Agenda:

1. NER → Bi-LSTM + CRF (code)
2. "Attention"-mechanism → LSTMs
   - Transformers
   - Multi-head Self attention
   - Terminology

```
[ ] print('\n ' )
    print('After processing, labels:\n', y[0])
```

(NER) → Health / Pharma

```
Raw Sample:
  Thousands of demonstrators have marched through London to protest the war in Iraq and demand the withdrawal of British troops from that


Raw Label:
  O O O O O O B-geo O O O O O B-geo O O O O O B-gpe O O O O O


After processing, sample:
 [10207  1277  6629 20616 15605 14764 14515 12779  1278 15048 17680 20918
 23613 32038 13909 15048  6336  1277 28724 32859  9404  3914  7714  5905
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0]


After processing, labels:
 [[0. 0. 0. ... 0. 0. 0.]
 [0. 0. 0. ... 0. 0. 0.]
 [0. 0. 0. ... 0. 0. 0.]
 ...
 [1. 0. 0. ... 0. 0. 0.]
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Model Building - Bi-LSTM + CRF

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Model Building - Bi-LSTM + CRF

+ Code + Text Connect

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Model: "model"
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 Layer (type)                 Output Shape              Param #
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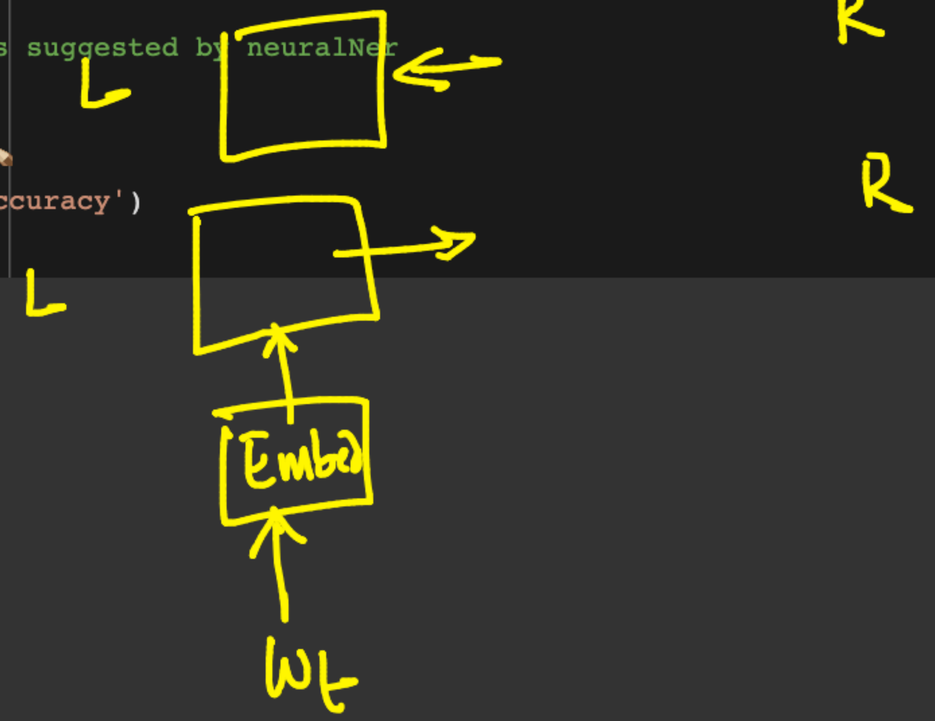
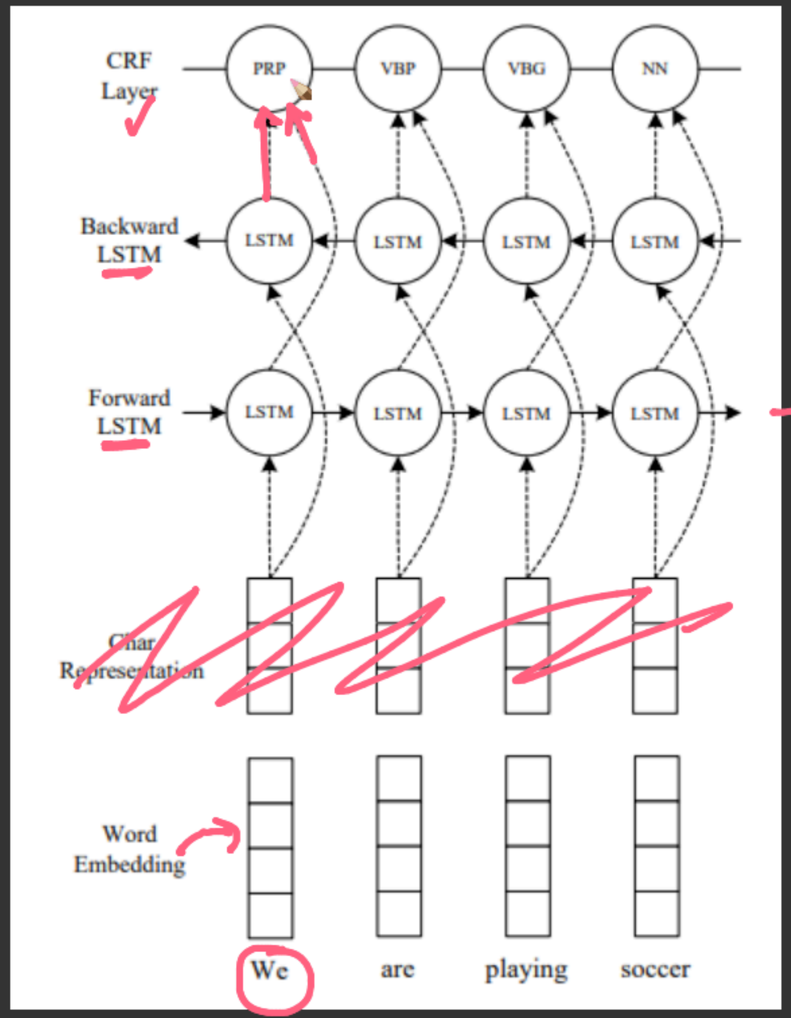
 time_distributed (TimeDistr  (None, 75, 50)           5050
```



- Therefore, we model label sequence jointly using a conditional random field (CRF) instead of decoding each label independently.



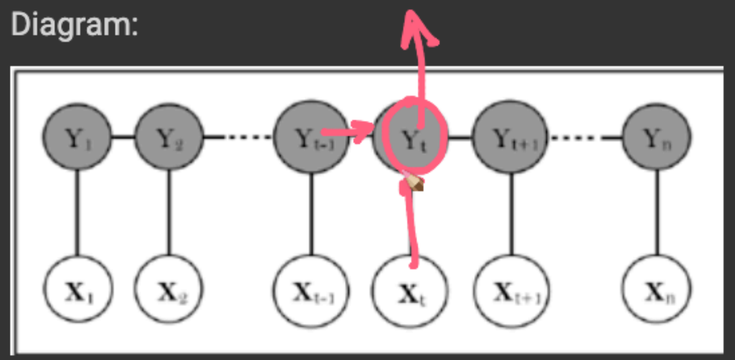
Hybrid

called as feature functions that will assist in generating unique features.

- These features function can consider any logic(depends on programmer) but the output has to be either True:1 or False:0.

Optional: Math of Linear CRF

Diagram:



Fundamental Equation:

Consider the below formula:

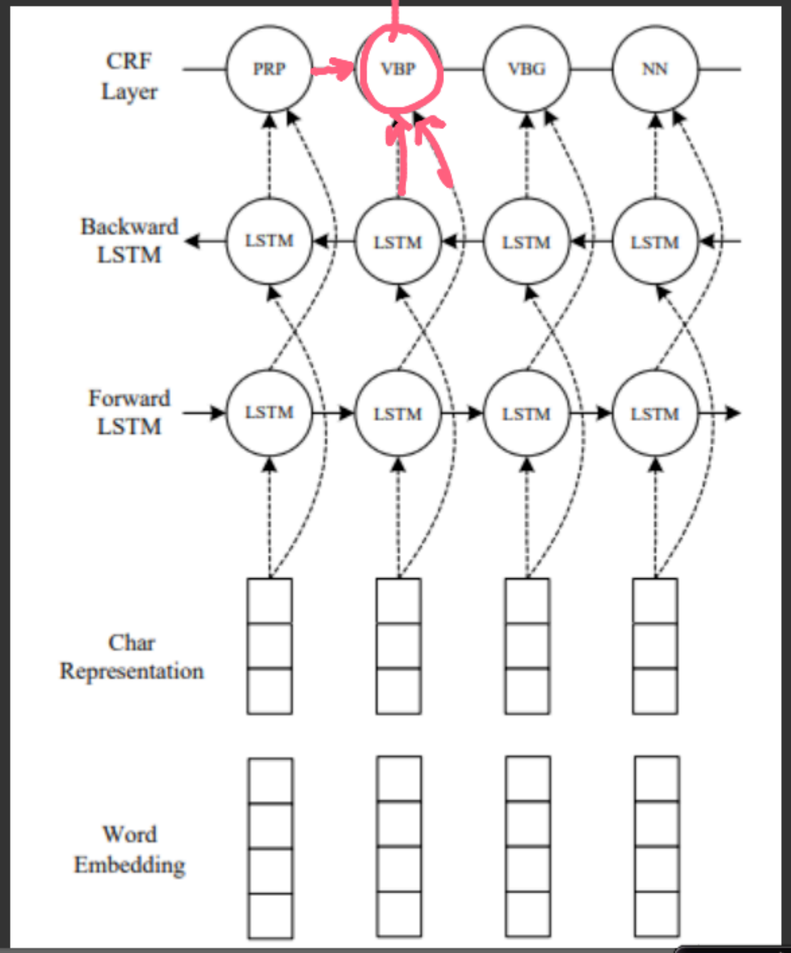
CRF:

$$p_\theta(y|x) = \frac{exp(\sum_j w_j F_j(x,y))}{\sum_{y'} exp(\sum_j w_j F_j(x,y'))}$$

, where $F_j(x,y) = \sum_{i=1}^{L} f_j(y_{i-1}, y_i, x, i)$

sentence.

