

5. To see when a particular animal dies, we can
 - a. Construct a graph connecting all the animals $[1...n]$, with edge weights of C_v . (Linear time). More specifically,
 - i. We have 2 states: the alive/just infected state and the contagious state.
 - ii. We can treat the alive/just infected state as a node a_i and the contagious state b_i , where $i \in [1...n]$.
 - iii. Then, connect a_i to b_i with an edge weight of C_v , showing the transition to contagion.
 - iv. Connect b_i to a_{i+1} with an edge of weight 0. This is because once an animal gets contagious, its neighbors will immediately become infected.
 - v. We can simplify this graph by just connecting all the animals $[1...n]$, with edge weights of C_v .
 - b. Create some source node s that connects to all $S \in [1...n]$. Make the edge weights of these 0. (Less or perhaps equal to than linear time)
 - c. Run Dijkstra, so we see which animals will die.
 - i. Runs in $O((|V| + |E|)\log(|V|))$; however, we assume each cage/animal is surrounded by at most 8 other animals/cages. We can restate the runtime:
 $O((|V| + 8|V|)\log(|V|)) \rightarrow O(9|V|\log(|V|)) \rightarrow O(n\log(n))$
 - d. Dijkstra tracks the shortest path to some node v using the array $d[v]$. Each entry in this array will be the sum of the weights (C_v). Whatever $d[v]$ is for some node, this will be the time of infection of this animal.
 - e. Death of an animal happens D_v after $C_{v(\text{aggregate})}$, where $C_{v(\text{aggregate})} = d[v]$.
 - f. Therefore, death of each animal happens $d[v] + D_v$.