

Testing whether the observed Iss is significantly lower than Iss.c.

Part I. For a symmetrical tree.

Prop. invar. sites	0.0000
Mean H	1.2595
Standard Error	0.0295
Hmax	1.8415
Iss	0.6839
Iss.c	0.8016
T	3.9866
DF	2153
Prob (Two-tailed)	0.0001
95% Lower Limit	0.6261
95% Upper Limit	0.7418

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

Iss.c	0.6382
T	1.5486
DF	2153
Prob (Two-tailed)	0.1216
95% Lower Limit	0.6261
95% Upper Limit	0.7418

Interpretation of results:

Significant Difference

Yes

No

Iss < Iss.c	Little saturation	Substantial saturation
Iss > Iss.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.