English summary

4.4 Emergency situations (continued)

- collective response (measurable by mobile-phone data)
- spatial patterns: decay with distance from event
- temporal pattern: sudden increase (catastrophes), slow increase (planned events)
- information cascades: many layers —— " ——, few layers —— " ——

5 Control & containment of outbreaks

5.1 Dataset

- EU regulations ⇒ database to monitor animal/livestock trade/movement
- Germany: HI-Tier
- Network: nodes ≙ agricultural premises (pig trade: 120.000)

  links ≙ trade contacts (—— " —— : 200.000/year)
- Structure of network: modularity $Q = \frac{1}{2m} \sum_{ij} \left[A_{ij} - \frac{k_i k_j}{2m} \right] \delta(c_i, c_j)$

  = # links within cluster − # expected links (for random connections)

5.2 Detection of outbreaks

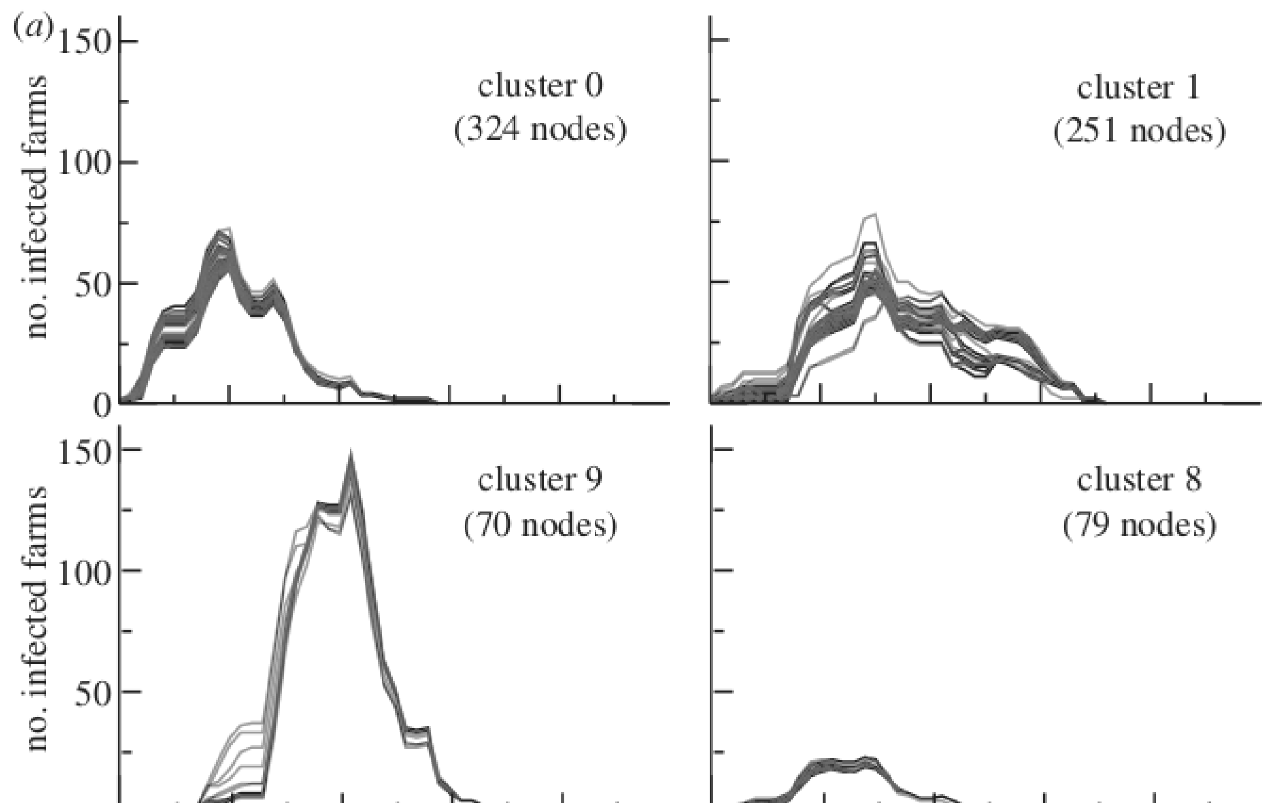
- goal: identify nodes that reliably detect many outbreaks (different origins) at an early stage.
- idea: compare overlap of paths Γ_1 and Γ_2 starting at different nodes

