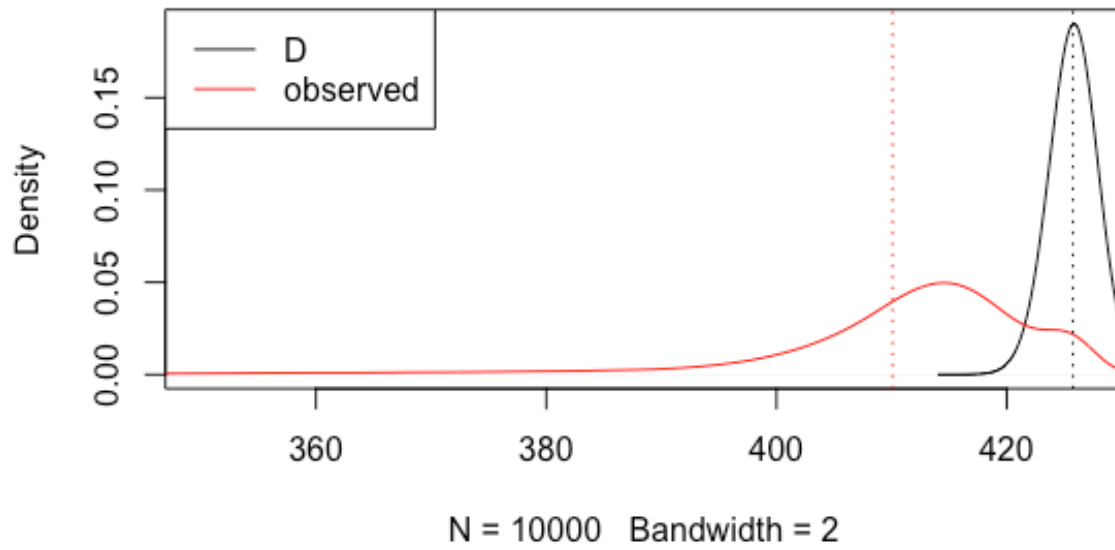
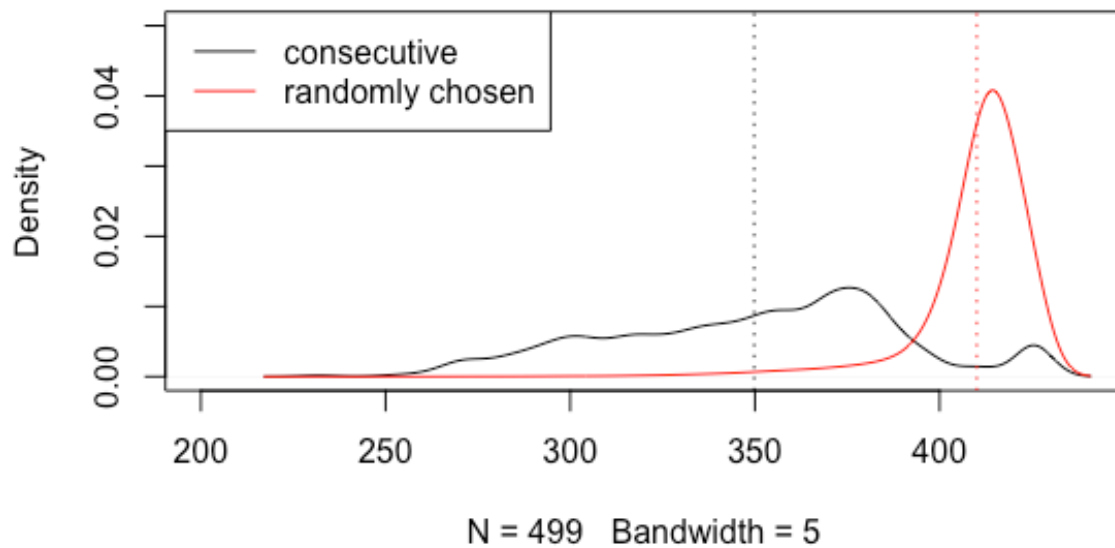


