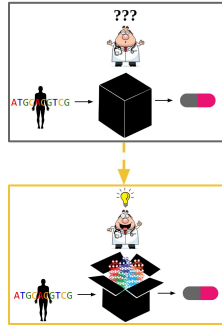
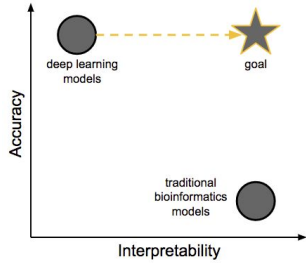
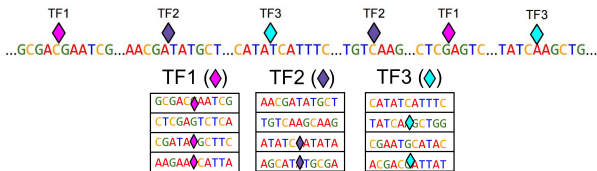


## 1. Motivation



## 2. Genomic Classification Task

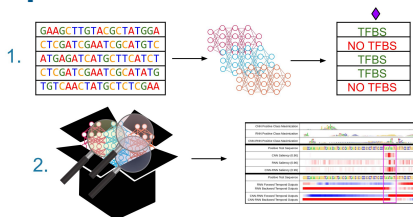
**Transcription Factors (TFs)** are proteins which bind to DNA and regulate gene expression. Predicting and understanding the **Transcription Factor Binding Sites (TFBSs)**, or subsequences where TFs bind is important to biologists.



The binding of a TF is triggered by local sequential patterns within TFBSs, known as **"motifs"**. Previous methods predicted TFBSs by constructing motifs using **position weight matrices** which best represented the binding sites.

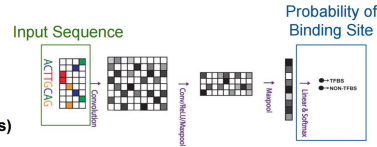


## 3. Deep Motif Dashboard

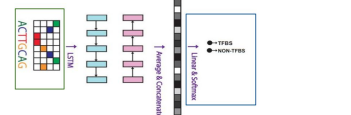


## 4. NN Models for TFBS Prediction

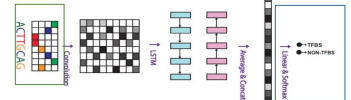
**1. Convolutional (CNN)**  
(short local patterns, or motifs)



**2. Recurrent (RNN)**  
(long term dependencies)



**3. Convolutional-Recurrent (CNN-RNN)**  
(long term dependencies among motifs)

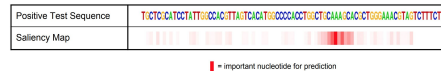


## 5. Visualization Methods

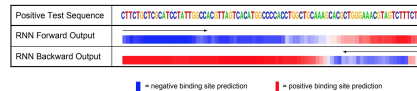
**1. Saliency Maps:** which nucleotides are most important for classification?

$$S_{+}(X) \approx w^T X + b = \sum_{i=1}^{|X|} w_i x_i$$

$$w = \frac{\partial S_{+}}{\partial X} \Big|_{X_0} \text{ "saliency map"}$$



**2. Temporal Output Scores:** what are the model's predictions at each timestep of the DNA sequence?



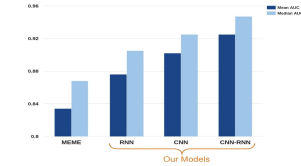
**3. Class Optimization:** for a particular TF, what does the optimal binding site sequence look like?

$$\arg \max_X S_{+}(X) + \lambda \|X\|_2^2$$

Where  $X$  is the input sequence and the score  $S_{+}$  is probability of sequence  $X$  being a positive binding site



## 6. Results



AUC on TFBS dataset from Alipanahi et al., 2015