$\Rightarrow$ Jaccard index $\Theta_{12} = \dfrac{|V_1 \cap V_2|}{|V_1 \cup V_2|}$ $\quad V_i$ = set of nodes on Γ_i, $|V_i|$ = # nodes

$\Rightarrow$ define clusters

- similarity of outbreaks for nodes of the same cluster

5.2 Detektion von Krankheitsausbrüchen (Fortsetzung)



ähnliches Verhalten

- Modell: deterministisches SIR-Modell

  ⇒ (i) Ansteckung mit Wahrscheinlichkeit 1 im nächsten Zeitschritt

  (ii) Erholung nach μ^{-1} Schritten

- Betrachte alle möglichen Startpunkte

- Berechne Wahrscheinlichkeit, dass Knoten k bei insgesamt n_k Ansteckungen bei Start in Cluster j erreicht wird: $\Pi_j(k)$

Bsp.: immer von einem einzigen Cluster angesteckt: $\Pi_j(k)=1$, $\Pi_{m\neq j}(k)=0$

immer von einem anderen Cluster angesteckt: $\Pi_j(k)=\frac{1}{n_k}$

⇒ Entropie : $S(k) = -\frac{1}{\log n_k}\sum_j \Pi_j(k)\log \Pi_j(k)$

→ 0 immer aus demselben Cluster