- For example, in POS tagging an adjective is more likely to be followed by a noun than a verb,
- In NER with standard BIO2 annotation I-ORG cannot follow I-PER.
- Therefore, we model label sequence jointly using a conditional random field (CRF) instead of decoding each label independently.



```
Downloading tensorflow_addons-0.18.0-cp37-cp37m-manylinux_2_17_x86_64.manylinux2014_x86_64.whl (1.1 MB)
     |████████████████████████████████| 1.1 MB 6.7 MB/s
Requirement already satisfied: typeguard>=2.7 in /usr/local/lib/python3.7/dist-packages (from tensorflow_addons) (2.7.1)
Requirement already satisfied: packaging in /usr/local/lib/python3.7/dist-packages (from tensorflow_addons) (21.3)
Requirement already satisfied: pyparsing!=3.0.5,>=2.0.2 in /usr/local/lib/python3.7/dist-packages (from packaging->tensorflow_addons) (3.0
Installing collected packages: tensorflow-addons
Successfully installed tensorflow-addons-0.18.0
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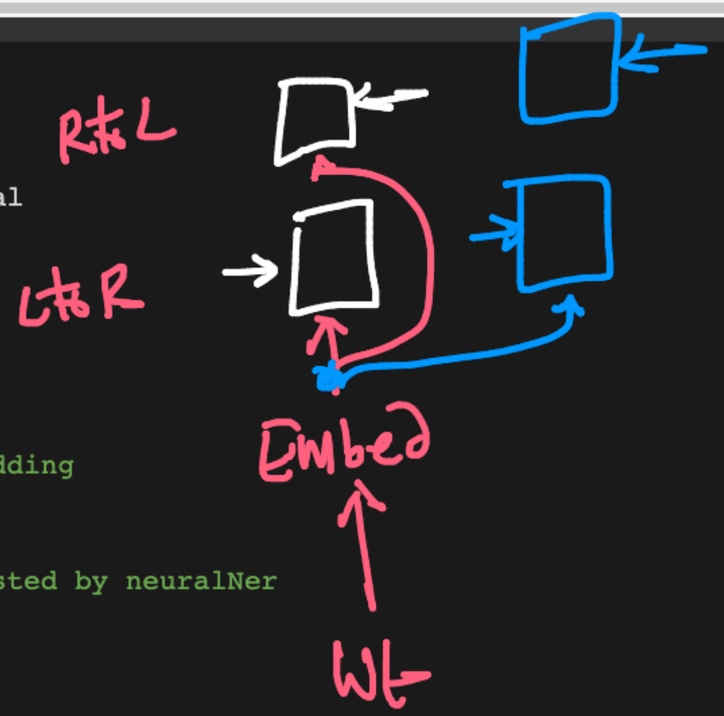


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L08_NER_re.ipynb - Colaborat | tfa.rnn.LayerNormLSTMCell | 1603.05118.pdf | Intro_to_Attention_Mechanism | Attention (machine learning) -

colab.research.google.com/drive/1XGu6sNmU2PN7bD6PsG30kM_nN6GsgYa5#scrollTo=ftiqfF8BLroi

+ Code + Text Connect

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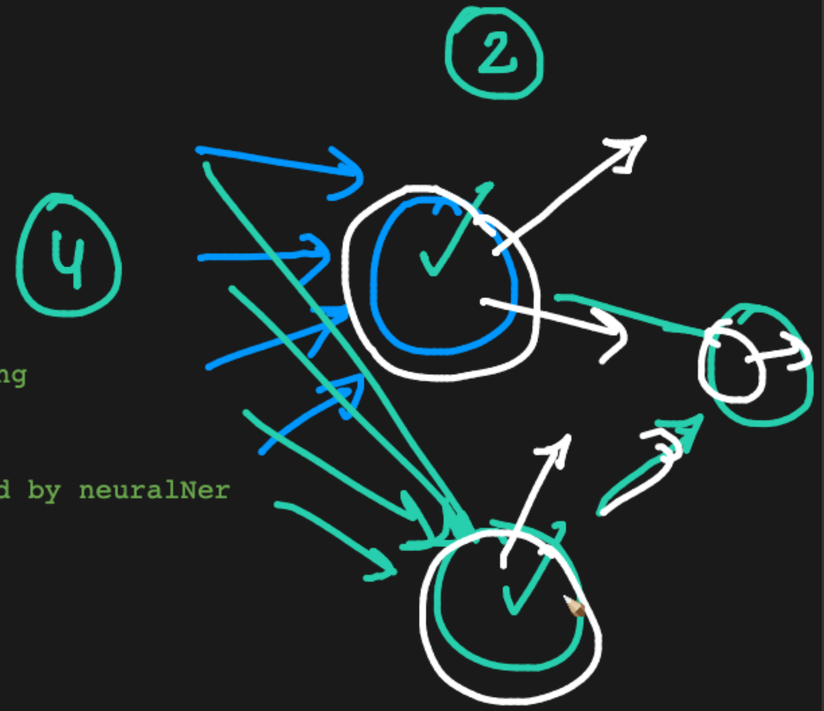


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10 / 11

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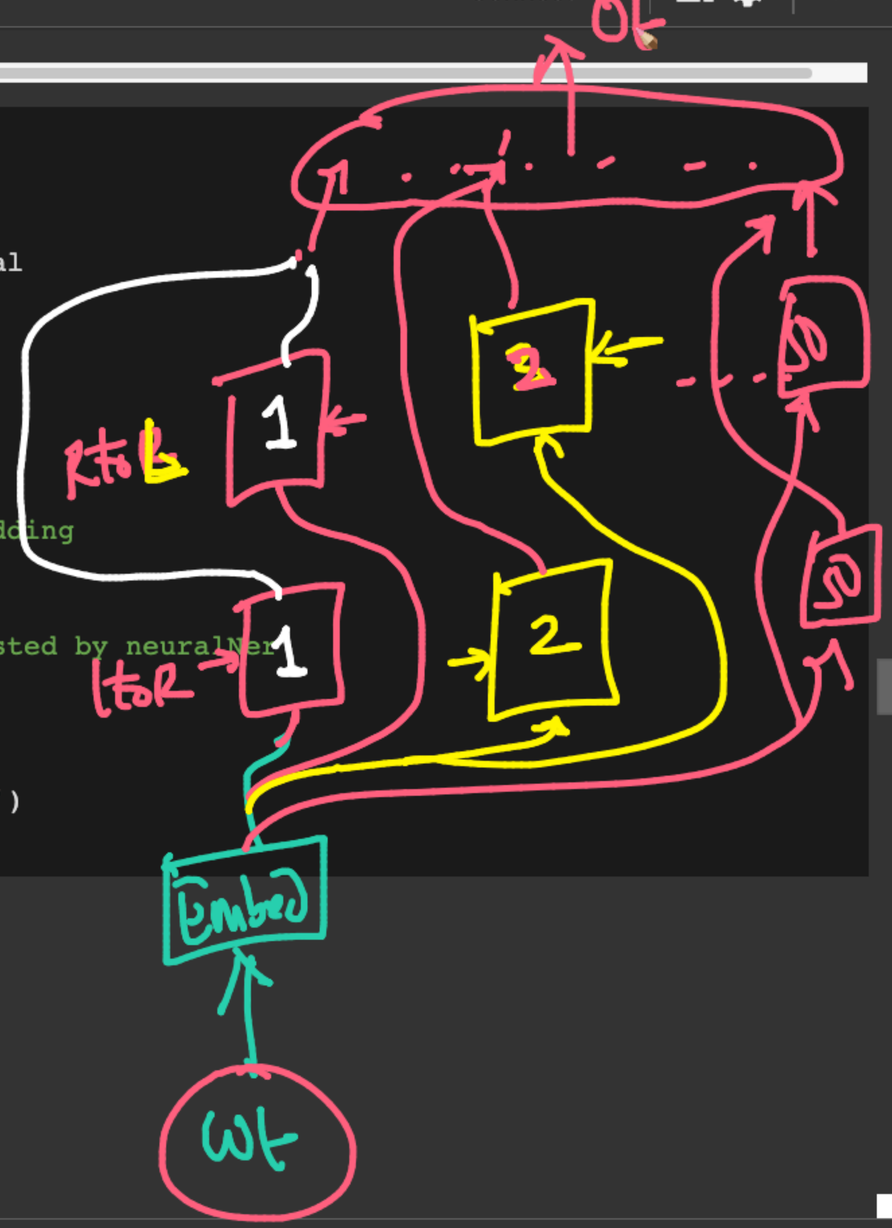

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+ Code + Text

Connect

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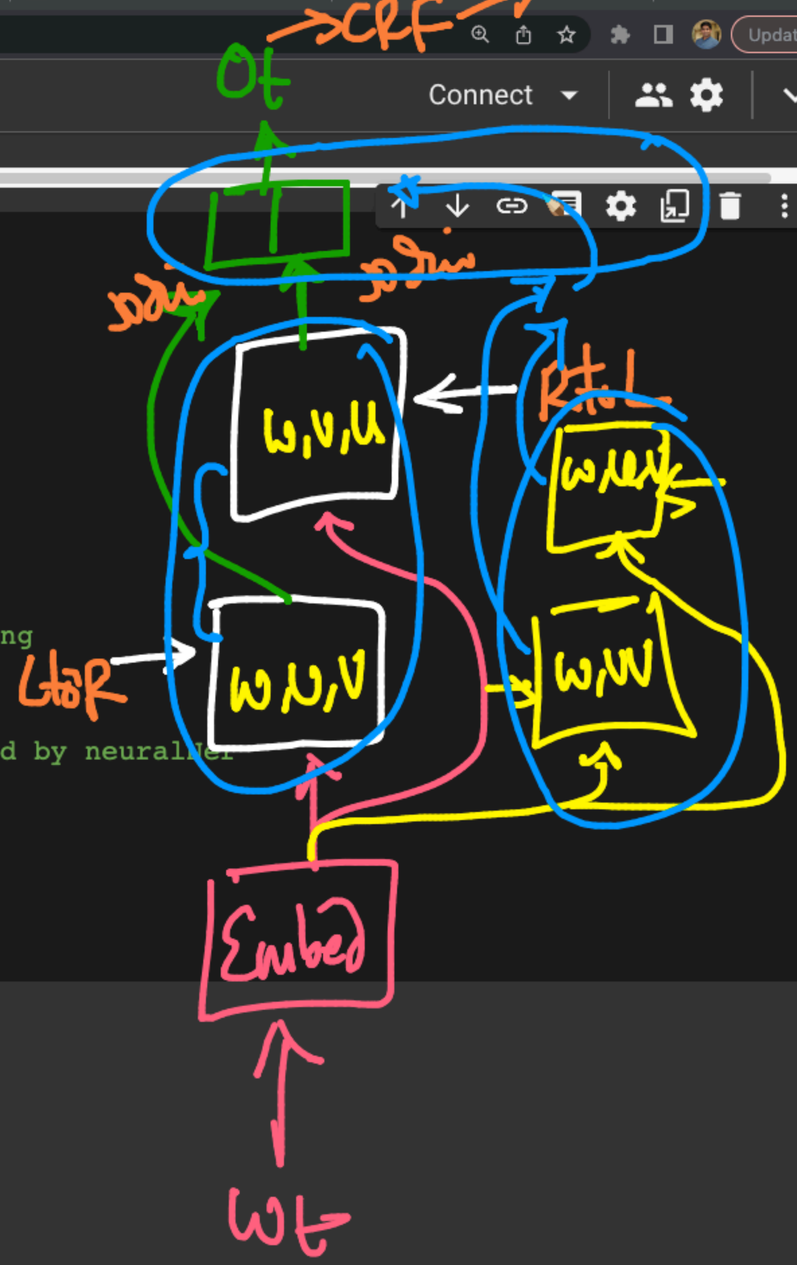


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✓ Functional API ✓

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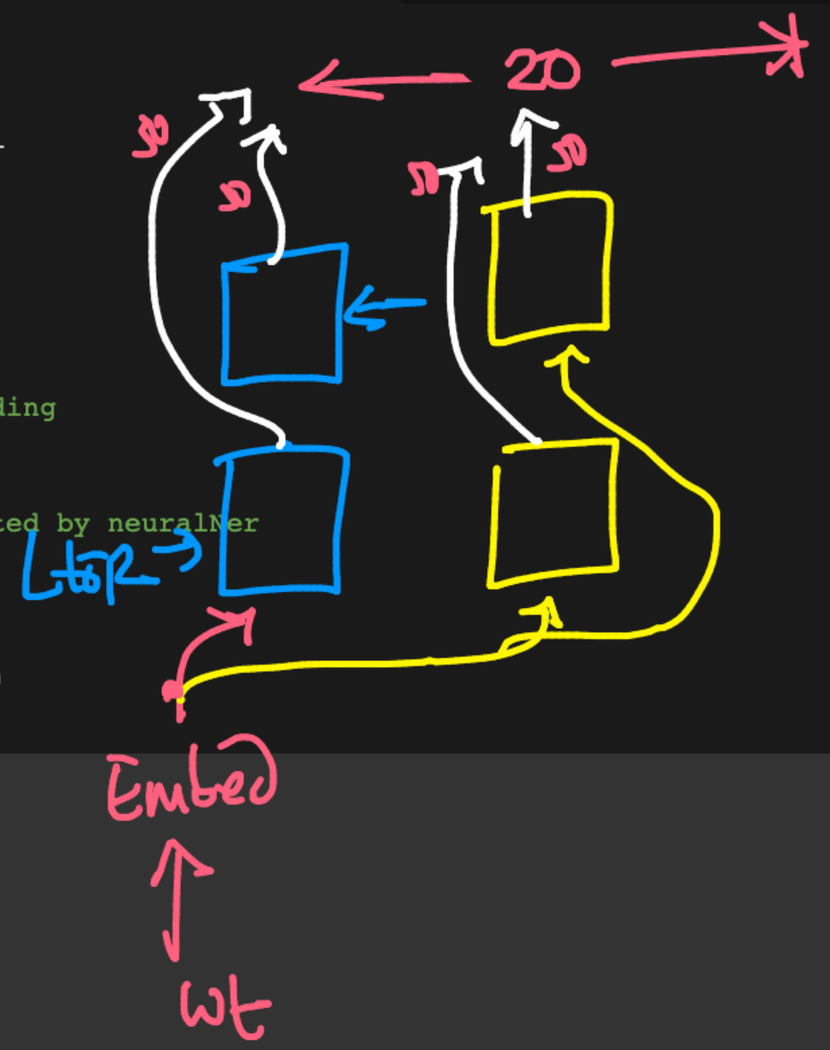


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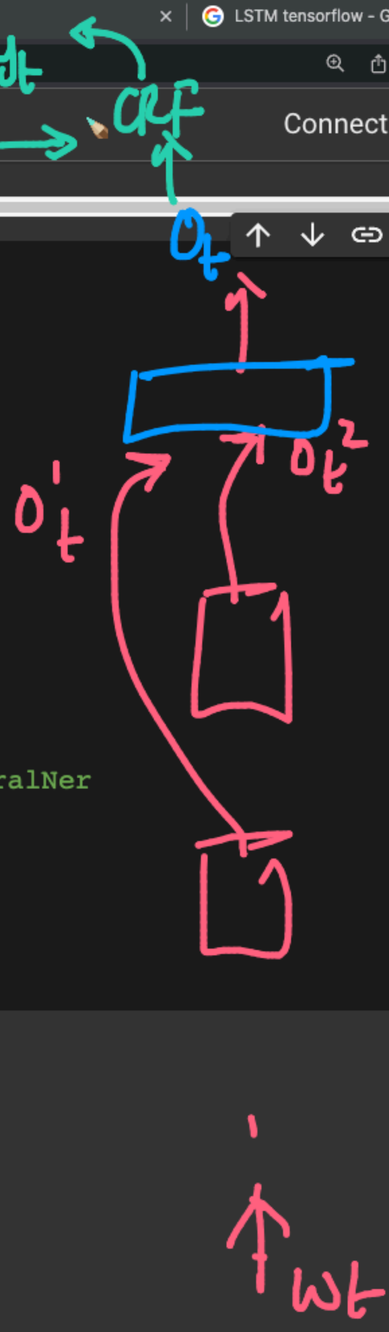


1. **drugName**
2. **condition**
3. **review** Let's take a look at one of review, and understand how a **SME would have labelled it manually.**

Sentence — NER

