**List of Functions Used in Ortho\_Detection V-1\_Old**

1. **GetMatrixNumber()**

Receive the info about matrix Number and Return the Matrix name Like "\n1. BLOSUM45\n2. BLOSUM62\n3. BLOSUM82\n4. Quit"

1. **GetQuerySequence(genome):**

Receive genome Fastaq File and return gene\_sequence\_list

1. **WriteQuery(query, Parallel\_num)**
2. **RunBlast(subject, Parallel\_num)**
3. **Get\_Same\_Species\_Forward\_Best\_Hit(blastp\_score)**
4. **GetForwardBesthit(blastp\_score)**
5. **DivisionParallelQuery(queryV,query\_division\_value, cpu\_count, queryV\_len)**
6. **RunParallelQuery(species\_of\_query , species\_of\_subject , queryV, parallel\_num)**
7. **Oneway\_Threshold\_Best\_hit(mode)**
8. **Backward\_Best\_Hit(args)**
9. **Search\_Equal\_BBH\_Data(target\_A)**
10. **Search\_Unequal\_BBH\_Data(target\_B)**
11. **Matching\_BBH(target)**
12. **Generating\_Matrix\_Clustering\_Ortholog(element\_set, bar)**
13. **Parallel\_MCL(score\_matrix)**
14. **MCL(score\_matrix)**
15. **Clustering(row\_data, col\_data, score\_matrix)**
16. **Parallel\_Matrix\_Multiplication\_Using\_Numpy(data)**
17. **Parallel\_Matrix\_Power\_Using\_Numpy(matrix\_element)**
18. **Parallel\_Matrix\_Divide\_Using\_Numpy(data)**
19. **Read\_Species\_List(pr=0)**
20. **Del\_File(path, file)**
21. **Check\_File(File)**
22. **Read\_Equal\_BBH(path)**
23. **Read\_Unequal\_BBH(path)**
24. **Read\_species\_List()**

**Blastp\_score is output file produced by runblast()**

**Blastp\_score = RunBlast(selected\_species\_dic[Species\_of\_object, parallel\_num]**

**Parallel\_num is number of CPU**