Part 7: Expected Fitness Change After Mutation

Given a initial genome sequence in which the following conditions are met:

a) The genome sequence can be split into w elements, each having k possible permutations.
b) The mutation rate r per element is consistent across the genome.
c) A single mutation can transform any given element into any of the other possible element permutations.

If $F(h_x)$ is the fitness contribution of an individual element, and if $F_e(h)_{rnd}$ is the expected fitness for a random element, (the average combined fitness of all of the permutations possible for an element,) we have:

$$\boxed{F_e(g)_{rnd}=w\cdot F_e(h)_{rnd}}$$

That is, the expected fitness for a random genome is equal to the expected fitness for a random element times the number of elements in the genome.

Now, for a given element, $F(h_x)$, the expected fitness for a random element can be expressed as follows:

$$F_e(h)_{rnd}=\frac{1}{k}F(h_x)+\sum_{i=1,i\neq x}^{k}\frac{1}{k}F(h_i)$$

$$\boxed{F_e(h)_{rnd}=\frac{1}{k}(F(h_x)+\sum_{i=1,i\neq x}^{k}F(h_i))}$$

Therefore,

$$\boxed{\sum_{i=1,i\neq x}^{k}F(h_i)=k\cdot F_e(h)_{rnd}-F(h_x)}$$

Now on mutation, for a true mutation to occur, the element must change from what it was before into one of the other possible element permutations. Thus, the expected fitness after mutation ($F_e(t_x)_{mut}$) must be:

$$F_e(t_x)_{mut}=\sum_{i=1,i\neq x}^{k}\frac{F(h_i)}{(k-1)}$$

$$\boxed{F_e(t_x)_{mut}=\frac{1}{(k-1)}\sum_{i=1,i\neq x}^{k}F(h_i)}$$

And, from what we discovered above, this means:

$$\boxed{F_e(t_x)_{mut}=\frac{k\cdot F_e(h)_{rnd}-F(h_x)}{(k-1)}}$$

The fitness change per element can then be calculated fairly easily:

$$F_e(t_x)_{mut}=F(h_x)+\Delta F_e(t_x)_{mut}$$

$$\Delta F_e(t_x)_{mut}=F_e(t_x)_{mut}-F(h_x)$$

$$\Delta F_e(t_x)_{mut}=\frac{k\cdot F_e(h)_{rnd}-F(h_x)}{(k-1)}-F(h_x)$$

$$\Delta F_e(t_x)_{mut}=\frac{k\cdot F_e(h)_{rnd}-F(h_x)-(k-1)\cdot F(h_x)}{(k-1)}$$

$$\Delta F_e(t_x)_{mut}=\frac{k\cdot F_e(h)_{rnd}-k\cdot F(h_x)}{(k-1)}$$

$$\boxed{\Delta F_e(t_x)_{mut}=\frac{k}{(k-1)}(F_e(h)_{rnd}-F(h_x))}$$

Given that r is the mutation rate per element, the expected fitness change per element for the next generation will then be:

$$\Delta F_e(t_x)=r\cdot\Delta F_e(t_x)_{mut}$$

$$\boxed{\Delta F_e(t_x)=\frac{r\,k}{(k-1)}(F_e(h)_{rnd}-F(h_x))}$$

Summing over the entire genome, we have:

$$\Delta F_e(m_x)=\sum_{i=1}^{w}(\frac{r\,k}{(k-1)}(F_e(h)_{rnd}-F(h_x)))$$

$$\Delta F_e(m_x)=\frac{r\,k}{(k-1)}\sum_{i=1}^{w}(F_e(h)_{rnd}-F(h_x))$$

$$\Delta F_e(m_x)=\frac{r\,k}{(k-1)}(\sum_{i=1}^{w}F_e(h)_{rnd}-\sum_{i=1}^{w}F(h_x))$$

$$\Delta F_e(m_x)=\frac{r\,k}{(k-1)}(w\cdot F_e(h)_{rnd}-F(g_x))$$

$$\boxed{\Delta F_e(m_x)=\frac{r\,k}{(k-1)}(F_e(g)_{rnd}-F(g_x))}$$

To get the average expected change over the entire population, we simply take the sum of the changes in the population, and divide by the population size.

Since our calculations assume a fixed number of children per parent, we can calculate the expected average according to the parents' size as follows:

$$\Delta F_e(m_{avg})=\frac{1}{n_g}\sum_{i=1}^{n_g}\frac{r\,k}{(k-1)}(F_e(g)_{rnd}-F(g_x))$$

$$\Delta F_e(m_{avg})=\frac{r\,k}{n_g(k-1)}\sum_{i=1}^{n_g}(F_e(g)_{rnd}-F(g_x))$$

$$\Delta F_e(m_{avg})=\frac{n_g\cdot r\cdot k}{n_g(k-1)}F_e(g)_{rnd}-\frac{r\,k}{n_g(k-1)}\sum_{i=1}^{n_g}F(g_x)$$

$$\Delta F_e(m_{avg})=\frac{r\,k}{(k-1)}F_e(g)_{rnd}-\frac{n_g\cdot r\cdot k}{n_g(k-1)}F(g_{avg})$$

$$\boxed{\Delta F_e(m_{avg})=\frac{r\,k}{(k-1)}(F_e(g)_{rnd}-F(g_{avg}))}$$

The function that results is linear, with a maximum value of:

$$\frac{r\,k}{(k-1)}F_e(g)_{rnd}\quad\text{for}\quad F(g_{avg})=0$$

And a minimum value of:

$$\frac{r\,k}{(k-1)}(F_e(g)_{rnd}-F(g)_{max})\quad\text{for}\quad F(g_{avg})=F(g)_{max}$$

A value of zero is attained when $F(g_{avg})=F_e(g)_{rnd}$.

As long as $F(g_{avg})$ is less than the expected random value, the fitness can be expected to increase. After a fitness value above the expected random value is obtained, natural selection must be utilized in order to overcome the negative trend.