Methodological approaches for the prediction or early detection of drug-use associated public-health outbreaks in the United States: a narrative review

Charles Marks, Derek Johnson, Gabriel Carrasco, Rocio Carrasco-Hernandez, Dan Ciccarone, Steffanie Strathdee, Davey Smith, Annick Borquez.

Word limit 300 (298)

Aim: A narrative review was conducted to identify quantitative approaches aimed at forecasting publichealth outbreaks associated to drug-use in the United States; relevant approaches were characterized.

Methods: We implemented a Pubmed search using the following terms: ("Substance-Related Disorders" [Mesh] OR drug use [tiab]) AND (outbreak [tiab] OR "Epidemics" [Mesh] OR "Disease Outbreaks" [Mesh]) AND ("Statistics as Topic" [Mesh] OR "Regression Analysis" [Mesh] OR statistic* [tiab] OR predictive [tiab] OR model [tiab]). We included studies aiming to anticipate drug-use associated outbreaks at the population level in the United States, and extracted the following information: approach, discipline, objective, health outcome, drug type, geographic unit of analysis, data sources and validation method.

Results: Approaches, identified in 15 selected studies, belonged to six overarching disciplines: statistical regression, epidemiological surveillance, phylogenetic surveillance, geospatial analyses, machine learning or internet search-trends analyses. Studies addressed three objectives: outbreak "risk assessment", "detection" or "prediction", and were implemented at the national, state, county or local/ZIP-code levels. Health outcomes included drug-use disorders (DUD), overdose, HCV, HIV and tuberculosis. Drugs included: "any drug", opioids or "novel drugs". Statistical and machine learning studies combined multiple data sources (socio-demographic, law enforcement, health systems) to assess or predict outbreak risk based on observed patterns. Epidemiological studies detected rapid localized increases in infectious diseases or overdose incidence using local surveillance, poison call-center, emergency department and vital statistics data. Phylogenetic studies detected growing drug-use associated transmission clusters using genetic sequences from national surveillance. Geospatial analyses detected clusters and spread of inappropriate prescription practices, prescription DUD and overdoses using prescription and DUD treatment data. Internet search-trend data analyses predicted overdoses and novel drug-use based on Google searches. Few studies validated their outputs.

Conclusion: Several approaches have been used to forecast drug-use associated outbreaks, relying on different data sources and providing unique strengths. A coordinated implementation of multiple, complementary approaches would likely increase our ability to successfully anticipate outbreak risk and respond preemptively.