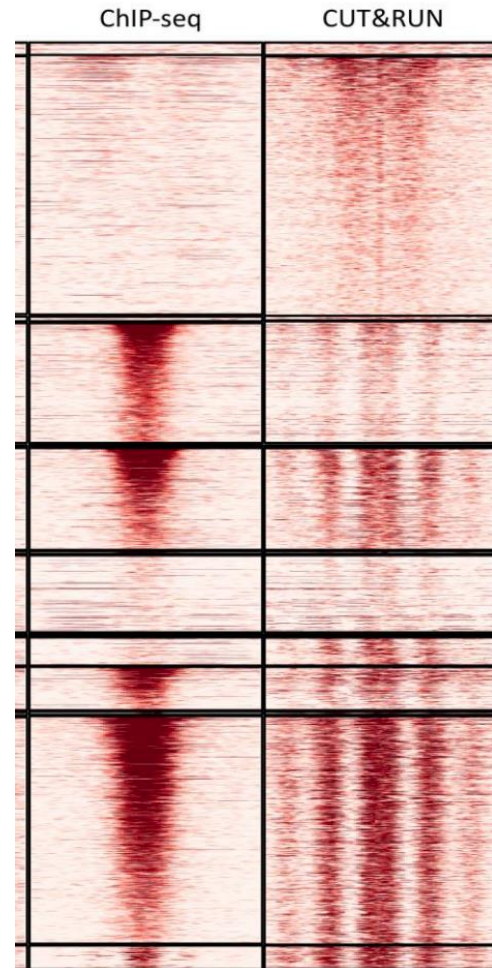


Goal: Compare ChIP-seq vs. CUT-N-RUN assays

Plan:

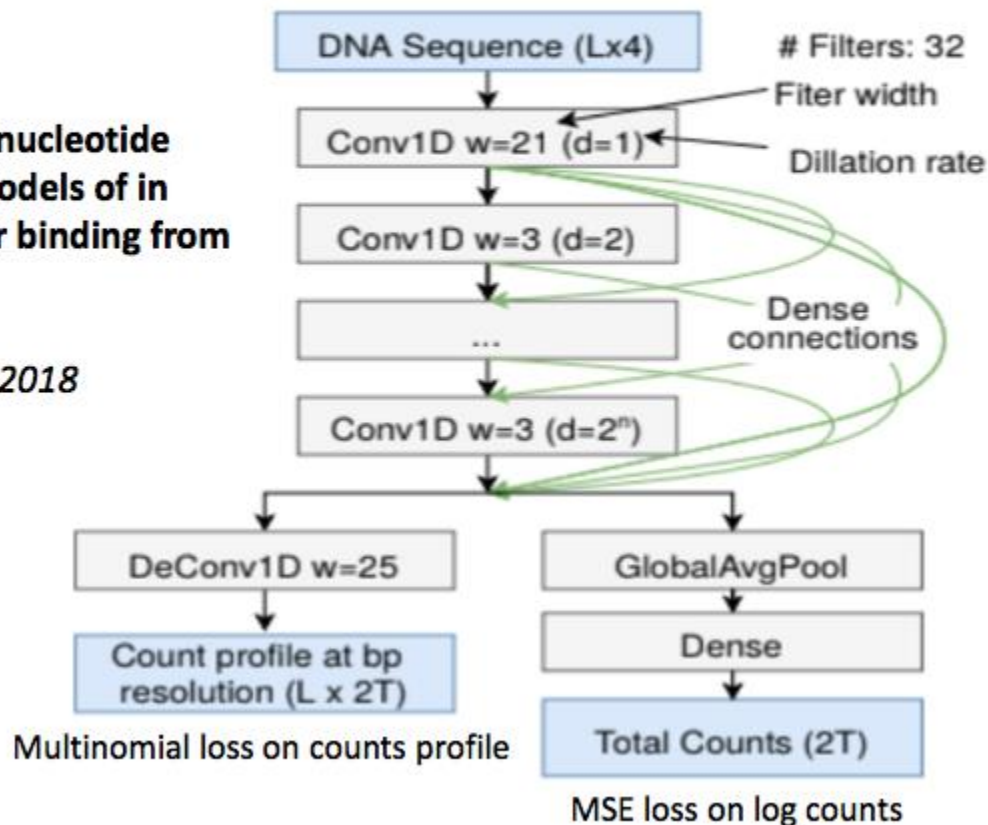
- Train profile-prediction models on ChIP-seq and CUT-N-RUN data for same cell line and factor
- Interpret models



