



Workshop on Advances on Epidemics in Complex Networks

Hidden Interactions of Social Populations & Epidemic Dynamics

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Outline

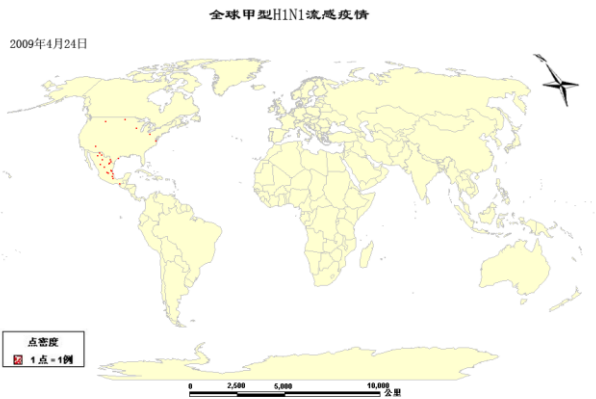
- **Brief review and motivation**
- **Familiar Stranger: overlooked social interactions**
Familiar stranger classifier, location prediction, immunization strategies
- **Invasion pathways: inference before prediction**
Invasion case, observability, identifiability
- **Outlook with extensions**

History repeats itself. ——Thucydides

- Smallpox, black-death,....., AIDS,....., SARS(2003), , A-H1N1(2009),*E.Coli*(2011),.....Ebola/Zika,.....?

- *The modern medical technology can save more patients before, while failed more effectively stopping a virus prevalence than before...*

<Science>, June 20, 2003:
Modeling the SARS Epidemic Transmission Dynamics and Control of SARS

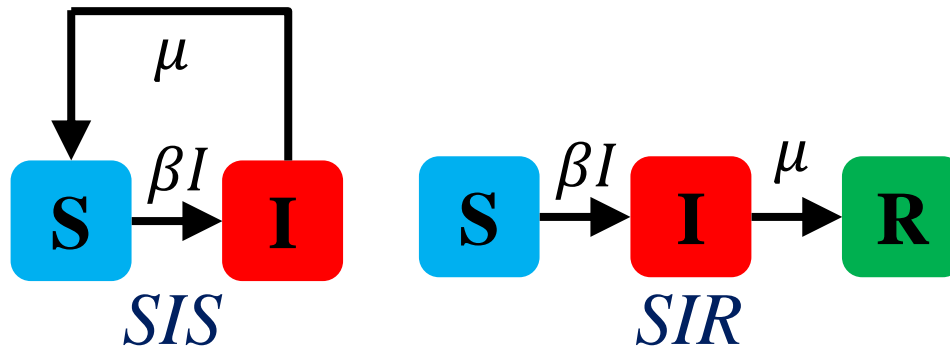


Epidemic models in a population



Daniel Bernoulli, *on smallpox inoculation, 1766*

Prototype of compartment model



mass action principle

An incremental infection depends on the rate of contact between susceptible and infectious individuals.

$$\Delta I = \beta \cdot S \cdot I$$



William Heaton Hamer
(1862-1936)

Epidemics on complex network (single population)

- **Analytic thresholds**

R. Pastor-Satorras, A. Vespignani (2001), Epidemic spreading in scale-free networks, *Physical Review Letters*, 86, 3200.

C. Castellano, R. Pastor-Satorras (2010), Thresholds for epidemic spreading in networks, *Physical Review Letters*, 105, 218701.

P. Van Mieghem and R. van de Bovenkamp (2013), Non-Markovian infection spread dramatically alters the SIS epidemic threshold, *Physical Review Letters*, 110, 108701.

.....

- **Evolution dynamics**

T. Gross, C.J.D. D'Limma, B. Blasius (2006). Epidemic dynamics on an adaptive network. *Physical Review Letters*, 96: 208701.

X. Li, X.F. Wang (2006), Controlling the spreading in small-world evolving networks: stability, oscillation, and topology. *IEEE Trans. Automatic Control*, 51(3): 534-540.

.....

- **Latest survey**

R. Pastor-Satorras, C. Castellano, P. Van Mieghem and A. Vespignani (2015), Epidemic processes in complex networks, *Review of Modern Physics*, 87(3), 925-979.

From single population to meta-population

- Richard Levins (1969), Bull. Entomol. Soc. Am. 15, 237. (**Spatial ecology**)
- Metapopulation: Divide the whole population (country/world) into several sub-populations (cities), a subpopulation is connected with others via public transportation networks, e.g., the air-line web, high-way web.

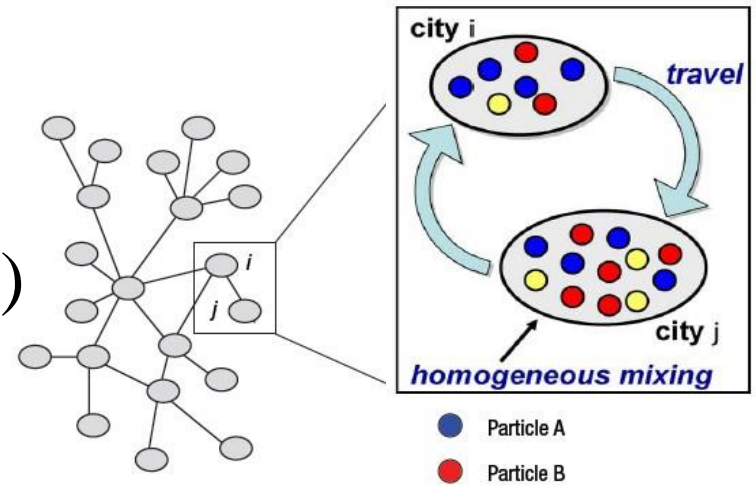


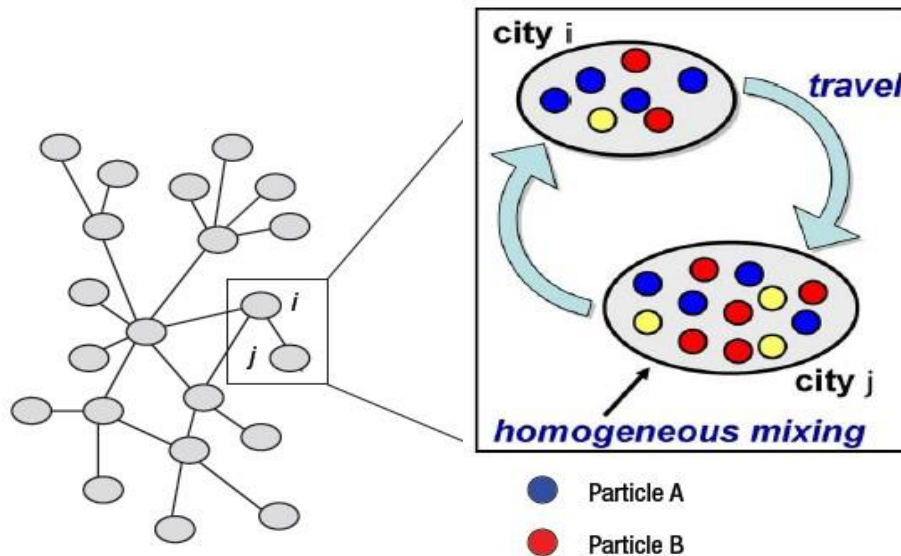
Figure 1 | Interconnected networks of human mobility in North America. The blue network represents short-range commuting flows by car, train and other means of transportation and transport infrastructures. Yellow-to-red lines denote airline flows for a few selected cities; red corresponds to greater traffic intensity. Population density is identified on the grey/white colour scale, with white corresponding to areas of higher density. All features in this map were obtained from real data¹⁰.

V. Colizza, et al. The role of the airline transportation network in the prediction and predictability of global epidemic. PNAS 103(2006): 2015-2020.

Too many stories,
leave for a new book



Spatial epidemics on meta-population



Computational models:
SI/SIS/SIR/SIRS/.....

Infectious parameters:
 R_0 /.....

Assumptions and data-driven **availability**:

- **Subpopulation** (node): Homogeneous mixing, human resident structure, human interactive patterns,
- **Path** (edge): Human travel mobility, local commuting patterns, invasion tree,

Our continuous concerns

- Subpopulations (nodes):

How is the temporal effect of social interactive patterns on network epidemics?

- Paths (edges):

How to infer the invasion trees before predicting network epidemics?

Our continuous concerns

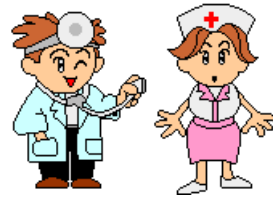
- Subpopulations (nodes):

How is the temporal effect of social interactive patterns on network epidemics?

- Paths (edges):

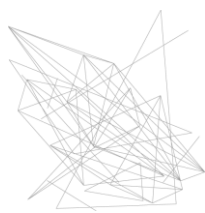
How to infer the invasion trees before predicting network epidemics?

Towards Human Interactions



- **Data Proxy**: Cell phones (bluetooth), Wireless Sensors, RFIDs, Wi-Fi.....
- **Temporal complexity**: interaction frequency, durations, intervals, time-stamps,
- **Temporal information**, more than ‘time-varying’, ‘time-switching’, ‘time-evolving’,.....

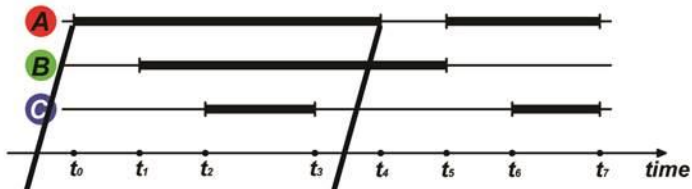
Human Interactive Dynamics: Proxy Datasets



	RFID	Wireless Sensor	Bluetooth	WiFi-Fudan
Number of attendee	25~14000	788	100	18715(46669)
Experiment period(day)	2~69	18	270 (9 months)	84 (3 months)
Time accuracy(second)	20	20	300 (5 minutes)	60 (1 minute)
Space accuracy(meter)	1~5	3	25	20
Agent awareness (Hawthorne effect)	Y	Y	Y	N



- FudanWiFi09
- HT09
- SGInfectious
- SMS-1
- SMS-2
- Sex6yr



The individual trace begins at the time of login passed.

The individual trace ends at the time of access signal lost.



