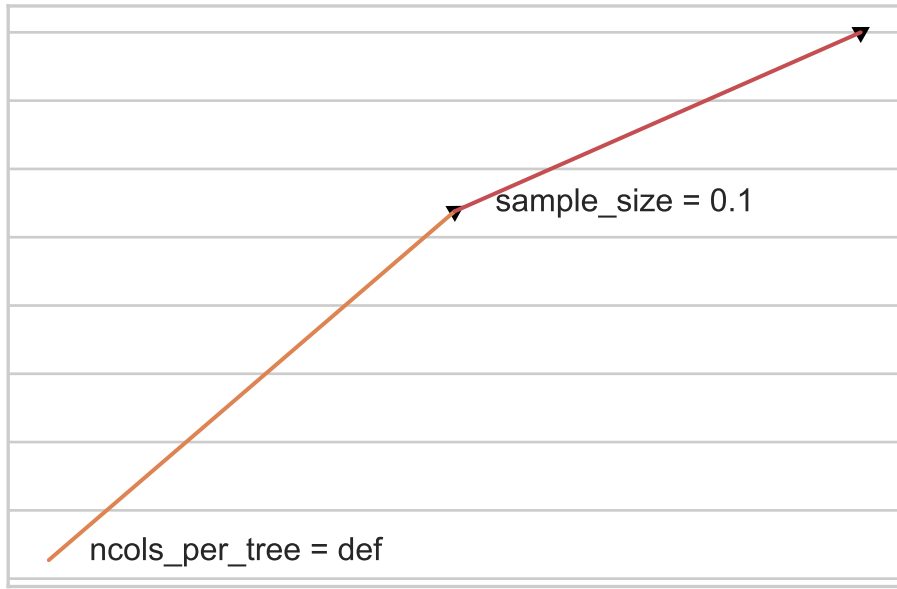


breastw

Cross-run ARI

1.0000
0.9975
0.9950
0.9925
0.9900
0.9875
0.9850
0.9825
0.9800



ncols_per_tree = def

sample_size = 0.1

standardize_data = FALSE