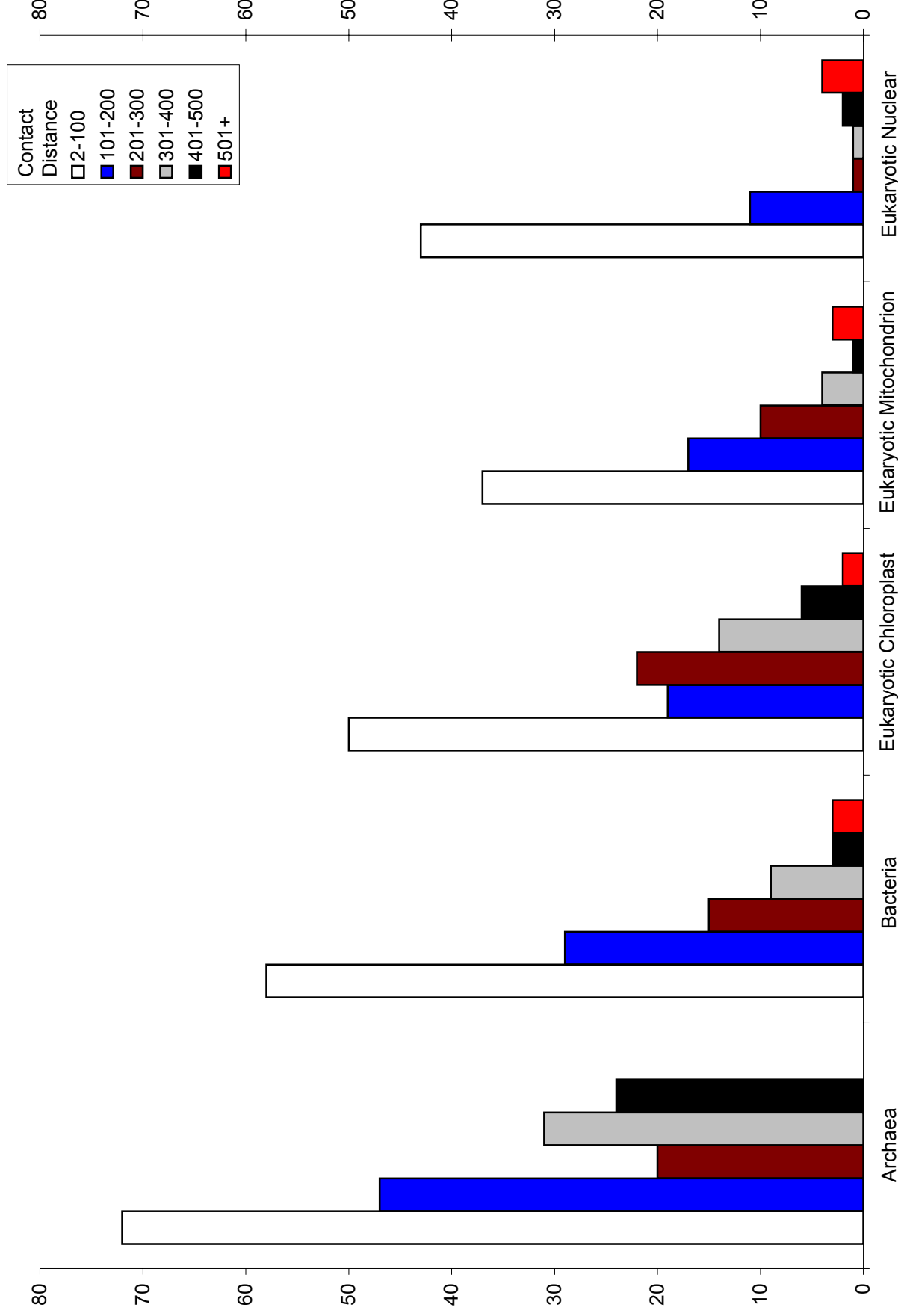


% of Comparative, Canonical Base-pairs with a Given Contact Distance Predicted Correctly

Accuracy of Base-pair Prediction by MFold as a Function of RNA Contact Distance and Phylogeny for 16S rRNA



% of Comparative, Canonical Base-pairs with a Given Contact Distance Predicted Correctly

This chart shows the prediction accuracy for comparative, canonical base-pairs of a given RNA contact distance for 16S rRNA grouped by phylogeny. RNA Contact Distance is defined as the number of nucleotides intervening between the 5' and 3' halves of a base-pair. Folding parameters for Mfold 3.1 were window size (W)=1, max suboptimal (MAX)=750, and percent suboptimality (P)=5%.