UserName, password, MAC address...

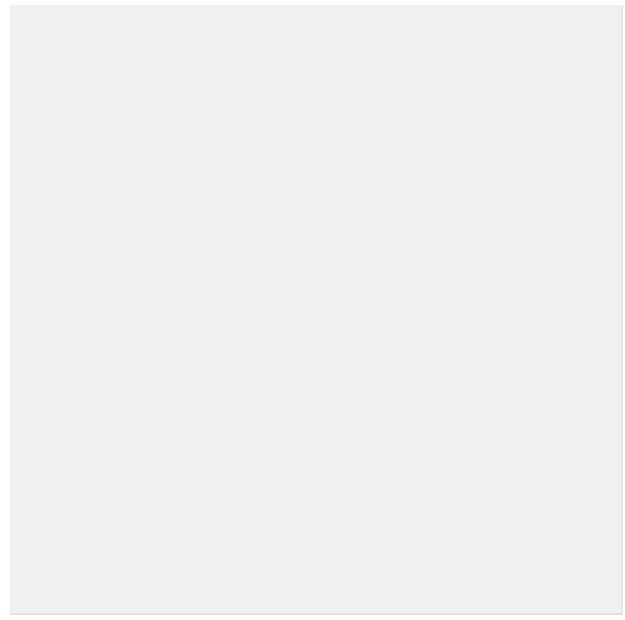
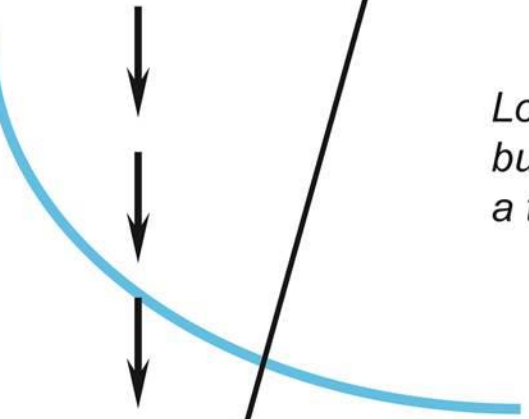


Login & building a trace

Scan & trace ending



out of range



Contributed publications

- X. Li, Y.Q. Zhang, A. V. Vasilakos, Discovering and Predicting Temporal Patterns of WiFi-Interactive Social Populations, in Opportunistic Mobile Social Networks, CRC Press, 2015, 99-122.
- D. Liang, X. Li, Y.Q. Zhang, Identifying familiar strangers in human encounter networks, EPL, 2016, 116, 18006.
- Y.Q. Zhang, J. Cui, S. Zhang, Q. Zhang, X. Li, Modelling temporal networks of human face-to-face contacts with public activity and individual reachability, European Physical Journal B, 2016, 89:26
- Y.Q. Zhang, X. Li, D. Liang, J. Cui, Characterizing bursts of aggregate pairs with individual poissonian activity and preferential mobility. IEEE Communication Letters, 2015, 19(7), 1225-1228.
- Y.Q. Zhang, X. Li, J. Xu, A. V. Vasilakos, Human interactive patterns in temporal networks, IEEE Trans. Systems, Man & Cybernetics: Systems, 2015, 45(2), 214-222.
- Y. Zhang, X. Li, Temporal dynamics and impact of event interactions of cyber-social populations, Chaos, 2013, 23, 013131.
- Y. Zhang, L. Wang, Y.Q. Zhang, X. Li, Towards a temporal network analysis of interactive WiFi users, EPL, 2012, 98, 68002.

Social ties

Acquaintances

friends, in-role, ...



Familiar strangers

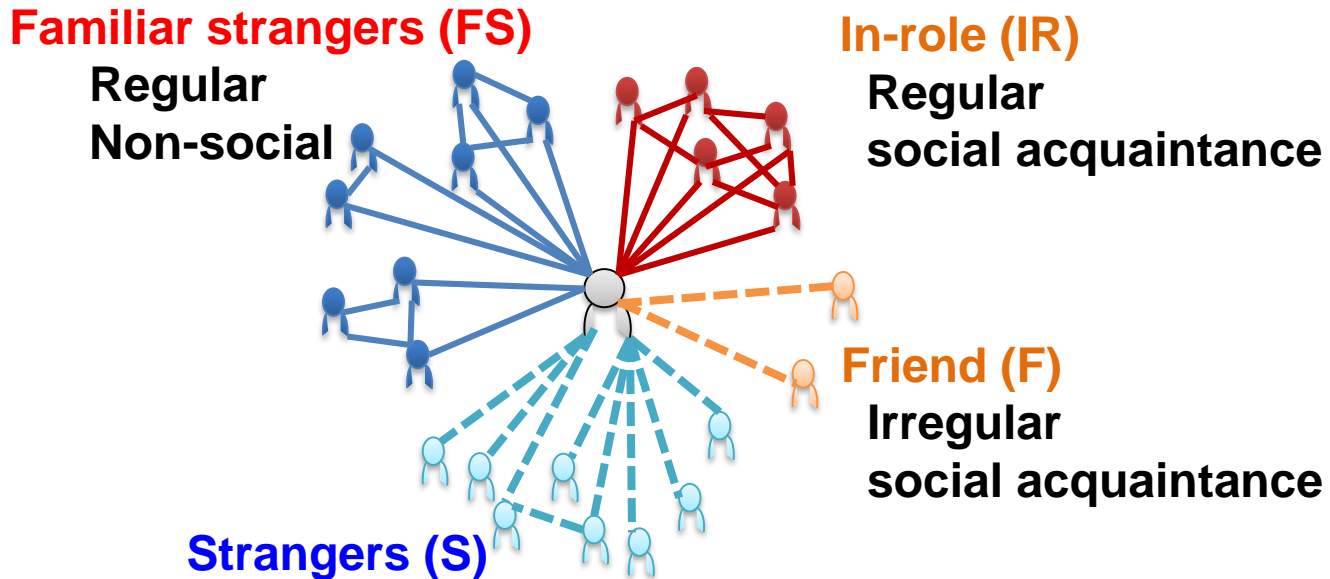


Strangers



Familiar Stranger

- Milgram (1970): Familiar Strangers are two persons who have repeatedly encountered but might never have been acquainted with each other.



Encounters with 'familiar strangers' play overlooked role in human interactions

9 December 2016, by Lisa Zyga

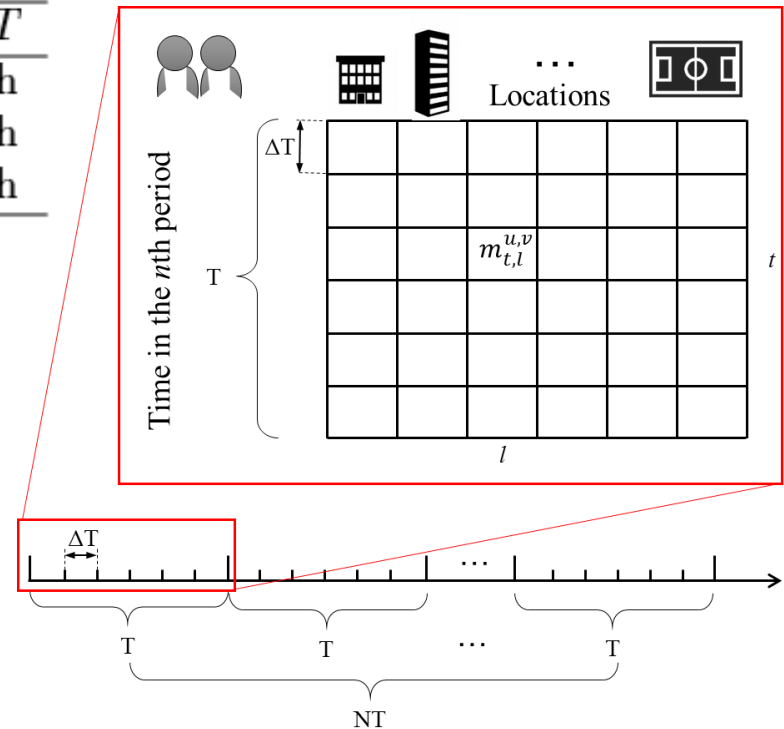
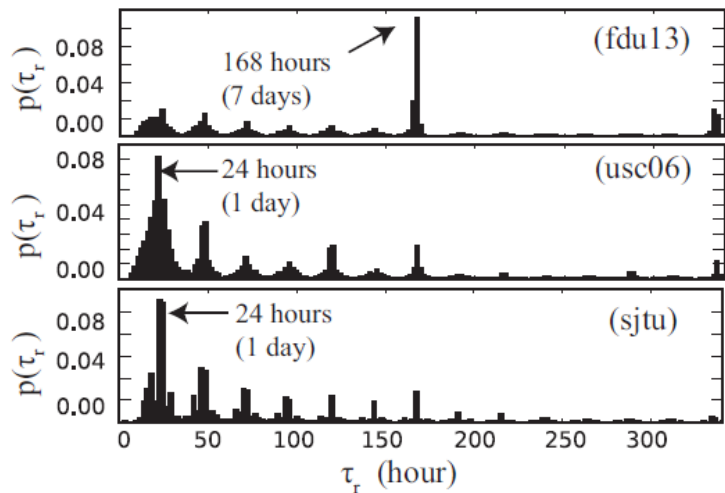
PHYS.ORG

D. Liang, X. Li, Y.Q. Zhang, Identifying familiar strangers in human encounter networks, EPL, 2016, 116, 18006.

Data and Encounter network

Data	$ U $	$ L $	Records #	N	T	ΔT
fdu13	10,146	1,452	3,825,382	12	7 d	3 h
usc06	5,185	137	808,015	84	1 d	3 h
sjtu	14,755	85	4,050,267	92	1 d	6 h

$|U|$: Number of users
 $|L|$: Number of locations
 Records #: Total number of records
 N : number of time cycles
 T : length of one time cycle
 ΔT : length of time step



$$m_{t,l}^{u,v} = (w_{t,l}^{u,v}, prop_{t,l}^{u,v})$$

$w_{t,l}^{u,v}$: **encounter weight**. The number of cycles that individual u and v encounter at location l and time step t .

$prop_{t,l}^{u,v}$: **encounter probability**. The empirical probability that individual u and v encounter at location l and time step t .

