

03 - Baseline Summarization using Transformer model

In this notebook file, we will do a transformer baseline model:

- read data from mini evaluation set (10% random sampling)
- extract abstract text (first paragraph)
- do summarization with model "Falconsai/medical_summarization"

```
In [1]: !pip install pandas  
!pip install transformers
```

Requirement already satisfied: pandas in c:\users\minh ubc\miniconda3\lib\site-packages (2.2.1)

Requirement already satisfied: numpy<2,>=1.23.2 in c:\users\minh ubc\miniconda3\lib\site-packages (from pandas) (1.25.2)

Requirement already satisfied: python-dateutil>=2.8.2 in c:\users\minh ubc\miniconda3\lib\site-packages (from pandas) (2.9.0)

Requirement already satisfied: pytz>=2020.1 in c:\users\minh ubc\miniconda3\lib\site-packages (from pandas) (2024.1)

Requirement already satisfied: tzdata>=2022.7 in c:\users\minh ubc\miniconda3\lib\site-packages (from pandas) (2024.1)

Requirement already satisfied: six>=1.5 in c:\users\minh ubc\miniconda3\lib\site-packages (from python-dateutil>=2.8.2->pandas) (1.16.0)

Requirement already satisfied: transformers in c:\users\minh ubc\miniconda3\lib\site-packages (4.38.1)

Requirement already satisfied: filelock in c:\users\minh ubc\miniconda3\lib\site-packages (from transformers) (3.13.1)

Requirement already satisfied: huggingface-hub<1.0,>=0.19.3 in c:\users\minh ubc\miniconda3\lib\site-packages (from transformers) (0.19.4)

Requirement already satisfied: numpy>=1.17 in c:\users\minh ubc\miniconda3\lib\site-packages (from transformers) (1.25.2)

Requirement already satisfied: packaging>=20.0 in c:\users\minh ubc\miniconda3\lib\site-packages (from transformers) (24.0)

Requirement already satisfied: pyyaml>=5.1 in c:\users\minh ubc\miniconda3\lib\site-packages (from transformers) (6.0.1)

Requirement already satisfied: regex!=2019.12.17 in c:\users\minh ubc\miniconda3\lib\site-packages (from transformers) (2023.10.3)

Requirement already satisfied: requests in c:\users\minh ubc\miniconda3\lib\site-packages (from transformers) (2.31.0)

Requirement already satisfied: tokenizers<0.19,>=0.14 in c:\users\minh ubc\miniconda3\lib\site-packages (from transformers) (0.15.2)

Requirement already satisfied: safetensors>=0.4.1 in c:\users\minh ubc\miniconda3\lib\site-packages (from transformers) (0.4.1)

Requirement already satisfied: tqdm>=4.27 in c:\users\minh ubc\miniconda3\lib\site-packages (from transformers) (4.66.1)

Requirement already satisfied: fsspec>=2023.5.0 in c:\users\minh ubc\miniconda3\lib\site-packages (from huggingface-hub<1.0,>=0.19.3->transformers) (2023.10.0)

Requirement already satisfied: typing-extensions>=3.7.4.3 in c:\users\minh ubc\miniconda3\lib\site-packages (from huggingface-hub<1.0,>=0.19.3->transformers) (4.10.0)

Requirement already satisfied: colorama in c:\users\minh ubc\miniconda3\lib\site-packages (from tqdm>=4.27->transformers) (0.4.6)

Requirement already satisfied: charset-normalizer<4,>=2 in c:\users\minh ubc\miniconda3\lib\site-packages (from requests->transformers) (3.3.2)

Requirement already satisfied: idna<4,>=2.5 in c:\users\minh ubc\miniconda3\lib\site-packages (from requests->transformers) (3.6)

Requirement already satisfied: urllib3<3,>=1.21.1 in c:\users\minh ubc\miniconda3\lib\site-packages (from requests->transformers) (2.2.1)

Requirement already satisfied: certifi>=2017.4.17 in c:\users\minh ubc\miniconda3\lib\site-packages (from requests->transformers) (2024.2.2)

```
In [2]: import pandas as pd
        from transformers import pipeline
        import torch
```

```
In [3]: # checking if GPU is available
        print(torch.cuda.is_available())
```

```
print(torch.cuda.current_device())
```

