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Protocol for the computation of figures 7 and 8 of the article "High precision detection of conserved segments from synteny blocks" Version 3

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Abstract

This protocol was used to compute figures 7 and 8 in the manuscript: 'High precision detection of conserved segments from synteny blocks'

Protocol

Install LibsDyogen, i-ADHoRe 3.0 and Cyntenator
Step 1.

All the steps are explained in https://github.com/DyogenIBENS/LibsDyogen/blob/master/README.txt. From now on we assume that the main folder of LibsDyogen is in the PYTHONPATH.

The README.txt also explains all the steps necessary to install and plug i-ADHoRe 3.0 and Cyntenator.

We used the release v2.0.0-alpha of the github deposit of LibsDyogen.

Install PhylDiag
Step 2.

All the steps are explained in https://github.com/DyogenIBENS/PhylDiag/blob/master/README.txt
From now on we assume that the main folder of PhylDiag is in PHYLDIAG

We used the release v2.0.0-alpha of the github deposit of PhylDiag

Take note of the data corresponding to the simulation made with MagSimus
Step 3.

In PHYLDIAG/data/benchmark :

* speciesTree.phylTree is the species tree of the simulation

* genes.<name>.list.bz2 are the simulated genomes (initial genome, intermediary genomes and

extant genomes)

* ancGenes.<name>.list.bz2 are the corresponding gene families

* cs.<name1>.<name2>.list.bz2 are the conserved segments between two species, <name1> and <name2>

* specRates_OptWith_InvDist_gamma_shape0.1_scale800_max1330_thesis contains the number of events on the branches of the species tree used for the simulation

* parameters_InvDist_gamma_shape0.1_scale800_max1330_thesis contains the parameters used for the simulation

The simulation used is from the release v2.0.0-alpha of the github deposit of the PhylDiag deposit

Compare conserved segments of PhylDiag and base_clusters of i-ADHoRe 3.0 with the reference simulated conserved segments

Step 4.

In the folder PHYLDIAG/data/benchmark

launch the command line :

> PHYLDIAG/src/benchmark/comparePhylDiagAndADHORESbsToSimulatedSbs.py speciesTree.phylTree Mus.musculus Gallus.gallus Amniota -pSimGenomes=genes.%s.list.bz2 -pAncGenes=ancGenes.%s.list.bz2 -pSimulatedSbs=sbs.genes.%s.%s.list.bz2 -preComputePairwiseSbs -oriented

The image is identical to the figure 7 of the article.

By default, the python script comparePhylDiagAndADHORESbsToSimulatedSbs.py loads previously computed values.

If you want to recompute in local the conserved segments of PhylDiag and the base_clusters of i-ADHoRe 3.0, change the boolean value

LOAD_PRECOMPUTED_BENCHMARK = False

at the beginning of PHYLDIAG/src/benchmark/comparePhylDiagAndADHORESbsToSimulatedSbs.py. Once more, after computation, the image is identical to the figure 7, otherwise contact me.

Compare the RBMs (Representative Synteny Blocks) of Cyntenator with the reference simulated conserved segments

Step 5.

In the folder PHYLDIAG/data/benchmark

launch the command line :

> PHYLDIAG/src/benchmark/compareCyntenatorSbsToSimulatedSbs.py speciesTree.phylTree
Mus.musculus Gallus.gallus Amniota -pSimGenomes=genes.%s.list.bz2 -
pAncGenes=ancGenes.%s.list.bz2 -pSimulatedSbs=sbs.genes.%s.%s.list.bz2 -preComputePairwiseSbs
-oriented

The image is identical to the figure 8 of the article.

Here also, by default, the python script compareCyntenatorSbsToSimulatedSbs.py loads previously
computed values.

If you want to recompute in local the RSBs of Cyntenator, change the boolean value

LOAD_PRECOMPUTED_BENCHMARK = False

at the beginning of PHYLDIAG/src/benchmark/compareCyntenatorSbsToSimulatedSbs.py.
Once more, after computation, the image is identical to the figure 8 of the article, otherwise contact
me.