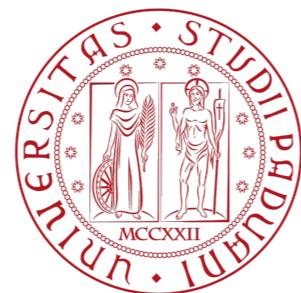


# Diversity in humans and pathogens: implications for the dynamics of epidemics and the impact of interventions

Chiara Poletto

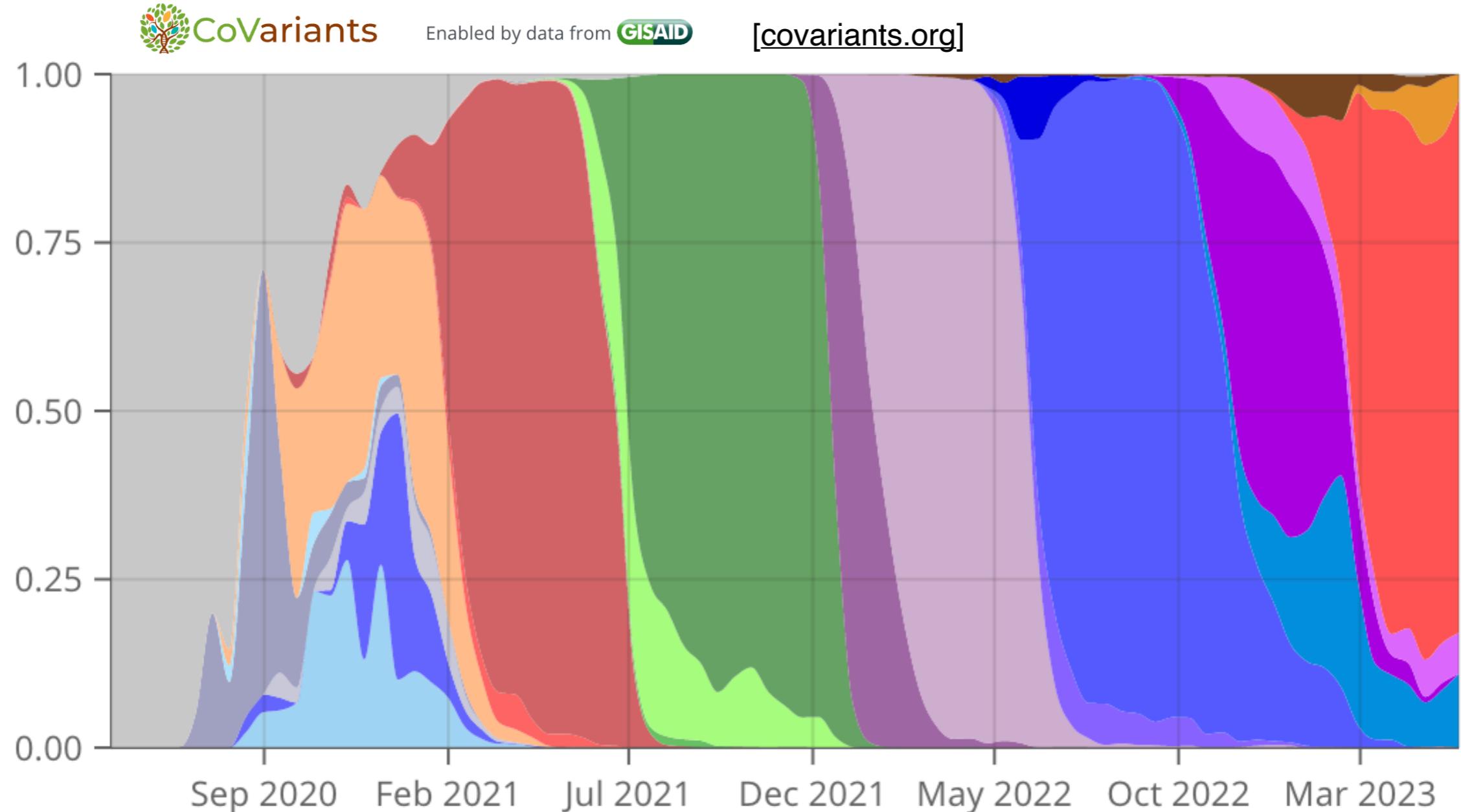
[chiara-poletto.github.io](https://chiara-poletto.github.io)  
[@chpoletto](https://twitter.com/chpoletto)



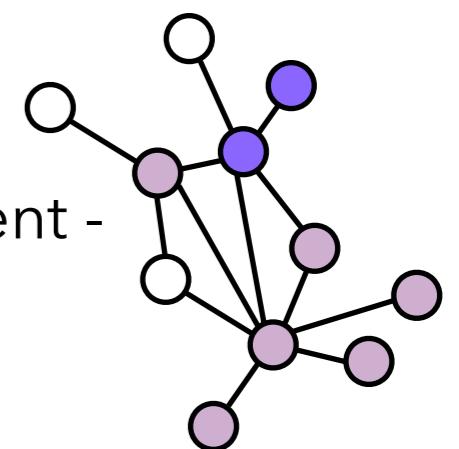
Institut Pierre Louis d'Épidémiologie et de Santé Publique  
Pierre Louis Institute of Epidemiology and Public Health

**Unifying the epidemiological and evolutionary  
dynamics of pathogens - Nordita - 13 June 2023**

# patterns of strain co-circulation



strain traits - strain interaction - host heterogeneities - treatment - vaccination - **contact/spatial structure**

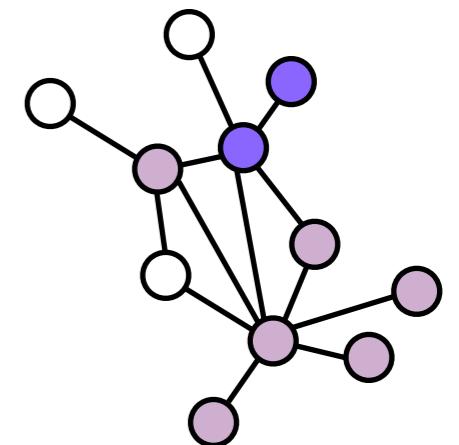


# patterns of strain co-circulation

contact and mobility  
networks determine the  
pattern of strain emergence

resident strains *alter* the  
network substrate

depending on hosts'  
interaction time-scale,  
either one of the two  
strains is advantaged



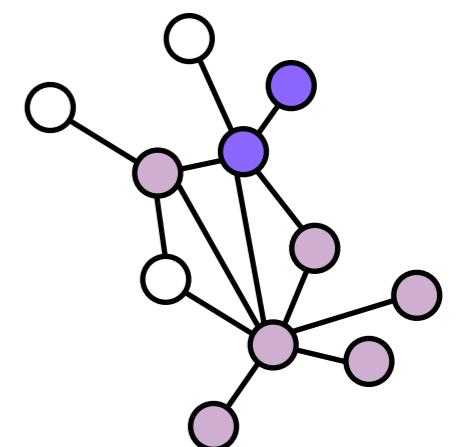
# patterns of strain co-circulation

contact and mobility  
networks determine the  
pattern of strain emergence

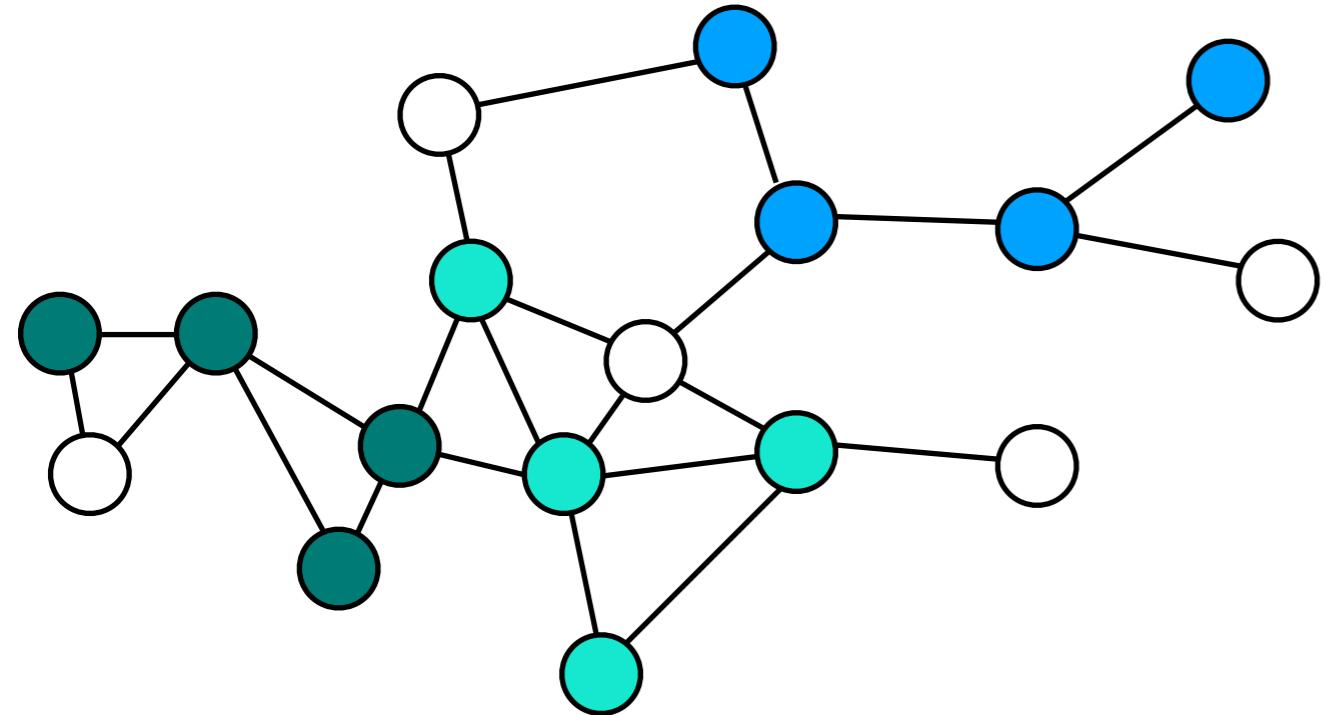
resident strains *alter* the  
network substrate