True
0

```
In [4]: # set up summarization model
model = pipeline("summarization",
                  model="Falconsai/medical_summarization",
                  device=-1 # run on GPU
                  )
```

```
In [5]: s = 'The evolutionary origins of the hypoxia-sensitive cells that trigger amniote resp  
s
```

```
Out[5]: 'The evolutionary origins of the hypoxia-sensitive cells that trigger amniote resp  
iratory reflexes - carotid body glomus cells , and 'pulmonary neuroendocrine cell  
s' ( PNECs ) - are obscure . Homology has been proposed between glomus cells , whi  
ch are neural crest-derived , and the hypoxia-sensitive 'neuroepithelial cells' (   
NECs ) of fish gills , whose embryonic origin is unknown . NECs have also been lik  
ened to PNECs , which differentiate in situ within lung airway epithelia . Using g  
enetic lineage-tracing and neural crest-deficient mutants in zebrafish , and physi  
cal fate-mapping in frog and lamprey , we find that NECs are not neural crest-deri  
ved , but endoderm-derived , like PNECs , whose endodermal origin we confirm . We  
discover neural crest-derived catecholaminergic cells associated with zebrafish ph  
aryngeal arch blood vessels , and propose a new model for amniote hypoxia-sensitiv  
e cell evolution: endoderm-derived NECs were retained as PNECs , while the carotid  
body evolved via the aggregation of neural crest-derived catecholaminergic ( chrom  
affin ) cells already associated with blood vessels in anamniote pharyngeal arches  
 . '
```

```
In [6]: result = model(s,
                        max_length=500,
                        min_length=100
                        )
summ = result[0]["summary_text"]
print(len(summ))
print(summ)
```

Your max_length is set to 500, but your input_length is only 354. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=177)

783
the evolutionary origins of the hypoxia-sensitive cells that trigger amniote respiratory reflexes - carotid body glomus cells , and 'pulmonary neuroendocrine cells' (PNECs) - are obscure . we find that endoderm-derived neuroepithelial cells (nEC) are not neural crest , but endodermal , like PNCEs , whose endodermale origin we confirm . here we propose a new model for amnium-sensitive cell evolution : endodermm-derived catecholaminergic cells associated with zebrafish pharyngeal arch blood vessel s , while the aggregation of chromaffin) cells already associated with blood vessel s in anamniotic arches has been proposed between the gills . ncs have also been likened to nephrine , which differentiate in situ within lung airway epithelia . the phenotypic origin is unknown .

```
In [7]: # put in a function
def summarize(text, model=model, min_length=100, max_length=500):
    """
```

```

        summarize a text using a transformer model,
        with min_length and max_length are number of tokens limits for the output
        """
    doc = model(text,
                 max_length=max_length,
                 min_length=min_length
                )
    summ = doc[0]["summary_text"]
    return summ

summarize(s)

```

Your max_length is set to 500, but your input_length is only 354. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=177)

Out[7]: 'the evolutionary origins of the hypoxia-sensitive cells that trigger amniote respiratory reflexes - carotid body glomus cells , and 'pulmonary neuroendocrine cells' (PNECs) - are obscure . we find that endoderm-derived neuroepithelial cells (nEC) are not neural crest , but endodermal , like PNCEs , whose endodermale origin we confirm . here we propose a new model for amnium-sensitive cell evolution : endodermm-derived catecholaminergic cells associated with zebrafish pharyngeal arch blood vessels , while the aggregation of chromaffin) cells already associated with blood vessels in anamniotic arches has been proposed between the gills . ncs have also been likened to nephrine , which differentiate in situ within lung airway epithelia . the phenotypic origin is unknown .'

In [8]: *# Load data*

```

filepath = "../data/mini_dataset/"
filename = "eLife_val_mini_milestone3.jsonl"
df = pd.read_json(filepath + filename,
                  orient="records",
                  lines=True
                 )

print(len(df))
df.head()

