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Epidemic spreading under exploration & preferential return mobility

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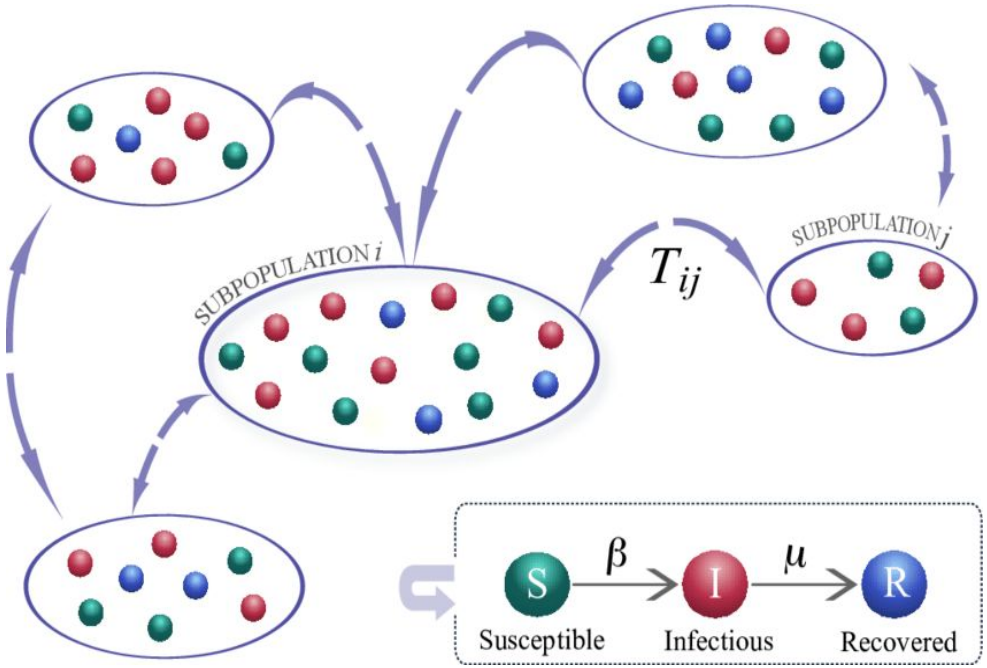
東京都、日本
８月７日・８月１１日「２０２３年」

Background: Epidemics on Metapopulations



Metapopulation scheme [from Ventura et al. (2022)]

Mobility models (typically) assume:

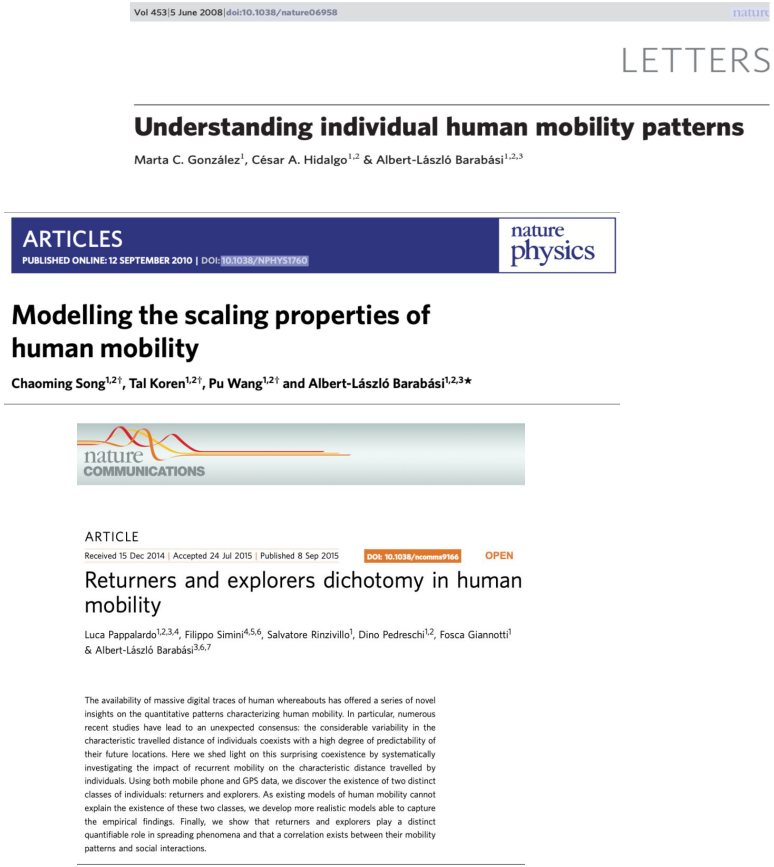
- Markovian random walks.
- Indistinguishable agents.

Background: Advances in human mobility

- Last decade: Exploration and preferential return models.

- Analysis of human mobility datasets reveal two main types of behaviors:

EXPLORERS & **RETURNERS**



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LETTERS

Understanding individual human mobility patterns

Marta C. González[1], César A. Hidalgo[1,2] & Albert-László Barabási[1,2,3]

ARTICLES
PUBLISHED ONLINE: 12 SEPTEMBER 2010 | DOI: 10.1038/NPHYS1760
nature physics

Modelling the scaling properties of human mobility

Chaoming Song[1,2†], Tal Koren[1,2†], Pu Wang[1,2†] and Albert-László Barabási[1,2,3*]

nature COMMUNICATIONS

ARTICLE

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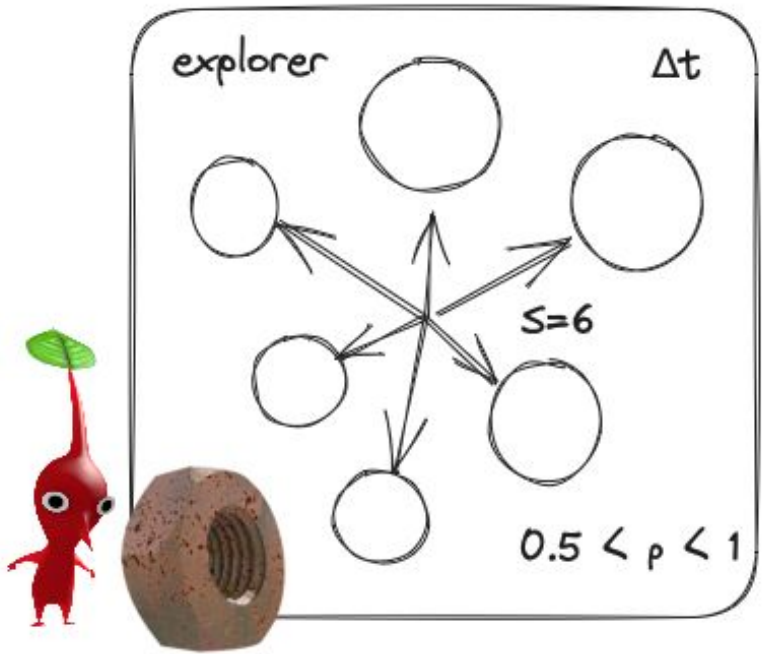
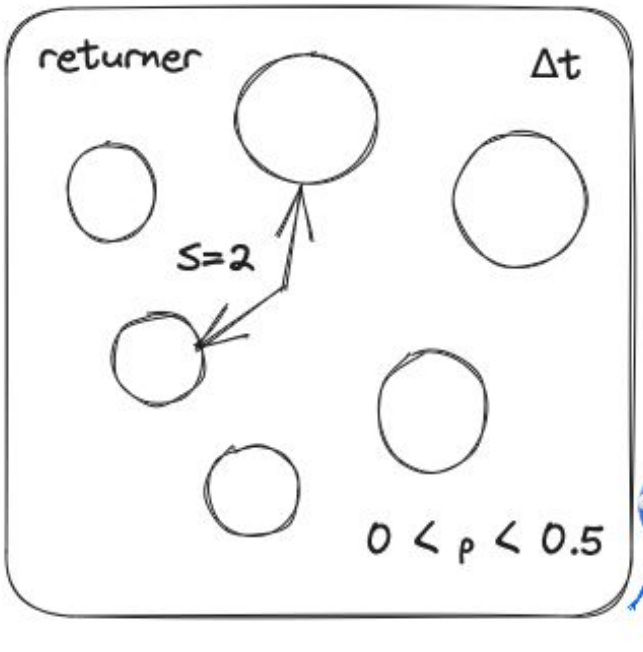
Returners and explorers dichotomy in human mobility

Luca Pappalardo[1,2,3,4], Filippo Simini[4,5,6], Salvatore Rinzivillo[1], Dino Pedreschi[1,2], Fosca Giannotti[1] & Albert-László Barabási[3,6,7]

The availability of massive digital traces of human whereabouts has offered a series of novel insights on the quantitative patterns characterizing human mobility. In particular, numerous recent studies have lead to an unexpected consensus: the considerable variability in the characteristic travelled distance of individuals coexists with a high degree of predictability of their future locations. Here we shed light on this surprising coexistence by systematically investigating the impact of recurrent mobility on the characteristic distance travelled by individuals. Using both mobile phone and GPS data, we discover the existence of two distinct classes of individuals: returners and explorers. As existing models of human mobility cannot explain the existence of these two classes, we develop more realistic models able to capture the empirical findings. Finally, we show that returners and explorers play a distinct quantifiable role in spreading phenomena and that a correlation exists between their mobility patterns and social interactions.

