

Phylogenetic Analysis of Isolated Influenza A Strains

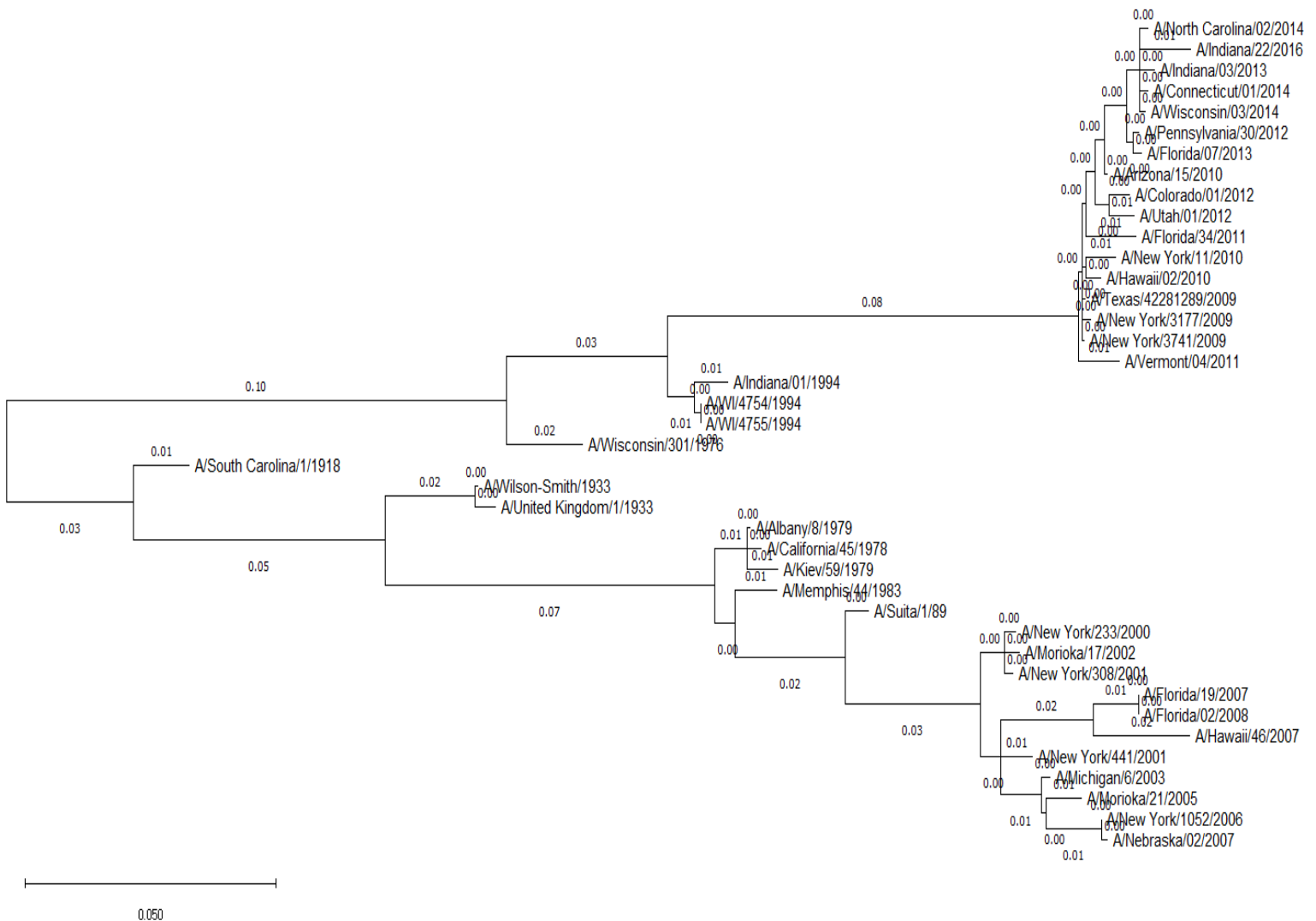


Figure: Molecular Phylogenetic analysis of all known isolated strains of Influenza A. Branch lengths are shown. Combination of large sample size and branch length indicators has caused some portions of figure to be distorted. For summary statistics, please look at table below.

Table:

[General Info]

Data Type	= unknown
No. of Taxa	= 40

No. of Sites = 1779

[Analysis Settings]

Model/Method = Tamura=Nei model

Select Codon Positions = 1st,2nd,3rd,Non=Coding

Initial Tree for ML = Make initial tree automatically (Default = NJ/BioNJ)

[Analysis Statistics]

Execution Time = 10.406 (seconds)

Peak Memory Used(Working Set) = 266.559 (MB)

Sum of branch lengths = 0.680

Model = Tamura-Nei (1993) model

Num of params = 82

Num of rates = 1

AICc = 16627.011

BIC = 17376.493

LnL = -8231.407

Invar = n/a

Gamma = n/a

Ts/Tv = 3.964