Author Set Identification via Quasi-Clique Discovery

A presentation for DAA 2022/2023

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- Introduction
 - Motivation
 - Important Concepts
- 2 Proposed Approach
 - Weighted Paper-Ego-Network Construction
 - Optimal Quasi-Clique with Constraint Extraction
- 3 Results
 - Experimental Setup
 - Comparison and Analysis
- 4 Conclusion

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Author Identification

The problem of author identification has been extensively studied, which aims to learn a model to rank potential authors for an anonymous paper based on public information.



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Possible Uses

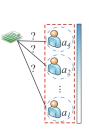
- Author identification
- Relevance search
- Personalized recommendations
- Reviewer recommendation
- Collaboration discovery

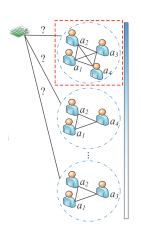


Problem formulation

Current approaches:

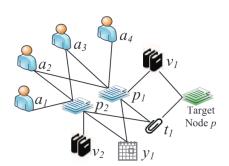
- Focus on single author identification
- Do not account for the optimal number of writers
- Do not take into account the relation between possible authors





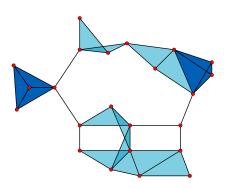
Heterogeneous Information Network (HIN)

- Directed graph
- Nodes and edges have types



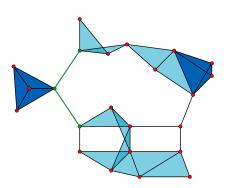
Clique (Graph Theory)

- Undirected graph
- Subset of vertices such that every two distinct vertices are adjacent



Quasi-Clique (Graph Theory)

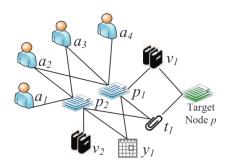
A set of nodes S is an α -quasi-clique if the edge density of the subgraph induced by S exceeds a threshold parameter $\alpha \in (0,1)$



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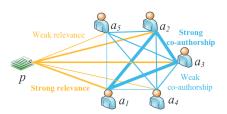
Heterogeneous Information Network (HIN)

- HINs are complex structures
- Complex structures lead to complex algorithms
- How to simply this HIN without removing relevant information?



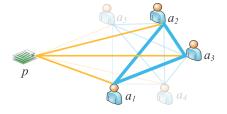
Weighted Paper-Ego-Network

- Extraction of a task-guided embedding to learn the low-dimensional representation of a network
- Creation of a simpler weighted graph



Optimal Author Subset

- To find an optimal author subset that is related to the anonymous paper is an NP-hard problem
- Discovering the largest clique is inapproachable and the clique concept is in practice too strict to miss a single edge in an otherwise dense subgraph
- Quasi-clique has been significantly used to discover dense subgraphs
- Maximum quasi-clique discovery is also an NP-hard problem



Algorithm description

- Optimization problem
- Local search algorithm
- Density calculation

```
Algorithm 1: OQCCE
 Input : Weighted paper ego network G_p = (V, E, W);
              maximum number of iterations I_{max}; the
              constrained node p
 Output: A subset of nodes S \subseteq V and p \in S
 S \leftarrow p, b_1 \leftarrow \text{TRUE}, i \leftarrow 1;
 while b_1 and i \leq I_{max} do
       b_2 \leftarrow TRUE:
       while bo do
            if there exists u \in V \setminus S and g_{\alpha,\beta}(S \cup \{u\}) \ge g_{\alpha,\beta}(S)
             then
                 S \leftarrow S \cup \{u\}:
            else
              b_2 \leftarrow FALSE;
       if there exists u \in S and u \neq p and g_{\alpha,\beta}(S \setminus \{u\}) \ge g_{\alpha,\beta}(S)
         then
            S \leftarrow S \setminus \{u\}:
       else
            b_1 \leftarrow FALSE:
       i \leftarrow i + 1:
```

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Datasets Used

Large scale datasets

Dataset	# papers	# authors	# terms	# venues
AMiner-I	8821	12660	12467	5
AMiner-II	35349	36247	31446	14

Evaluation Metrics

$$P = \frac{|S_a' \cap S_a|}{|S_a'|}$$

 Not sensitive to false negatives

$$\bullet R = \frac{|S_a' \cap S_a|}{|S_a|}$$

Not sensitive to false positives

•
$$F1 = \frac{2*P*R}{P+R}$$

- \circ S_a real author set
- S_a' returned author set

Dataset	# papers	# authors	# terms	# venues
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Results

