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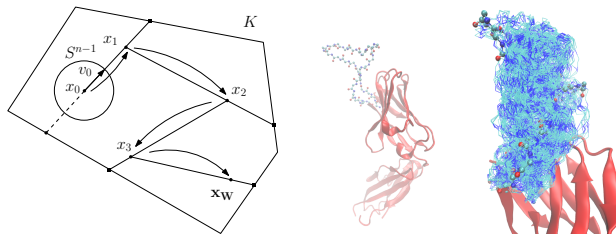


Figure 1: (Left) Hit-and-Run in a 2D polygon [1]. (Middle, right) Conformations of a long flexible protein loop [2, 3].

MASTER INTERNSHIP PROPOSAL

SAMPLING ALGORITHMS IN HIGH-DIMENSIONAL SPACES CODING THE GEOMETRY OF PROTEINS

Keywords: sampling algorithms, Monte Carlo Markov Chain, volume calculations, statistical physics, conformational spaces, protein structure analysis.

Context. A well studied problem in geometry is the calculation of the volume of a high-dimensional polytope. While this problem is NP-hard, probabilistic algorithms based on Monte Carlo Markov Chain techniques and random walks of the Hit-and-Run type have been developed [1]. Currently, state-of-the-art random walks compute volumes in hundreds of dimensions within minutes on a laptop [2, 3].

In structural biology, a central problem is the prediction of the function of a protein, which requires understanding its dynamics—see e.g. AI, molecular design and the Covid19. A key achievement in protein structure analysis is the **AlphaFold** by Deepmind, which predicts a plausible structure from the amino acid sequence [4]. However, a single structure falls short from providing insights in the function of a protein. (For a metaphor, consider getting a single picture for an entire movie.) The generation of exhaustive molecular conformations is therefore a major challenge, and we recently contributed state-of-the-art algorithms for flexible loops, based on Hit-and-Run like algorithms working in high dimensional curved spaces coding the geometry of proteins [5, 6].

Goals. The work envisioned encompasses the analysis of our sampling algorithms, and their extension to compute provably correct averages in the so-called NVT ensemble. The analysis are likely to suggest modifications and improvements, which will also be implemented in C++ in the scope of the Structural Bioinformatics Library, an advanced software environment providing both low level algorithmic classes, and applications for end-users.

Conditions. Internship with *gratification*. Possibility to follow-up with a PhD thesis.

References

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