

What is the Protein Side-Chain Positioning Problem?

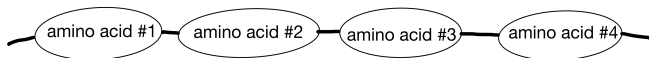
Protein Side-Chain Positioning, (SCP), is one of the most important subproblems of the protein structure prediction problem. SCP has many applications, e.g. to e.g., [Bur15]: ligand binding; and protein-protein docking with backbone flexibility. We now see how to formulate it as a mixed integer program, (MIP).

What is a Protein?

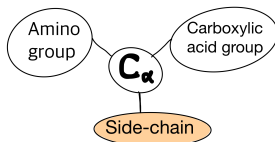
A protein

A collection of chains of amino acids

- **Chain:**
a sequence of amino acids



- **Amino acid:**
building blocks of a protein
consists of $\{C, H, O, N\}$



Protein Side-Chain Positioning Problem (SCP)

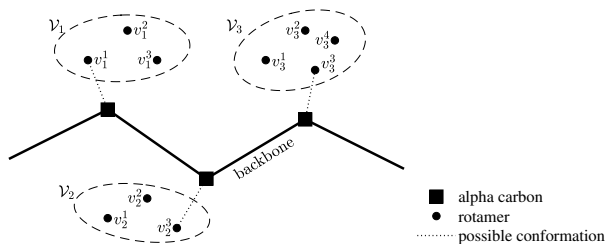
Task

Given

- a collection of sets of candidates for each side-chain of an amino acid
- pair-wise energy values between all candidates

Do

- Pick exactly ONE candidate from each set
- while yielding the minimum energy



Applications & Roadmap

Applications

- One of the most important subproblems of the protein structure prediction problem.
- Examples: ligand binding, protein-protein docking, etc

Roadmap

- Formulate as a quadratic integer program
- Relax the hard problem
- Solve using continuous optimization methods
- Round the approximate solution
- Use branch and bound and cutting planes to improve solution

Problem Formulation as IQP

Given a collection of disjoint sets $\mathcal{V}_i, i \in [p]$. $|\mathcal{V}_i| = m_i$,

$n_0 = \sum_{i=1}^p m_i$ and $\mathcal{V} = \cup_{i=1}^p \mathcal{V}_i$.

\mathcal{V}_i : rotamer set, elements in \mathcal{V}_i rotamers.

Goal

- 1 Select *exactly one* rotamer v_i from each set \mathcal{V}_i ,
- 2 Minimize the sum of
 - 1 the weights (energy) on the edges between chosen rotamers, and
 - 2 the energy between each chosen rotamer and the backbone

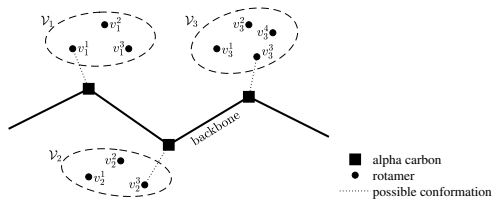


Figure: A Diagram of the Protein Side-Chain Positioning Problem

Problem Formulation as IQP

$$\begin{aligned} \rho_{\text{IQP}}^* := \min & \sum_{u,v} E_{uv} x_u x_v \\ \text{s.t.} & \sum_{u \in \mathcal{V}_k} x_u = 1, \quad k = 1, \dots, p \\ & x = (x_u) \in \{0, 1\}^{n_0}. \end{aligned}$$

Equivalently,

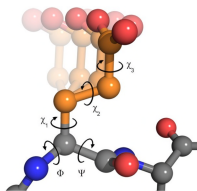
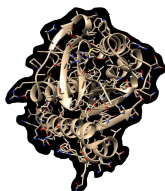
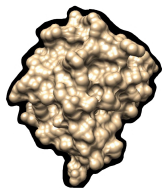
$$\begin{aligned} \text{(IQP)} \quad \rho_{\text{IQP}}^* := \min & x^T E x \\ \text{s.t.} & A x = \bar{e}_p \\ & x = [v_1^T \quad v_2^T \quad \dots \quad v_p^T]^T \in \{0, 1\}^{n_0} \\ & v_i \in \{0, 1\}^{m_i}, \quad i = 1, \dots, p, \end{aligned}$$

where

$$A := \text{blkdiag}(\bar{e}_{m_1}^T, \bar{e}_{m_2}^T, \dots, \bar{e}_{m_p}^T) \in \mathbb{R}^{p \times n_0},$$

Strategy

The **SCP** problem is NP-hard \rightarrow Work with e.g., **SDP** relaxation



F.J. Burkowski.

Computational and Visualization Techniques for Structural Bioinformatics Using Chimera.

Chapman & Hall/CRC mathematical and computational biology series. Chapman and Hall/CRC, London, 2015.