ACCELERATION OF EVOLUTIONARY SPREAD BY LONG-RANGE DISPERSAL

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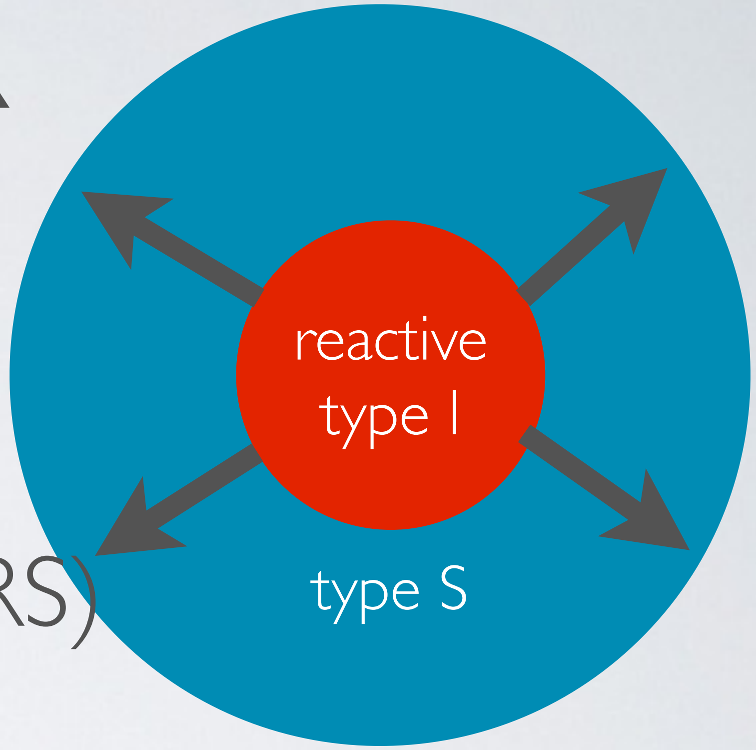
joint work with Daniel S. Fisher
(Stanford)

DISPLACING ONE TYPE BY ANOTHER

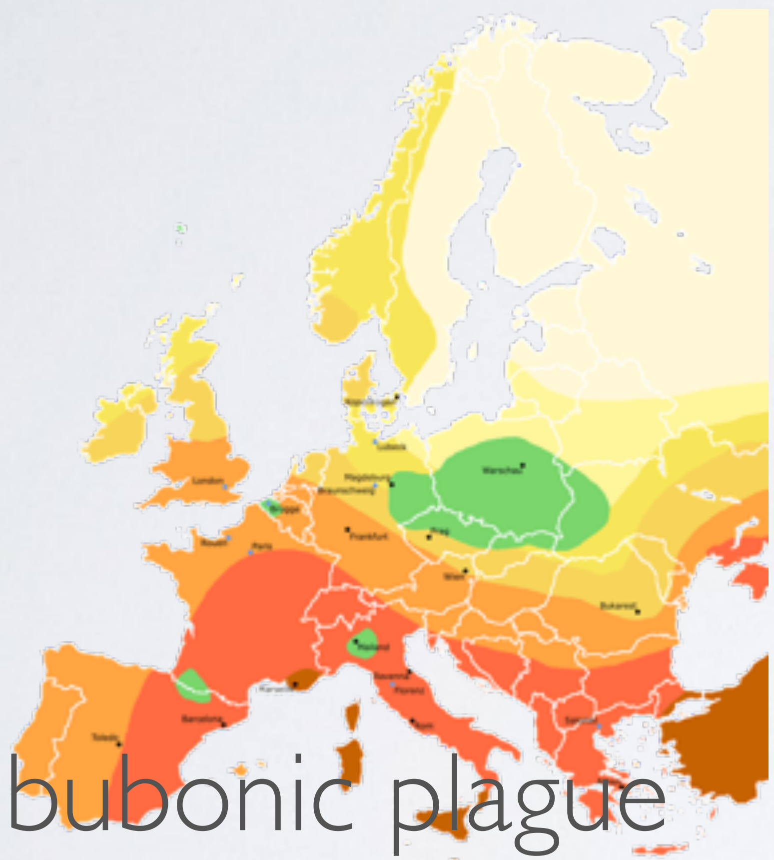


- Spread of an advantageous gene
- Spread of infectious disease (influenza, SARS) ~ chemical reaction, e.g. S+I->2I
- Spread of invasive species (gypsy moth, cane toad)
- Spread of information, gossip …

How fast?

