

Testing whether the observed I<sub>ss</sub> is significantly lower than I<sub>ss.c</sub>.

Part I. For a symmetrical tree.

Prop. invar. sites	0.0000
Mean H	0.3396
Standard Error	0.0101
Hmax	1.7203
I <sub>ss</sub>	0.1974
I <sub>ss.c</sub>	0.8118
T	60.7988
DF	2066
Prob (Two-tailed)	0.0000
95% Lower Limit	0.1776
95% Upper Limit	0.2172

Part II. For an extreme asymmetrical (and generally very unlikely) tree.

I <sub>ss.c</sub>	0.7053
T	50.2605
DF	2066
Prob (Two-tailed)	0.0000
95% Lower Limit	0.1776
95% Upper Limit	0.2172

Interpretation of results:

Significant Difference

Yes No

I <sub>ss</sub> < I <sub>ss.c</sub>	Little saturation	Substantial saturation
I <sub>ss</sub> > I <sub>ss.c</sub>	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.