## Attention and Transformer Models for Genomics

**BMI/CS 776** 

www.biostat.wisc.edu/bmi776/

Spring 2025

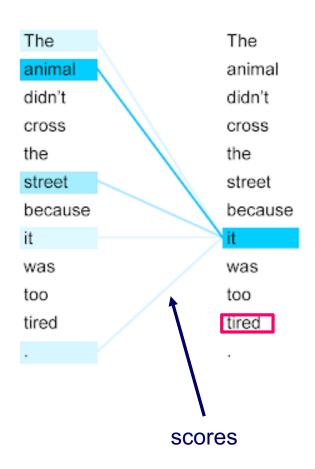
Daifeng Wang

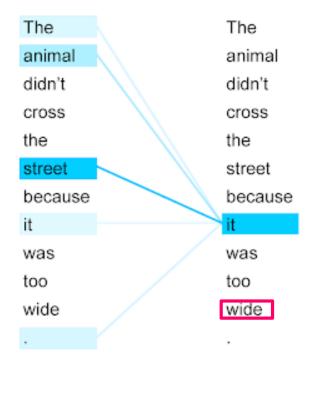
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#### Goals for lecture

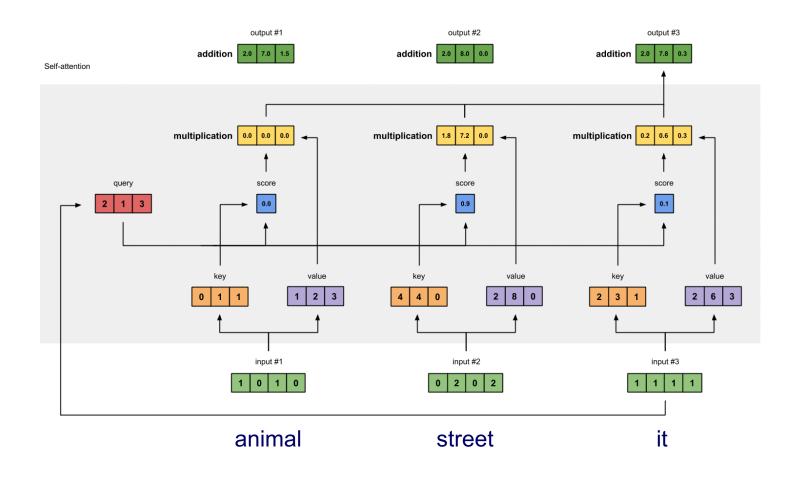
- Attentions
  - Interpretation
  - Self and Cross-Attention Calculation
  - Multi-Head Attention
- Transformer architecture
  - Positional Encoding
  - Generative Output
- Applications to bioinformatics