“BPNet” architecture from Avsec et al., 2018

BPNet: Learning single-nucleotide resolution predictive models of in vivo transcription factor binding from CHIP-nexus data

Avsec et al., ICML WCB, 2018

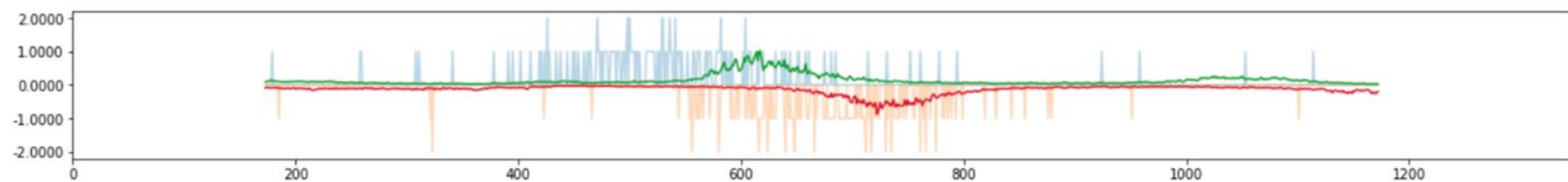


Žiga Avsec

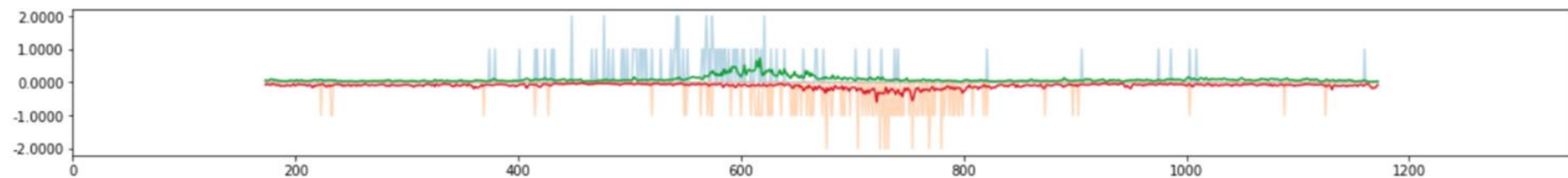
Initial model: ChIP-seq and CUT-N-RUN in H1ESCs

- CUT-N-RUN from “Pioneer Factor-Nucleosome Binding Events during Differentiation Are Motif Encoded” (Meers et al., Henikoff lab)
- ChIP-seq from ENCODE
- Started with model predicting POU5F1/OCT4 and NANOG ChIP-seq, and POU5F1/OCT4 CUT-N-RUN, given **only dna sequence**

