

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	0.572	0.846	17.703	2714	0.0000	0.827	16.471	2714	0.0000
8	0.631	0.833	9.016	2714	0.0000	0.744	5.029	2714	0.0000
16	0.724	0.818	3.190	2714	0.0014	0.651	2.466	2714	0.0137
32	0.839	0.802	0.989	2714	0.3226	0.538	8.078	2714	0.0000

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.