Epidemic spreading under exploration & preferential return mobility

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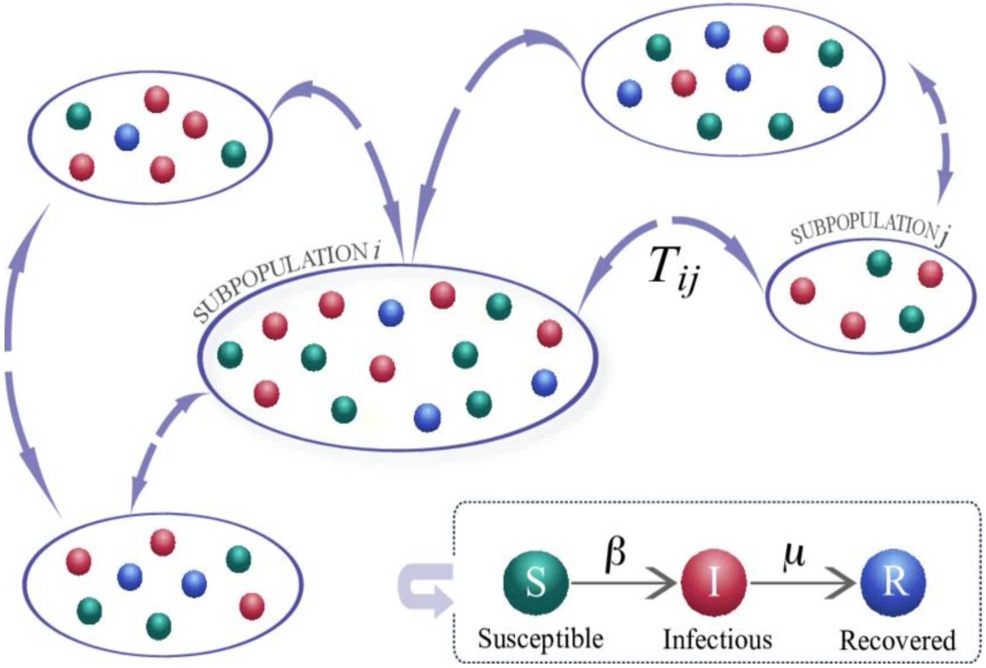
Background: Epidemics on Metapopulations



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
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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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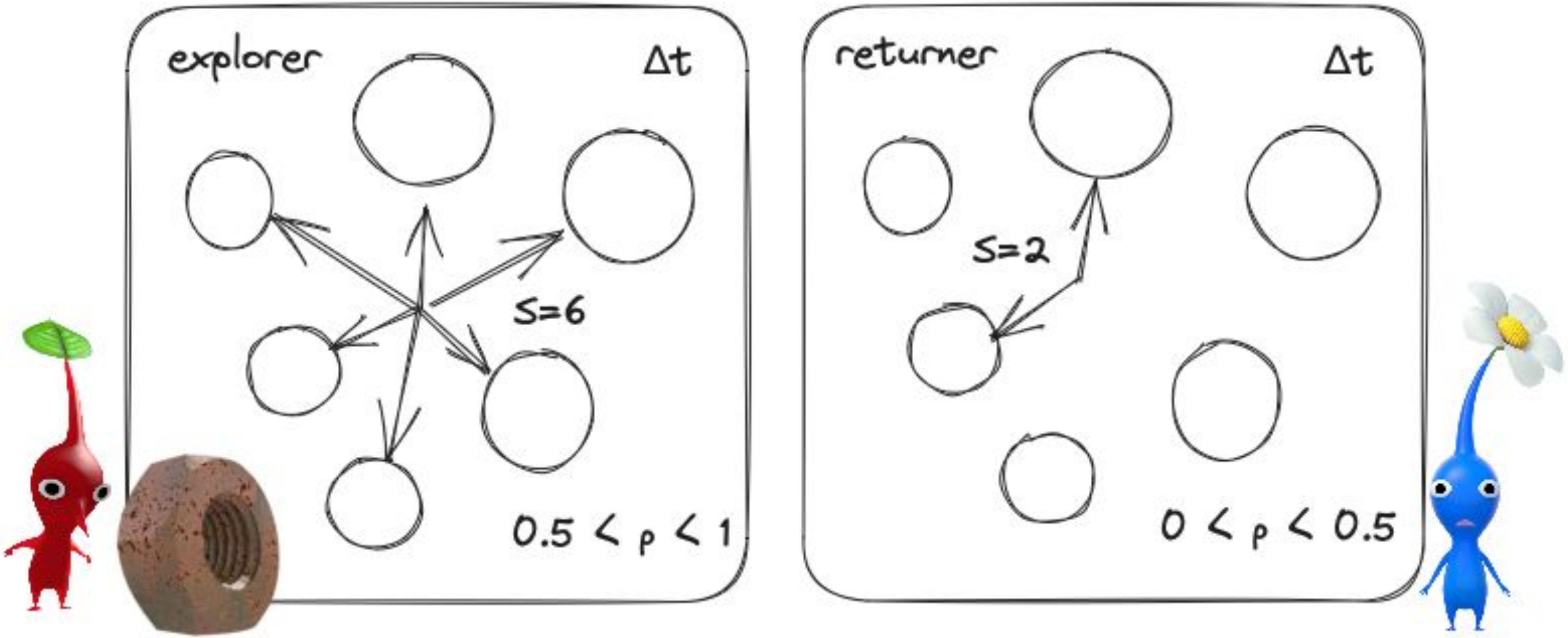
Returners and explorers dichotomy in human mobility

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.