```

Out[8]:

	lay_summary	article	headings	keywords	id
0	It can take several months , or even years , f...	Mature neural networks synchronize and integra...	[Abstract, Introduction, Results, Discussion, ...	[neuroscience]	elife-69011-v2
1	Many of our decisions are made on the basis of...	Many decisions are thought to arise via the ac...	[Abstract, Introduction, Results, Discussion, ...	[neuroscience]	elife-17688-v1
2	Oculo-Cerebro-Renal syndrome of Lowe (Lowe sy...	Mutations in the inositol 5-phosphatase OCRL c...	[Abstract, Introduction, Results, Discussion, ...	[cell biology]	elife-02975-v2
3	When an embryo develops , its cells must work ...	Gradients of signaling proteins are essential ...	[Abstract, Introduction, Results, Discussion, ...	[developmental biology]	elife-38137-v3
4	Our genomes contain a record of historical eve...	Similarity between two individuals in the comb...	[Abstract, Introduction, Results, Discussion, ...	[evolutionary biology, genetics and genomics]	elife-15266-v1

In [9]:

```
# extract abstract (first paragraph)
df["abstract"] = df["article"].apply(lambda text: text.split("\n")[0])
print(df["abstract"].iloc[3])
df.head()
```

Gradients of signaling proteins are essential for inducing tissue morphogenesis . However , mechanisms of gradient formation remain controversial . Here we characterized the distribution of fluorescently-tagged signaling proteins , FGF and FGFR , expressed at physiological levels from the genomic knock-in alleles in *Drosophila* . FGF produced in the larval wing imaginal-disc moves to the air-sac-primordium (ASP) through FGFR-containing cytonemes that extend from the ASP to contact the wing-disc source . The number of FGF-receiving cytonemes extended by ASP cells decreases gradually with increasing distance from the source , generating a recipient-specific FGF gradient . Acting as a morphogen in the ASP , FGF activates concentration-dependent gene expression , inducing pointed-P1 at higher and cut at lower levels . The transcription-factors Pointed-P1 and Cut antagonize each other and differentially regulate formation of FGFR-containing cytonemes , creating regions with higher-to-lower numbers of FGF-receiving cytonemes . These results reveal a robust mechanism where morphogens self-generate precise tissue-specific gradient contours through feedback regulation of cytoneme-mediated dispersion .

Out[9]:

	lay_summary	article	headings	keywords	id	abstract
0	It can take several months , or even years , f...	Mature neural networks synchronize and integra...	[Abstract, Introduction, Results, Discussion, ...	[neuroscience]	elife-69011-v2	Mature neural networks synchronize and integra...
1	Many of our decisions are made on the basis of...	Many decisions are thought to arise via the ac...	[Abstract, Introduction, Results, Discussion, ...	[neuroscience]	elife-17688-v1	Many decisions are thought to arise via the ac...
2	Oculo-Cerebro-Renal syndrome of Lowe (Lowe sy...	Mutations in the inositol 5-phosphatase OCRL c...	[Abstract, Introduction, Results, Discussion, ...	[cell biology]	elife-02975-v2	Mutations in the inositol 5-phosphatase OCRL c...
3	When an embryo develops , its cells must work ...	Gradients of signaling proteins are essential ...	[Abstract, Introduction, Results, Discussion, ...	[developmental biology]	elife-38137-v3	Gradients of signaling proteins are essential ...
4	Our genomes contain a record of historical eve...	Similarity between two individuals in the comb...	[Abstract, Introduction, Results, Discussion, ...	[evolutionary biology, genetics and genomics]	elife-15266-v1	Similarity between two individuals in the comb...

```
In [10]: # apply summarization
df["baseline_summary"] = df["abstract"].apply(lambda text: summarize(text))
df.head()
```

Your max_length is set to 500, but your input_length is only 226. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=113)

Your max_length is set to 500, but your input_length is only 206. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=103)

Your max_length is set to 500, but your input_length is only 318. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=159)

Your max_length is set to 500, but your input_length is only 321. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=160)

Your max_length is set to 500, but your input_length is only 237. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=118)

Your max_length is set to 500, but your input_length is only 296. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=148)

Your max_length is set to 500, but your input_length is only 369. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=184)

Your max_length is set to 500, but your input_length is only 317. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=158)

C:\Users\Minh UBC\miniconda3\Lib\site-packages\transformers\pipelines\base.py:1157: UserWarning: You seem to be using the pipelines sequentially on GPU. In order to maximize efficiency please use a dataset

warnings.warn(
Your max_length is set to 500, but your input_length is only 287. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=143)

Your max_length is set to 500, but your input_length is only 281. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=140)

Your max_length is set to 500, but your input_length is only 244. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=122)

Your max_length is set to 500, but your input_length is only 249. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=124)

