## Practical 5:

1- Simulate 50000 data sets with the some conditions of Practical 4 and using the following summary statistics:

Symbol	Description
$\pi$	Mean of the pairwise difference
S	Number of segregating sites
k	Number of different haplotypes
sH	Shannon's index
mMFS	Mean of the Mutation Frequency Spectrum
sdMFS	Standard Deviation of the Mutation Frequency Spectrum

- 2 Plot the summary statistics against Ne.
- 3 Calculate Cp index between Ne and the used summary statistics.