



# Mathematical Modeling of Mutation Rate and Population Size

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Submitted: 05-06-2021

Revised: 18-06-2021

Accepted: 20-06-2021

**ABSTRACT:** Assuming  $F_n$  to be the probability that the system will fail in the future when it is now at population level  $n$ , I had obtained a recurrence relation and solved it completely for all values of  $n$  in three different cases. Obtaining the value of  $1 - F_n$ , I computed  $F_1$  for which I had computed the optimal value. The calculation of  $F_n$  and minimum value of  $F_1$  are dealt in detail in this paper. From these calculations, we can understand an important concept regarding the shifting of proliferation to hyper-mutation of cells.

**Keywords:** Population Level, Relative Rate, Steady Rate, Recurrence Relation, Lagrange Parameters.

## I. INTRODUCTION

Beginning with a somewhat impressionistic version of this model, in which exposure to antigen (with T-cell help implied) starts the process by activating a medium affinity B-cell of a population, one mutation away from high affinity. Such a cell proliferates after

$$F_n = \frac{r}{\lambda n + mnP_n + r} + \frac{\lambda n}{\lambda n + mnP_n + r} F_{n+1} + \frac{(m-1)nP_n}{\lambda n + mnP_n + r} F_{n-1} \quad (2.1)$$

## III. SOLUTION TO THE RECURRENCE RELATION

I now choose  $\{P_n\}$  to minimize  $F_1$  by imposing the "equations of motion" with Lagrange parameters, and since these equations can be written as linear in  $P_n$ , optimal strategy will be achieved if either  $P_{\min} = 0$  or  $P_{\max} = \infty$  (finite  $P_{\max}$  gives similar results) at each  $n$ . There will then be one—and only one, it can be shown—switch point, say at  $n = n_0$ , we have

$$P_n = 0, \quad n \leq n_0 \quad (3.1) \quad \text{and}$$

$$P_n = \infty, \quad n > n_0 \quad (3.2).$$

Now using (3.2) in (2.1) by observing the fact as  $P_n = \infty$ , the first two terms in the right hand side

activation at steady rate  $\lambda$ , while the antigen is killing the infected organism at steady rate  $r$ . The population of interest is one mutated site, out of  $m$  relevant DNA sites, away from the high-affinity Ab, whose production neutralizes the Ag and so annuls the death rate  $r$ ; we assume that the mutation rate  $P_n$  is controlled by the population size  $n$ . We want to choose the repertoire  $\{P_n\}$  to minimize the probability  $F_1$  that the initially activated system fails due to death of the host organism before settling into steady high-affinity production.

## II. DEVELOPING THE MODEL

Let  $F_n$  be the probability that the system will fail in the future when it is now at population level  $n$ . The next event can either be death of the host at relative rate  $r$ , proliferation at relative rate  $\lambda n$ , or mutation of one of the  $m$  relevant DNA sites at relative rate  $mnP_n$ . But  $m - 1$  of the  $m$  mutations produce a still lower affinity cell, which is eliminated from the population and so we have the following recurrence relation

of (2.1) vanish whereas the doesn't vanish giving

$$F_n = \frac{m-1}{m} F_{n-1}, \quad n > n_0 \quad (3.3)$$

If  $n = n_0$  then from (3.1), we have  $P_n = 0$ . Using this in (2.1), we get

$$F_{n_0} = \frac{r}{\lambda n_0 + r} + \frac{\lambda n_0}{\lambda n_0 + r} F_{n_0+1}, \quad n = n_0 \quad (3.4)$$

Similarly if  $n < n_0$  using (3.1) in (2.1), we get

$$F_n = \frac{r}{\lambda n + r} + \frac{\lambda n}{\lambda n + r} F_{n+1}, \quad n < n_0 \quad (3.5)$$

Now taking  $n = n_0 + 1$  in (3.3), we get

$$F_{n_0+1} = \frac{m-1}{m} F_{n_0} \quad (3.6)$$



Substituting (3.6) in (3.4), we have

$$F_{n_0} = \frac{r}{\lambda n_0 + r} + \frac{\lambda n_0}{\lambda n_0 + r} \times \frac{m-1}{m} F_{n_0} \quad \text{from}$$

$$\text{which we get } F_{n_0} = \frac{mr}{\lambda n_0 + mr} \quad (3.7)$$

Now from (3.3), we get

$$F_n = \frac{m-1}{m} F_{n-1} = \left(\frac{m-1}{m}\right)^2 F_{n-2} = \left(\frac{m-1}{m}\right)^3 F_{n-3} = \dots = \left(\frac{m-1}{m}\right)^{n-n_0} F_{n_0} \quad (3.8)$$

where  $F_{n_0}$  is given by (3.7).

Similarly, for  $n < n_0$ , (3.5) can be written as

$$1 - F_n = 1 - \frac{r}{\lambda n + r} - \frac{\lambda n}{\lambda n + r} F_{n+1} = \frac{\lambda n}{\lambda n + r} (1 - F_{n+1}) = \frac{n}{n + \frac{r}{\lambda}} (1 - F_{n+1}) \quad (3.9)$$

Using the pattern obtained in (3.9) for  $n$  up to  $n_0 - 1$  and using (3.7) we have

$$1 - F_n = \frac{n}{n + \frac{r}{\lambda}} \times \frac{n+1}{\left(n+1 + \frac{r}{\lambda}\right)} \times \frac{n+2}{\left(n+2 + \frac{r}{\lambda}\right)} \times \dots \times \frac{n_0-1}{\left(n_0-1 + \frac{r}{\lambda}\right)} (1 - F_{n_0})$$

$$= \frac{(n_0-1)!}{(n-1)!} \times \frac{\left(n-1 + \frac{r}{\lambda}\right)!}{\left(n_0-1 + \frac{r}{\lambda}\right)!} \times \frac{\lambda n_0}{\lambda n_0 + mr}, \quad n \leq n_0 \quad (3.10)$$

In particular, for  $n = 1$ , we have

$$F_1 = 1 - \left(\frac{r}{\lambda}\right)! \frac{(n_0-1)! \times \lambda n_0}{\left(n_0-1 + \frac{r}{\lambda}\right)! \times (\lambda n_0 + mr)} \quad (3.11)$$

Now in the denominator of (3.11) we find the term

$$\left(n_0-1 + \frac{r}{\lambda}\right)!$$

Hence  $F_1$  in (3.11) will attain minimum if

$$n_0 = m \left(1 - \frac{r}{\lambda}\right) \quad (3.12).$$

Substituting the optimal value of  $n_0$  obtained in (3.12) to (3.7), we find that

$$F_{n_0} = \frac{mr}{\lambda n_0 + mr} = \frac{mr}{m(\lambda - r) + mr} = \frac{r}{\lambda} \quad (3.13)$$

#### IV. CONCLUSION

In this paper, I had derived the expression for the probability that the system will fail in the future when it is now at population level  $n$ . After

doing so, I had obtained  $F_1$  and tried to minimize it. From the minimum value of  $F_1$  obtained in (3.13), we see that one doesn't shift from proliferation to hyper-mutation until each of the  $m$  closest sequences has had its chance.

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