# Structural Biology: Assignment 3

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June 6, 2017

## Preface

This is an assignment report in connection to the *Structural Biology* module in the Computational Biology course at the University of Cambridge, Lent term 2017. All related code is as of June 6, 2017 available through a Github repository by contacting hpa22@cam.ac.uk.

## Exercises

### 1

Figure 1a shows the frequency distribution of the weighted pairwise distances between sequences, given that their similarity fraction is > 70%. Figure 1b shows the predicted protein contact map between the residues in each sequence, i.e. how correlated certain positions are with each other based on the evolutionarily inferred contact (EIC) scores. Figure 1c in turn depicts the minimal distance between the amino acids in the crystal as a function of the corresponding DI rank. Lastly, fig. 1d shows the overlap between the experimentally observed structure and the predicted tertiary interactions.
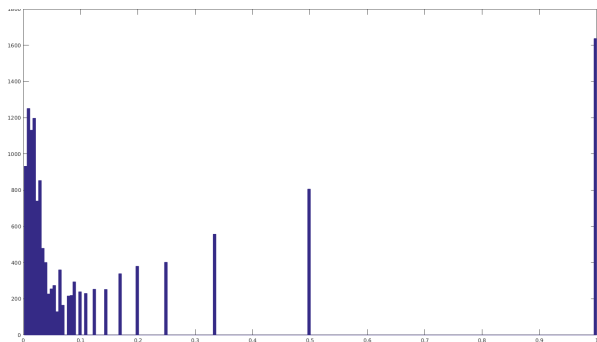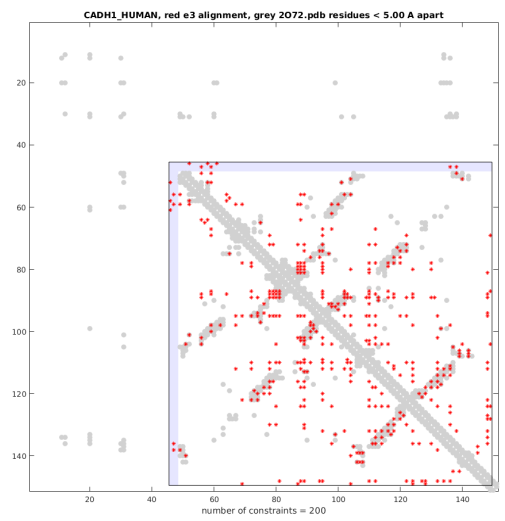
(a) Figure1
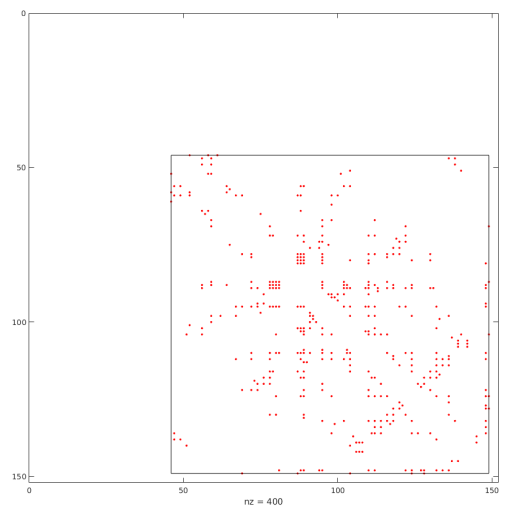


(b) Figure2
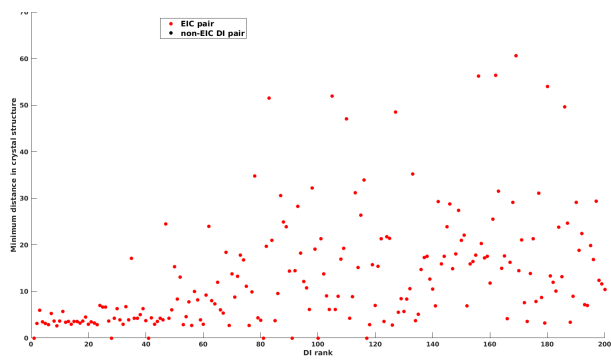


(c) Figure3



(d) Figure4

Figure 1: Figure of figures