→ 1 immer verschieden

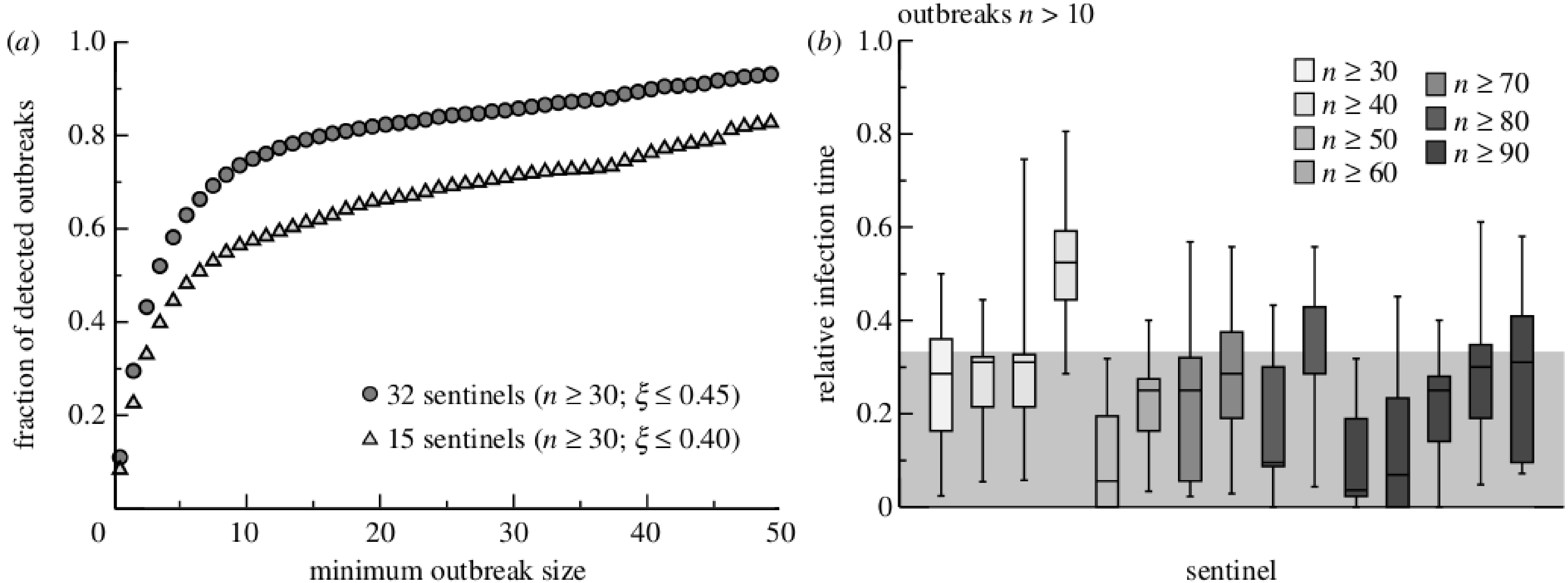


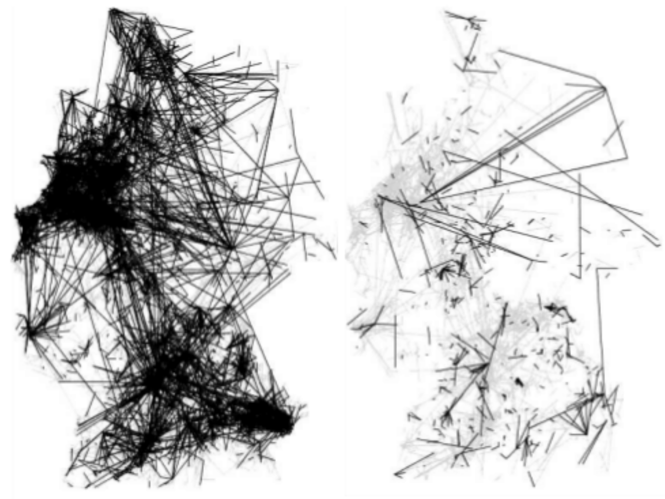
Figure 8. Properties of the surveillance system based on sentinel premises. (*a*) Fraction of outbreaks detected by the sentinels as a function of the minimum outbreak size of the epidemic, for two sets of sentinels (of 15 and 32 sentinels), corresponding to ($n_s = 30$, $\xi_s = 0.4$) and ($n_s = 30$, $\xi_s = 0.45$), respectively. (*b*) Boxplot of the time of infection of the 15 sentinels relative to the full duration of the outbreak, considering the detected outbreaks with final size being larger than 10. Each box is coloured according to the number of times n that the sentinel has been infected and a grey shaded area indicates 33% of the relative infec-

Einige wenige Knoten (geschickt gewählt) detektieren fast alle Ausbrüche zu einem frühen Zeitpunkt.