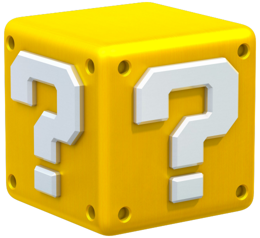
Explorers & returners



High exploration probability,
High S -> Low visit frequency

Low exploration probability,
Low S -> High visit frequency

Our work

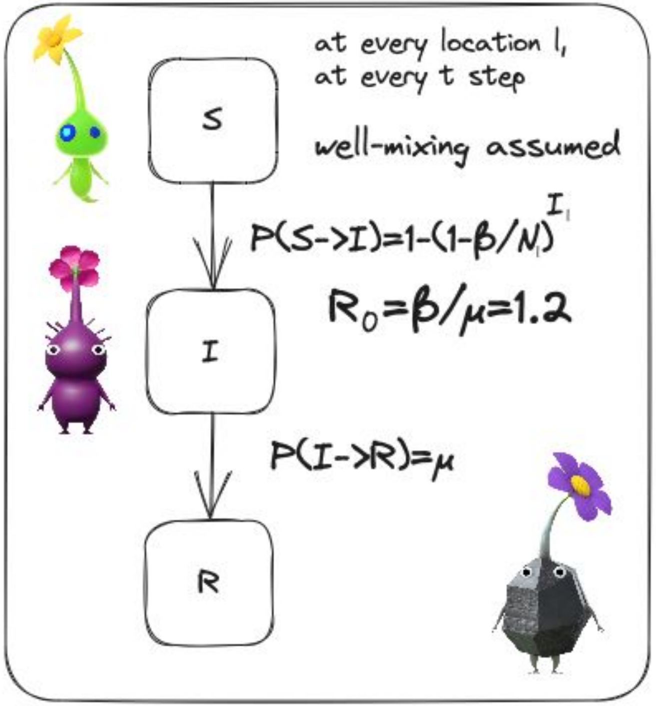


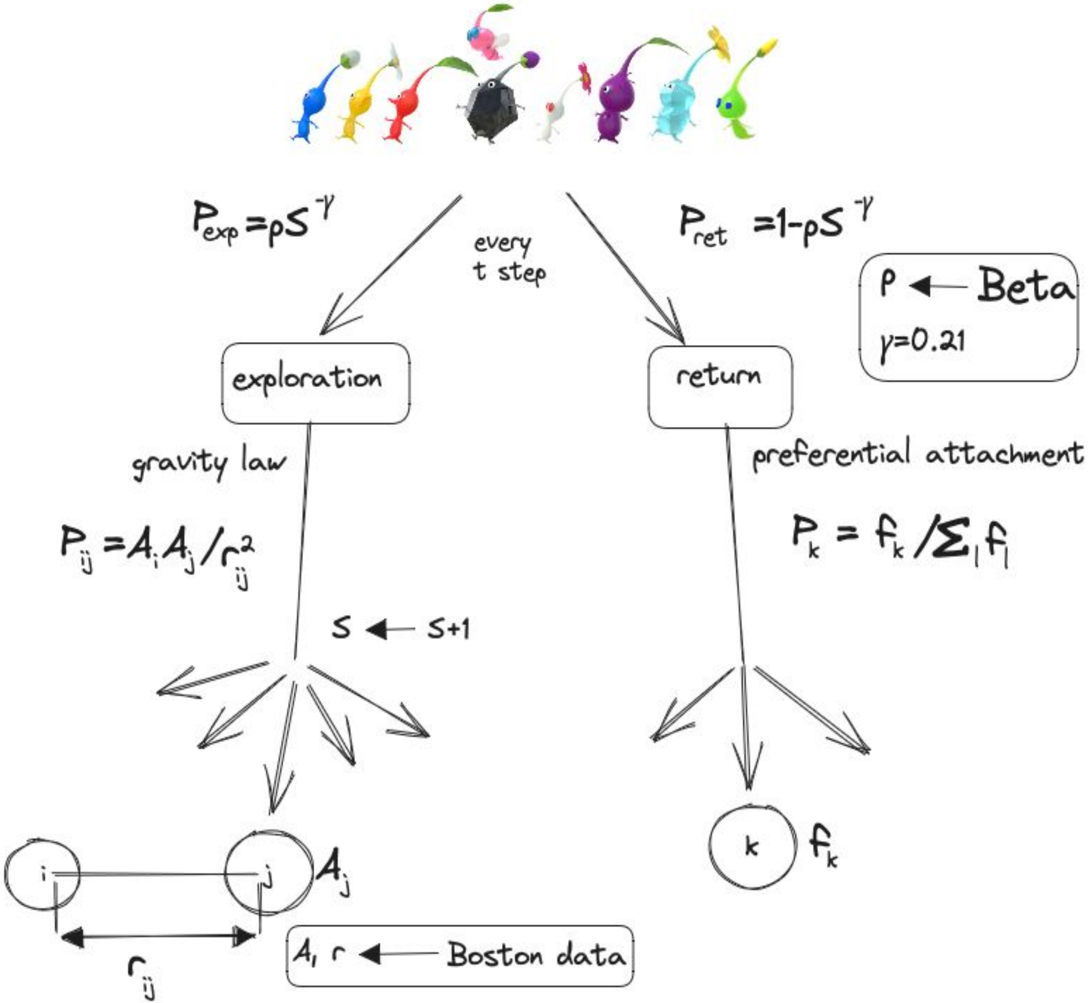
- Literature mentions the relevance of these discoveries to epidemics, but have not been thoroughly explored.

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

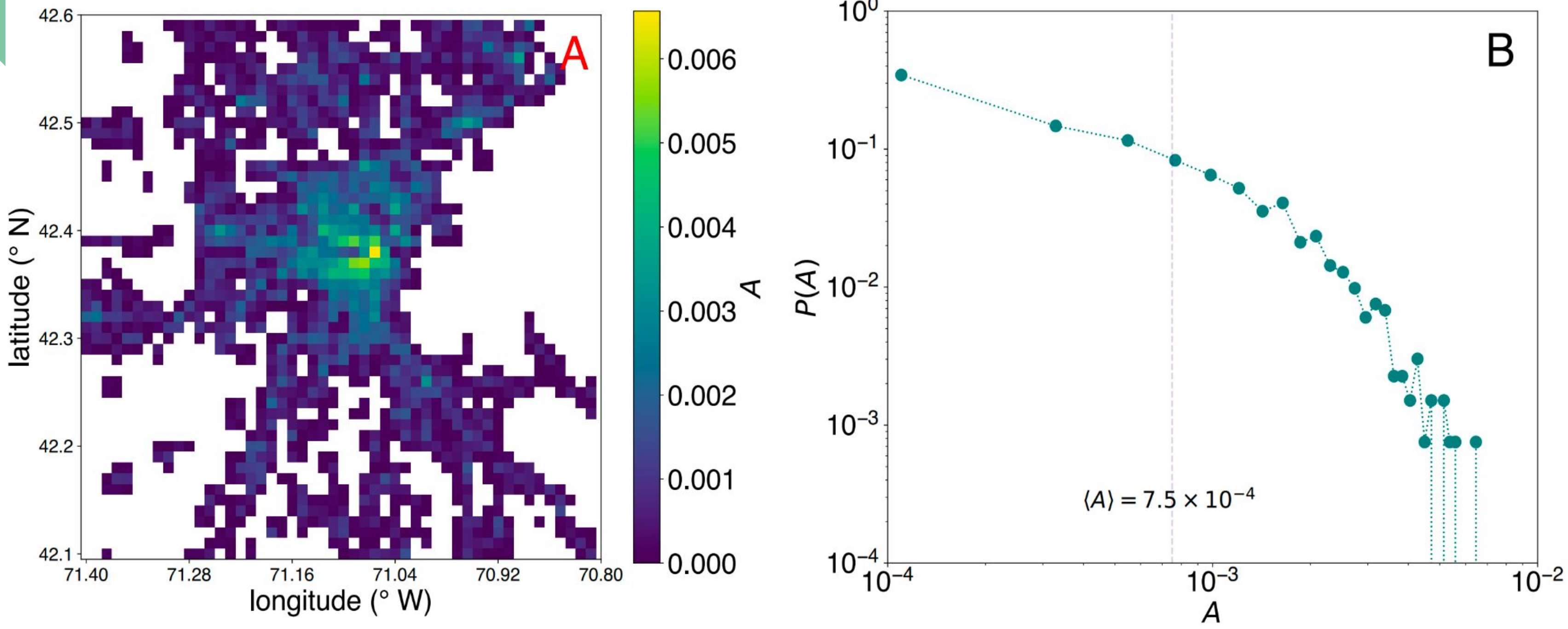
- Determine the role of explorers & returners in the spreading of an epidemic disease

SIR model
+ d-EPR model





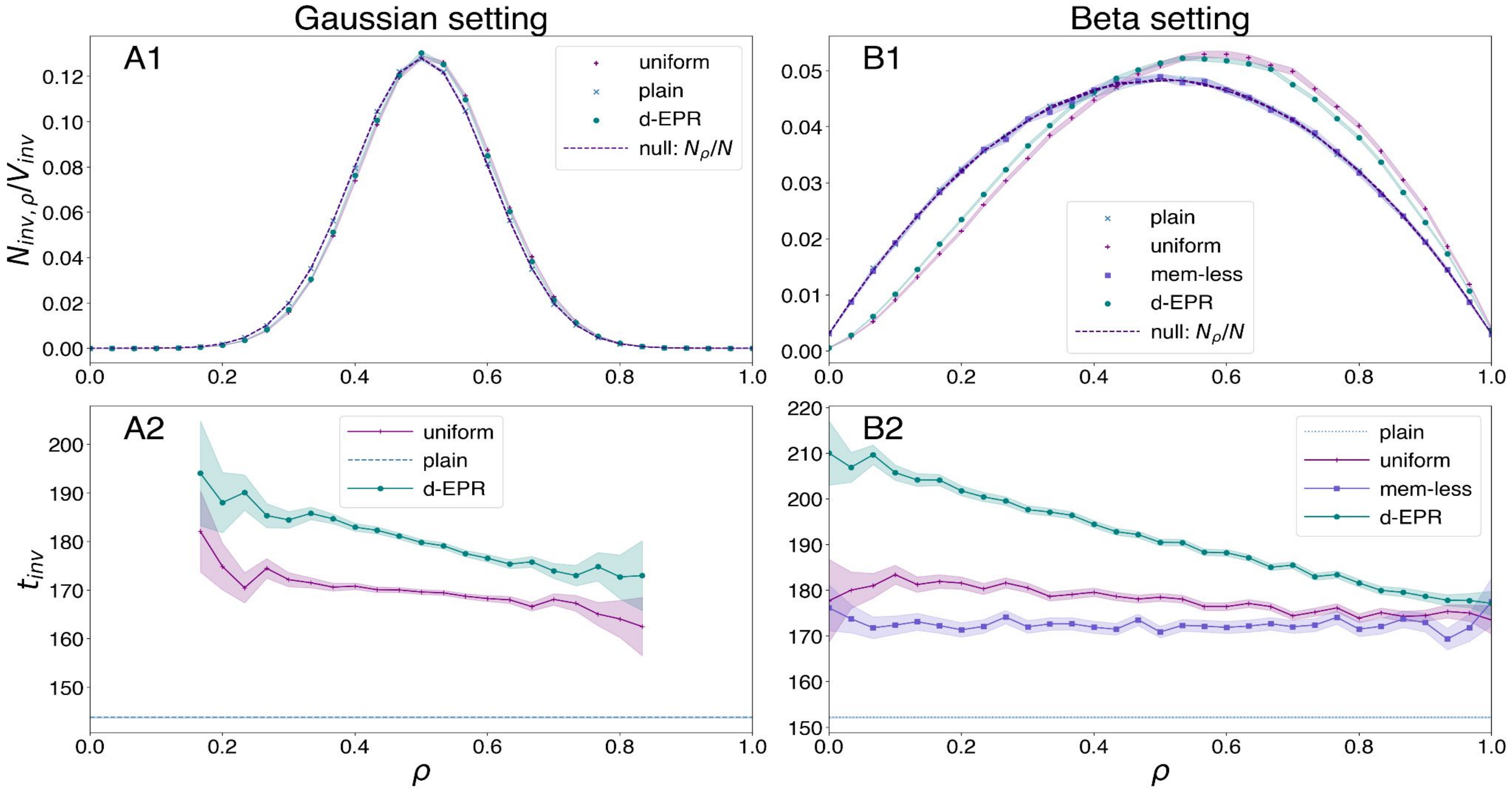
Spatial structure: Locations’ attractiveness