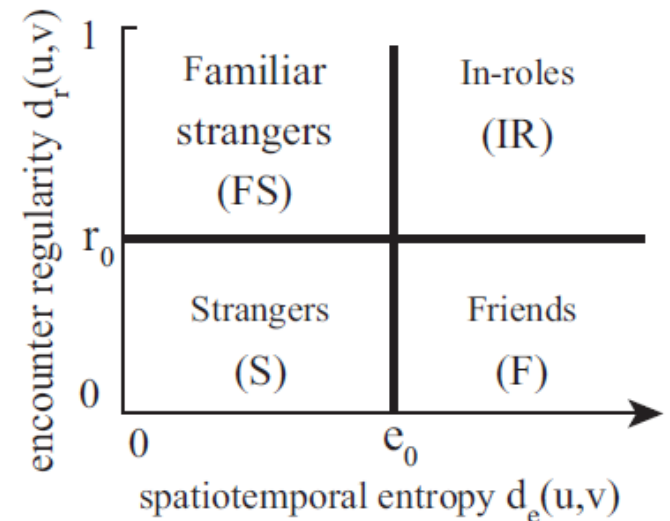
Social ties and Entropy

spatiotemporal entropy $d_e(u, v) = \log_2 \sum_l \sum_t \text{sign}(w_{t,l}^{u,v})$

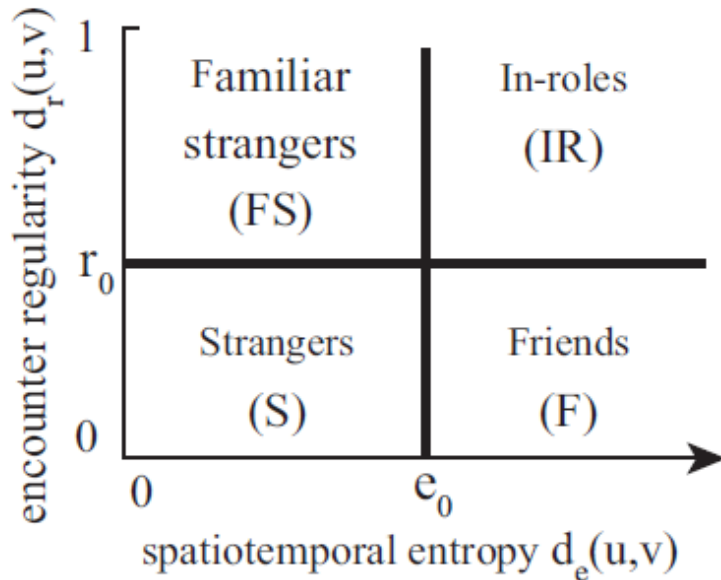
The spatiotemporal entropy measures **the degree of social similarity**. The spatiotemporal entropy between acquaintances will be larger than that of other pairs with random social similarity.

encounter regularity $d_r(u, v) = \frac{\sum_l \sum_t (w_{t,l}^{u,v} \times \text{prop}_{t,l}^{u,v})}{\sum_l \sum_t w_{t,l}^{u,v}}$

Encounter regularity measures to what degree the encounter events between a pair of users are generated obeying the **periodic life routines**



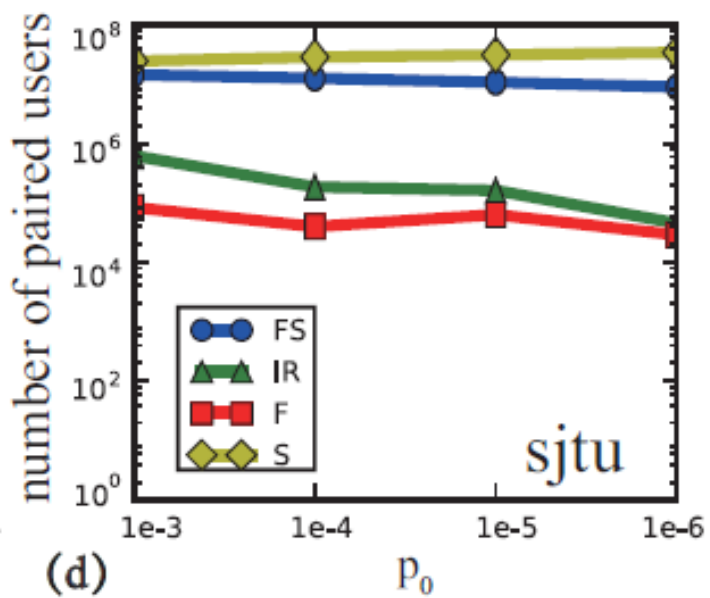
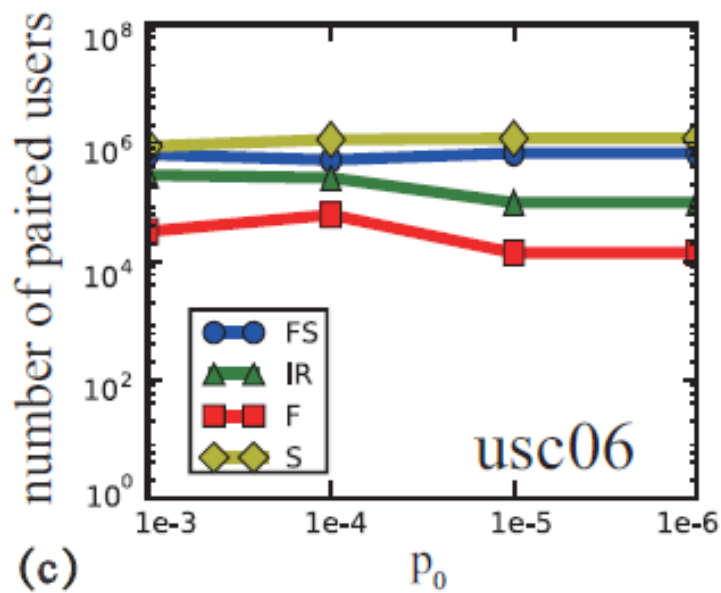
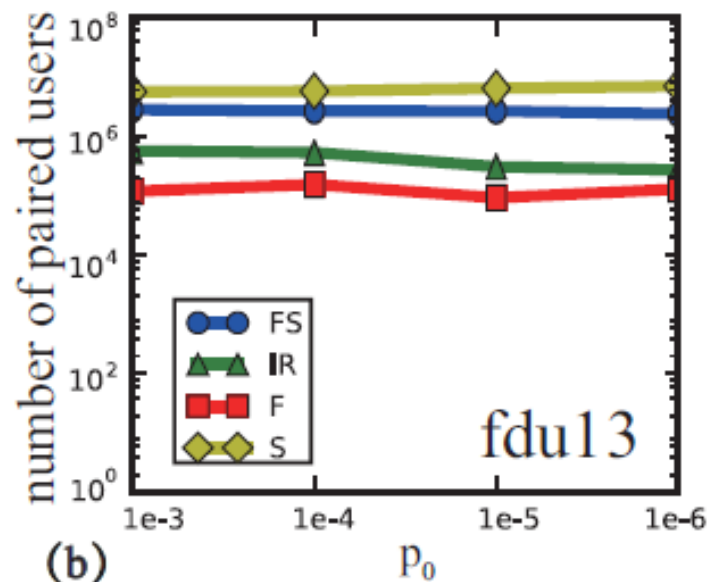
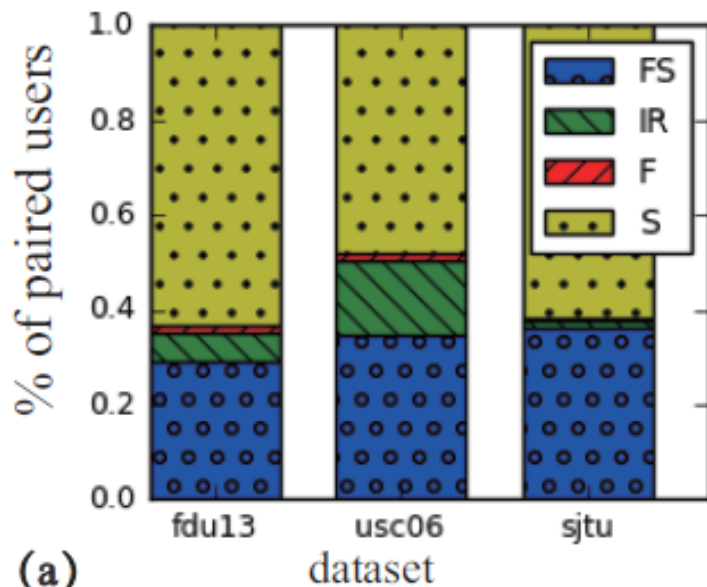
Familiar Stranger Classifier



