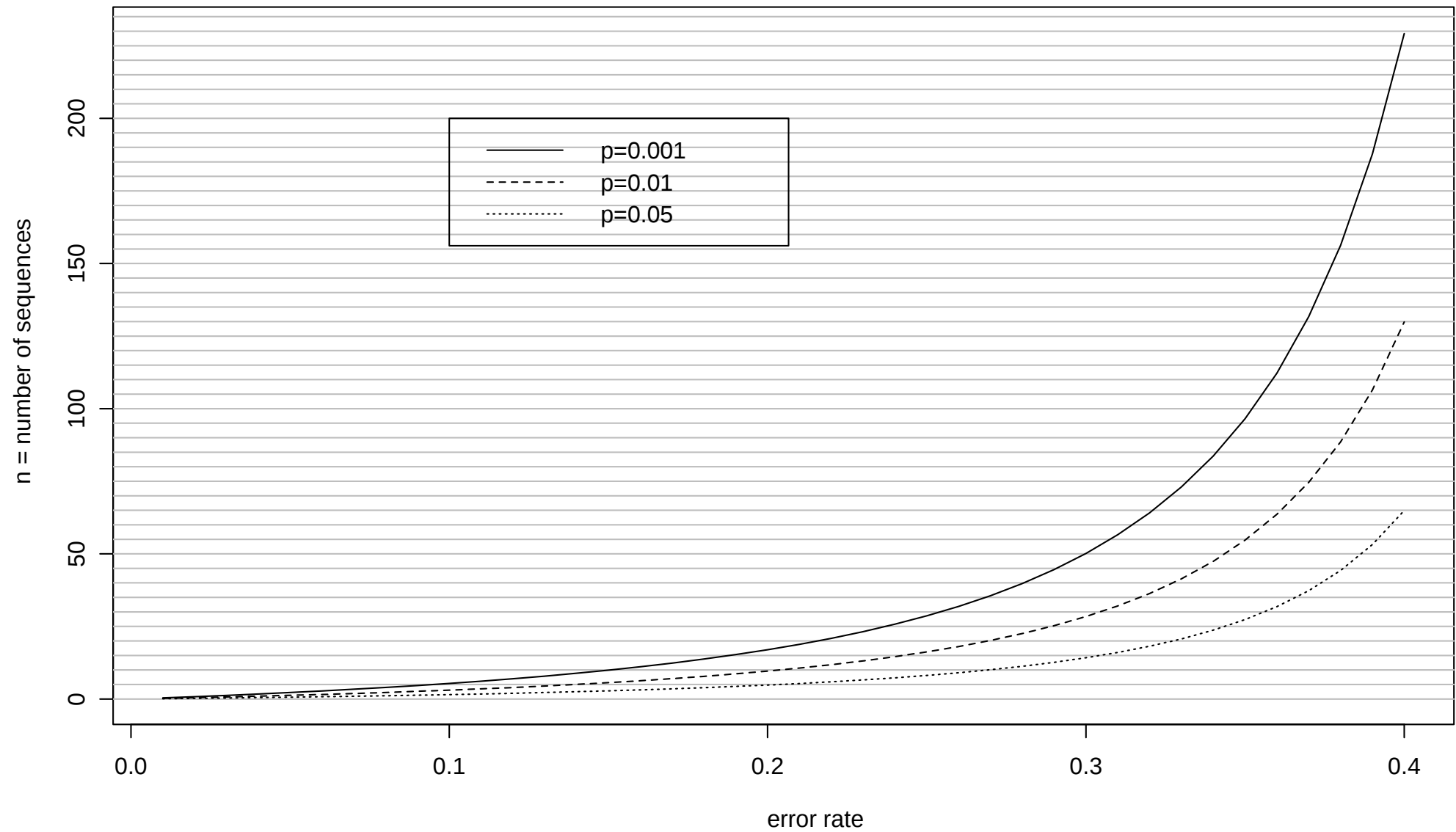


A Number of sequences necessary to obtain a majority of sequences identical to the reference



b

