

# **Program of identificate species dividing line manual**

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Documentation

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# 1 Introduction

We coding this program to solve problem that identification of the species dividing line,input a sequence file (.fasta ...) and output a bar chart(.png file type) about frequency distribution of distance,so we can get a frist gap,this gap corssponding a pecentage that we need.Like under bar chart Figure 1,the frist gap corssponding a 2.5 percentage that read is automatic by program,when we get the dividing line(a percentage),so using it to modify previous construted phylogenetic tree that we can get species tree.

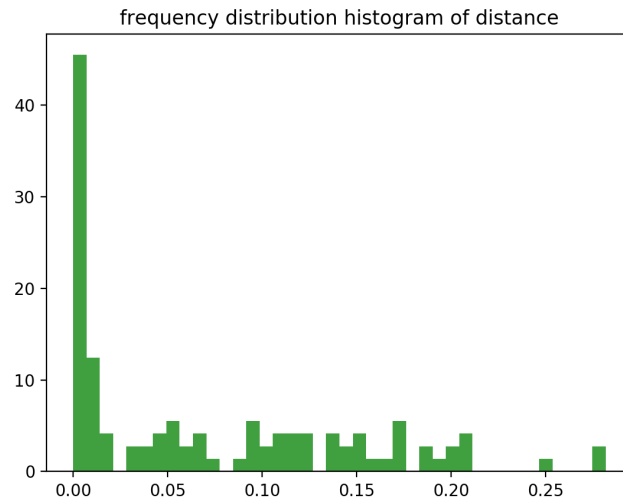
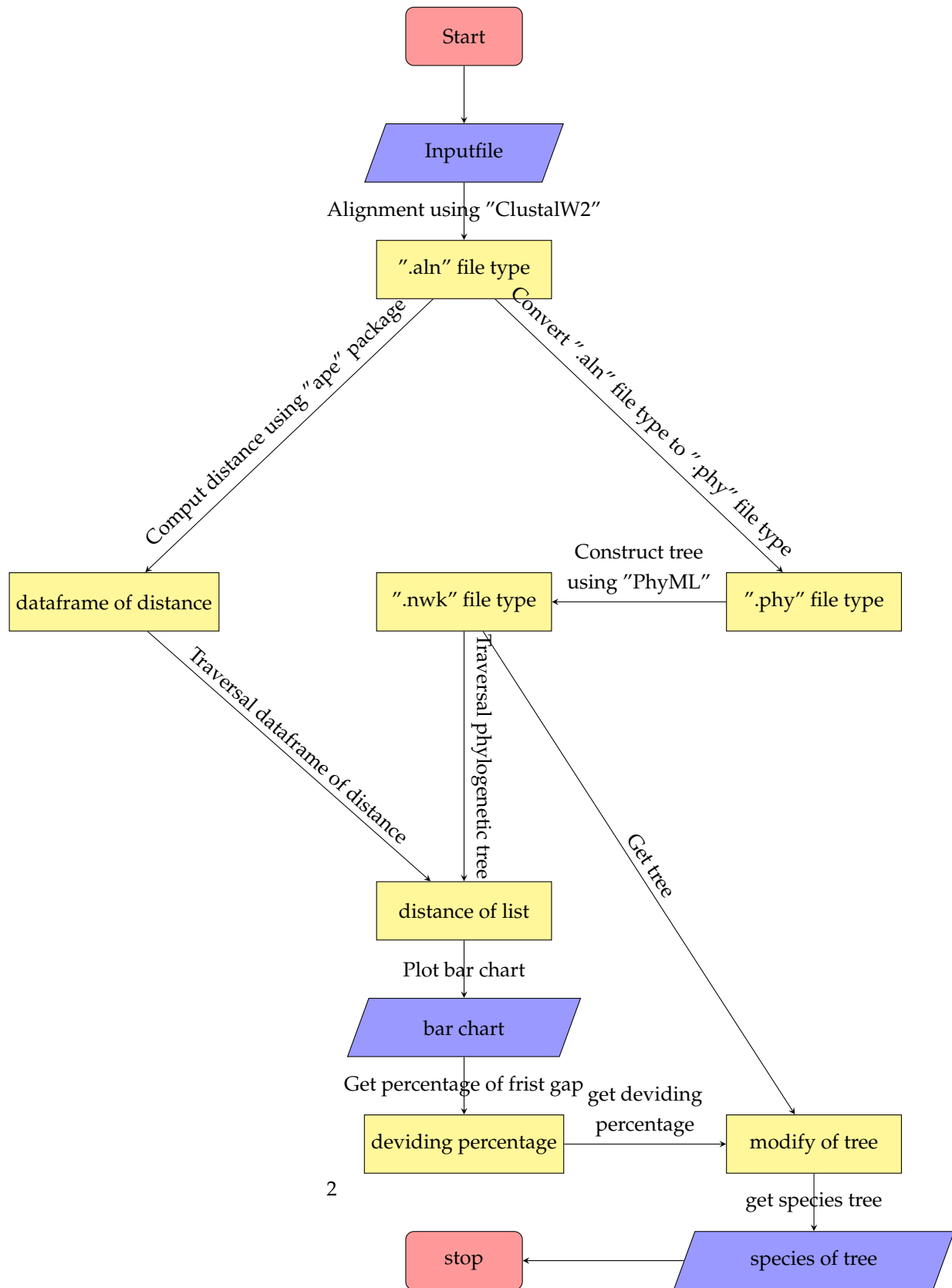


Figure 1: bar chart

# 2 algorithm

Here we describe the details of program,this program is mainly coded by python language( python3.6 distribustion ),using PhyML[GG03] to construt phylogenetic tree,using rpy2 module to concatenate python and ape package[PCS04]( a R language package ),cluswtal2[LBB<sup>+</sup>07] be used for building phylogenetic tree,the software flow chart is as follows:



## 2.1 what python packages we used?

We used Biopython[EBPB12](but we need import Bio,not Biopython in python program),rpy2[rpy],itertools,pandas,numpy,maltplotlib,copy and pydot;You can look for them if you aren't familiar with these python package.

## 2.2 How to use it?

We provide a website(...) for you, you only need a browser and open the url to upload your file(must be ".fasta, ..." type file),email and so on,we will send the results to you by email,the normal results include a picture of bar chart and a species tree file that is ".nwk" type file.

## References

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