

# Test run

url: <https://dongzhang0725.github.io/dongzhang0725.github.io/example/>

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# 1. PhyloSuite installation

Please see <https://dongzhang0725.github.io/dongzhang0725.github.io/installation/>.

## 2. Install plugins

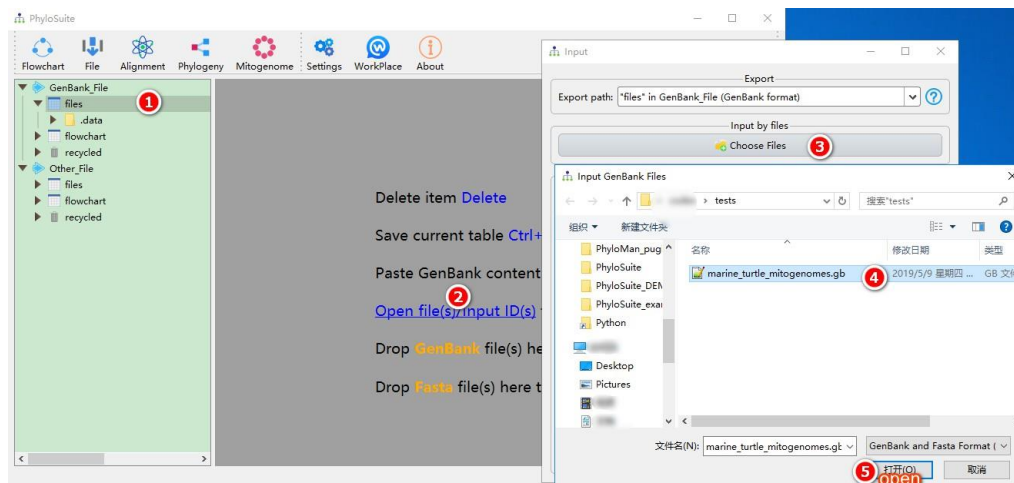
Please see <https://dongzhang0725.github.io/dongzhang0725.github.io/PhyloSuite-demo/how-to-configure-plugins/>.

## 3. Run the test

Here I use 31 marine turtle mitogenomes as an example. For the original paper see <https://www.sciencedirect.com/science/article/pii/S1055790312002242#t0005>.

### 3.1 Import mitogenomes

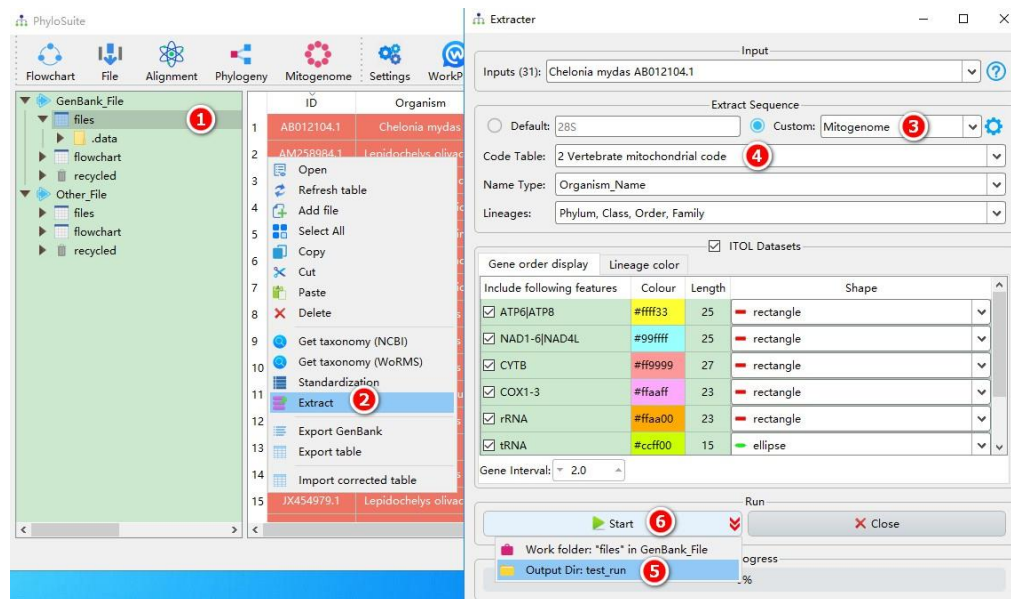
1. Select any of the work folders (here I chose **files**);
2. Click **Open file(s)/Input ID(s)** to open the input window;
3. Click **Choose Files** in the **Input by files** box;
4. Go to PhyloSuite root folder, open the **tests** folder, then choose **marine\_turtle\_mitogenomes.gb**;
5. Click **Open** to import.



