Scalable tensor methods for multirelational learning across graphs

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Outline

- Task description: multi-relational learning among heterogeneous graphs
 - Examples
 - Formal definition
- Review: label propagation and tensor product graph
 - Label propagation algorithm
 - Tensor product graph
- Scalable tensor methods for multi-relational learning
 - Low-rank label propagation algorithm on tensor product graph
 - Sparse label propagation algorithm on tensor product graph
 - Tensor decomposition with graph constraint
- Experiments: Aligning multiple PPI networks, CT scans and DBLP data

Task description: examples



- Blue edges: within graph interactions
- Red edges: cross graph interactions

"Chemical compound (drug) A is targeting on protein B." (Compound: A, Protein: B) "John publish a reinforcement learning paper at ICML." (Author: John, Paper: RL, Venue: ICML)

Task description: examples

- Aligning protein-protein interaction networks across species.
- Nodes are proteins
- Edges connect interacting proteins.
- The relations are evolutionary relations.



Task description: examples

• Align the same organ (color) across the CT scans of human body



Slice -1264



Slice -1273





Slice -1267



Slice -1276







Task description: definition

- Given:
 - Individual graph $W^{(i)} \in \mathbb{R}^{I_i \times I_i}, i = 1, \dots n$.
 - A tensor $\mathcal{Y} \in \mathbb{R}^{I_1 \times I_2 \times \ldots \times I_n}$ storing (parts of) the initial scores of the multirelations (tuples) between the nodes from different graphs.
- Task:
 - Predict the scores of the unscored tuples.
 - Correct the scores of the scored tuples based on the graph structures.

Task description: definition





Background: label propagation



$$y^{t+1} = \alpha S y^t + (1 - \alpha) y^0$$

$$S = D^{-\frac{1}{2}} W D^{-\frac{1}{2}}$$



Zhou, Denny, et al. (NIPS, 2004)

Background: label propagation

• Objective function

$$\begin{aligned} \mathcal{J}(y) &= \sum_{i,j} w_{ij} (\frac{y_i}{\sqrt{d_{ii}}} - \frac{y_j}{\sqrt{d_{jj}}})^2 + \mu ||y - y^0||^2 \\ &= y^T L y + \mu ||y - y^0||^2, \\ \end{aligned}$$
where $\mu = \frac{1 - \alpha}{\alpha}, \ L = I - S.$

• Closed-form solution

$$y^* = (1 - \alpha)(I - \alpha S)^{-1}y^0$$

PageRank (random walk with restart)

- Define a Markov Chain to represent the web surfing jumping probability
- Start with a random page and take random walks.
- The stationary distribution of the Markov Chain gives the probability of stopping at a particular page (a good rank!)
- Label propagation is a very similar algorithm.



ID=2

Background: tensor product graph (TPG)



 $W = W^{(1)} \otimes W^{(2)} \otimes W^{(3)} \in \mathbb{R}^{I_1 I_2 I_3 \times I_1 I_2 I_3}$

$$W_{(1,I,A),(2,II,B)} = W_{1,2}^{(1)} W_{I,II}^{(2)} W_{A,B}^{(3)}$$

Revisit the learning task

- Given:
 - Individual graph $W^{(i)} \in \mathbb{R}^{I_i \times I_i}, i = 1, \dots n$.
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 - Correct the scores of the scored tuples based on the graph structures.

Revisit the learning task $\overrightarrow{\mathcal{V}} \in \mathbb{R}^{I_1 I_2 I_3 \times 1}$) 3.II.C 3.I.B 3.II.B 3.11.A 4.II.C 3.I.C (2)(3)• Task: • Predict the scores of the unscored tuples =

- Predict the labels of the unlabeled nodes of W.
- Correct the scores of the scored tuples based on the graph structures =
- Correct the labels of the labeled nodes of W based on the graph structures

Revisit the learning task



$$\vec{Y}^{t+1} = \alpha (S^{(1)} \otimes S^{(2)}) \vec{Y}^{t} + (1-\alpha) \vec{Y}^{0}$$
$$Y^{t+1} = \alpha S^{(2)} Y^{t} S^{(1)} + (1-\alpha) Y^{0}$$



$$\begin{vmatrix} \vec{\mathcal{Y}}^{t+1} = \alpha(\bigotimes_{i=1}^{n} S^{(i)}) \vec{\mathcal{Y}}^{t} + (1-\alpha) \vec{\mathcal{Y}}^{0} \\ \mathcal{Y}^{t+1} = \alpha \mathcal{Y}^{t} \times_{1} S^{(n)} \times_{2} S^{(n-1)} \cdots \times_{n} S^{(1)} + (1-\alpha) \mathcal{Y}^{0} \end{vmatrix}$$

A simple simulation









Scalability issue

• Iterative approach:

$$\vec{\mathcal{Y}}^{t+1} = \alpha(\bigotimes_{i=1}^{n} S^{(i)})\vec{\mathcal{Y}}^{t} + (1-\alpha)\vec{\mathcal{Y}}^{0}$$
$$\mathcal{Y}^{t+1} = \alpha\mathcal{Y}^{t} \times_{1} S^{(n)} \times_{2} S^{(n-1)} \cdots \times_{n} S^{(1)} + (1-\alpha)\mathcal{Y}^{0}$$