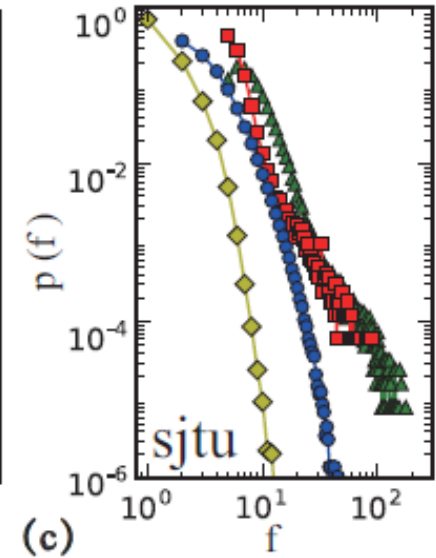
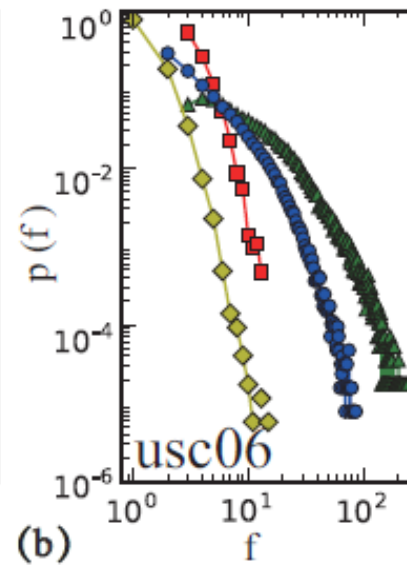
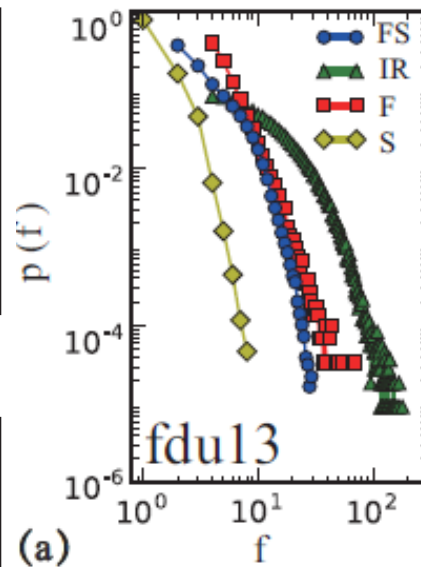
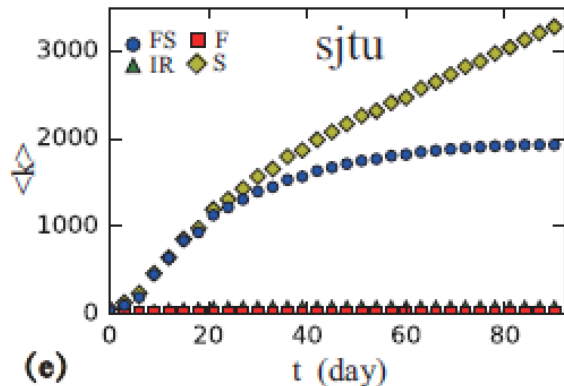
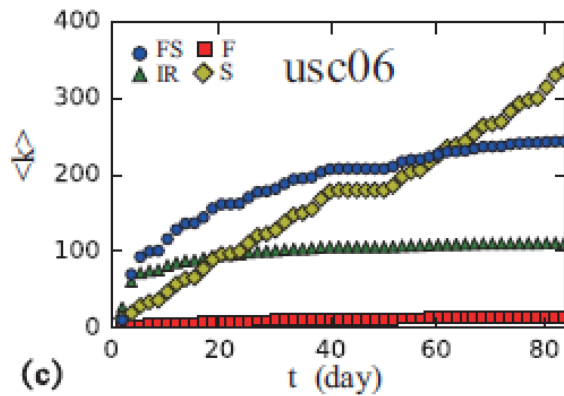
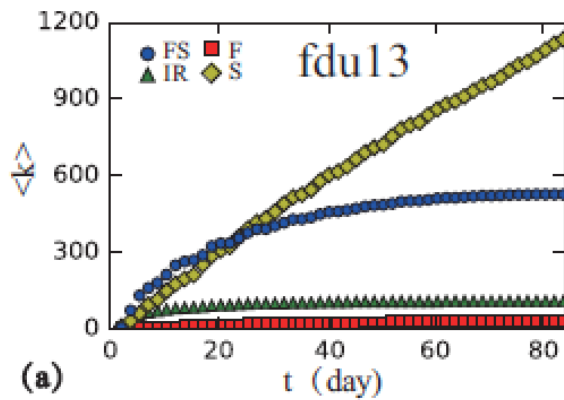
- (1) Obtain encounter matrix $M_{u,v}$ and $M_{u,v}^{null}$ from the empirical dataset and the null model.
- (2) Calculate $d_e(u, v)$ and $d_r(u, v)$ from $M_{u,v}$. Calculate $d_e^{null}(u, v)$ and $d_r^{null}(u, v)$ from $M_{u,v}^{null}$.
- (3) Get e_0 and r_0 , where

$$P(d_r^{null}(u, v) > r_0) =$$

$$P(d_e^{null}(u, v) > e_0) = p_0.$$
- (4) Get pairwise relationship according to the diagram on the left.

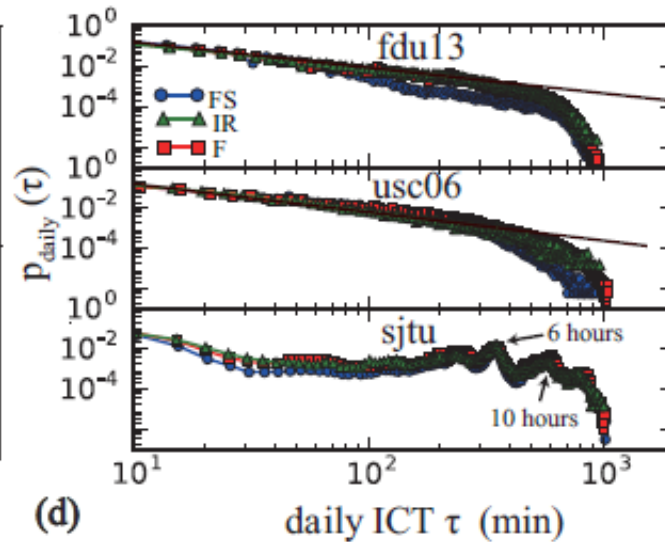
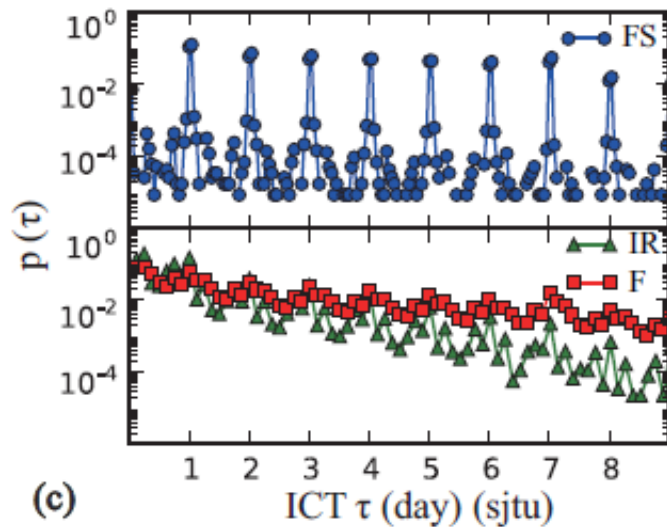
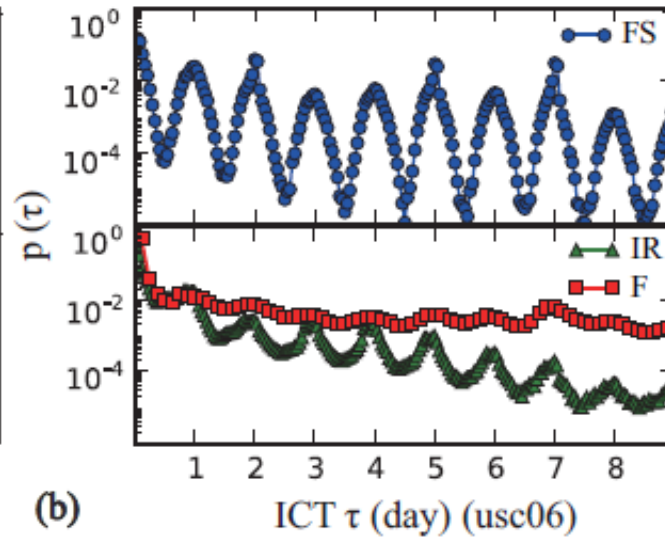
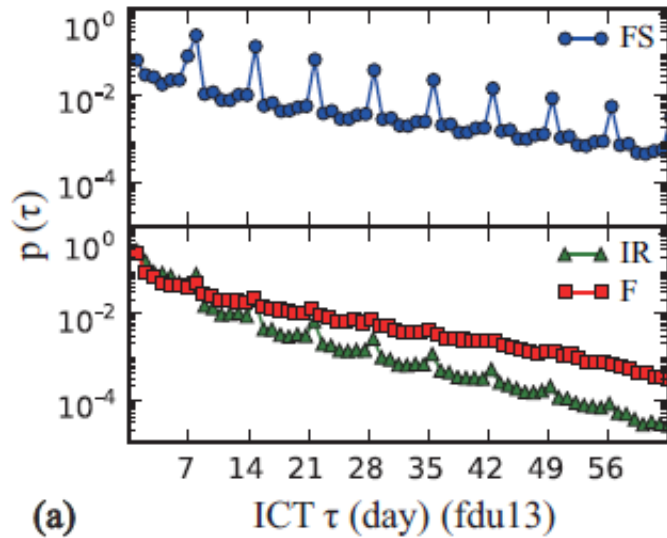


FS degree characteristics



- FS' average degree is finite but larger than the Dunbar Number (150).
- FS' encounters are structurally stable with higher encounter frequencies than those of strangers.

FS temporal (ICT) characteristics



Our continuous concerns

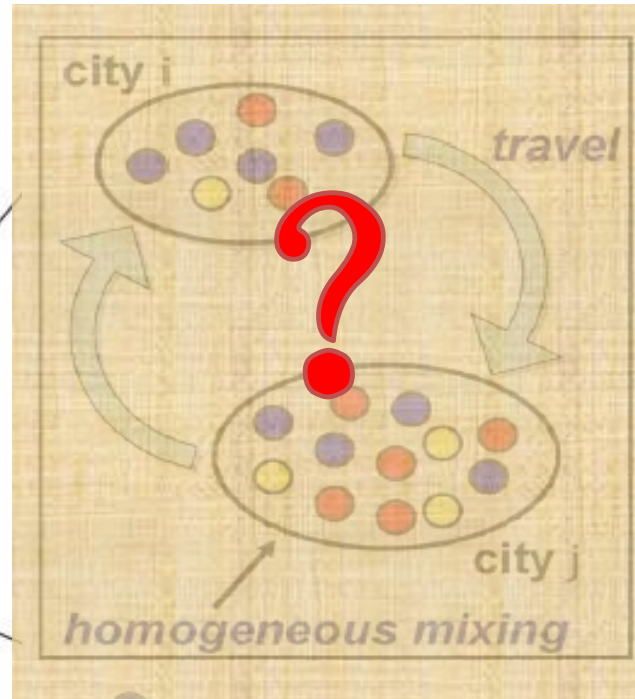
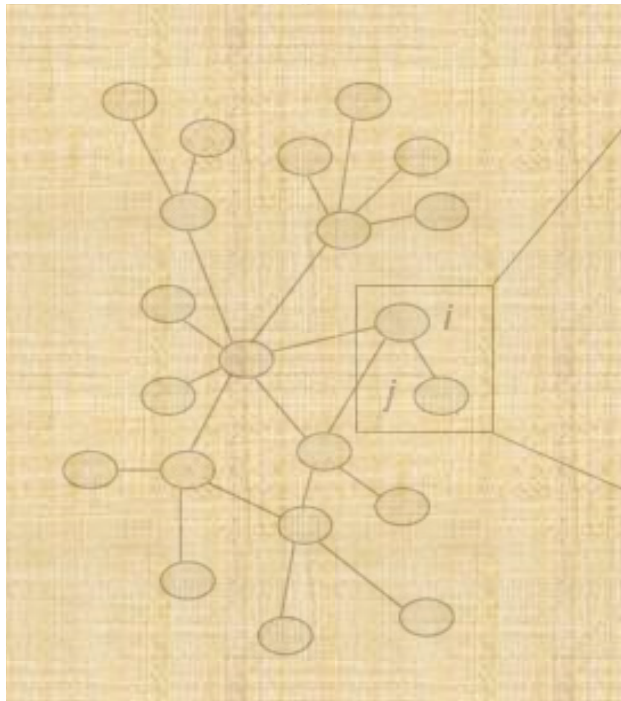
- Subpopulations (nodes):

How is the temporal effect of social interactive patterns on network epidemics?

