S.O. + functional (only component A)

Let us go back to the information given by the initial condition. Given that the *complexity* is given by $\sim \frac{1}{q}$, the equation is:

$$k = n(1 - H(q))$$

and we may rewrite n in the form of α and n_0 as:

$$n = \frac{n_0}{1 - \alpha}$$

Now going back to the image of the Self Organised plus the functional Component.

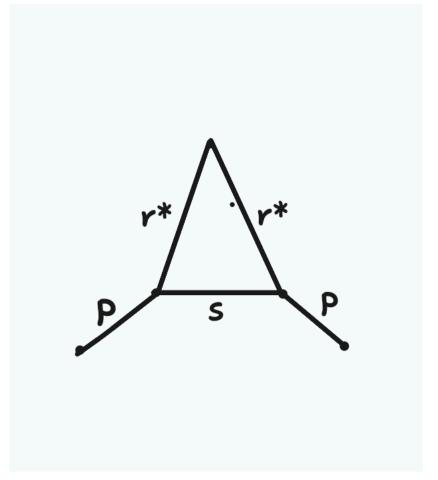


Figure 1: The constraint diagram for self organised copying with a functional constraint, note that the r^* in the figure is just \hat{r} . I didn't have the functionality to add hat on top of a variable in the paint software that was used to create the image.

We define r to be the following (note that $r^* = \hat{r}$).

$$\begin{split} r &= \hat{r} \oplus p \\ \hat{r} &= \left(\frac{1}{2}\right) \frac{r-p}{\frac{1}{2}-p} \end{split}$$

if the strings are generated iid with bernoulli trials, of length l_s each then the probability of finding a string with some empirical probability distribution of the element as $\{q\}$ when the probability of the underlying thing is given by $\{p\}$ is:

$$\mathcal{P} = 2^{-l_s D_{KL}(\tilde{q} \| p)}$$

Thus the probability of finding two strings with the relative distance s with each other while both mutually being at a distance \hat{r} from some other string (calculation can be done for a string of all zeros).

from the normalisation condition,

$$\tilde{q}_1 + \tilde{q}_2 + \tilde{q}_3 + \tilde{q}_4 = 1$$

and the conditions on relative distances will give three more equations,

$$\begin{split} \hat{r} &= \tilde{q}_2 + \tilde{q}_3 \\ \hat{r} &= \tilde{q}_3 + \tilde{q}_4 \\ s &= \tilde{q}_2 + \tilde{q}_3 \end{split}$$

one can solve for \tilde{q} 's and then get the following,

$$\begin{split} \tilde{q}_1 &= 1 - \frac{1}{2}(2\hat{r} + s), \\ \tilde{q}_2 &= \tilde{q}_3 = \frac{s}{2}, \\ \tilde{q}_4 &= \hat{r} - \frac{s}{2} \end{split}$$

for a randomly drawn string with bernulli trial and $p_0=p_1=\frac{1}{2}$ then, we can compute the $D_{KL}(q\|p)$ easily,

$$\begin{split} D(q\|p) &= \sum q_i \log \left(\frac{q_i}{p_i}\right) \\ D(q\|p) &= \sum q_i \log(4q_i) \\ D(q\|p) &= 2 + \sum q_i \log(q_i) \\ D(q\|p) &= 2 - H(\{q\}) \end{split}$$

thus the probability of finding these strings is:

$$\begin{split} \mathcal{P} &= 2^{-\alpha n(2-H(\{\tilde{q}\}))} \\ &\log \left(\frac{1}{\mathcal{P}}\right) = \alpha n(2-H(\tilde{q})) \end{split}$$

and the number of initial condition and genomic information bits:

$$\begin{split} k + l &= \alpha n (2 - H(\{\tilde{q}_i\})) \\ l &= \alpha n (2 - H(\{\tilde{q}_i\})) - k \\ l &= n (\alpha (2 - H(\{\tilde{q}_i\})) - (1 - H(q))) \\ l &= \left(\frac{n_0}{1 - \alpha}\right) [\alpha [2 - H(\{\tilde{q}_i\})] - [1 - H(q)]] \end{split}$$