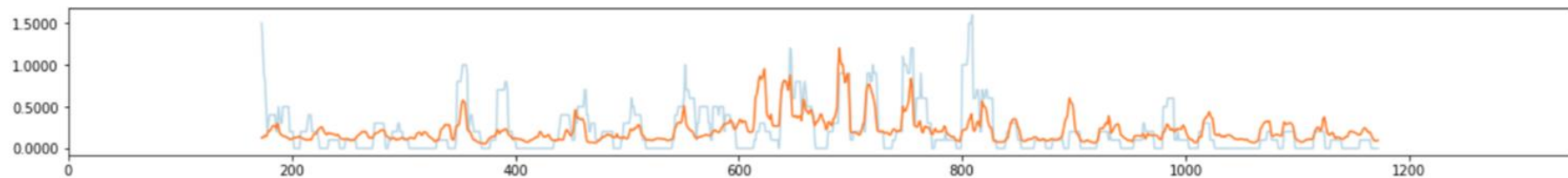
NANOG ChIPseq preds



POU5F1 ChIPseq preds

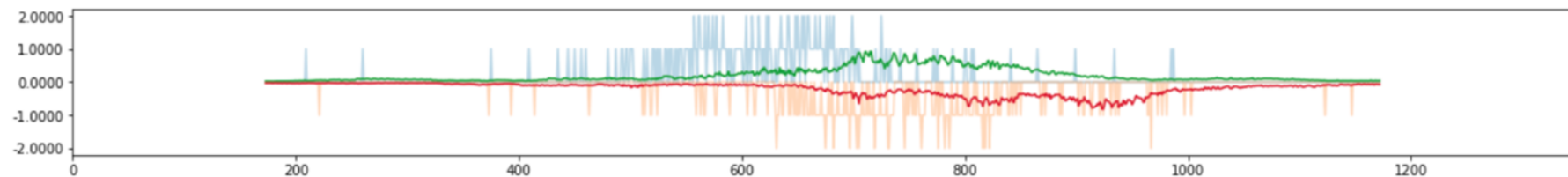


POU5F1 CUTNRUN preds

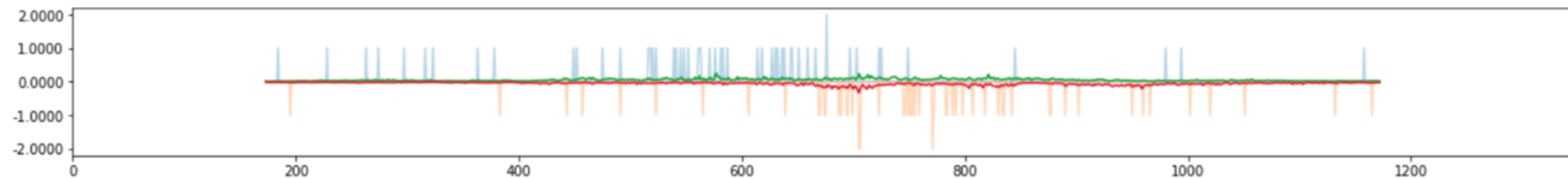


1923

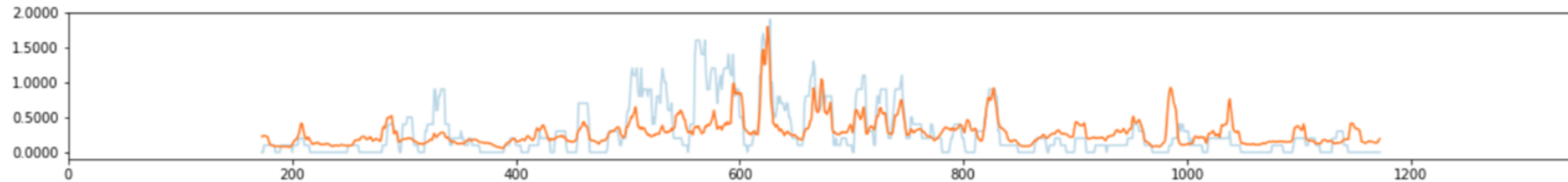
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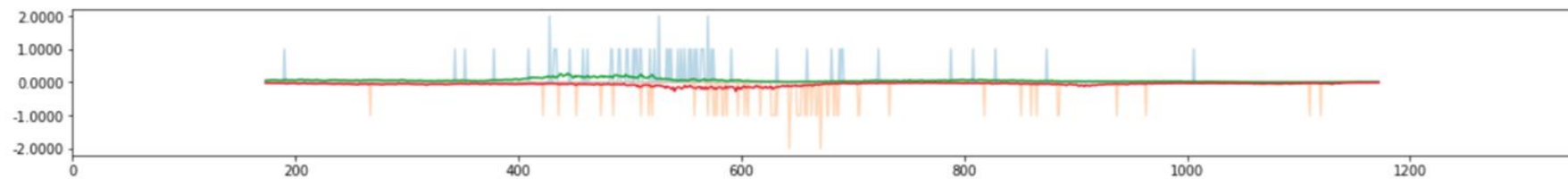
POU5F1 ChIPseq preds



