Big Bird, Transformers for Longer Sequences

(NeurIPS 2020)

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Agenda

- Transformers
 - Universality, Turing Completeness
- Sparse Transformers
 - Universality, Turing Completeness, Graph Theory
- Applications
 - NLP, Genomics

Transformers



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Transformers: Permutation Invariant



Transformers: Proportion Invariant



Transformers: Sequence Modeling



Are Transformers Universal Approximators of Sequence-to-sequence Functions? (ICLR 2020)

• Theorem

For every $f: \mathbb{R}^{n \times d} \to \mathbb{R}^{n \times d}$ with a compact support,

there exists a transformer t

s.t. d(f, t) is as small as desired

(Distance between functions)

$$\mathsf{d}_p(f_1, f_2) := \left(\int \|f_1(\boldsymbol{X}) - f_2(\boldsymbol{X})\|_p^p d\boldsymbol{X}\right)^{1/p}$$



• Key proposition 1

 $\forall C \subset R^{n \times d}$, C compact, there exists a transformer t,

s.t. $\forall U, V \in C, t(U)_i \neq t(V)_j \text{ if } U_i \neq V_j \text{ or } U \neq_p V$

(by constructing specific ATT)

 $(\neq_p : not proportionally equivalent)$

• Key proposition 1

 $\forall C \subset \mathbb{R}^{n \times d}$, C compact, there exists a transformer t,

s.t. $\forall U, V \in C, t(U)_i \neq t(V)_j \text{ if } U_i \neq V_j \text{ or } U \neq_p V$



• Key proposition 2

For every $f: \mathbb{R}^d \to \mathbb{R}^d$ with a compact support,

there exists a feed-forward network t

s.t. d(f, t) is as small as desired



• Transformers are universal sequence models

(through the cooperation of POS + ATT + FF)



• A Turing machine

 $\delta: Q \times \Sigma \to Q \times \Sigma \times \{L, R\}$

current	current	next	symbol	move
state	memory	state	to	left/right
	symbol		write	



• Church-Turing Thesis

Any effectively calculable function can be realized by some Turing machines

- -> A computer is either as powerful as Turing machines or less powerful
- -> Those who are as powerful are said to be *Turing-complete*

On the Turing Completeness of Modern Neural Network Architectures (ICLR 2019)

• Theorem

The class of transformers is Turing-complete

• The key proposition

Every Turing machine can be directly realized (state transition, memory read/write, move left/right) by a sequence-to-sequence transformer with

- a 1-layer encoder,
- a 3-layer decoder,

a vector dimension of $2|Q| + 4|\Sigma| + 11$

Transformers



Transformer Layer

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Sparse Transformers



Sparse Transformers: Adjacency Matrices









Sparse Transformers: Adjacency Matrices



Sparse Transformers: Complexity



Sparse Transformers: Universality

• Theorem

For every $f: \mathbb{R}^{n \times d} \to \mathbb{R}^{n \times d}$ with a compact support,

there exists a sparse transformer t with a global adjacency matrix

s.t. d(f, t) is as small as desired

• Theorem

The class of the sparse transformers with O(n) adjacency matrices is

Turing-complete



complete

star

circular

ER(5,2)

The Average Distances in Random Graphs with Given Expected Degrees (PNAS 2002)



The average distance (shortest paths between nodes) in

ER(n, d) are almost surely in $O(\log n / \log d)$



Erdős-Rényi ER(5,2)



• Graph Expansion

Expansion(G) :=
$$\min_{S} \frac{|B|}{|S|}$$

• Theorem 2.1

The expansion of a regular graph is bounded

by $\lambda_1 - \lambda_2$, where λ_i is the *i*th largest

eigenvalue of the adjacency matrix

-> Expansion of a graph is related to its spectral properties



• Theorem 2.2

An Erdős-Rényi graph approximates its corresponding complete graph spectrally

-> Sparse transformers expand contexts fast like full transformers



• Masked Language Modeling (MLM)

Self-supervised learning to give each word a contextualized embedding



• Masked Language Modeling (MLM)

Table 9: Dataset used for pre training.					
Dataset	# tokens	Avg. doc len.			
Books [111]	1.0 B	37K			
CC-News [34]	7.4B	561			
Stories [90]	7.7B	8.2K			
Wikipedia	3.1B	592			

Table 10: MLM performance on held-out set.

Model	Base	Large
RoBERTa (sqln: 512)	1.846	1.496
Longformer (sqln: 4096)	1.705	1.358
BIGBIRD-ITC (sqln: 4096)	1.678	1.456
BIGBIRD-ETC (sqln: 4096)	1.611	1.274

• Question Answering (QA)

Find the answer and its supporting evidence in a paragraph, a document, or multiple documents Paragraph A:

Return to Olympus is the only album by the alternative rock band Malfunkshun. It was released after the band had broken up and after lead singer Andrew Wood (later of Mother Love Bone) had died of a drug overdose in 1990. Stone Gossard, of Pearl Jam, had compiled the songs and released the album on his label, Loosegroove Records.