Explorers & returners

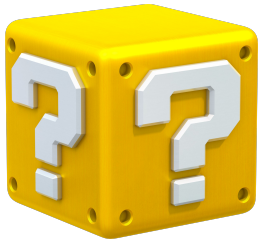




High exploration probability,
High S -> Low visit frequency

Low exploration probability,
Low S -> High visit frequency

Our work

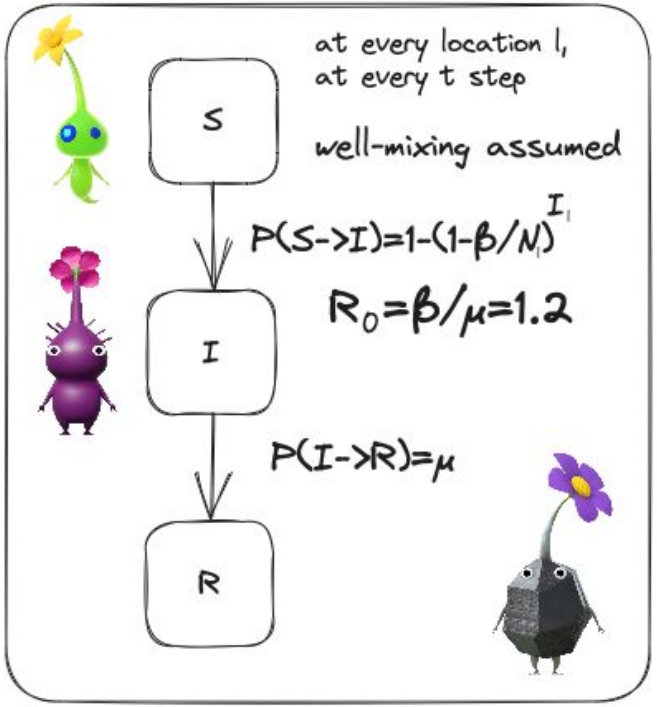


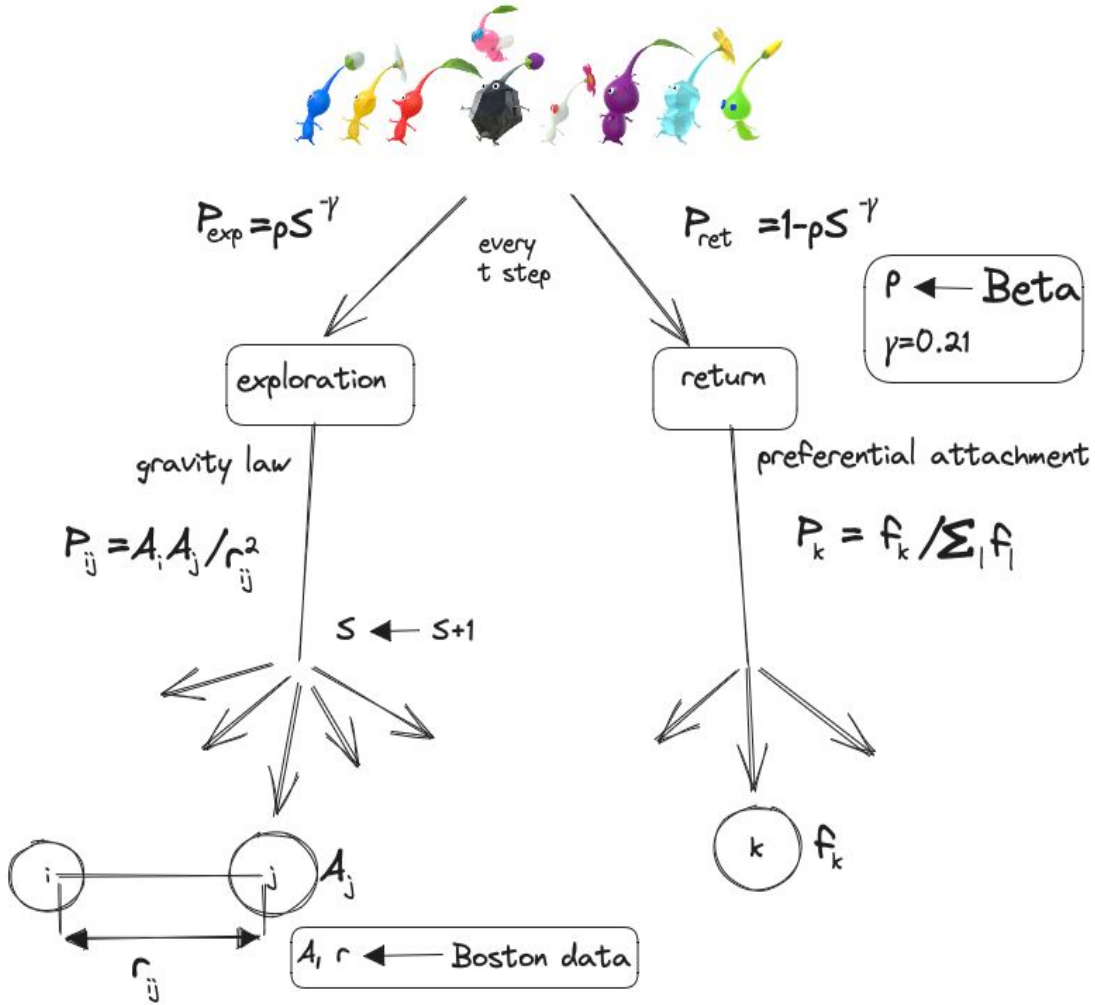
- Literature mentions the relevance of these discoveries to epidemics, but have not been thoroughly explored.

- Explore & characterize an epidemic spreading under an EPR mobility model.

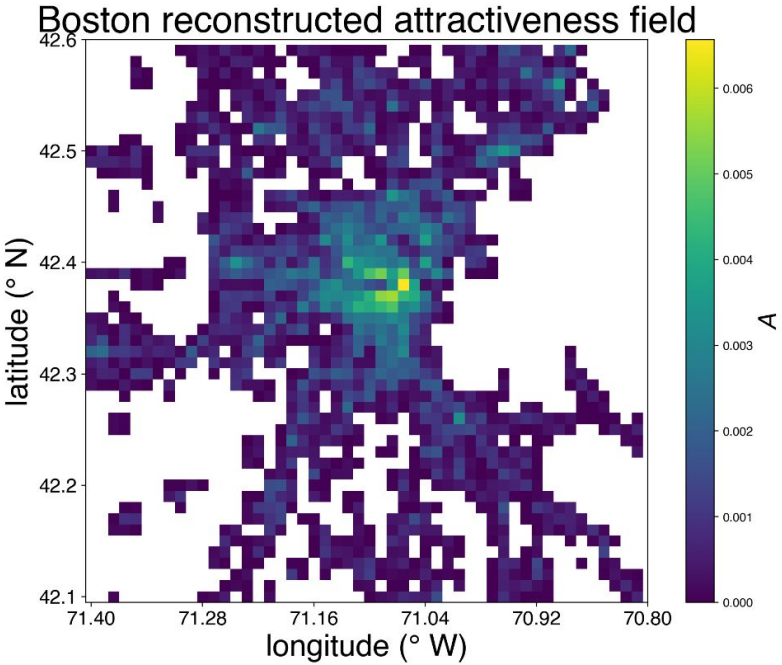
- Determine the role of explorers & returners in the spreading of an epidemic disease