```
[ ] print('Review Number:',raw_df['uniqueID'][0])
    print('Drug Name:',raw_df['drugName'][0])
    print('Review:',raw_df['review'][0])
```

```
Review Number: 206461.0
Drug Name: Valsartan
Review: "It has no side effect, I take it in combination of Bystolic 5 Mg and Fish Oil"
```

And we see, for review number 206461, there were **no side-effects or problem** being caused by the drug Valsartan. Let's take a look at another example.

```
[ ] print('Review Number:',raw_df['uniqueID'][15])
    print('Drug Name:',raw_df['drugName'][15])
    print('Review:',raw_df['review'][15])
```

```
Review Number: 81890.0
Drug Name: Liraglutide
Review: "I have been taking Saxenda since July 2016.  I had severe nausea for about a month once I got up to the 2.6 dosage.  It has since
```

Liraglutide is a molecule used to treat type 2 diabetes and chronic weight management. Now, we can see there are some side-effects attached to it

	Disease		
	S800	s800	SPECIES
Clinical	i2b2-2010	i2b2	PROBLEM, TEST, TREATMENT
	Radiology	radiology	ANATOMY, OBSERVATION, ANATOMY_MODIFIER, OBSERVATION_MODIFIER, UNCERTAINTY

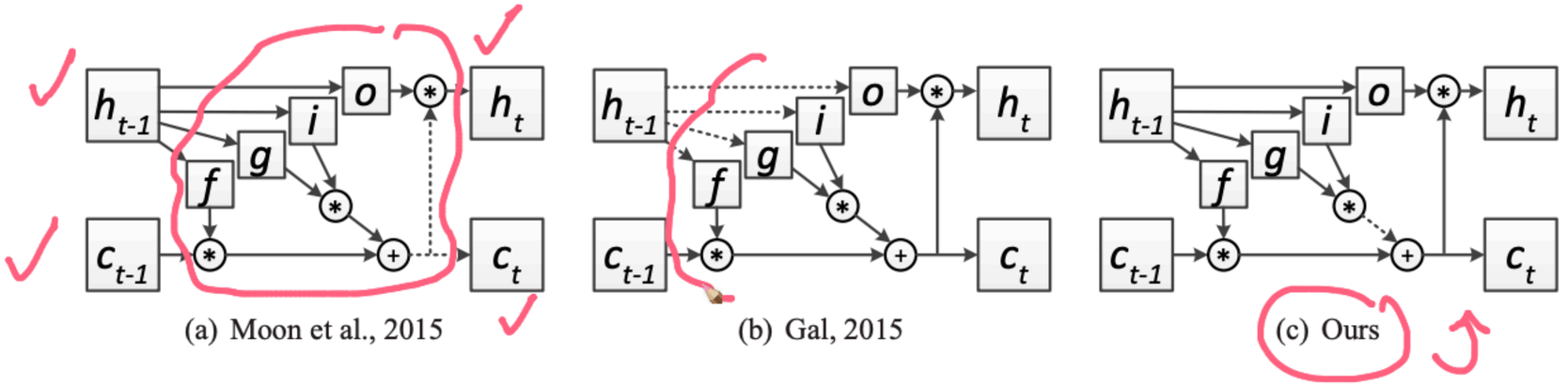
The 16 entity types in the BioNLP13CG model include, some of which are:

- ORGAN
- ORGANISM
- PROBLEM
- TREATMENT
- DISEASE
- CHEMICAL

Let's import stanza