Your max_length is set to 500, but your input_length is only 213. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=106)

Your max_length is set to 500, but your input_length is only 229. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=114)

Your max_length is set to 500, but your input_length is only 246. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=123)

Your max_length is set to 500, but your input_length is only 246. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=123)

Your max_length is set to 500, but your input_length is only 344. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=172)

Your max_length is set to 500, but your input_length is only 306. Since this is a su

mmarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=153)
 Your max_length is set to 500, but your input_length is only 266. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=133)
 Your max_length is set to 500, but your input_length is only 227. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=113)
 Your max_length is set to 500, but your input_length is only 250. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=125)
 Your max_length is set to 500, but your input_length is only 286. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=143)
 Your max_length is set to 500, but your input_length is only 293. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=146)
 Your max_length is set to 500, but your input_length is only 256. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=128)

Out[10]:

	lay_summary	article	headings	keywords	id	abstract	baseline_si
0	It can take several months , or even years , f...	Mature neural networks synchronize and integra...	[Abstract, Introduction, Results, Discussion, ...	[neuroscience]	elife-69011-v2	Mature neural networks synchronize and integra...	we investi progr large
1	Many of our decisions are made on the basis of...	Many decisions are thought to arise via the ac...	[Abstract, Introduction, Results, Discussion, ...	[neuroscience]	elife-17688-v1	Many decisions are thought to arise via the ac...	a novel mani mimics the
2	Oculo-Cerebro-Renal syndrome of Lowe (Lowe sy...	Mutations in the inositol 5-phosphatase OCRL c...	[Abstract, Introduction, Results, Discussion, ...	[cell biology]	elife-02975-v2	Mutations in the inositol 5-phosphatase OCRL c...	the in phosphata is reci
3	When an embryo develops , its cells must work ...	Gradients of signaling proteins are essential ...	[Abstract, Introduction, Results, Discussion, ...	[developmental biology]	elife-38137-v3	Gradients of signaling proteins are essential ...	gradient fc controvers
4	Our genomes contain a record of historical eve...	Similarity between two individuals in the comb...	[Abstract, Introduction, Results, Discussion, ...	[evolutionary biology, genetics and genomics]	elife-15266-v1	Similarity between two individuals in the comb...	back similarity two inc


```
In [11]: # write to output
output_path = "../data/milestone3/transformer_baseline/"
output_file = "elifе.csv"
df.to_csv(output_path+output_file,
          index=False,
          )
print("Output file completed")
```

Output file completed

```
In [12]: # write to txt file
output_file_txt = "elifе.txt"

# write the baseline_summary column to txt file
txt_df = df['baseline_summary']
txt_df.to_csv(output_path+output_file_txt,
              index=False,
              header=False,
              sep="\n"
              )
print("Output file completed")
```

Output file completed

```
In [13]: # repeat for PLOS dev set
# Load data
filepath = "../data/mini_dataset/"
filename = "PLOS_val_mini_milestone3.jsonl"
df = pd.read_json(filepath + filename,
                  orient="records",
                  lines=True
                  )

print(len(df))
df.head()
```

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Out[13]:	lay_summary	article	headings	keywords	id
0	Yersinia pestis , the bacterial agent of plagu...	Fleas can transmit Yersinia pestis by two mech...	[Abstract, Introduction, Results, Discussion, ...	[united states, invertebrates, medicine and he...	journal.ppat.1006859
1	The genome of all vertebrates is heavily colon...	Endogenous retroviruses (ERVs) are remnants ...	[Abstract, Introduction, Results, Discussion, ...	[viruses, sheep, virology]	journal.ppat.0030170
2	The molecular mechanisms underlying directed c...	The Drosophila embryonic gonad is assembled fr...	[Abstract, Introduction, Results, Discussion, ...	[]	journal.pgen.1003720
3	Contrary to the long-standing belief that no n...	Recently , we presented a study of adult neuro...	[Abstract, Introduction, Model, Results, Discu...	[computational biology/computational neuroscie...	journal.pcbi.1001063
4	Embryonic stem cells have two remarkable prope...	Understanding the transcriptional regulation o...	[Abstract, Introduction, Results, Discussion, ...	[developmental biology, cell biology, mammals,...	journal.pgen.0030145

```
In [14]: # extract abstract (first paragraph)
df["abstract"] = df["article"].apply(lambda text: text.split("\n")[0])
print(df["abstract"].iloc[3])
df.head()
```

