

<u>Task</u>	<u>Test</u>	<u>Site strategy</u>	<u>Branch strategy</u>	<u>Complexity</u>	<u>Effective sample size</u>	<u>Parallelization</u>	<u>Practical # sequences limit</u>
Gene-wide selection	BUSTED	Random Effects	Random Effects	Fixed	~sites x taxa	SMP	~2,000
Site-level selection / episodic	MEME	Fixed Effects	Random Effects	Fixed	~ taxa	SMP/MPI	~25000 (cluster)
Site-level selection / pervasive	FEL	Fixed Effects	Fixed Effects	Fixed	~ taxa	SMP/MPI	~25000 (cluster)
Branch-level selection	aBSREL	Random Effects	Fixed Effects	Adaptive	~ sites	SMP/MPI	~ 1,000
Compare selective regimes between sets of branches	RELAX	Random Effects	Mixed Effects	Fixed	~sites x (branch set size)	SMP	~ 1,000
Compare selective pressure between sets of branches on individual sites	Contrast-FEL	Fixed Effects	Fixed Effects	Fixed	~ branch set	SMP/MPI	~25000 (cluster)

Current suggested best practices.

There are lots of methods you could use to study positive selection, including >10 developed by our group. The field is still evolving, and this is our current suggestions of what to do with your data, depending on the question you want to answer.

Question	Method	Output
Is there episodic selection anywhere in my gene (or along a set of branches known a priori)?	Branch-site unrestricted statistical test of episodic diversification (BUSTED).	<ul style="list-style-type: none"> • p-value for gene-wide selection • inferred dN/dS distributions • a “quick and dirty” scan of sites where selection could have operated.
Are there branches in the tree where some sites have been subject to diversifying selection? Also: inferring ancient divergence times.	Adaptive branch site random effects likelihood (aBSREL)	<ul style="list-style-type: none"> • p-values for each branch • dN/dS distributions for each branch • evolutionary process complexity
Are there sites in the alignment where some of the branches have experienced diversifying selection?	Mixed effects model of evolution (MEME)	<ul style="list-style-type: none"> • p-values for each site • dN/dS distributions for each site
Intra-species viral analyses for sites under selection	MEME/FEL internal branches	<ul style="list-style-type: none"> • p-values for each site • dN/dS distributions for each site
Are there sites which have experiences diversifying selection and my alignment is large?	Fast unconstrained bayesian analysis of selection (FUBAR)	<ul style="list-style-type: none"> • Posterior probabilities of selection at each site • An estimate of the the gene-wide dN/dS distribution
Are parts of the tree evolving with different selective pressures relative to other parts of the tree?	RELAX (a test for relaxed selection)	<ul style="list-style-type: none"> • p-value for whether or not there is relaxed or intensified selection • inferred dN/dS distributions for different branch sets • more flexible distribution companions possible