### Attention Interpretation

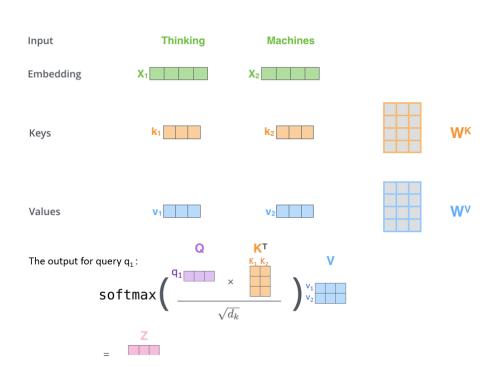




### **Attention Calculation**

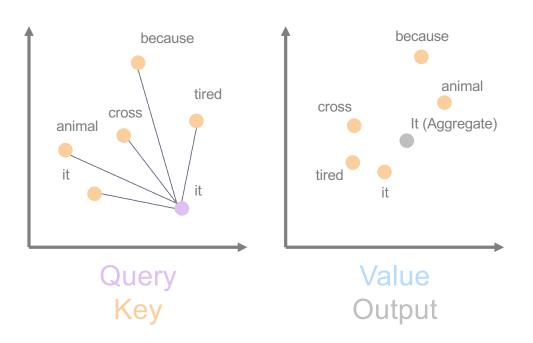


#### **Attention Calculation**



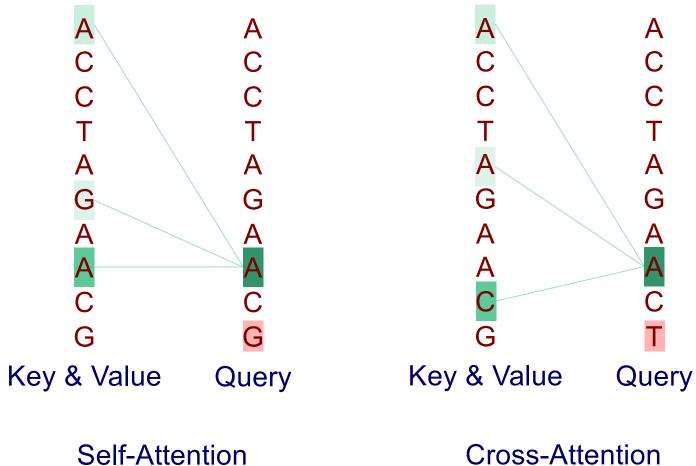
- Embeddings are passed through feed-forward networks to produce a query vector, as well as key and value vectors
- Value vectors are summed proportionally to the similarity between their corresponding keys and the query

### **Attention Calculation**



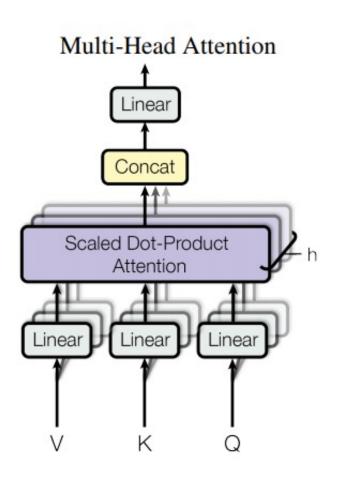
- Key and query vectors can be thought of as sharing a latent space
- The distance between the query and keys then determines the final output in value space

## Types of Attention



**Cross-Attention** 

#### Multi-Head Attention

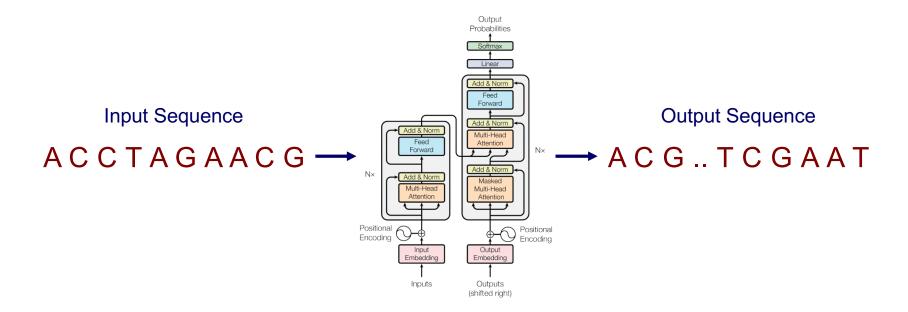


Each attention module is known as a 'head'

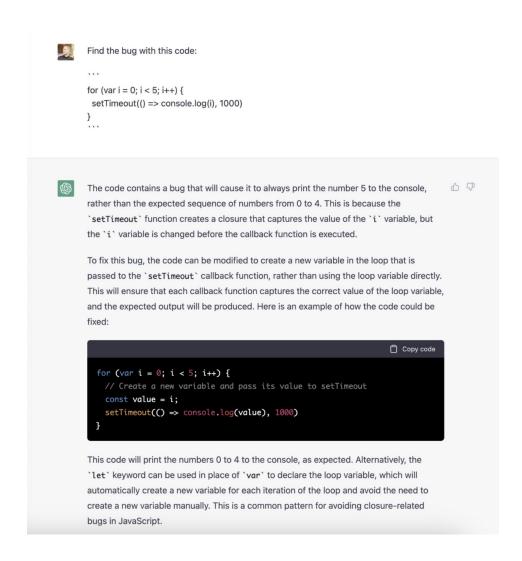
Multi-head attention involves aggregating multiple heads, usually culminating in average pooling

This allows each head to prioritize differing features of the sequence (e.g. noun-noun relationships, noun-verb relationships)

