1. In the folder summer programming, there are 3 programs that were used to generate the initial database
   1. Writing sequence and known polymorphisms updated (all sheets)
   2. Write known pathogenic mutations from mitomap (all sheets) (working)
      1. The program doesn’t catch insertion mutation so they have to be manually entered (7471)
      2. Also doesn’t catch deletions listed as “:” (3271 and 15944)
   3. Write all polymorphisms from mtDB (all sheets)
2. Run the “Alignment inserter without addition and only polymorphic transition scoring” program in the folder Alignment and that will insert data from the first three sheets into the last three as appropriate.
   1. If a new mutation is found that is pathogenic it needs to be inserted into the large pathogenic database sheet as well as individually entered into the appropriate sheet for each tRNA and then the program needs to be run again
3. The “Modifier for addition of conservation score” will add the conservation score
   1. It is found in the Conservation test folder and it takes the file “tRNA database alignment test” and adds the conservation score it it
   2. NOTE: for this program to work, the program “page reading” must be run first so that the data is in the memory to be used for insertion
4. Use “alignment analysis for all tRNA” to look at the windows of interest for all tRNA
5. Use “Mapping score to tRNA structure” to map scores to tRNA structure
6. Run prediction testing and prediction testing appended to get prediction data