depending on hosts'  
interaction time-scale,  
either one of the two  
strains is advantaged

[Poletto et al PLoS  
Comp Biol 2013; Poletto  
et al Sci Rep 2015]

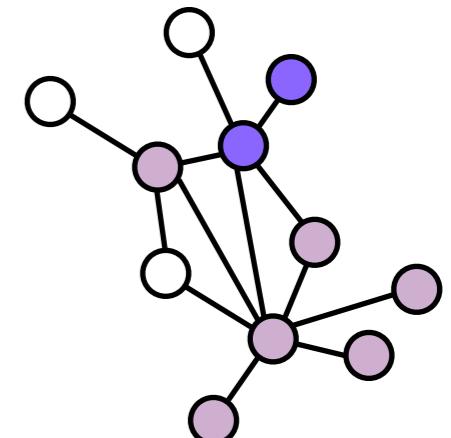


# patterns of strain co-circulation



# **resident strains alter the network substrate**

strain responsible for past infections/  
resident strain/ fastest strain occupies a  
portion of nodes  
*emerging spread on a residual network*



# patterns of strain co-circulation

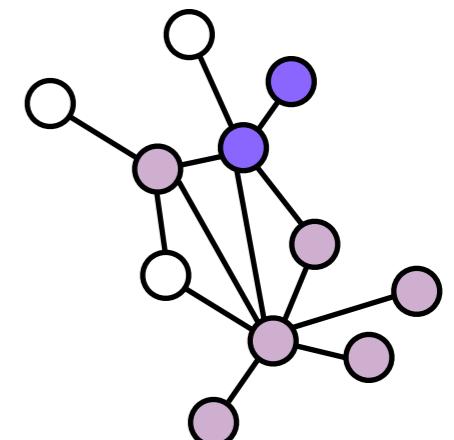


ecology of many strains on a network

[F. Pinotti, É. Fleury, D. Guillemot, P.-Y. Böelle, C. Poletto,  
PLoS Computational Biology 15(5) 2019]

[F. Pinotti et al in preparation]

**resident strains alter  
the network substrate**



# emergence/dominance/co-existence of *S aureus* strains

contact spatial structure in hospitals:

- small population  
(strong stochastic effects)
- high patient turn-over  
(strain introduction from the outside)
- ward composition
- host heterogeneities  
(patients/health care workers)

[Kouyos et al, PLOS Pathogens 2013; Kouyos et al PLOS Pathogens 2011; Cooper et al, PLOS Comput Biol 2012; Bonten et al CID 2001]



# emergence/dominance/co-existence of *S aureus* strains

contact spatial structure in hospitals:

- small population  
(strong stochastic effects)
- high patient turn-over  
(strain introduction from the outside)
- ward composition
- host heterogeneities  
(patients/health care workers)



[Kouyos et al, PLOS Pathogens 2013; Kouyos et al PLOS Pathogens 2011; Cooper et al, PLOS Comput Biol 2012; Bonten et al CID 2001]

## network data: face-to-face contacts / patient transfer

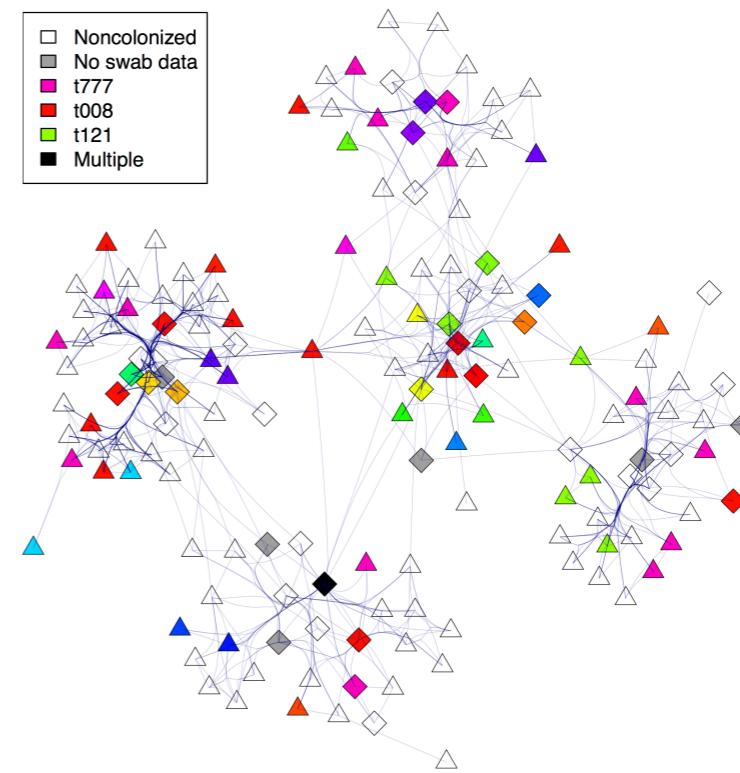
[Liljeros et al Math Popul Stud 2007; Obadia et al. PLOS Comput Biol 2015; Isella et al PLoS ONE 2011; Donker et al PLoS ONE 2012; Nekkab et al PLOS Comput Biol 2017 ]

# Individual-Based Investigation of Resistance Dissemination (I-Bird)

- long term health care facility
- 5 wards
- duration 4 months

## Close Proximity Interaction data

- RFID technology
- 329 Patients - 261 Health-Care-Workers
- temporal resolution 30s



# Individual-Based Investigation of Resistance Dissemination (I-Bird)

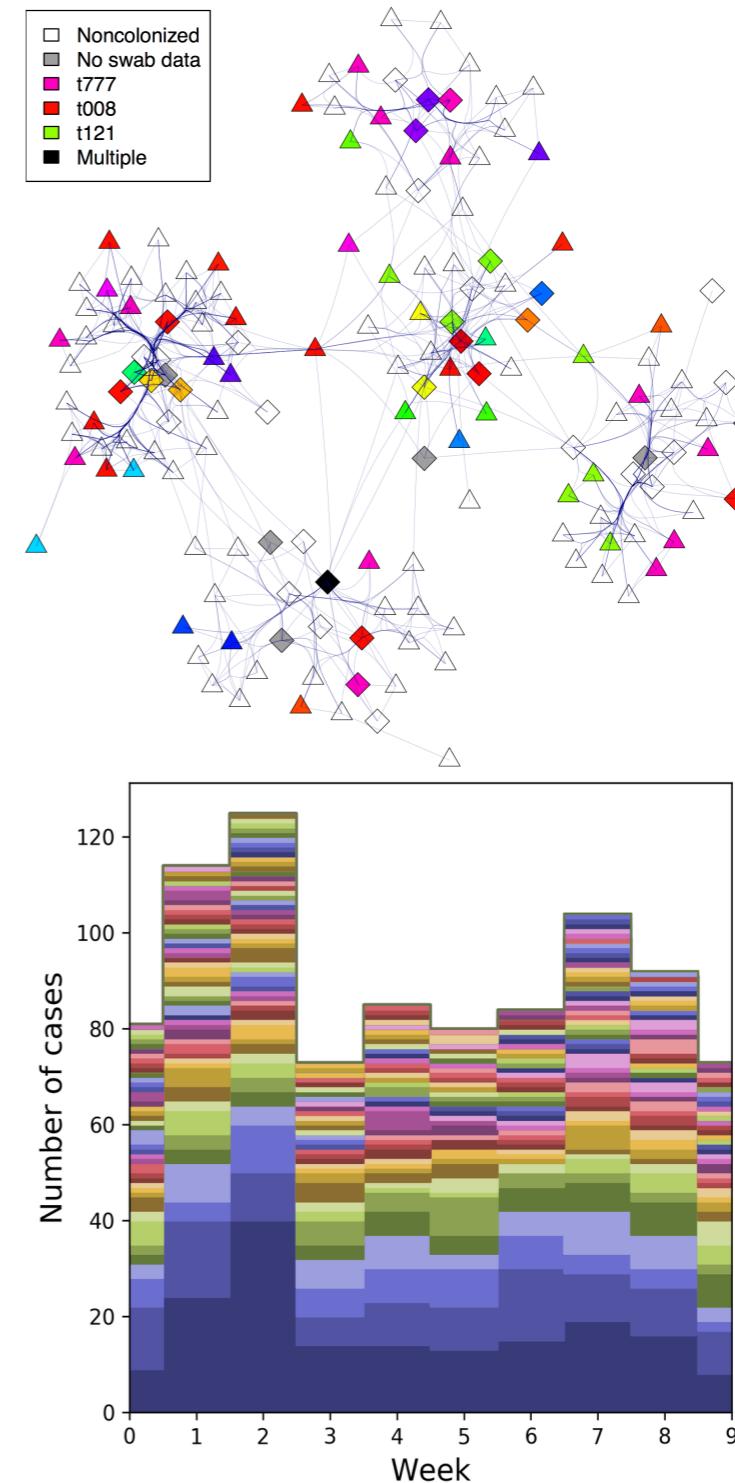
- long term health care facility
- 5 wards
- duration 4 months