Paragraph B:

Mother Love Bone was an American rock band that formed in Seattle, Washington in 1987. The band was active from 1987 to 1990. Frontman Andrew Wood's personality and compositions helped to catapult the group to the top of the burgeoning late 1980s/early 1990s Seattle music scene. Wood died only days before the scheduled release of the band's debut album, "Apple", thus ending the group's hopes of success. The album was finally released a few months later.

Q: What was the former band of the member of Mother Love Bone who died just before the release of "Apple"?

A: Malfunkshun

• Question Answering (QA)

Table 2: QA Dev results using Base size models. We report accuracy for WikiHop and F1 for HotpotQA, Natural Questions, and TriviaQA.

Model	HotpotQA			Natu	ıralQ	TriviaQA	WikiHop
model	Ans	Sup	Joint	LA	SA	Full	MCQ
RoBERTa	73.5	83.4	63.5	-	-	74.3	72.4
Longformer	74.3	84.4	64.4	-	-	75.2	75.0
BIGBIRD-ITC	75.7	86.8	67.7	70.8	53.3	79.5	75.9
BIGBIRD-ETC	75.5	87.1	67.8	73.9	54.9	78.7	75.9

• Question Answering (QA)

Table 3: Fine-tuning results on **Test** set for QA tasks. The Test results (F1 for HotpotQA, Natural Questions, TriviaQA, and Accuracy for WikiHop) have been picked from their respective leaderboard. For each task the top-3 leaders were picked not including BIGBIRD-etc. For Natural Questions Long Answer (LA), TriviaQA, and WikiHop, BIGBIRD-ETC is the new state-of-the-art. On HotpotQA we are third in the leaderboard by F1 and second by Exact Match (EM).

Model	HotpotQA				NaturalQ			TriviaQA		WikiHop
hiodel	Ans	Sup	Joint	-	LA	SA	Fu	111	Verified	MCQ
HGN [26]	82.2	88.5	74.2		-	-		-	-	-
GSAN	81.6	88.7	73.9		-	-		-	-	-
ReflectionNet 32	-	-	-		77.1	64.1		-	-	-
RikiNet-v2 61	-	-	-		76.1	61.3		-	-	-
Fusion-in-Decoder [39]	-	-	-		-	-	84	1.4	90.3	-
SpanBERT [42]	-	-	-		-	-	79).1	86.6	-
MRC-GCN [88]	-	-	-		-	-		-	-	78.3
MultiHop [14]	-	-	-		-	-		-	-	76.5
Longformer [8]	81.2	88.3	73.2		-	-	77	7.3	85.3	81.9
BIGBIRD-ETC	81.2	89.1	73.6		77.8	57.9	8 4	1.5	92.4	82.3

Classification

Table 15: Classification results. We report the F1 micro-averaged score for all datasets. Experiments on smaller IMDb and Hyperpartisan datasets are repeated 5 times and the average performance is presented along with standard deviation.

Model	IMDb [64]	Yelp-5 [109]	Arxiv [35]	Patents [53]	Hyperpartisan [47]
# Examples	$\begin{array}{c} 25000\\ 2\\ 0.14\end{array}$	650000	30043	1890093	645
# Classes		5	11	663	2
Excess fraction		0.04	1.00	0.90	0.53
SoTA	[89] 97.4	[3] 73.28	69) 87.96	69) 69.01	40 90.6
RoBERTa	95.0 \pm 0.2	71.75	87.42	67.07	87.8 \pm 0.8
BIGBIRD	95.2 \pm 0.2	72.16	92.31	69.30	92.2 \pm 1.7

*Excess fraction: proportion of samples longer than 512 words

Summarization

Abstractive summarization via seq2seq learning

Document

PEGASUS is a great model for abstractive summarization tasks. It achieves close to state-of-the-art results with little training data. The results are ...

Extractive Summarization

PEGASUS is a great model for abstractive summarization tasks.

Abstractive Summarization

PEGASUS model achieves close to state-of-the-art results for abstractive summarization tasks with little resources.

