

# Just How Hopeless Is Trying to Learn about Contagion from Social Network Data?

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Joint work with Andrew Thomas

Details: <http://arxiv.org/abs/1004.4704>

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- 5 yes: because sometimes jumping off a bridge is the only sane thing to do (external causation)



Wikipedia, s.v. "Tacoma Narrows Bridge (1940)"

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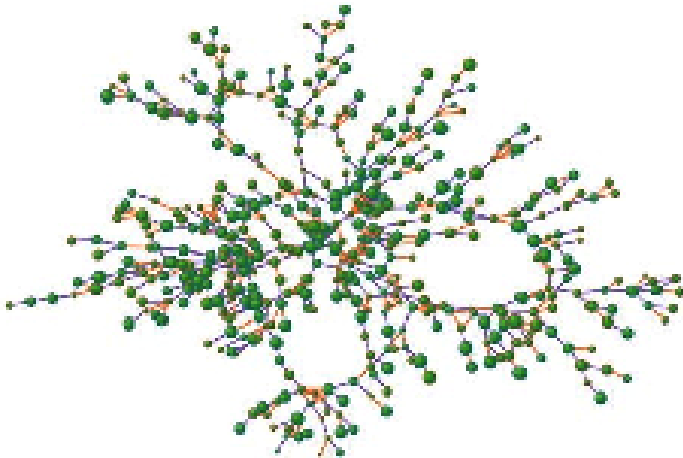
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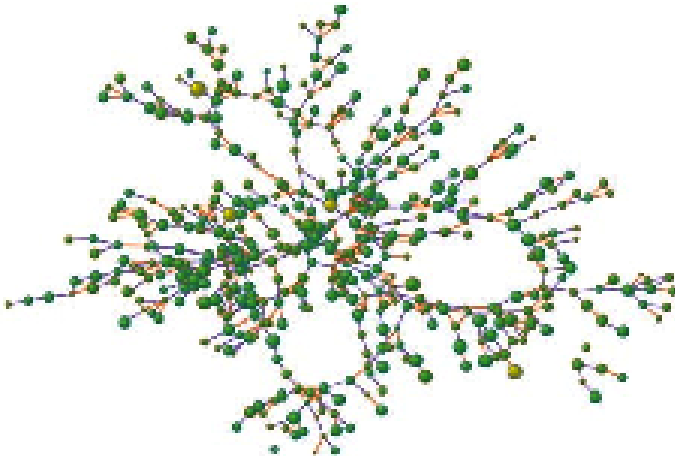
Whether Irene does something is predicted by whether Irene's neighbors had already done it

- Diffusion of innovations
- Diffusion of ideologies
- Infectious diseases
- Not-obviously-infectious conditions (e.g., obesity, loneliness, divorce) . . .