## Close Proximity Interaction data

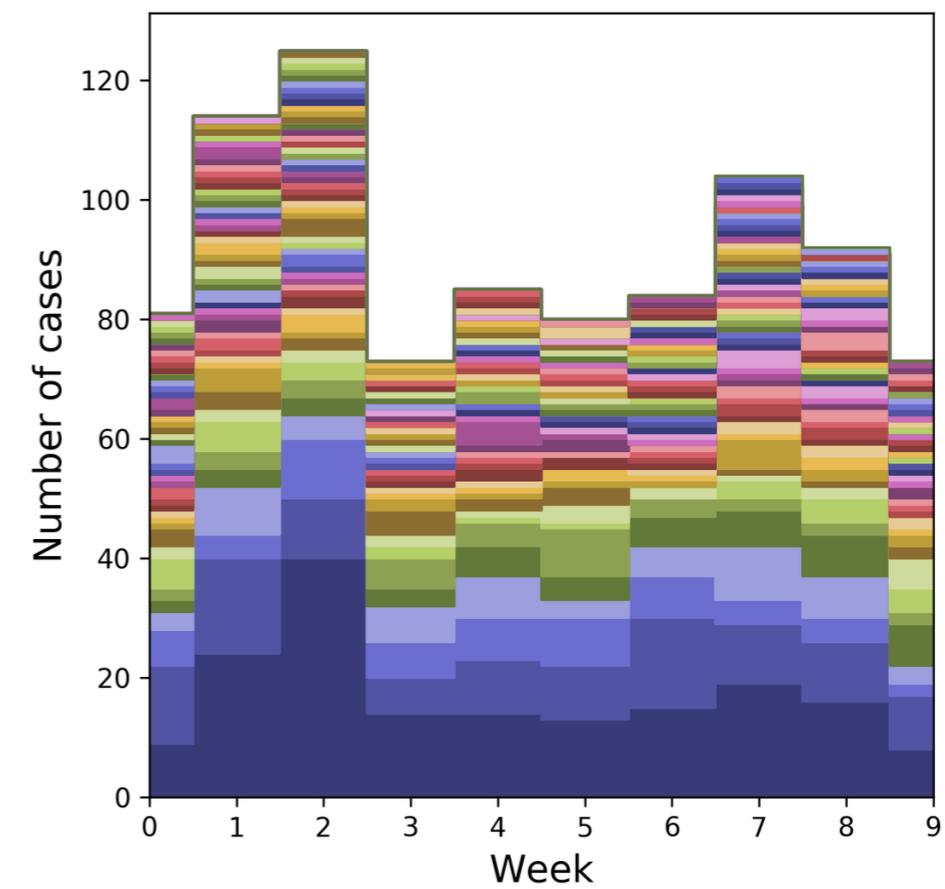
- RFID technology
- 329 Patients - 261 Health-Care-Workers
- temporal resolution 30s

## Colonisation

- weekly nasal swabs
- colonisation of *S. aureus*
- information of spa type + resistance profile

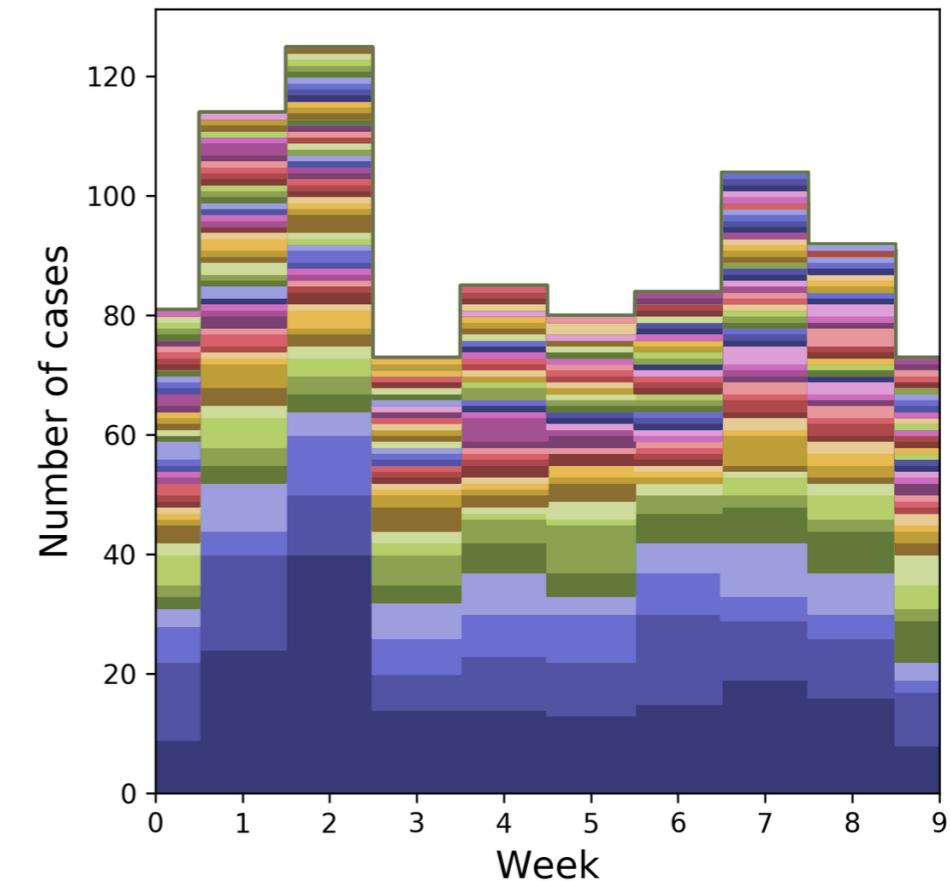
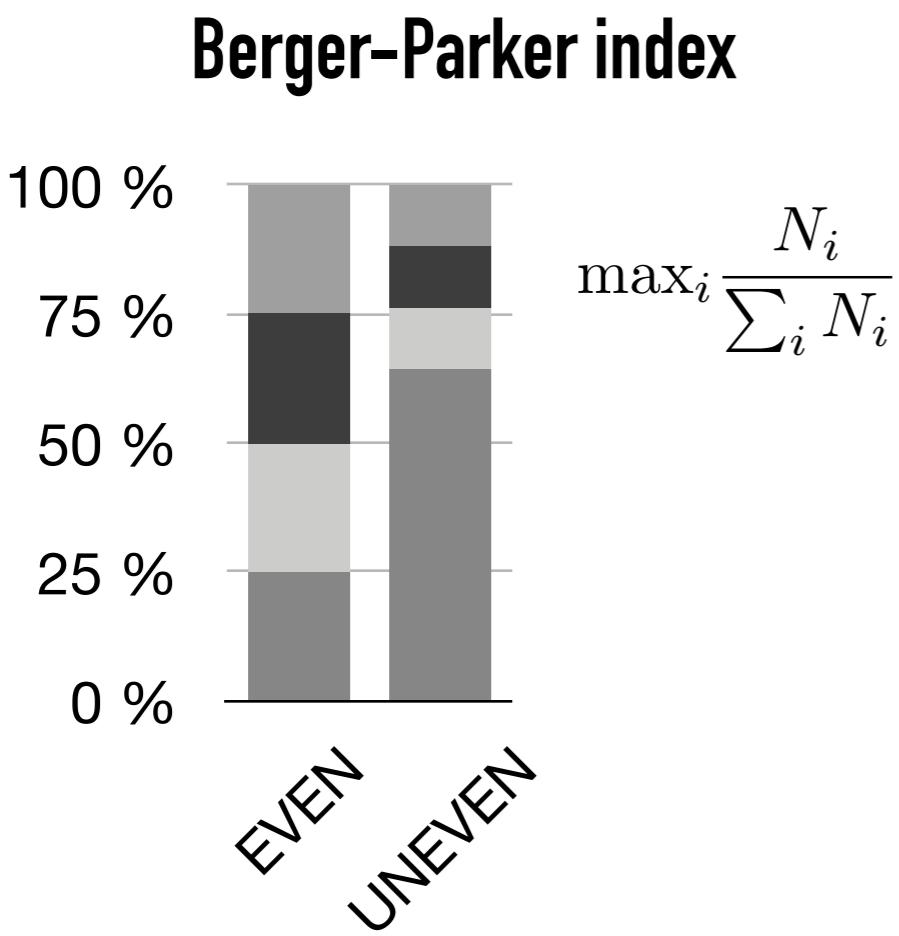


