

# CS440 Project Description: Motion Planning for Closed Chains

Hamidreza Chitsaz

## 1 Overview

Closed chains are ubiquitous. Look at your feet while standing or at your hand when you hold a door handle to open; see Figure 1. Look at your both hands while manipulating an object or when you shake hands with a friend. Also, biomolecules almost always contain multiple nested closed chains, ranging from carbon hexagons to amino-acid bonds and base pairing in nucleic acids; see Figure 2. Motions of closed chains play critical role in our day to day life. Particularly, in this interactive world, robots ought to be able to reason and plan for closed chain motion arising from interaction with other robots, humans (e.g. hand shaking), articulated objects, etc. In this class of projects, you will develop uniform configuration sampling and implement RRT\* and PRM for closed chains.

There have been a number of studies on motion planning for closed chains [1, 2, 3, 4, 5, 6]. For instance, Trinkle and Milgram characterized the geometry and topology of closed chains in 2D and 3D without considering (self or obstacle) collisions [4]. Recently, Zhang and others gave a configuration sampling algorithm for closed kinematic chains [6]. In almost all of those works, sampling-based path planners are deployed to study motion of closed kinematic chains. A key component of sampling based planners is a uniform configuration sampler as it has been shown that sampling bias can significantly affect the performance of such planners [7].

## 2 Uniform sampling

An efficient, uniform sampler for closed kinematic chains can potentially elevate the performance of path planners particularly for highly articulated chains. Recently, an efficient and provably uniform configuration sampling algorithm for closed chains in 3D has been given [8, 9].

The idea is to decompose the configuration of a closed chain into three components: (i) a rotation in  $SO(3)$ , (ii) a point in a convex polytope, and (iii) dihedral angles that lie on a high dimensional torus; see Figure 3. A theorem states that uniform sampling of each of the three components will result in uniform sampling of the entire configuration [9]. We know how to uniformly sample  $SO(3)$ ; we know how to uniformly sample a torus; it remains to uniformly sample a convex polytope. Cantarella and Shonkwiler showed that when the closed chain is equilateral, i.e. link lengths are all equal, the convex polytope can be transformed into a hypercube in which case uniform sampling would be trivial. Otherwise, an algorithm called hit-and-run (Monte Carlo) can be used to sample the convex polytope [8]. The convex polytope arises from triangle inequality on all the interior edge lengths, i.e.  $1 \leq d_1 + d_2$  in Figure 3 as the link lengths are all assumed to be 1.



Figure 1: Opening a door by the Boston Dynamics robot. Notice multiple closed chains formed by the legs, arm, and the door.

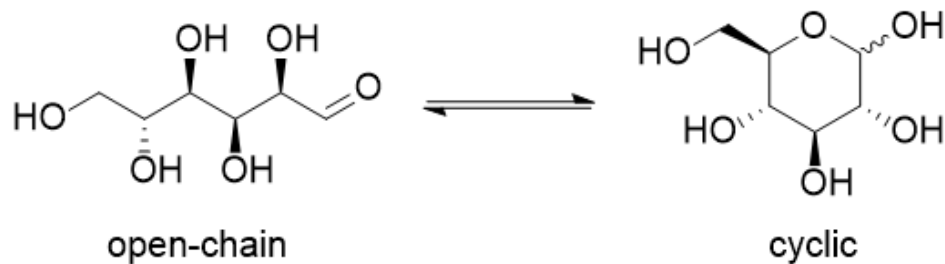


Figure 2: Open and closed chain configurations of an organic molecule.

