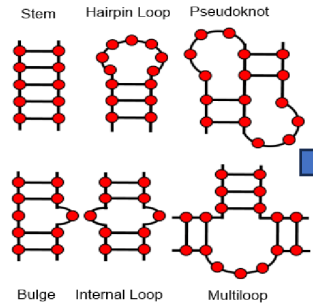


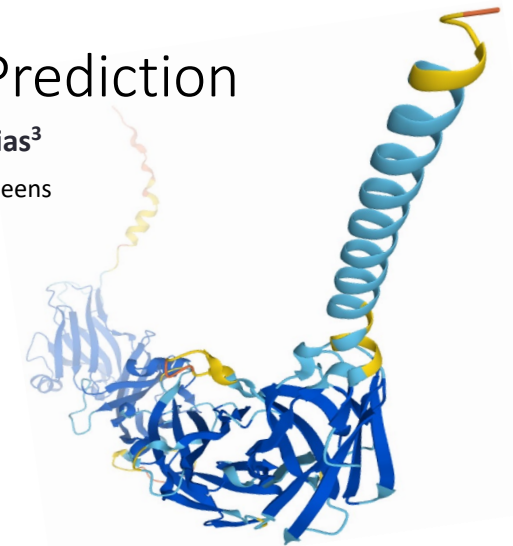
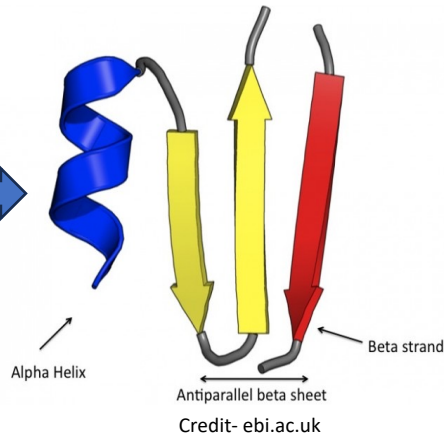
Adapting NU-ResNet and NUMO-ResNet for Peptide Stability Prediction

Owen Krueger¹, Mohit Malu³, Rebecca Sutcliffe⁴, Nicholas Dunne², You Zhou¹, Giulia Pedrielli¹, Andreas Spanias³

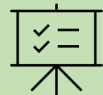
1. SCAI at Arizona State University 2. Bidesign Europe at Dublin City University 3. School of ECEE at Arizona State University 4. Queens University Belfast



Credit- Chheda, Nilay & Gupta, Manish. (2014). RNA as a Permutation.



Objective:



- ❑ Current deep ML model successfully predicts RNA structure stability
- ❑ Adapt and Train model to predict peptide stability

Sub-Goals:



- ❑ Change NU-ResNet to utilize Amino acids
- ❑ Pull and format Peptide training data for model
- ❑ Implement Peptide Motif recognition for NUMO-ResNet

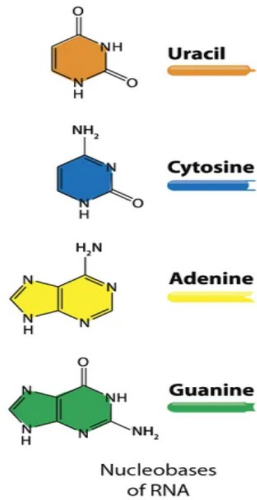
Purpose:



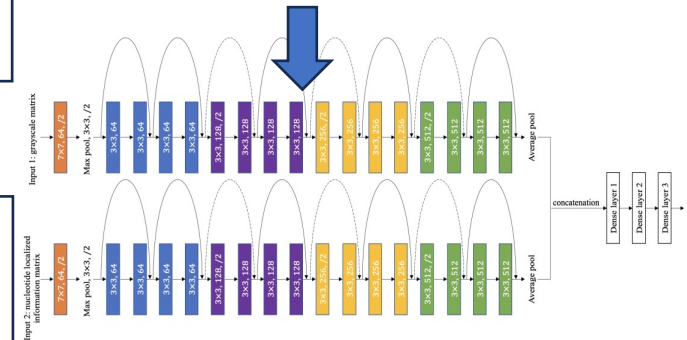
- ❑ Assess Model's capability to predict other molecules
- ❑ Potentially provide researchers with tool to evaluate peptides

Amino acids

Ala	Alanine
Arg	Arginine
Asn	Asparagine
Asp	Aspartic acid
Cys	Cysteine
Gln	Glutamine
Glu	Glutamic acid
Gly	Glycine
His	Histidine
Ile	Isoleucine
Leu	Leucine
Lys	Lysine
Met	Methionine
Phe	Phenylalanine
Pro	Proline
Ser	Serine
Thr	Threonine
Trp	Tryptophan
Tyr	Tyrosine
Val	Valine



WORLDWIDE
PDB
PROTEIN DATA BANK



Credit- Y. Zhou, G. Pedrielli, F. Zhang, T. Wu
"Deep learning to predict RNA Stability: NU-ResNet and NUMO-ResNet," unpublished.