# ecological indicators



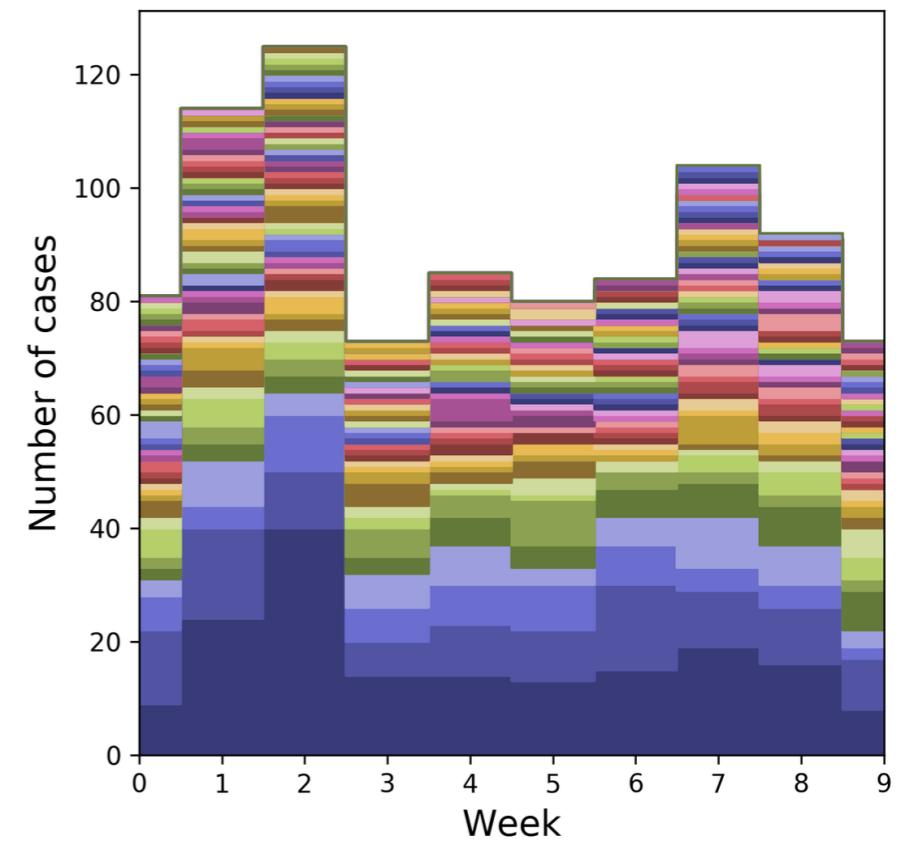
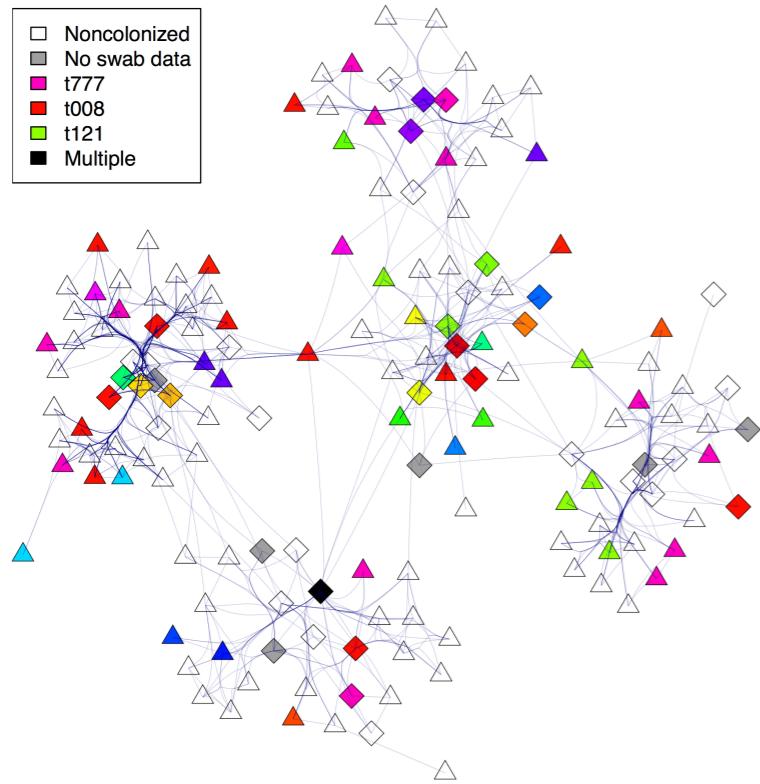
- prevalence
  - richness : # strains
  - evenness/dominance

# ecological indicators



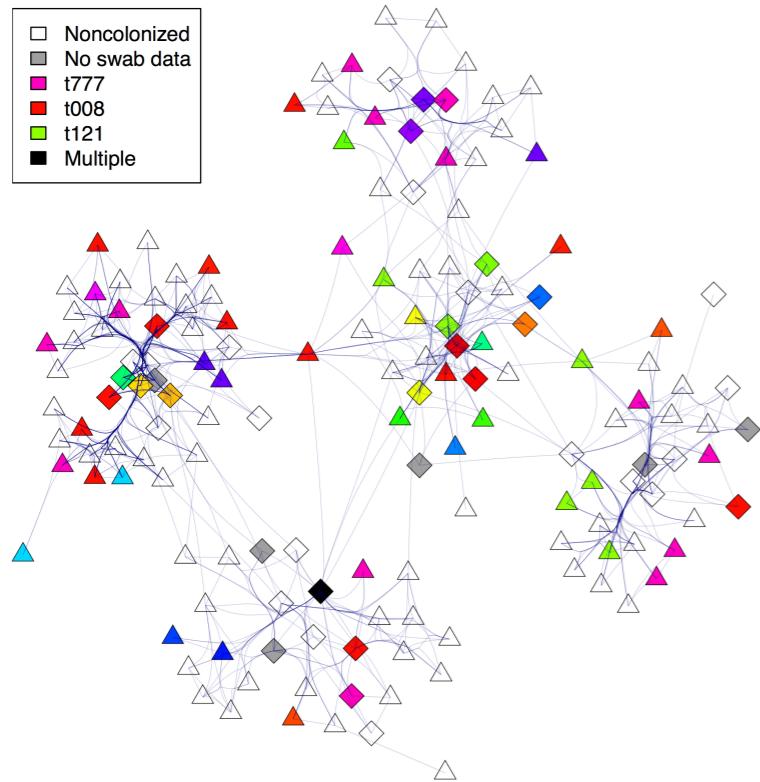
- prevalence
- richness : # strains
- evenness/dominance