A 1975

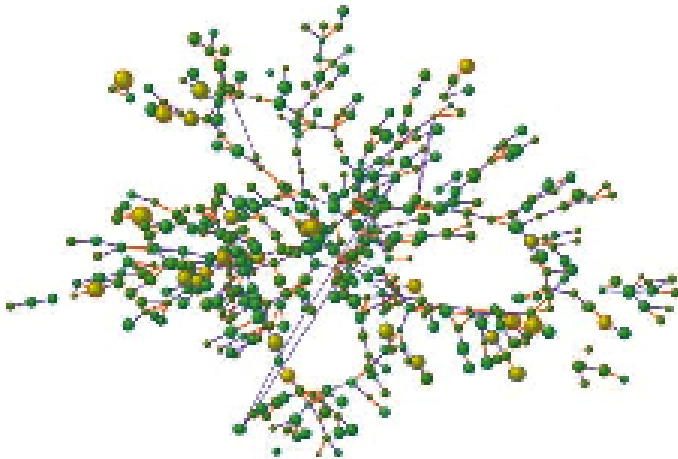


B 1980

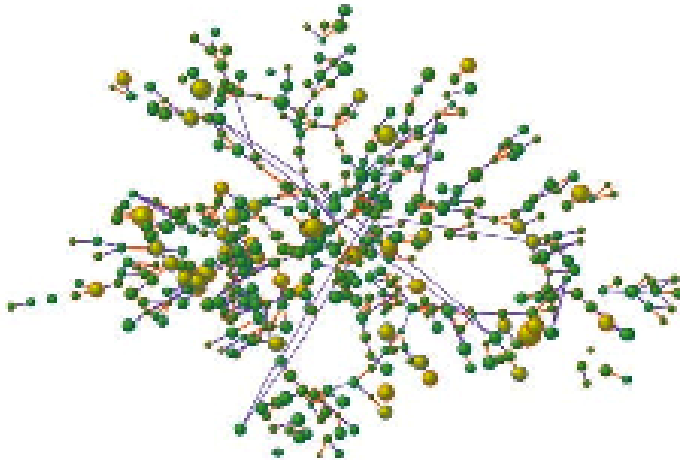




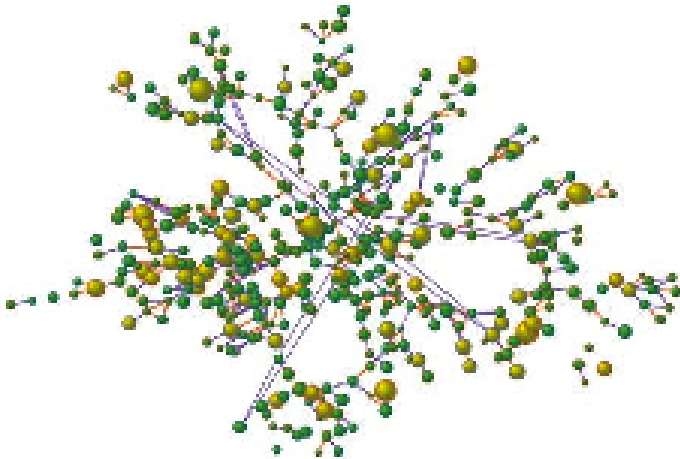
1985



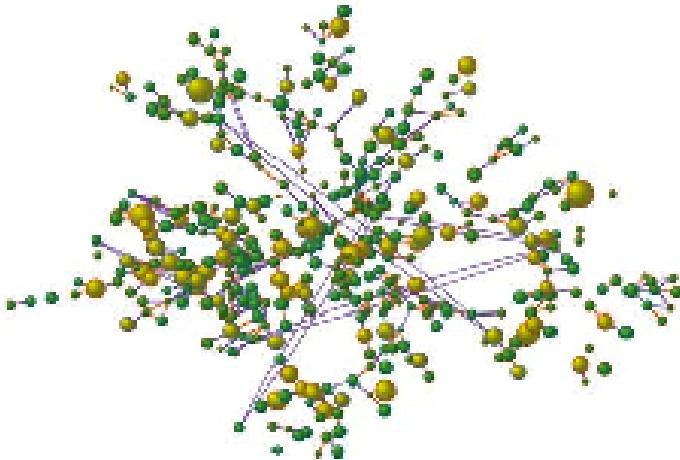
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- Social engineering by targeting influential people
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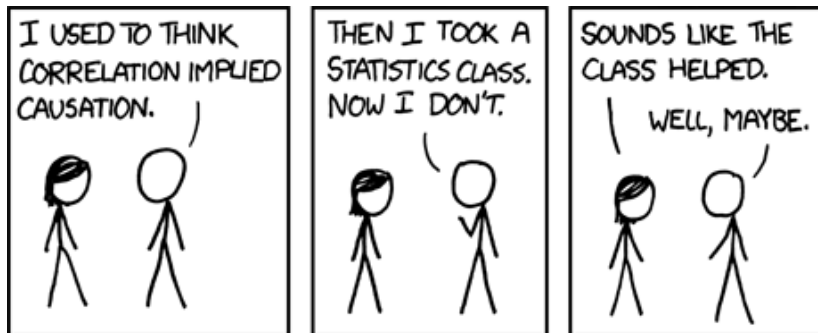
Can we actually figure out how influence/contagion there is?

