



- Partition a pathogen tree into terminal and internal branches
- Terminal branches potentially include “dead-end” lineages, i.e. those which are maladaptive
- Internal branches include at least one “*transmission*” (intra-species) or “*replication*” (intra-host) events: stronger action of selection
- Focusing on a subset of branches can allow one to interpret dN/dS more precisely

Codon	Partition	alpha	beta+	p+	LRT	Episodic selection detected?	# branches	Most common codon substitutions at this site
367	1	0.000	98.114	0.459	9.062	Yes, p = 0.0047	2	[2]Gtc>Ttc
439	1	0.000	35.271	1.000	4.990	Yes, p = 0.0379	1	[1]aaC>aaA
452	1	0.000	30.877	1.000	5.520	Yes, p = 0.0288	1	[4]cTg>cGg [1]Ctg>Atg
477	1	0.000	51.490	0.460	4.334	Yes, p = 0.0532	1	[1]aGc>aAc
501	1	0.000	271.405	0.145	3.460	Yes, p = 0.0839	1	[3]Aat>Tat [1]aAt>aCt,Tat>Aat
614	1	0.000	49.307	0.464	3.187	Yes, p = 0.0968	1	[1]Gat>Aat,gGt>gAt

hyphy meme --alignment data/spike.fas --tree data/spike.tree --branches Internal