Recently , we presented a study of adult neurogenesis in a simplified hippocampal memory model . The network was required to encode and decode memory patterns despite changing input statistics . We showed that additive neurogenesis was a more effective adaptation strategy compared to neuronal turnover and conventional synaptic plasticity as it allowed the network to respond to changes in the input statistics while preserving representations of earlier environments . Here we extend our model to include realistic , spatially driven input firing patterns in the form of grid cells in the entorhinal cortex . We compare network performance across a sequence of spatial environments using three distinct adaptation strategies: conventional synaptic plasticity , where the network is of fixed size but the connectivity is plastic; neuronal turnover , where the network is of fixed size but units in the network may die and be replaced; and additive neurogenesis , where the network starts out with fewer initial units but grows over time . We confirm that additive neurogenesis is a superior adaptation strategy when using realistic , spatially structured input patterns . We then show that a more biologically plausible neurogenesis rule that incorporates cell death and enhanced plasticity of new granule cells has an overall performance significantly better than any one of the three individual strategies operating alone . This adaptation rule can be tailored to maximise performance of the network when operating as either a short- or long-term memory store . We also examine the time course of adult neurogenesis over the lifetime of an animal raised under different hypothetical rearing conditions . These growth profiles have several distinct features that form a theoretical prediction that could be tested experimentally . Finally , we show that place cells can emerge and refine in a realistic manner in our model as a direct result of the sparsification performed by the dentate gyrus layer .

Out[14]:

	lay_summary	article	headings	keywords	id	
0	Yersinia pestis , the bacterial agent of plagu...	Fleas can transmit Yersinia pestis by two mech...	[Abstract, Introduction, Results, Discussion, ...	[united states, invertebrates, medicine and he...	journal.ppat.1006859	Y by
1	The genome of all vertebrates is heavily colon...	Endogenous retroviruses (ERVs) are remnants ...	[Abstract, Introduction, Results, Discussion, ...	[viruses, sheep, virology]	journal.ppat.0030170	
2	The molecular mechanisms underlying directed c...	The Drosophila embryonic gonad is assembled fr...	[Abstract, Introduction, Results, Discussion, ...	[]	journal.pgen.1003720	as
3	Contrary to the long-standing belief that no n...	Recently , we presented a study of adult neuro...	[Abstract, Introduction, Model, Results, Discu...	[computational biology/computational neuroscie...	journal.pcbi.1001063	l s
4	Embryonic stem cells have two remarkable prope...	Understanding the transcriptional regulation o...	[Abstract, Introduction, Results, Discussion, ...	[developmental biology, cell biology, mammals,...	journal.pgen.0030145	Ur tr n

```
In [15]: # apply summarization
df["baseline_summary"] = df["abstract"].apply(lambda text: summarize(text))
df.head()
```

```
C:\Users\Minh UBC\miniconda3\Lib\site-packages\transformers\pipelines\base.py:1157:
UserWarning: You seem to be using the pipelines sequentially on GPU. In order to max
imize efficiency please use a dataset
    warnings.warn(
Token indices sequence length is longer than the specified maximum sequence length f
or this model (531 > 512). Running this sequence through the model will result in in
dexing errors
Your max_length is set to 500, but your input_length is only 461. Since this is a su
mmarization task, where outputs shorter than the input are typically wanted, you mig
ht consider decreasing max_length manually, e.g. summarizer('...', max_length=230)
Your max_length is set to 500, but your input_length is only 398. Since this is a su
mmarization task, where outputs shorter than the input are typically wanted, you mig
ht consider decreasing max_length manually, e.g. summarizer('...', max_length=199)
Your max_length is set to 500, but your input_length is only 359. Since this is a su
mmarization task, where outputs shorter than the input are typically wanted, you mig
ht consider decreasing max_length manually, e.g. summarizer('...', max_length=179)
Your max_length is set to 500, but your input_length is only 417. Since this is a su
mmarization task, where outputs shorter than the input are typically wanted, you mig
ht consider decreasing max_length manually, e.g. summarizer('...', max_length=208)
Your max_length is set to 500, but your input_length is only 239. Since this is a su
mmarization task, where outputs shorter than the input are typically wanted, you mig
ht consider decreasing max_length manually, e.g. summarizer('...', max_length=119)
Your max_length is set to 500, but your input_length is only 267. Since this is a su
mmarization task, where outputs shorter than the input are typically wanted, you mig
ht consider decreasing max_length manually, e.g. summarizer('...', max_length=133)
Your max_length is set to 500, but your input_length is only 371. Since this is a su
mmarization task, where outputs shorter than the input are typically wanted, you mig
ht consider decreasing max_length manually, e.g. summarizer('...', max_length=185)
Your max_length is set to 500, but your input_length is only 345. Since this is a su
mmarization task, where outputs shorter than the input are typically wanted, you mig
ht consider decreasing max_length manually, e.g. summarizer('...', max_length=172)
Your max_length is set to 500, but your input_length is only 392. Since this is a su
mmarization task, where outputs shorter than the input are typically wanted, you mig
ht consider decreasing max_length manually, e.g. summarizer('...', max_length=196)
Your max_length is set to 500, but your input_length is only 449. Since this is a su
mmarization task, where outputs shorter than the input are typically wanted, you mig
ht consider decreasing max_length manually, e.g. summarizer('...', max_length=224)
Your max_length is set to 500, but your input_length is only 285. Since this is a su
mmarization task, where outputs shorter than the input are typically wanted, you mig
ht consider decreasing max_length manually, e.g. summarizer('...', max_length=142)
Your max_length is set to 500, but your input_length is only 497. Since this is a su
mmarization task, where outputs shorter than the input are typically wanted, you mig
ht consider decreasing max_length manually, e.g. summarizer('...', max_length=248)
Your max_length is set to 500, but your input_length is only 361. Since this is a su
mmarization task, where outputs shorter than the input are typically wanted, you mig
ht consider decreasing max_length manually, e.g. summarizer('...', max_length=180)
Your max_length is set to 500, but your input_length is only 358. Since this is a su
mmarization task, where outputs shorter than the input are typically wanted, you mig
ht consider decreasing max_length manually, e.g. summarizer('...', max_length=179)
Your max_length is set to 500, but your input_length is only 414. Since this is a su
mmarization task, where outputs shorter than the input are typically wanted, you mig
ht consider decreasing max_length manually, e.g. summarizer('...', max_length=207)
Your max_length is set to 500, but your input_length is only 269. Since this is a su
mmarization task, where outputs shorter than the input are typically wanted, you mig
ht consider decreasing max_length manually, e.g. summarizer('...', max_length=134)
Your max_length is set to 500, but your input_length is only 229. Since this is a su
```

