

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} | I _{ss} Sym | T | DF | P | I _{ss.c} Asym | T | DF | P |
|--------|-----------------|-------------------|---------------------|------|--------|-------|------------------------|------|--------|---|
| 4 | 0.613 | 0.830 | 10.028 | 1319 | 0.0000 | 0.798 | 8.579 | 1319 | 0.0000 | |
| 8 | 0.680 | 0.803 | 3.954 | 1319 | 0.0001 | 0.701 | 0.667 | 1319 | 0.5049 | |
| 16 | 0.767 | 0.786 | 0.477 | 1319 | 0.6336 | 0.598 | 4.086 | 1319 | 0.0000 | |
| 32 | 0.870 | 0.767 | 1.989 | 1319 | 0.0469 | 0.477 | 7.559 | 1319 | 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.