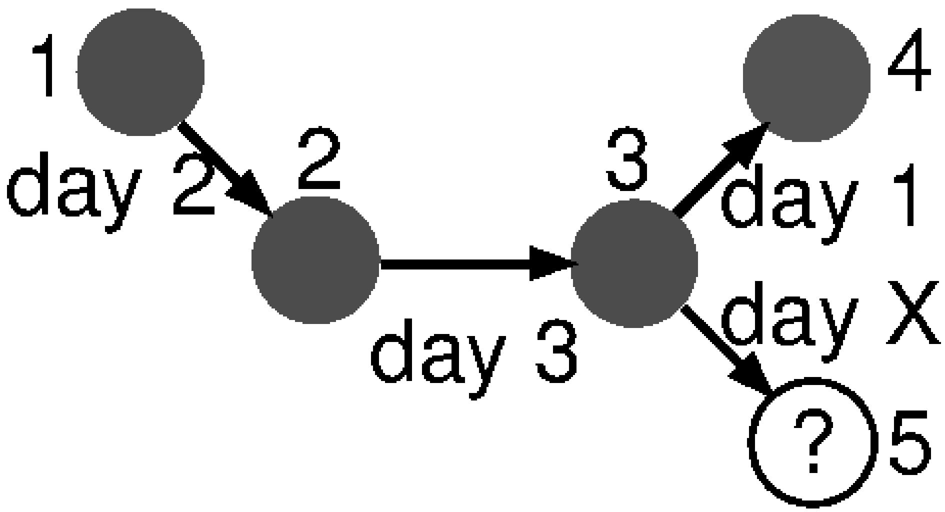
5.3 Kontrolle von Ausbreitungen

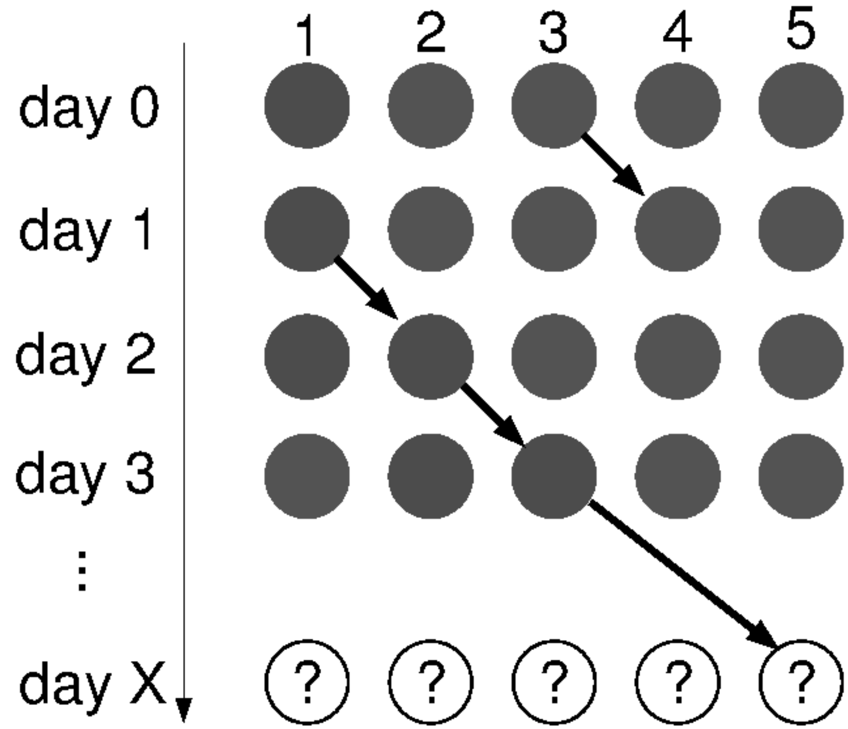
- Daten: deutsche Schweinehandel
- zeitlich abhängiges/veränderliches Netzwerk

