

User manual of the Exploration program

Jean-Philippe Doyon, Sylvie Hamel, Cedric Chauve

No Institute Given

1 Running the program

Author: Jean-Philippe Doyon

exploration D repository [Options]

Repository contains speciesTree, geneTree, and edgeValues files

Options:

P : Output reconciliation to primetv format

E : perform explorations

L : compute likelihood

H : read and consider true reconciliation

Q : compute posterior probabilities

C : Check that the enumeration algorithm is consistant with the space set

M : Maximal depth

S : Print to logfile each n steps

D : Compute the prob for each mapping $\text{rec}(u) = x$

Fig. 1: Help message of the *Exploration* program.

A typical call of the program is as follows: “./Exploration D ../INPUT_FILES/DATA3 E L Q D”. Here is a brief description:

- The folder “./INPUT_FILES/DATA3” contains the species and gene trees, and the rates and branch lengths of the species tree.
- “E”: explore the space of reconciliations;
- “L”: compute the likelihood of each visited reconciliation;
- “Q”: compute the (posterior) probability of each visited reconciliation;
- “D”: compute the (posterior) probability for mapping a node of the gene tree on a cell (vertex/branch) of the species tree.

Calling the program as above generates a file “exploration.results”, which is described in the following pages.

Exploration statistics

Indicates if the LCA Rec is also
the Most Likely one

Deviation from minRec likelihood
Nb of rec s.t. $\text{lik}(\text{rec}) > \text{lik}(\text{minrec})$: 0
Likelihood of minRec: 0.00774128
Dev Count
80 1

Likelihood of the LCA reconciliation

All likelihoods

Posterior probabilities distribution

Prob #Rec

17 1

82 1

Distribution: Posterior probability / nb. of Rec.

MinRec

NMC / Sum Post Prob

0 0.82857

1 0.17143

Sum of the posterior probability
overall Rec located at n NMCs to
the LCA Rec.

RealRec

NMC / Sum Post Prob

0 1

1 0

Idem: ... to the Real Reconciliation
(only for simulated gene trees)

LikRec

NMC / Sum Post Prob

0 0.82857

1 0.17143

Idem: to the Most Likely Rec.

MinRec

NMC / Prob Mass

Probability mass overall Rec.
located at at most n NMCs to the
LCA Rec.

RealRec
Dist #Rec
0 2
1 0

Idem: ... to the Real Reconciliation
(only for simulated gene trees)

LikRec
Dist #Rec
0 1
1 1

Idem: to the Most Likely Rec.

Distances NMC # Diff. Mapping
MinRec , LikRec : 0 0

Total number of rec: 2

Deviation = | diam/2 - d_nmc(MinRec , rec) |

Sum of deviation: 1

GeneFam 0

Informations on the input trees

Species tree
((0,1),2);

Genes tree
((0,1),2*);
Covers all species: 1
Nb of reconciliations: 2
Space diameter: 1

Info. on the Reconciliation Space

- size
- diameter

Check Stat Set Option: F
State Set size: 0

All reconciliations

Max depth 1

CPU time 0.001696 Overall Runing Time