Conventional Kinesin is an important motor protein in axonal transport. It is well studied through gliding motility assays and bead motility assays. However, the stepping chemical cycle is complex. This makes it difficult to predict how changes in rate constants within the cycle may affect processivity, velocity, or stall force. To probe this, I have written a simulation of kinesin walking using a Markov Chain Monte Carlo method. The transition to each state is the kinetic rate constant. This model allows for interactions between each head, and it does not exclude states that do not appear on the average cycle. The paths to these states are unlikely, but the probability to reach them is not zero. The simulation allows for a force to aid and inhibit the stepping process, and the concentration of ATP, ADP, and Pi can be adjusted to match experiments. Because of this back stepping and other rare phenomenon of kinesin processivity can be studied. The simulation can be set to match lab conditions and thus can provide greater insight into experiments.