EPIDEMIC SPREAD

Historic scenario

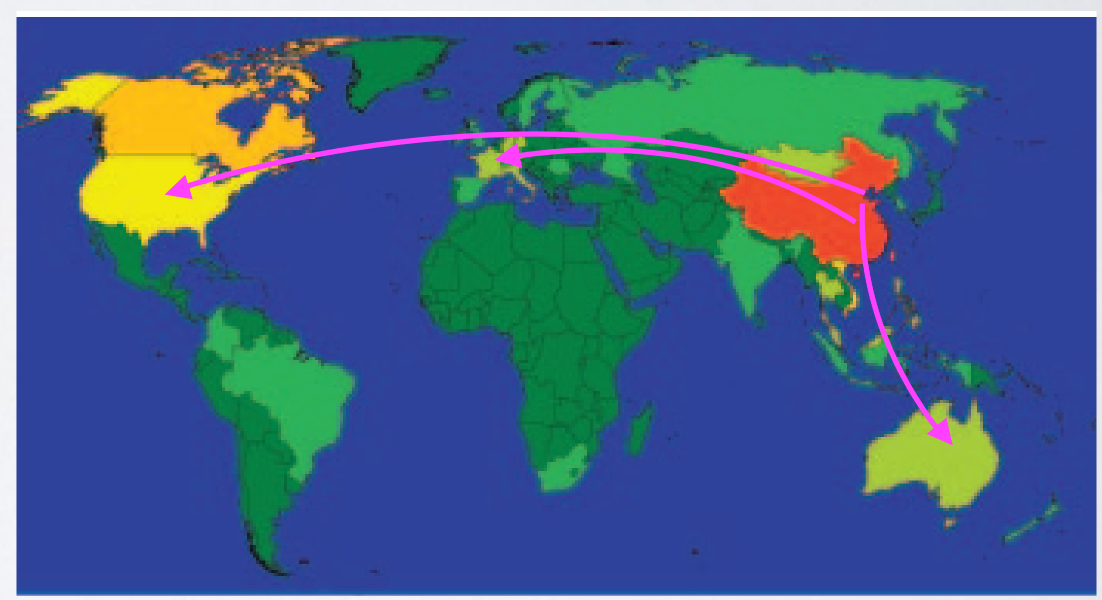


bubonic plague

J. V. Noble, Nature **250**, 726 (1974).

300-600km/yr

Modern scenario



SARS

L Hufnagel et al., PNAS **101,** 15124 (2004)

