Exercise 3: Run your code. How do your results differ from your simulation of bond vibrations for an isolated HF molecule? Does our system reach thermal equilibrium with a well-defined temperature: i.e. do the energies seem to converge to some sort of steady state? If so, is the well-defined temperature to which our system converges the temperature used in the simulation?

**The results different from the stimulation of bond vibrations for an isolated HF molecule is that its separate closed. This system that is show its not as isolated as the one we did before. The system that we are doing is shown through drag or random perturbation that are computed for the BBK system.**

Exercise 4: Rerun the code a few times, exploring what happens when you change the length of the timestep and change the value of gamma. Do the ranges for the initial conditions make sense? How would you evaluate the reasonability of the initial conditions or other parameters such as the length of the timestep or value of gamma?

**The ranges of the initial conditions make sense when running the codes a few times. When the gamma changes, the graph changes by increasing the size and decreasing.**