

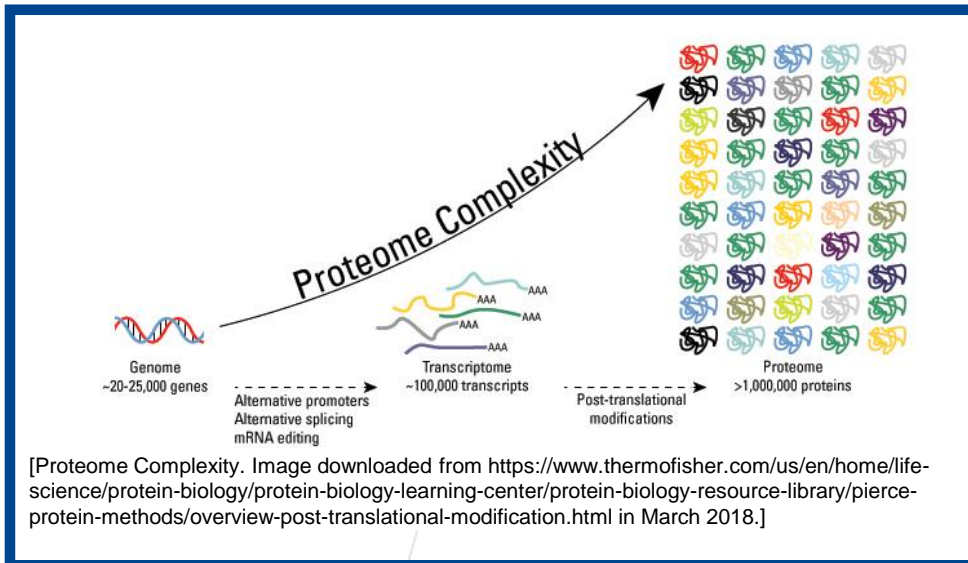
Clarence R. White Jr.

Department: *Computational Science and Engineering*

Dissertation Title: *In Silico Prediction of Protein
Sequence Classification and Post Translational
Modification Site Prediction using Deep Neural
Networks*

Major Professor: *Dr. Dukka KC*

Co-advisor: *Dr. Robert Newman*



RESEARCH QUESTIONS / PROBLEMS:

- In order to bridge the gap between protein sequences and attributes, in a timely manner, prompts the challenge to develop computational methods for prediction various attributes of proteins based on their sequence information alone.

METHODS:

1. Extracting a comprehensive feature set from protein sequences,
2. The prediction of β -lactamase enzymes; S-glutathionylation sites and phosphorylation sites in the *Chlamydomonas reinhardtii* (*C. reinhardtii*) organism.

RESULTS / FINDINGS:

- We developed an accurate, precise, and a specific classification methods. These methods significantly outperformed existing methods

SIGNIFICANCE / IMPLICATIONS:

- The predictions using our method can be performed in silico. In silico methods are promising in that they can be used as preliminary analysis to drive further in vivo and in vitro experiments. Thus, they save significant time and money.