

Keeping our graphs attentive

Petar Veličković

Artificial Intelligence Group Department of Computer Science and Technology, University of Cambridge, UK

AMLab Seminar

10 April 2018

Introduction

- In this talk, I will present a survey of recent developments in applying attentive mechanisms to improving the exploitation of nontrivial graph structure in data.
- This will involve a discussion of:
 - Graph Attention Networks.
 - Subsequently released generalisations and improvements (EAGCN, GaAN, DeepInf, Attention Solves your TSP).
 - Applications to relational reasoning, multi-agent interaction, cortical mesh segmentation and paratope prediction.
 - An ongoing project in graph classification (with Thomas Kipf).



Graphs are everywhere!





Mathematical formulation

We will focus on the node classification problem:

- ▶ Input: a matrix of *node features*, $\mathbf{F} \in \mathbb{R}^{N \times F}$, with *F* features in each of the *N* nodes, and an *adjacency matrix*, $\mathbf{A} \in \mathbb{R}^{N \times N}$.
- ► Output: a matrix of node class probabilities, Y ∈ ℝ^{N×C}, such that Y_{ij} = ℙ(Node i ∈ Class j).
- We also assume, for simplicity, that the edges are unweighted and undirected:

► That is,
$$A_{ij} = A_{ji} = \begin{cases} 1 & i \leftrightarrow j \\ 0 & otherwise \end{cases}$$

but many algorithms we will cover are capable of generalising to weighted and directed edges.

► There are two main kinds of learning tasks in this space...



Transductive learning



Training algorithm sees all features (including test nodes)!



Inductive learning

- Now, the algorithm does not have access to all nodes upfront!
- This often implies that either:
 - Test nodes are (incrementally) inserted into training graphs;
 - Test graphs are disjoint and completely unseen!
- A much harder learning problem (requires generalising across arbitrary graph structures), and many transductive methods will be inappropriate for inductive problems!



Explicit graph neural network methodologies

We will restrict our attention solely to methods that *directly* leverage the graph structure when extracting features.

• Main idea: Compute node representations \vec{h}_i based on the initial features \vec{f}_i and the graph structure, and then use \vec{h}_i to classify each node independently.



The silver bullet—a convolutional layer

It would be, in particular, highly appropriate if we could somehow generalise the *convolutional operator* (as used in CNNs) to operate on arbitrary graphs!

A "common framework" for many of the approaches to be listed now has been presented in "Neural Message Passing for Quantum Chemistry", by Gilmer et al. (ICML 2017).



















Challenges with graph convolutions

Desirable properties for a graph convolutional layer:

- Computational and storage efficiency ($\sim O(V + E)$);
- Fixed number of parameters (independent of input size);
- Localisation (acts on a local neighbourhood of a node);
- Specifying different importances to different neighbours;
- Applicability to inductive problems.
- Fortunately, images have a highly rigid and regular connectivity pattern (each pixel "connected" to its eight neighbouring pixels), making such an operator trivial to deploy (as a small kernel matrix which is slided across).
- Arbitrary graphs are a much harder challenge!



Spectral graph convolution

- A large class of popular approaches attempts to define a convolutional operation by operating on the graph in the spectral domain, leveraging the *convolution theorem*.
- These approaches utilise the graph Laplacian matrix, L, defined as L = D A, where D is the degree matrix (diagonal matrix with D_{ii} = deg(i)) and A is the adjacency matrix.
- ► Alternately, we may use the **normalised graph Laplacian**, $\tilde{L} = I D^{-1/2}AD^{-1/2}$.



Graph Laplacian example





Graph Fourier Transform

- The Laplacian is symmetric and positive semi-definite; we can therefore diagonalise it as L = UΛU^T, where Λ is a diagonal matrix of its eigenvalues.
- This means that multiplying the feature matrix by U^T allows us to enter the spectral domain for the graph! Therein, convolution just amounts to pointwise multiplication.
- This "Graph Fourier Transform" is the essence of the work of Bruna et al. (ICLR 2014).



Graph Fourier Transform, cont'd

To convolve two signals using the convolution theorem:

$$conv(\vec{x}, \vec{y}) = \mathbf{U} \left(\mathbf{U}^T \vec{x} \odot \mathbf{U}^T \vec{y} \right)$$

► Therefore, a *learnable convolutional layer* amounts to:

$$ec{h}_i' = \mathbf{U}\left(ec{w} \odot \mathbf{U}^T \mathbf{W} ec{h}_i
ight)$$

where \vec{w} is a learnable vector of weights, and $\mathbf{W} \in \mathbb{R}^{F' \times F}$ is a shared, learnable, feature transformation.