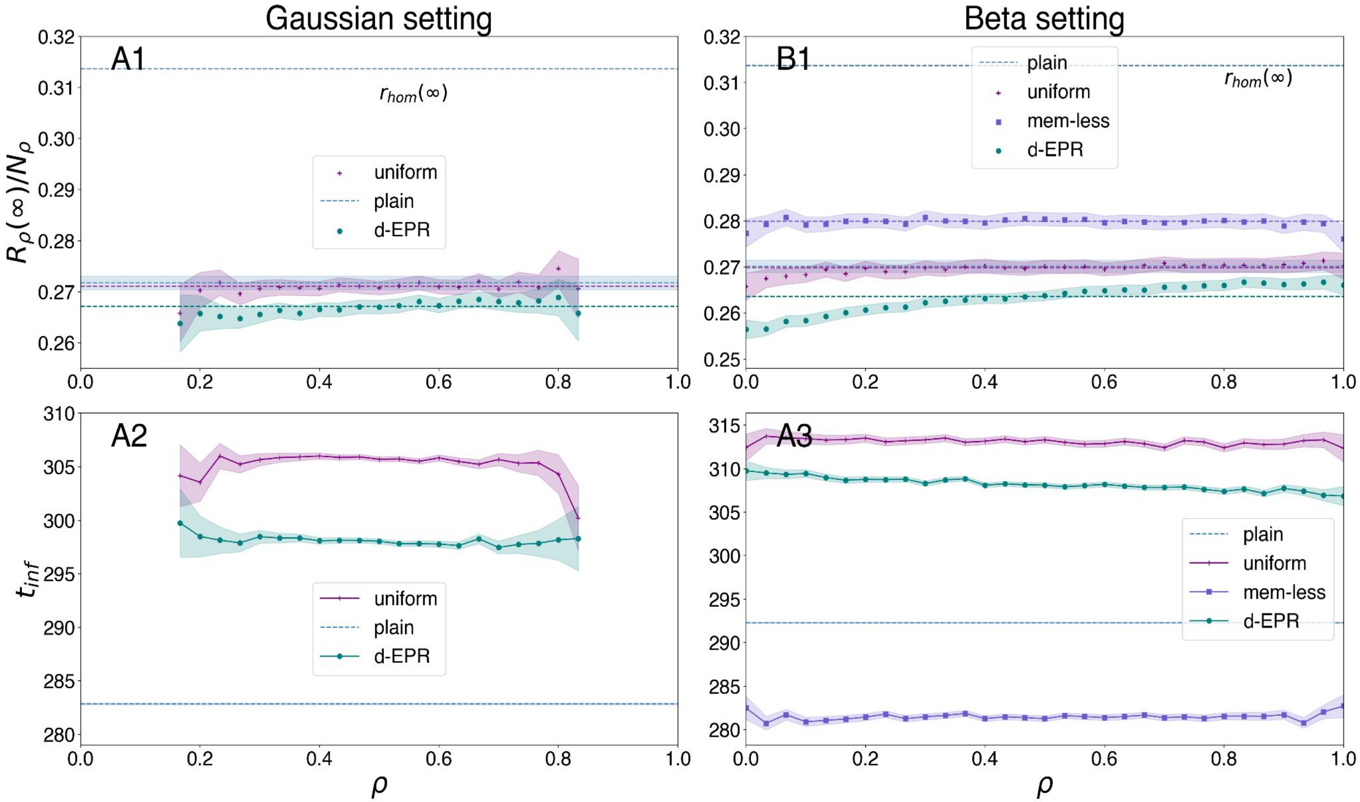
Left: Field reconstruction from high-resolution individual anonymized trajectories.
Right: Attractiveness distribution (log-log).

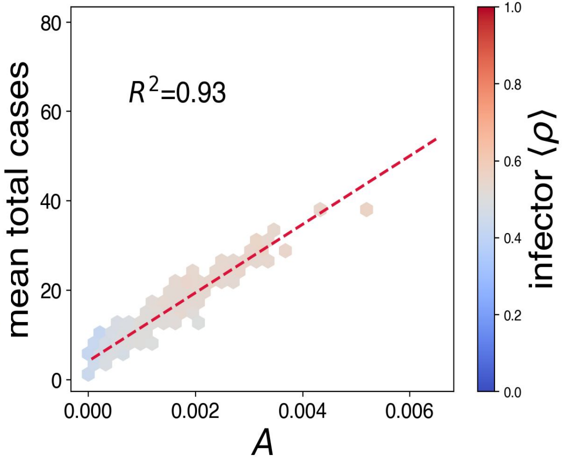
Effective system size V~1300 of $1km^2$.

