

Laboratory of Bioinformatics 1 part B - Capriotti

Saul Pierotti

March 14, 2020

- There will be a project for the final, to be submitted for may 18
- Protein structure is more conserved than sequence
- When sequence identity is sufficiently high, we can transfer structural information
- A structural alignment is a rigid body transformation of 2 subsets from 2 sets of points that maximizes a given distance metric
 - Finding the correspondence set is an NP-hard problem
 - Finding the optimal rigid transformation of the correspondence set is $\Theta(n)$