C Appendix: Arbitrary Initial Distribution

The solution for an arbitrary initial distribution: $N_{init}(m)$, requires solving (22) subject to different boundary conditions at $t = 0$; the terms proportional to $A_m$ are the same, the term proportional to $N_0$ is replaced by the superposition of new terms describing the propagation of each bin of initial histogram:

$$F(m, t) = \sum_{i=1}^{\infty} N_{init}(i) \psi_i(m, t) + A_m(\phi - \phi^{-\frac{m}{i+\pi}}) - \sum_{i=1}^{m-1} A_i \psi_i(m, t)$$

$$\psi_i(m, t) = \begin{cases} 0 & \text{if } m < i \\ \beta_i^{i-\frac{m}{i+\pi}} (1 - \phi^{-\frac{m}{i+\pi}})^{m-i} & \text{for } m \geq i \end{cases}$$  (35)

with the same definitions for $A_{m}$ and $\beta_{m}^{i}$ as before. These are derived by following by successive integration in the same way as was done in Appendix A.

The fact that $\psi_i(m, t) = 0$ for $m < i$ reflects the fact that there is no gene deletion; genes that start in bin $i$ may either stay put or advance to bins corresponding to larger fold sizes, but will never populate bins of fold size less than $i$.

One important conclusion may be drawn from the full solution: all initial distributions ultimately lead to the the same limiting distribution determined by the $A_m$. Just as before, the dependence on the initial fold distribution $N_{init}(m)$ decays with time, leading to the same asymptotic distribution as was found for an initial distribution of $N_0$ folds of size 1 in (9). Of course, the details of how the crossover happens will depend on the particular form of $N_{init}(m)$.  

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