# *S. aureus* spread in hospitals



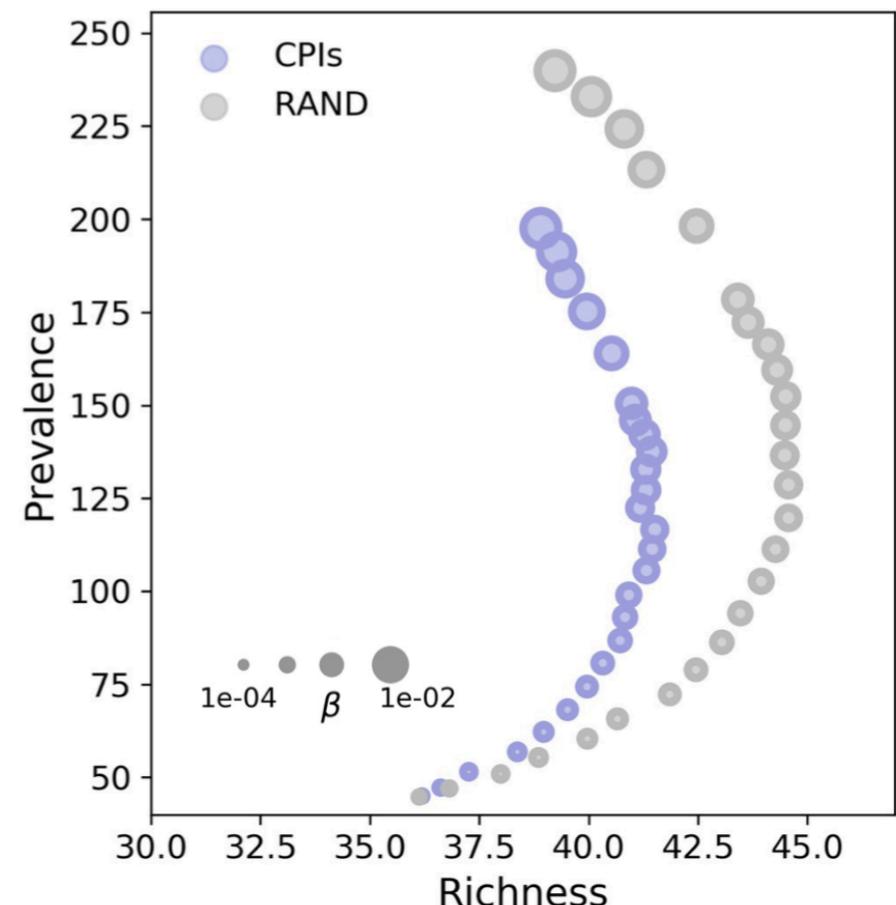
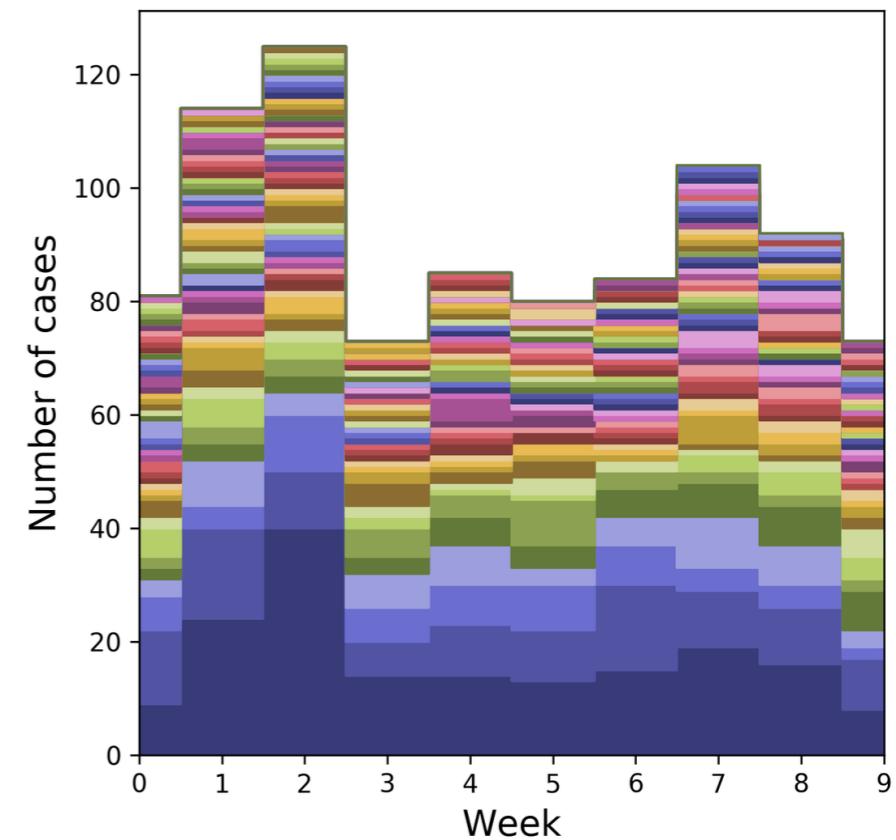
- multi-strain SIS model as simple model of *S. aura* colonisation
- mutual exclusion
- strain injection
- neutral hypothesis: strains have same transmissibility and duration of colonisation
- simulation on the CPIs network
- compare with a randomisation (RAND)

# *S. aureus* spread in hospitals

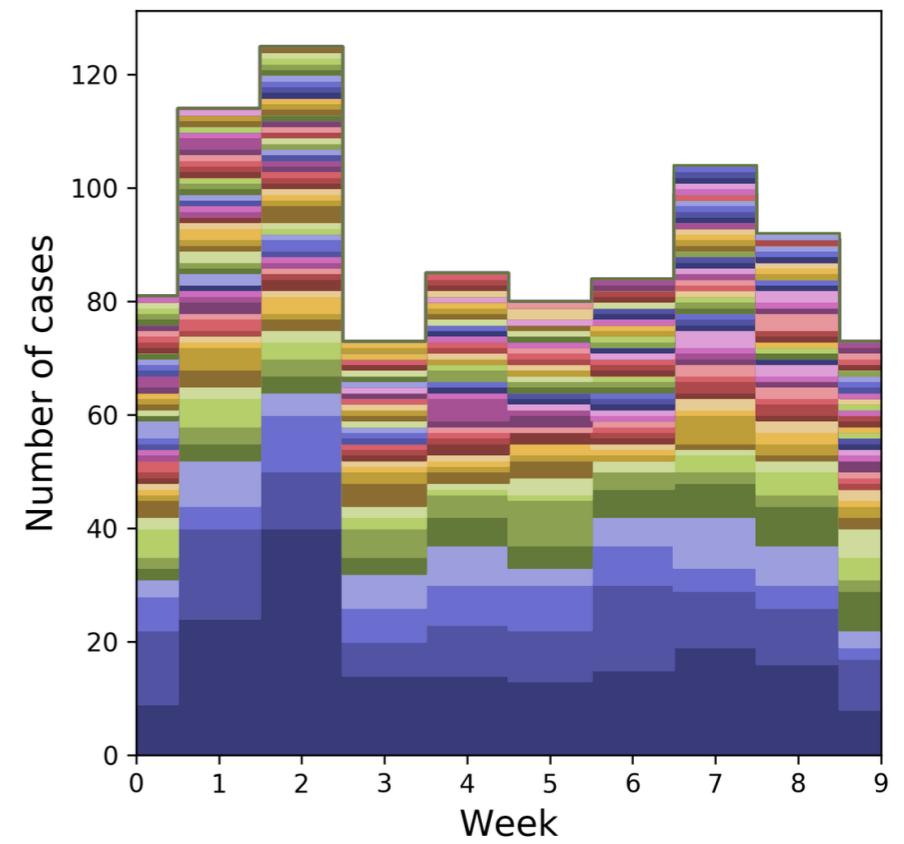


- multi-strain SIS model as simple model of *S. aurea* colonisation
- mutual exclusion
- strain injection
- neutral hypothesis: strains have same transmissibility and duration of colonisation
- simulation on the CPIs network
- compare with a randomisation (RAND)

[Pinotti et al, PLoS Comp Biol, 2019 ]