- Paths (edges):

How to infer the invasion trees before predicting network epidemics?

To identify such epidemic processes?



- Particle A
- Particle B

Epidemic parameter?
Invasion trees?

.....

when such epidemic processes are unknown with only (partial) observed data?



Contributed publications

- X. Li, J.B. Wang, and C. Li, “Towards identifying and predicting spatial epidemics on complex meta-population networks”, Springer, 2017, in press.
- J.B. Wang, L. Wang, and X. Li, “Identifying spatial invasion of pandemics on meta-population networks via anatomizing arrival history,” IEEE Trans. Cybernetics, 2016, 46(12), 2782-2795.
- X. J. Li, C. Li, and X. Li, “Vaccinating SIS epidemics in networks with zero-determinant strategy,” IEEE Int. Symposium on Circuits and Systems (ISCAS 2017), 2275-2278, 2017.
- X. Li, J.B. Wang, and C. Li, “Towards identifying epidemic processes with interplay between complex networks and human populations”, 2016 IEEE Conference on Norbert Wiener in the 21st Century. 67-71, 2016.
- J.B. Wang, C. Li, and X. Li, “Predicting spatial transmission at the early stage of epidemics on a networked metapopulation,” 12th IEEE International Conference on Control & Automation (ICCA), 116-121, 2016.
- J.B. Wang, X. Li, and L. Wang, “Inferring spatial transmission of epidemics in networked metapopulations”, IEEE Int. Symposium on Circuits and Systems (ISCAS 2015), 906-909, 2015.
- J.B. Wang, L. Cao, and X. Li, “On estimating spatial epidemic parameters of a simplified metapopulation model,” 13th IFAC Symposium on Large Scale Complex Systems, 383–388, 2013.

Exploring Epidemic Shortest Paths

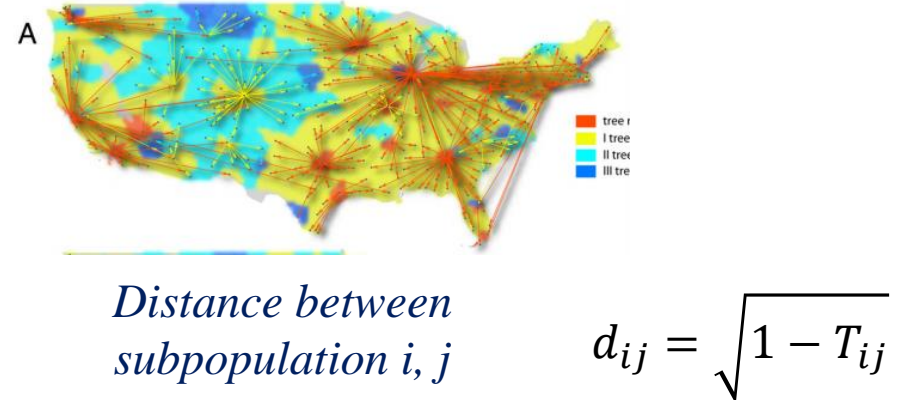
Average-Arrival-Time (ARR)-Based Shortest Paths Tree (SPT) [1]

Shortest path between subpopulation s, j

$$\lambda\langle t_j \rangle \approx \chi(j|s)$$

$$\equiv \min_{\{P_{s,j}\}} \sum_{(k,l) \in P_{s,j}} \left[\ln \left(\frac{N_k \lambda}{w_{kl}} \right) - \gamma \right]$$

Monte Carlo-Maximum-Likelihood (MCML)-Based Epidemic Invasion Tree [2]



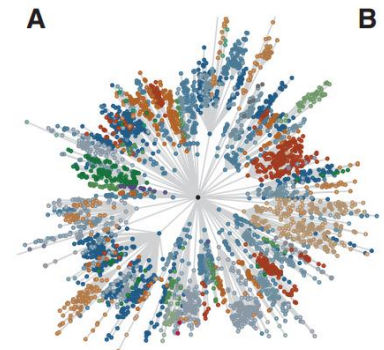
Effective (EFF)-Distance-Based Most Probable Paths Tree [3]

Effective distance between subpopulation m, n

$$d_{mn} = (1 - \log P_{mn}) \geq 1$$

Shortest paths between subpopulation m, n

$$D_{mn} = \min_{\Gamma} \lambda(\Gamma)$$



[1] A. Gautreau, A. Barrat, and M. Barthelemy. "Global disease spread: statistics and estimation of arrival times," *Journal of theoretical biology*, vol. 251, no. 3, pp. 509–522, Apr. 2008.

[2] D. Balcan, V. Colizza, B. Gonçalves, H. Hu, J. J. Ramasco and A. Vespignani, "Multiscale mobility networks and the spatial spreading of infectious diseases." *Proc. Natl. Acad. Sci.*, vol. 106 no. 51, pp. 21484–21489, Dec. 2009.

[3] D. Brockmann and D. Helbing, "The Hidden Geometry of Complex, Network-Driven Contagion Phenomena," *Science*, vol. 342, no. 6164, pp. 1337–1342, Dec. 2013.

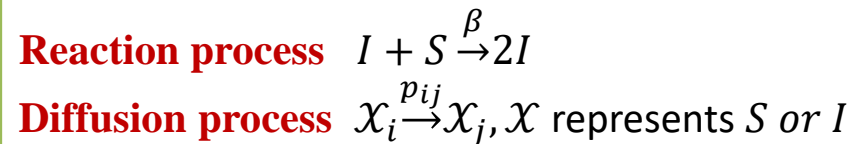
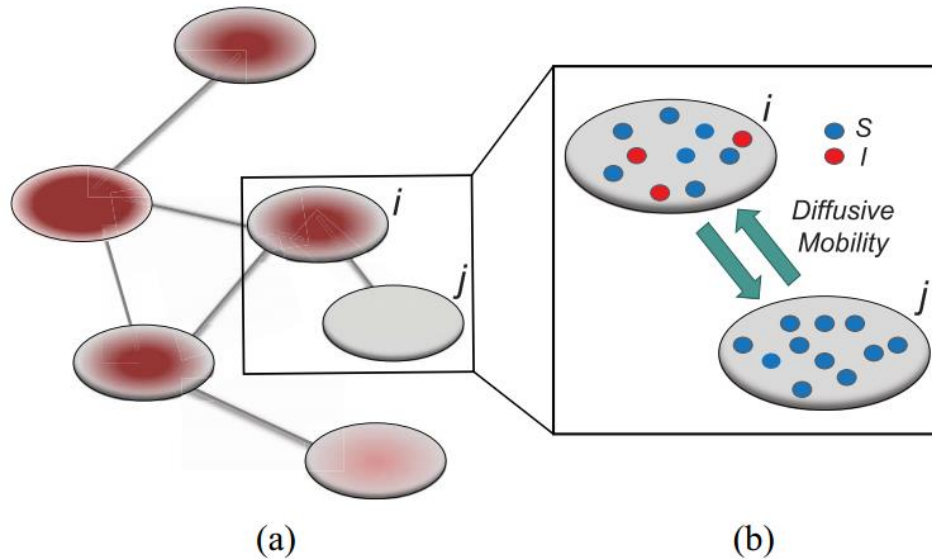
Q: is it possible to retrospect the stochastic pandemic spatial paths among a networked metapopulation?

Our answer:

Invasion Pathways Identification Algorithm Based on Dynamical Programming and Maximum Likelihood Estimation

J.-B. Wang, L. Wang, and X. Li, “Identifying spatial invasion of pandemics on meta-population networks via anatomizing arrival history,” *IEEE Trans. Cybernetics*, 2016, 46(12), 2782-2795.

Problem Statement with SI dynamics



- [1] Hufnagel L, Brockmann D, Geisel T., PNAS, 101: 15124-15129, 2004.
[2] Colizza, V., Pastor-Satorras, R. & Vespignani A., Nature Phys.3, 276-282, 2007.