Handelsnetz an 2 verschiedenen Tagen →

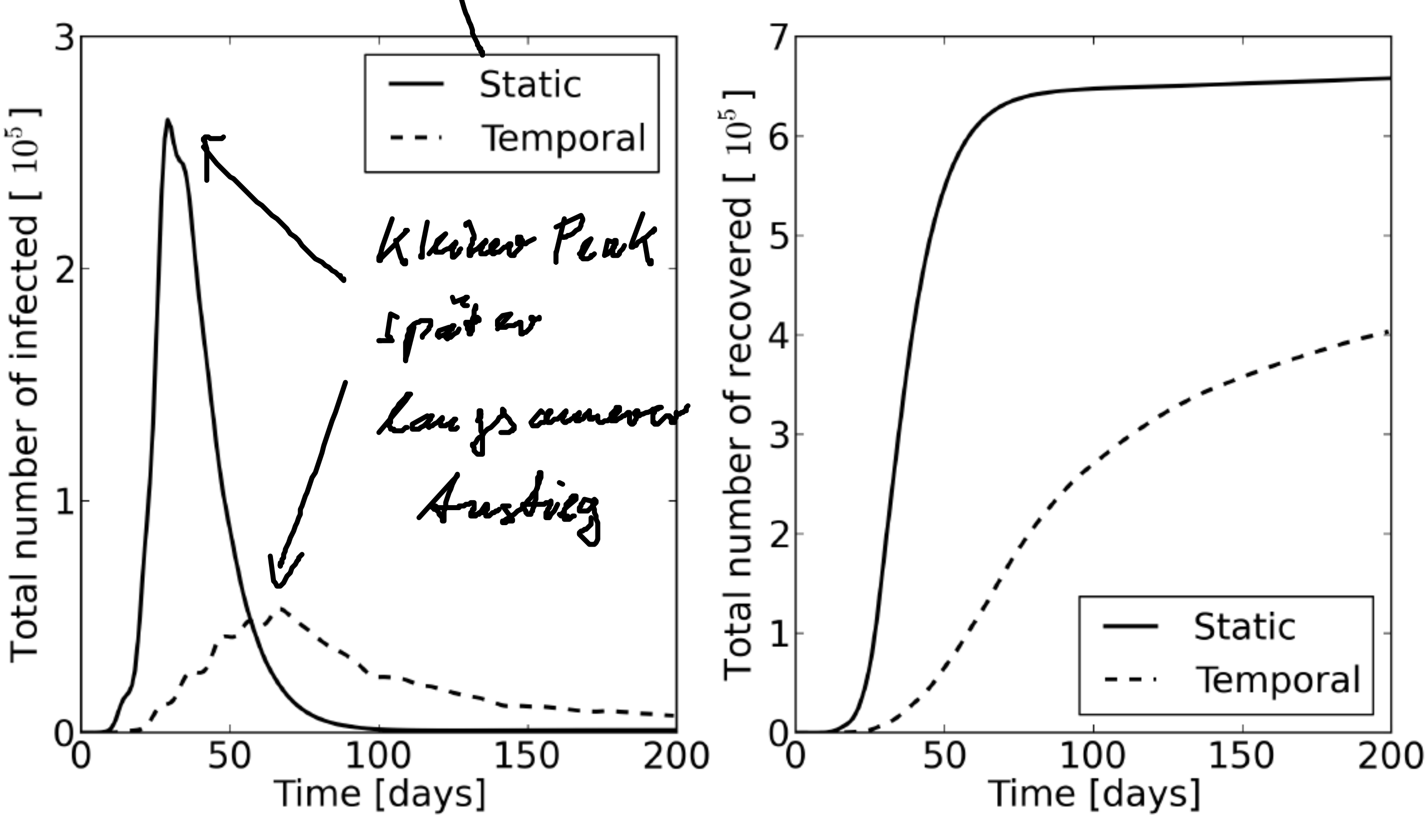


- Kausalität



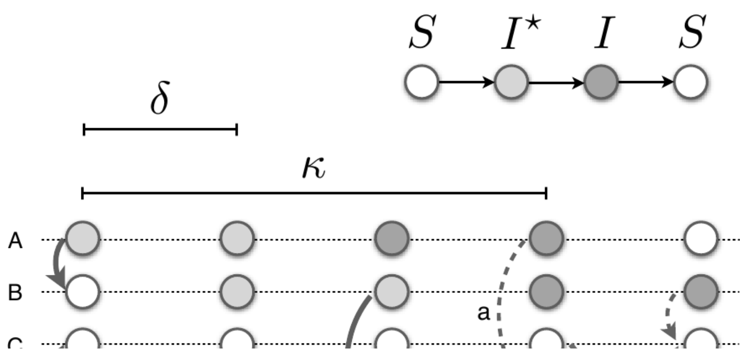


zeitlich aggregiert



SIR-Modell

$$\beta = 1,$$
$$\gamma = 0.1,$$
$$\varepsilon = 10^{-4},$$
$$n = 3218,$$
$$N_\mu(0) = 100,$$
$$S_\mu(0) = 100,$$
$$S_1(0) = 99$$