[illegible]

[illegible]

[illegible]

[illegible]

Your max_length is set to 500, but your input_length is only 356. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=178)

Your max_length is set to 500, but your input_length is only 303. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=151)

Your max_length is set to 500, but your input_length is only 463. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=231)

Your max_length is set to 500, but your input_length is only 294. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=147)

Your max_length is set to 500, but your input_length is only 385. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=192)

Your max_length is set to 500, but your input_length is only 348. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=174)

Your max_length is set to 500, but your input_length is only 366. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=183)

Your max_length is set to 500, but your input_length is only 445. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=222)

Your max_length is set to 500, but your input_length is only 461. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=230)

Your max_length is set to 500, but your input_length is only 412. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=206)

Your max_length is set to 500, but your input_length is only 423. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=211)

Out[15]:	lay_summary	article	headings	keywords	id	
0	Yersinia pestis, the bacterial agent of plagu...	Fleas can transmit Yersinia pestis by two mech...	[Abstract, Introduction, Results, Discussion, ...	[united states, invertebrates, medicine and he...	journal.ppat.1006859	Y by
1	The genome of all vertebrates is heavily colon...	Endogenous retroviruses (ERVs) are remnants ...	[Abstract, Introduction, Results, Discussion, ...	[viruses, sheep, virology]	journal.ppat.0030170	I
2	The molecular mechanisms underlying directed c...	The Drosophila embryonic gonad is assembled fr...	[Abstract, Introduction, Results, Discussion, ...	[]	journal.pgen.1003720	as
3	Contrary to the long-standing belief that no n...	Recently , we presented a study of adult neuro...	[Abstract, Introduction, Model, Results, Discu...	[computational biology/computational neuroscie...	journal.pcbi.1001063	I s
4	Embryonic stem cells have two remarkable prope...	Understanding the transcriptional regulation o...	[Abstract, Introduction, Results, Discussion, ...	[developmental biology, cell biology, mammals,...	journal.pgen.0030145	Ur tr r

```
In [16]: # write to output
output_path = "../data/milestone3/transformer_baseline/"
output_file = "plos_mini.csv"
df.to_csv(output_path+output_file,
          index=False,
          )
print("Output file completed")
```