• Summarization

		Arxiv		PubMed			BigPatent			
M	odel	R-1	R-2	R-L	R-1	R-2	R-L	R-1	R-2	R-L
	SumBasic [68]	29.47	6.95	26.30	37.15	11.36	33.43	27.44	7.08	23.66
	LexRank 25	33.85	10.73	28.99	39.19	13.89	34.59	35.57	10.47	29.03
	LSA [98]	29.91	7.42	25.67	33.89	9.93	29.70	-	-	-
Ħ	Attn-Seq2Seq [86]	29.30	6.00	25.56	31.55	8.52	27.38	28.74	7.87	24.66
A	Pntr-Gen-Seq2Seq [77]	32.06	9.04	25.16	35.86	10.22	29.69	33.14	11.63	28.55
ior	Long-Doc-Seq2Seq [20]	35.80	11.05	31.80	38.93	15.37	35.21	-	-	-
Ρ	Sent-CLF [82]	34.01	8.71	30.41	45.01	19.91	41.16	36.20	10.99	31.83
	Sent-PTR [82]	42.32	15.63	38.06	43.30	17.92	39.47	34.21	10.78	30.07
	Extr-Abst-TLM [82]	41.62	14.69	38.03	42.13	16.27	39.21	38.65	12.31	34.09
	Dancer [31]	42.70	16.54	38.44	44.09	17.69	40.27	-	-	-
	Transformer	28.52	6.70	25.58	31.71	8.32	29.42	39.66	20.94	31.20
se	+ RoBERTa [76]	31.98	8.13	29.53	35.77	13.85	33.32	41.11	22.10	32.58
Ba	+ Pegasus [108]	34.81	10.16	30.14	39.98	15.15	35.89	43.55	20.43	31.80
	BIGBIRD-RoBERTa	41.22	16.43	36.96	43.70	19.32	<u>39.99</u>	55.69	37.27	<u>45.56</u>
e	Pegasus (Reported) [108]	44.21	16.95	38.83	45.97	20.15	41.34	52.29	33.08	41.75
arg	Pegasus (Re-eval)	43.85	16.83	39.17	44.53	19.30	40.70	52.25	33.04	41.80
Ľ	BIGBIRD-Pegasus	46.63	19.02	41.77	46.32	20.65	42.33	60.64	42.46	50.01

Table 4: Summarization ROUGE score for long documents.

• DNA MLM

Self-supervised learning to give each DNA word a contextualized embedding according to its DNA sentence

-> DNA words: learned via Byte-Pair Encoding (BPE)

• DNA MLM

Self-supervised learning to give each DNA word a contextualized embedding according to its DNA sentence

- 1. Start with empty document set $D = \emptyset$.
- 2. For each chromosome C, repeat the following procedure 10 times.
- -> DNA sentences:
- (a) Pick uniformly at random a starting point q between base pairs 0 and 5000 from the 5' end.
- (b) Repeat until q > |C|
 - i. Pick uniformly at random *s* a number between 50 and 100 to denote number of sentences per document.
 - ii. Constructs a document d containing s sentences using consecutive base pairs (bps). The length of each sentence is chosen uniformly at random between 500-1000. Thus the resulting document has 25,000 100,000 bps.

iii.
$$D = D \bigcup d$$

iv. $q = q + |d|$

• DNA MLM

Model	BPC
SRILM 58 BERT (sqln. 512)	1.57 1.23
BIGBIRD (sqln. 4096)	1.12

*SRILM: n-gram (k-mer) models

Table 5: MLM BPC

• Promoter Region Prediction

Learning to classify a given DNA fragment as a promoter or a non-promoter

sequence

DeePromoter: Robust Promoter Predictor Using Deep Learning (Frontiers in genetics 2019)



• Promoter Region Prediction

Model	F1
CNNProm [91] DeePromoter [71]	69.7 95.6
BigBird	99.9

Table 6: Comparison.

*DeePromoter: CNN + LSTM

• Chromatin-Profile Prediction

Learning to predict chromatin-profiling from non-coding genomic sequence

Predicting Effects of Noncoding Variants with Deep Learning-based Sequence Model (Nat Methods 2015)

- 2.4M noncoding variants
- 919 chromatin-profile
 - 690 transcription factors (TF) binding profiles for 160 different TFs
 - 125 DNase I sensitivity (DHS) profiles
 - 104 histone-mark (HM) profiles

Chromatin-Profile Prediction

Model	TF	HM	DHS
gkm-SVM [30]	89.6	-	

95.8

96.1

DeepSea [110]

BIGBIRD

92.3

92.1

85.6

88.7

Table 7: Chromatin-Profile Prediction



Earth Day 2022

Energy and Policy Considerations for Deep Learning in NLP (ACL 2019)

Consumption	CO_2e (lbs)
Air travel, 1 person, NY↔SF	1984
Human life, avg, 1 year	11,023
American life, avg, 1 year	36,156
Car, avg incl. fuel, 1 lifetime	126,000
Training one model (GPU)	
NLP pipeline (parsing, SRL)	39
w/ tuning & experiments	78,468
Transformer (big)	192
w/ neural arch. search	626,155

Table 1: Estimated CO₂ emissions from training common NLP models, compared to familiar consumption.¹