Disease invasion: Explorers drive it



Disease prevalence



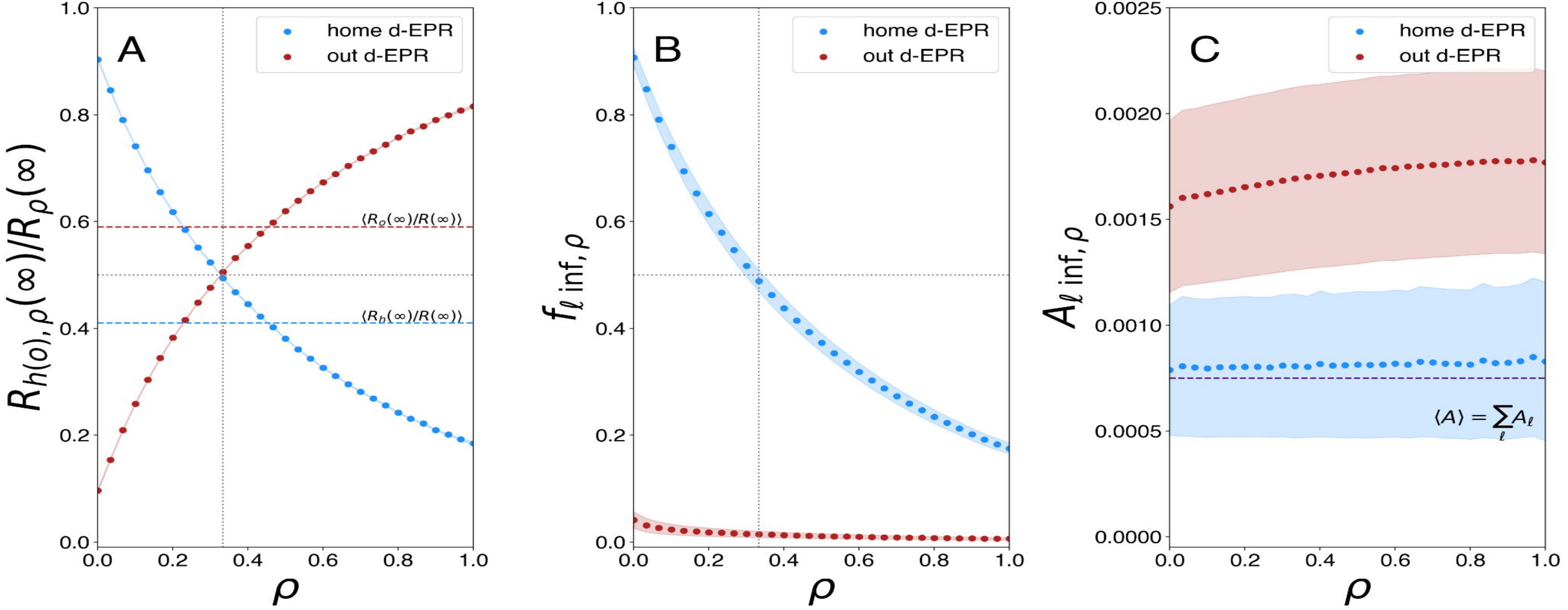


Explorers & returners deviate from the global average.

Infection times differ much less than invasion times

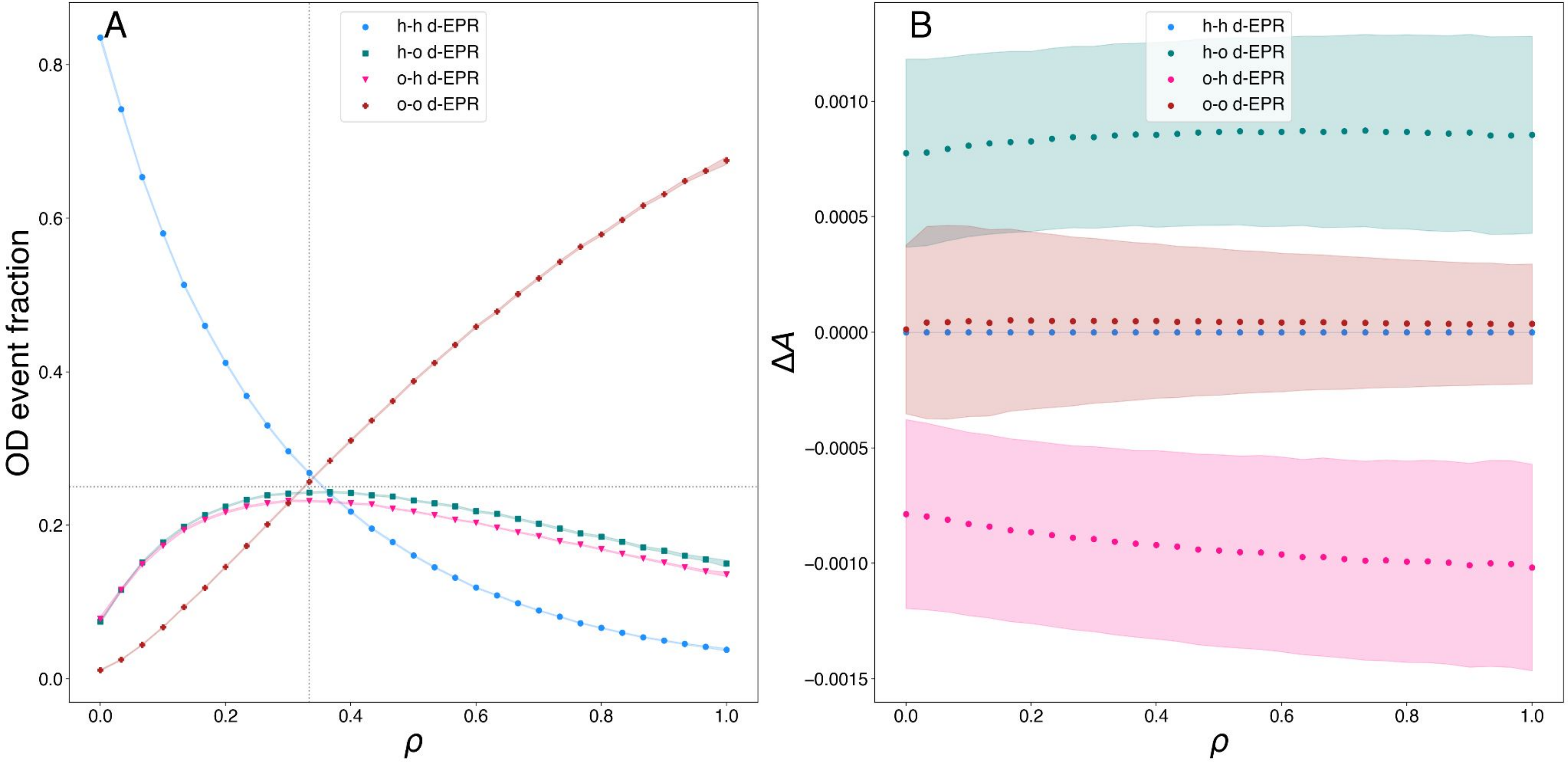
Explorers tend to be infected in most attractive locations.

Origin of infection, recurrence & attractiveness

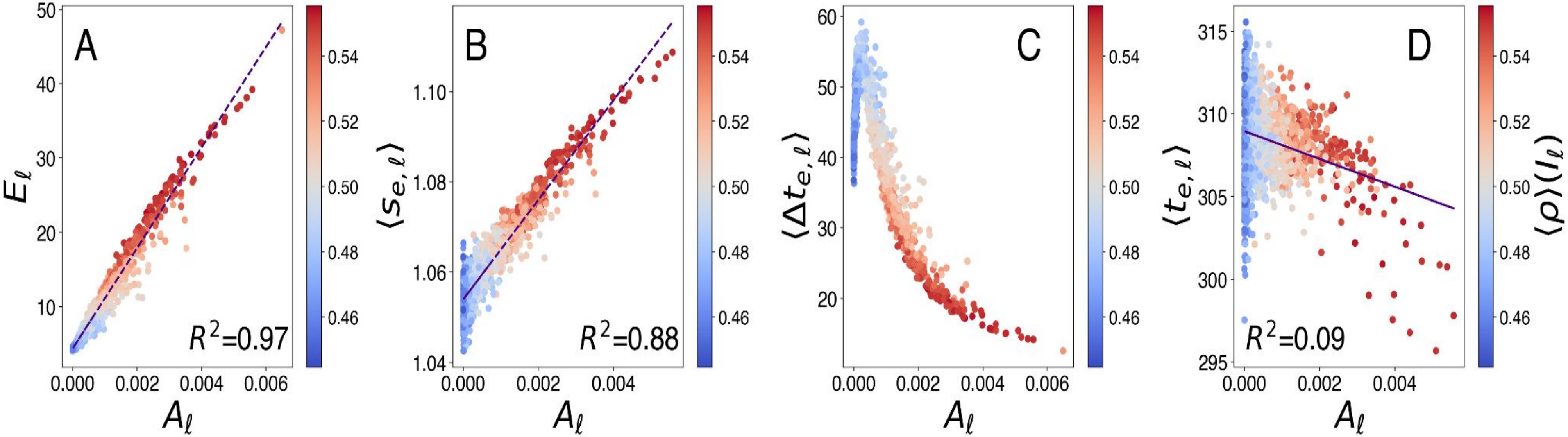


Majority of infections occur outside home location → Very small recurrence → Bad luck?
Agents were just wandering around very attractive locations

Spreading the disease
(from origin to destination)



Contagion events & attractiveness



- [A & B] More attractiveness → more events, but size differences are not a thing. (?)
- [C] More attractiveness → Shorter inter-event times. But with also less attractiveness!
- Top A locations sustain the epidemic in time, bottom A locations show a short-lived outbreak
- [D] High synchronization

What we learned & Future work

Main conclusions:

- Heterogeneous populations & recurrence are fundamental to obtain richer behavior.
- Explorers deliver the disease across the system, they do it faster & are impacted more than returners.
- Returners are prone to get the infection at home, whereas explorers outside.
- Even for low rho values, an important number of trips is established with high attractiveness locations.
- High attractiveness locations constantly sustain the epidemic, while this occurs like a *burst* in the lowest attractiveness locations.