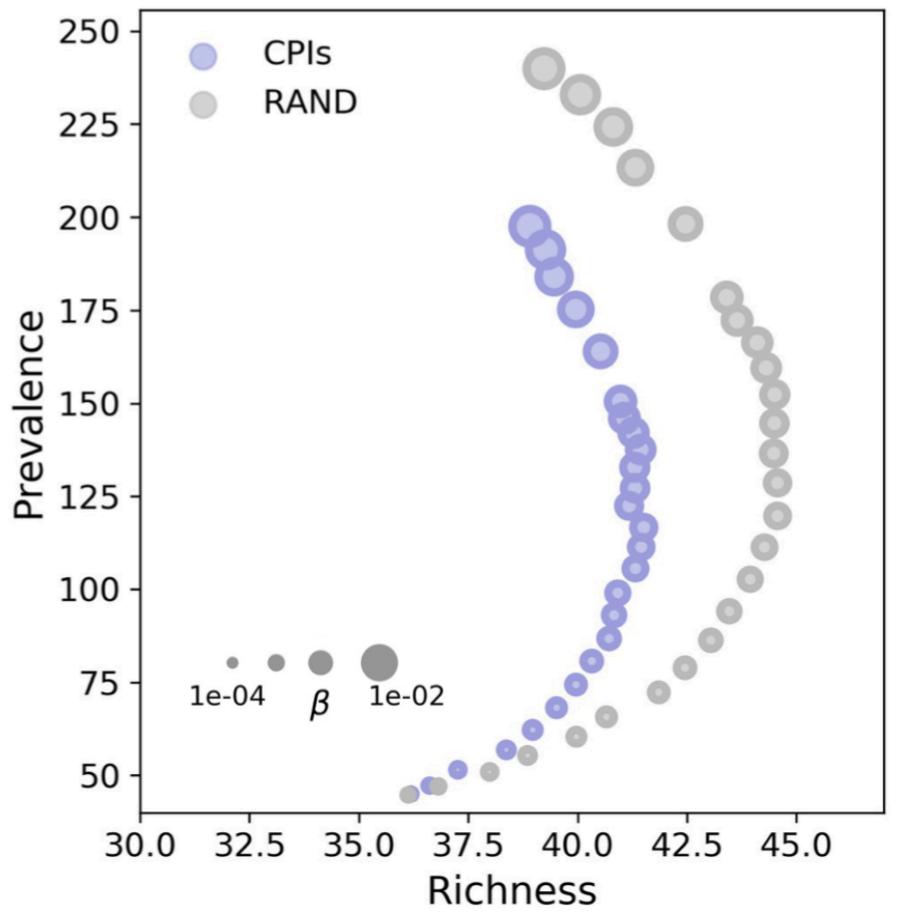
# *S. aureus* spread in hospitals



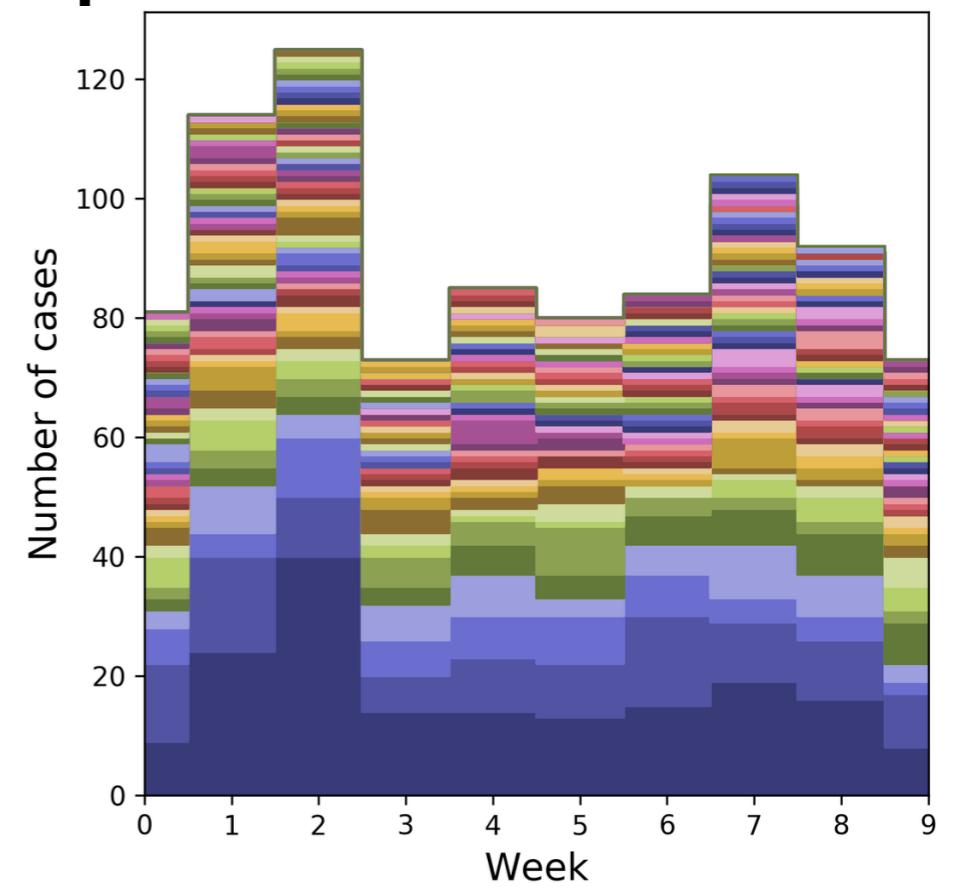
## **richness and prevalence**

Comparison between RAND and CPIs done at same parameters

**CPIs has smaller richness at same prevalence**



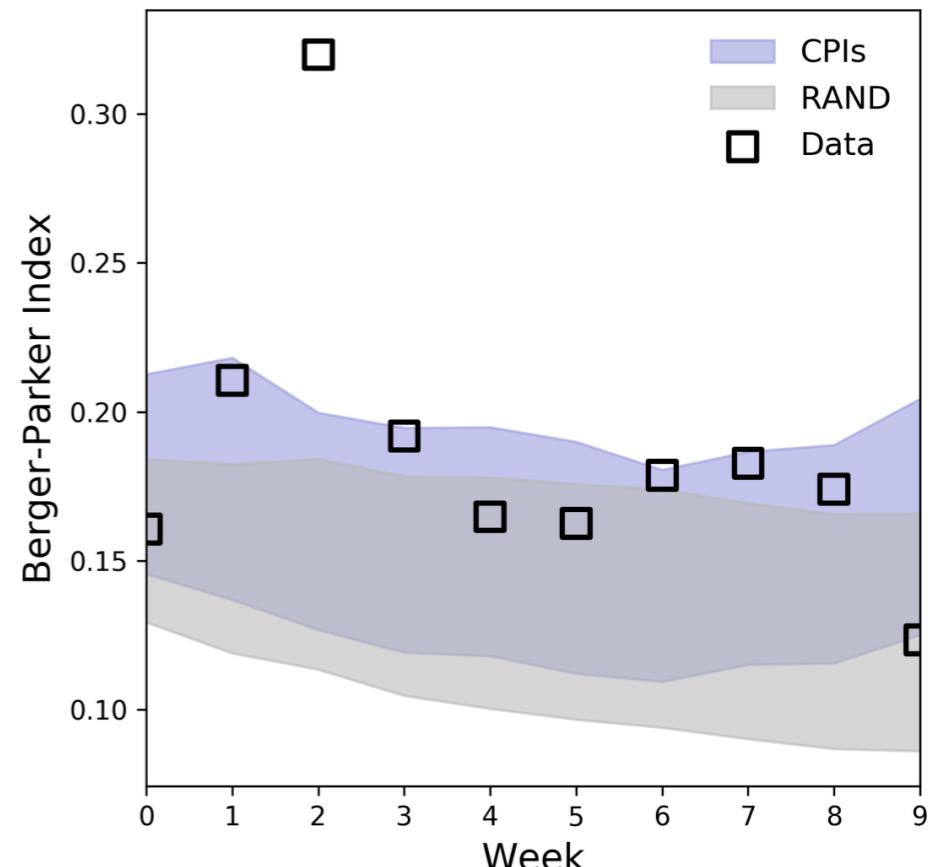
# *S. aureus* spread in hospitals



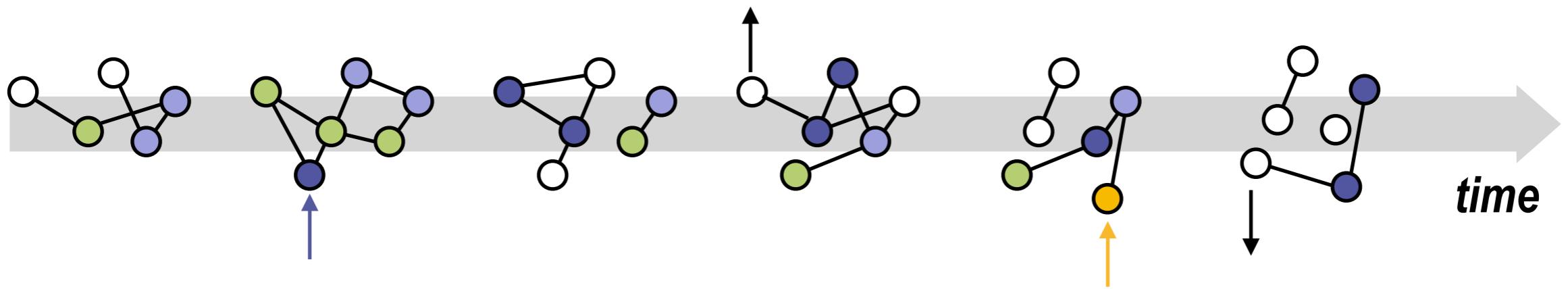
## **dominance**

Comparison between RAND and CPIs done at same richness and prevalence

