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	0.4730
Standard Error	0.0251
Hmax	1.8656
Iss	0.2535
Iss.c	0.7628
T	20.3133
DF	926
Prob (Two-tailed)	0.0000
95% Lower Limit	0.2043
95% Upper Limit	0.3027

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

Iss.c	0.5286
T	10.9715
DF	926
Prob (Two-tailed)	0.0000
95% Lower Limit	0.2043
95% Upper Limit	0.3027

Interpretation of results:

	Significant Difference	
	Yes	No
Iss < Iss.c	Little saturation	Substantial saturation
Iss > Iss.c	Useless sequences	Very poor 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.