- Downsides:
 - Computing **U** is $O(V^3)$ —infeasible for large graphs!
 - One independent weight per node—not fixed!
 - Not localised!



Chebyshev networks

- These issues have been overcome by *ChebyNets*, the work of Defferrard *et al.* (NIPS 2016).
- ► Rather than computing the Fourier transform, use the related family of *Chebyshev polynomials* of order k, T_k:

$$ec{h}_i' = \sum_{k=0}^K w_k T_k(\mathbf{L}) \mathbf{W} ec{h}_i$$

These polynomials have a recursive definition, highly simplifying the computation:

$$T_0(x) = 1$$
 $T_1(x) = x$ $T_k(x) = 2xT_{k-1}(x) - T_{k-2}(x)$



Properties of Chebyshev networks

• Owing to its recursive definition, we can compute the output iteratively as $\sum_{k=0}^{K} w_k \vec{t}_k$, where:

$$\vec{t}_0 = \mathbf{W}\vec{h}_i$$
 $\vec{t}_1 = \mathbf{L}\mathbf{W}\vec{h}_i$ $\vec{t}_k = 2\mathbf{L}\vec{t}_{k-1} - \vec{t}_{k-2}$

where each step constitutes a sparse multiplication with L.

- The number of parameters is **fixed** (equal to K weights).
- ► Note that T_k(L) will be a (weighted) sum of all powers of L up to L^k. This means that T_k(L)_{ij} = 0 if dist(i, j) > k!
 ⇒ The operator is K-localised!



Properties of Chebyshev networks, cont'd

To avoid issues with exploding or vanishing signals, typically a scaled version of L is fed into the algorithm:

$$ilde{\mathsf{L}} = rac{2\mathsf{L}}{\lambda_{max}} - \mathsf{I}$$

where λ_{max} is the largest eigenvalue of L.

- ► This constrains all eigenvalues to lie in the range [-1, 1], therefore making the norm of all results controllable.
- ► Major limitation: unable to specify different weights to different nodes in a neighbourhood! All k-hop neighbours will receive weight w_k + w_{k+1} + ··· + w_K.



Going back to the image scenario, under the assumption that each pixel of an image is connected to its immediate four neighbours, this would constrain our 3×3 convolutional kernel to be of the form:

$$\begin{bmatrix} w_2 & w_1 + w_2 & w_2 \\ w_1 + w_2 & w_0 + w_1 + w_2 & w_1 + w_2 \\ w_2 & w_1 + w_2 & w_2 \end{bmatrix}$$

severely limiting the variety of patterns that can be usefully extracted from the image.





- The Graph Convolutional Network (GCN) of Kipf & Welling (ICLR 2017) further fine-tunes the Chebyshev framework.
- Setting K = 1 and assuming λ_{max} ≈ 2 allows for redefining a single convolutional layer as simply:

$$\vec{h}_i' = \tilde{\mathbf{D}}^{-1/2} \tilde{\mathbf{A}} \tilde{\mathbf{D}}^{-1/2} \mathbf{W} \vec{h}_i$$

which significantly improves computational performance on larger graphs and predictive power on small training sets.

► However, the previous issue is *still there...*



Applicability to inductive problems

- Another *fundamental* constraint of all spectral-based methods is that the learnt filter weights are assuming a particular, fixed, graph Laplacian.
- This makes them theoretically inadequate for arbitrary inductive problems!
- We have to move on to non-spectral approaches...



Molecular fingerprinting networks

- An early notable approach towards such methods is the work of Duvenaud *et al.* (NIPS 2015).
- ► Here, the method adapts to processing with various degrees by learning a *separate* weight matrix H_d for each node degree d.
- The authors dealt with an extremely specific domain problem (molecular fingerprinting), where node degrees could never exceed five; this does not scale to graphs with very wide degree distributions.





- Conversely, the recently-published GraphSAGE model by Hamilton *et al.* (NIPS 2017) aims to restrict every degree to be the same (by sampling a *fixed-size* set of neighbours of every node, during both training and inference).
- Inherently drops relevant data—limiting the set of neighbours visible to the algorithm.
- Impressive performance was achieved across a variety of inductive graph problems. However, the best results were often achieved with an LSTM-based aggregator, which is unlikely to be optimal.



