**Practical 3**

**Sanger Sequence Analysis by AliView**

1. Download and install FinchTV to visualize the Sanger results
2. Use Finch TV to clean the sequences
3. Use AliView to Align the sequences and create final merged sequence
4. BLAST and identification of best hits.

Download FinchTV from :

For windows:

<https://digitalworldbiology.com/sites/default/files/Basic%20page/upfiles/Windows_FinchTV_1_4_0.zip>

For MacOS

<https://digitalworldbiology.com/sites/default/files/Basic%20page/upfiles/MacOSX_FinchTV.zip>

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **S.N.** | **Query information** | **Blast Hit Information** | | | | |
| **Sequence ID** | **Query Length** | **Query Cover%\*** | **Identity%\*** | **Scientific Name** | **Species Hits with Accessions No** |
| 1 | PQ1 | 1492 | 100 | 99.85 | *Zeugodacus tau* | MH900081 (*Zeugodacus tau*),  MT121257 (*Zeugodacus tau*),  NC\_027290 (*Bactrocera tau*) |
| 2 | PQ2 |  | 100 |  |  |  |
| 3 | PQ3 |  |  |  |  |  |
| 4 | PQ4 |  |  |  |  |  |
| 5 | PQ5 |  |  |  |  |  |
| 6 | PQ6 |  |  |  |  |  |
| 7 | PQ7 |  |  |  |  |  |
| 8 | PQ8 |  |  |  |  |  |
| 9 | PQ9 |  |  |  |  |  |
| 10 | PQ10 |  |  |  |  |  |
| 11 | PQ11 |  |  |  |  |  |