I started by going over with Bryan what I discussed with Jing and Alex yesterday. Then I made a function in python that can convert the wig file into a dictionary mapping the nucleotide number to what letter it is and how many reads it has.

Now I will look into finding a way to turn a HashMap into a string and then back into a HashMap for the LoadAndSave for the Optimizer functions.

I had to create my own way of parsing the HashMap string. This method varied slightly between what the HashMaps contained. I also had to do this for ArrayLists.

I showed Jing the function that makes dictionaries from the wig files. I also added a function that complements the value stored if we are looking at the antisense strand. I am still not sure if we need to reverse it or not.

After many hours of work I think I was able to get the new version of optimizer working. Including the load function. I will try running it for nor up to 10 gates this weekend. If it appears successful, I will work on the ReadMe. And a function to delete the extra files when finished.

Note. You do not want to run this on a cloud that automatically syncs. It will cause lots of problems.

I also need to add a line of code that deletes all the saved work after it finishes. But before deleting the saved work for NOR, try doing a replace all in the file to switch . with @ and see if I can find all 256 with NAND.