Reminder: Self-attention

A recent development in attentional mechanisms concerns self-attention; a scenario where the input attends over itself:

$$lpha_{ij} = \mathbf{a}(\vec{h}_i, \vec{h}_j)$$

 $\vec{h}'_i = \sum_j \textit{softmax}_j(lpha_{ij})\vec{h}_j$

where $a(\vec{x}, \vec{y})$ is a neural network (the *attention mechanism*).

- Critically, this is parallelisable across all input positions!
- Vaswani et al. (NIPS 2017) have successfully demonstrated that this operation is self-sufficient for achieving state-of-the-art on machine translation.



Graph Attention Networks

- My ICLR 2018 publication, proposing Graph Attention Networks (GATs), leverages exactly the self-attention operator!
- In its naïve form, the operator would compute attention coefficients over all pairs of nodes.
- To inject the graph structure into the model, we restrict the model to only attend over a node's neighbourhood when computing its coefficient!



GAT equations

To recap, a single attention head of a GAT model performs the following computation:

$$\begin{aligned} \mathbf{e}_{ij} &= \mathbf{a}(\vec{h}_i, \vec{h}_j) \\ \alpha_{ij} &= \frac{\exp(\mathbf{e}_{ij})}{\sum_{k \in \mathcal{N}_i} \exp(\mathbf{e}_{ik})} \\ \vec{h}'_i &= \sigma \left(\sum_{j \in \mathcal{N}_i} \alpha_{ij} \mathbf{W} \vec{h}_j \right) \end{aligned}$$

Some further optimisations (like *multi-head attention* and *dropout* on the α_{ij} values) help further *stabilise* and *regularise* the model.



A single GAT step, visualised





GAT analysis

- Computationally efficient: attention computation can be parallelised across all edges of the graph, and aggregation across all nodes!
- ► Storage efficient—a sparse version does not require storing more than O(V + E) entries anywhere;
- Fixed number of parameters (dependent only on the desirable feature count, not on the node count);
- Trivially localised (as we aggregate only over neighbourhoods);
- Allows for (implicitly) specifying different importances to different neighbours.
- Readily applicable to inductive problems (as it is a shared edge-wise mechanism)!



GAT performance

It seems that we have finally satisfied all of the major requirements for our convolution!

How well does it perform?



Datasets under study

Summary of the datasets used in our experiments.

	Transductive			Inductive
	Cora	Citeseer	Pubmed	PPI
# Nodes	2708	3327	19717	56944 (24 graphs)
# Edges	5429	4732	44338	818716
# Features/Node	1433	3703	500	50
# Classes	7	6	3	121 (multilabel)
# Training Nodes	140	120	60	44906 (20 graphs)
# Validation Nodes	500	500	500	6514 (2 graphs)
# Test Nodes	1000	1000	1000	5524 (2 graphs)



Results on Cora/Citeseer/Pubmed

Transductive					
Method	Cora	Citeseer	Pubmed		
MLP	55.1%	46.5%	71.4%		
ManiReg	59.5%	60.1%	70.7%		
SemiEmb	59.0%	59.6%	71.7%		
LP	68.0%	45.3%	63.0%		
DeepWalk	67.2%	43.2%	65.3%		
ICA	75.1%	69.1%	73.9%		
Planetoid	75.7%	64.7%	77.2%		
Chebyshev	81.2%	69.8%	74.4%		
GCN	81.5%	70.3%	79.0%		
MoNet	$81.7 \pm \mathbf{0.5\%}$	—	$\textbf{78.8} \pm \textbf{0.3\%}$		
GCN-64*	$81.4 \pm \mathbf{0.5\%}$	$\textbf{70.9} \pm \textbf{0.5\%}$	$\textbf{79.0}\pm0.3\%$		
GAT (ours)	$\textbf{83.0}\pm0.7\%$	$\textbf{72.5}\pm0.7\%$	$\textbf{79.0} \pm 0.3\%$		



Results on PPI

Inductive					
Method	PPI				
Random	0.396				
MLP	0.422				
GraphSAGE-GCN	0.500				
GraphSAGE-mean	0.598				
GraphSAGE-LSTM	0.612				
GraphSAGE-pool	0.600				
GraphSAGE*	0.768				
Const-GAT (ours)	0.934 ± 0.006				
GAT (ours)	$\textbf{0.973} \pm 0.002$				

Here, *Const-GAT* is a GCN-like inductive model.



t-SNE + attention coefficients on Cora





Incorporating edge context

- The attentional setup of GAT treats each edge equally.
- This will not be appropriate for inputs such as chemical compounds, wherein the same atom can possess identical neighbourhoods but with different bonds!