□ Known:

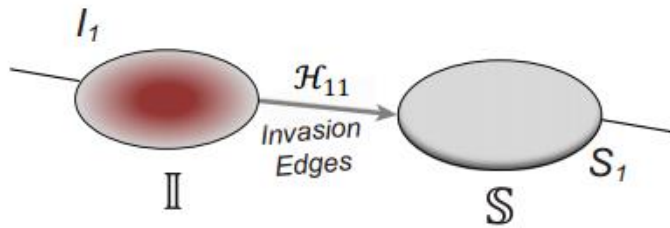
- Number of infected individuals of each infected subpopulation $I_i(t)$ at time step t , network topology (including diffusion rates)

□ Unknown (to identify):

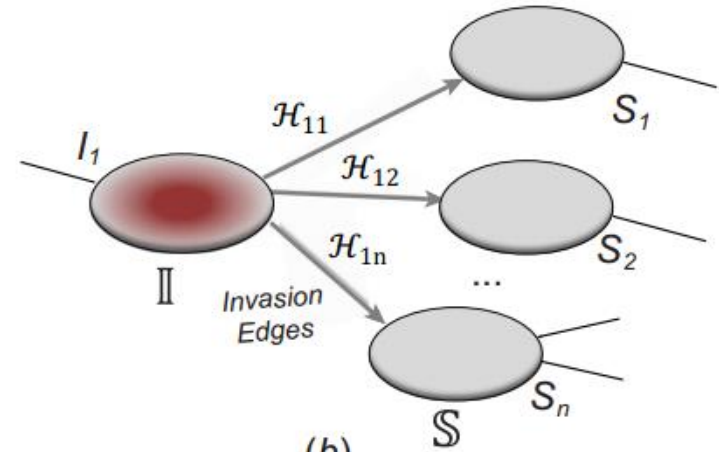
- Spatial invasion pathways



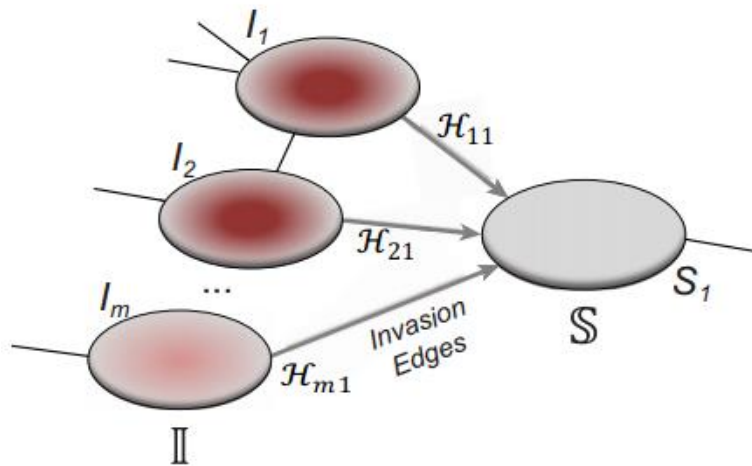
Four Invasion Cases



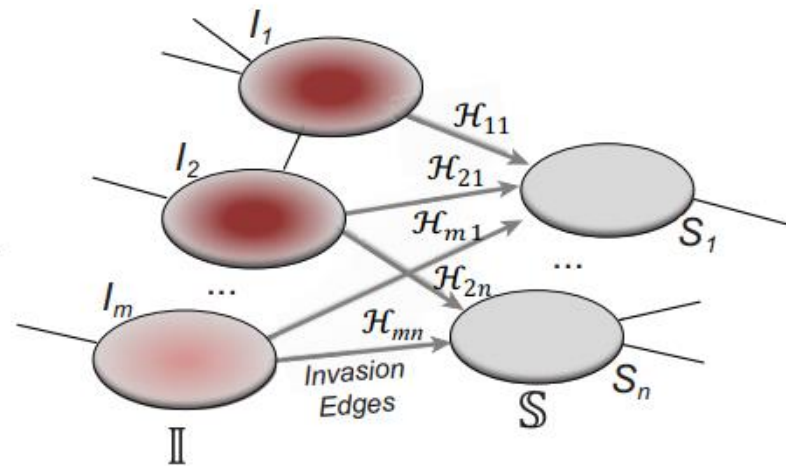
(a)



(b)



(c)



(d)

Invasion Pathways Identification Algorithm

Algorithm steps:

1) Invasion Partition (Dynamic Programming)

The whole invasion pathway T is anatomized into (at each epidemic arrival time (EAT)) four classes of invasion cases with number of Λ :

$$I \mapsto S, I \mapsto nS, mI \mapsto S, mI \mapsto nS$$

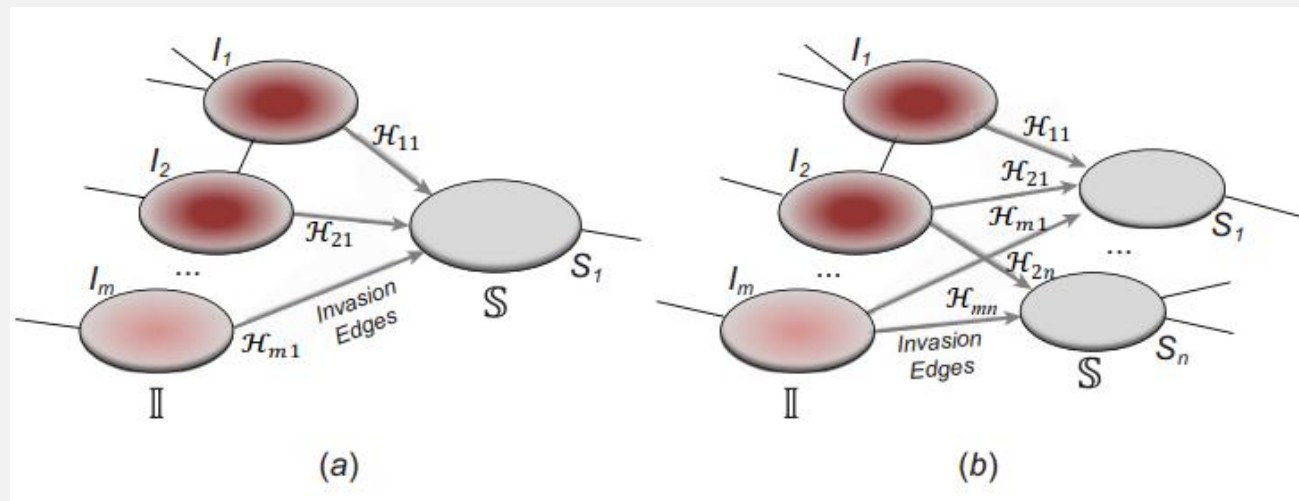
$$T_{\text{whole invasion pathways}} = \text{opt} \sum_{i=1}^{\Lambda} \hat{a}_i$$

2) Identifying Each Invasion Case

Accurate identification + optimal identification (Maximum Likelihood Estimation)

$$\hat{a}_i = \arg \max_{a_i \in G_{INC_i}} P(a_i | G_{INC_i})$$

Invasion Cases (INCs)



$$mI \mapsto S$$

$$mI \mapsto nS$$

Subpopulations' observability

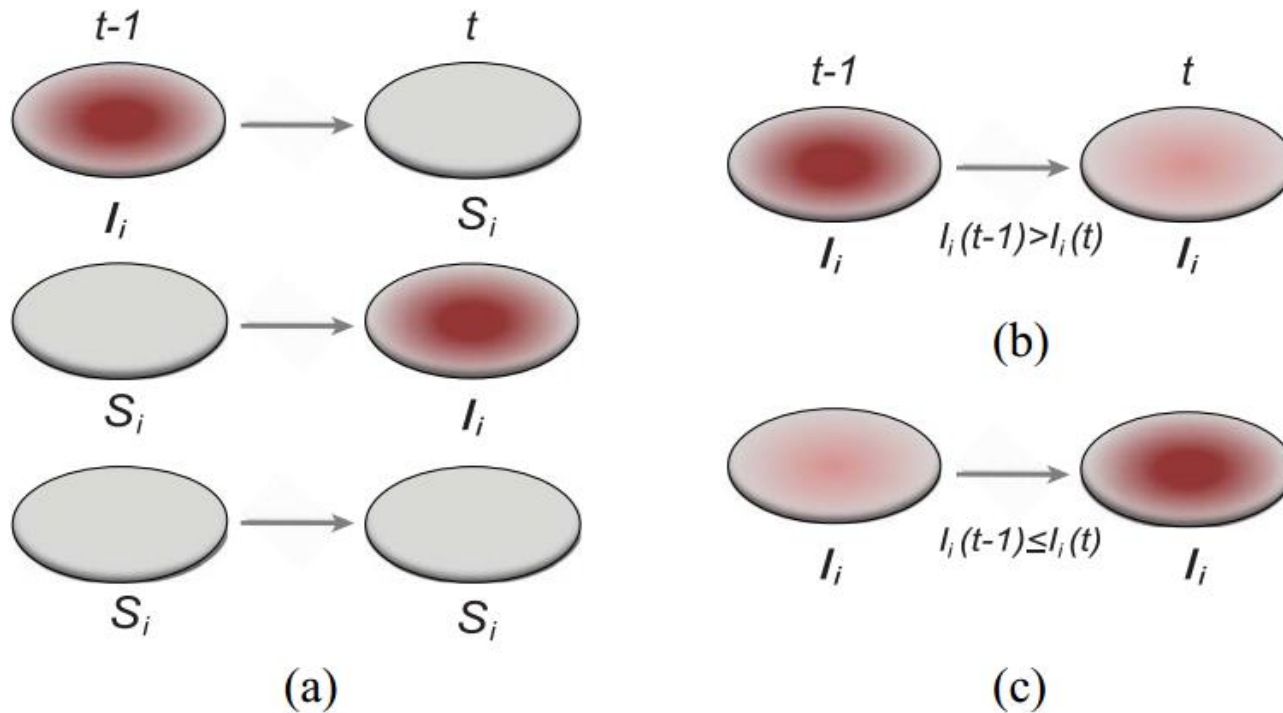
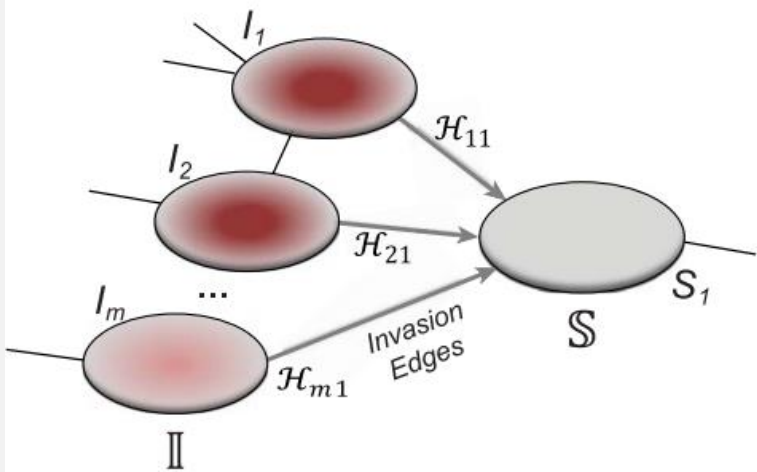


Illustration of neighbors subpopulation classification in terms of status transitions from $t - 1$ to t :

(a) Observable subpopulation i . (b) Partially observable subpopulation i . (c) Unobservable subpopulation i .