Ongoing/future work...

- Priority: Compare spreading under real trajectories with model predictions.
- Export this analysis to other cities/urban settlements.

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Universidad Zaragoza

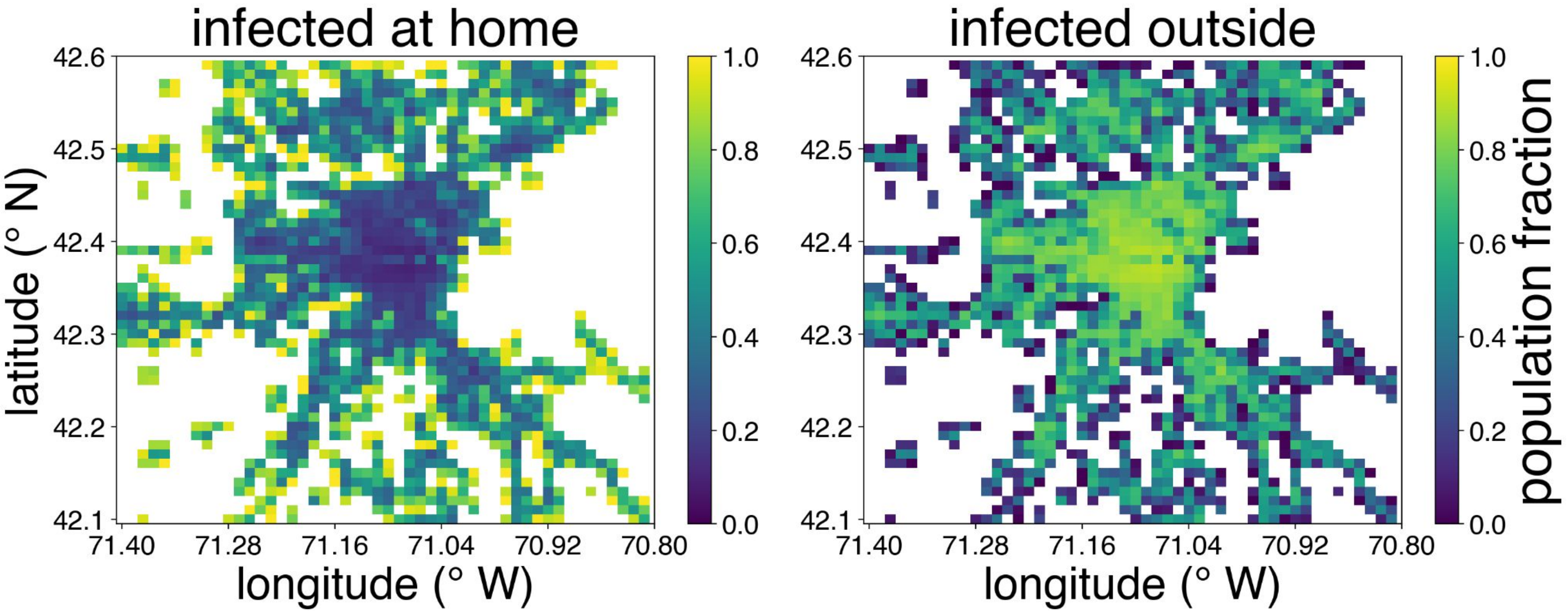
Cosnet

cuebiq

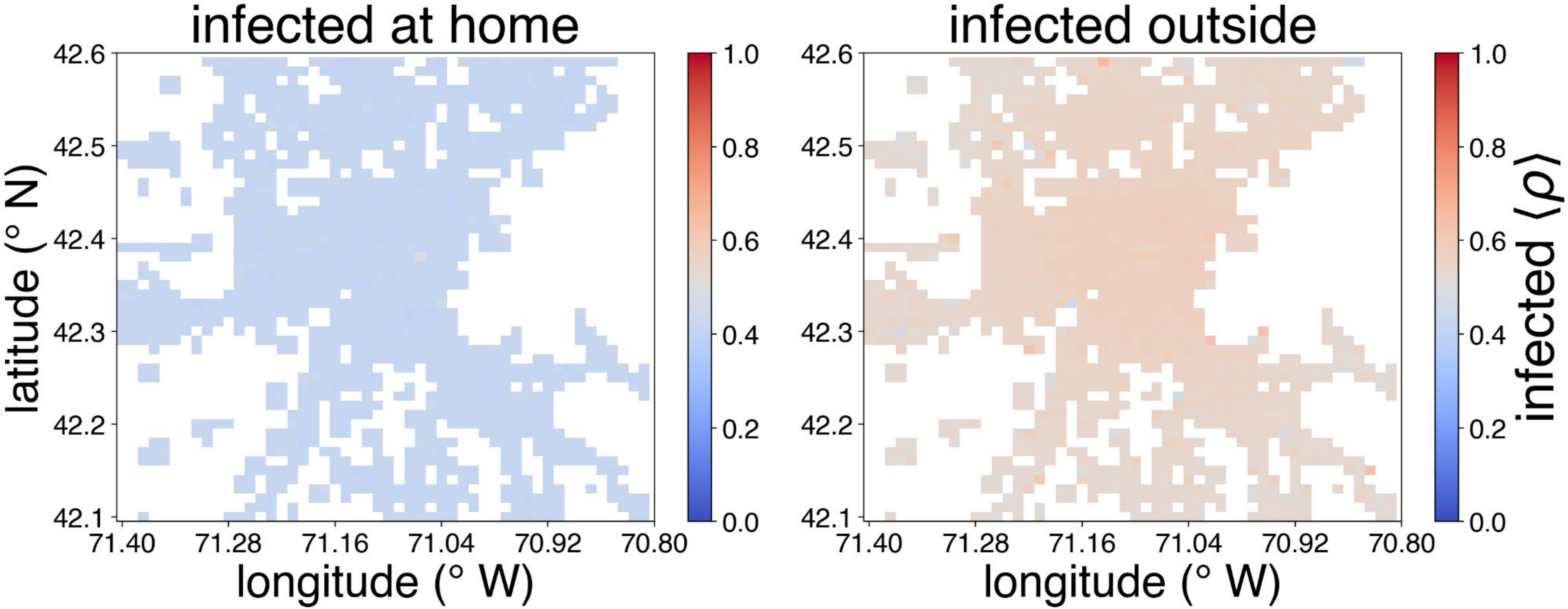
AccelNet
MultiNet

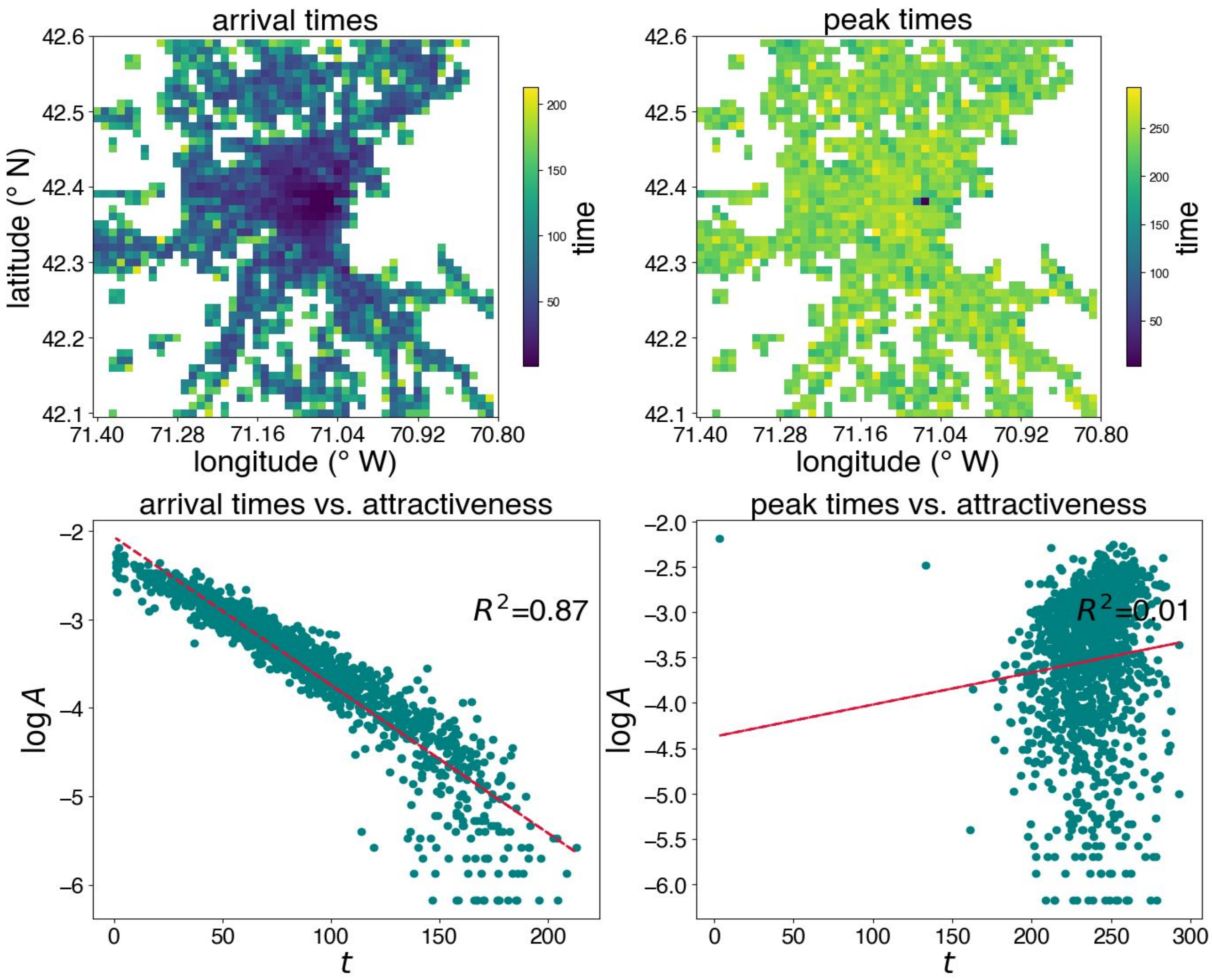
Thank you!

Home/outside infection map

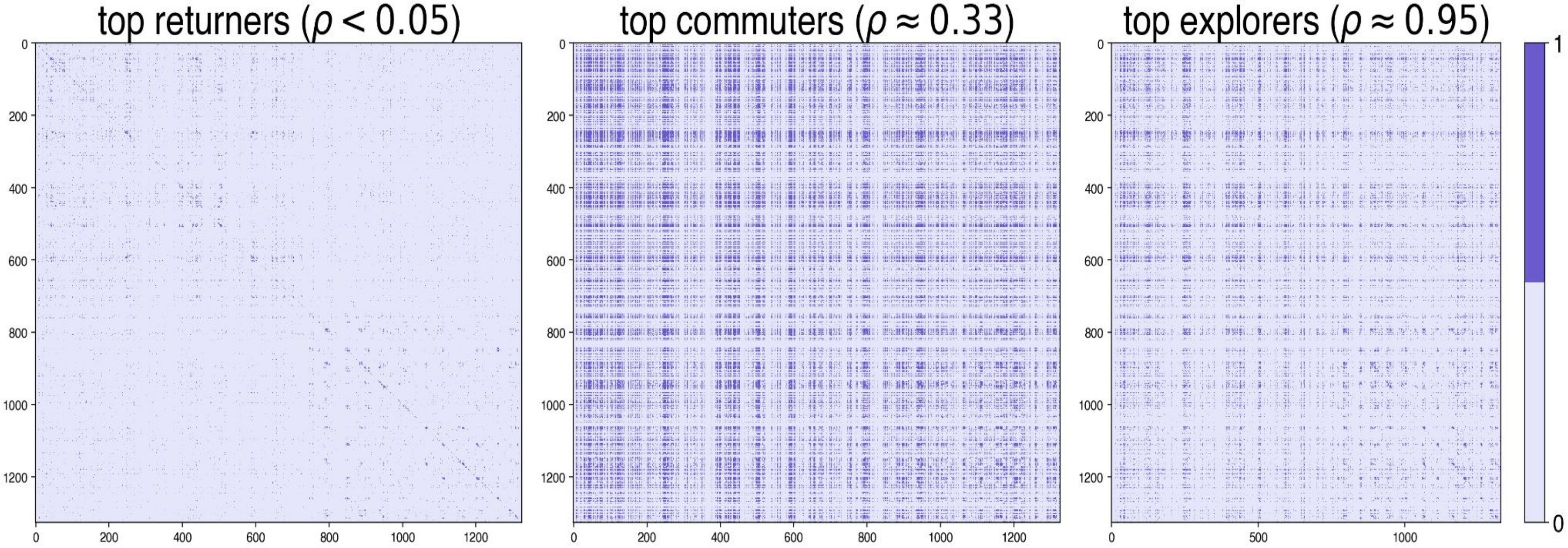


Home/outside infection map (II)

