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356       "AIC-c":12923.31524090407,
357       "Confidence Intervals":{
358         "non-synonymous/synonymous rate ratio":{
359           "LB":0.006858130361216103,
360           "UB":0.01057945031810191
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363       "Log Likelihood":-6413.456800779904,
364       "Rate Distributions":{
365         "Substitution rate from nucleotide A to nucleotide C":0
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367         "Substitution rate from nucleotide A to nucleotide T":0
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368         "Substitution rate from nucleotide C to nucleotide G":0
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369         "Substitution rate from nucleotide C to nucleotide T":1
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370         "Substitution rate from nucleotide G to nucleotide T":0
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371         "non-synonymous/synonymous rate ratio":0.008593681136758865
372       },
373       "display order":1,
374       "estimated parameters":48
375     }
376   },
377   "input":{
378     "file name":"/Users/sergei/Dropbox/Talks/VEME-2021/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,(CHIN_01
            ,EG101)Node17)Node15)Node7,(((ITALY_1998_EQUINE,PAAN001)Node22
            ,(RO97_50,VLG_4)Node25)Node21,KN3829)Node20)Node6,AST99)Node5
            ,PAH001)Node4,IS_98)Node3,MEX03)"
384     }
385   },
386   "test results":{
387     "non-synonymous/synonymous rate ratio":{
388       "LRT":2512.583763184408,
389       "p-value":0
390     }
391   },
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WNV NS3

Model	Log L	# p	dN/dS	LRT	p-value
Null	-7668.7	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
Null	-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
Null	-9311.0	176	1		
Alternative	-9292.0	177	0.54 [0.48-0.61]	37.94	~0

Very strongly conserved