**Caiya Zhang**

**10.19 Weekly Report**

**What you have done in the past week:**

1. I finished the final draft of my proposal this week, and I plan to submit it after this week's meeting. Since the instructor has postponed the proposal submission deadline until Nov 7th and we can resubmit in unlimited times, I can still revise it if there’s any change of the main approach.
2. I'm preparing the report on the two key papers. This week I'm mostly combing through the proposed framework in “plos comb”, and I may need some more time on the other one.
3. I'm browsing some GNN frameworks that focus on interpretability, and I'm still studying about how to implement and evaluate a interpretable method.

**What are major challenges/issues you need to discuss in the meeting:**

Regarding the interpretability of the pre-training, I am looking at some data visualization methods, such as Maximum Mean Discrepancy (MMD), and I wonder if this is a viable idea for the database I will use. Of course, I am also learning about this, and I’m learning more about methods to achieve interpretability in the middle or later stages of training. I wonder if there’s any relevant suggestions.

**What you want to accomplish in the next week/weeks:**

1. Continue in-depth reading the two papers and focus more on the “nature method” to complete the report slides on the interpretation of the two articles.
2. I may need to schedule a meeting with Yan to make sure my understanding is accurate and to see if there is any other paper that may has significant instruction to my model.

**10.12 Weekly Report**

**What you have done in the past week:**

1. This week, I mainly focused on completing the draft proposal. During the process of writing proposal, I sorted out several goals that I need to achieve in order to complete the project, and I’m a little bit clearer about the overall time schedule.

2. I have quickly read over the two articles on Plos Computational Biology and Nature Methods. So far, I think GeoPPI can be an alternative to the baseline method or project for comparison, and the SKEMPI 2.0 dataset mentioned in several papers may also be an alternative to the baseline dataset.

**What are major challenges/issues you need to discuss in the meeting:**

I wrote my draft based on structure of the sample given by the instructor, combined with the proposal I received, and I found there is no module that requires me to describe the method and data sets in the given outline, which was what I might need to show from my perspective. So far, I have only mentioned them in the Abstract and Objectives, which are relatively brief and general, so I was wondering if I need to explain more about methods and datasets I may use in this project.

**What you want to accomplish in the next week/weeks:**

1. Continue to modify and improve my proposal.
2. Continue doing literature review and collect some ideas about choosing specific graph neural network structure in my work.
3. Carefully understand the feature extraction methods in the two key papers, as well as learn more about the use of AlphaFold database.

**Reference**

Jankauskaitė, J., Jiménez-García, B., Dapkūnas, J., Fernández-Recio, J., & Moal, I. H. (2018). SKEMPI 2.0: An updated benchmark of changes in protein–protein binding energy, kinetics and thermodynamics upon mutation. *Bioinformatics*, *35*(3), 462–469. https://doi.org/10.1093/bioinformatics/bty635

Liu, X., Luo, Y., Li, P., Song, S., & Peng, J. (2021). Deep geometric representations for modeling effects of mutations on protein-protein binding affinity. *PLOS Computational Biology*, *17*(8). <https://doi.org/10.1371/journal.pcbi.1009284>

Tubiana, J., Schneidman-Duhovny, D., & Wolfson, H. J. (2022). Scannet: An interpretable geometric deep learning model for structure-based protein binding site prediction. *Nature Methods*, *19*(6), 730–739. <https://doi.org/10.1038/s41592-022-01490-7>

