to 0, then all of the exons would be shifted back by the length of the first exon, reducing the number of exons overall and displacing their location in the genomic sequence.

Another noteworthy change is the rather different transcribe() function in my project. Besides adjusting it to take the dna strand type as an argument—and transform the exon positions accordingly—I also needed to add an argument for the mRNA's coding sequence location. This was something of a sticking point in the creation of this project. Despite verifying my computed exons with NCBI, the website I had pulled the original genome from, my translate function kept returning an incorrect (and lengthened) peptide chain. I tried quite a few different things to troubleshoot—computing the exon locations differently, using a different database, transcribing the complement st

evolutionary truth 6