EAGCN (Shang et al., 2018)

- The edge context was incorporated for the first time in the edge attention-based multi-relational GCN (EAGCN) model.
- ► Assume that there are K different edge attributes (e.g. atom pair type, bond order...) and that the *i*-th attribute has d_i possible values.
- A separate attention coefficient α_{ij} is learned for every value of every attribute (i ∈ {1,...,K}, j ∈ {1,...d_i}), as a simple scalar embedding.



EAGCN attention mechanism

These embeddings then form the (unnormalised) attention coefficient matrices Aⁱ for each edge attribute *i*:

$$oldsymbol{\mathsf{A}}_{st}^i = egin{cases} lpha_{ij} & oldsymbol{s} o t ext{ of type } j ext{ in attr. } i \ -\infty & oldsymbol{s}
eq t \end{cases}$$

which are then softmax-normalised:

$$\widetilde{\mathbf{A}}_{st}^{i} = \frac{\exp\left(\mathbf{A}_{st}^{i}\right)}{\sum_{k}\exp\left(\mathbf{A}_{kt}^{i}\right)}$$

We can then use each of these as a separate attention head, and e.g. concatenate their outputs (for node features H):

$$\mathbf{H}' = \prod_{i=1}^{K} \sigma\left(\widetilde{\mathbf{A}}^{i} \mathbf{H} \mathbf{W}\right)$$



EAGCN in action: computing \mathbf{A}^{i}





EAGCN in action: single layer



Evaluated on molecular property classification and regression, outperforming several standard graph-based baselines.



GaAN (Zhang et al., 2018)

- The multi-head attention of GAT treats each attention head equally. However, not all heads necessarily convey equally important or meaningful feature spaces.
- The Gated Attention Network (GaAN) architecture introduces a gating mechanism on top of a key-value attention (as in Vaswani et al.), to control the impact of each output of each attention head.
- Evaluated on inductive node classification (Reddit/PPI) and traffic speed forecasting (METR-LA), outperforming many challenging baselines.



GaAN dataflow

- Assume we have node *features* \vec{h}_i and node *reference vectors* \vec{z}_j (useful to decouple when working on **temporal graphs**).
- ► First, derive queries, keys and values for the attention:

$$\vec{q}_i = \mathbf{W}_q \vec{h}_i$$
 $\vec{k}_i = \mathbf{W}_k \vec{z}_i$ $\vec{v}_i = \mathbf{W}_v \vec{z}_i$

Now, use the queries and keys to derive coefficients:

$$\alpha_{ij} = \frac{\exp\left(\langle \vec{q}_i, \vec{k}_j \rangle\right)}{\sum_{m \in \mathcal{N}_i} \exp\left(\langle \vec{q}_i, \vec{k}_m \rangle\right)}$$



GaAN dataflow, cont'd

At the same time, compute the gating for each node (using max-pool and average-pool information):

$$\vec{g}_{i} = \sigma \left(\mathbf{W}_{g} \left[\vec{h}_{i} \parallel \max_{j \in \mathcal{N}_{i}} \mathbf{W}_{m} \vec{z}_{j} \parallel \frac{\sum_{j \in \mathcal{N}_{i}} \vec{z}_{j}}{|\mathcal{N}_{i}|} \right] \right)$$

Finally, attend over the values and apply the gating (distributed over K independent heads)—including a skip connection:

$$\vec{h}_{i}' = \sigma \left(\mathbf{W}_{o} \left[\vec{h}_{i} \parallel \bigsqcup_{k=1}^{K} \vec{g}_{i}^{(k)} \odot \sum_{j \in \mathcal{N}_{i}} \alpha_{ij}^{(k)} \vec{v}_{j}^{(k)} \right] \right)$$



GaAN in action





DeepInf (Qiu et al., 2018)

- ► Modelling influence locality within large social networks.
- Let s^t_u ∈ {0,1} denote whether node u has performed an action at any time t' < t.</p>
- ► Aim to predict whether node v ever performs the action (s_v^{+∞}), given the action statuses of all of its r-hop neighbours at time t.
- First study where attentional mechanisms (such as GAT) appear to be *necessary* for surpassing baseline approaches (such as logistic regression or SVMs).