Methods		Evaluation					Avg.		
		P (†)	R (†)	J (†)	F1 (†)	$MAP (\uparrow)$	RMSE (↓)	- Avg.	
Top-5 Feature method	Similarity	PTPA	0.2716 (2)	0.5007 (7)	0.2310(2)	0.3356 (2)	0.6109 (1)	0.1714 (2)	2.67
	measure	PCPA	0.2098 (7)	0.3937 (11)	0.1680 (7)	0.2614 (7)	0.4718 (9)	0.1714 (2)	7.16
		LR	0.2160 (5)	0.3915 (12)	0.1827 (6)	0.2657 (4)	0.4834 (7)	0.1714 (2)	6.00
	method	SVM	0.2493 (3)	0.4562 (9)	0.2154 (4)	0.3081(3)	0.5451(3)	0.1714 (2)	4.00
		Bayesian	0.2209 (4)	0.4075 (10)	0.1888 (5)	0.2733 (5)	0.4951 (6)	0.1714 (2)	5.33
	NetE	0.2123 (6)	0.3870 (13)	0.1669 (8)	0.2616 (6)	0.4571 (11)	0.1714 (2)	7.66	
	Similarity	PTPA	0.1555 (9)	0.5779 (2)	0.1454 (10)	0.2365 (9)	0.5897 (2)	0.5023 (3)	5.83
	measure	PCPA	0.1388 (11)	0.5066 (5)	0.1257 (13)	0.2110 (11)	0.4517 (12)	0.5023 (3)	9.10
		LR	0.1358 (13)	0.5005 (8)	0.1270 (12)	0.2059 (13)	0.4664 (10)	0.5023(3)	9.83
Top-10	Feature	SVM	0.1629 (8)	0.5988 (1)	0.1538 (9)	0.2477 (8)	0.5296 (4)	0.5023(3)	5.50
	method	Bayesian	0.1364 (12)	0.5010 (6)	0.1277 (11)	0.2069 (12)	0.4767 (8)	0.5023 (3)	8.67
	Heth	NetE	0.1506 (10)	0.5347 (3)	0.2269(3)	0.2275 (10)	0.4435 (13)	0.5023(3)	7.00
	ASI			0.5284 (4)	0.4009 (1)	0.4712 (1)	0.5295 (5)	0.1123 (1)	2.00
					Fl.	a til a sa			
	Methods		D (4)	D (4)	Evalu		MAD (4)	DMCE (I)	Avg.
	Methods		P (†)	R (†)	J (†)	F1 (↑)	MAP (†)	RMSE (↓)	
	Methods Similarity	PTPA	0.3391 (2)	0.5899 (6)	J (†) 0.2886 (2)	F1 (†) 0.4108 (2)	0.7165 (3)	0.2880 (2)	2.83
		PCPA	0.3391 (2) 0.3287 (3)	0.5899 (6) 0.5743 (8)	J (†) 0.2886 (2) 0.2776 (4)	F1 (↑) 0.4108 (2) 0.3986 (3)	0.7165 (3) 0.6595 (6)	0.2880 (2) 0.2880 (2)	2.83
Ton 5	Similarity measure	PCPA LR	0.3391 (2) 0.3287 (3) 0.3113 (4)	0.5899 (6) 0.5743 (8) 0.5400 (9)	J (†) 0.2886 (2) 0.2776 (4) 0.2645 (5)	F1 (↑) 0.4108 (2) 0.3986 (3) 0.3769 (4)	0.7165 (3) 0.6595 (6) 0.6605 (5)	0.2880 (2) 0.2880 (2) 0.2880 (2)	2.83 4.33 4.83
Top-5	Similarity measure Feature	PCPA LR SVM	0.3391 (2) 0.3287 (3) 0.3113 (4) 0.2202 (7)	0.5899 (6) 0.5743 (8) 0.5400 (9) 0.4553 (12)	J (†) 0.2886 (2) 0.2776 (4) 0.2645 (5) 0.1674 (11)	F1 (↑) 0.4108 (2) 0.3986 (3) 0.3769 (4) 0.2803 (9)	0.7165 (3) 0.6595 (6) 0.6605 (5) 0.9948 (1)	0.2880 (2) 0.2880 (2) 0.2880 (2) 0.2880 (2)	2.83 4.33 4.83 7.00