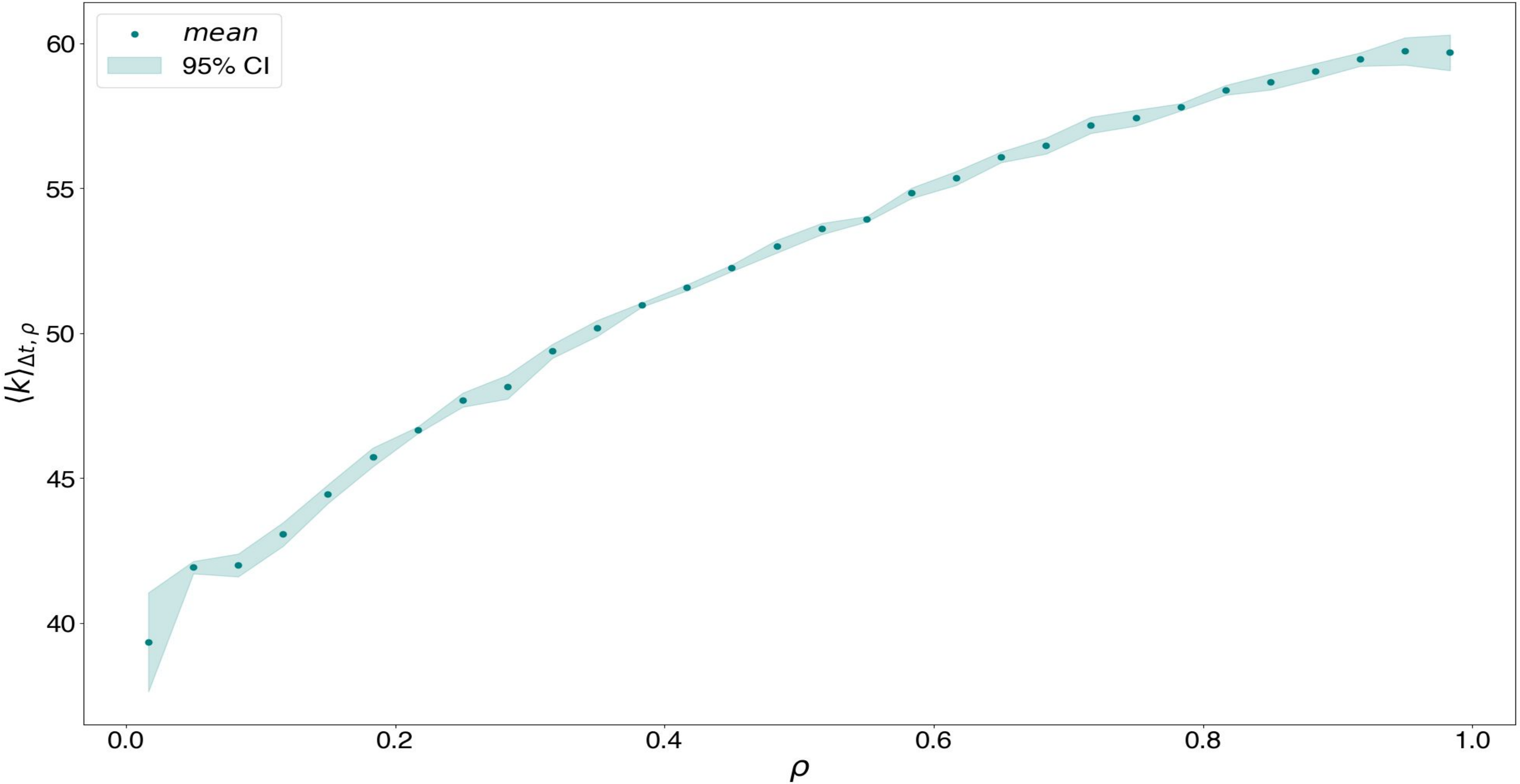



arrival times
peak times
latitude (° N)
longitude (° W)
time
arrival times vs. attractiveness
peak times vs. attractiveness
$\log A$
t
R^2=0.87
R^2=0.01