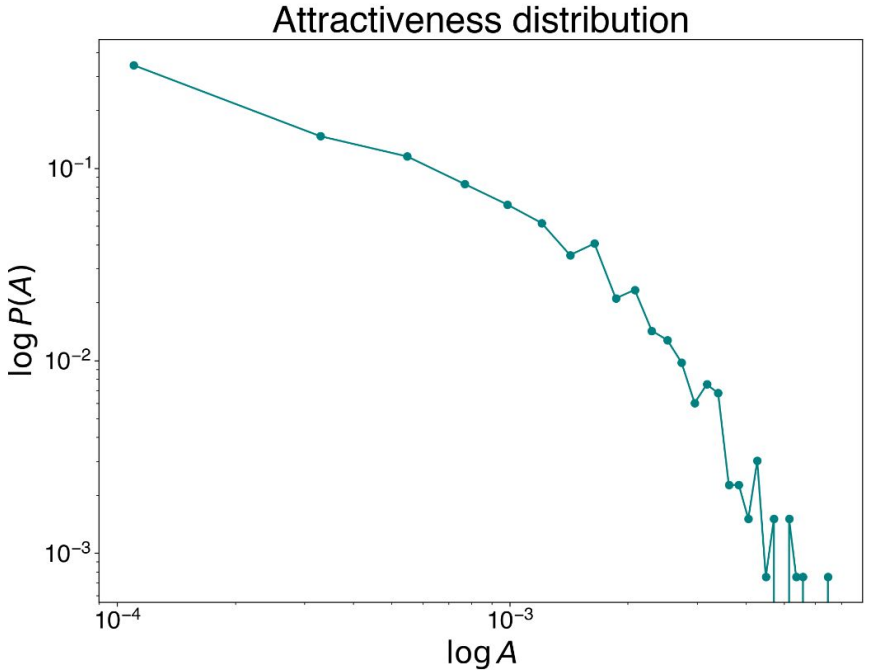
SIR model
+ d-EPR model





Spatial structure: Locations' attractiveness

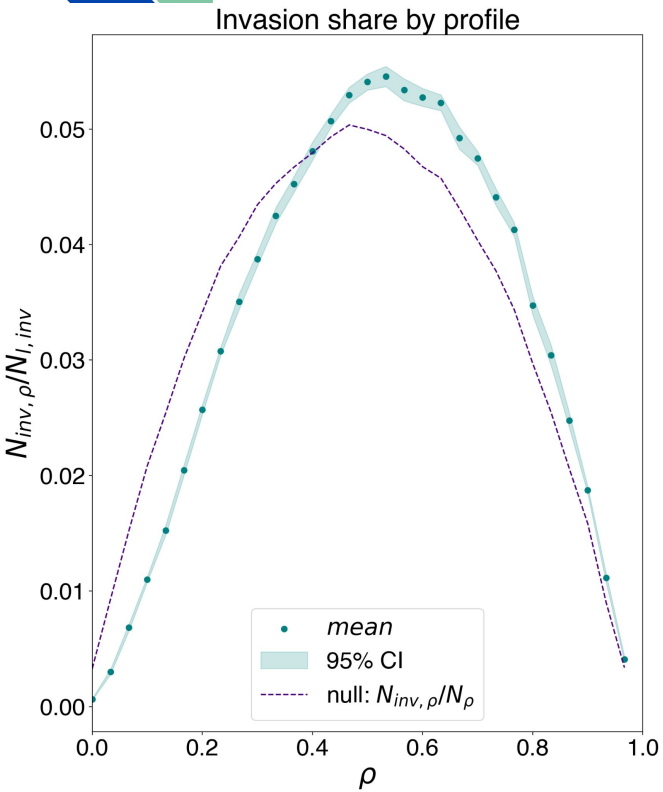


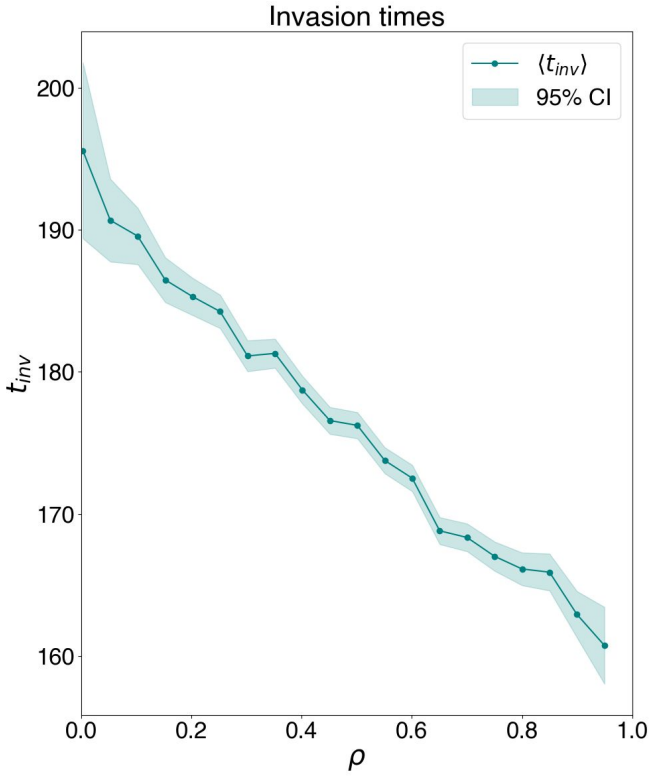


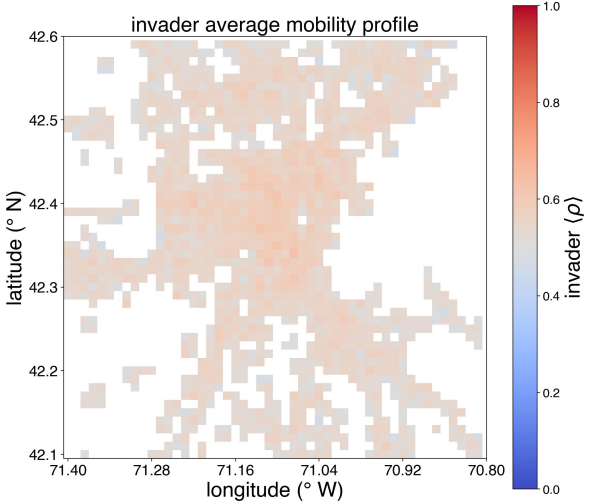
Left: Field reconstruction from high-resolution individual anonymized trajectories.
Right: Attractiveness distribution (log-log).

Effective system size V~1300 of 1km^2.

Invasions: who, when & where



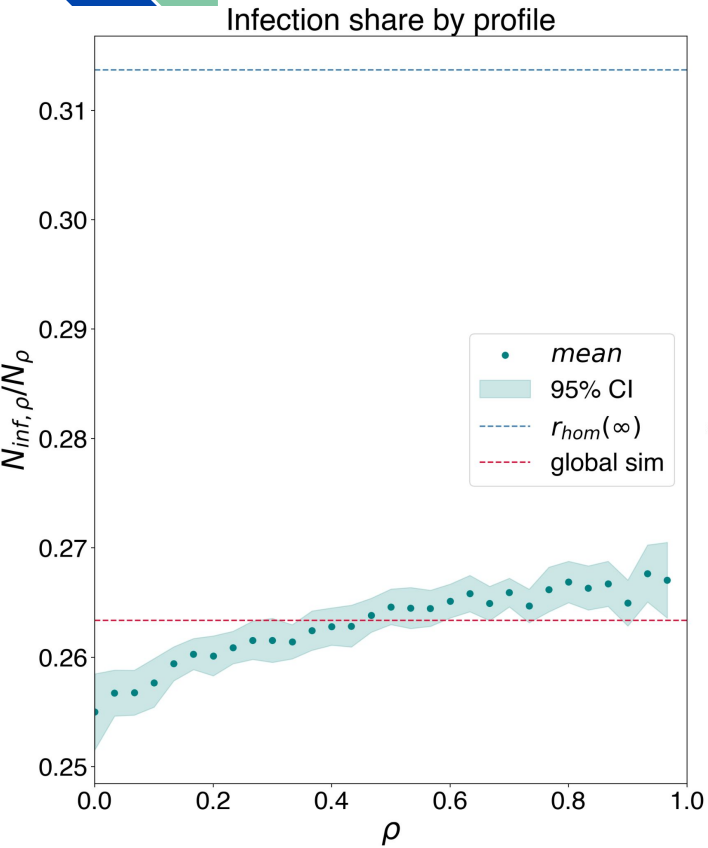


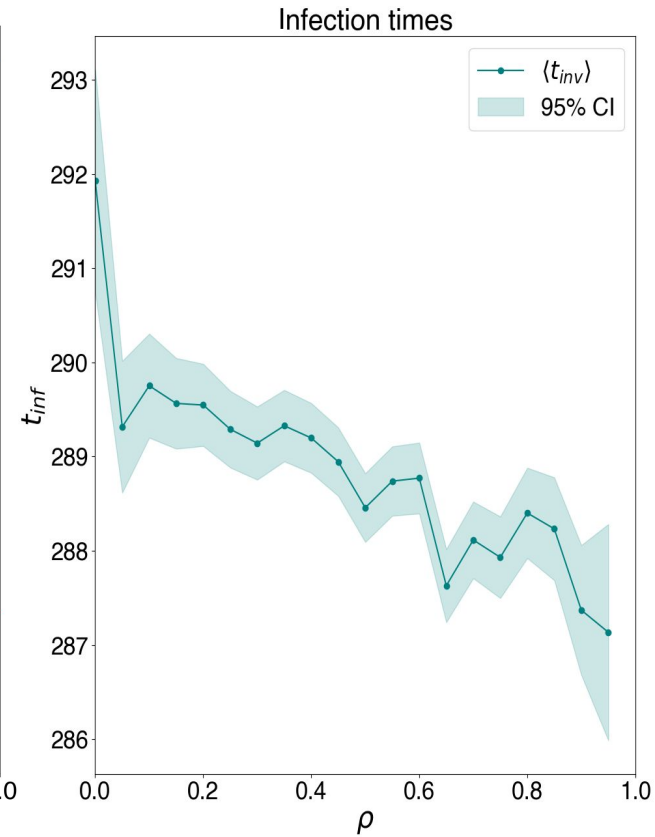


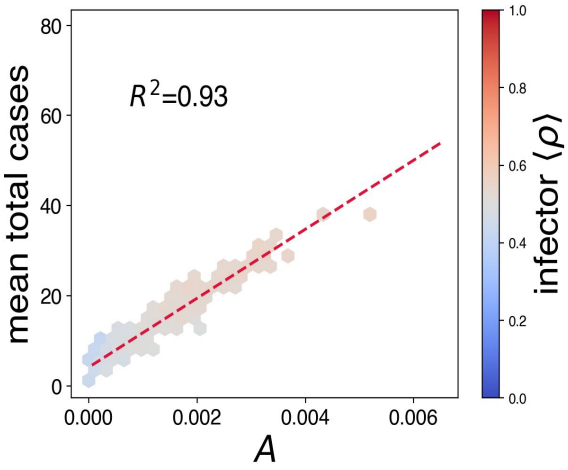
Explorers outperform returners

Explorers invade substantially earlier.

