Robustness

The methods that can be downloaded here are developed to explore the robustness of the parsimonious host-symbiont tree reconciliation method under editing or small perturbations of the input. The editing involves making different choices of unique symbiont mapping to a host in the case where multiple associations exist and re-rootings of the symbiont tree.

Rerooting

This method takes in input the nexus file of EUCALYPT (containing the host tree, the symbiont tree and the associations between their leaves) and a cost vector. It considers all the possible re-rooting of the symbiont tree and for each of them outputs the cost of the optimal acyclic solutions (if any), the corresponding event vectors with their multiplicities, and also the number of plateaux obtained together with some additional information. An example of an output file is given below.

Testing all possible acyclic rootings of the symbiont tree reconciliation (beta version)
This software tests all possible acyclic rooting of the symbiont tree reconciliation.
To obtain the beta test of the software, please click here:
http://team.inria.fr/erable/files/2020/11/Eucalypt_Acyclic_Rerooting.jar_.gz
The general command line for using Eucalypt_Acyclic_Rerooting is:

```
$ Eucalypt_Acyclic_Rerooting.jar -i <input_file > -task 5 [options] -o <output_file >
```

Testing all possible rootings of the symbiont tree reconciliation
This software tests both cyclic and acyclic rooting of the symbiont tree reconciliation.
To obtain the software, please click here:
http://team.inria.fr/erable/files/2020/11/Eucalypt_Rerooting.jar_.gz
The general command line for using Eucalypt_Rerooting is:

```
$ Eucalypt_Rerooting.jar -i <input_file > -task 5 [options] -o <output_file >
```

Example of output_file:

```
--------------------------------------------------------
Task 5 - Re-Rooting.
Input file                  : inputfile.nex                # general information
Output file                 : outputfile
Co-speciation cost          : 0.000
Duplication cost            : 1.000
Host-switch cost            : 1.000
Loss cost                   : 1.000
Maximum jump                : No limit
Root-to-root                 : Yes
Random sampling             : No
Number of solutions         : No limit
--------------------------------------------------------
Node: !P54                                                 # reconciliation obtained rooting the symbiont tree in !P54 node
((a_elynae,a_curvulae)!P54,((((((a_karii,(a_turfusa, …    # symbiont tree obtained rooting the tree in !P54 node
Number of distinct event vectors  = 2                      # number of different acyclic event vectors
{[6, 0, 14, 8]=376, [7, 0, 13, 11]=96}                     # acyclic event vectors obtained with their cardinality
Optimum cost = 50.000                                      # acyclic optimum cost obtained
--------------------
Node: a_sempervirentis                                     # reconciliation obtained rooting the symbiont tree in a_sempervirentis node
(a_sempervirentis,(((a_inclusa,a_subinclusa)!P25,…         # symbiont tree obtained rooting the tree in a_sempervirentis node
Number of distinct event vectors  = 0                      # number of different acyclic event vectors
Optimum cost = 1,000.000                                   # when there is no acyclic solution the optimum cost obtained is 1,000.000
--------------------
 [a_karii, a_turfusa, a_bigelowii, a_pratensis, !P10, !P8,…# all roots tried
[52.0, 57.0, 60.0, 54.0, 54.0, …                           # acyclic optimum costs obtained
nb plateaux: 2                                             # number of plateaux obtained
plateaux: [[!P49], [!P3]]                                  # closest nodes from each plateaux

Distance plateau0 plateau1: 3                              # closest nodes from each plateaux
```

```
distance between plateaux                              # distance between plateaux
--------------------------------------------------------
```

Multiple Associations

These methods take in input the nexus file of EUCALYPT (containing the host tree, the symbiont tree and the associations between their leaves). For each dataset, we considered all the datasets that can be obtained by resolving the multiple associations in all the possible ways. More precisely, for each symbiont associated with more than one host, we chose one and only one of the possible associations, and we did this in all the possible ways.

Solving multiple associations

This software creates all datasets obtained by solving all multiple associations in all possible ways
To obtain the code, please click here:
http://team.inria.fr/erable/files/2020/11/solveMultipleAssociations.py_.pdf.
The general command line for using solveMultipleAssociations.py is:

```
$ python solveMultipleAssociations.py <input_file >
```

Pruning the host tree

This software takes out the leaves without associations.
To obtain the code, please click here:
http://team.inria.fr/erable/files/2020/11/prune.py_.pdf.
The general command line for using prune.py is:

```
$ python prune.py <input_file >
```

Paper datasets

Here you can download the Nexus files which were used in our study:
http://team.inria.fr/erable/files/2020/11/PaperDatasets-Robustness.zip.