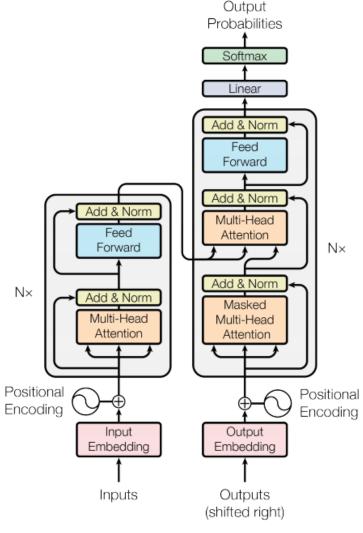
### **Transformer Outline**



## **Example: Generative Text**

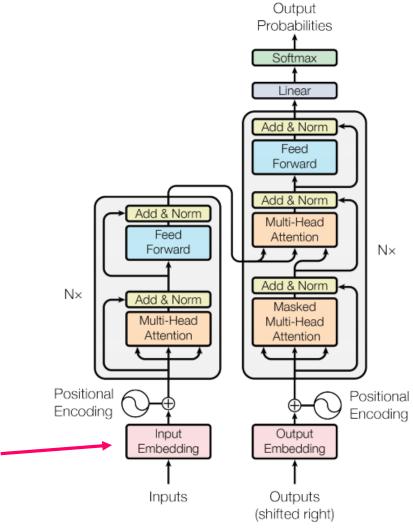


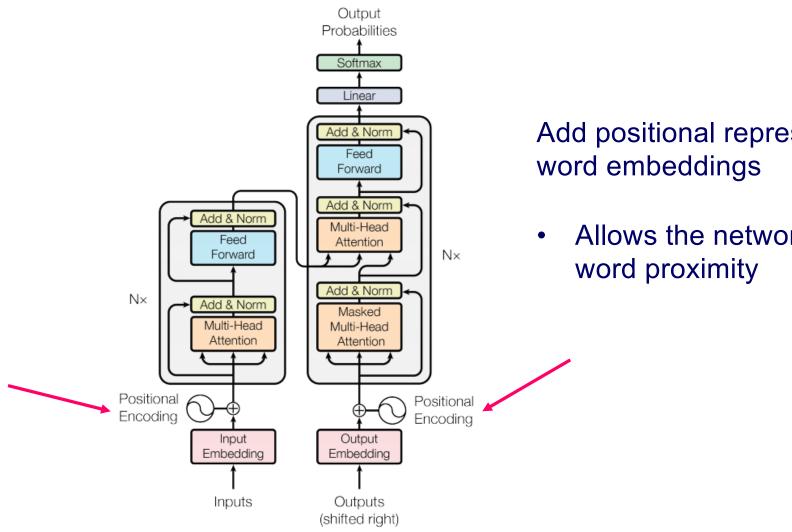
### **Transformer Architecture**



Encoder Decoder

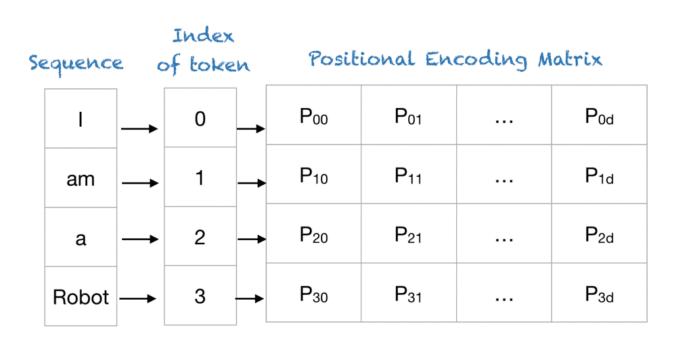
## Input Embedding





Add positional representations to

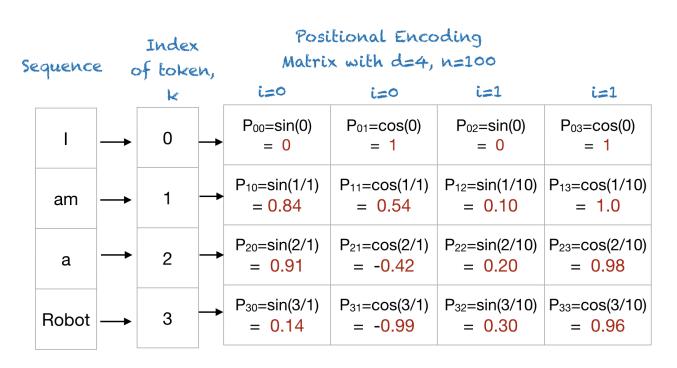
Allows the network to consider



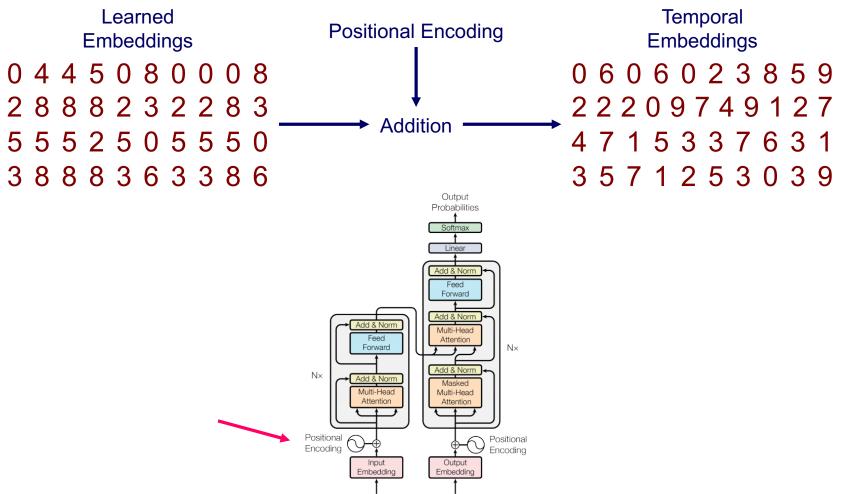
Positional Encoding Matrix for the sequence 'I am a robot'