***CPIs has stronger dominance***

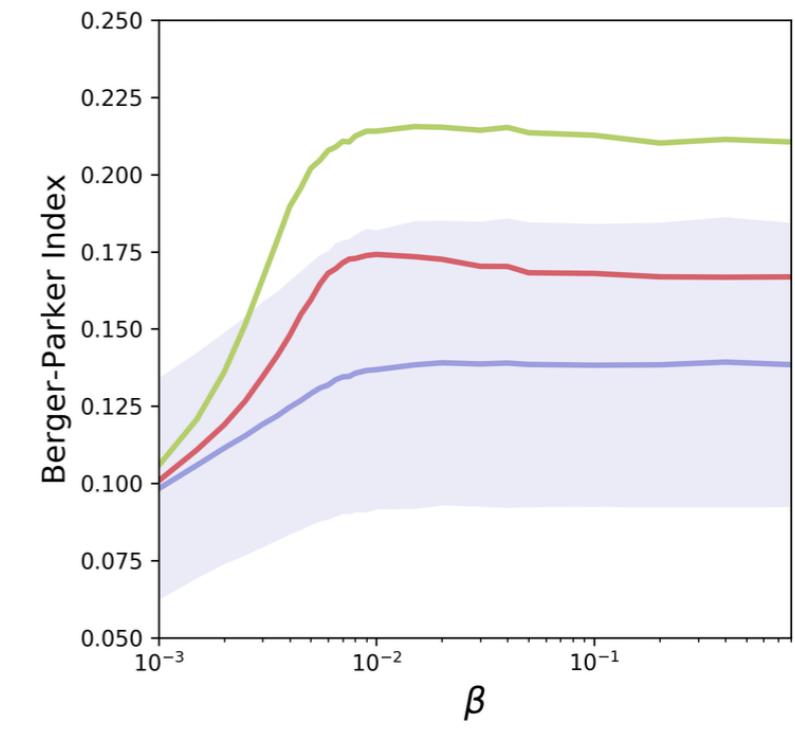
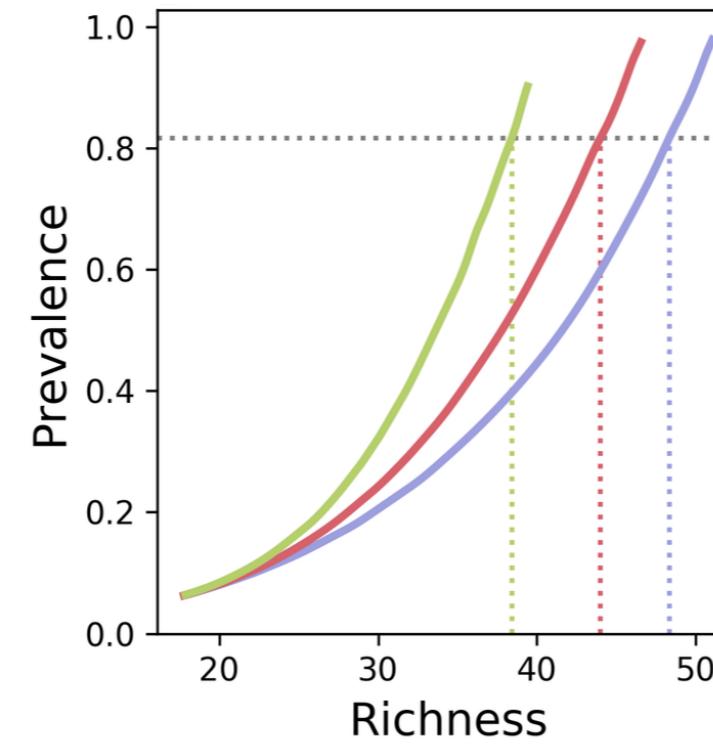
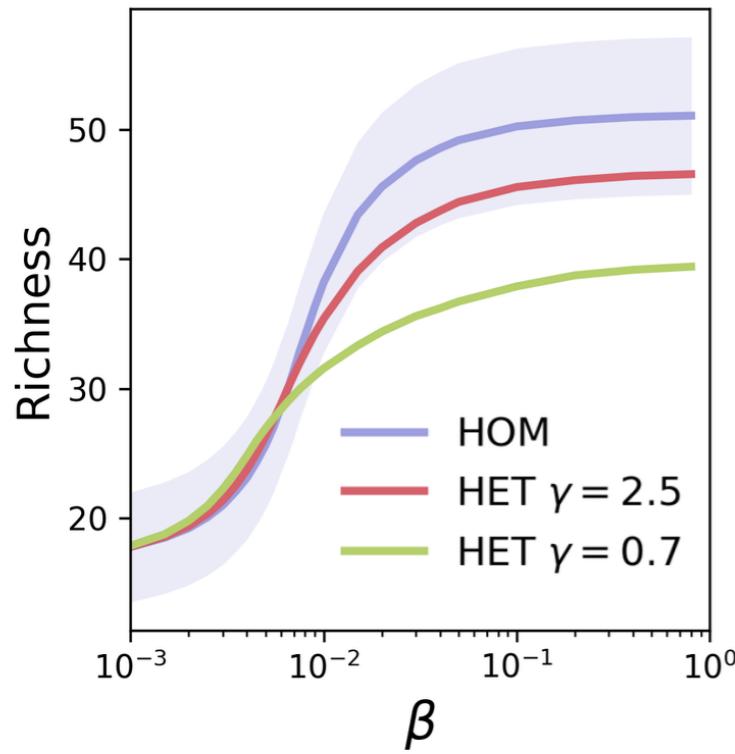
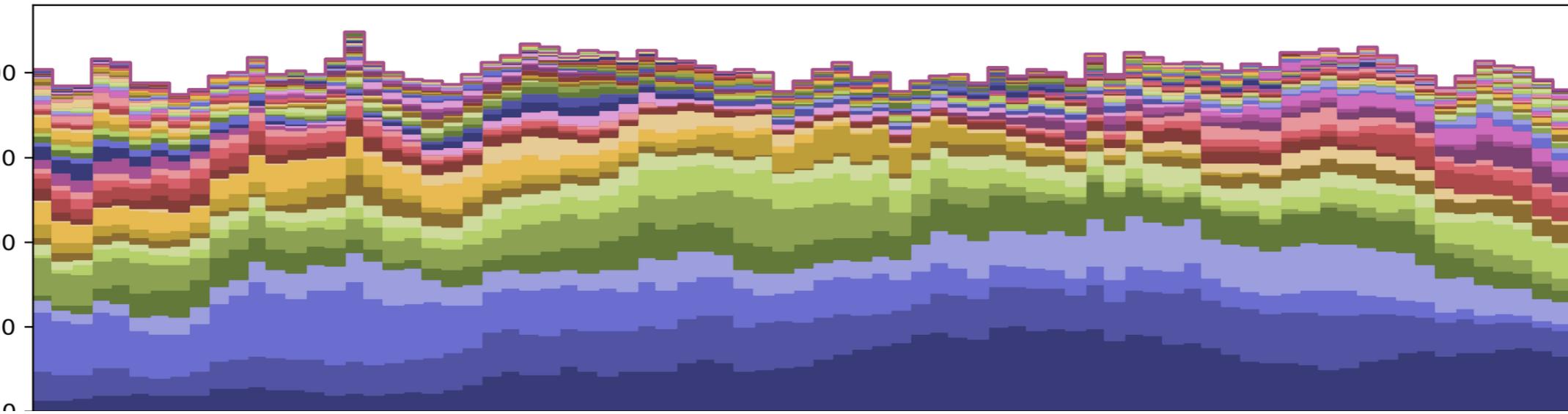


# synthetic network model



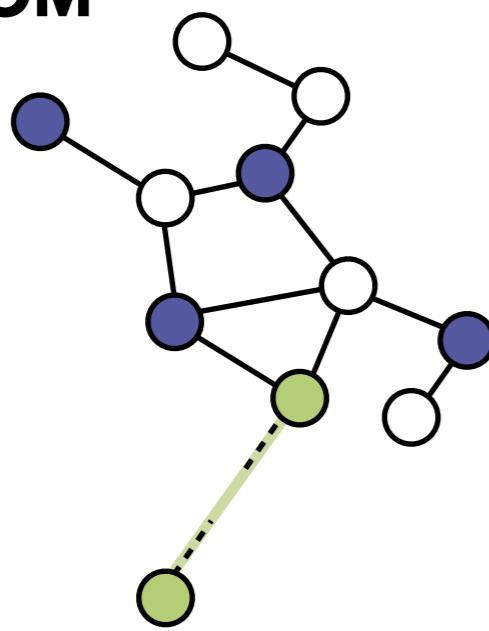
- nodes entering and leaving
- community structure
- forming contacts
  - **HET** heterogeneous activity
  - **HOM** homogeneous activity

