

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

Part I. For a symmetrical tree.

Prop. invar. sites	0.0000
Mean H	1.6929
Standard Error	0.0293
Hmax	1.8780
Iss	0.9014
Iss.c	0.8044
T	3.3177
DF	2570
Prob (Two-tailed)	0.0009
95% Lower Limit	0.8441
95% Upper Limit	0.9588

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

Iss.c	0.6159
T	9.7575
DF	2570
Prob (Two-tailed)	0.0000
95% Lower Limit	0.8441
95% Upper Limit	0.9588

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.