Motions for Complex and High-Dimensional Robots

Lydia Tapia\(^1\), Aleksandra Faust\(^2\), Nick Malone\(^3\), and Kasra Manavi\(^1\)
Collaborators: Nancy Amato\(^1\), Rafael Fierro\(^4\), Ron Lumia\(^5\), Shawna Thomas\(^4\), and John Wood\(^3\)

\(^1\)University of New Mexico, Department of Computer Science
\(^2\)University of New Mexico, Department of Electrical and Computer Engineering
\(^3\)University of New Mexico, Department of Mechanical Engineering
\(^4\)Texas A&M University, Department of Computer Science and Engineering

Contact: Lydia Tapia, tapia@cs.unm.edu

Tasks performed by robots, such as swarms of flying robots carrying valuable cargo, or robot arms learning to control several interconnected joints while interacting with humans, can require the orchestrated control and/or learning of many degrees of freedom. Similarly, antibodies aggregating on cell surfaces in order to initiate a cell-signaling response, need a correct sequence of molecular motions. The difficulty of studying these types of motion-based problems is that they are often very complex of high dimensionality, and require considerable computing power. For example, a single antibody consists of tens of thousands of atoms and aggregation can involve tens of thousands of antibodies. Our research aims to understand how to simulate these complex and high-dimensional motion-based search problems with intelligent motion planning techniques. This work addresses important questions of analysis and feasibility in both robotic and biological domains. While these sound like divergent domains, we use a single approach to solve these high-dimensional, complex problems. This approach entails the search of high-dimensional representations, the space of all possible configurations or actions, for each type of problem.

Molecular Motion Modeling

In order to computationally study interesting, large, and biologically relevant molecules, we have used a robotics-based technique for studying molecular motions. This method is derived from probabilistic roadmap methods (PRMs) that build a graph, or roadmap, where conformations are represented as vertices and transitions between conformations represent edges. The roadmap we construct approximates a molecule’s energy landscape. As shown (right), the energy landscape relates conformations to energy. While each molecule has its own unique landscape, the global minimum of each landscape is the lowest energy point, the native state. The unique physical features of a folding landscape, e.g., the hills and valleys, determine the folding behavior for that molecule. Our approximate map of the landscape quickly and efficiently captures the principal features of the landscape through both global views of the folding process and microscopic views of many (typically thousands) folding pathways. Our new techniques have been able to capture kinetic events that have been shown in lab experiments, such as the folding rates for protein G and its mutants, NuG1 and NuG2. We are currently extending this work to study molecular interaction problems.
Planning with Model Uncertainty

Safety-PRM is a method for roadmap construction that can be used in robotic workspaces with uncertainties in the model. For example, these can be inaccuracies that are caused by sensor error when an environment model was constructed. The uncertainty is encoded into the roadmap directly through the incorporation of non-binary collision detection values, i.e., a probability of collision. We refer to this new roadmap as a Safety-PRM because it allows tunability between the expected safety of the robot and the distance along a path.

To validate Safety-PRM, we have explored the distortion of known environments by different error models with varying amounts of error and compared Safety-PRM’s performance to standard planning methods that do not account for model error. Paths are planned on the distorted environments and then tested against the known (error-free) environments. We have shown that we can generate paths that guarantee collision avoidance and that allow the robot to maintain high clearance from obstacles, with less computation time than comparable methods. Roadmap construction has been shown to be embarrassingly parallel, and often several runs are required to evaluate the impact of the stochasticity of the underlying PRM.

Motion-based Task Learning

Robots and agents, especially multi-agent systems, operate in high-dimensional state and action spaces. To perform complex motion-based tasks autonomously, they need to first learn the task, and later to plan a trajectory that accomplishes the goal. To learn a task, the agents observe large number of samples. Between ten and one-hundred thousand samples are typically needed. The system examines each sample for all possible outcomes to select the best one and build an internal policy. After the task is learned, planning motion selects a series of actions that transition the system from a start state to the goal state. At each planning step, all possible outcomes are examined and the best one is selected according to the learned policy. The number of possible outcomes for each sample grows exponentially with the dimensionality of the agent’s action space. Action space of a single agent system can be 3 dimensional, and the action space for multi-agent system can be represented by the sum of the dimensionality of individual agents. For high-precision tasks, even for a single agent, over 1 million outcomes are possible. For example, a quadrotor carrying a suspended load with minimal residual oscillations, has a 3-dimensional action space, and 2.2 million outcomes that it must examine at every step. Since it requires 90,000 samples to learn the task, the learning takes over 200 billion operations. In the planning phase, to create a 10 second trajectory at 50Hz, the agent must examine over 1 billion operations. Fortunately, the samples and outcomes can be examined independently and in parallel. High performance computing brings the processing into practically feasible realm for offline motion-based task learning.

References

Website: http://www.cs.unm.edu/amprg/

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