At first glance, robots and molecules have little in common. Robots are commonly thought of as tools that perform tasks such as vacuuming the floor, while molecules play essential roles in many biochemical processes. However, the functionality of both robots and molecules is highly dependent on their motions. In the case of robots, complex spaces and many specialized planning methods can make finding feasible motions an expert task. In the case of protein molecules, several diseases such as Alzheimer's, Parkinson's, and Mad Cow Disease are associated with protein misfolding and aggregation. Understanding of molecular motion is still very limited because it is difficult to observe experimentally. Therefore, computational tools are essential to enable researchers to plan and understand motions.

In this talk, we draw from our unique perspective from robotics to present a novel computational approach to approximate complex motions of protein and RNA molecules. We will show results that capture biological findings for several protein and RNA molecules.