```
[ ]  !pip install stanza
```

```
Looking in indexes: https://pypi.org/simple, https://us-python.pkg.dev/colab-wheels/public/simple/
Collecting stanza
  Downloading stanza-1.4.2-py3-none-any.whl (691 kB)
     |                                | 691 kB 6.9 MB/s
```



(a) Moon et al., 2015 (b) Gal, 2015 (c) Ours

Figure 1: Illustration of the three types of dropout in recurrent connections of LSTM networks. Dashed arrows refer to dropped connections. Input connections are omitted for clarity.

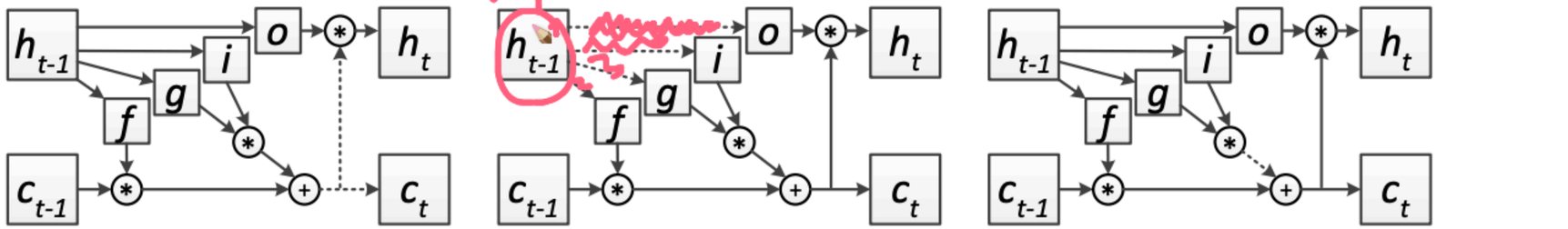
$$\mathbf{h}_t = (1 - \mathbf{z}_t) * \mathbf{h}_{t-1} + \mathbf{z}_t * \mathbf{g}_t \quad (12)$$

Similarly to the LSTMs, we propoose to apply dropout to the hidden state updates vector $\mathbf{g}_t$:

$$\mathbf{h}_t = (1 - \mathbf{z}_t) * \mathbf{h}_{t-1} + \mathbf{z}_t * d(\mathbf{g}_t) \quad (13)$$

We found that an[illegible] behave as binary switches. vious hidden states directly as proposed in The fact that Moon et al. (2015) have achieved an

the network is able to learn long-term dependencies, it is not capable of exploiting them during test phase. Note that our assumption of all gates being equal to 1 helps the network to preserve hidden state, since in a real network gate values lie within (0, 1) interval. In practice trained networks tend to saturate gate values (Karpathy et al., 2015)



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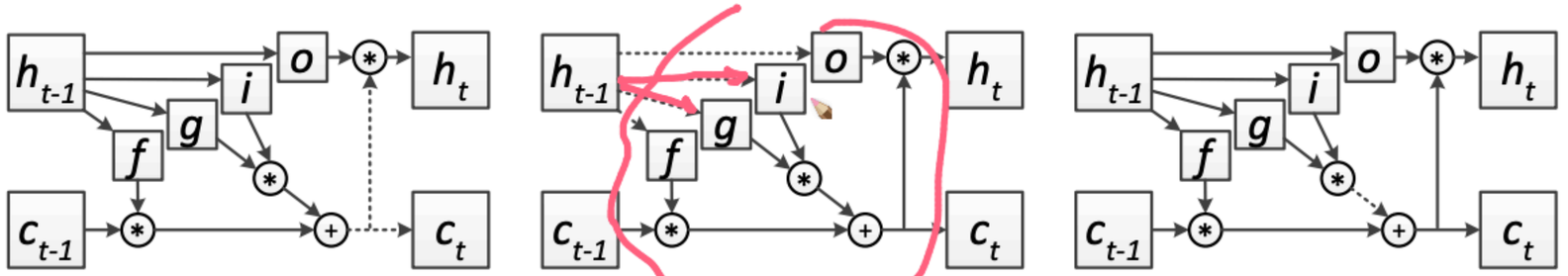

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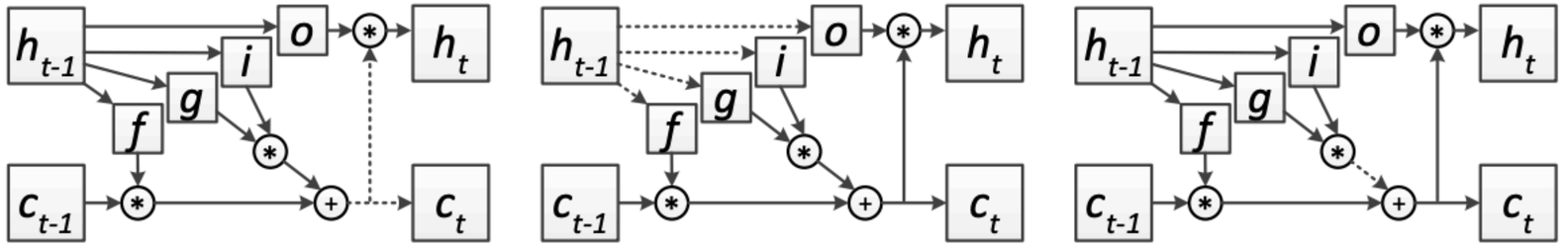

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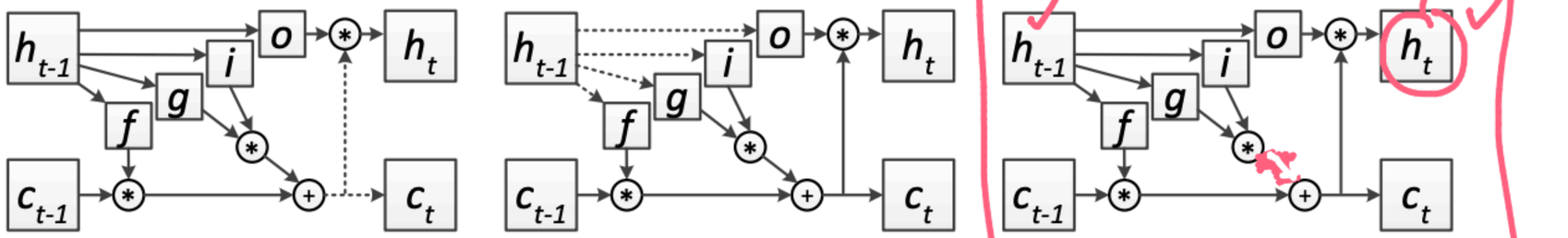

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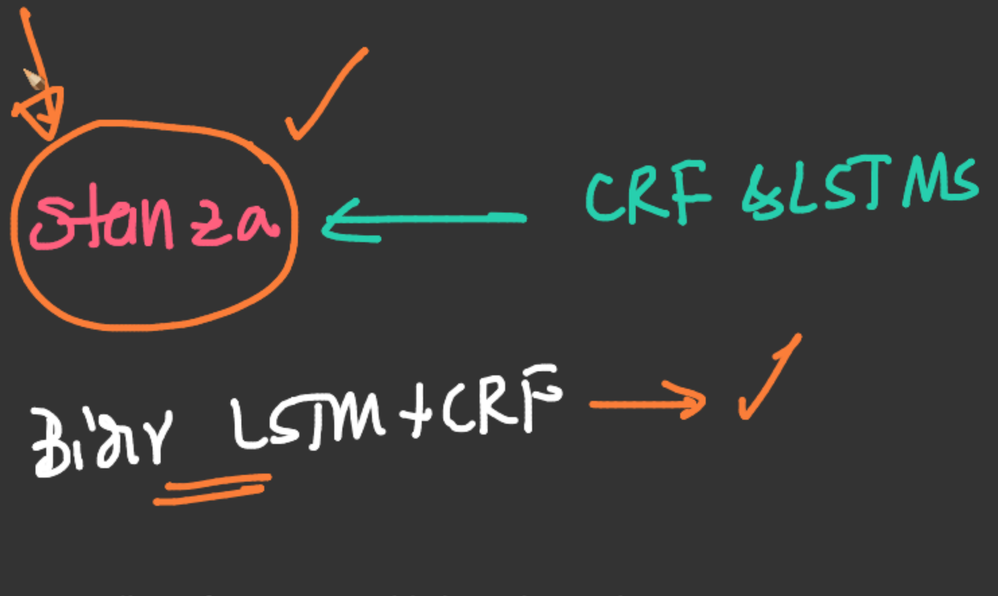
```
Name: drugName, dtype: int64
```

So we see the top 5 drugName with the highest number of side-effects are :

- **Trazodone**
- **Lamotrigine**
- **Tamsulosin**
- **Amitriptyline**
- **Dulcolax**



Scope for improvement

1. Use BIO-Bert for Relationship extraction We can see some the problems are solved by that Drug as well, so if we can establish a relationship between the drugName and the side-effect that will give us a much refined insight about the drug

Further more we can also involve

2. Knowledge Graph for Question and Answering purpose

Conclusion summary

Links:

https://www.persistent.com/blogs/building-named-entity-recognition-models-for-healthcare/

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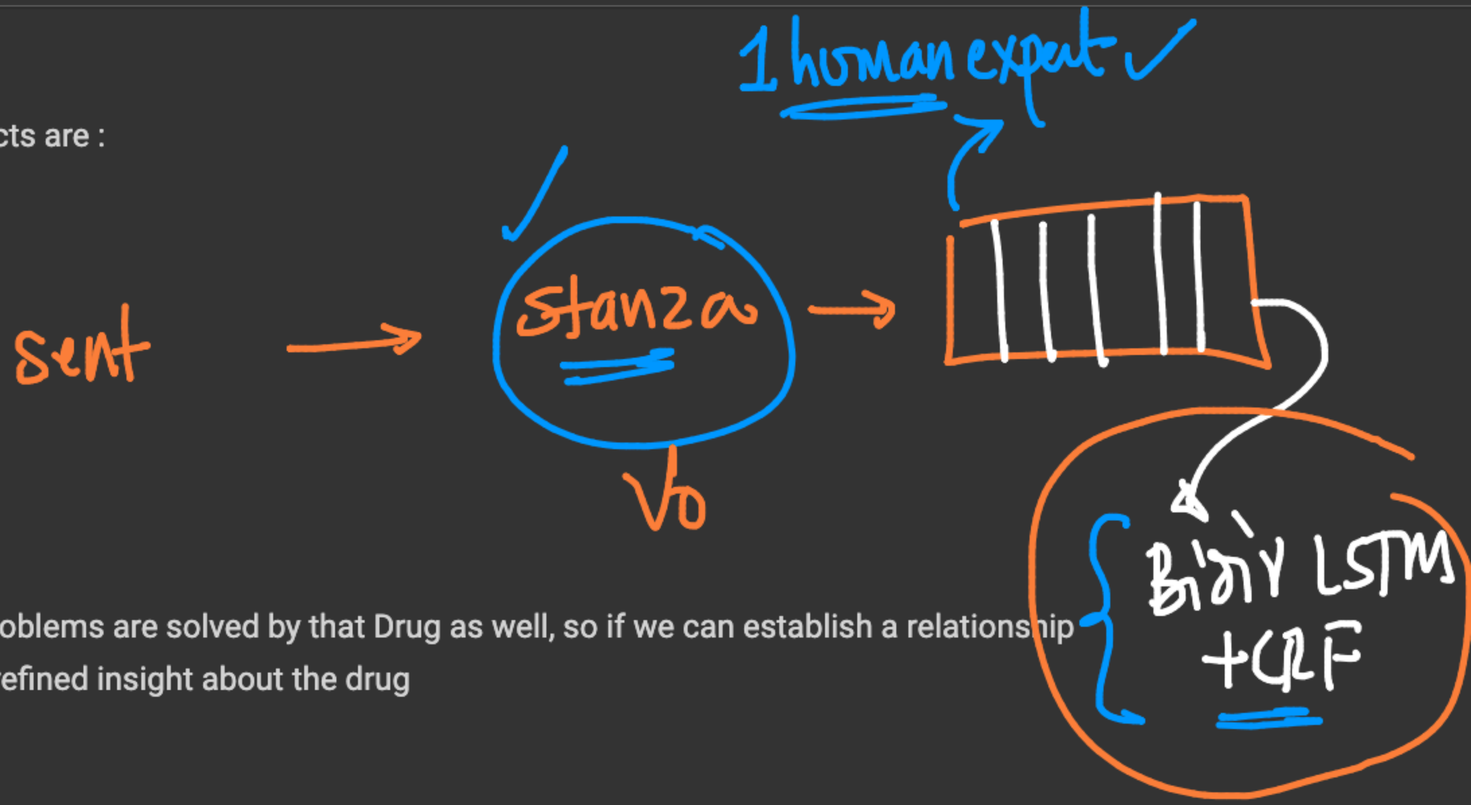

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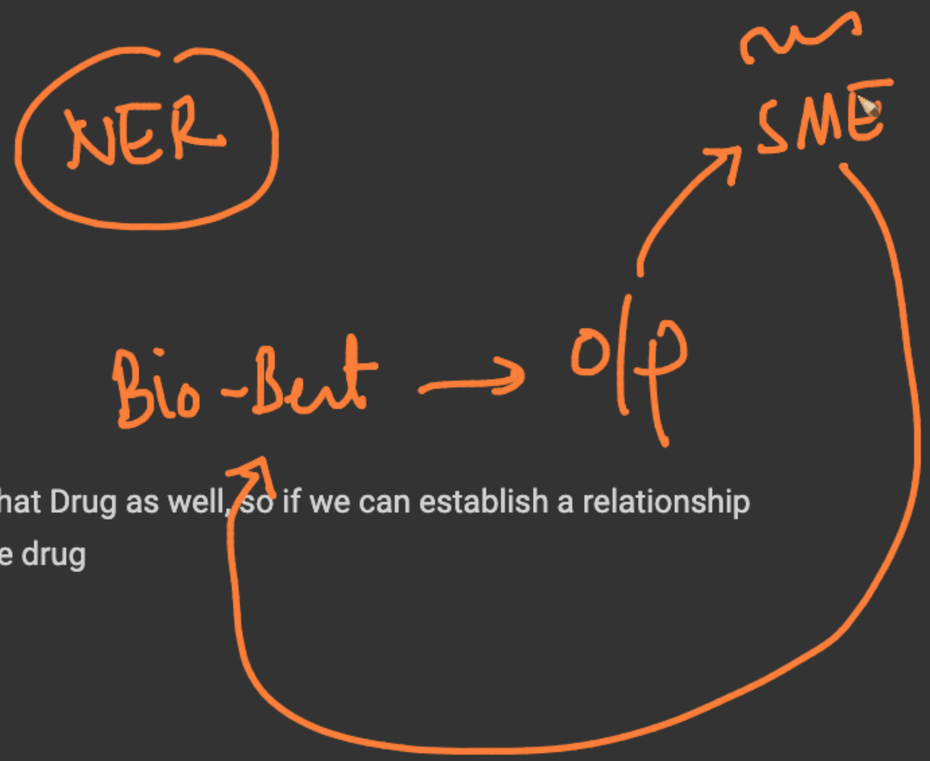

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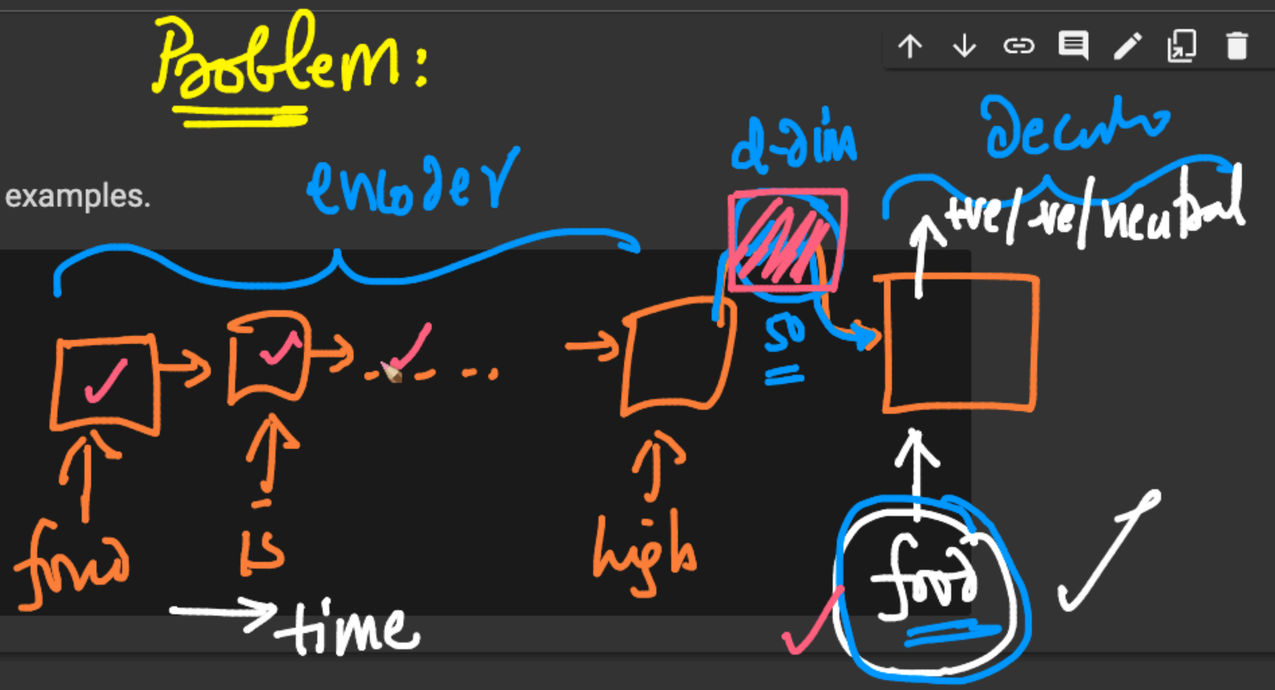
what is 'aspect' in ML?

- the way in which a problem, idea, etc., may be considered
- like your goal is to do classification based on some aspect. see below examples.