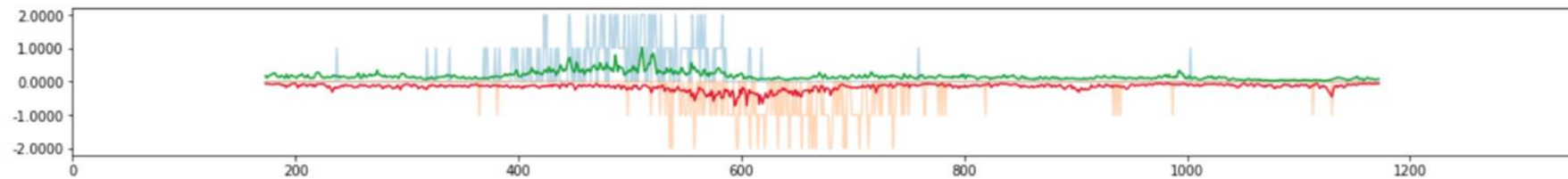
POU5F1 CUTNRUN preds



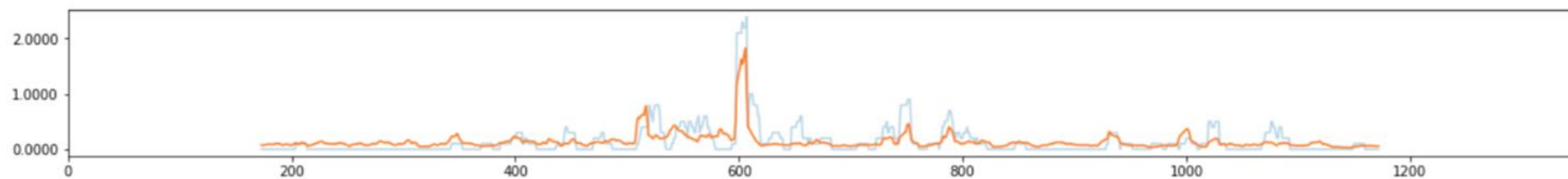
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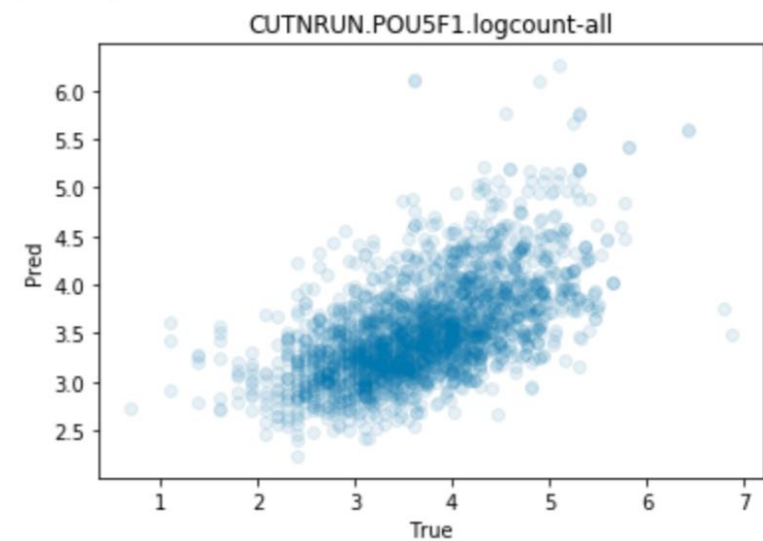
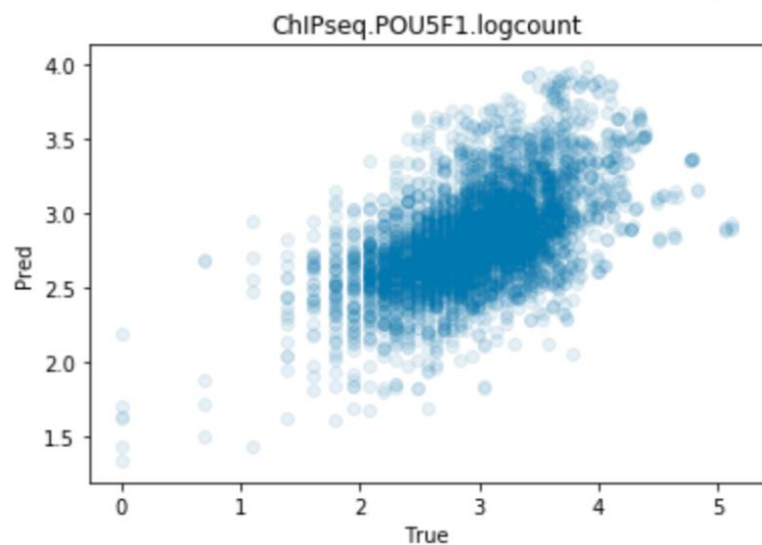
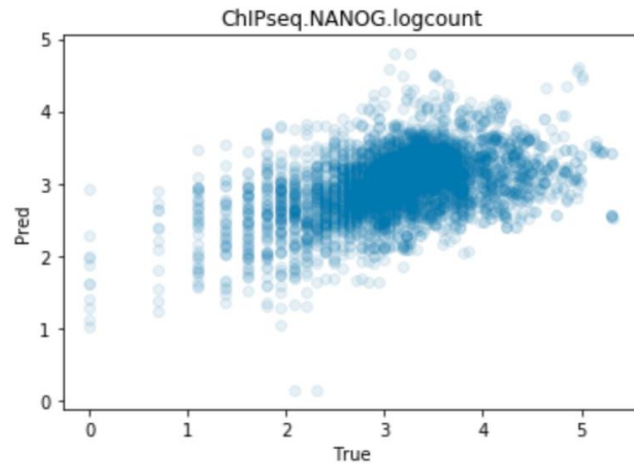


POU5F1 ChIPseq preds



POU5F1 CUTNRUN preds





SpearmanrResult(correlation=0.5488101936918638,

SpearmanrResult(correlation=0.5945533452203494,