**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~~**

**#Steps of Program to run**

1. **Read\_Species\_List(pr =1) Run first and return 3 values**
2. **GetMatrixNumber() 🡪 blastp\_matrix**
3. **Check\_file(Cluster\_out) # Cluster\_out = command\_options.Cluster\_out**
4. **Del\_File(Score\_file, “\*”) # Score\_File = command\_options.Score\_file**
5. **Starting Log file Write**
6. **Backward\_best\_hit\_work\_list = Oneway\_Threshold\_Best\_Hit(mode) # mode = command\_options.mode**
7. **Read\_Equal\_BBH(Score\_file+selected\_species\_dic[i]+”\_”+selected\_specied\_dic[k])**
8. **Read\_unequal\_BBH(Score\_file+selected\_species\_dic[i]+”\_”+selected\_species\_dic[k])**
9. **Matchin\_BBH(unequal\_RBH\_element)**
10. **Generating\_Matrix\_Clustering\_Ortholog(data, bar)**

**## variable Name with Running Process**

1. **Mode:. Is user input to select mode among 3 that is Blastp , Blastp Using precalculated data and Clustering**
2. **Second Variable is to select Name of Genome to analyze (Suppose Only one Selected)**

**Genome\_name selected is passed to selected\_number and converted to sorted set and also program exit if input greater than number of Genome available**

1. **Blastp\_matrix = GetMatrix() Function run and Output is “BLOSUM45” , “BLOSUM62” or “BLOSUM” default is BLOSUM62**

**BLOSUM80 is used for closely related alignment databases, BLOSUM45 is used for more distantly related alignments BLOSUM62 is the Matrix built using sequences with more than 62 % Similarity (Sequences with >= 62 %identically were clustered. Note BLOSUM62 is the default matrix for protein BLAST. Experimentation has shown that the BLOSUM-62 matrix is among the best for detecting most weak protein similarities.**