### 3.2 Gene extraction

1. In the main interface, choose **files** work folder, select all sequences;
2. Right-click and choose **Extract** to enter the extraction interface;
3. Select the predefined **Mitogenome** as the sequence type;

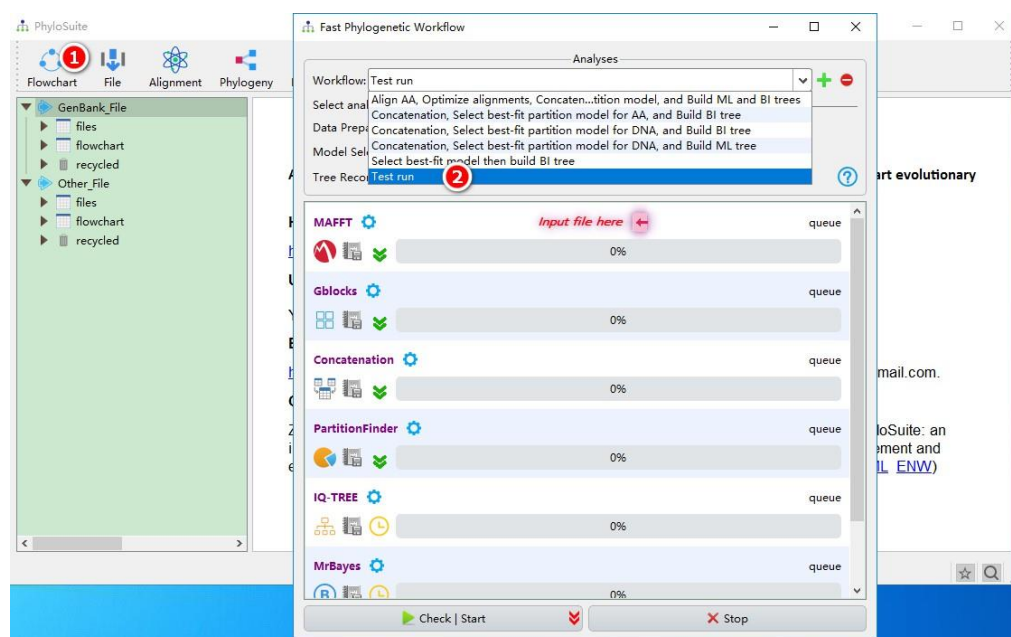
4. Select **2 Vertebrate mitochondrial code**;
5. Click to rename the output dir name as **test\_run**;
6. Click **Start** to extract.



