

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	1.1530
Standard Error	0.0198
Hmax	1.6282
I <sub>ss</sub>	0.7082
I <sub>ss.c</sub>	0.8288
T	6.1026
DF	2819
Prob (Two-tailed)	0.0000
95% Lower Limit	0.6694
95% Upper Limit	0.7469

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

I <sub>ss.c</sub>	0.7561
T	2.4233
DF	2819
Prob (Two-tailed)	0.0154
95% Lower Limit	0.6694
95% Upper Limit	0.7469

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.