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                      1.2807
Standard Error              0.0293
Hmax                        1.6458
Iss                         0.7781
Iss.c                       0.8008
T                           0.7725
DF                          1271
Prob (Two-tailed)           0.4400
95% Lower Limit             0.7207
95% Upper Limit             0.8356


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Part II. For an extreme asymmetrical (and generally very
unlikely) tree.
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Iss.c                       0.6982
T                           2.7300
DF                          1271
Prob (Two-tailed)           0.0064

95% Lower Limit             0.7207
95% Upper Limit             0.8356


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Interpretation of results:
            Significant Difference
            ----------------------
            Yes          No
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Iss < Iss.c   Little       Substantial
              saturation   saturation
--------------------------------------------------------
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.