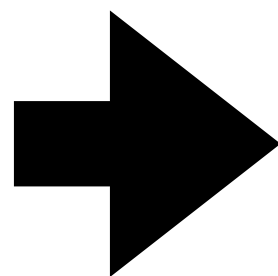


```

354 },
355 "Standard MG94":{
356   "AIC-c":12923.31190785199,
357   "Confidence Intervals":{
358     "non-synonymous/synonymous rate ratio":{
359       "LB":0.006844594453196991,
360       "UB":0.01055858911944712
361     }
362   },
363   "Log Likelihood":-6413.455134253863,
364   "Rate Distributions":{
365     "Substitution rate from nucleotide A to nucleotide C":0.2433728512340663,
366     "Substitution rate from nucleotide A to nucleotide G":1,
367     "Substitution rate from nucleotide A to nucleotide T":0.3060223183303938,
368     "Substitution rate from nucleotide C to nucleotide G":0.02087667707983453,
369     "Substitution rate from nucleotide C to nucleotide T":1.979133076079397,
370     "Substitution rate from nucleotide G to nucleotide T":0.2305847598841325,
371     "non-synonymous/synonymous rate ratio":0.008575064843083209
372   },
373   "display order":1,
374   "estimated parameters":48
375 }
376 },
377 "input":{
378   "file name":"/Users/sergei/Dropbox/Talks/VEME-current/data/WestNileVirus_NS3.fas",
379   "number of sequences":19,
380   "number of sites":619,
381   "partition count":1,
382   "trees":{
383     "0":"(HNY1999,NY99_EQHS,NY99_FLAMINGO,((((((RABENSBURG_ISOLATE,(WNFCG,SPU116_89)Node11)Node9,KUNCG)Node8,(ETHAN4766,
384       (CHIN_01,EG101)Node17)Node15)Node7,(((ITALY_1998_EQUINE,PAAN001)Node22,
385       (RO97_50,VLG_4)Node25)Node21,KN3829)Node20)Node6,AST99)Node5,PAH001)Node4,IS_98)Node3,MEX03)"
386   }
387 },
388 "test results":{
389   "non-synonymous/synonymous rate ratio":{
390     "LRT":2512.58476730381,
391     "p-value":0
392   }
393 },

```



WNV NS3

| Model | Log L | # p | dN/dS | LRT | p-value |
|-------------|----------|-----|------------------------|--------|---------|
| <i>Null</i> | -7745.48 | 49 | 1 | | |
| Alternative | -6413.5 | 50 | 0.009 [0.007-0.011] | 2512.6 | ~0 |

Very strongly conserved

HIV-1 env

| Model | Log L | # p | dN/dS | LRT | p-value |
|-------------|---------|-----|----------------------|------|---------|
| <i>Null</i> | -2078.3 | 40 | 1 | | |
| Alternative | -2078.2 | 41 | 1.122 [0.94-1.33] | 0.33 | ~0.6 |

Not significantly different from neutral

SARS-CoV-2 spike

| Model | Log L | # p | dN/dS | LRT | p-value |
|-------------|---------|-----|---------------------|-------|---------|
| <i>Null</i> | -9311.0 | 176 | 1 | | |
| Alternative | -9292.0 | 177 | 0.54 [0.48-0.61] | 37.94 | ~0 |

Very strongly conserved