In the Wright-Fisher model, the $2N$ copies of a locus in consideration could come either from $N$ diploid individuals (who have two copies of their genetic material in each cell) or $2N$ haploid individuals (who have one copy of their genetic material in each cell). Consider Moran model with one type of mutation. We think of $n = 2N$ haploid individuals, and a genetic locus with two alleles $A$ and $a$ that have the same fitness. This model evolves as following:

(i) At each time step, an individual chosen uniformly at random out of $n$ individuals is being “replaced”.

(ii) To replace individual $x$, we choose at random from the set of individuals, including $x$ itself.

(iii) An allele $A$ that is chosen mutates to allele $a$ with probability $\rho > 0$, while $a$ doesn’t mutate to $A$.

**Problem 1.** Let $S = \{0, 1, 2, \ldots, n\}$ be the sample space and $X_t$ be the number of alleles $A$ at time $t$. Write down the transition probabilities for the Markov chain $X_t$ over the state space $S$. Next, properly define the fixation time $T_f$.

**Problem 2.** Compute the average fixation time given that the Markov chain begins with $j$ alleles $A$, i.e. find

$$E[T_f \mid X_0 = j].$$

Is there a differential equations approach?