## Shuffling Cards and Genes

Let us consider the following modified version of the card shuffle. As before, the card shuffle is a Markov chain on the permutation group $\mathrm{S}_{n}$, but this time the permutation $\sigma_{t}$ obeys the following Markov chain: at each time step, pick an index $i_{t+1}$ uniformly from $\{1, \ldots, n-1\}$ and set

$$
\sigma_{t+1}(j)=\left\{\begin{array}{ll}
\sigma_{t}(j+1) & j=i_{t+1} \\
\sigma_{t}(j-1) & j=i_{t+1}+1 \\
\sigma_{t}(j) & \text { otherwise }
\end{array} .\right.
$$

If we were allowed to transpose any two elements at random, we found that this had a mixing time $\tau \sim$ $n \log n$. In this problem, we will show that the above Markov chain, with only neighboring transpositions allowed, has a mixing time $\tau \lesssim n^{3} \log n$.

To solve this problem, we will use coupling. The chains we will couple will be the forward and backward chains $\sigma_{t}^{\mathrm{F}}$ and $\sigma_{t}^{\mathrm{B}}$, which start from the initial conditions $\sigma_{0}^{\mathrm{F}}(a)=\sigma_{0}^{\mathrm{B}}=(n-a)$. The chains will each evolve as the chain above, except in the case where $\sigma_{t}^{\mathrm{F}}\left(i_{t+1}\right)=\sigma_{t}^{\mathrm{B}}\left(i_{t+1}+1\right)$ or $\sigma_{t}^{\mathrm{B}}\left(i_{t+1}\right)=\sigma_{t}^{\mathrm{F}}\left(i_{t+1}+1\right)$. In this case, one of the chains is picked uniformly at random, and only that chain is switched.
(a) Let us denote $D_{t}(a)$ as the (positive-valued) distance between $a$ in the F and B chains. Show that $\left|D_{t+1}(a)-D_{t}(a)\right| \leq 1$, and that

$$
\begin{aligned}
& \mathrm{P}\left(D_{t+1}(a)=D_{t}(a)+1 \mid D_{t}(a), \sigma_{t}^{\mathrm{F}}, \sigma_{t}^{\mathrm{B}}\right)=\frac{1}{n-1} \quad\left(0<D_{t}(a) \leq n-1\right) \\
& \mathrm{P}\left(D_{t+1}(a)=D_{t}(a)+1 \mid D_{t}(a), \sigma_{t}^{\mathrm{F}}, \sigma_{t}^{\mathrm{B}}\right) \leq \frac{1}{n-1} \quad\left(0<D_{t}(a)<n-1\right)
\end{aligned}
$$

and show that $D_{t}(a)=0$ is an absorbing state.
(b) Let $X_{t}$ be a random walk on $\{0, \ldots, n-1\}$ with the same transition rules as above (but with the latter equation replaced by an equality): i.e., with probability $(n-1)^{-1}$, the walker will move either left or right, except at a boundary or at 0 . Let

$$
\begin{aligned}
\tau_{a} & =\inf \left(t: D_{t}(a)=0\right), \\
\tau_{a}^{X} & =\inf \left(t: X_{t}=0 \mid X_{0}=n+1-2 a\right) .
\end{aligned}
$$

Show that $\tau_{a} \leq \tau_{a}^{X}$, if we appropriately match the steps of the random walk to the shuffle.
(c) Using techniques that we used for random walks on the line, find the explicit expression for $\tau_{a}^{X}$.
(d) Use Markov's inequality to show that $\mathrm{P}\left(\tau_{a}>n^{3}\right)<1 / 2$ for any $a$, and use this result to determine a good upper bound for $\mathrm{P}\left(\tau_{a}>2 n^{3} \log _{2} n\right)$.
(e) Conclude that the mixing time $\tau \lesssim 2 n^{3} \log n$ in the limit of $n$ large.

With some clever techniques for estimating lower bounds on mixing times, one can show that $\tau \sim n^{3} \log n$ precisely, although this is above the scope of this problem.

This is also a toy model for the biological problem of mutations in DNA. As DNA. which is a long sequence of base pairs, is replicated in cells, sometimes the cell makes a mistake, and may transpose two base pairs. We thus have a rough time scale for how long it should take for us to "lose track" of what our ancestors' DNA was.