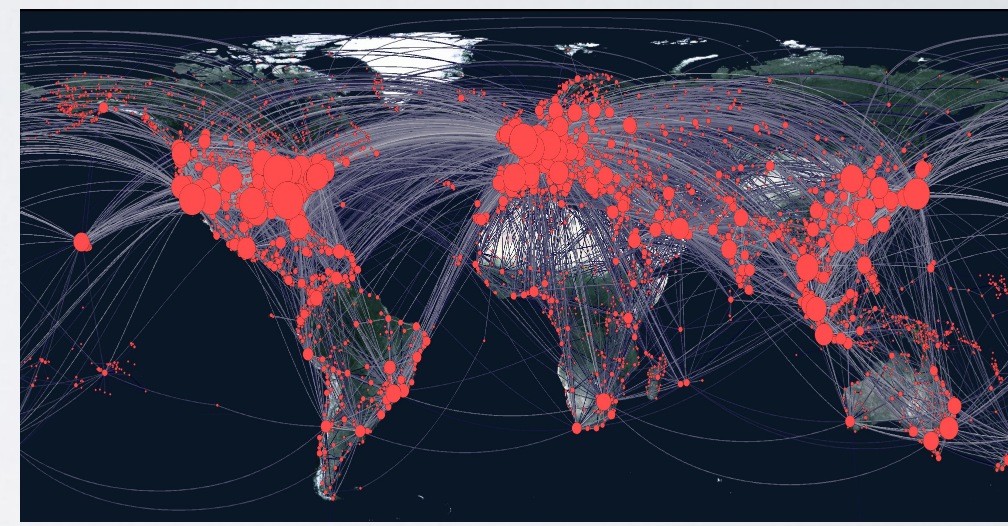
Around the world
in ~6 months

SPREAD DEPENDS ON DISPERSAL PATTERNS

Historic scenario

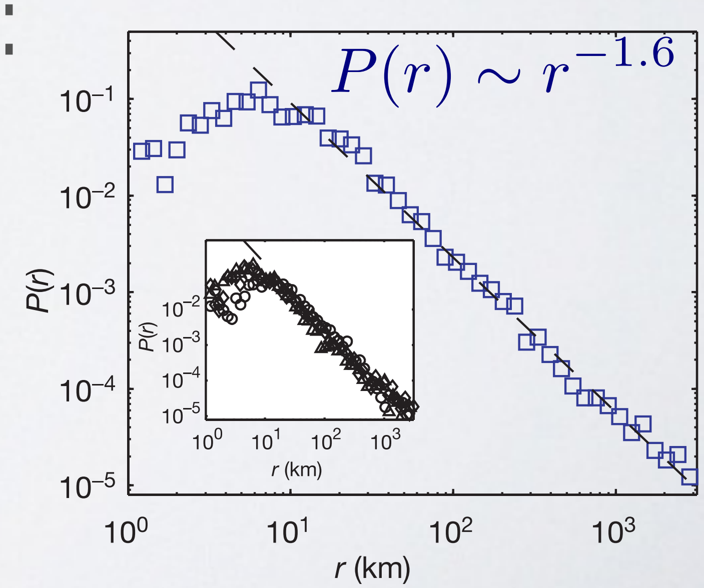
Qualitative Difference?

Modern scenario



Helbing, Brockmann, et al. ArXiv:1402.7011 (2014)

Tracking $ bills: broad tails ...



Brockmann, et al. Nature (2006)

SPREAD DEPENDS ON DISPERSAL PATTERNS

Short distance dispersal (SDD)

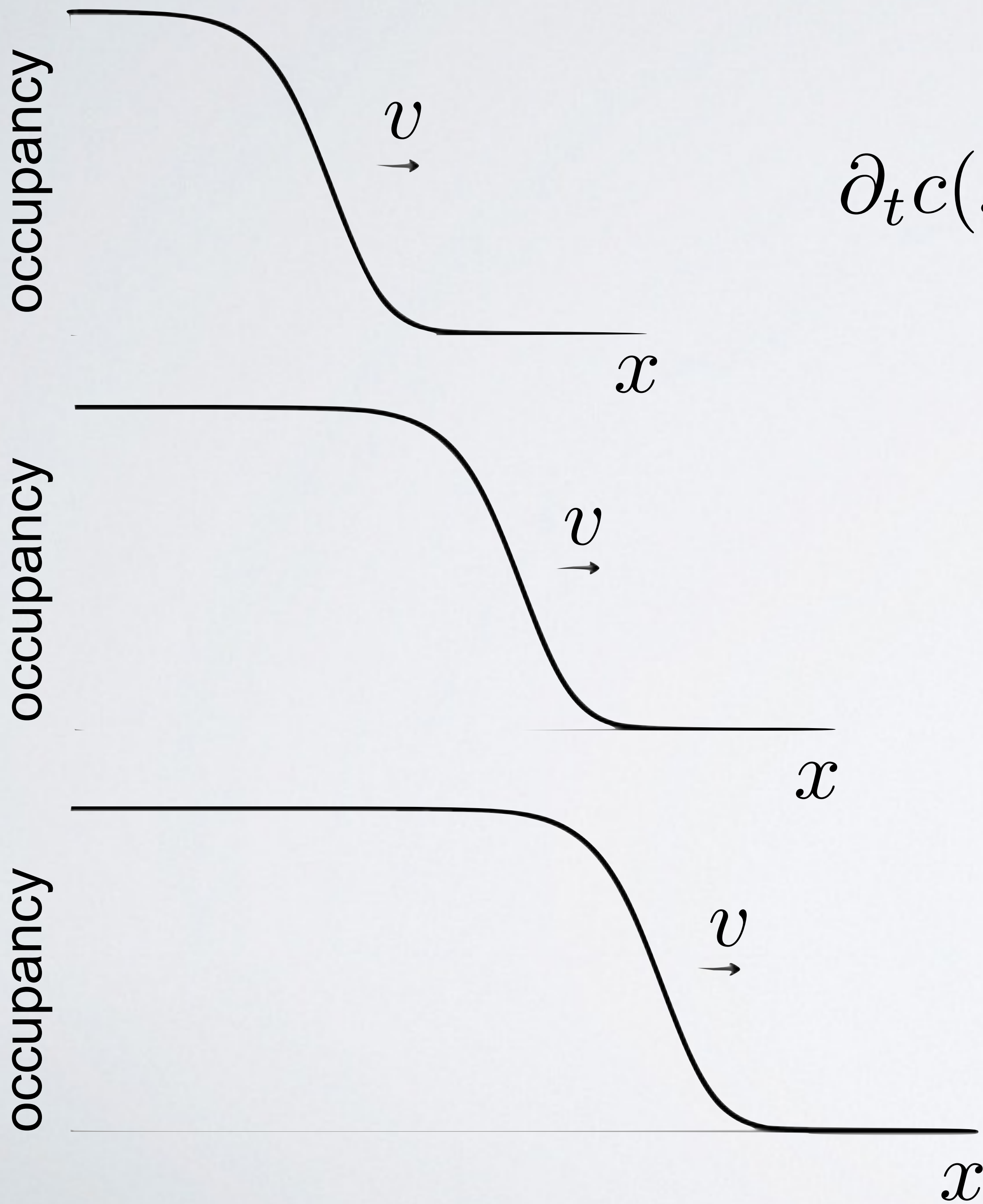
Long distance dispersal (LDD)

