



At G_1 , avg length = 1, prob k_1 it transitions out of G_1

At G_2 , avg $l = 2$, prob k_2 it transitions, $1 - k_2$ it stays in gene

$$k_2 = \frac{P_2}{1 - k_1}$$

$$k_3 = \frac{P_3}{(1 - k_1)(1 - k_2)}$$

$$k_{999} = \frac{P_{999}}{(1 - k_1)(1 - k_2) \dots}$$

$$k_{1000} = 1$$

Gene is subdivided into 1000 substates according to their lengths, the probability of the gene staying inside the gene is $1 - \frac{1}{v}$ where v = average length of the gene.

We choose a variable k such that our probability of getting a gene of size k is P_k .

The transitioning k has values compounding. The probability of length 2- P_2 is $(1 - k_1) \times k_2$. Thus $k_2 = \frac{P_2}{1 - k_1}$. This can be expanded to include the entire distribution.