```
INPUT = {'text': 'food is delicious but price is high',
            'aspect':'food',

  }

  OUTPUT = {'aspect_Sentiment' : 'Positive'
              }
```



```
[ ] #load glove word embedding vectors
    glove_vectors = gensim.downloader.load('glove-twitter-25')
```

1. Get KEY

> $SourceSentence$ = "food is delicious but price is high"
> $Tokenized$ = [food, is, delicious, but, price, is, high]
> $Key = representation(Tokenized)$

Here, *representation* is nothing but a word embedding model or output from recurrent model.

```
[ ] #Input
    sentences = ['food', 'is', 'delicious', 'but', 'price', 'is', 'high']

    #Dimensionality reduction for easy visualization.
    pca = PCA(n_components=5)

    # Key sequence
    KEY = [glove_vectors[i].tolist() for i in sentences]
    KEY = pca.fit_transform(KEY)

    # PLot
    plt.figure(figsize=(10.5, 7.5))
    key_df = pd.DataFrame(np.transpose(np.matrix(KEY)), columns = sentences)
```

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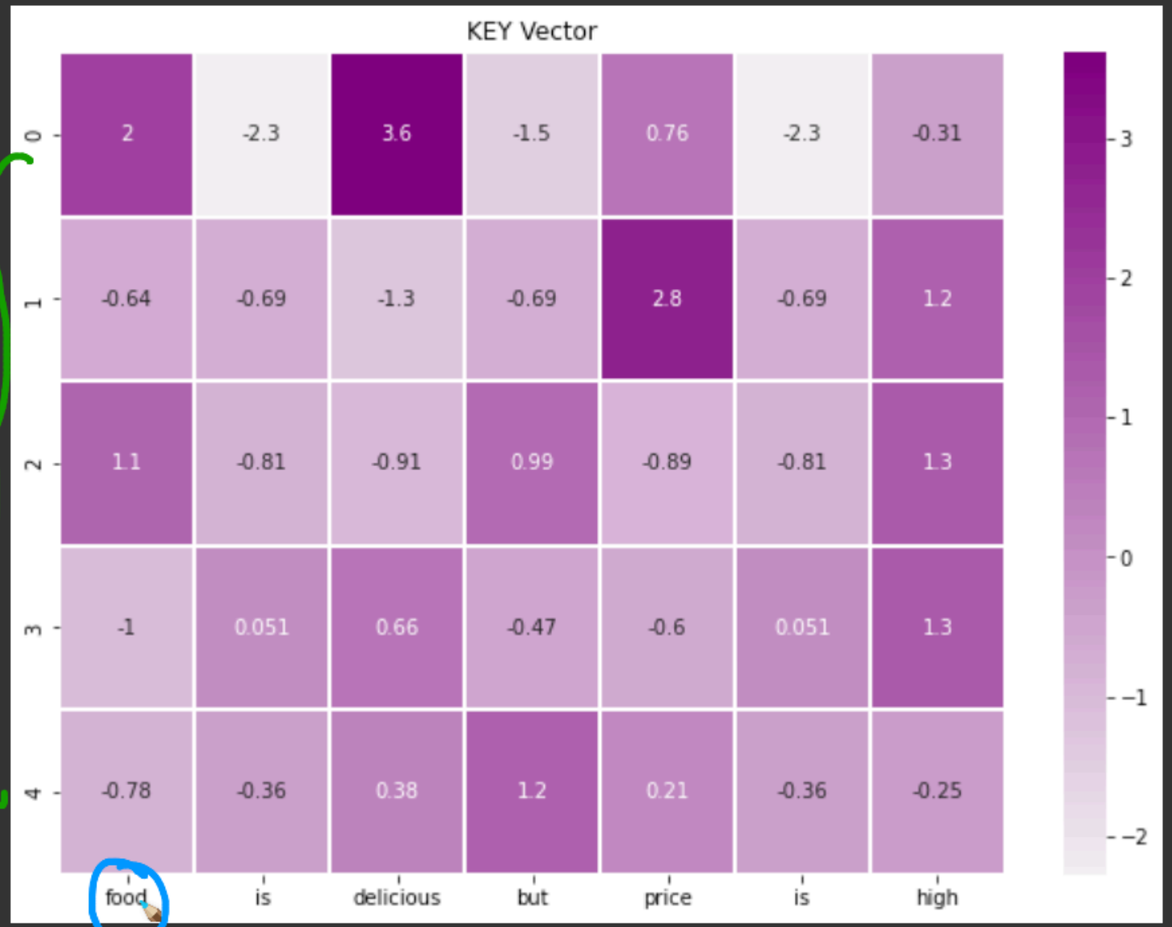

5-dim of each w_i

↓

PCA (dim-red) on w2vec

2. Get Query

target = [tasty, cost]

$Tokenized$ = [food, is, delicious, but, price, is, high]

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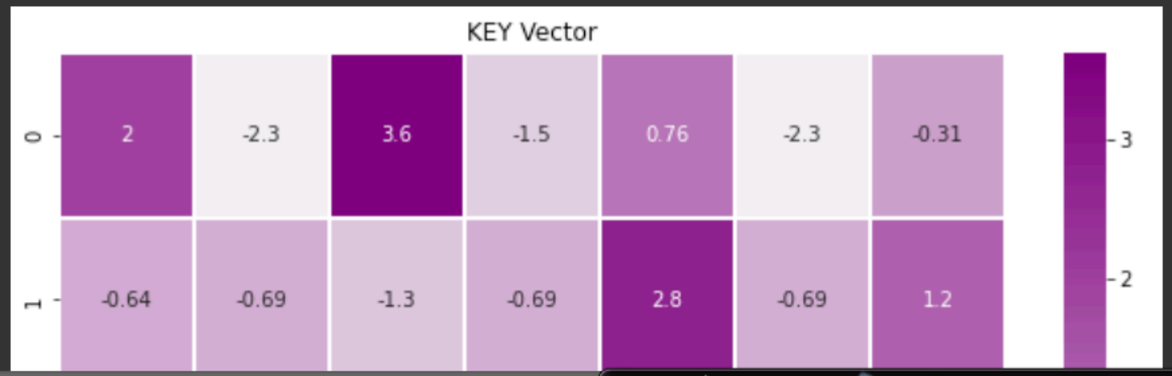
ax = sns.heatmap(key_df, annot=True, cmap=sns.light_palette("purple", as_cmap=True), linewidths=1, ).set_title('KEY Vector')
```



target : ---

ABSA

2. Get Query

target = [tasty, cost]

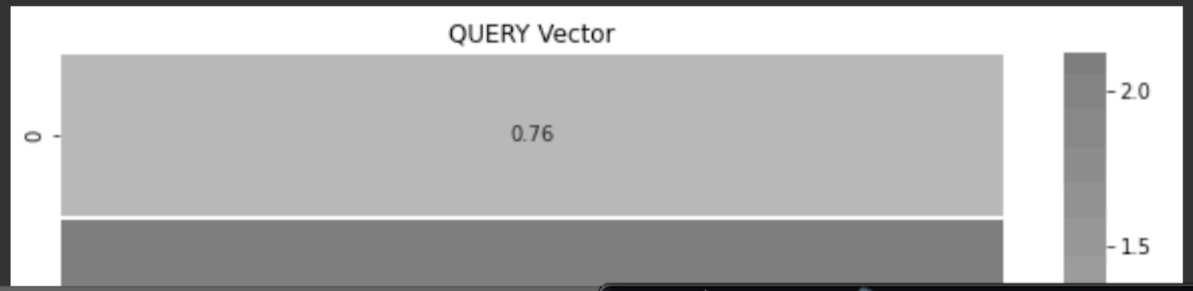
$QUERY = representation(target)$

Here, *representation* is nothing but a word embedding model.

```
#Query text
target = [ 'cost']

#Query embedding and dimensionality reduction
QUERY = [glove_vectors[i].tolist() for i in target]
QUERY = pca.transform(QUERY)


#Plot
plt.figure(figsize=(10.5, 7.5))
query_df = pd.DataFrame(np.transpose(QUERY), columns = target)
ax = sns.heatmap(query_df, annot=True, cmap=sns.light_palette("grey", as_cmap=True), linewidths=1, ).set_title('QUERY Vector', )
```



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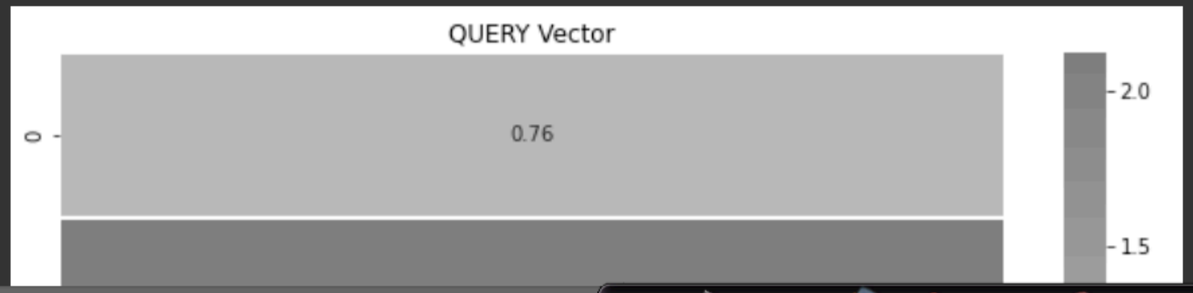

```
attn_df = pd.DataFrame(ATTN_WEIGHTS, index = sentences, columns = target)

plt.figure(figsize=(14.5, 7.5))
ax = sns.heatmap(attn_df , annot=True, cmap=sns.light_palette("green", as_cmap=True), linewidths=1).set_title('ATTN_WEIGHTS', )
```

K dxm ← sentence. length
5 = 7

Q dxm ← #aspects
5 = 1

Atten fn: dot

Energy/Attn score = $K^T \cdot Q$
nxd dxm

A = nxm = 1
7

$Softmax(K^T \cdot Q)$

```
ax = sns.heatmap(np.array(applied_attention_1).reshape(7, 5), annot=True, cmap=sns.light_palette("indigo", as_cmap=True), linewidths=1).s
```

