

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

Part I. For a symmetrical tree.

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=====
Prop. invar. sites      0.0000
Mean H                  1.9094
Standard Error          0.0401
Hmax                   1.9206
Iss                     0.9942
Iss.c                   0.7972
T                       4.9127
DF                      2630
Prob (Two-tailed)      0.0000
95% Lower Limit        0.9156
95% Upper Limit        1.0728
=====
```

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

```
=====
Iss.c                   0.5613
T                       10.7964
DF                      2630
Prob (Two-tailed)      0.0000
95% Lower Limit        0.9156
95% Upper Limit        1.0728
=====
```

Interpretation of results:

Significant Difference

Yes No

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Iss < Iss.c   Little      Substantial
             saturation   saturation
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Iss > Iss.c   Useless      Very poor
             sequences     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.