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This is a causal inference question

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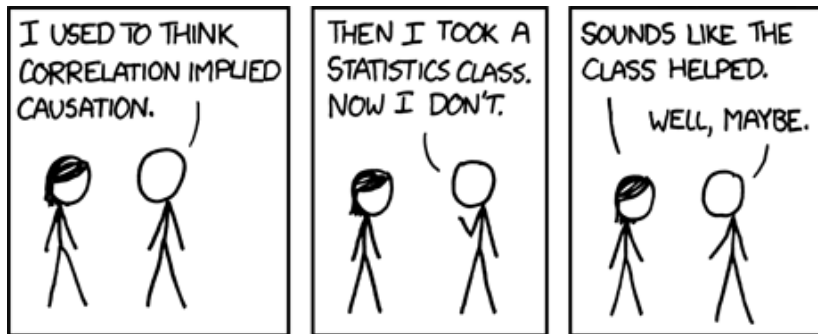
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# Causal Inference

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“Correlation doesn’t imply causation, but it does waggle its eyebrows suggestively and gesture furtively while mouthing ‘look over there’”

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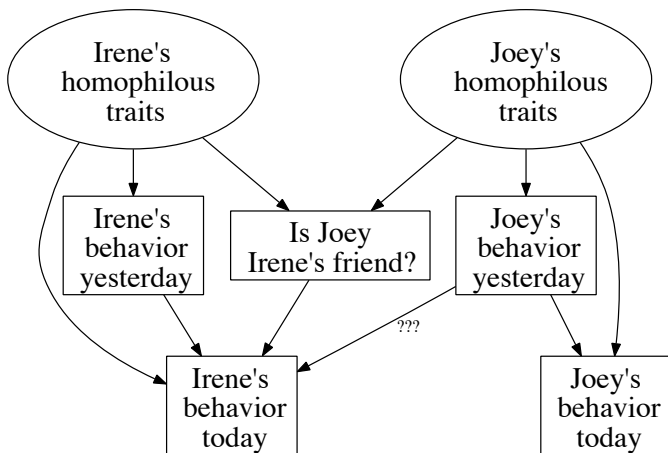
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Do controls *activate* indirect paths?

Separate question: what causal diagrams are compatible with the correlation pattern?

(Spirtes *et al.*, 2001)





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- 5  $\therefore$  Homophily is confounded with contagion

# Failed Escape Attempts

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Letting social ties change over time *really* doesn't help

(Noel and Nyhan, 2010)

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... fails if senders and receivers have systematically different trait values

e.g., people similar friends but also like median friends

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*Gellner: “Social structure is who you can marry, culture is what you wear at the wedding.”*

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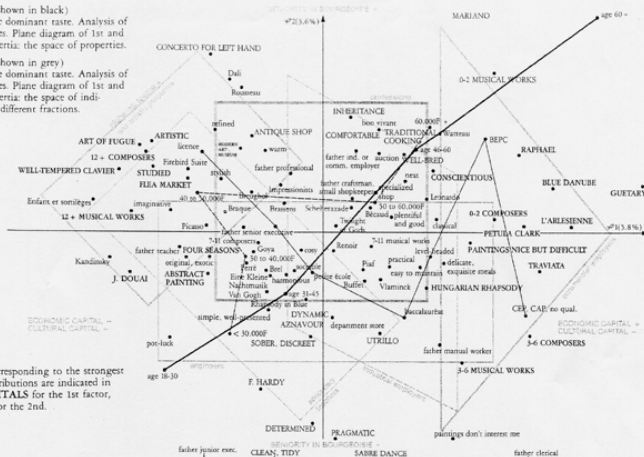
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- Correlation/regression analyses; cultural choices are predictable from social statuses (e.g. Bourdieu (1984))

