

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

Part I. For a symmetrical tree.

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Prop. invar. sites	0.0000
Mean H	0.1982
Standard Error	0.0112
Hmax	1.8348
I _{ss}	0.1080
I _{ss.c}	0.7664
T	59.0192
DF	1034
Prob (Two-tailed)	0.0000
95% Lower Limit	0.0861
95% Upper Limit	0.1299

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

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I _{ss.c}	0.5566
T	40.2148
DF	1034
Prob (Two-tailed)	0.0000
95% Lower Limit	0.0861
95% Upper Limit	0.1299

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.

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