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Fix N . Let $\{z_1, z_2, \dots\}$ be an i.i.d. sequence of random choices from the set $\{1, 2, \dots, 2N\}$. Let $(y_{n,1}, y_{n,2}, \dots, y_{n,2N}) = (z_{2N(n-1)+1}, z_{2N(n-1)+2}, \dots, z_{2Nn})$. We construct a process (X^n) as follows: $X^0 = (1, 2, \dots, 2N)$, and $X_i^{n+1} = X_{y_{n+1,i}}^n$; i.e. the sequence X^{n+1} is obtained by random sampling from X^n .

We can think of the process (X^n) as a sequence of “populations”. (X^n) is a Markov chain having the constant sequences as absorbing states. (X^n) can also be used as a base structure for the construction of other Markov Chains. For example, if we initially label some of the elements of $\{1, 2, \dots, 2N\}$ as a certain type of allele, then the sequence which counts that allele in each population is a Markov Chain with state space $\{0, 1, 2, \dots, 2N\}$. This is the well-known Wright-Fisher model of pure genetic drift.

We will analyze other objects related to the the chain (X^n) , such as the distribution of the absorption time. This research is part of a grant, “Who Pulls the Random Strings in Neural Evolution”, at Samford University, which concerns evolving genomes that generate neural networks. In the general case, successive populations are determined using a genetic algorithm. (Received September 16, 2014)