# impact of heterogeneous contact activity

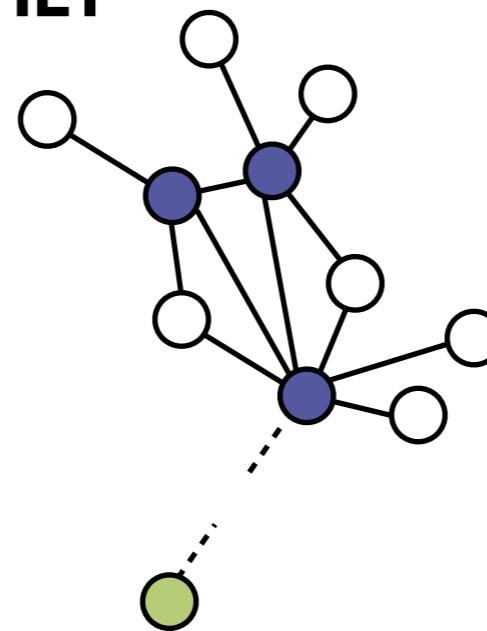


# impact of heterogeneous contact activity

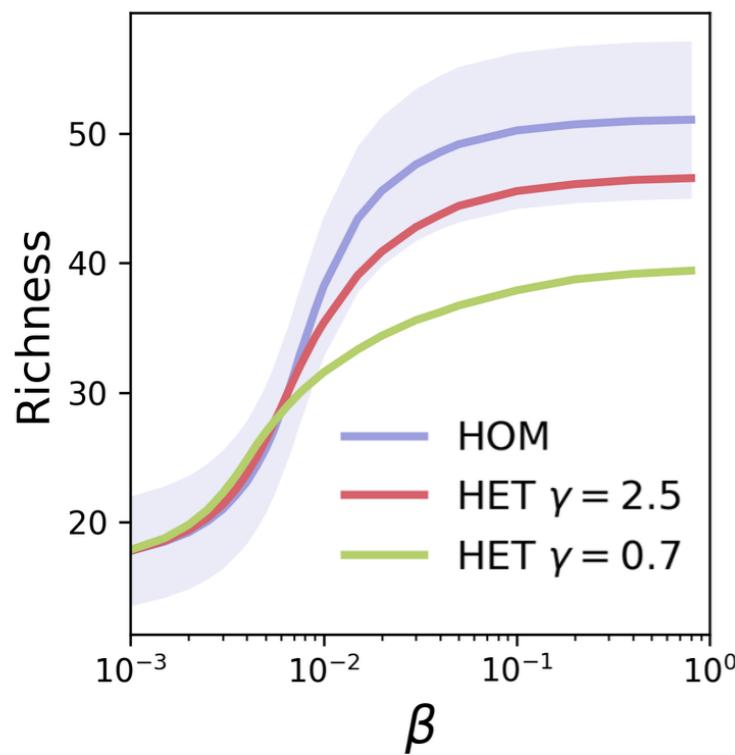
HOM



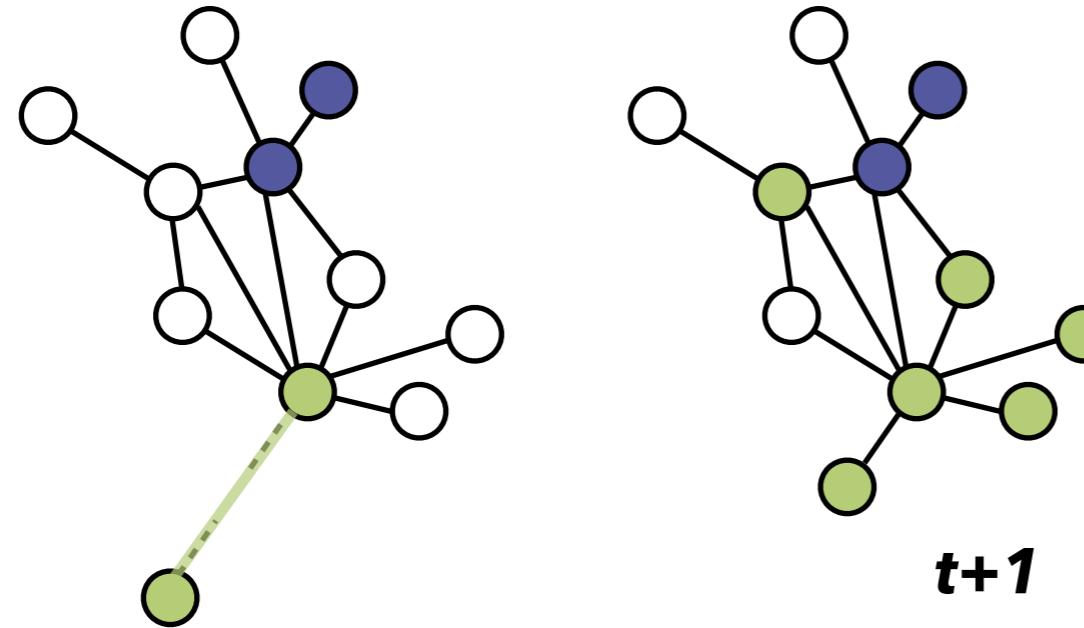
HET



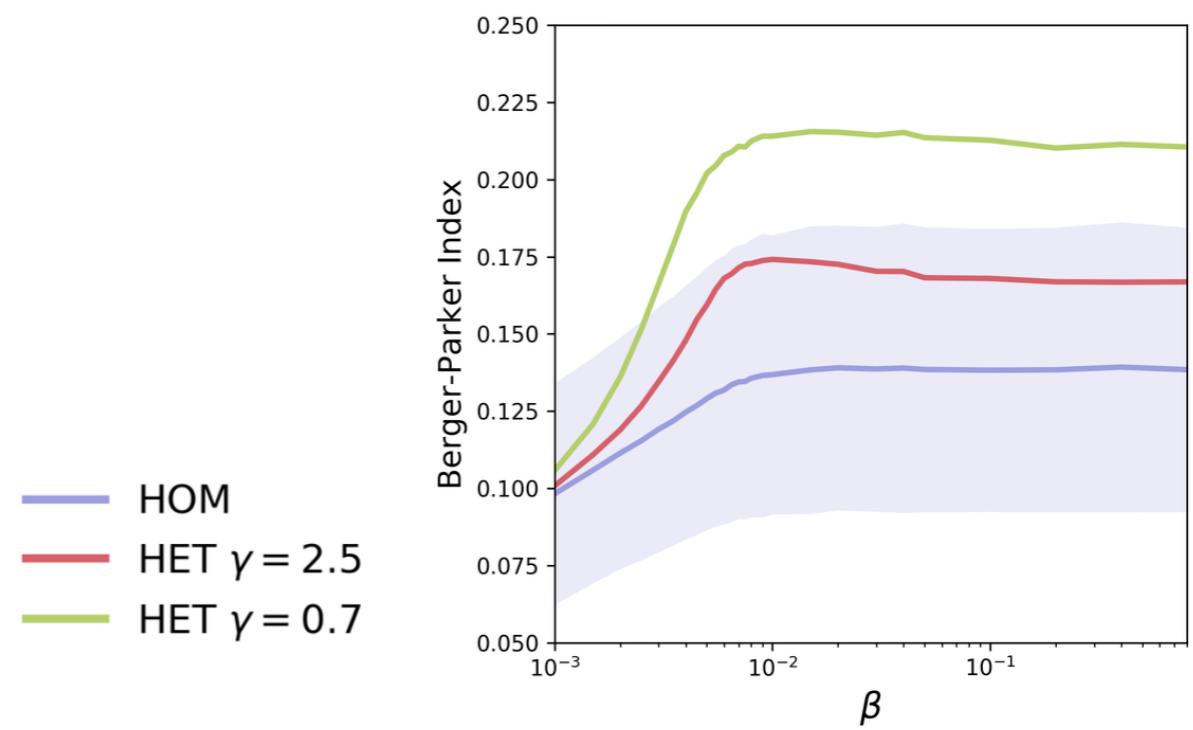
highly active nodes act  
as ***super-blocker***  
hinder the emergence  
of a strain  
[Leventhal et al. Nat Comm 2015]



# impact of heterogeneous contact activity



highly active nodes act  
as ***super-spreader***  
enhance the spread of  
few lucky strains



# Conclusions

- ecological perspective to characterise strain population
- contact heterogeneities:
  - hinder the introduction of strains from the outside [Leventhal et al Nature Comm 2015]
  - amplify certain strains, making outbreaks more likely
- importance of contact network to properly interpret ecological data

# ack:

Francesco Pinotti  
Pierre-Yves Boëlle  
Éric Fleury  
Didier Guillemot  
Benjamin Faucher  
Chiara E.lisa Sabbatini

Peter Czuppon  
Moritz U.G. Kraemer  
Philippe Lemey  
Vittoria Colizza  
Francois Blanquart,

# ref:

F. Pinotti, É. Fleury, D. Guillemot, P.-Y. Böelle, C. Poletto,  
PLoS Computational Biology 15(5) 2019

@chpoletto

[chiara-poletto.github.io](https://chiara-poletto.github.io)