Infections: who, when & where







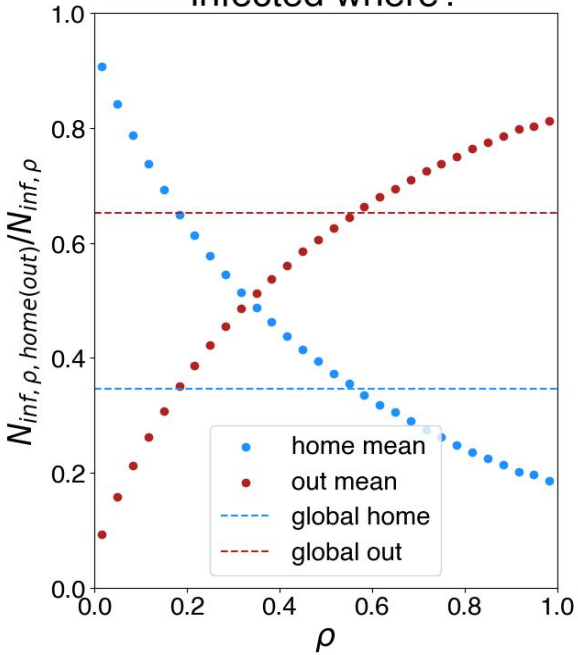
Explorers & returners deviate from the global average.

Infection times differ much less than invasion times

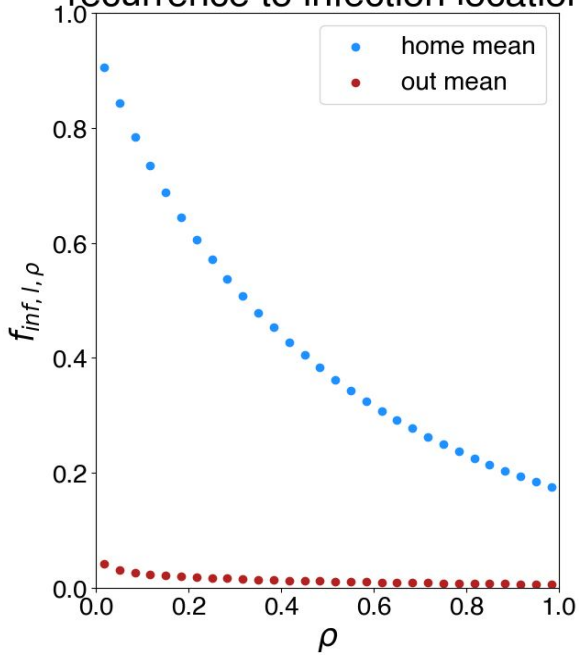
Explorers tend to be infected in most attractive locations.

Origin of infection, recurrence & attractiveness

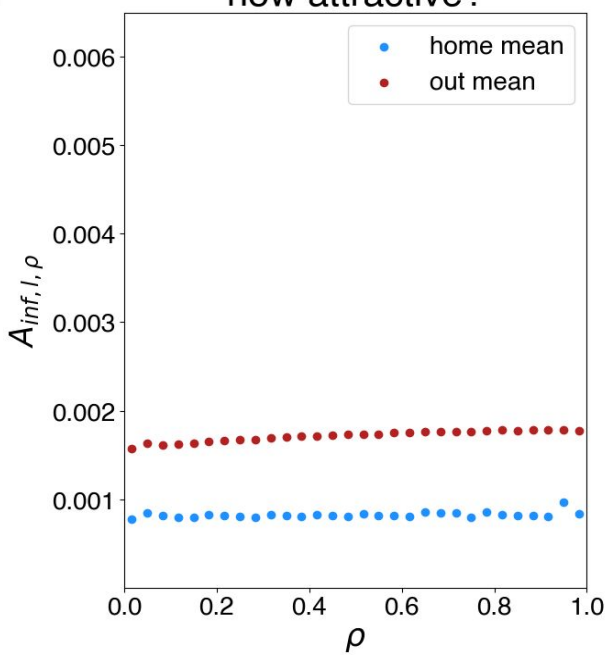
infected where?



recurrence to infection location

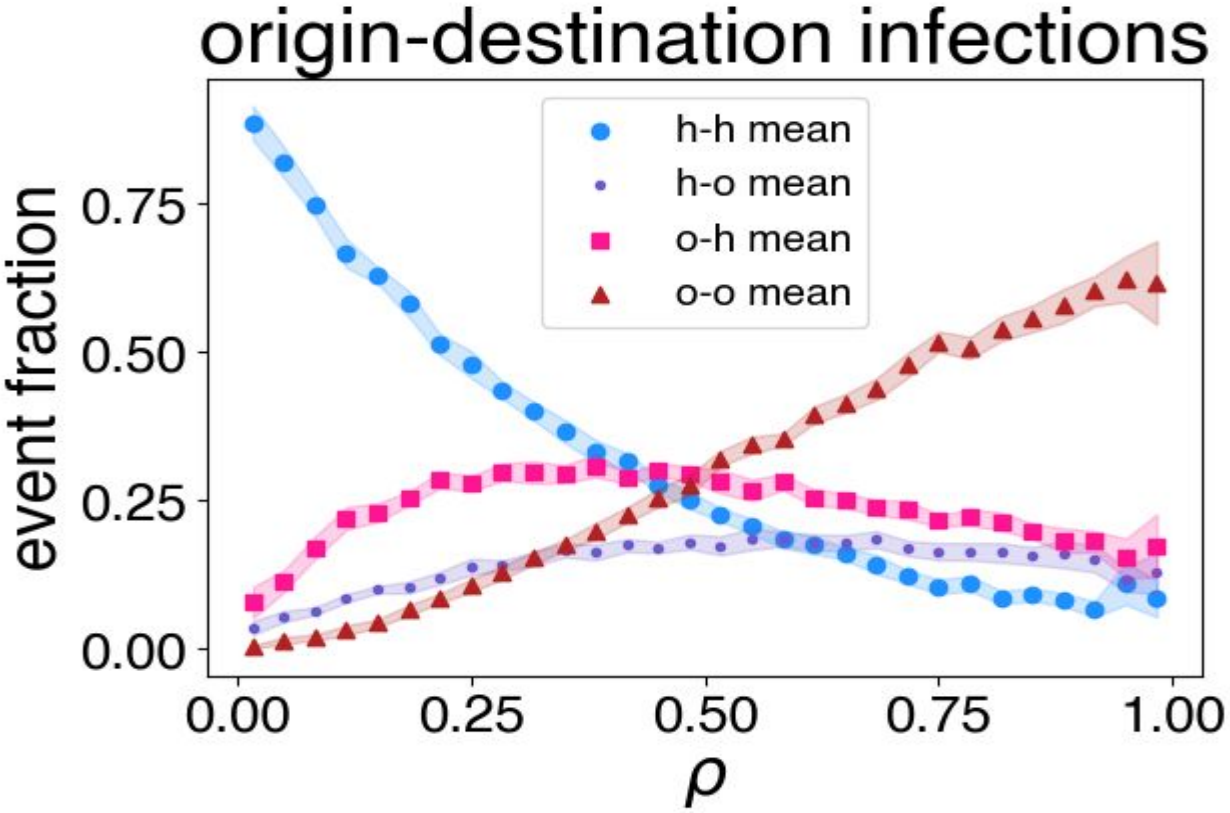


how attractive?