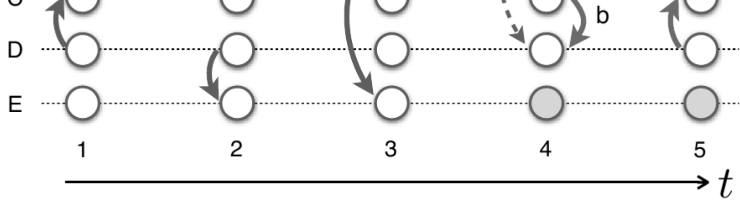


Figure 2. Infection model and adaptation mechanism. Nodes are arranged vertically with links between them for each day. Nodes can be in three states: susceptible, S (empty circles), undetected infected, $I^\star$ (yellow), and detected infected, I (red). After δ days, infected nodes are detected and for $t \in [t^\star + \delta, t^\star + \kappa]$ – with $t^\star$ being the time of infection – all out-going links from the detected nodes (red) are randomly rewired to other susceptible or undetected nodes as starting point, e.g. the link **a** is destroyed and instead the link **b** is created. After κ days, infected nodes recover.

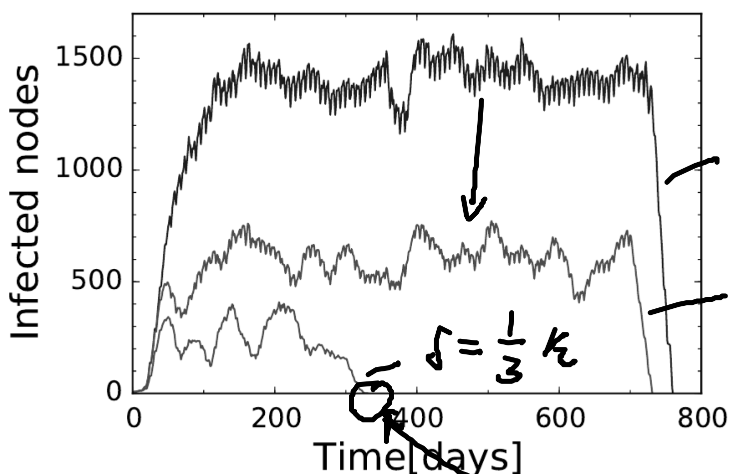


Figure 3. Typical time course of an epidemic. Prevalence (number of infected nodes, daily resolution) for a fixed infectious period $\kappa = 30$ d and different detection times δ: unadapted $\delta = \kappa$ (blue), adapted $\delta = 15$ d (red) and $\delta = 10$ d (green).

B10
SFB 910

Hövel:
Control of networks with time-varying topologies and applications to epidemiology

Goals and visions
→ Characteristics/analysis of time-dependent networks
→ Early detection of epidemics, identification of most influential nodes in spreading processes
→ Epidemic spreading on generic and real-world networks
→ Adaptation rules of the network to counteract epidemics

Compartmental model of disease spreading
Susceptible-Infected-Recovered (SIR)

$S \xrightarrow{\beta} I \xrightarrow{\gamma} R$

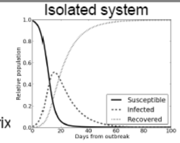
Transmission rate: β
Recovery rate: γ

$$\frac{dS_\mu}{dt} = -\beta S_\mu \frac{I_\mu}{N_\mu} + f^{(in)}_{S_\mu} - f^{(out)}_{S_\mu}$$
$$\frac{dI_\mu}{dt} = \beta S_\mu \frac{I_\mu}{N_\mu} - \gamma I_\mu + f^{(in)}_{I_\mu} - f^{(out)}_{I_\mu}$$
$$\frac{dR_\mu}{dt} = \gamma I_\mu + f^{(in)}_{R_\mu} - f^{(out)}_{R_\mu}$$

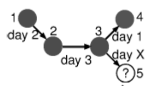
Coupling term → in and out fluxes:

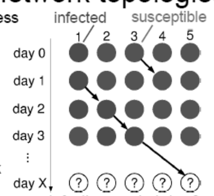
$$f^{(in)}_{S_\mu} = \varepsilon \sum_{\nu=1}^{n} a_{\mu\nu}(t) S_\nu, \qquad f^{(out)}_{S_\mu} = \varepsilon \sum_{\nu=1}^{n} a_{\nu\mu}(t) S_\mu$$