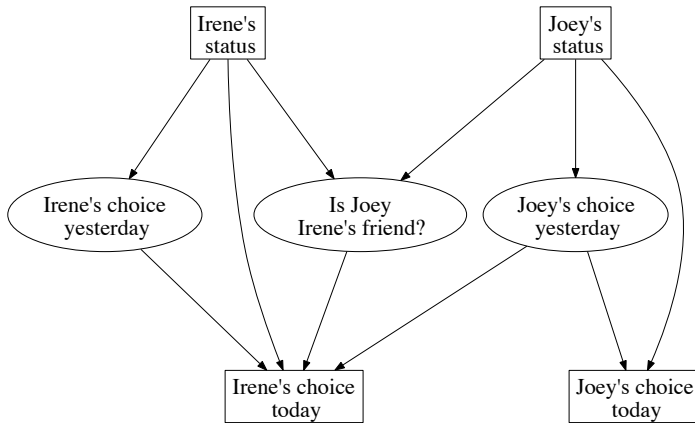
The items corresponding to the strongest absolute contributions are indicated in **BOLD CAPITALS** for the 1st factor, **CAPITALS** for the 2nd.



## Homophily, Contagion, Confounding

Probably true a lot of the time

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BUT usually ignores social networks and just looks at surveys



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- Data departing from neutral model  $\Rightarrow$  evidence of adaptation

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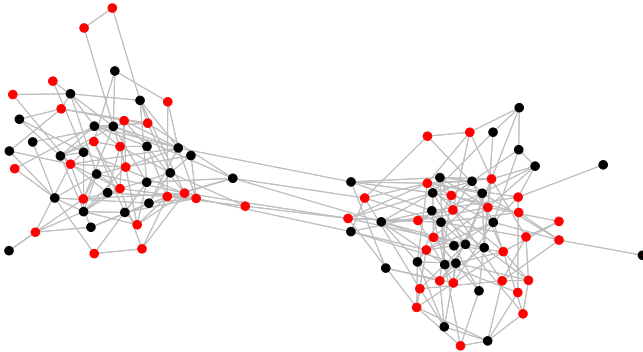
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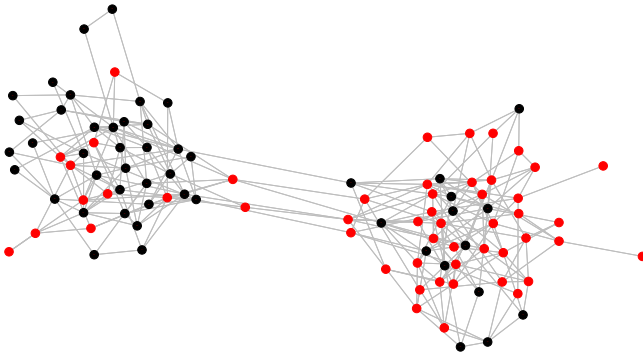
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(= “voter model” of statistical mechanics)

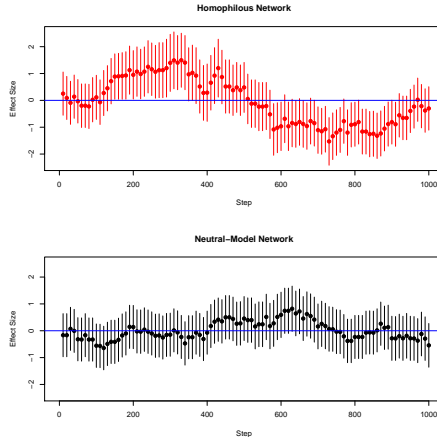


100 node network, homophily for status (2 groups), initial choices



After 300 updates





Coefficients for logistic regression of choice on status,  $\pm$  95% confidence intervals.  
Red, homophilous network; black, matched non-assortative network

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- Need to control for neighbors' *previous choices*

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- Clustering: figure out the traits from the social network

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Work in progress, only negative results so far. . .

