* Hey! So I noticed that all my ACM emails were in the trash and I just noticed it now so I do not have the code for this coding challenge but I will be walking through how I would solve this problem.
* As we can see, each gene contains a name , locus-tag and reference number
* The important way to distinguish between these genomes is the locus. (Classify them based on location)
* Next to source there is a number that for example shows (1..2766). This shows the number of base pairs that are occupied by this gene
* When we map the circle, the one with the most base pairs will have a thicker part of the circle.
* Firstly, I would come up with a TXT file with the base pairs and the name of the genome.
* Then I would come up with a scale for this circle. For this project I think we can dp 1- 3000 because that’s the max number of base pairs
* I would do this program in python, so I would start by drawing a circle to this scale.
* I am not quite sure how I can write code that matches each one of these genes with that particular base pair sequence so I would love to learn ☺