Test of substitution saturation (Xia et al. 2003; Xia and Lemey 2009)

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   1.2954
Standard Error   0.0472
Hmax   1.8895
Iss   0.6856
Iss.c   0.7645
T   1.6736
DF   1229
Prob (Two-tailed)   0.0945
95% Lower Limit   0.5931
95% Upper Limit   0.7781

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Part II. For an extreme asymmetrical (and generally very
unlikely) tree.
==
Iss.c   0.4898
T   4.1513
DF   1229
Prob (Two-tailed)   0.0000

95% Lower Limit   0.5931
95% Upper Limit   0.7781

==

Interpretation of results:
            Significant Difference

            Yes   No

Iss < Iss.c   Little   Substantial
              saturation   saturation

Iss > Iss.c   Useless   Very poor
              sequences   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.