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.
==
Prop. invar. sites   0.0000
Mean H   0.7326
Standard Error   0.0326
Hmax   1.7453
Iss   0.4197
Iss.c   0.7813
T   11.0795
DF   1193
Prob (Two-tailed)   0.0000
95% Lower Limit   0.3557
95% Upper Limit   0.4838

==
Part II. For an extreme asymmetrical (and generally very
unlikely) tree.
==
Iss.c   0.6513
T   7.0951
DF   1193
Prob (Two-tailed)   0.0000

95% Lower Limit   0.3557
95% Upper Limit   0.4838

==

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.