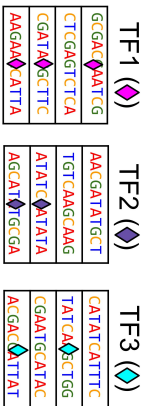


## 1. Genomic Classification Task

Transcription Factors (TFs) are proteins which bind to certain locations of DNA, and in turn regulate gene expression.

XYZ1  $\blacklozenge$  AACC GTATGCT...CATTTCATC...GATTCGT.C.CTCGAGTC...TATCACGG...  
XYZ1  $\blacklozenge$  AACGATATGCT



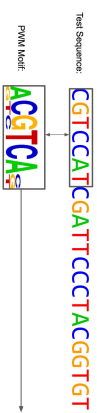
Predicting and understanding the **Transcription Factor Binding Sites** (TFBSs), or subsequences where TFs bind is important to biologists.

## 2. Motifs (Templates) and PWMs

The binding of a TF is triggered by local sequential patterns within TFBSs, known as "motifs".



Researchers first predicted TFBSs by constructing motifs using **position weight matrices** (PWMs) which best represented the positive binding sites, and then compared the test sequence to the PWMs. However, constructing good PWMs is difficult.

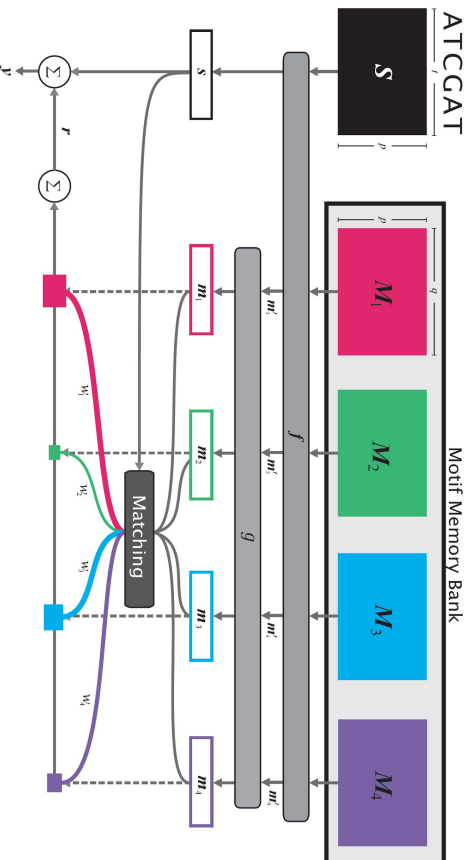


## 3. Memory Matching Network: Automatically Learning Motif Templates

Matching Networks

In the Matching Network (MN) model by Vinyals et al. (2016), they train a differentiable nearest neighbor model to find the closest matching image of a new unseen image from a support set of images.

In Memory Matching Networks (MMN), we replace the fixed support set with a memory template support set. MMNs are for a general classification setting (i.e. not one-shot) and we seek to instead learn the support set, which remains constant for every new test classification.

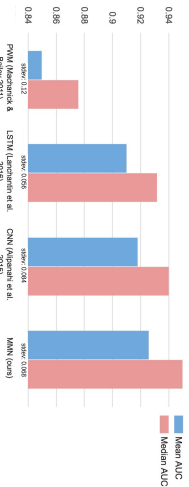


$$\begin{aligned}
 S &= \text{LookupTable}_S(x) \\
 M_i &= \text{LookupTable}_{M_i}(1, \dots, q) \\
 s &= f(S) = \text{attLSTM}(S) \\
 m'_i &= f(M_i) = \text{attLSTM}(M_i) \\
 m_{1..L} &= g(m'_1, \dots, m'_L) = \text{LSTM}(m'_1, \dots, m'_L) \\
 u_i &= \frac{\exp(K[s, m_i])}{\sum_j \exp(K[s, m_j])} \\
 r &= \sum_i u_i m_i \\
 y &= W(r + \mathbf{r})
 \end{aligned}$$

$$\begin{aligned}
 \text{attLSTM}(Z) &= \sum_n \alpha_n h_n \\
 h_{1..N} &= \text{LSTM}(g_1, \dots, g_N) \\
 \alpha_n &= \frac{\exp(h_n \cdot u)}{\sum_j \exp(h_j \cdot u)}
 \end{aligned}$$

## 4. Results

We use the 61 leukemia cell TF datasets from Alipanahi et al. (2015) which had a training set of at least 10,000 sequences. Each dataset has 1,000 testing sequences with an even positive/negative split. We train a separate model for each TF dataset. The reported AUC statistics are across all 61 datasets. We also show the attention weights of a specific positive "ATF1" sample.



character attention weights  $\alpha$

GGGGTCACTCTCAACGGGCTGGCGGTGGCGGAAGATGACGACACAGGGCTGGGTGGCGCTTTGTG

TACCGTCA

memory comparison weights  $w$

