Purpose of programs:

1- Yah\_BinGenerator.py

*It takes the sequence and cut it into small bins according to user request.*

2- Yah\_main\_M\_cat.py *and* Yahya\_sample\_pLine.py:

*Align the FASTA file to reference genome and sort and merge the output SAM file.*

*It also runs Yah*\_M\_CAT\_Final.py *as a pip line command.*

3- Yah\_M\_CAT\_Final.py:

*Take merged sorted SAM file and calculate the BIN hit generated for reference genome and tells which organism belongs to which genome.*

*It implements Tax score and 5%rule and other method to do that.*

Files Descriptions:

bowtie2SamtoolsToAlignSortMerg:

It is a word document file. It describes how to align sort and merge manually using the command line.

The other files:

*Either sample input file to the programs or sample output.*