Documentation for mergeDistMats Program

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Running Title: mergeDistMats

0.1 Introduction

This is the first version of documentation for the program mergeDistMats. This program is designed to merge phylogenetic distance matrices for subsequent input to phylogenetic distance analysis programs sch as Wag2020 (https://githib.com/wardwheeler/wag2020).

All source code, precompiled binaries, test data, and documentation are available from https://githib.com/wardwheeler/mergeDistMats.

This first version is brief.

0.2 Input Distance Matrix Format

Input distance matrices should be in CVS format (can be exported from spreadsheet programs), with first line of taxon (terminal) names and square matrix following. First column (from second row) contains distances, not repeat of names.

Matrices must be symmetrical and non-negative, but may have different (if overlapping) taxon (terminal) sets.

Beware of the MS-Excel non-conforming CVS output. A final line feed needs to be added to Excel created CVS files.

0.3 Output Formats

The program outputs (to stdout) a unified matrix in CVS format.

0.4 Command options

There is a single command line option to be specified. Either "normalize" or 'weight". This parameter specifies whether the input matrices (and output matrix) are scaled on [0,1] ("normalize") to force an equal weighting on each input matrix. The alternative, "weight" leaves the input values as they are and simply adds them together.

The program requires a single argument and at least one input matrix file.

0.5 Program Use

The program is invoked from the command-line as in:

mergeDistMats normalize testData2.csv > ouputMatrix.csv

mergeDistMats weight testData.csv testData2.csv > ouputMatrix.csv

Execution in Parallel

By default the program will execute using a single process core. By specifying the options '+RTS -NX -RTS' where 'X' is the number of processors offered to the program. These are specified after the program as in (for 4 parallel threads):

mergeDistMats + RTS - N4 - RTS other options...

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