chromosome2 part(a) with mean



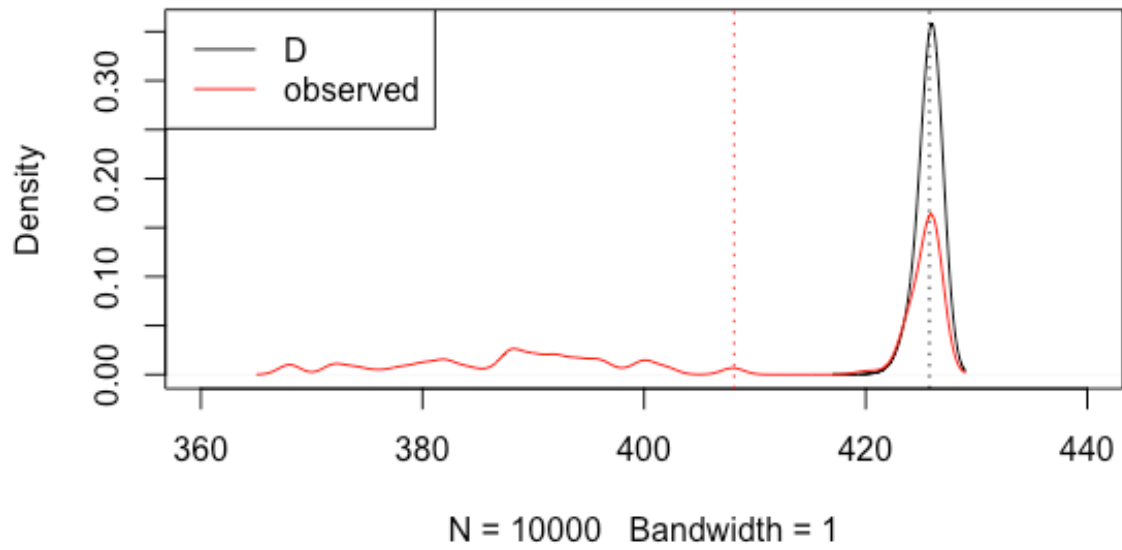
For chr2, the observed tree distances are closer to 0 than expected if the 2 trees were chosen at random uniformly.

chromosome2 part(b) with mean



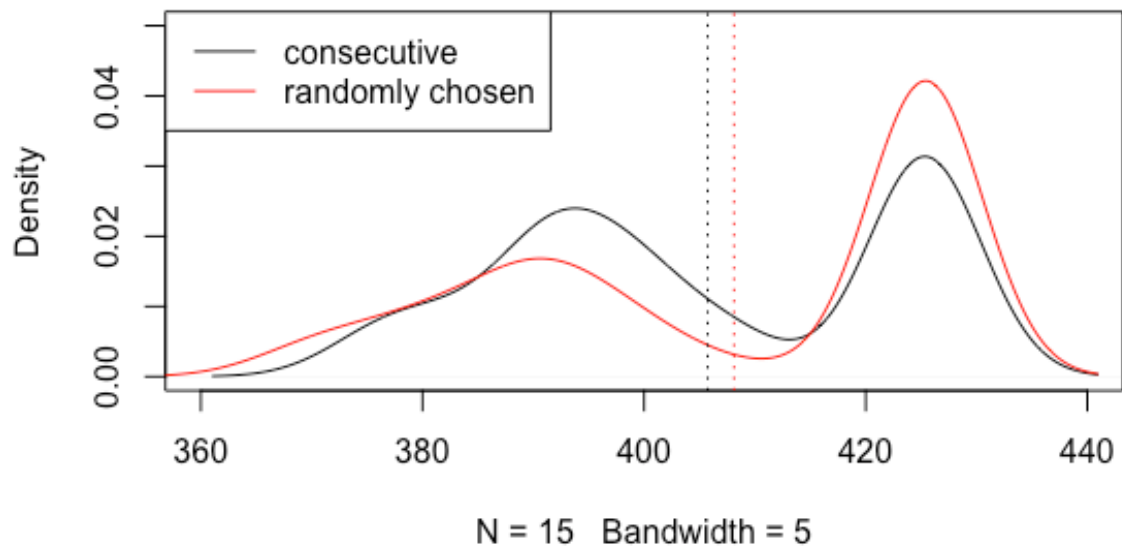
For chr2, trees from 2 consecutive blocks tend to be more similar to each other than trees from 2 randomly chosen blocks.

chromosomeC part(a) with mean



For chrC, the observed tree distances are closer to 0 than expected if the 2 trees were chosen at random uniformly.

