on parsTxt.py to parse out the thermocouple data from the DAVE .txt file.
  + PCR\_TI.py reads files from the “dataPCR” folder and TC\_TI.py reads from the “dataTC” folder.
* PCR\_TI.py has two functions: “denature” and “anneal”. Call “denature” to analyze denature data and “anneal” for anneal data.
* Both scripts print the tolerance interval and confidence interval for each run in the data folder and whether it would pass the given criteria. It also plots the TI and CI to visually illustrate if the run passes criteria.
* PCR\_rampRate.py can be used to determine the ramp rate of heating and cooling while cycling the PCR stage.
  + This script is dependent on parsTxt.py to parse the required data and it pulls the desired files from the “dataPCR” folder.
* Multiple files can be analyzed simultaneously.
* Within the scripts, the following variables are defined as:
  + “instListShort” is a list of instruments that are in the “dataPCR” or “dataTC” folder.
  + “replicate” is the number of runs on each instrument (should generally be 1).
  + “alpha” is the significance level, or 1-confidence level (for 95% confidence, α=0.05).
  + “p” is the reliability, or what percentage of all data points that are within the tolerance interval (p=0.90 for 90% reliability).
  + “deviationCrit” is the acceptance criteria (1.5 for PCR, 2.5 for TC).
  + “heatRRlimit” is the minimum heating ramp rate.
  + “coolRRlimit” is the minimum cooling ramp rate.

INSTRUCTIONS

* The .txt file can be produced using the DAVE tab in RCade.
  1. Promptly after the run has finished, select “console”.
  2. In the text box under “Output File Name” type the desired name of the file. Generally, the naming convention is as follows: “unit\_thermocouple\_date\_run#” (ex: Adv13\_w86\_230216\_Run1).
  3. Select “Read Console” then “Write Log to File”.
  4. This file can then be moved to the data folder.
* After moving the desired txt file to the data folder, open the script for the desired analysis.
  1. In the “instListShort” list, include all instruments in alphanumerical order as they appear in the data folder when sorted by “Name”.
  2. If there are multiple files for each instrument, change “replicate” to the number of runs of each instrument.
  3. All other variables should remain unchanged.
  4. Ensure that either the anneal or denature function is called at the end of the script.
  5. Run the script and record the desired data.
* For PCR\_TI and TC\_TI, the run passes if the tolerance interval is completely enclosed by the acceptance criteria, 1.5 and 2.5 respectively.
* For PCR\_rampRate, the run passes if the entire tolerance interval is greater than the acceptance criteria.