## 3.3 Phylogenetic workflow

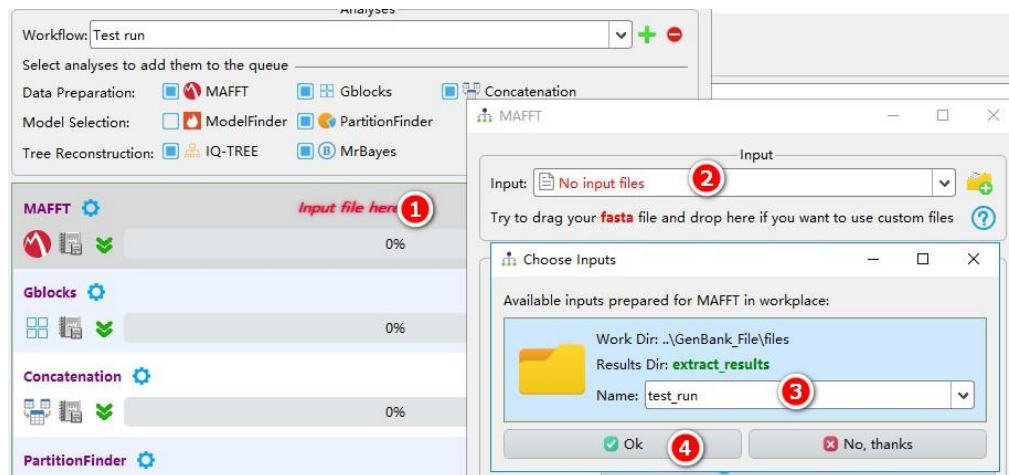
### 3.3.1 Choose workflow

1. Click **Flowchart** in the menu bar;
2. Choose **Test run** in the **Workflow** menu;

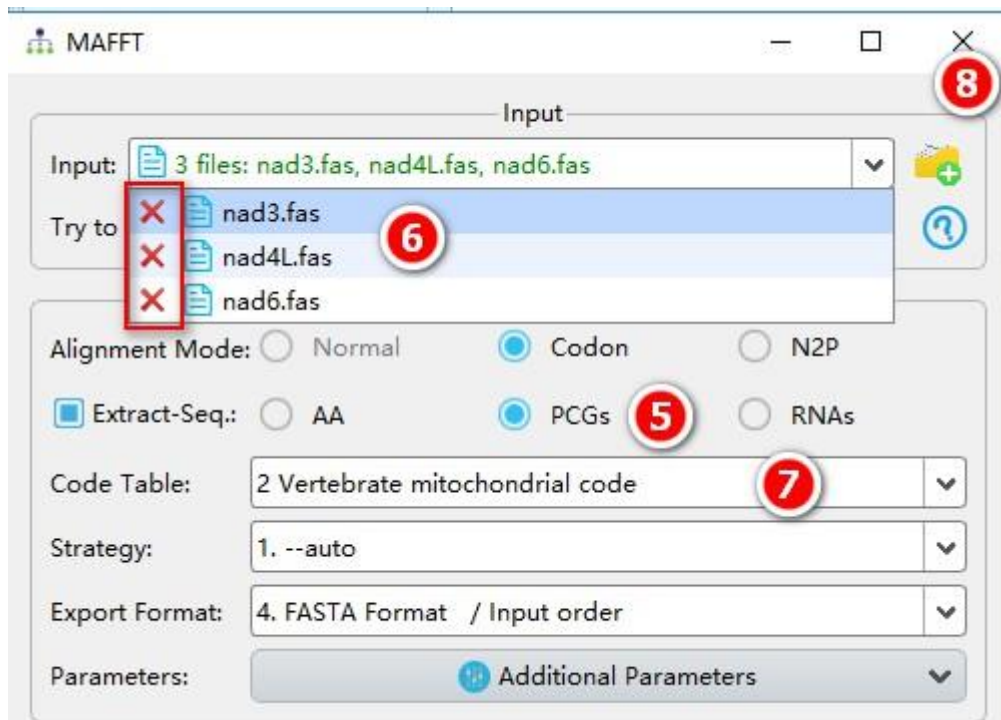


### 3.3.2 Input file and parameter setting

1. Only the first program needs an input file, so click the red **Input file here** to open the MAFFT program window;
2. Click the file input box of MAFFT to view the automatically prepared input files (you may opt to use a different file via **No, thanks**);
3. Select the results that you extracted in section 3.2 (**test\_run** in **extract\_results**);
4. Click **Ok** to import.