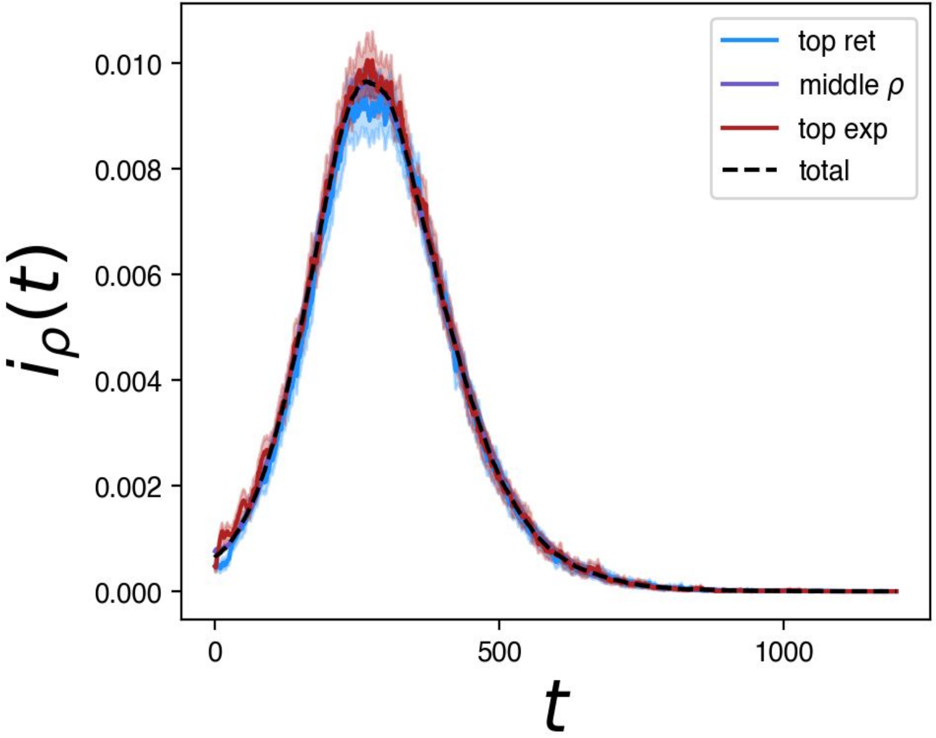
Mobility adjacency matrices

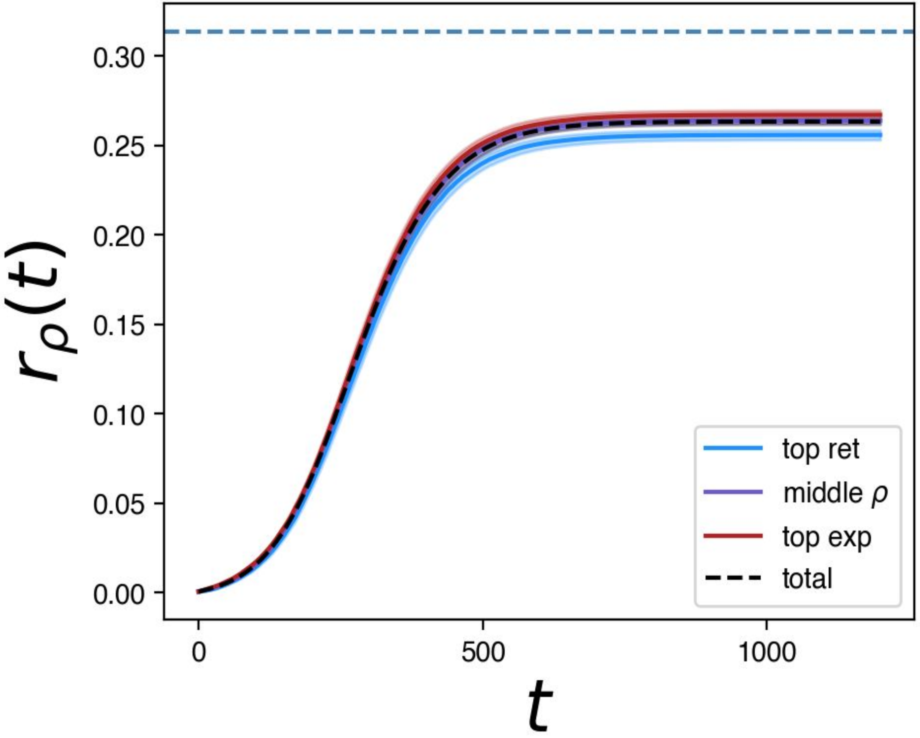


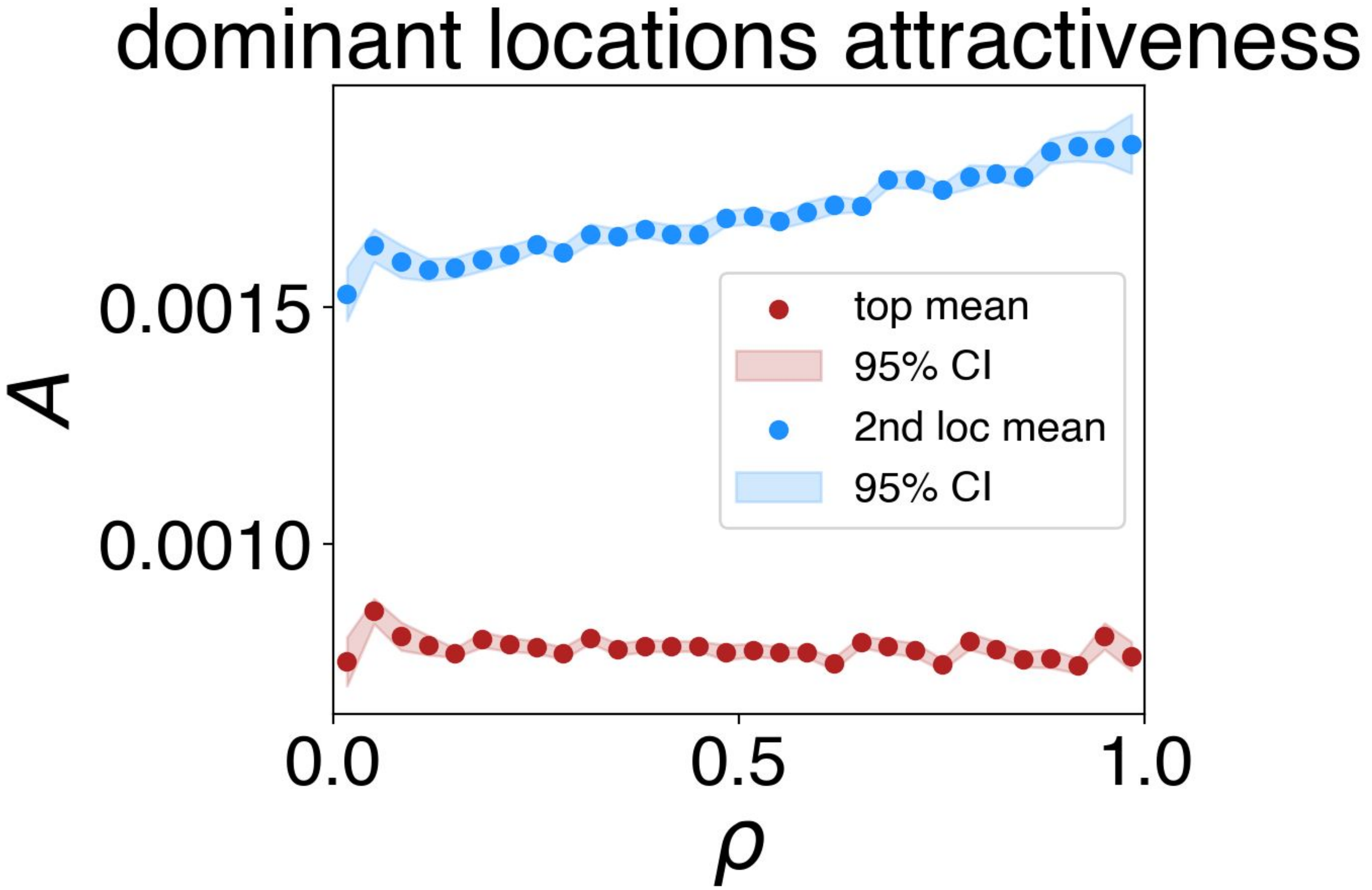
Average degree



Time evolution for incidence & prevalence

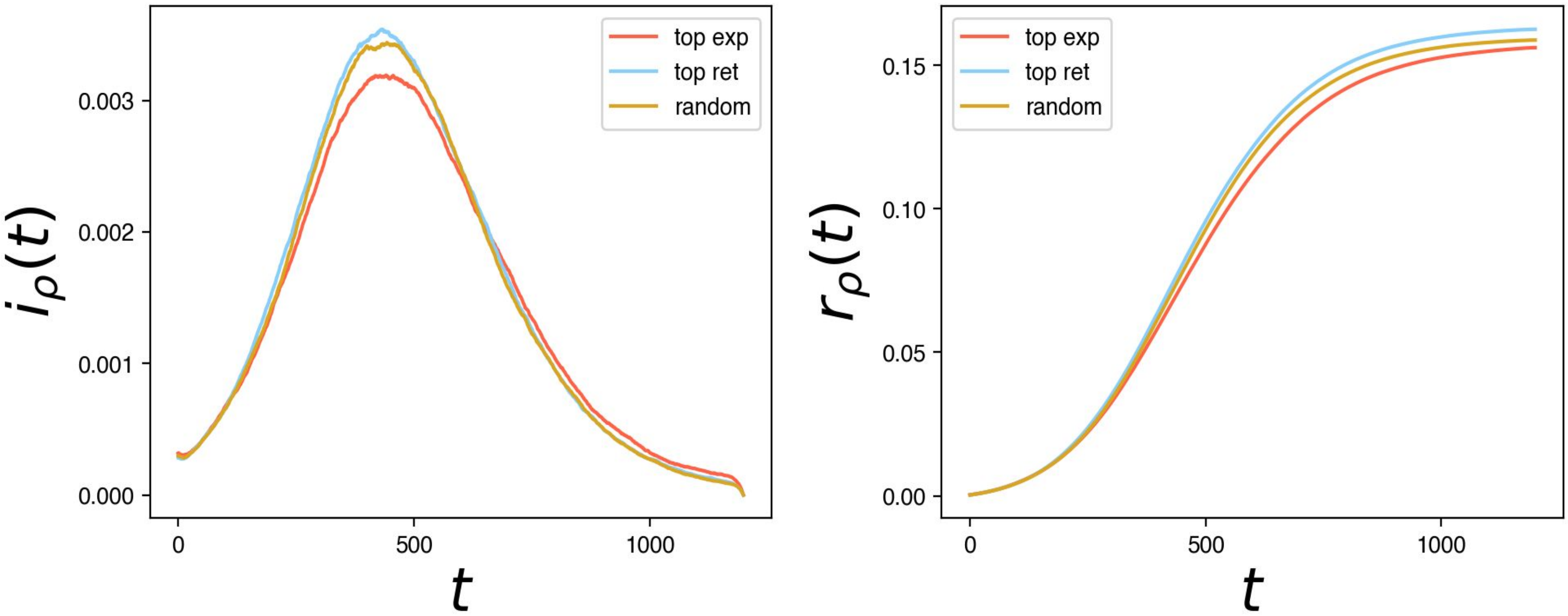




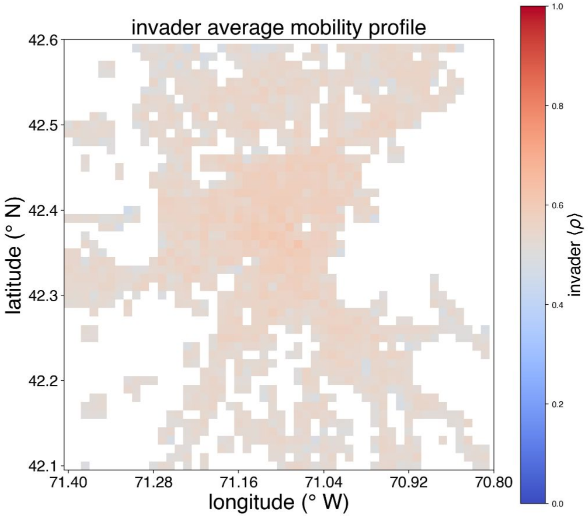


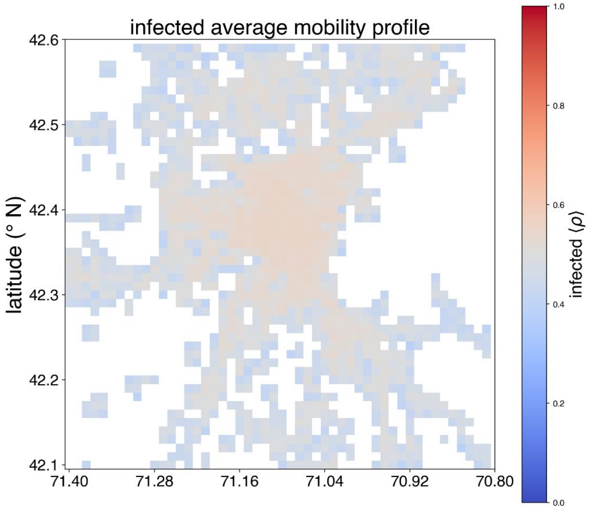
