DACTYLOPIUS IDENTIFIER

Created by Clarke van Steenderen

1

The user can choose from 4 gene databases, or upload their own in FASTA format

Select File

Own file upload

- 12S.fas
- 18S.fas
- COI(DTOM).fas
- COI(PCOFI).fas
- Own file upload

User manual ?

Click to view the help file:

Upload a .fas file

Browse... No file selected

Select File

Own file upload

Enter sequence name:

QUERY

2

Enter nucleotide sequence:

AAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAA

Query sequence input

Distance correction method

Jukes-Cantor

- none
- Jukes-Cantor

Distance correction method

Jukes-Cantor

Agglomeration method

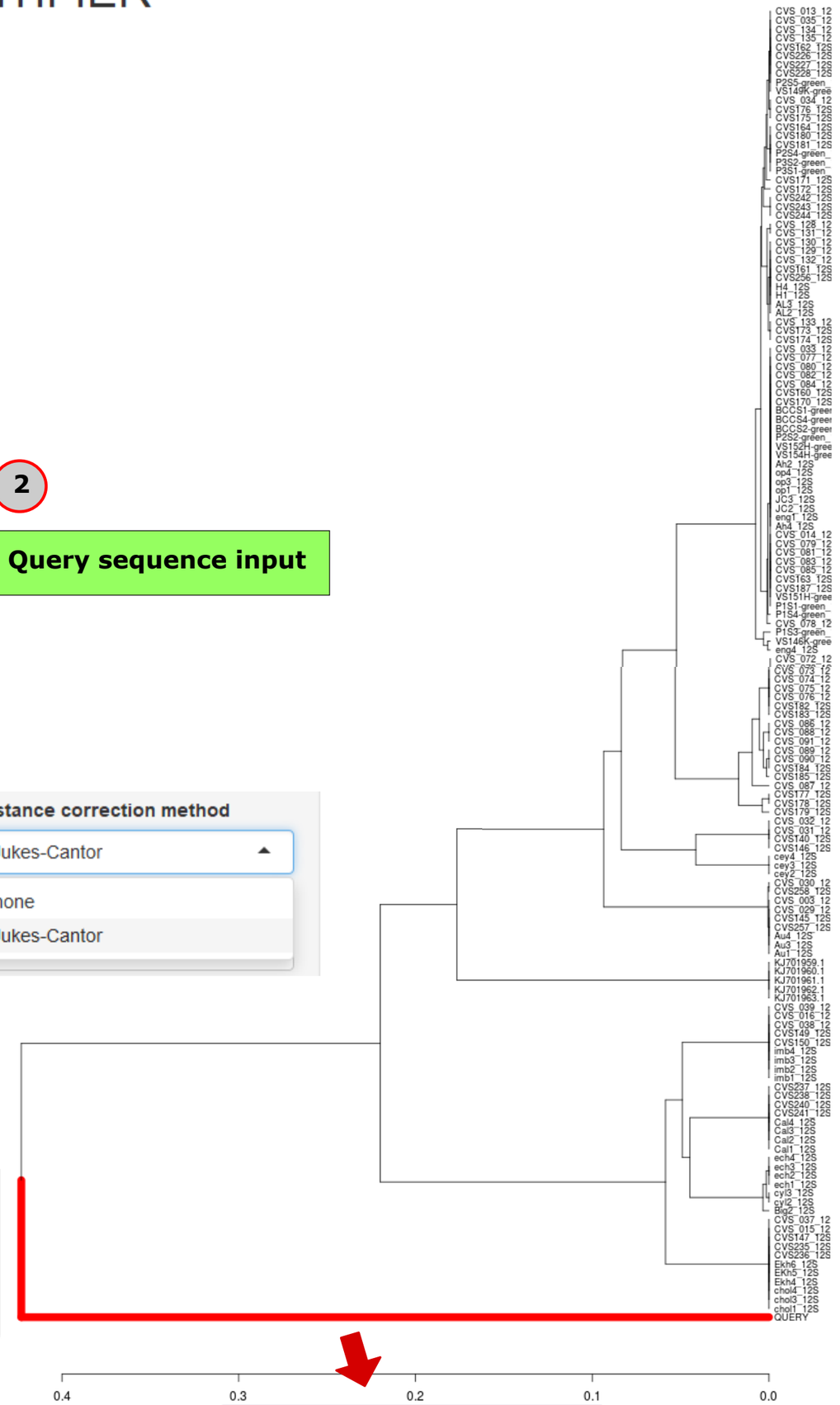
UPGMA

3 Submit

Agglomeration method

UPGMA

- complete
- single
- UPGMA
- WPGMA
- NJ
- ML



Query sequence shown in red. Its placement is relative to the selected database

DACTYLOPIUS IDENTIFIER

USER GUIDE

Created by:

Clarke van Steenderen

Department of Zoology and Entomology

The Centre for Biological Control

Rhodes University, Grahamstown, Eastern Cape, South Africa

2019

e-mail: vsteenderen@gmail.com

OVERVIEW

This program is designed for the quick identification of *Dactylopius* species (Hemiptera: Dactylopiidae), but can be applied to any taxon if the relevant database of genetic sequences is supplied. The user can either upload a database of their choice, or can select from those provided under the 'Select File' drop down menu (12S, 18S, and two COI markers). The sequences provided were obtained by Clarke van Steenderen as part of his M.Sc. degree, under the supervision of Dr. Iain Paterson and Dr. Shelley Edwards. A query nucleotide sequence is entered into the search box, and a phylogenetic tree is created where the query sequence is matched to the database, and highlighted in red.

UPLOADING YOUR OWN FILE