CS 6474/CS 4803 Social Computing: Prediction & Forecasting II

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Week 14 | April 10, 2023
Examples of many successes...
### Incomplete history of cascade prediction

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<th>Who</th>
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<th>Features</th>
<th>Metric</th>
<th>Conclusion</th>
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<td>Is item retweeted?</td>
<td>Topic Models</td>
<td>F1=0.47</td>
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<td>Content</td>
<td>F1&gt;0.9</td>
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<td>Which of two does better?</td>
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<td>Accu=65.6%</td>
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<td>ChengADKL 14</td>
<td>Will cascade double?</td>
<td>Temporal</td>
<td>AUC=0.88</td>
<td>Predictable</td>
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Lerman, Yang, Petrovic, Romero, Kupavskii, Ma, Weng, Zhao, Yu, etc
Progress?

All of this work examines a different question with a different measure of success, evaluated on a different subset of data, making it difficult to assess overall progress\(^1\)

\(^1\)http://hunch.net/?p=22
Predicting success on Twitter?

Bakshy, Hofman, Mason, Watts (2011):
How viral will my tweet be?
“Cascades are unpredictable!”
Reasons behind the inconsistencies
Meaningless comparisons lead to false optimism in medical machine learning

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July 21, 2017

Abstract

A new trend in medicine is the use of algorithms to analyze big datasets, e.g. using everything your phone measures about you for diagnostics or monitoring. However, these algorithms are commonly compared against weak baselines, which may contribute to excessive optimism. To assess how well an algorithm works, scientists typically ask how well its output correlates with medically assigned scores. Here we perform a meta-analysis to quantify how the literature evaluates their algorithms for monitoring mental wellbeing. We find that the bulk of the literature (~77%) uses meaningless comparisons that ignore patient baseline state. For example, having an algorithm that uses phone data to diagnose mood disorders would be useful. However, it is possible to over 80% of the variance of some mood measures in the population by simply guessing that each patient has their own average mood - the patient-specific baseline. Thus, an algorithm that just predicts that our mood is like it usually is can explain the majority of variance, but is, obviously, entirely useless. Comparing to the wrong (population) baseline has a massive effect on the perceived quality of algorithms and produces baseless optimism in the field. To solve this problem we propose "user lift" that reduces these systematic errors in the evaluation of personalized medical monitoring.
Exploring limits to prediction in complex social systems
A unified framework: Luck vs. skill\(^2\)

- Model success \(S\) as a mix of skill \(Q\) and luck \(\varepsilon\):
  \[
  S = f(Q) + \varepsilon
  \]

- Measure the fraction of variance remaining after conditioning on skill:
  \[
  F = \frac{\mathbb{E}[\text{Var}(S|Q)]}{\text{Var}(S)} = 1 - R^2
  \]

- \(R^2 = 1\) in a pure skill world, \(R^2 = 0\) in pure luck world

\(^2\text{Formalizes Maboussin (2012)}\)
Data

- Examined all 1.4B tweets containing URLs posted in February 2015
- Eliminated spam using internal Microsoft classifier
- Restricted attention to tweets containing URLs from the top 100 English-speaking domains with the most unique adopters
- Resulted in 850M tweets from 50M distinct users covering news, entertainment, videos, images, and products
- Measured the total cascade size for each seed tweet
Predictive features

Used a random forest to estimate success (cascade size) given skill (available features)

- **Basic content features**: URL domain, time of tweet, spam score, ODP category
- **Basic user features**: number of followers, number of friends, number of posts, account creation time
- **Topic features**: the most probable Latent Dirichlet Allocation topic for each user and tweet, along with an interaction term
- **Past success**: the average number of retweets received by each URL and user in the past
Predictive performance

Our best model explains roughly half of the variance in outcomes.

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![Graph showing R² values for different models](image)

- **Red line**: All tweets
- **Dashed red line**: Past user success only

- **Y-axis**: $R^2$ values
- **X-axis**: Features (Basic content, Content: topic, Basic user, User: topic, User: past succ., Content & user, All features)
Content features alone perform poorly
Predictive performance

Basic user features provide a reasonable boost in performance

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![Graph showing $R^2$ values for different feature sets]
### Predictive performance

Past user success alone accounts for almost all of predictive power.

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![Graph showing R² values for different models](image)

Legend:
- Red solid line: All tweets
- Red dashed line: Past user success only

Graph: R² values for different models ranging from 0.0 to 1.0 across various feature sets.
• Both models derive their **predictive power** from the same simple feature: a user’s **past success**

• **Content features** are only **weakly informative**

• **Performance plateaus** as we add more features, suggesting a possible limit to the **predictability** of diffusion outcomes
How can you prove a limit?