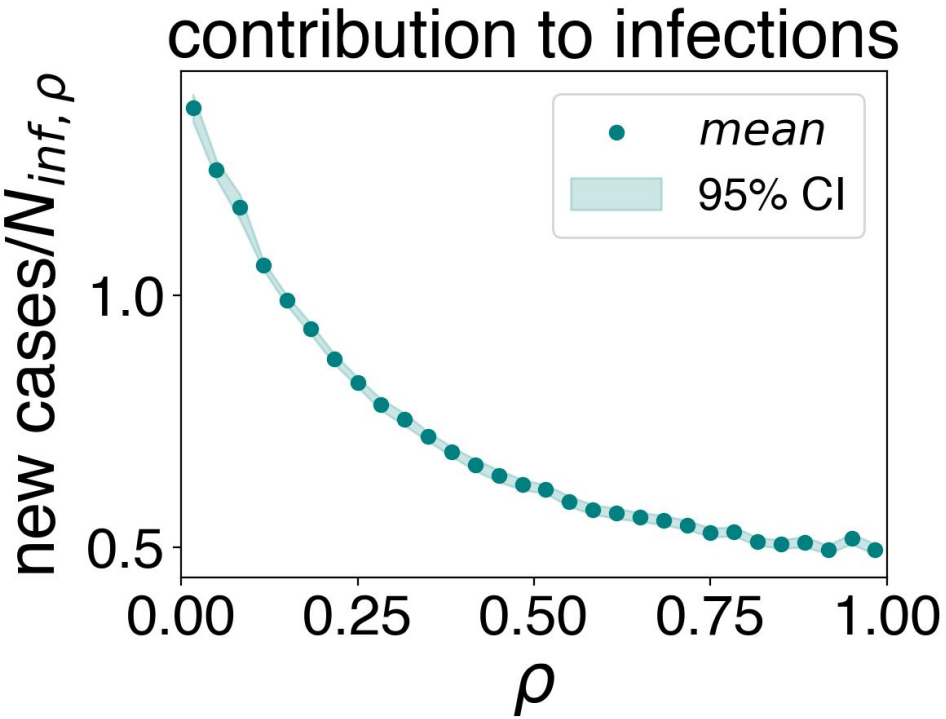


Majority of infections occur outside home location → Very small recurrence → Bad luck?
Agents were just around very attractive locations

Where were you infected & where did you infect?



Which groups contribute the most to new infections?



Under the well-mixing assumption, every infected agent contributes to the force of infection → new infected cases generation.

Adjusted by size, there is a clear trend: Returners contribute more to trigger contagion events and thus new cases.

Conclusions & Future work

Conclusions:

- **Explorers** deliver the disease across the system, they do it faster & are impacted more.
- Opposite for **returners**. But they also proportionally contribute more to sustain contagion chains.
- Important part of contagions occurs **outside home** locations.
- Size of effects may depend on:
    - How far we are from homogeneous mixing.
    - Attractiveness distribution & spatial geometry.

Ongoing/future work…

- Compare results with conventional metapopulations models.
- Compare spreading under real trajectories with model predictions.
- Export this analysis to other cities/urban settlements.

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Universidad Zaragoza
Cosnet
cuebiq
AccelNet MultiNet

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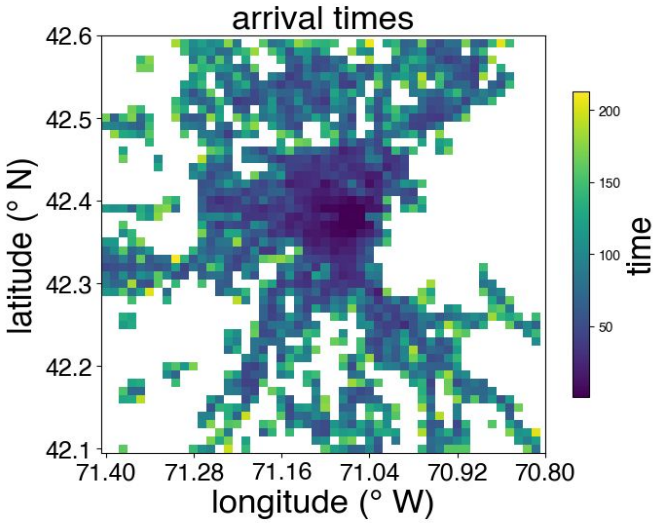
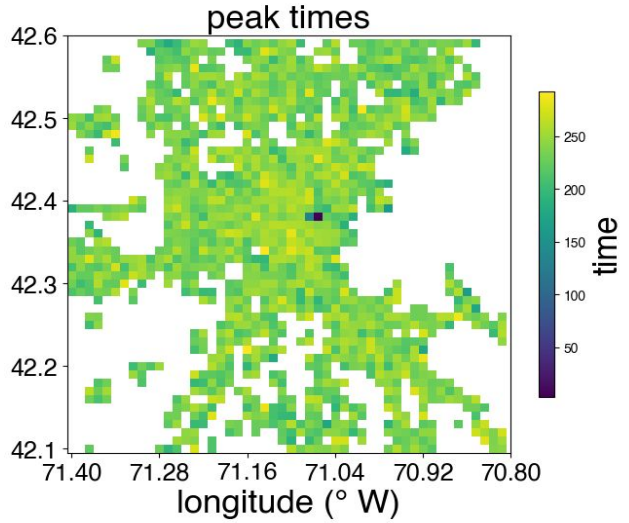
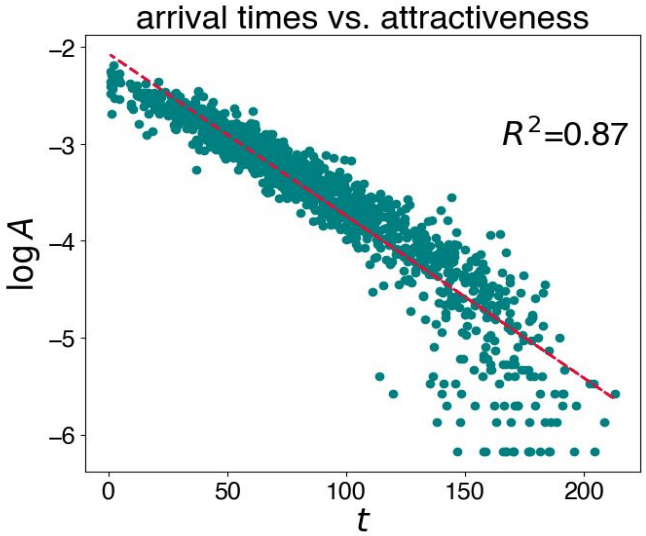
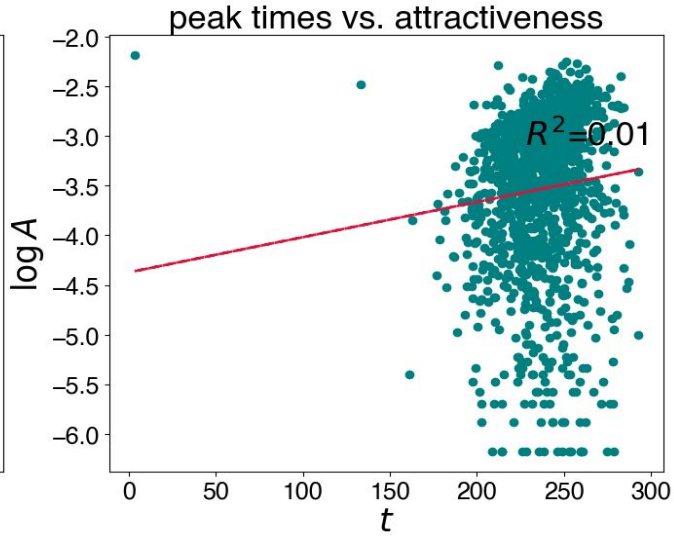
Thank you!

