GraphProtDeep

Project overview

# GraphProtDeep Model Specificity

# Literature

## Overviews of Proteins and Binding Preferences

### Paper: Sequence, Structure, and Context Preferences of Human RNA Binding Proteins, Molecular Cell 2018

[(Dominguez et al. 2018)](https://paperpile.com/c/1eMWMs/nvpA)

### Paper: Deciphering human ribonucleoprotein regulatory networks, BioArXiv 2018

[(Mukherjee et al. 2018)](https://paperpile.com/c/1eMWMs/qaXe)

Thorough investigation of binding preferences of 64 RBPs. They reanalysed many PAR-CLIP experiments and after quality control kept 114 of 173 libraries corresponding to 64 RBPs.

Figure 2 shows a nice clustering of sequence binding preferences. See [this table](https://docs.google.com/spreadsheets/d/1rnm1pCWECogyhisJ5Ml471Cc7YPLiFIsBZECZVRN-7U/edit?usp=sharing) for an overview of the clustered data and dataset availability. Good for selecting proteins from different sequence specificity clusters when checking that models are specific to the protein of interest and not just the technical bias.

## RBP Sequence and Structure Preferences

* SSMART: “RNA motif finder that simultaneously models the primary sequence and the structural properties of the RNA targets sites”
  + [(Munteanu et al. 2018)](https://paperpile.com/c/1eMWMs/m26X)

## Deep Learning Approaches

* [(Alipanahi et al. 2015)](https://paperpile.com/c/1eMWMs/NQ2V)
* [(Zhang et al. 2016)](https://paperpile.com/c/1eMWMs/sWLo)
* [(Gandhi 2017)](https://paperpile.com/c/1eMWMs/uGh9)
* [(Li et al. 2017)](https://paperpile.com/c/1eMWMs/UPzT)
* [(Pan and Shen 2017)](https://paperpile.com/c/1eMWMs/1nVS)
* [(Pan et al. 2018)](https://paperpile.com/c/1eMWMs/0aYR)
* [(Busia et al. 2018)](https://paperpile.com/c/1eMWMs/Ld0p)
* [(Pan and Shen 2018)](https://paperpile.com/c/1eMWMs/s6pz)
* [(Pan and Shen 2018)](https://paperpile.com/c/1eMWMs/bqUp)
* [(Ko o et al. 2018)](https://paperpile.com/c/1eMWMs/gazG)
* Zheng, J. *et al.* Deep-RBPPred: Predicting RNA binding proteins in the proteome scale based on deep learning. *Sci. Rep.* **8,** 15264 (2018). [(Zheng et al. 2018)](https://paperpile.com/c/1eMWMs/SQhR)
  + Identifies RNA-binding proteins, not their targets.

## Integrative Approaches

* Eggeling, R. Disentangling transcription factor binding site complexity. *Nucleic Acids Res.* (2018). doi:10.1093/nar/gky683 [(Eggeling 2018)](https://paperpile.com/c/1eMWMs/ytSY)
* Mukherjee, N. *et al.* Deciphering human ribonucleoprotein regulatory networks. *bioRxiv* 295097 (2018). doi:10.1101/295097 [(Mukherjee et al. 2018)](https://paperpile.com/c/1eMWMs/qaXe)

## Competing Approaches

* Munteanu, A., Mukherjee, N. & Ohler, U. SSMART: Sequence-structure motif identification for RNA-binding proteins. *Bioinformatics* 287953 (2018).[(Munteanu et al. 2018)](https://paperpile.com/c/1eMWMs/m26X)

## Recent Overview

* Dominguez, D. *et al.* Sequence, Structure, and Context Preferences of Human RNA Binding Proteins. *Mol. Cell* **70,** 854–867.e9 (2018). [(Dominguez et al. 2018)](https://paperpile.com/c/1eMWMs/nvpA)

## Other References

* Experimental evidence that regulation by RBPs is specific to cell-type
  + Yuan, Y. *et al.* Cell type-specific CLIP reveals that NOVA regulates cytoskeleton interactions in motoneurons. *Genome Biol.* **19,** 117 (2018). [(Yuan et al. 2018)](https://paperpile.com/c/1eMWMs/HL69)