GENETIC BARCODE TESTER

USER GUIDE

Created by:

Clarke van Steenderen

Based upon the algorithms derived from the R package SPIDER

Department of Zoology and Entomology

The Centre for Biological Control

Rhodes University, Grahamstown, Eastern Cape, South Africa

2019

e-mail: vsteenderen@gmail.com

OVERVIEW

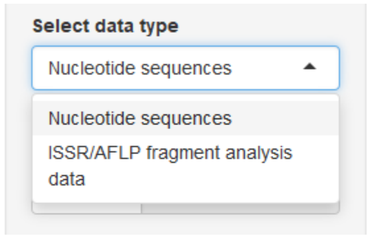
This program enables the user to test how efficient a set of genetic sequences are in allowing for their correct identification. The barcode testing algorithms implemented here are derived from the R package SPIDER, (**SP**ecies **ID**entity and **E**volution in **R**) developed by Brown *et al.* (2012). The program has been encoded to allow for both nucleotide and binary data input (such as ISSRs and AFLPs), which are subsequently converted into distance matrices.

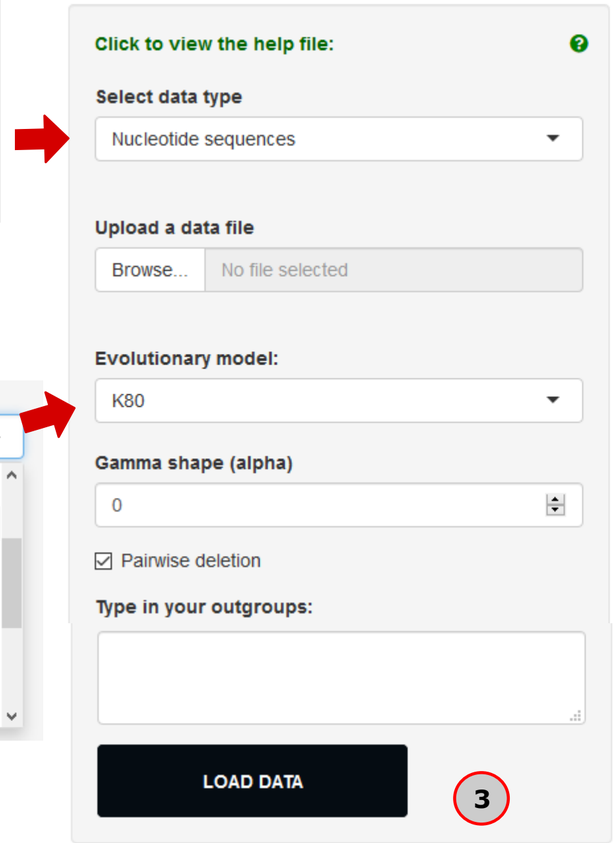
A highly useful function is that of the setting of distance thresholds in order to minimise the occurrence of false positive and false negative identifications. This attempts to help answer the question of "How different must the specimens be before they are considered different species/lineages/haplotypes etc.?".

User manual ?

1

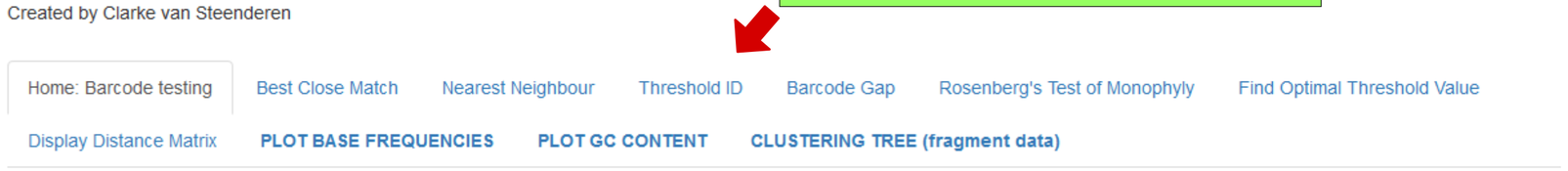
The user can upload nucleotide sequences or binary data

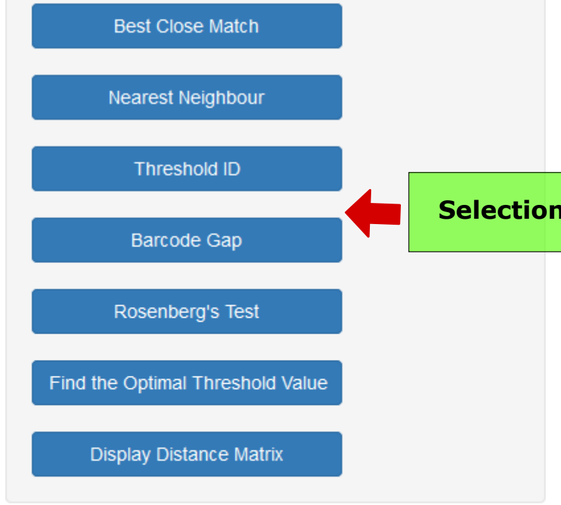




3

Results of the barcode testing algorithms are viewed in the tabs at the top of the screen





Selection of tests

4

2

	row.names(data1)
1	ech
2	ech
3	ech
4	ech
5	cyl
6	cyl
7	chol
8	chol
9	chol
10	chol
11	cal
12	cal
13	cal
14	cal
15	big
16	big

After the data is uploaded, the sequence names appear in a table. These need to be edited such that all the same species/taxa of interest have the same name.