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Geometry Of The Space Of Phylogenetic TreesTwo Of The Most Common Methods, The Maximum Likelihood Methods And The Parsimony Methods (Foulds And Graham, 1982). As A Consequence Bi-ologists Have To Use Approximate Optimization Algorithms That Use Random Starting Points And Certain Random Moves Between Trees. The Resulting Trees Thus Vary From Run To Run. The Geometric Model We Introduce In Feb 1th, 2024Statistical Science Bootstrapping Phylogenetic Trees ...BOOTSTRAPPING PHYLOGENETIC TREES 243 1870) Different Ones] Number Of Combinatorial Tree Forms. I Denote The Metric Tree Estimate By τ[^], The True Tree By τ And The Space Of Metric Trees T , Sometimes With An Index N To Denote The Number Of Leaves. After Deciding Which Estimator To Use, A Natural Jun 1th, 2024Bootstrapping Phylogenetic Trees: Theory And MethodsStatistical Science 2003, Vol. 18, No. 2, 241-255 C) Institute Of Mathematical Statistics, 2003 Bootstrapping Phylogenetic Trees: Theory And Methods Susan Holmes Abstract. This Is A Survey Of The Use Of The Bootstrap In The Area Of Systematic And Evolutionary Biology. I Present The Current Usage By Biologists Jun 2th, 2024.

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