- Option to do several randomized tree searches on a fixed starting tree.
- Options for sequence-similarity-based alignment size red

Graham Jones (http://www.sightsynthesis.co.uk/

function on a finite machine we will unavoidably obtain round

```
[-y]
[-z multipleTreesFile]
[-# numberOfRuns]
```

-f m: RAxML will compare bipartitions between two bunches of trees passed via `-t` and `-z` respectively. The program will return the Pearson correlation between all bipartitions found in the two tree files. A file called `RAxML_bipartitionFrequencies.outpuFileNam5 -11.8801 Td [( )-5.6477(m5 -11.8801 Td [353T bipartition freentestofEAxampl:`

Specify a threshold for sequence similarity clustering. RAxML will then print out an alignment to a file called

-m PROTCATmatrixName[F]:

Specify a random number seed for the parsimony inferences. This allows you and others to reproduce your results (reproducible/verifiable experiments) and will help me debug the program. This option **HAS NO EFFECT in the parallel MPI version**.
Example: `raxmlHPC -s alg -m GTRGAMMA -p 12345 -n TEST`.

`-q multipleModelFileName`

This allows you to specify the regions of your alignment for which an individual model of nucleotide substitution should be estimated. This will typically be useful to infer trees for long (in terms of ase–pairs) multigene alignments. If, e.g., `-m GTRGAMMA` is used, individual -shape parameters, GTR-rates, and empirical base frequencies will be estimated and optimized for each partition. IMPORTANT: ous RAxML

Example: raxmlHPC -s alg -m GTRGAMMA -q part -n TEST.

-r constraintFileName

If you want to only compute a randomized parsimony starting tree with RAxML and not execute an ML analysis of the tree specify `-y`

Here, we use the GTRMIX model, i.e. inference under GTRCAT and evaluation of the final tree under GTRGAMMA such that we can compare the final likelihoods for the ting FI0-FI4 and the automatically determined setting

in his very good GARLI code (