Nucleosome positioning

Statistical null model
- specifically placed nucleosome
- others randomly distributed
- but don't overlap

How do we quantify the resulting distribution?
How do we compare to experimental data?

Density with distance from fixed nucleosome

\[ P(r) \iff P(r, 1 \text{ nuc at } r) \]

\[ P(r) \]

\[ d_1 \quad d_2 \quad d_3 \quad d_4 \quad \ldots \quad r \]

The distribution of \( d_i \): \( e^{-d_i} \)

\[ \Rightarrow \text{ easy to calculate the distribution of } \sum d_i \]

\[ P_h(r = \sum d_i) = \prod d_i e^{-d_i} S(r - \sum \frac{d_i}{r}) \]
solve by hand or Laplace transform

\[ \hat{P}(s) = \int_{0}^{\infty} dr \ e^{-sr} \hat{P}(r) = \int_{0}^{\infty} dr \ e^{-sr} \sum_{i} \delta(r-\Sigma_{i}d_{i}) \]

\[ = e^{-sr} \sum_{i} \delta(r-\Sigma_{i}d_{i}) \]

\[ = \frac{1}{(s+\xi)^{k-\xi}} \]

- this laplace transform has a known inverse

\[ P(r = \Sigma_{i}d_{i}) = \frac{1}{(k-\xi)!} (\xi r)^{k-\xi} e^{-\xi r} \]

- put back the excluded volume blocks

\[ \hat{q}_{a}(r) = \hat{P}(r-kb) = \frac{1}{(k-1)!} (\xi (r-kb))^{k-1} e^{-\xi (r-kb)} \Theta(r-kb) \]

- the total distribution is

\[ P(r) = e^{-\xi (r-kb)} \sum_{k=1}^{\infty} \frac{(\xi (r-kb))^{k-1}}{(k-1)!} \Theta(r-kb) \]

- at short distances only \( k=1,2 \ldots \) contribute

- at large distances, the distribution becomes flat