Summary

- BPNet can map raw DNA sequence to nucleotide-resolution binding profiles with high accuracy

- Interpretation frameworks enable discovery of novel and subtle properties of the cis-regulatory code

  - DeepLIFT: base-resolution inference of key nucleotides and motif instances in individual regulatory elements and retrotransposons

  - TF-MoDISco: novel motif representations
    - Known and novel motifs associated with distinct combinatorial footprints
    - Tethered binding
    - Subtle flanking sequence patterns

  - Synthetic and in-silico perturbation experiments:
    - higher-order motif syntax
    - Soft motif spacing constraints (helical and nucleosome range)
    - asymmetric cooperative influence of TFs

- Binding models adapt to accurately predict reporter expression activity of regulatory elements