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Biology 131
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Locating OriCs within a Genome

URL: https://repl.it/@jademello/Independent-Project

Motivation:

    I was motived to take on this project, because I found the discussion of skew diagrams in class interesting. Moreover, when such an independent project was presented as a possibility, I immediately started trying to think of a way to solve it. Lastly, it has major implications for helping scientists address a real-life problem: finding the location of OriCs within a given genome after that genome has been sequenced.

Data Formatting:

    Originally, the *S. solfataricus* genome was obtained from NCBI. However, this genome sequence proved too long to work with. So, three toy sequences were made by myself to be used as th

The results showed that it is possible to predict possible OriCs, at least within the toy sequences. That being, given the somewhat arbitrary inputs for backrange and skewdrop, this program can successfully identify what would visually appear on the corresponding skew diagram to be a valley representing an OriC (Fig. 1A, Fig. 1B). However, given these predetermined parameters, there is some limit to size of the valley that can be detected. This is shown with the small valley just before the 200th nucleotide in Figure 1B and at the start of the sequence in Figure 1C.

Since the toy sequences 1 and 2 are vaguely mimic actual genomes, the assumption is that this program could potentially identify actual OriCs. Nevertheless, it would take a long time to complete a single run. Therefore, further tuning of the program would be necessary before applying it to a full-sized genome.