K_{dxn} , Q_{dxM}

7×1

$ATTN\text{-}WEIGHTS = Softmax(K^T_{nxd} Q_{dxM})$

$7 \times M \times 1$

$V = key = V = K_{dxn}$

V^T_{7x5}

$V_{nxd=5}$

$= 7$

```
[ ] def calculate_attention_vector(applied_attention):
      return np.sum(applied_attention, axis=0)
```

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6. Context Vectors

$V^T_{7\times5}$

$A = \text{softmax}(K^T Q)$

```
def apply_attention_scores(attention_weights, annotations):
 # Multiple the annotations by their attention weights
 return  [  annotations[:, i] * attention_weights[i] for i in range(len(attention_weights))]


applied_attention_1 = apply_attention_scores(ATTN_WEIGHTS, np.transpose(VALUE))

plt.figure(figsize=(14.5, 7.5))
ax = sns.heatmap(np.array(applied_attention_1).reshape(7, 5), annot=True, cmap=sns.light_palette("indigo", as_cmap=True), linewidths=1).s
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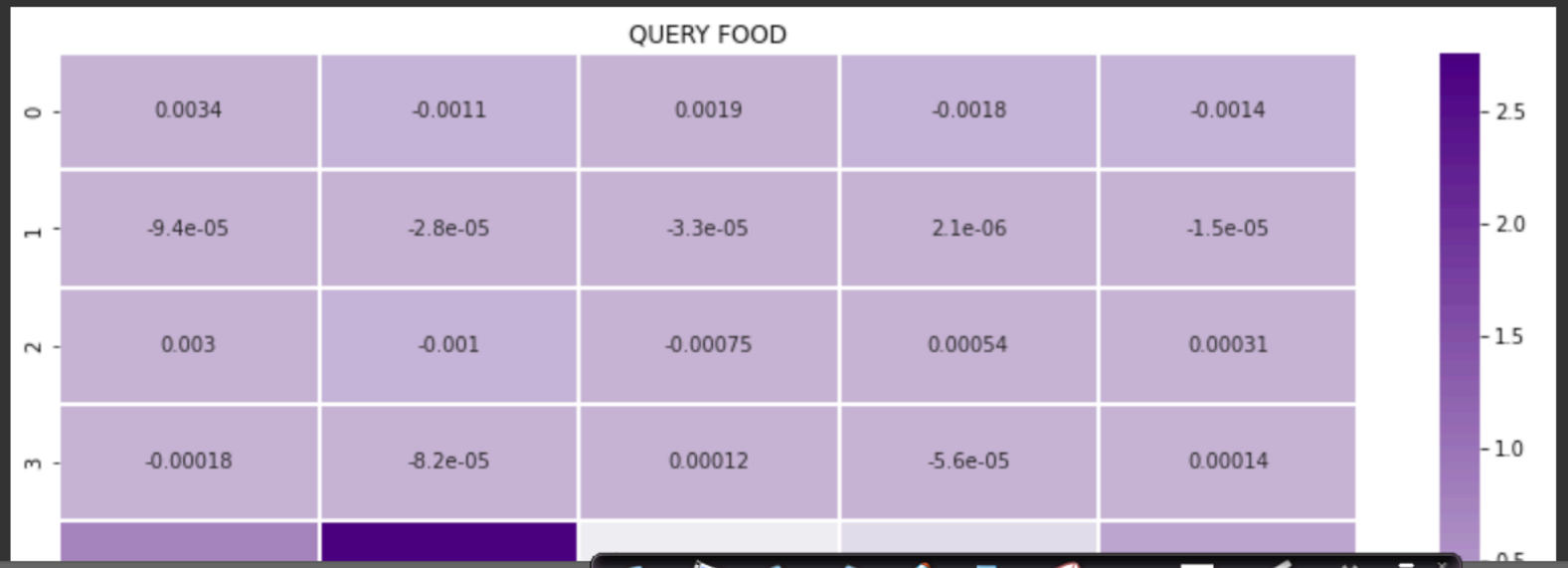

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$softmax(K^T \cdot Q) \cdot V$

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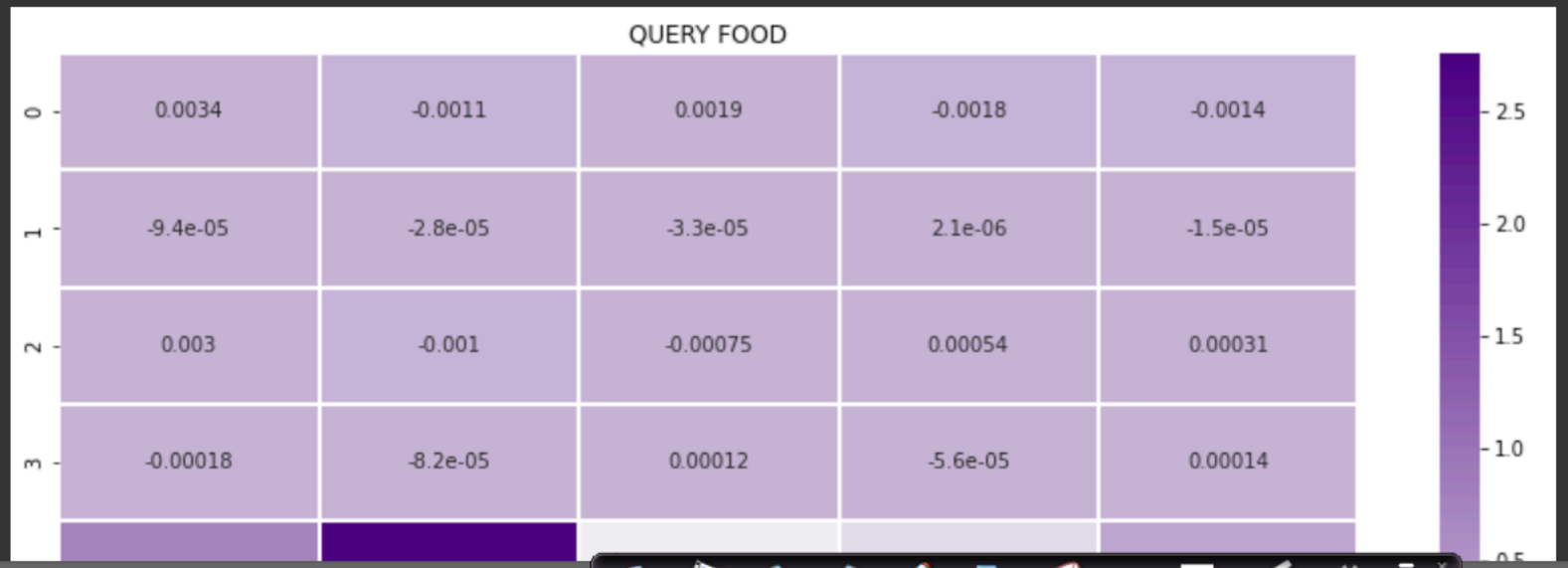

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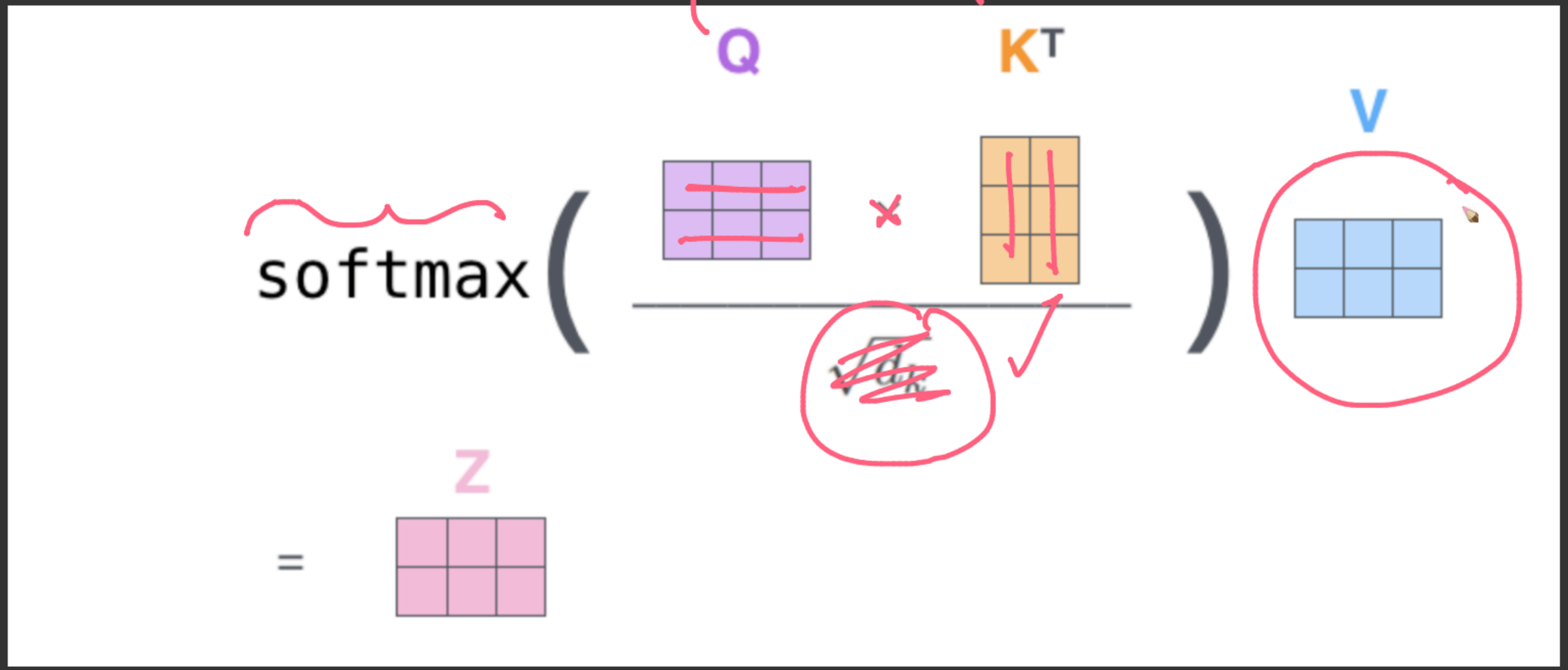
$K = Key,$
$V = Value,$
$where \ \ K == Q == V$

K=V

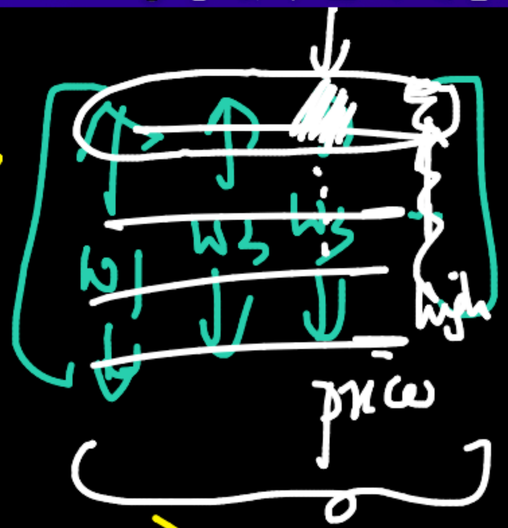