Qualitative Difference?

Traveling waves

'Metastatic growth'

TRAVELING WAVES (1D)



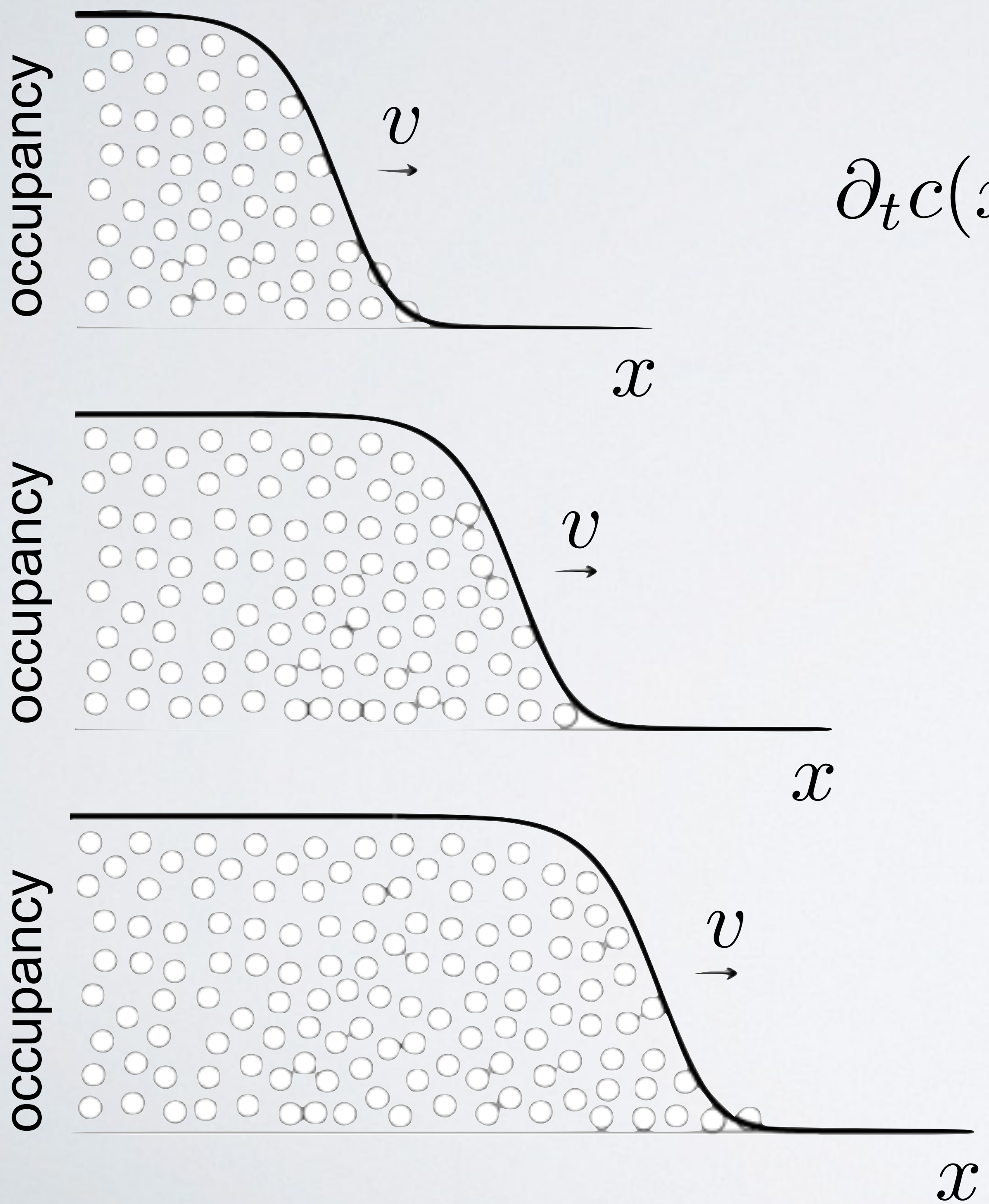
$$\partial_t c(x,t) = D\Delta c + rc\left(1 - \frac{c}{K}\right)$$