- Time complexity of one iteration $O((\prod_{i=1}^{n} I_i)(\sum_{i=1}^{n} I_i))$
- Space complexity $O(\prod_{i=1}^n I_i)$
- Closed form solution:

$$\overrightarrow{\mathcal{Y}}^* = (1-\alpha)(I-\alpha S)^{-1}\overrightarrow{\mathcal{Y}}^0$$
$$= (1-\alpha)(\otimes_{i=1}^n Q^{(i)})(I-\alpha(\otimes_{i=1}^n \Lambda^{(i)}))^{-1}(\otimes_{i=1}^n Q^{(i)T})\overrightarrow{\mathcal{Y}}^0$$

Proposition 1: Low rank approximation of TPG

• Idea:

minimize $||(I - \alpha S)^{-1} - (I - \alpha S_k)^{-1}||_{2,F}$ subject to rank $(S_k) = k$

Lemma. Let $\lambda_1, \ldots, \lambda_n$ be eigenvalues of A with corresponding eigenvectors x_1, \ldots, x_n , and let μ_1, \ldots, μ_m be eigenvalues of B with corresponding eigenvectors y_1, \ldots, y_m . Then the eigenvalues and eigenvectors of $A \otimes B$ are $\lambda_i \mu_j$ and $x_i \otimes y_j$, $i = 1, \ldots, n$, $j = 1, \ldots, m$.

Solved by eigenvalue selection method

Proposition 1: Low rank approximation of TPG



Experiment 1 – CT Scan Image Alignment

- 134 CT Scan images of size 512 x 512.
- Each image was segmented into regions (features).
- Sampled spots are aligned across the images.



Proposition 2: keep the tensor sparse

- Tensor becomes dense after every propagation step
- Adding L1-norm regularizer to keep the sparsity $\mathcal{J}_{L1}(\overrightarrow{\mathcal{Y}}) = \mathcal{J}(\overrightarrow{\mathcal{Y}}) + \beta \sum_{i=1}^{N} |\overrightarrow{\mathcal{Y}}_i|.$
- Apply FISTA (fast iterative shrinkage-thresholding algorithm)

$$\mathcal{Y}^{t+1} = \frac{1}{L_J} (\mathcal{Y}^t \times_1 S^{(n)} \times_2 S^{(n-1)} \cdots \times_n S^{(1)}) + (1 - \frac{1+\mu}{L_J}) \mathcal{Y}^t + \frac{\mu}{L_J} \mathcal{Y}^0.$$

where the step size $L_J = 1 + \mu - \min(\bigotimes_{i=1}^n [\lambda_{\min}(S^{(i)}), \lambda_{\max}(S^{(i)}]))$

• Use METTM (Memory-Efficient Tensor Times Matrix) for matrixtensor multiplication

Experiment 2 – PPI Network Alignment

- PPI subnetworks of four species Human (HSA), Mouse (MMU), Fly (DME) and Yeast (SCE).
- Four pathways (subnetworks) are tested.

Pathway	DME	HSA	MMU	SCE
00020	43/332	30/257	32/312	32/265
00190	144/208	133/292	134/315	72/284
00564	63/151	95/318	94/187	18/192
04320	28/226	28/300	26/228	-

• Validation:

Checking the agreement of the alignment scores and the protein functional similarities returned by Gene Ontology (Consortium et al., 2015)

Experiment 2 – PPI Network Alignment

3

3

Rank

Seq-Sim ← LowrankTLP

---- Approx-LinkProp

4

Rank

4

5

5

×10⁴

×10⁴



Experiment 2 – PPI Network Alignment



Future work: tensor decomposition

Revisit objective function

$$\begin{aligned} \mathcal{J}(y) &= \sum_{i,j} w_{ij} \left(\frac{y_i}{\sqrt{d_{ii}}} - \frac{y_j}{\sqrt{d_{jj}}}\right)^2 + \mu ||y - y^0||^2 \\ &= y^T L y + \mu ||y - y^0||^2, \end{aligned}$$

where $\mu = \frac{1-\alpha}{\alpha}, \ L = I - S.$

Future work: tensor decomposition

• CPD form assumption

$$\mathcal{J}(A, B, C) = vec(\llbracket A, B, C \rrbracket)^T Lvec(\llbracket A, B, C \rrbracket) + \mu ||\llbracket A, B, C \rrbracket - \mathcal{Y}^0||^2$$
$$= \mathbf{1}^T (C \odot B \odot A)^T L (C \odot B \odot A) \mathbf{1} + \mu ||\mathcal{Y}^0 - \llbracket A, B, C \rrbracket ||^2$$

$$\frac{\partial \mathcal{J}}{\partial A} = 2(AM_1 - \mu S^{(1)}AM_2 - (1 - \mu)M_3)$$

$$M_1 = C^T C * B^T B, M_2 = C^T S^{(3)}C * B^T S^{(2)}B \text{ and } M_3 = Y_{(1)}^0 (C \odot B).$$

Experiment 3 – DBLP dataset

- 13823 Authors, 11372 papers and 10167 venues.
- 12066 tuples.
- Experiment setting: randomly sampling 0.1%, 1%, 5%, 10%, 50% and 90% of tuples to be the training data. The rest are testing data.

Liu, H., & Yang, Y. (ICML, 2016)



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THANKS !