```
[ ] #softmaxing
```

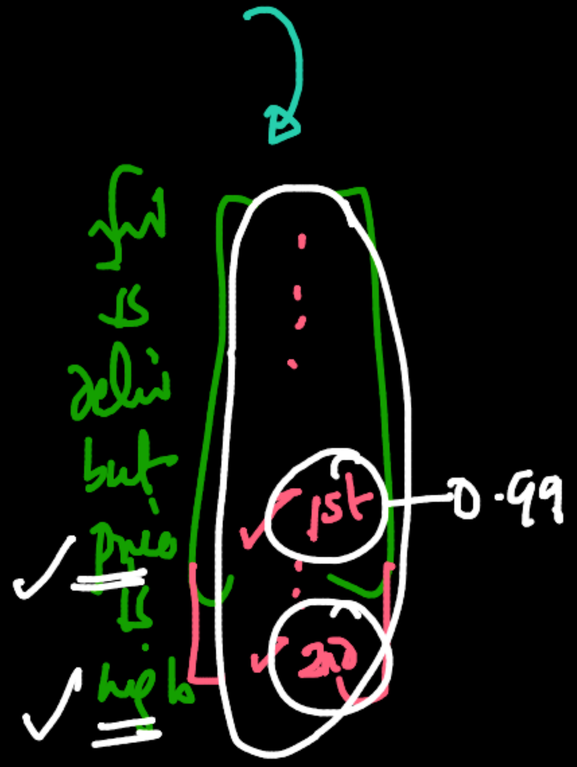
ABSA

aspects

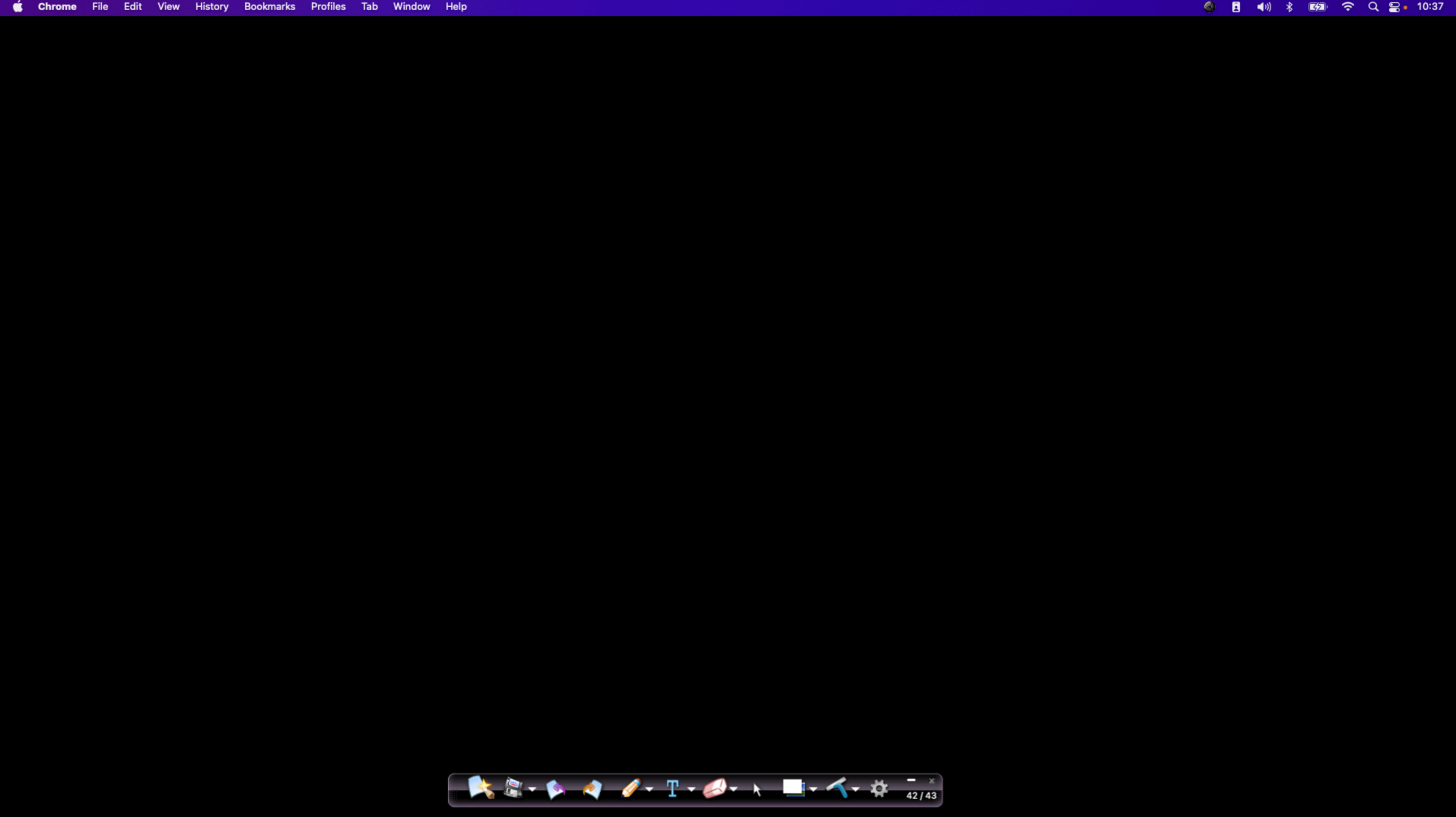
$$\text{softmax}\left(\frac{Q \times K^T}{\sqrt{d}}\right) \cdot V$$



vec. rep of each word in my Sent



fr every aspect, which words in the Sent are most similar


Chrome File Edit View History Bookmarks Profiles Tab Window Help
10:37
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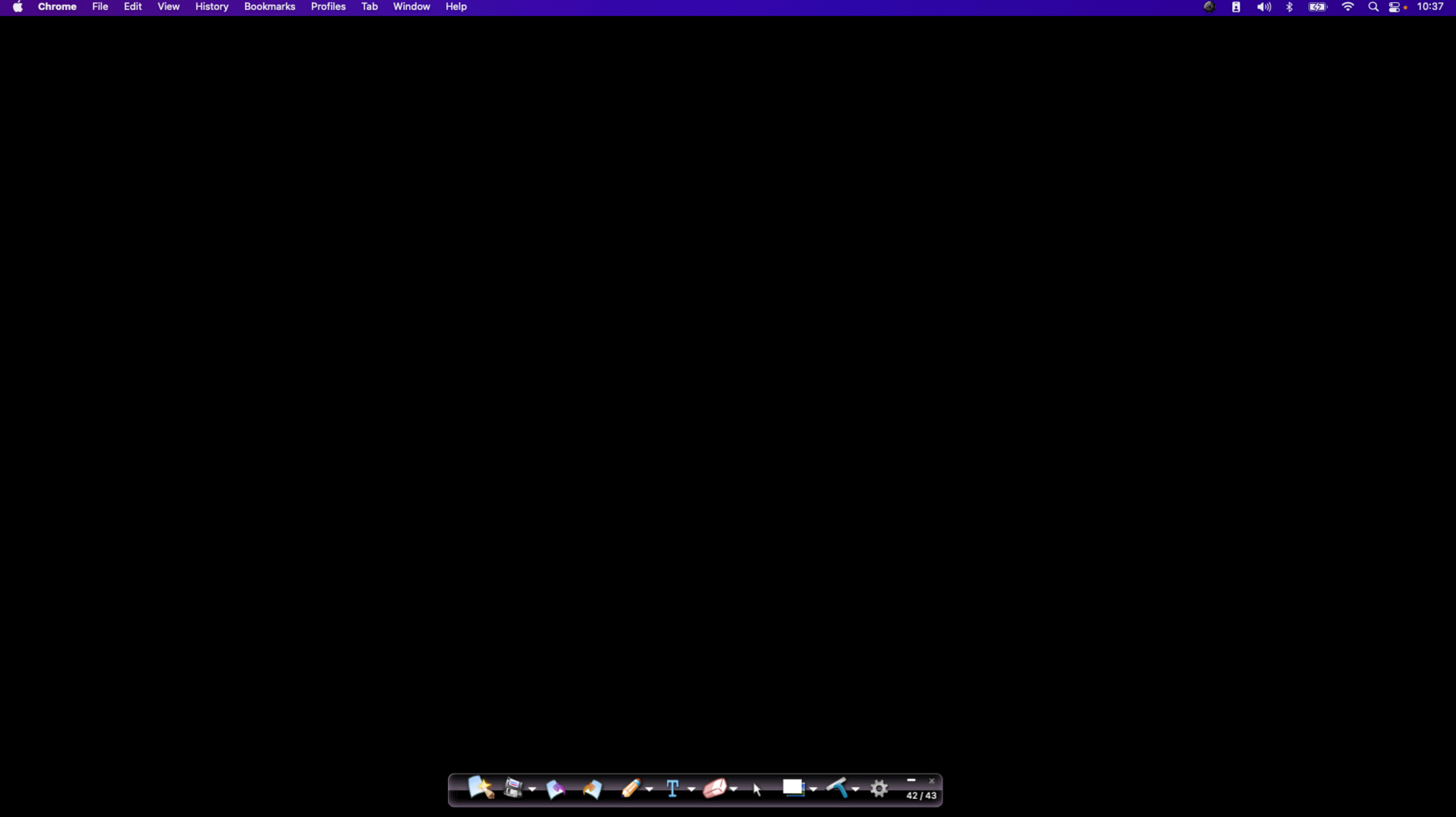
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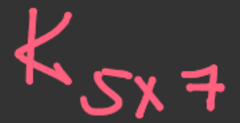
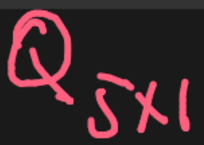
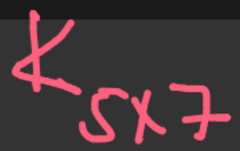
10:37
42 / 43

3. Compute Energy Function.

> Here, Energy Function is *Dot Product*.







```
[ ] def compute_energy_function(vect, mat):
      # calculate energy/attention fuction
      return np.matmul( mat, np.transpose(vect),)

    ENERGY_SCORE = compute_energy_function(QUERY, KEY)
    ENERGY_SCORE
```

```
array([[ 0.51131411],
       [-3.23661494],
       [-0.24969932],
       [-2.17613397],
       [ 6.85134696],
       [-3.23661494],
       [ 1.53640209]])
```

4. Compute Attention weights

```
[ ] def softmax(x):
        # Compute attention weights
        x = np.array(x, dtype=np.float64)
        e_x = np.exp(x)
```

6. Context Vectors

```
def apply_attention_scores(attention_weights, annotations):
 # Multiple the annotations by their attention weights
 return  [  annotations[:, i] * attention_weights[i] for i in range(len(attention_weights))]


applied_attention_1 = apply_attention_scores(ATTN_WEIGHTS, np.transpose(VALUE))

plt.figure(figsize=(14.5, 7.5))
ax = sns.heatmap(np.array(applied_attention_1).reshape(7, 5), annot=True, cmap=sns.light_palette("indigo", as_cmap=True), linewidths=1).s
```

food way del but pic way high

Q: Cost

```
[ ] def calculate_attention_vector(applied_attention):
      return np.sum(applied_attention, axis=0)
```

food →
good →
1. pizza →
2 high →

K
V
Softmax $(K^T Q)$ · V
Cost ✓