**10.5 Weekly Report**

**What you have done in the past week:**

1. Based on last week's session, this week I first continued my understanding of the mCSM -PPI2 [1] dataset.
   1. I reviewed the modeling approach of the original mCSM [2] project and supplemental files of mCSM-PPI2, which are both predecessors of the target project, and specifically understood the idea of "Graph-based structural signatures" construction relied on in these projects.
   2. Then I focused back to the mCSM-PPI2 paper, to understand the six features presented in “Modelling effects of mutation” section. With previous understanding of mCSM-PPI2 data, I found the graph modeling ideas of above-mentioned projects are invariant, all of them represent atoms as nodes and their interactions as edges, and use pharmacological features to illustrate the effects of physicochemical changes caused by point mutations. Regarding the six newly proposed features in mCSM-PPI2, they are different effects on single point mutations, and are used to combine with their well-established graph-based signatures for regression and classification.
2. I discussed the investigated dataset with Yan in our meeting, and we found, although this project uses a graph-based structure, its most dominant predictive model is still a traditional machine learning algorithm, where there may not much guidance on our GNN-based framework. So we still need to spend some time doing some literature review in the next weeks.
3. Yan has sent me three papers she found on related work, of which I am following one to understand how to generate the graph [3].
4. I was also preparing a short report for presentation in this week's meeting.

**What are major challenges/issues you need to discuss in the meeting:**

1. There is not much concern so far, since I’m still in progress of accumulating knowledge of relevant works.

**What you want to accomplish in the next week/weeks:**

1. Continue studying the papers Yan sent me, while I can also find one or two similar projects that may give me some inspirations.
2. Based on the ideas that have been accumulated so far and the proposal I received at the very beginning, I’m going to write a draft for the formal proposal I need to submit two weeks later.

**Reference**

[1] Rodrigues, C. H. M., Myung, Y., Pires, D. E. V., & Ascher, D. B. (2019). mCSM-PPI2: Predicting the effects of mutations on protein–protein interactions. *Nucleic Acids Research*, *47*(W1), W338–W344. <https://doi.org/10.1093/nar/gkz383>

[2] Pires, Ascher, D. B., & Blundell, T. L. (2014). mCSM: predicting the effects of mutations in proteins using graph-based signatures. Bioinformatics, 30(3), 335–342. <https://doi.org/10.1093/bioinformatics/btt691>

[3] Liu, Luo, Y., Li, P., Song, S., & Peng, J. (2021). Deep geometric representations for modeling effects of mutations on protein-protein binding affinity. *PLoS Computational Biology*, *17*(8), e1009284–. <https://doi.org/10.1371/journal.pcbi.1009284>

**9.28 Weekly Report**

**What you have done in the past week:**

1. This week I focused on the dataset in mCSM-PPI2 and went through the general structure of input data for that project;
2. To understand how to get and prepare similar data in real code, I referred to a github project called GeoPPI, which was recommended by Yan;
3. Tried to retrieve one of the csv files in mCSM dataset (S4169) on Google Colab, and split each row of data according to the method used in GeoPPI;
4. Prepare for the short presentation of describing and handling the data.

**What are major challenges/issues you need to discuss in the meeting?**

1. I wonder is there a specific type of graph neural network is recommended for PPI prediction, such as GCN or CGAT, etc.

**What you want to accomplish in the next week/weeks:**

1. In next week, my plan is to reproduce the data preparation part of mCSM on Colab, following the idea of GeoPPI to obtain data and build graphs, and check the results by printing the matrix;
2. Ready to start writing a formal thesis proposal, which will be due on Oct 20th.

**9.21 Weekly Report**

**What you have done in the past week:**

1. Quickly read over the four papers mentioned in “Literature Review”, and I’ve had a general understanding of the task mentioned in the proposal.
2. A github repository was created to upload weekly report, and this is the repo link: <https://github.com/Caiya-Zhang/gnn_pro_mut>

**What are major challenges/issues you need to discuss in the meeting?**

1. Whether I can develop my project basing on the code of the recommended project, or is there a recommended framework. If I need to start from scratch, I may first build the framework as I'm used to and may modify later.

**What you want to accomplish in the next week/weeks:**

1. For the binding affinity changes equation given in the proposal, I am not particularly sure how this equation is actually applied in code. I may need Frederic's help.
2. Focus on reading and understanding the DATA and METHOD parts of mCSM-PPI2 and MutaBind2. Hopefully, through these, I can **have an initial idea of the form of data I need to use for training and how to apply the objective function**. I hope I can get some inspiration from this.