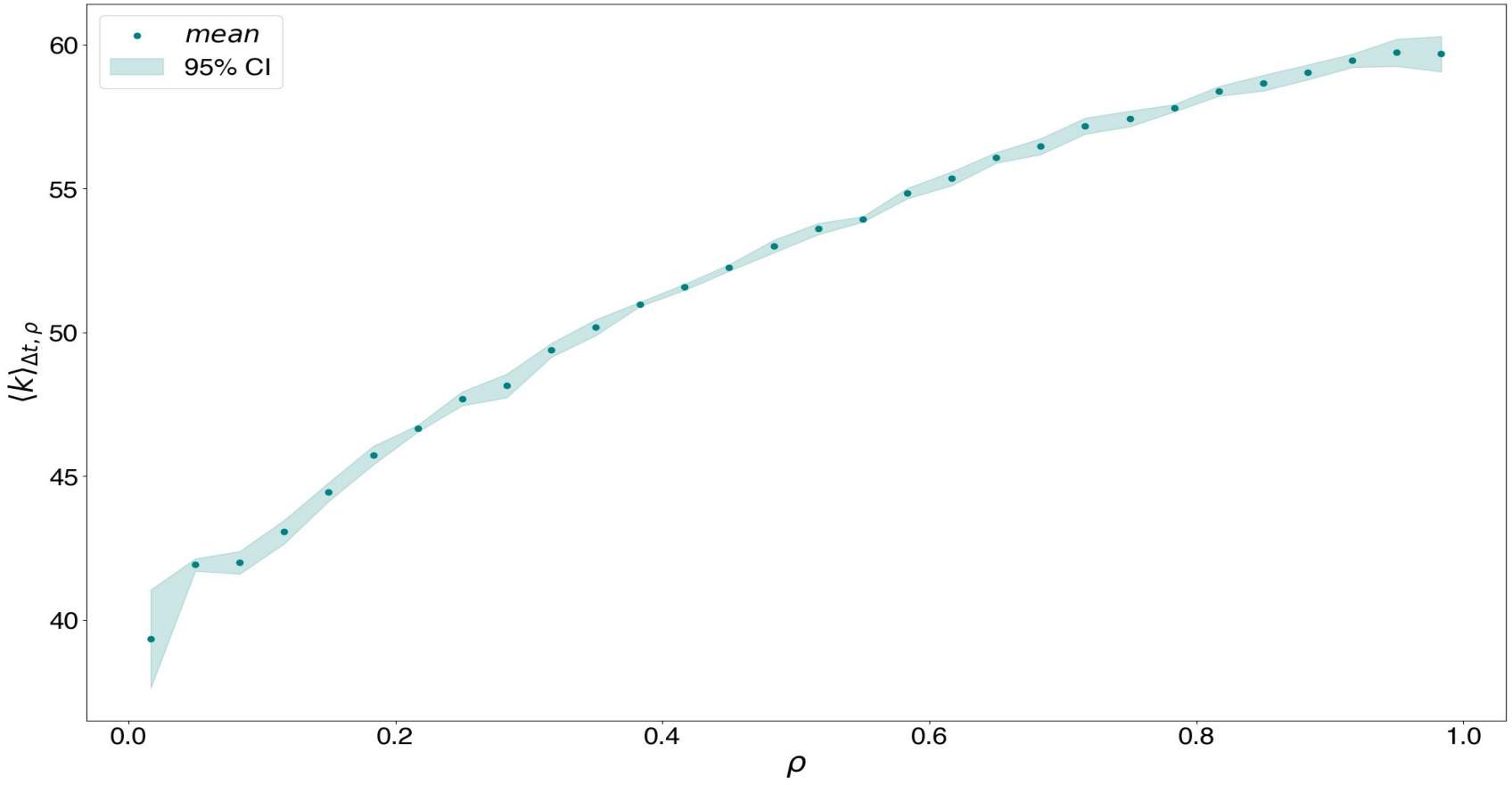

arrival times
42.6
42.5
42.4
42.3
42.2
42.1
latitude (° N)
71.40
71.28
71.16
71.04
70.92
70.80
longitude (° W)
200
150
100
50
time


peak times
42.6
42.5
42.4
42.3
42.2
42.1
71.40
71.28
71.16
71.04
70.92
70.80
longitude (° W)
250
200
150
100
50
time

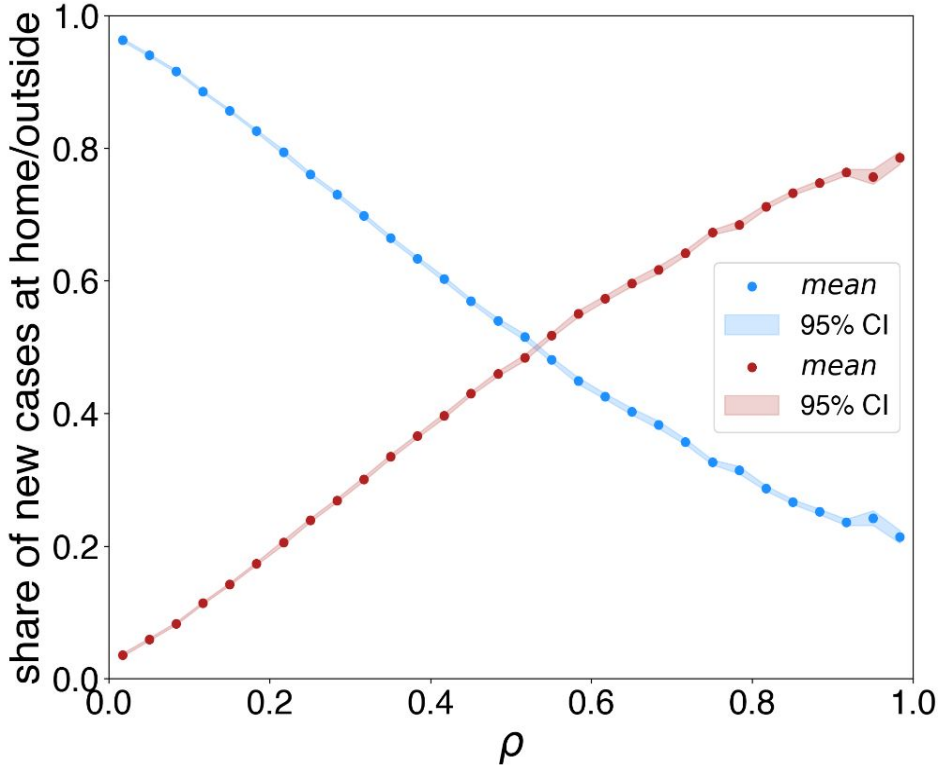

arrival times vs. attractiveness
R^2=0.87
log A
−2
−3
−4
−5
−6
0
50
100
150
200
t

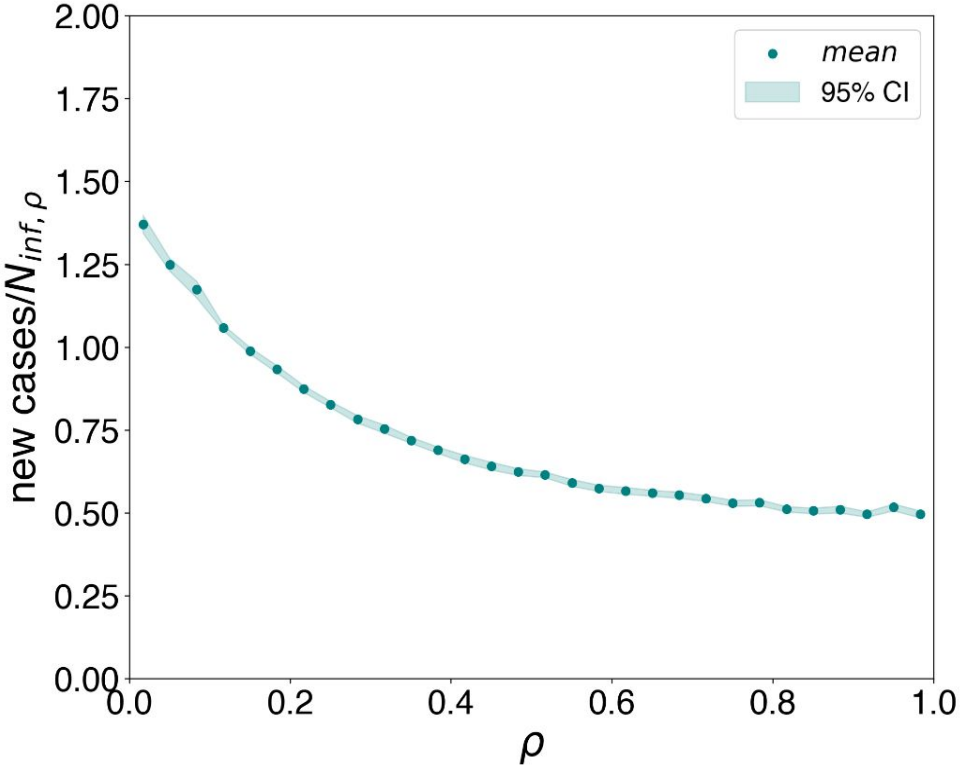

peak times vs. attractiveness
R^2=0.01
log A
−2.0
−2.5
−3.0
−3.5
−4.0
−4.5
−5.0
−5.5
−6.0
0
50
100
150
200
250
300
t

