



- 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 | 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 |