Identification of $mI \mapsto S$

Step 1 Accurate Identification



Theorem 1 (Accurate Identification of Invasion Pathway):
 With the following conditions: 1) among m possible sources illustrated in set \mathbb{I} , there are only m' ($m' \leq m$) partially observable subpopulations \mathbb{I}' , whose neighboring subpopulations (excluding the invasion destination S_1) only experience the transition S to S or I to S at that EAT and 2) $\sum_{i \in \mathbb{I}'} [I_i(t-1) - I_i(t)] = \mathcal{H}$, the invasion pathway of an INC $mI \mapsto S$ ($m > 1$) can be identified accurately.

Step 2 Optimal Identification

Decompose the number of first arrival infected individuals

$$\sum_{i=1}^m \mathcal{H}_{i1} = \mathcal{H}$$

Compute the likelihood of each potential solution:

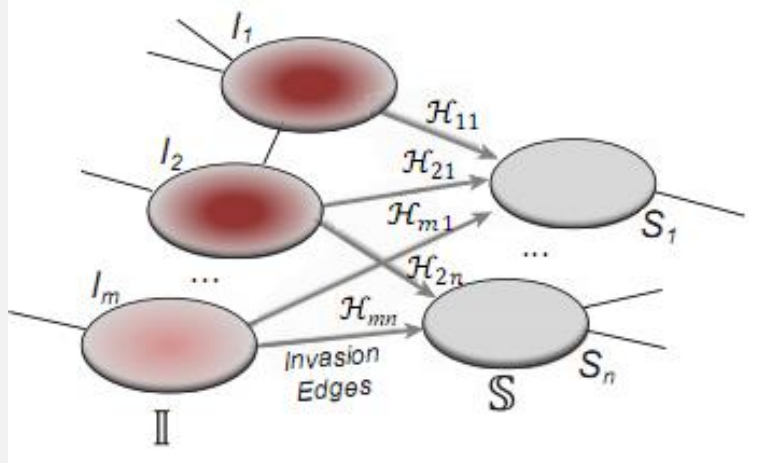
$$\begin{aligned} P(\sigma_j | \mathcal{E}_{mIS}) &= P(\mathcal{E}_{mIS} | \sigma_j) P(\sigma_j) / P(\mathcal{E}_{mIS}) \\ &= P(\mathcal{E}_{mIS} | \sigma_j) P(\sigma_j) / \sum_{j=1}^M [P(\mathcal{E}_{mIS} | \sigma_j) P(\sigma_j)] \\ &= P(\sigma_j) / \sum_{j=1}^M [P(\sigma_j)] \\ &= \prod_{k=1}^m \Omega(\mathcal{H}_{k1}^{(j)}) / \sum_{i=1}^M \prod_{k=1}^m \Omega(\mathcal{H}_{k1}^{(i)}) \end{aligned}$$

Choose the maximal one

$$\begin{aligned} \hat{a}^{mIS} &= \arg \max_{\sigma_i} P(\sigma_i | \mathcal{E}_{mIS}) \\ &= \arg \max_{a_i} P(a_i | G_{mIS}) \end{aligned}$$

Identification of $mI \mapsto nS$

Step 1 Accurate Identification:



Theorem 2 (Accurate Identification of Invasion Pathway):
 With the following conditions: 1) the number of invasion edges $E_{in} \leq n + m$; 2) the neighbor subpopulations of each subpopulation in set \mathbb{I} are with the transition S to S or I to S except their neighbor subpopulations in set \mathbb{S} during t_{EAT-1} to t_{EAT} ; and 3) $\sum_{i=1}^m \Delta I_i(t) = \sum_{k=1}^n \mathcal{H}_k$, the invasion pathway of an INC $mI \mapsto nS (m, n > 1)$ can be identified accurately.

Step 2 Optimal Identification:

Decompose the number of first arrival infected individuals

$$\sum_{i \in Y_k} \mathcal{H}_{ik} = \mathcal{H}_k$$

Compute the likelihood of each potential solution:

$$P(\sigma_j | \mathcal{E}_{mInS}) = \prod_{k=1}^m \Omega(\mathcal{H}_{kk\bar{h}}^{(j)}) / \sum_{i=1}^M \prod_{k=1}^m \Omega(\mathcal{H}_{kk\bar{h}}^{(i)})$$

Choose the maximal one

$$\begin{aligned} \hat{a}^{mInS} &= \arg \max_{\sigma_i} P(\sigma_i | \mathcal{E}_{mInS}) \\ &= \arg \max_{a_i} P(a_i | G_{mInS}) \end{aligned}$$

Analysis

Denote π the probability corresponding to the most likely pathways for a given INC. Thus we have $\pi(\sigma) = \sup\{P(\sigma_i|\mathcal{E})\}$.

Property 1: Given an INC $mI \mapsto S$ or $mI \mapsto nS$, $P(\sigma_i|\mathcal{E}) = (\prod_{k=1}^m \Omega / \sum_{i=1}^M \prod_{k=1}^m \Omega)$. there must exist P_{min} and P_{max} satisfying $P_{min} \leq \pi(\sigma) \leq P_{max}$

Identifiability

Definition 1 (Entropy of Transferring Likelihoods of M Potential Solutions): According to Shannon entropy, we define the normalized entropy of transferring likelihood $P(\sigma_1|\mathcal{E}), \dots, P(\sigma_M|\mathcal{E})$ as

$$\mathcal{S} = -\frac{1}{\log M} \sum_{i=1}^M P(\sigma_i|\mathcal{E}) \log P(\sigma_i|\mathcal{E})$$

Define *identifiability* of invasion pathways to characterize the difficulty level an INC can be identified $\Pi = \pi(\sigma)(1 - \mathcal{S})$.

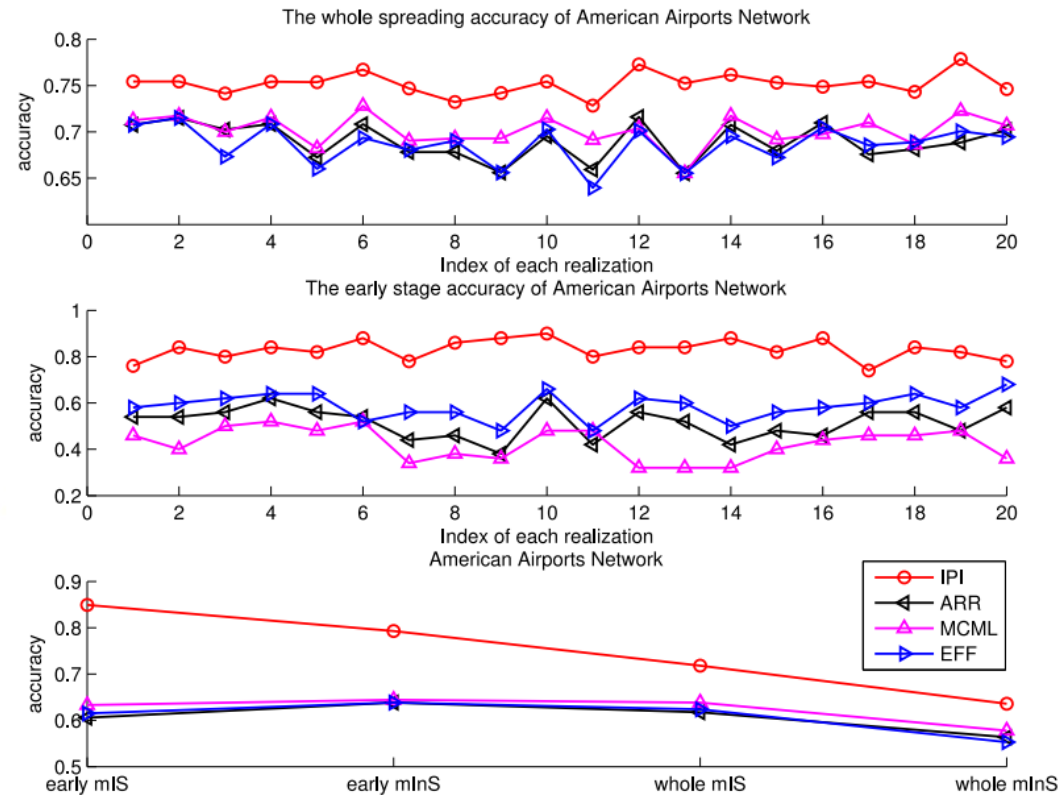
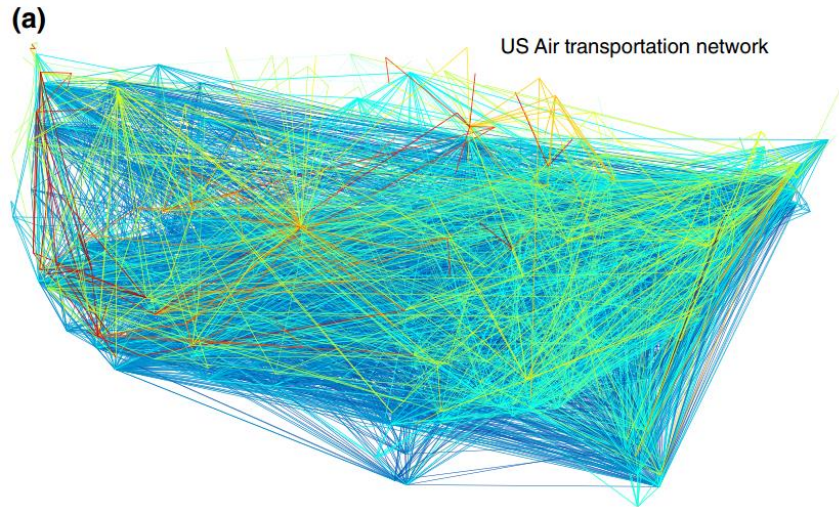
Theorem 3: Given an INC $mI \mapsto S$ or $mI \mapsto nS$, Π is the identifiability computed by the IPI algorithm. There exist a lower boundary $\Pi_{min} = 1/M (1 - \mathcal{S}')$ and $\Pi_{max} = \pi - \mathcal{S}(\pi(\sigma))$ that

$$\Pi_{min} \leq \Pi \leq \Pi_{max},$$

where $\mathcal{S}' = -\left(\frac{1}{\log M}\right)(\pi \log(\pi) + \sum \left(\frac{1-\pi}{M-1}\right) \log\left(\frac{1-\pi}{M-1}\right))$.