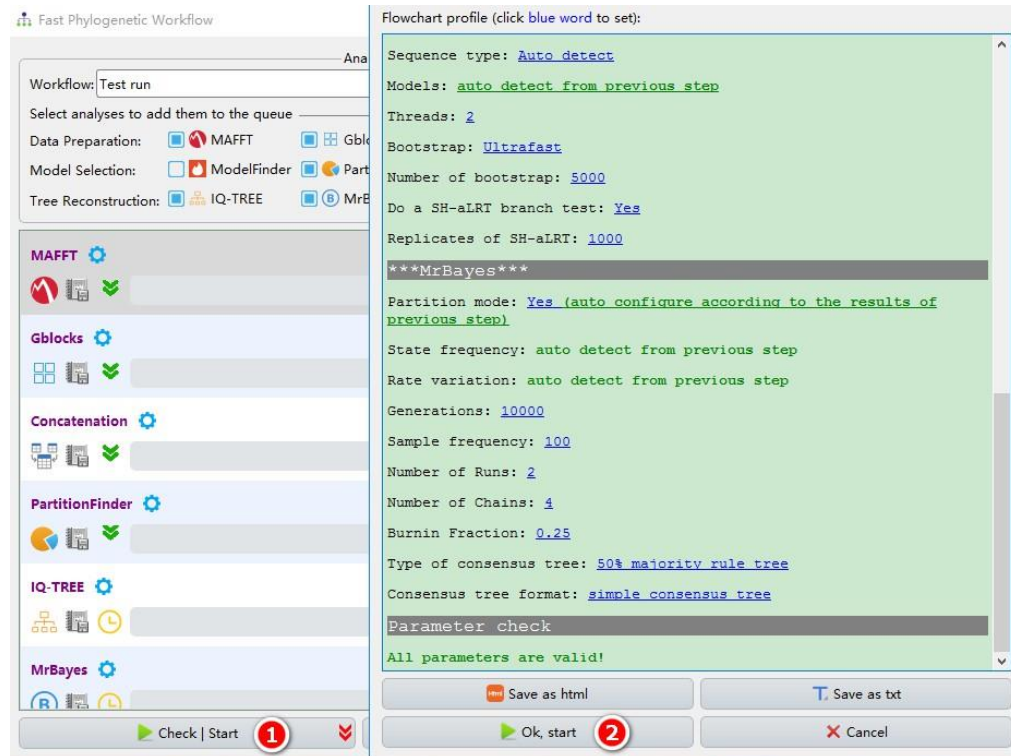


5. Tick **Extract-Seq** option and then tick **PCGs**, and the nucleotide sequences of protein-coding genes will be imported automatically;
6. To speed up the test, you may pop-up the files menu and remove all files but 'nad3.fas', 'nad4L.fas' and 'nad6.fas' files (using the **remove button** [red x sign]);
7. Select **2 Vertebrate mitochondrial code**;
8. Just close the window to save the imported files and parameters.