• Results robust to other ML models
  – Decision tree, linear regression
• Consistent with prior work
• Asymptote, dependency between features
• Can’t rule everything out
  – Simulation
Simulation

- SIR disease model
- Scale free network similar to Twitter
  - 7M users, $\alpha = 2.05$
  - 8B simulated cascades
- **Quality**: $R_0 =$ average neighbors infected
  - $p$(infect over edge) $\times$ mean-degree
- Prediction task
  - Given (possibly noisy) estimate of $R_0$ and the seed node, predict cascade size
Conclusions

Most things don’t spread, but when they do, it’s difficult to predict success.
Conclusions

Despite a great deal of research on the topic, it’s difficult to assess long-term progress in predicting success.
Conclusions

State-of-the-art models explain roughly half of the variance in outcomes, based primarily on past success.
Conclusions

This is likely due to randomness in diffusion process itself, rather than our ability to estimate or model it.
Detecting influenza epidemics using search engine query data

Jeremy Ginsberg, Matthew H. Mohebbi, Rajan S. Patel, Lynnette Brammer, Mark S. Smolinski & Larry Brilliant

Nature 457, 1012–1014 (2009) | Cite this article

Abstract

Seasonal influenza epidemics are a major public health concern, causing tens of millions of respiratory illnesses and 250,000 to 500,000 deaths worldwide each year. In addition to seasonal influenza, a new strain of influenza virus against which no previous immunity exists...
RESEARCH ARTICLE

Accurate estimation of influenza epidemics using Google search data via ARGO

Shihao Yang, Mauricio Santillana, and S. C. Kou
+ See all authors and affiliations

PNAS November 24, 2015 112 (47) 14473-14478; first published November 9, 2015;
https://doi.org/10.1073/pnas.1515373112

Edited by Wing Hung Wong, Stanford University, Stanford, CA, and approved September 30, 2015 (received for review August 6, 2015)

Significance

Big data generated from the Internet have great potential in tracking and predicting massive social activities. In this article, we focus on tracking influenza epidemics. We introduce ARGO (A Real-time system for the Estimation of the Geographical spread of online queries), a real-time system that utilizes publicly available Google search data to estimate influenza activity.
Reassessing Google Flu Trends Data for Detection of Seasonal and Pandemic Influenza: A Comparative Epidemiological Study at Three Geographic Scales

Donald R. Olson, Kevin J. Konty, Marc Paladini, Cecile Viboud, Lone Simonsen

Published: October 17, 2013 • https://doi.org/10.1371/journal.pcbi.1003256

Abstract

The goal of influenza-like illness (ILI) surveillance is to determine the timing, location and magnitude of outbreaks by monitoring the frequency and progression of clinical case incidence. Advances in computational and information technology have allowed for automated collection of higher volumes of electronic data and more timely analyses than previously possible. Novel surveillance systems, including those based on internet search query data like Google Flu Trends (GFT), are being used as surrogates for clinically-based reporting of influenza-like-illness (ILI). We investigated the reliability of GFT during the last decade (2003 to 2013), and compared weekly public health surveillance with search query data to characterize the timing and intensity of seasonal and pandemic influenza at the national (United States), regional (Mid-Atlantic) and local (New York City) levels. We identified substantial flaws in the original and updated GFT models at all three geographic scales, including completely missing the first wave of the 2009 influenza A/H1N1 pandemic, and greatly overestimating the intensity of the A/H3N2 epidemic during the 2012/2013 season. These results were obtained for both the original (2008) and the updated (2009) GFT algorithms. The performance of both models was...
The parable of google flu
Big data hubris
Algorithmic Dynamics
It's Not Just About Size of the Data
The era of Big Data has begun. Computer scientists, physicists, economists, mathematicians, political scientists, bio-informaticists, sociologists, and other scholars are clamoring for access to the massive quantities of information produced by and about people, things, and their interactions. Diverse groups argue about the potential benefits and costs of analyzing genetic sequences, social media interactions, health records, phone logs, government records, and other digital traces left by people. Significant questions emerge. Will large-scale search data help us create better tools, services, and public goods? Or will it usher in a new wave of privacy incursions and invasive marketing? Will data analytics help us understand online communities and political movements? Or will it be used to track protesters and suppress speech? Will it transform how we study human communication?
Deeper data: a response to boyd and Crawford

Andre Brock

First Published August 24, 2015  |  Research Article  |  https://doi.org/10.1177/0163443715594105

Abstract

Data analysis of any sort is most effective when researchers first take account of the complex ideological processes underlying data’s originating impetus, selection bias, and semiotic affordances of the information and communication technologies (ICTs) under examination.

Keywords

Big Data, critical cultural informatics, critical information studies, data and society, digital sociology, social media and society

In 2013, Lois Scheidt and I organized a panel for the International Congress of Qualitative Inquiry titled ‘Small data in a big data world’ as a response to ‘Six Provocations for Big Data’. Our panelists presented incredible work conceptualizing new approaches in an age of ‘big data’ to qualitative social media research,
Class Exercise

Assess what “small” or “deep” data, in each of the following cases might be considered.

i) Predict how people react on a new product release (e.g., the latest version of iPhone), as observed on social media

ii) Predict whether greater anonymity leads to greater hate speech on social media

iii) Predict whether following recommended videos on YouTube leads down a more politically extreme rabbit hole

iv) Predict whether deplatforming reduces misinformation on social media
Prediction and explanation in social systems

Abstract

Historically, social scientists have sought out explanations of human and social phenomena that provide interpretable causal mechanisms, while often ignoring their predictive accuracy. We argue that the increasingly computational nature of social science is beginning to reverse this traditional bias against prediction; however, it has also highlighted three important issues that require resolution. First, current practices for evaluating predictions must be better standardized. Second, theoretical limits to predictive accuracy in complex social systems must be better...