Top-5	Similarity measure Feature method	PCPA LR SVM Bayesian	0.3391 (2) 0.3287 (3) 0.3113 (4) 0.2202 (7) 0.2964 (5)	0.5899 (6) 0.5743 (8) 0.5400 (9) 0.4553 (12) 0.5144 (10)	J (↑) 0.2886 (2) 0.2776 (4) 0.2645 (5) 0.1674 (11) 0.2491 (6)	F1 (↑) 0.4108 (2) 0.3986 (3) 0.3769 (4) 0.2803 (9) 0.3587 (5)	0.7165 (3) 0.6595 (6) 0.6605 (5) 0.9948 (1) 0.6458 (8)	0.2880 (2) 0.2880 (2) 0.2880 (2) 0.2880 (2) 0.2880 (2)	2.83 4.33 4.83 7.00 6.00
Top-5	Similarity measure Feature	PCPA LR SVM Bayesian JetE	0.3391 (2) 0.3287 (3) 0.3113 (4) 0.2202 (7)	0.5899 (6) 0.5743 (8) 0.5400 (9) 0.4553 (12)	J (†) 0.2886 (2) 0.2776 (4) 0.2645 (5) 0.1674 (11)	F1 (↑) 0.4108 (2) 0.3986 (3) 0.3769 (4) 0.2803 (9)	0.7165 (3) 0.6595 (6) 0.6605 (5) 0.9948 (1)	0.2880 (2) 0.2880 (2) 0.2880 (2) 0.2880 (2)	2.83 4.33 4.83 7.00 6.00 7.33
Top-5	Similarity measure Feature method	PCPA LR SVM Bayesian JetE PTPA	0.3391 (2) 0.3287 (3) 0.3113 (4) 0.2202 (7) 0.2964 (5)	0.5899 (6) 0.5743 (8) 0.5400 (9) 0.4553 (12) 0.5144 (10)	J (↑) 0.2886 (2) 0.2776 (4) 0.2645 (5) 0.1674 (11) 0.2491 (6)	F1 (↑) 0.4108 (2) 0.3986 (3) 0.3769 (4) 0.2803 (9) 0.3587 (5)	0.7165 (3) 0.6595 (6) 0.6605 (5) 0.9948 (1) 0.6458 (8)	0.2880 (2) 0.2880 (2) 0.2880 (2) 0.2880 (2) 0.2880 (2)	2.83 4.33 4.83 7.00 6.00
Top-5	Similarity measure Feature method HetN Similarity	PCPA LR SVM Bayesian JetE	0.3391 (2) 0.3287 (3) 0.3113 (4) 0.2202 (7) 0.2964 (5) 0.2645 (6)	0.5899 (6) 0.5743 (8) 0.5400 (9) 0.4553 (12) 0.5144 (10) 0.4561 (11)	J (↑) 0.2886 (2) 0.2776 (4) 0.2645 (5) 0.1674 (11) 0.2491 (6) 0.2078 (7)	F1 (↑) 0.4108 (2) 0.3986 (3) 0.3769 (4) 0.2803 (9) 0.3587 (5) 0.3191 (6)	0.7165 (3) 0.6595 (6) 0.6605 (5) 0.9948 (1) 0.6458 (8) 0.6021 (12)	0.2880 (2) 0.2880 (2) 0.2880 (2) 0.2880 (2) 0.2880 (2) 0.2880 (2)	2.83 4.33 4.83 7.00 6.00 7.33
	Similarity measure Feature method Heth Similarity measure	PCPA LR SVM Bayesian NetE PTPA PCPA LR	0.3391 (2) 0.3287 (3) 0.3113 (4) 0.2202 (7) 0.2964 (5) 0.2645 (6) 0.1927 (8)	0.5899 (6) 0.5743 (8) 0.5400 (9) 0.4553 (12) 0.5144 (10) 0.4561 (11) 0.6624 (1)	J (†) 0.2886 (2) 0.2776 (4) 0.2645 (5) 0.1674 (11) 0.2491 (6) 0.2078 (7) 0.1795 (8)	F1 (↑) 0.4108 (2) 0.3986 (3) 0.3769 (4) 0.2803 (9) 0.3587 (5) 0.3191 (6) 0.2884 (7)	0.7165 (3) 0.6595 (6) 0.6605 (5) 0.9948 (1) 0.6458 (8) 0.6021 (12) 0.6913 (4)	0.2880 (2) 0.2880 (2) 0.2880 (2) 0.2880 (2) 0.2880 (2) 0.2880 (2) 0.2880 (3)	2.83 4.33 4.83 7.00 6.00 7.33 5.16