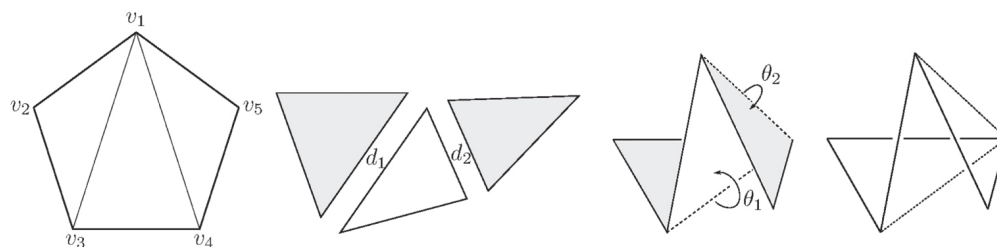


Figure 3: Demonstration of interior edge lengths and dihedral angles. Obtained from [8].

### 3 Probabilistic planners: RRT and PRM

You will develop and use the uniform sampler explained above in RRT and PRM and will compare the results with those of RRT and PRM with off-the-shelf sampling algorithms. We would like to test the hypothesis that dynamic domain RRT with uniform sampling outperforms all other planners. You will test on highly entangled closed chains with multiple nested ones, e.g. RNAs, RNA-RNA interaction [10, 11], proteins, multi-arm manipulation, etc.

### 4 Practical considerations

You would benefit from some ROS packages such as *chomp*, *MoveIt!*, *ompl*, and *sbpl*. It is recommended that you download and install ROS and some of the motion planning packages that come with ROS. Try to create a simple closed kinematic chain model and run some off-the-shelf planning algorithms such as RRT\* and PRM. Finally, implement uniform sampling in those planners and compare with the naïve sampling performance.

### References

- [1] S. M. LaValle, J. Yakey, and L. E. Kavraki. A probabilistic roadmap approach for systems with closed kinematic chains. In *Proc. IEEE Int'l Conf. on Robotics and Automation*, pages 1671–1676, 1999.
- [2] J. Yakey, S. M. LaValle, and L. E. Kavraki. Randomized path planning for linkages with closed kinematic chains. *IEEE Transactions on Robotics and Automation*, 17(6):951–958, December 2001.
- [3] J. Cortes, T. Simeon, and J.P. Laumond. A random loop generator for planning the motions of closed kinematic chains using PRM methods. In *Robotics and Automation, 2002. Proceedings. ICRA '02. IEEE International Conference on*, volume 2, pages 2141–2146, 2002.
- [4] R. James Milgram and J. C. Trinkle. The geometry of configuration spaces for closed chains in two and three dimensions. *Homology Homotopy Appl.*, 6(1):237–267, 2004.
- [5] A. Yershova and S. M. LaValle. Planning for closed chains without inverse kinematics. In *IEEE International Conference on Robotics and Automation*, 2007. Under review.
- [6] Yajia Zhang, K. Hauser, and Jingru Luo. Unbiased, scalable sampling of closed kinematic chains. In *2013 IEEE International Conference on Robotics and Automation*, pages 2459–2464, May 2013.
- [7] A. Yershova, L. Jaillet, T. Simeon, and S. M. LaValle. Dynamic-domain RRTs: Efficient exploration by controlling the sampling domain. In *Proceedings IEEE International Conference on Robotics and Automation*, 2005.
- [8] Jason Cantarella, Bertrand Duplantier, Clayton Shonkwiler, and Erica Uehara. A fast direct sampling algorithm for equilateral closed polygons. *Journal of Physics A: Mathematical and Theoretical*, 49(27):275202, 2016.
- [9] Jason Cantarella and Clayton Shonkwiler. The symplectic geometry of closed equilateral random walks in 3-space. *Ann. Appl. Probab.*, 26(1):549–596, 02 2016.

- [10] Hamidreza Chitsaz, Raheleh Salari, S.Cenk Sahinalp, and Rolf Backofen. A partition function algorithm for interacting nucleic acid strands. *Bioinformatics*, 25(12):i365–i373, 2009. Also ISMB/ECCB proceedings.
- [11] Elmirasadat Forouzmand and Hamidreza Chitsaz. The RNA Newton polytope and learnability of energy parameters. *Bioinformatics*, 29(13):i300–i307, 2013. Also ISMB/ECCB proceedings.