BS6213

Protein function prediction

Professor Wong Limsoon

30 January 2022

This session is an opportunity for students to apply what they have learned in the previous sessions, as well as to engage in a more reflective and contemplative approach to reading reported results. We do this in the context of protein function prediction. Each student should read the materials below beforehand.

Background

- Wiki page on protein function prediction, https://en.wikipedia.org/wiki/Protein_function_prediction
- Twilight zone of protein sequence alignments, https://academic.oup.com/peds/article/12/2/85/1550637
- Seo et al. "DeepFam: Deep learning-based alignment-free method for protein family modelling and prediction", Bioinformatics 34(13):i254-i262, 2018 https://academic.oup.com/bioinformatics/article/34/13/i254/5045722

Pre- & post-session reports assignment

Before the session (submit before 30 January 2023):

- The report should address what the Seo et al. paper is talking about, and what analysis or methodological bugs you think the paper might have.

After the session (submit by 3 February 2023):

- Summarize any new insight you have gained from the session's discussion on the paper, and also comment on what you write in your pre-session report.