DeepInf pipeline



Datasets:

- ► OAG (network: coauthorship; action: citation)
- Digg (network: friendship; action: vote up)
- ► Twitter (network: follow; action: retweet "Higgs")
- Weibo (network: follow; action: retweet)



DeepInf: qualitative analysis of attention





Attention Solves Your TSP (Kool & Welling, 2018)

- Successfully demonstrated the viability of attentional mechanisms on graphs to solving combinatorial problems (*Euclidean TSP*—each node is specified by (x, y) coordinates).
- A decoder computes the probability distribution for the next node to visit, π_t, based on:
 - a fixed-size encoding of the graph, \vec{h}_G (obtained by an *encoder*);
 - the embeddings of the first and last visited node: \vec{h}_{π_1} , $\vec{h}_{\pi_{t-1}}$.
 - the embeddings \vec{h}_i of all nodes *i* still in the graph.
- Then this probability distribution is optimised using REINFORCE (with a greedy rollout baseline).



Attention Solves Your TSP: Encoder



- Uses the key-value attention mechanism, as in GaAN.
- Every node attends over all others.
- We obtain node embeddings \vec{h}_i , as well as the graph embedding \vec{h}_G (as their average).



Attention Solves Your TSP: Decoder

- First, create a **context node** containing $[\vec{h}_G, \vec{h}_{\pi_{t-1}}, \vec{h}_{\pi_1}]$.
- Then this node (multi-head) attends over all remaining nodes.
- Finally, the context node single-head attends over all remaining nodes, with the coefficients interpreted as probabilities.





Relational reasoning



Relation Networks (Santoro et al., 2017)



Modelling multi-agent interactions





The VAIN framework (Hoshen, 2017)



Neighbourhood attention



One-shot imitation slearning (Duan et al., 2017)



Mesh-based cortical parcellation



with Guillem Cucurull, Konrad Wagstyl et al. (NIPS BigNeuro 2017)



Motivation for antibody design

Antibodies are

- Y-shaped proteins
- a critical part of our immune system
- They neutralise pathogenic bacteria and viruses by tagging the antigen in a "lock and key" system.
- Designing our own arbitrary antibodies would be a big step towards personalised medicine.





Towards personalised medicine

- Generating an antibody requires first predicting the specific amino acids (the **paratope**) which participate in the neutralisation of the antigen.
- Input: a sequence of (one-hot encoded) antibody amino acids. (+ a sequence of (one-hot encoded) antigen amino acids)
- Output: probability for each amino acid to participate in the binding with the antigen.



Paratope prediction





Related work

- i-Patch (Krawczyk *et al.* (2013)) is a hard-coded physical model which requires expensive data (e.g. positional information of each atom of both antibody and antigen).
- ProABC (Olimpieri *et al.* (2013)) uses a shallow classifier on antibody sequence data only.
- I have contributed to the two first viable deep learning architectures in this space, setting the new state-of-the-art without requiring positional information:
 - ► **Parapred** (Bioinformatics) (*with Edgar Liberis*), using a convolutional-recurrent neural network architecture.
 - AG-Fast-Parapred (with Andreea Deac), replacing these layers with dilated convolutions and (self-)attention, allowing for faster execution and integrating antigen sequence data.



The Parapred and Fast-Parapred architecture



Fast-Parapred (with Andreea Deac)



Cross-modal attentive Parapred



Fast-Parapred (with Andreea Deac)



Cross-modal attentive Parapred



AG-Fast-Parapred (with Andreea Deac)



Attention!

► Input:

- antibody computed residue features $\mathbf{b} = \{\vec{b}_1, \vec{b}_2, ... \vec{b}_k\}, \vec{b}_i \in \mathbb{R}^N$
- antigen computed residue features $\mathbf{g} = \{\vec{g}_1, \vec{g}_2, ... \vec{g}_l\}, \vec{g}_j \in \mathbb{R}^M$
- for each \vec{b}_i a set of neighbouring residues ν_i
- ► The attention coefficients are then computed using the shared attentional mechanism a: ℝ^N × ℝ^M → ℝ and a new feature vector is obtained:

$$ec{m{b}'} = \sigma \left(\sum_{j \in
u_i} m{a}(ec{m{b}}_i, ec{m{g}}_j) ec{m{g}}_j
ight)$$



Quantitative results



95% confidence intervals, after 10 runs of 10-fold crossvalidation.



Qualitative results





Qualitative results



- The model learns the antibody/antigen geometry without being given any positional information.
- This could enable us to build an epitope predictor!





Questions?

petar.velickovic@cst.cam.ac.uk http://www.cst.cam.ac.uk/~pv273/ https://cAT

https://github.com/PetarV-/GAT

