



- 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

SARS CoV-2 Spike
Internal Branches Only

Codon	Partition	alpha	beta+	p+	LRT	Episodic selection detected?	# branches	Most common codon substitutions at this site
:-----:	:-----:	:-----:	:-----:	:-----:	:-----:	:-----:	:-----:	:-----:
367	1	0.000	97.046	0.481	9.056	Yes, p = 0.0047	2	[2]GTC>TTC
439	1	0.000	35.187	1.000	4.987	Yes, p = 0.0380	1	[1]AAC>AAA
452	1	0.000	30.833	1.000	5.519	Yes, p = 0.0289	1	[4]CTG>CGG [1]CTG>ATG
477	1	0.000	51.490	0.460	4.330	Yes, p = 0.0533	1	[1]AGC>AAC
501	1	0.000	271.405	0.145	3.456	Yes, p = 0.0840	1	[3]AAT>TAT [1]AAT>ACT, TAT>AAT

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