Rice iGEM team, 2018

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Software GUI usage instructions

1. Download the entire folder called “Rice iGEM 2018 Orthogonal Algorithm” from GitHub.
2. Open the file orthoriboalgorithm.py in the IDE of your choice (e.g., PyCharm, Atom, etc.) Make sure you have Anaconda 3 installed.
3. Run the code. A separate application (our GUI) should open in a few seconds.
4. Ensure that Vienna RNA is installed and is in the same folder as orthoriboalgorithm.py
5. Collect the following inputs for the algorithm:
   1. The name of the CDS file for the organism (e.g., EColiCDS.txt). If the bacteria has an extra plasmid CDS file, just grab the one containing information about the chromosomal sequences.
      1. The CDS file must be in .txt format and stored in the same folder on your computer as orthoriboalgorithm.py
   2. The name of the genome file for the same organism (e.g., EColiGenome.txt)
      1. The genome file must be in .txt format and stored in the same folder on your computer as orthoriboalgorithm.py.
      2. Delete the introduction text and only keep the sequence in the file.
   3. The name of the organism (e.g., E. coli)
   4. The start and ending indices of the 16s rRNA, both positive integers.
      1. These can be obtained from resources such as https://biocyc.org/
   5. The number of threads to generate to process the program, a positive integer.
      1. Increasing the number of threads for parallel processing generally decreases program run times.
      2. Around 4-8 threads are recommended for moderate to powerful computers. Using greater than 8 threads is not recommended and could lead to the CPU operating at 100% for long periods of time along with increased computer temperatures, and possible computer damage.
6. Type the inputs into the GUI, and click “Start Algorithm”.
7. The algorithm generally takes 1-2 hours to complete on a 2.8 GHz CPU powered computed
8. The output will be displayed in the blue output box.