Average degree

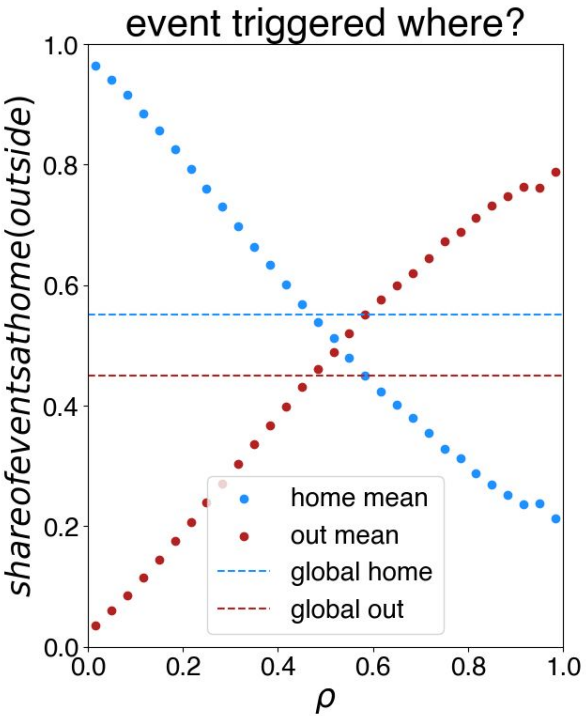


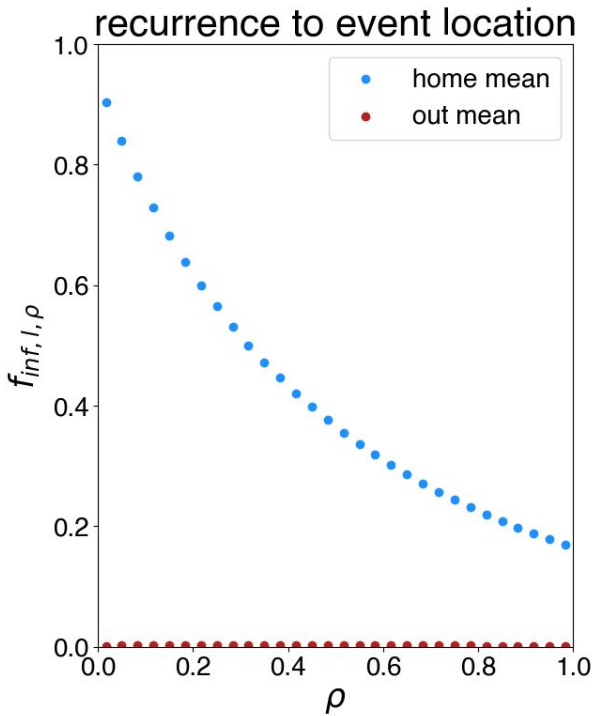
Contribution to new cases

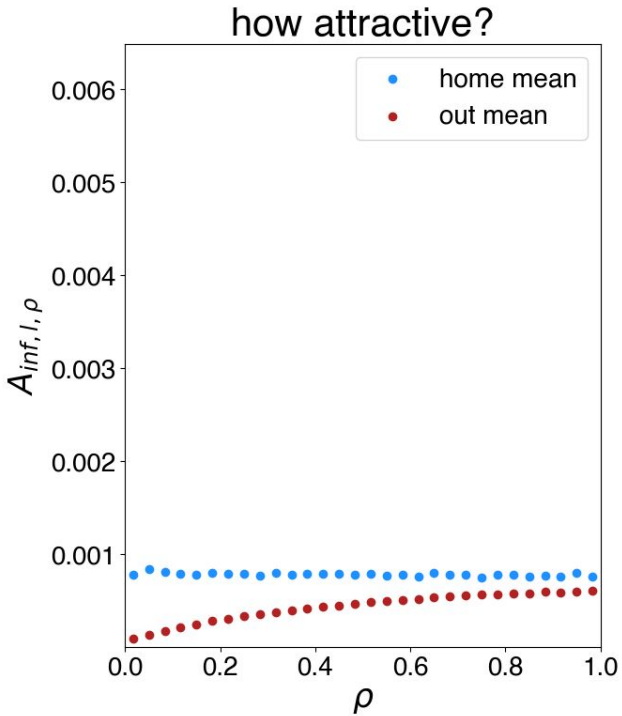




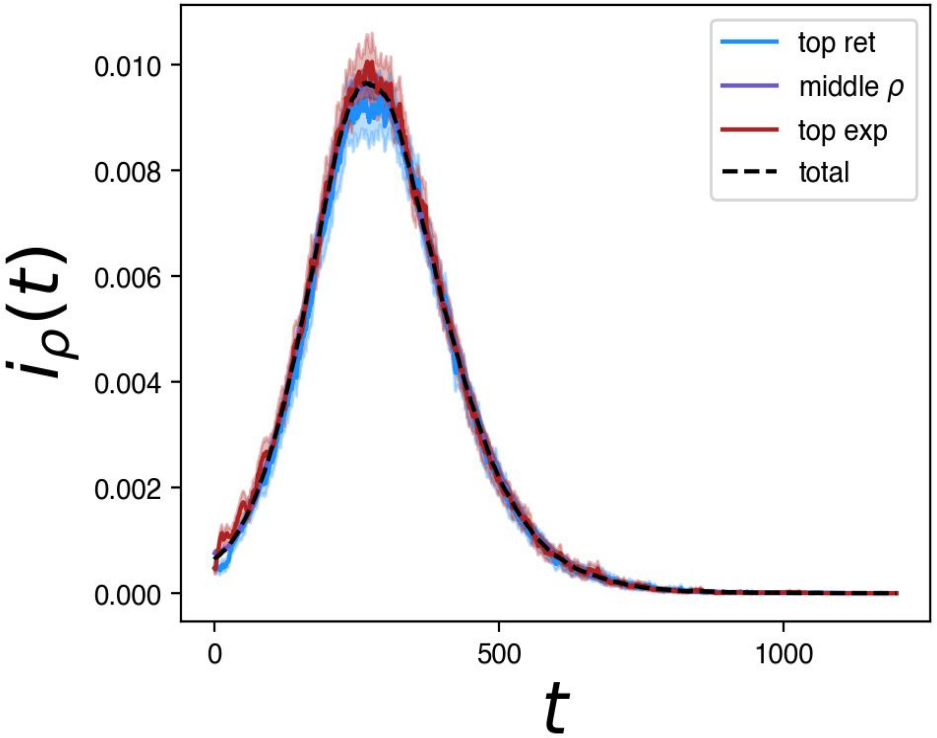
Where do agents infect?