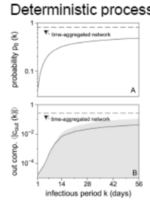
coupling strength (time-varying) adjacency matrix

Isolated system


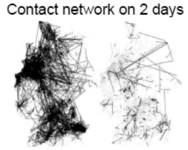
I. Empirical networks, deterministic processes

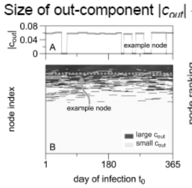
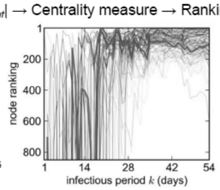
Time-varying network topologies
Schematic spreading process

State of node 5 depends on evolution of the network

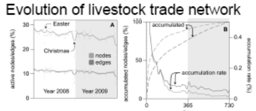

Infectious period: k = 3

Deterministic process: 100% chance of infection

Static networks overestimate probability p_0 of secondary infection and outbreak size $|c_{out}|$.

Network extraction and deterministic model
Data set: number of nodes > 100,000 (in 2 years) **B1** **B8** **B9**
aggregated number of edges = 267,702
daily mean = 4929
Data source: *Herkunfts- und Informationssystem Tier* (HI-Tier)

Contact network on 2 days


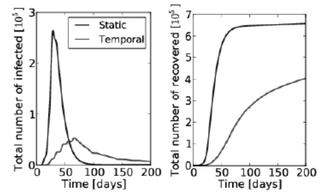
Size of out-component $|c_{out}|$ → Centrality measure → Ranking



Evolution of livestock trade network


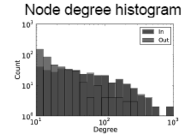
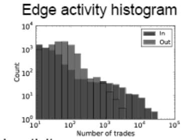
Sensitive dependence of out-component on day of primary infection t_0 and infectious period k
Konschake, Lentz, Conraths, Hövel, and Selhorst, PLoS ONE 8, e55223 (2013).

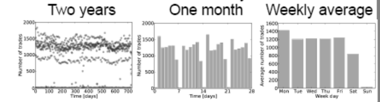
Experimental collaborations
Thomas Selhorst (Friedrich-Loeffler-Institut): data acquistion of livestock trade
Albert-László Barabási (Northeastern University): network science, controllability
Carlo Ratti (Massachusetts Institute of Technology): mobility networks, network analysis

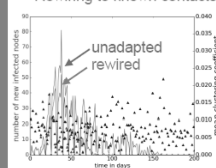
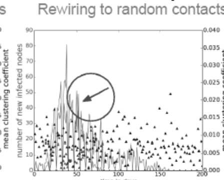
II. Numerical modeling of spreading diseases

Dynamics on temporal networks
Simulation of SIR model on empirical networks **B8**


$\beta = 1$, $N_\mu(0) = 100$, → Slower increase
$\gamma = 0.1$, $S_\mu(0) = 100$, → Smaller/later peak
$\varepsilon = 10^{-4}$, $S_1(0) = 99$ → Longer decay
$n = 3218$, ← number of nodes

Network diagnostics **B1** **B8** **B9**
Node degree histogram

Edge activity histogram


Network activity
Two years / One month / Weekly average


Control of dynamics and adaptation rules
Rewiring to known contacts

Rewiring to random contacts

→ Reduction/Increase of outbreak size

Control concepts:
→ Adaptive control: **A1**
Selivanov, Lehnert, Dahms, Hövel, Fradkov, Schöll, Phys. Rev. E (2012).
→ Controllability of networks **A4**
→ Temporal response of network **A9**

BSc thesis: Florian Fiebig (co-supervised by S. Yanchuk, **A3**)

Role within Collaborative Research Center

Biological systems and contagion processes as applications of control of temporal networks extracted from empirical, real-world datasets.
Collaboration and overlap with projects of groups A and B:
adaptive control **A1**, spatio-temporal delay systems **A3**, observation and control of networks **A4**
time-varying coupling with hysteresis **A9**, analysis of complex networks **B1** **B8** **B9**