

Analysis performed on all sites.

Testing whether the observed I_{ss} is significantly lower than I_{ss.c}.

I_{ss}Sym is I_{ss.c} assuming a symmetrical topology.

I_{ss}Asym is I_{ss.c} assuming an asymmetrical topology.

NumOTU	I _{ss}	I _{ss.c}	Sym	T	DF	P	I _{ss.c}	Asym	T	DF	P
4	0.221	0.824	33.683	1109	0.0000	0.792	31.896	1109	0.0000		
8	0.245	0.794	21.767	1109	0.0000	0.689	17.623	1109	0.0000		
16	0.275	0.777	15.402	1109	0.0000	0.583	9.440	1109	0.0000		
32	0.313	0.755	10.980	1109	0.0000	0.456	3.544	1109	0.0004		

Note: two-tailed t-tests are used.

Interpretation of results:

Significant Difference

Yes No

I _{ss} < I _{ss.c}	Little saturation	Substantial saturation
I _{ss} > I _{ss.c}	Useless sequences	Very poor for phylogenetics

Please cite:

Xia, X., Z. Xie, M. Salemi, L. Chen, Y. Wang. 2003. An index of substitution saturation and its application. *Molecular Phylogenetics and Evolution* 26:1-7.

Xia, X. and Lemey, P. 2009. Assessing substitution saturation with DAMBE. Pp. 615-630 in Philippe Lemey, Marco Salemi and Anne-Mieke Vandamme, eds. *The Phylogenetic Handbook: A Practical Approach to DNA and Protein Phylogeny*. 2nd edition Cambridge University Press.