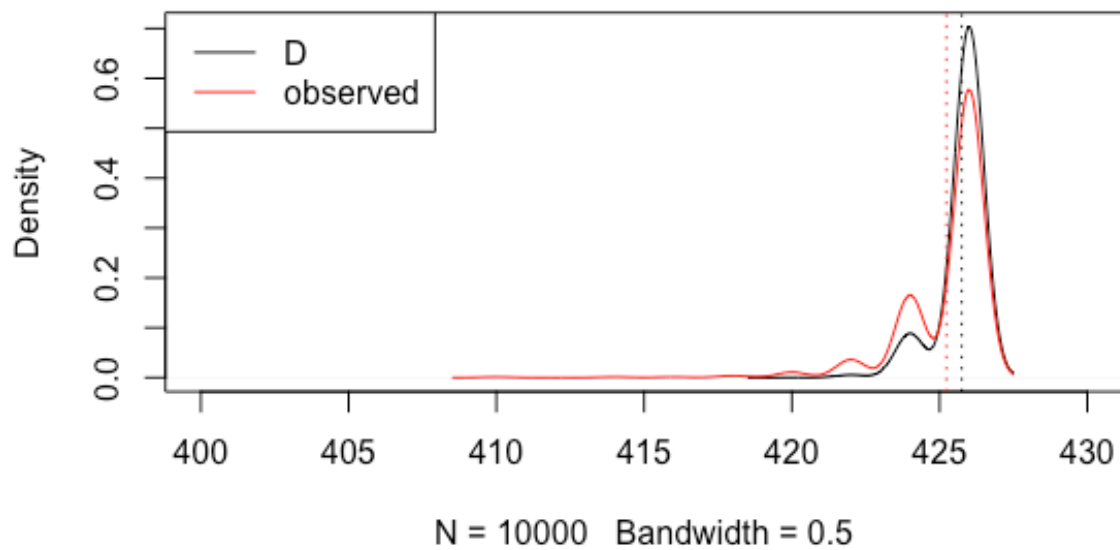
chromosomeC part(b) with mean



For chrC, trees from 2 consecutive blocks tend to be more similar to each other than trees

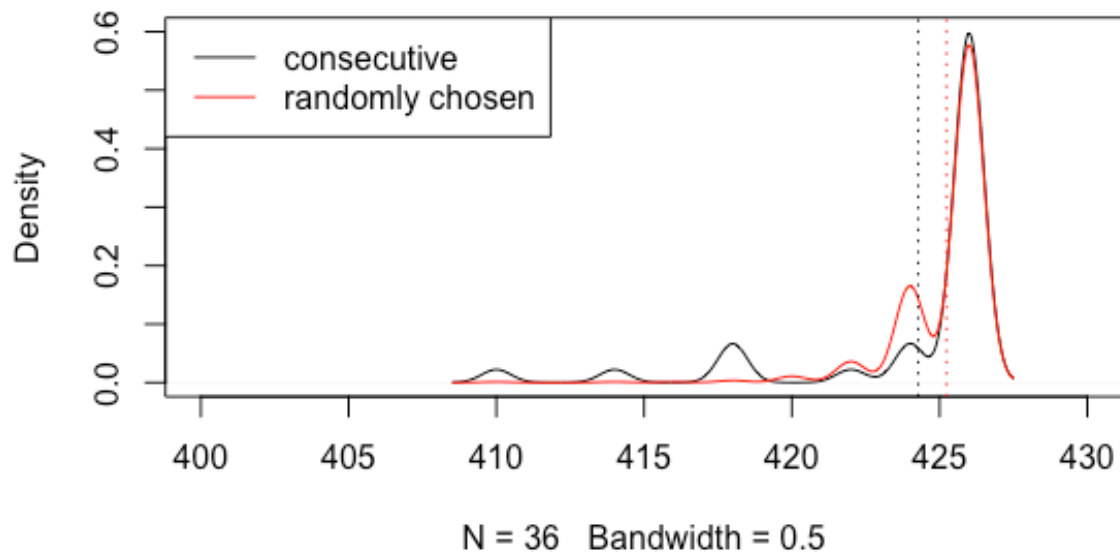
from 2 randomly chosen blocks, but the trend is much less than that of chr2.

chromosomeM part(a) with mean



For chrM, the observed tree distances closer to 0 than expected if the 2 trees were chosen at random uniformly, but the trend is much less than that of chr2.

chromosomeM part(b) with mean



For chrM, trees from 2 consecutive blocks tend to be more similar to each other than trees from 2 randomly chosen blocks, but the trend is much less than that of chr2.