

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

Part I. For a symmetrical tree.

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Prop. invar. sites	0.0000
Mean H	0.4494
Standard Error	0.0221
Hmax	1.4554
I <sub>ss</sub>	0.3088
I <sub>ss.c</sub>	0.8076
T	22.5912
DF	1142
Prob (Two-tailed)	0.0000
95% Lower Limit	0.2655
95% Upper Limit	0.3521

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

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I <sub>ss.c</sub>	0.7559
T	20.2536
DF	1142
Prob (Two-tailed)	0.0000
95% Lower Limit	0.2655
95% Upper Limit	0.3521

Interpretation of results:

Significant Difference		
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	Yes	No
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I <sub>ss</sub> < I <sub>ss.c</sub>	Little saturation	Substantial saturation
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I <sub>ss</sub> > I <sub>ss.c</sub>	Useless sequences	Very poor for phylogenetics
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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.