Example 1

American Airports Network (AAN)
 $N=404$; total population= 2.4×10^8 ,
 $\langle k \rangle = 16$.

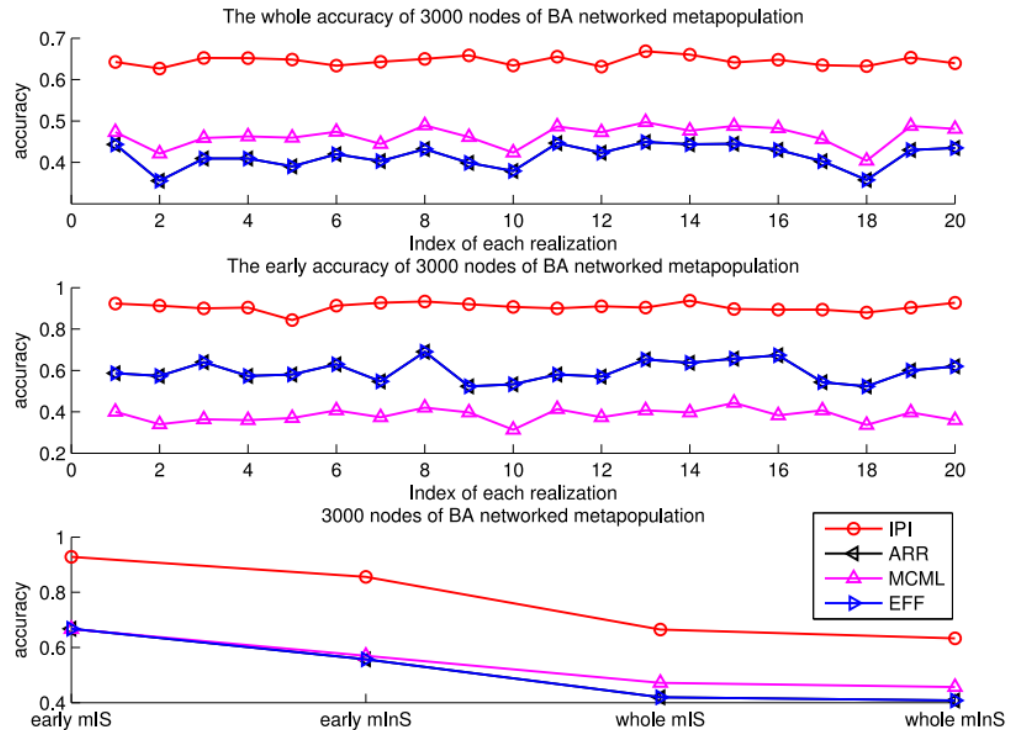
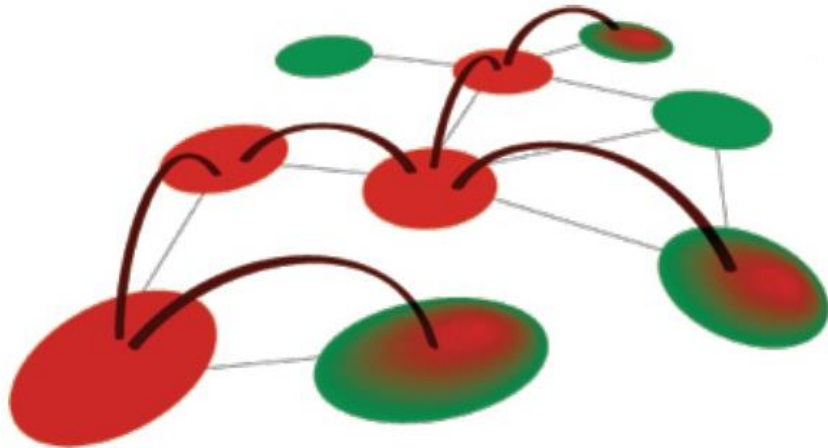


The figure shows various identified accuracy for the early stage and the whole invasion pathways on the AAN.

Example 2

Large-scale BA metapopulation network

$N=3000$; $N_i=6 \times 10^5$; total population= 1.8×10^9 , $\langle k \rangle = 16$.



The figure shows various identified accuracy for the early stage and the whole invasion pathways on 3000 subpopulations of the BA networked metapopulation.

Example 3

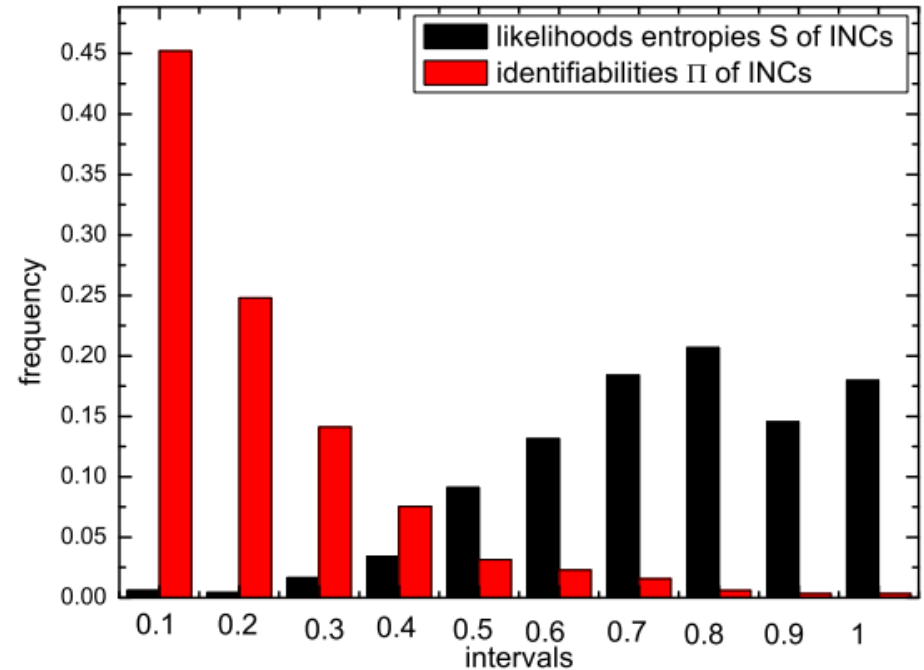
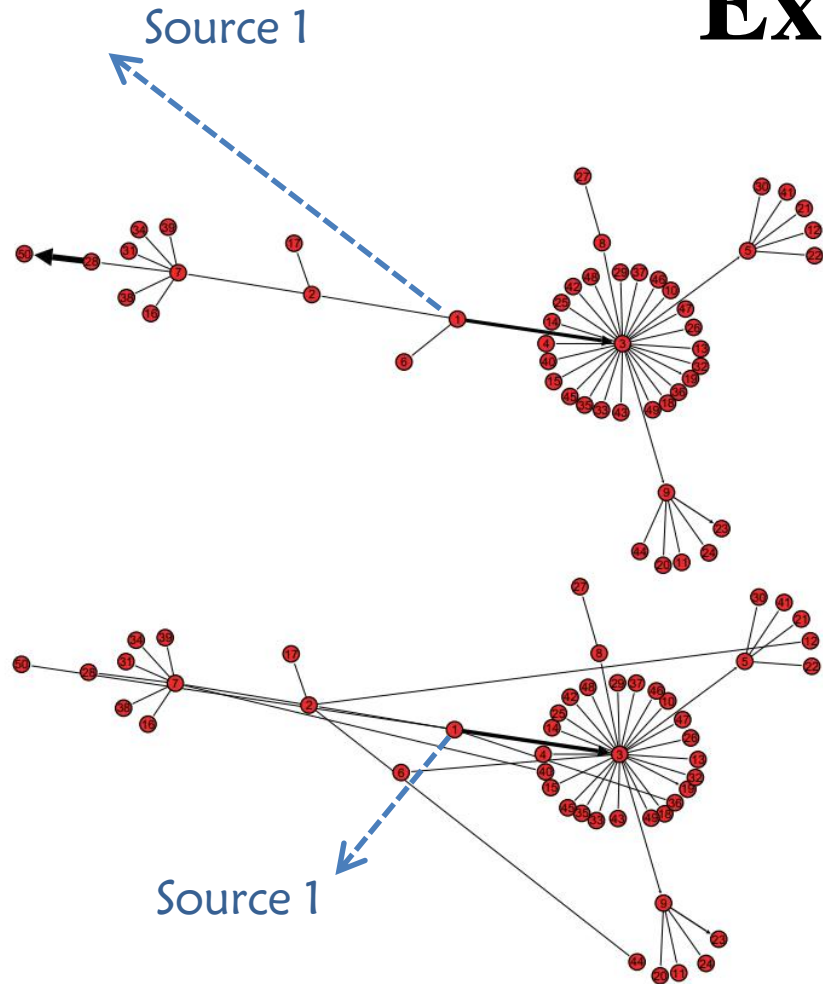


Illustration of the **actual** invasion pathways and the **most likely identified** invasion pathways on the AAN. Subpopulation 1 is the source.

Statistics analysis of the likelihoods entropy and identifiability of wrongly identified INCs on the AAN.

Extension to the **SIR** situation

Inferring SIR spatial invasion on meta-population networks, ready for submission.



Outlook with more extensions

- On reconstructing temporal networks (**null model**)

Reconstruction of stochastic temporal networks through diffusive arrival times, *Nature Communications*, 2017, 8, 15729.

- On optimizing vaccination social-cost (**ZD strategy**)

Minimizing social-cost of vaccinating network SIS epidemics, *IEEE Trans. Network Science and Engineering*, minor revision.

Vaccinating SIS epidemics in networks with zero-determinant strategy, *ISCAS 2017*, Baltimore, 2275-2278.

- On Temporal epidemic thresholds (**non-markovian**)

Spectral analysis of epidemic thresholds of temporal networks, *IEEE Trans. Cybernetics*, 2017, in press.

Acknowledgment Contributions

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Su Causeway in Spring Dawn



Lotus Flowers in the Breezing Winding
Courtyard



Autumn Moon over the Calm Lake



Lingering Snow on the Broken Bridge

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Evening Bell Ringing at Nanping Hill



Three Pools Mirroring the Moon



The Xixi Wetland Park





Thank you!

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