

Testing whether the observed I_{ss} is significantly lower than I_{ss.c}.

Part I. For a symmetrical tree.

=====	
Prop. invar. sites	0.0000
Mean H	0.3016
Standard Error	0.0112
Hmax	1.8839
I _{ss}	0.1601
I _{ss.c}	0.8050
T	57.8365
DF	2681
Prob (Two-tailed)	0.0000
95% Lower Limit	0.1382
95% Upper Limit	0.1820

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

=====	
I _{ss.c}	0.6128
T	40.5976
DF	2681
Prob (Two-tailed)	0.0000
95% Lower Limit	0.1382
95% Upper Limit	0.1820

Interpretation of results:

Significant Difference		

	Yes	No

I _{ss} < I _{ss.c}	Little saturation	Substantial saturation

I _{ss} > I _{ss.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.