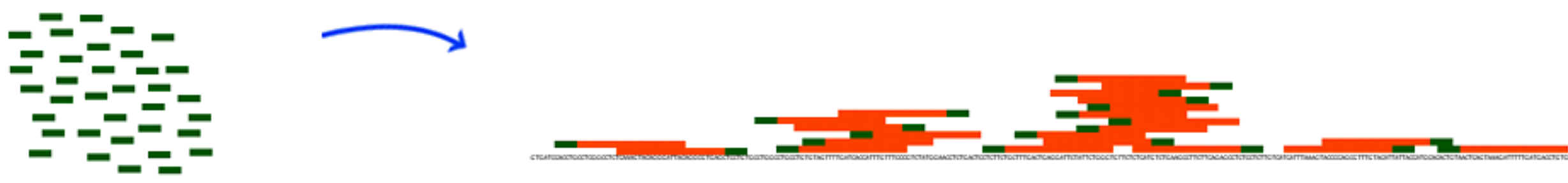
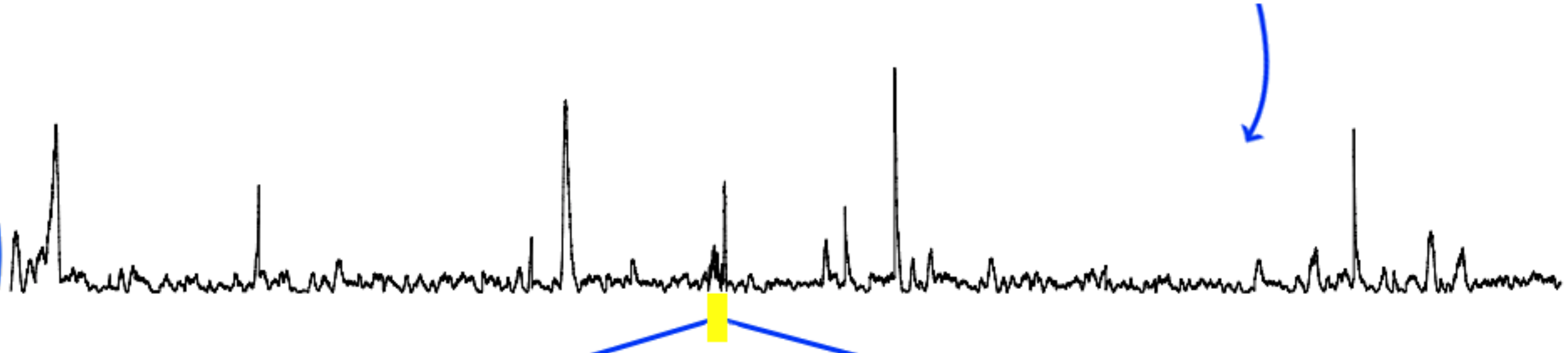


Extend aligned reads to the average fragment length.



Plot the number of extended reads containing each base pair.



Divide genome into regions and construct trees for each region.



Use tree shape statistic  $\mathcal{M}$  to call significant peaks.

