

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

Part I. For a symmetrical tree.

```
=====
Prop. invar. sites      0.0000
Mean H                  1.7014
Standard Error          0.0260
Hmax                    1.8307
Iss                     0.9294
Iss.c                   0.8100
T                       4.5833
DF                      2525
Prob (Two-tailed)       0.0000
95% Lower Limit         0.8783
95% Upper Limit         0.9804
=====
```

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

```
=====
Iss.c                   0.6566
T                       10.4727
DF                      2525
Prob (Two-tailed)       0.0000
95% Lower Limit         0.8783
95% Upper Limit         0.9804
=====
```

Interpretation of results:

Significant Difference

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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.