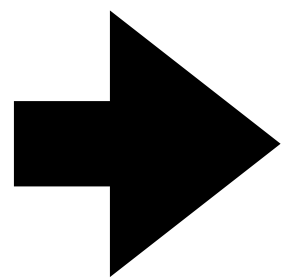


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354 },
355 "Standard MG94":{
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363   "Log Likelihood":-6413.455134253863,
364   "Rate Distributions":{
365     "Substitution rate from nucleotide A to nucleotide C":0.2433728512340663,
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371     "non-synonymous/synonymous rate ratio":0.008575064843083209
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373   "display order":1,
374   "estimated parameters":48
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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 },

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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