Test of substitution saturation (Xia et al. 2003; Xia and Lemey 2009)

Analysis performed on all sites.

Testing whether the observed Iss is significantly lower than Iss.c.
  IssSym is Iss.c assuming a symmetrical topology.
  IssAsym is Iss.c assuming an asymmetrical topology.

NumOTU	Iss	Iss.cSym	T	DF	P	Iss.cAsym	T	DF	P
4	0.579	0.835	10.925	1577	0.0000	0.805	9.657	1577	0.0000
8	0.678	0.811	3.815	1577	0.0001	0.712	0.976	1577	0.3292
16	0.808	0.795	0.289	1577	0.7724	0.614	4.173	1577	0.0000
32	0.956	0.777	3.049	1577	0.0023	0.497	7.838	1577	0.0000

Note: two-tailed t-tests are used.

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Interpretation of results:

        Significant Difference

        Yes   No

Iss < Iss.c   Little   Substantial
              saturation   saturation

Iss > Iss.c   Useless   Very poor
              sequences   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.