dominant locations attractiveness
0.0015
0.0010
A
top mean
95% CI
2nd loc mean
95% CI
0.0
0.5
1.0
ρ

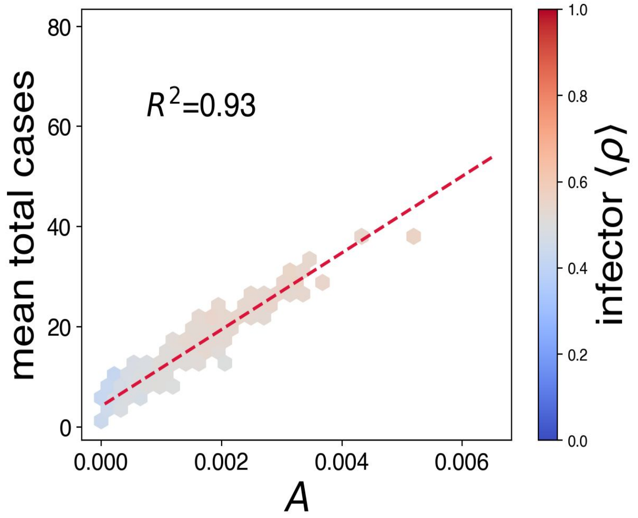
Targeted vaccination



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** ($\boldsymbol{\rho}$>0.5).
In the **least attractive** locations, the typical infected tends to be a returner **lower** ($\boldsymbol{\rho}$<0.5).