Top-5	Similarity measure Feature method HetN Similarity measure Feature	PCPA LR SVM Bayesian JetE PTPA PCPA	0.3391 (2) 0.3287 (3) 0.3113 (4) 0.2202 (7) 0.2964 (5) 0.2645 (6) 0.1927 (8) 0.1913 (9)	0.5899 (6) 0.5743 (8) 0.5400 (9) 0.4553 (12) 0.5144 (10) 0.4561 (11) 0.6624 (1) 0.6531 (2)	J (†) 0.2886 (2) 0.2776 (4) 0.2645 (5) 0.1674 (11) 0.2491 (6) 0.2078 (7) 0.1795 (8) 0.1778 (9)	F1 (↑) 0.4108 (2) 0.3986 (3) 0.3769 (4) 0.2803 (9) 0.3587 (5) 0.3191 (6) 0.2884 (7) 0.2860 (8)	0.7165 (3) 0.6595 (6) 0.6605 (5) 0.9948 (1) 0.6458 (8) 0.6021 (12) 0.6913 (4) 0.6363 (10)	0.2880 (2) 0.2880 (2) 0.2880 (2) 0.2880 (2) 0.2880 (2) 0.2880 (2) 0.8536 (3) 0.8536 (3)	2.83 4.33 4.83 7.00 6.00 7.33 5.16 6.83
	Similarity measure Feature method Heth Similarity measure	PCPA LR SVM Bayesian NetE PTPA PCPA LR	0.3391 (2) 0.3287 (3) 0.3113 (4) 0.2202 (7) 0.2964 (5) 0.2645 (6) 0.1927 (8) 0.1913 (9) 0.1857 (10)	0.5899 (6) 0.5743 (8) 0.5400 (9) 0.4553 (12) 0.5144 (10) 0.4561 (11) 0.6624 (1) 0.6531 (2) 0.5779 (7)	J (↑) 0.2886 (2) 0.2776 (4) 0.2645 (5) 0.1674 (11) 0.2491 (6) 0.2078 (7) 0.1795 (8) 0.1778 (9) 0.1729 (10)	F1 (↑) 0.4108 (2) 0.3986 (3) 0.3769 (4) 0.2803 (9) 0.3587 (5) 0.3191 (6) 0.2884 (7) 0.2860 (8) 0.2775 (10)	0.7165 (3) 0.6595 (6) 0.6605 (5) 0.9948 (1) 0.6458 (8) 0.6021 (12) 0.6913 (4) 0.6363 (10) 0.6382 (9)	0.2880 (2) 0.2880 (2) 0.2880 (2) 0.2880 (2) 0.2880 (2) 0.2880 (2) 0.2880 (3) 0.8536 (3) 0.8536 (3)	2.83 4.33 4.83 7.00 6.00 7.33 5.16 6.83 8.16
	Similarity measure Feature method HetN Similarity measure Feature	PCPA LR SVM Bayesian JetE PTPA PCPA LR SVM Bayesian	0.3391 (2) 0.3287 (3) 0.3113 (4) 0.2202 (7) 0.2964 (5) 0.2645 (6) 0.1927 (8) 0.1913 (9) 0.1857 (10) 0.1101 (13)	0.5899 (6) 0.5743 (8) 0.5400 (9) 0.4553 (12) 0.5144 (10) 0.4561 (11) 0.6624 (1) 0.6531 (2) 0.5779 (7) 0.4553 (12)	J (†) 0.2886 (2) 0.2776 (4) 0.2645 (5) 0.1674 (11) 0.2491 (6) 0.2078 (7) 0.1795 (8) 0.1778 (9) 0.1729 (10) 0.0943 (13)	F1 (†) 0.4108 (2) 0.3986 (3) 0.3769 (4) 0.2803 (9) 0.3587 (5) 0.3191 (6) 0.2884 (7) 0.2860 (8) 0.2775 (10) 0.1702 (13)	0.7165 (3) 0.6595 (6) 0.6605 (5) 0.9948 (1) 0.6458 (8) 0.6021 (12) 0.6913 (4) 0.6363 (10) 0.6382 (9) 0.9948 (1)	0.2880 (2) 0.2880 (2) 0.2880 (2) 0.2880 (2) 0.2880 (2) 0.2880 (2) 0.8536 (3) 0.8536 (3) 0.8536 (3)	2.83 4.33 4.83 7.00 6.00 7.33 5.16 6.83 8.16 5.00

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Conclusion

- Author identification is a very useful (and interesting) subject matter
- Simplification of HIN to solve a maximum quasi-clique problem is very ingenious
- Author set identification is a definite improvement over state of the art