$$P(k, 2i) = \sin\left(\frac{k}{n^{2i/d}}\right)$$

$$P(k, 2i + 1) = \cos\left(\frac{k}{n^{2i/d}}\right)$$



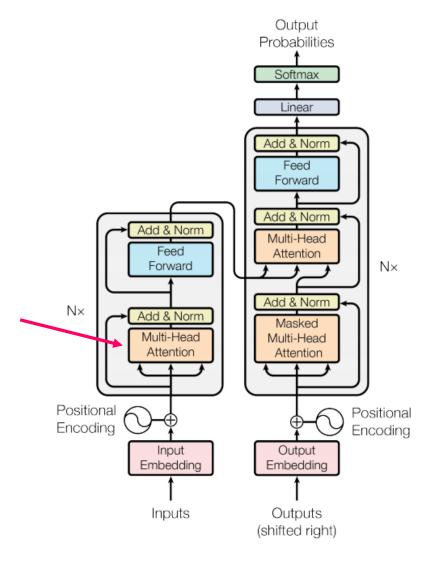
Positional Encoding Matrix for the sequence 'I am a robot'



Inputs

Outputs (shifted right)

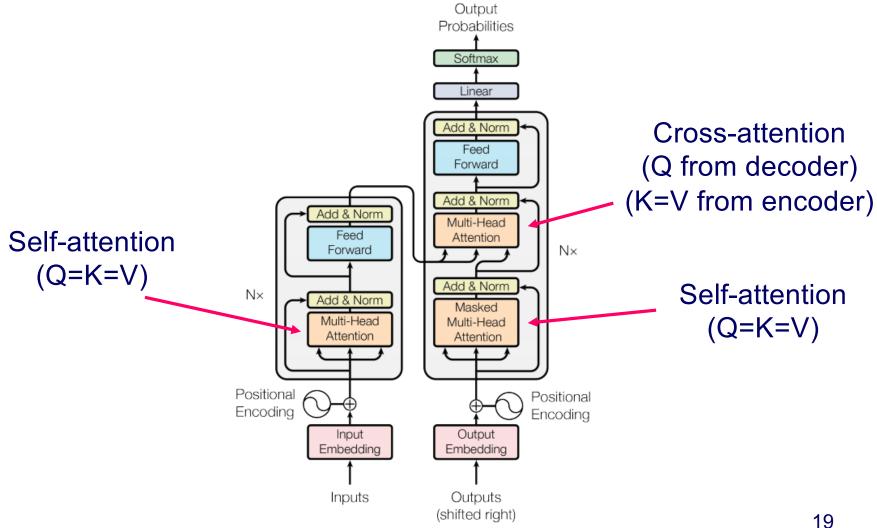
#### **Attention Modules**



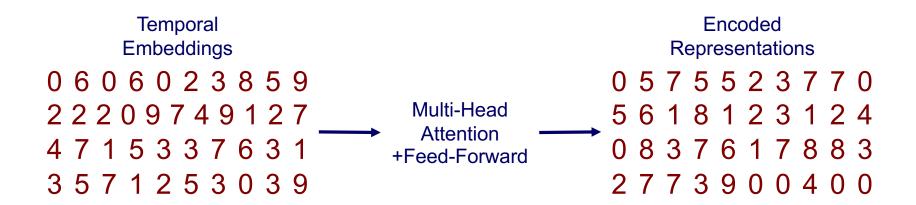
Prioritize bases relative to each other

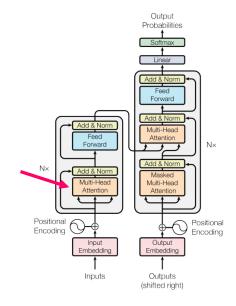
- This is the primary mechanism which allows transformers to work
- Essentially adds context to existing embeddings