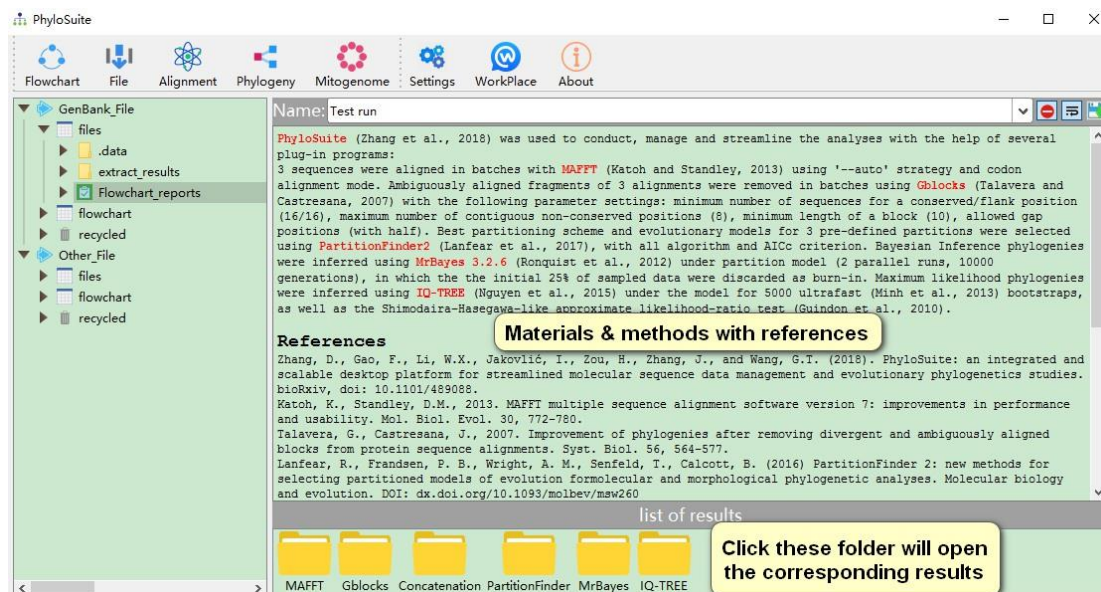
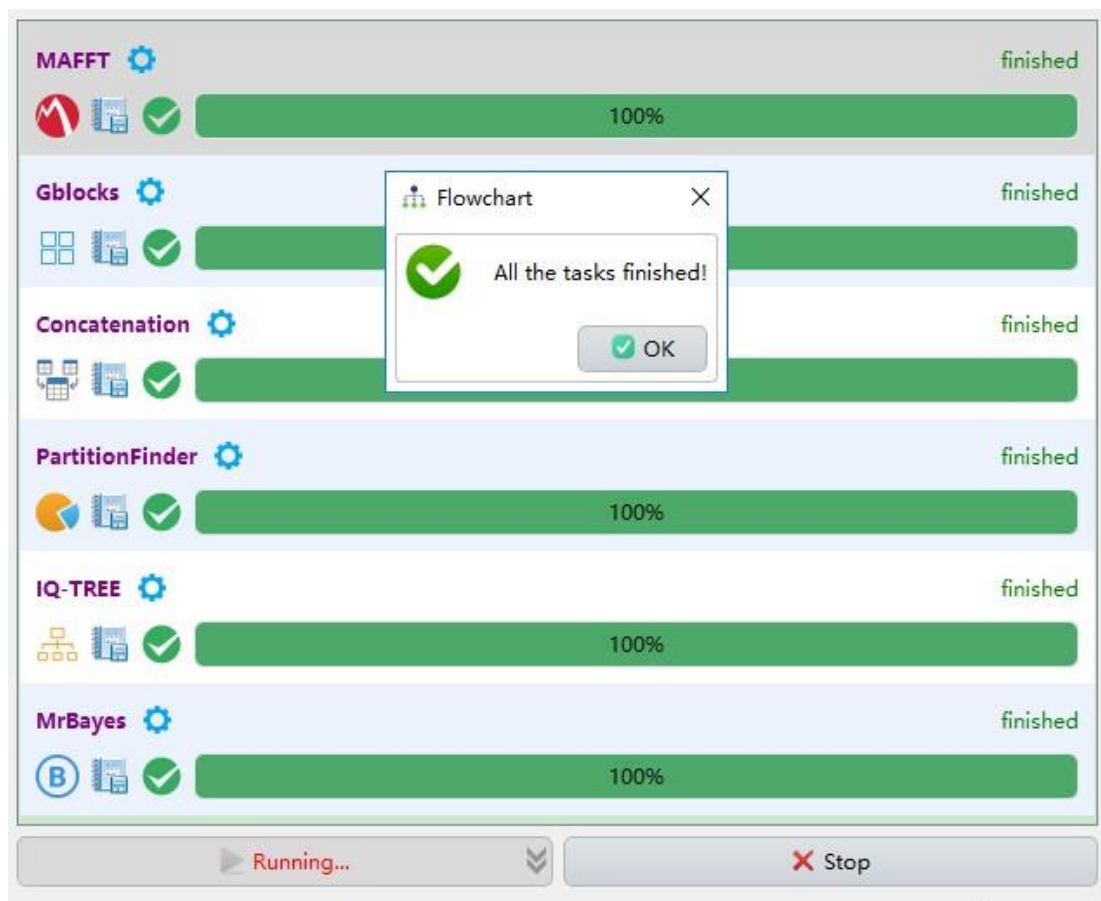
### 3.3.3 Start workflow