```
[ ] def calculate_attention_vector(applied_attention):
      return np.sum(applied_attention, axis=0)
```

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- These Alignment functions based on a notion of comparing query representations with key representations.
- compute either the cosine similarity or the dot product between the key and query representations.
- To account for varying lengths of representation, scaled dot product can be employed that normalizes the dot product by the representation vector length.
- Note that these functions assume that key and query have the same representation vector space.

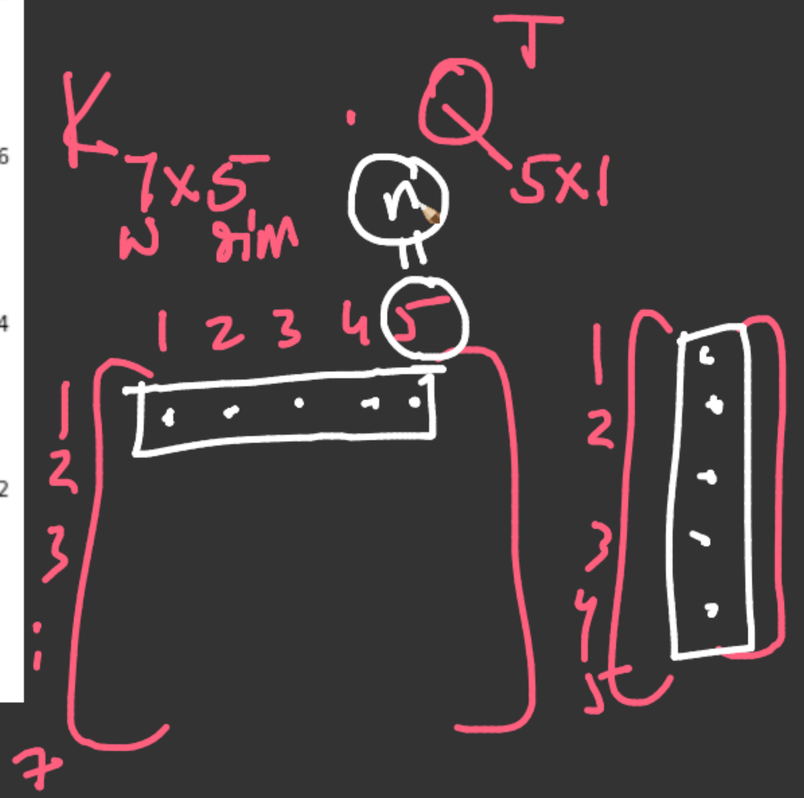
$Attention\_Function$	$Equation\ f(Q, K)$
$Similarity/(e.g.\ CosineSim)$	$Sim(Q, K)$
$DotProduct/Multiplicative$	$Q^T K$
$Scaled\_DotProduct$	$\frac{Q^T K}{\sqrt{n}}$

$\frac{Q^T k}{\sqrt{n}}$ or $k^T Q$

2. General alignment function

1. **General alignment**
2. **Biased general alignment**
3. Activated general alignment

- General alignment extends dot product to keys and queries with different representations by introducing a learnable transformation matrix W that maps queries to the vector space of keys.
- Biased general alignment allows to learn the global importance of some keys irrespective of the query by introducing a bias term.



5. VALUE

Here, VALUE = KEY

```
[ ]  VALUE = np.matrix(KEY)
```

1. Similarity based Alignment functions

1. **Similarity e.g. Cosine Similarity**
2. **Dot Product**
3. **Scaled Dot Product**

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- Biased general alignment allows to learn the global importance of some keys irrespective of the query by introducing a bias term.
- Activated general alignment adds a nonlinear activation layer such as hyperbolic tangent, rectifier linear unit, or scaled exponential linear unit.

$Attention\_Function$	$Equation\ f(Q, K)$
$General\_alignment$	$Q^T W K$
$Biased\_general\_alignment$	$K^T(W \cdot Q + b)$
$Activated\_general\_alignment$	$activation(Q^T W K + b)$

$$\text{softmax}\left(\frac{Q^T \cdot (W_k \cdot K)}{\sqrt{n}}\right) \cdot V$$

3. Additive alignment function

1. **Concat**
2. **Additive Alignment**
3. **Deep alignment**

- combine keys and query to form a joint representation.

2. **Dot Product**
3. **Scaled Dot Product**

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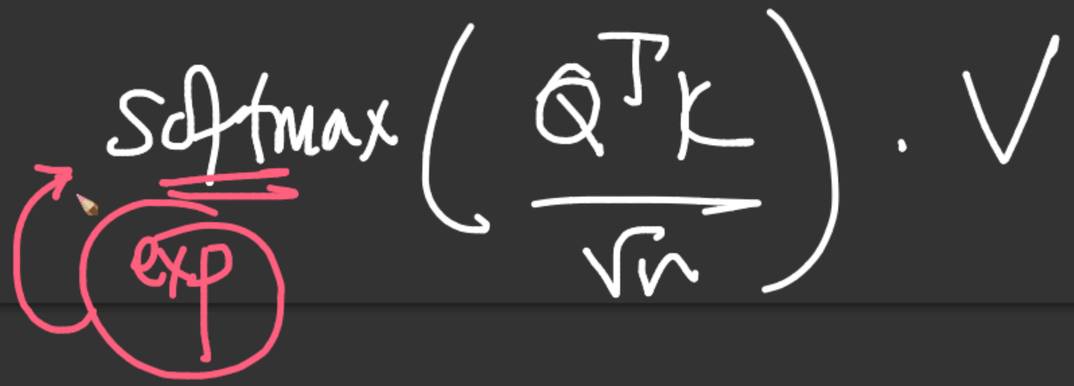

2. General alignment function

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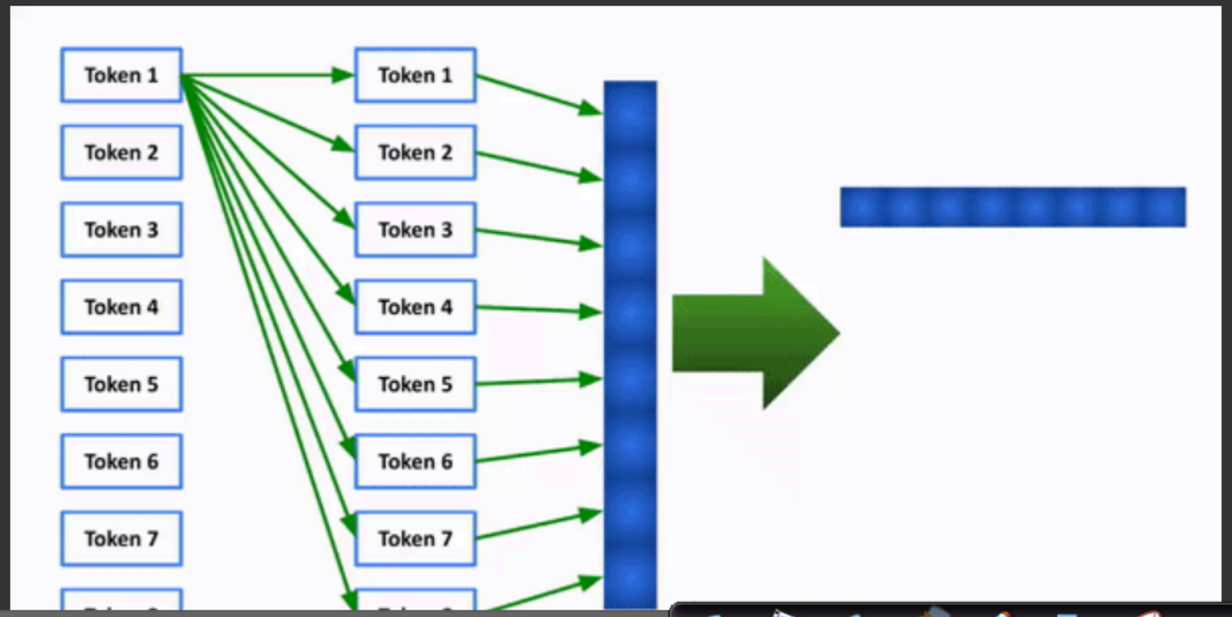
- General alignment extends dot product to keys and queries with different representations by introducing a learnable transformation matrix W that maps queries to the vector space of keys

2. Self Attention AM

- In Self-Attention both KEY and QUERY sequence is Same.
- Basically, QUERY = KEY = VALUE
- **How to Compute Self AM?**
  - Compute KEY, QUERY and VALUE Vectors
  - Compute Energy function
  - Compute Attention Score



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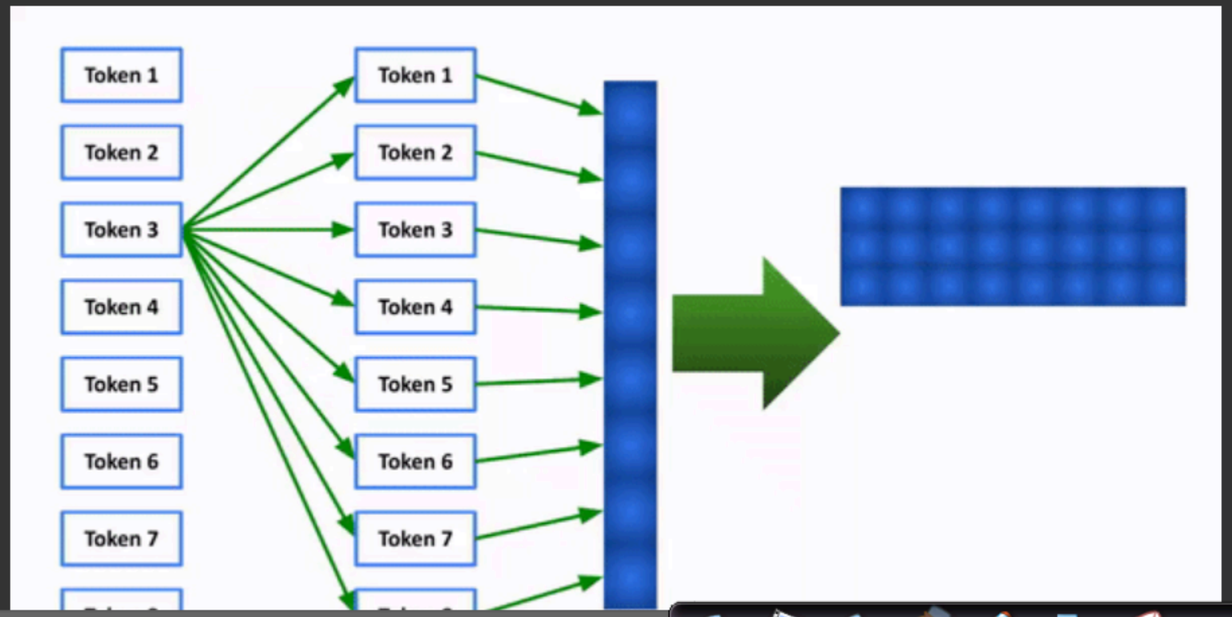

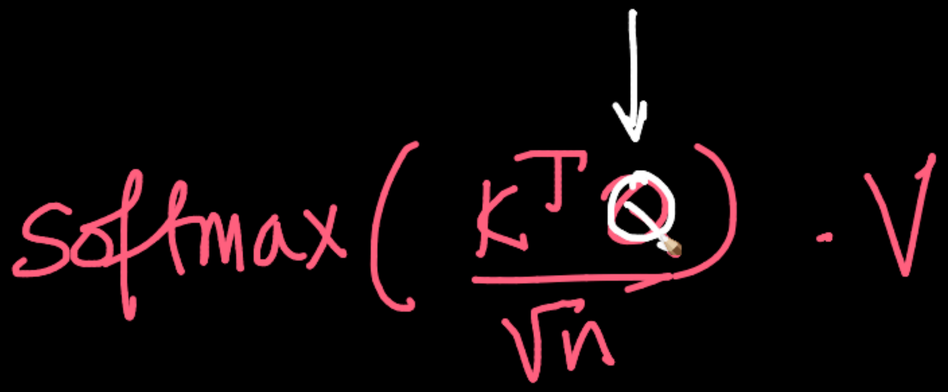

Intro_to_Attention_Mechanisms_V1.ipynb

Open in Colab

```
import pandas as pd
import numpy as np
import string
import re
import random
%matplotlib inline
import matplotlib.pyplot as plt
import seaborn as sns
from gensim.models import word2vec, FastText
import gensim.downloader
from sklearn.decomposition import PCA
```

Problem Statement

- You are a data scientist in travel agency company.
- Your company is trying to figure out the sentiment of people about the Hotel and Restaurant listed on their website on the basis of entity