Output file completed

```
In [17]: # write to txt file
output_file_txt = "plos.txt"

# write the baseline_summary column to txt file
txt_df = df['baseline_summary']
txt_df.to_csv(output_path+output_file_txt,
              index=False,
              header=False,
              sep="\n"
              )
print("Output file completed")
```

Output file completed

```

In [21]: # apply to test sets
filepath = "../data/biolaysumm2024_data/"
filenames = ["eLife_test.jsonl",
              "PLOS_test.jsonl"]
output_path = "../data/milestone3/transformer_baseline/test_set/"

output_csv_filenames = ["elife_test.csv",
                        "plos_test.csv"]

output_txt_filenames = ["elife.txt",
                        "plos.txt"]

for i, fname in enumerate(filenames):
    print("Loading file = ", fname)
    df = pd.read_json(filepath + fname,
                      orient="records",
                      lines=True
                      )
    print("n rows =", len(df))

    print("Extracting abstract...")
    df["abstract"] = df["article"].apply(lambda text: text.split("\n")[0])

    print("Making summaries....")
    df["baseline_summary"] = df["abstract"].apply(lambda text: summarize(text))

    print("Writing csv output...")
    df.to_csv(output_path+output_csv_filenames[i],
              index=False,
              )
    print("Output csv file completed")

    txt_df = df['baseline_summary']
    txt_df.to_csv(output_path+output_txt_filenames[i],
                  index=False,
                  header=False,
                  sep="\n"
                  )
    print("Output txt file completed")

print("---- All completed----")

```

C:\Users\Minh UBC\miniconda3\Lib\site-packages\transformers\pipelines\base.py:1157: UserWarning: You seem to be using the pipelines sequentially on GPU. In order to maximize efficiency please use a dataset

warnings.warn(

Your max_length is set to 500, but your input_length is only 394. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=197)

```
Loading file = eLife_test.jsonl  
n rows = 142  
Extracting abstract...  
Making summaries....
```

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

Your max_length is set to 500, but your input_length is only 334. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=167)

Your max_length is set to 500, but your input_length is only 381. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=190)

Your max_length is set to 500, but your input_length is only 327. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=163)

Your max_length is set to 500, but your input_length is only 283. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=141)

Your max_length is set to 500, but your input_length is only 418. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=209)

Your max_length is set to 500, but your input_length is only 269. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=134)

Your max_length is set to 500, but your input_length is only 290. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=145)

Your max_length is set to 500, but your input_length is only 306. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=153)

Your max_length is set to 500, but your input_length is only 354. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=177)

Your max_length is set to 500, but your input_length is only 379. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=189)

Your max_length is set to 500, but your input_length is only 347. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=173)

Your max_length is set to 500, but your input_length is only 411. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=205)

C:\Users\Minh UBC\miniconda3\Lib\site-packages\transformers\pipelines\base.py:1157: UserWarning: You seem to be using the pipelines sequentially on GPU. In order to maximize efficiency please use a dataset

```
warnings.warn(
```

Your max_length is set to 500, but your input_length is only 295. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=147)

Writing csv output...

Output csv file completed

Output txt file completed

Loading file = PLOS_test.jsonl

n rows = 142

Extracting abstract...

Making summaries....

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

mmarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=175)
Your max_length is set to 500, but your input_length is only 218. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=109)
Your max_length is set to 500, but your input_length is only 331. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=165)
Your max_length is set to 500, but your input_length is only 274. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=137)
Your max_length is set to 500, but your input_length is only 475. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=237)
Your max_length is set to 500, but your input_length is only 352. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=176)
Your max_length is set to 500, but your input_length is only 432. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=216)
Your max_length is set to 500, but your input_length is only 354. Since this is a summarization task, where outputs shorter than the input are typically wanted, you might consider decreasing max_length manually, e.g. summarizer('...', max_length=177)

Writing csv output...

Output csv file completed

Output txt file completed

---- All completed----