

The University of Texas Health Science Center at Houston

School of Biomedical Informatics



The University of Texas Health Science Center at Houston

School of Public Health

Modeling Influential Neighbors in Social Networks of Young MSM: An Application of Graph Attention Networks to Predict and Track HIV Infection

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An Ecosystem for Data Centered Informatics Research



Three major steps

Data Extraction (Text-mining and Natural Language Processing)



Data Standardization & Integration (Ontology and Semantic Technologies)



Data Processing and Analyses (Machine learning, Statistical, social network analysis)



Al-assisted HIV prevention/intervention



Background

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1981 to 2015 in the U.S.

HIV infected: > 1.8 million Died: 650,000

2015 in the U.S.

Men who have sex with men (MSM) in high risk of HIV infection: 30.7%

2016 in the U.S.

Young MSM (20-29) in new infections: 37.2%



Between 2010 and 2016, the annual number of HIV infections decreased but the number of YMSM remained stable or increased.

Background

President Trump announced his Administration's goal to end the HIV epidemic in the United States within 10 years

Intervention: Early identification of newly HIV infected cases is essential

- □ 162,500 (14%) persons whose infections had not been diagnosed
- □ Many persons with HIV are tested late in the course of infection
- □ Late testing results in missed opportunities for prevention and treatment of HIV and increased risk for transmission to their partners

Prevention: PrEP: (pre-exposure prophylaxis) is a daily medication taken to prevent HIV infection

- Public perception, awareness, misinformation, lack of education
- □ High risk population recruitment

Al-assisted HIV prevention/intervention

Deep learning based HIV infection risk prediction





Public perception analyses using social media

Electronic methods to recruit persons at high risk of HIV infections

Al-based personalized education and intervetion

Deep learning based HIV infection risk prediction



Data

Young Men's Affiliation Project (YMAP), includes individuals of YMSM, aged 16 to 29, in Houston and Chicago.

Data in this study came from 378 YMAP baseline participants in Houston collected between 2014 and 2016 using the respondent-driven sampling (RDS) method.

Our data includes combined social network information from peer referral and social/sexual partners, HIV testing results and survey data (sociodemographic, sexual behavior).

Motivation

Social network drives the individual HIV risks.

To make predictions upon the risk of HIV infection on each individual and perform early preventions.

Assumption

- Apart from individual-level variables, social network context also contributes significantly on HIV risks.
- Network neighborhood also provide important information for the prediction and influential neighbors should be identified.

Method

Graph Attention Network (GAT)



Input

- Graph: adjacency matrix
- Individual features: socio-demographic variables (race/ethnicity, age, etc.), sexual behaviors (condom use, number of recent sex partners, etc.), graph characteristics (diagonal, centrality, etc.)

Result

Evaluation metric: Area under the ROC Curve (AUC)

Baselines: Logistic Regression (LR), Random Forest (RF), Graph Convolutional Network (GCN) and Multi-layer Perceptron (MLP). Five independent realizations of train-test splits.

GAT outperforms baselines.

	AUC	Std (±)
LR	72.17	4.59
RF	75.59	3.73
GCN	57.34	5.84
MLP	67.50	6.04
GAT	80.6	6.56

Conclusion

We illustrated the capability of the GATs to increase the prediction of HIV and tracking the propagation of the disease in social network of YMSM.

Our study demonstrated the importance of focusing on the most influential neighbors on better predicting individual's HIV status.

Our study findings inform effective network-based interventions through identifying most influential neighbors.

Next step: Investigating the scalability of the machine learning model across cities.

Al-assisted HIV infection prevention/intervention

Deep learning based HIV infection risk prediction





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Electronic methods to recruit persons at high risk of HIV infections

AI-based education









Location

Sex orientation



User attributes inference





Real-time surveillance





Personalized intervention through tailored message

Al-assisted HIV prevention/intervention

Deep learning based HIV infection risk prediction





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AI-based personalized education

Mobile Health Dialogue System



Natural language interface

Ontology-based software architecture

Ontology-based software architecture

-HIV Ontology (HIVO) -Ontology of PrEP & PEP (OPP) -Patient dialogue ontology (PHIDO) -Visualized Emotion (VEO) -User Content Ontology (UCO)

Software Component

-Conversational Ontology Operator (COO)

-Question-answering component (FOQ-U)

.... AND THERE'S MORE



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