Modelling random hexamer binding

$$C_j = \sum_i [p_i t_j] = [t_j] \sum_i [p_i] \exp\left(\frac{\Delta G_{ij}}{k_B T}\right)$$

Coverage

Free binding energy

Free template sequence in the genome

Primer concentration
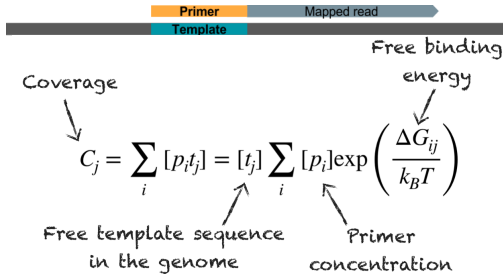
- High frequency of mismatching primer-template events
- Lack of tabulated ΔG values for non Watson-Crick base pairing
- Difficult to determine exact genomic kmer abundance for BS converted genome