1. Click the **Check | Start** button, and the parameter summary window will pop up, allowing you to check and modify the parameters;
2. Click **Ok, start** to start the workflow.



### 3.3.4 Get workflow results

When all the tasks are finished, click **Ok** to view the results, double-click the folders in the **list of results** box to open the corresponding results:





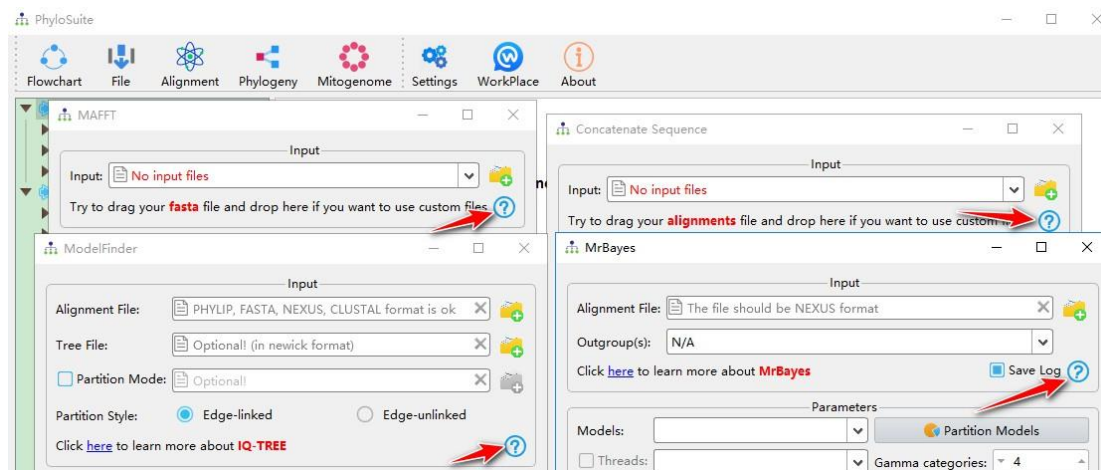
Scroll to the bottom of the results, and you will see that the whole workflow takes around 3 minutes (CPU: AMD Ryzen 7 1700; RAM: 8 G; OS: Windows 10 64 bit).

```
Flowchart start at: 2019-05-09 11:06:19.172226
Flowchart finish at: 2019-05-09 11:09:11.346319
Total time used for Flowchart: 0:02:52.174093
Time used for MAFFT: 0:00:05.153051
Time used for Gblocks: 0:00:00.133002
Time used for Concatenation: 0:00:00.050000
Time used for PartitionFinder: 0:02:26.088031
Time used for MrBayes: 0:00:11.684009
Time used for IQ-TREE: 0:00:20.614005
```

Note: to make this 'test run' very fast, I set a very low number of generations for MrBayes (10000) and IQ-TREE ultrafast bootstrap (5000).

## 4. Test run of each function

You may view a brief demo and/or test for each function via the inbuilt question mark button. For example:



## 5. Recommended reading

Other demo tutorials can be found [here](#).