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but *should* reduce it, tighten bounds

... or make it worse if the relationship isn't simple homophily

# Conclusion

- 1 Homophily + causal influence looks like contagion
- 2 Homophily + contagion looks like causal influence
- 3 Need scientific knowledge and/or blind faith in assumptions  
Technical trickery won't do (alas)
- 4 *May* be possible to *limit* confounding

## Toy Example

Try to predict  $Y(i, t)$  from  $Y(j, t)$  and vice versa when

$$A_{ij} = 1, A_{ji} = 0$$

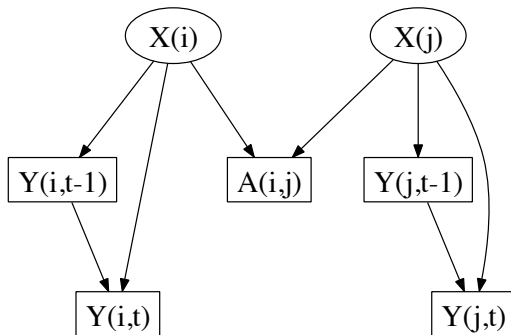
$$X(i) \sim \mathcal{U}(0, 1)$$

Edges form with probability  $\propto \text{logit}^{-1}(-3|X(i) - X(j)|)$

$i$  nominates  $j$  from among neighbors,  $\propto \text{logit}^{-1}(-|X(j) - 0.5|)$

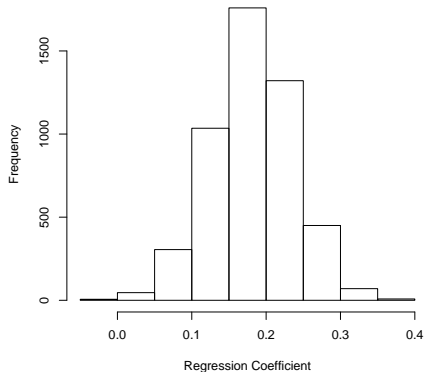
$$Y(i, 0) = (X(i) - 0.5)^3 + \mathcal{N}(0, (0.02)^2)$$

$$Y(i, 1) = Y(i, 0) + 0.3X_i + \mathcal{N}(0, (0.02)^2)$$

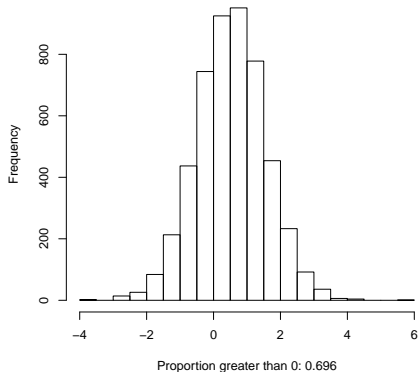


Causal graph of the model with no contagion, but asymmetry in regression coefficients

**Effect of Phantom 'Influencer' on 'Influenced' in Time Series**



**z-score of Directional Difference**



## Results:

- $Y(i, 1)$  is well-predicted from  $Y(j, 0)$
- *Nominees* are disproportionately in the middle;  $i \rightarrow j, j \nrightarrow i$  suggests  $i$  is more peripheral
- For asymmetric pairs, regression of sender on receiver differs from that of receiver on sender



## An Analogy For Community Control

Gene association studies: does having this genetic variant influence this trait/change this risk?

Real populations are structured

Sub-populations differ (due to reproductive isolation etc.)

⇒ genes are correlated

⇒ random biases and inflated variances (vs. usual formulas)

⇒ many bogus results

Population structure substantial even for e.g. Germany (Steffens *et al.*, 2006) or Italy, never mind “white Americans”

Responses: (1) pedigrees; (2) “genomic control” by estimating over-dispersion empirically (Devlin *et al.*, 2001); (3) clustering — the diffusion maps in Lee *et al.* (2009) look *a lot* like Newman (2006)

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