
LGT.dat

Column 1: Family identifier	Each protein family has a unique integer identifier.
Column 2: Congruent or Incongruent	Each protein tree is either congruent or incongruent with the reference tree. C: protein tree is congruent with reference I: protein tree is incongruent with reference (legal edit paths found) I(N): protein tree is incongruent with reference (legal edit paths NOT found) I(N)?: protein tree is incongruent with reference (legal edit paths NOT found)
Column 3: Edit distance	The minimum edit distance. If no legal edit paths were found, then edit distance is reported as 'n'.
Column 4: Total paths	The total number of legal paths. If no legal edit paths were found, then the number of legal paths is reported as 'n'
Column 5: Unique paths	The number of unique paths (counting paths that are permutations of each other only once). If no legal edit paths were found, then the number of unique paths is reported as 'n'
Column 6: Number of discordant regions.	Discordant regions are reconciled independent from one another.
Column 7: Obligate edits	A edit is defined as obligate if it is implied by every path in the set of most-parsimonious edit paths resolving the discordance between the reference tree and the protein tree.
Column 8: Possible edits	A transfer is defined as possible if it appears in some, but not necessarily all, of the most-parsimonious edit paths resolving the discordance between the protein tree and reference tree.