#### Self and Cross-Attention

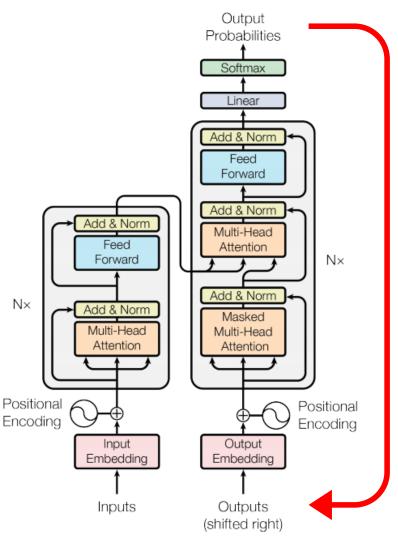


#### **Transformer Attention**





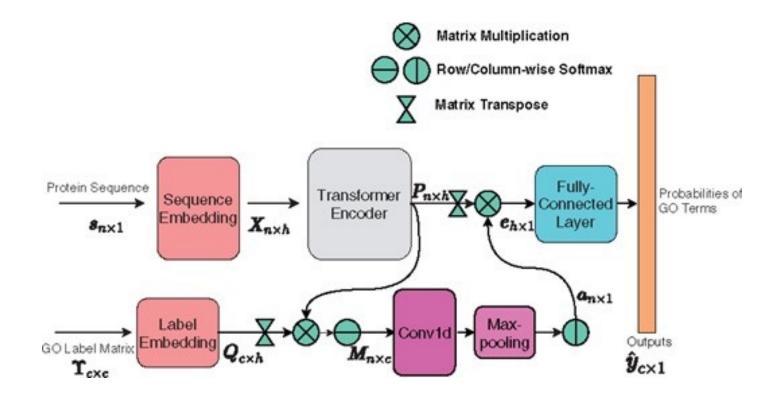
#### Transformer Decoder



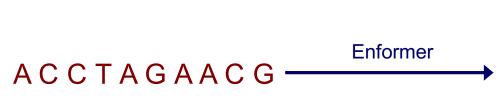
For generative outputs, repeatedly choose the most likely next element until the end of the sequence

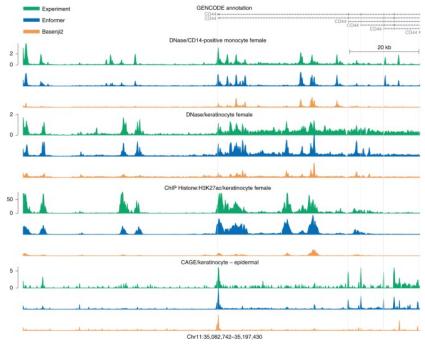
- 0. <start>
- 1. <start> A
- 2. <start> A T
- 3. <start> ATT
- 4. <start> ATTG
- 5. <start> A T T G <end>

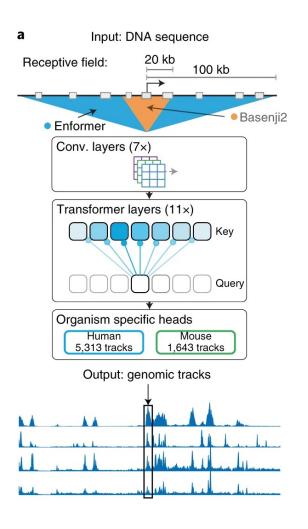
## Example: Protein Function Annotation



Transformers have applications other than sequence generation as well



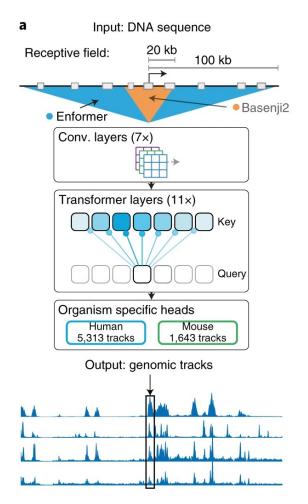




Instead of generating a DNA sequence, genomic tracks (e.g. TF binding, accessibility) can be generated instead

- Convolve 100kb to produce features for each base with attention pooling
- Feed to multiple selfattention blocks (transformer encoder)
- Apply final convolutions to predict tracks for humans or mice

Transformers allow for broader search regions with fewer computational limits



Predict attribute-correlated locations based on DNA sequence

After predicting tracks, known enhancers line up with calculated attention scores