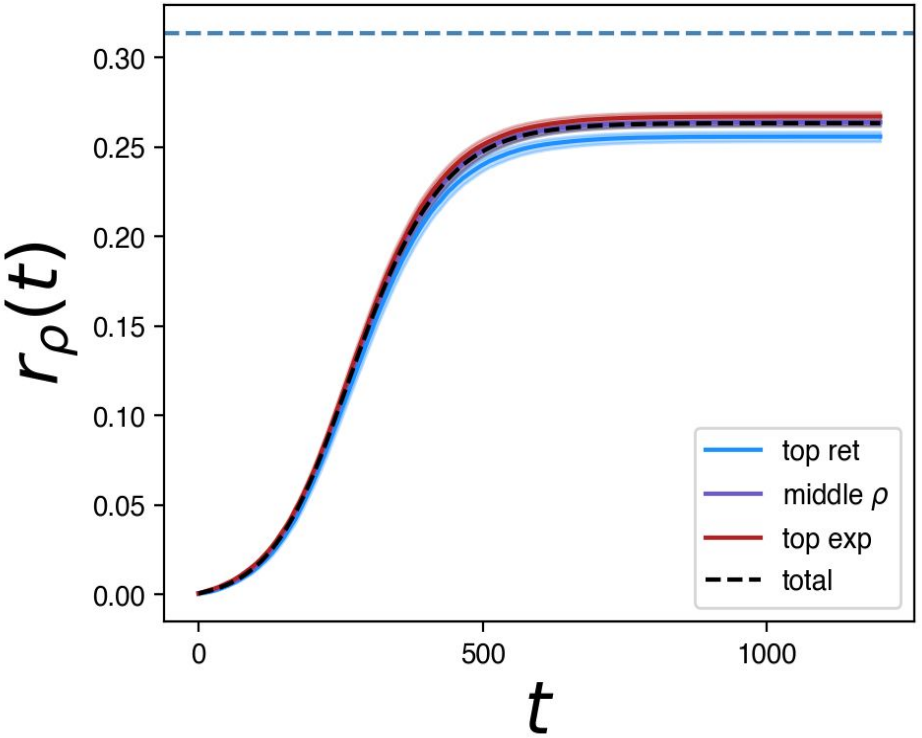




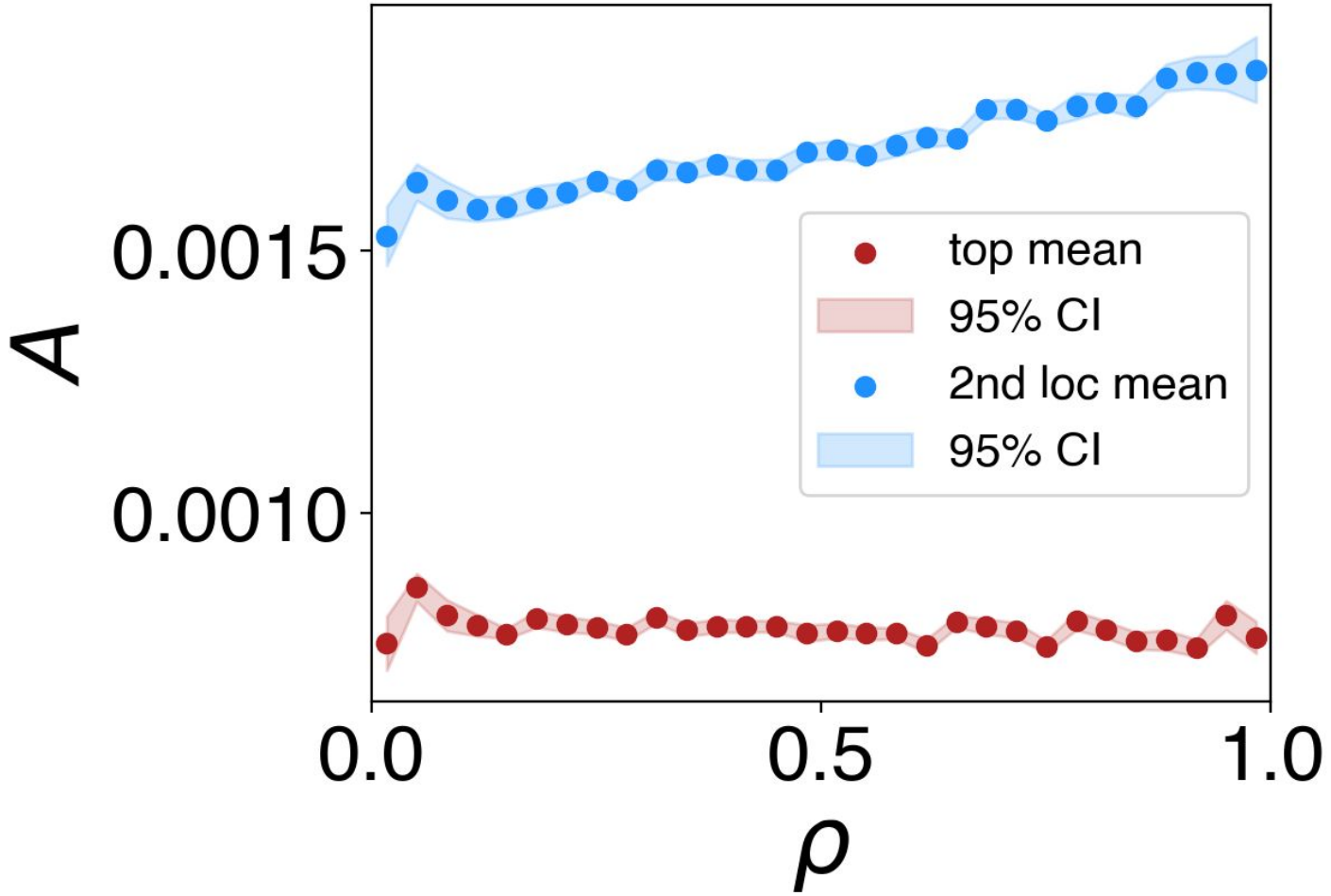


Time evolution for incidence & prevalence

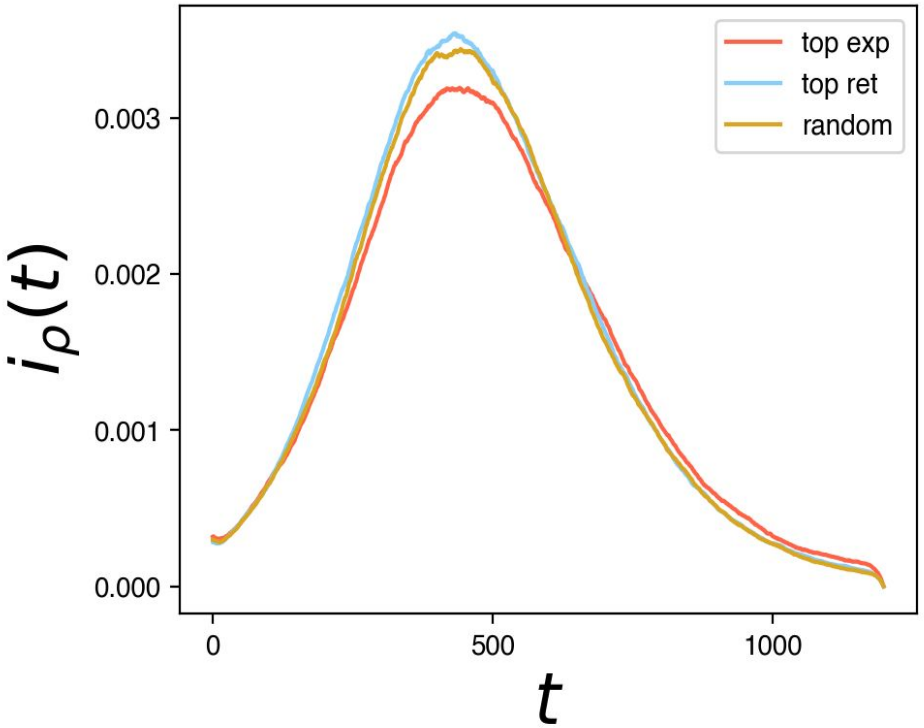


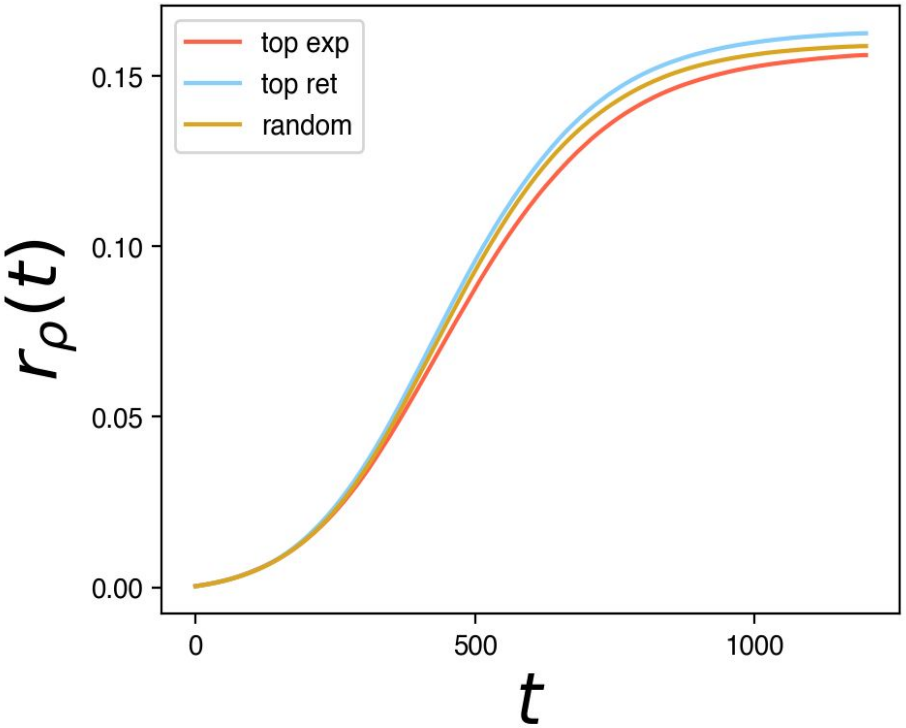


dominant locations attractiveness

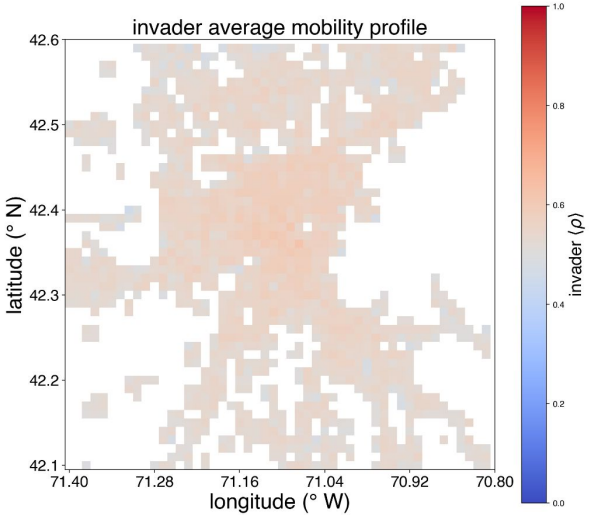


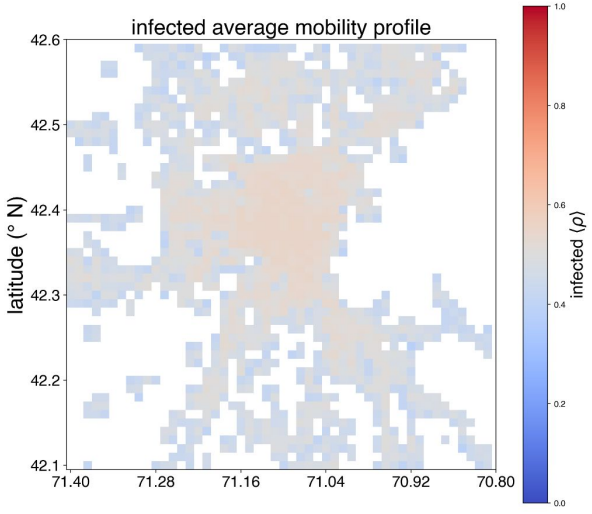
Targeted vaccination

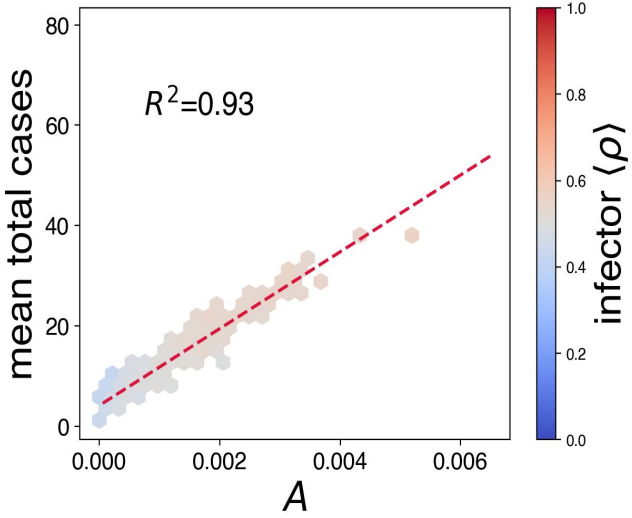




What's the average invader/infected mobility profile per location?







Explorers absolutely **dominate** when bringing the disease to a new location.

In the **most attractive** locations, the typical infected tends to be an **explorer** (***ρ***>0.5).
In the **least attractive** locations, the typical infected tends to be a returner **lower** (***ρ***<0.5).