diffusion growth

R.A. Fisher (1937), Kolmogorov et al. (1937)

$$v = 2\sqrt{Dr}$$

NOISY TRAVELING WAVES



$$\partial_t c(x,t) = D\Delta c + rc\left(1 - \frac{c}{K}\right) + \eta\sqrt{c}$$

diffusion growth noise

R.A. Fisher (1937), Kolmogorov et al. (1937)

Mueller, Tribe (1995)
Tsimring, et al (1995)
Brunet, Derrida (1998)

$$v = 2\sqrt{Dr} \times \left(1 - \pi^2 \ln^{-2} K\right)$$

weak noise: Brunet, Derrida, PRE (1998)

GENERALIZATION TO LONG DISTANCE DISP.

$$\partial_t c(x,t) = D\Delta c + rc\left(1 - \frac{c}{K}\right) + \eta\sqrt{c}$$

diffusion growth noise

$$\int_{\vec{x}'} G\left(\vec{x} - \vec{x}'\right) c(\vec{x}')$$

jump kernel

so far, mostly mean field approaches:

$$G(\vec{z}) \sim |z|^{-(\mu+d)}$$

$\mu < 2$ → exp. growth

e.g. Mancinelli, Vergni, Vulpiani, (2002), del Castillo-Negrete D (2003)

'fat tail cutoff' → lin. growth

Hufnagel, Brockmann (2008)

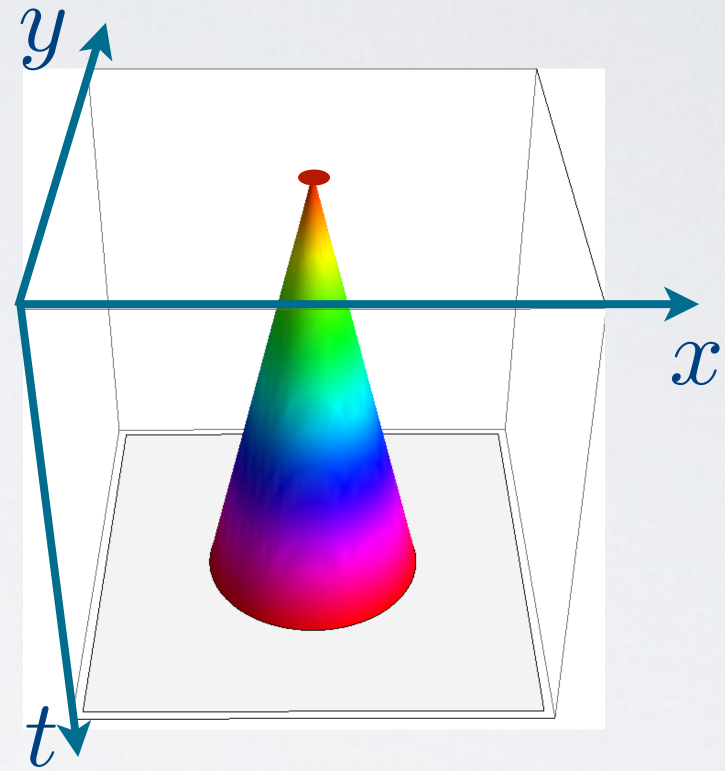
Mean-field approaches neglect the discreteness of long-range jumps

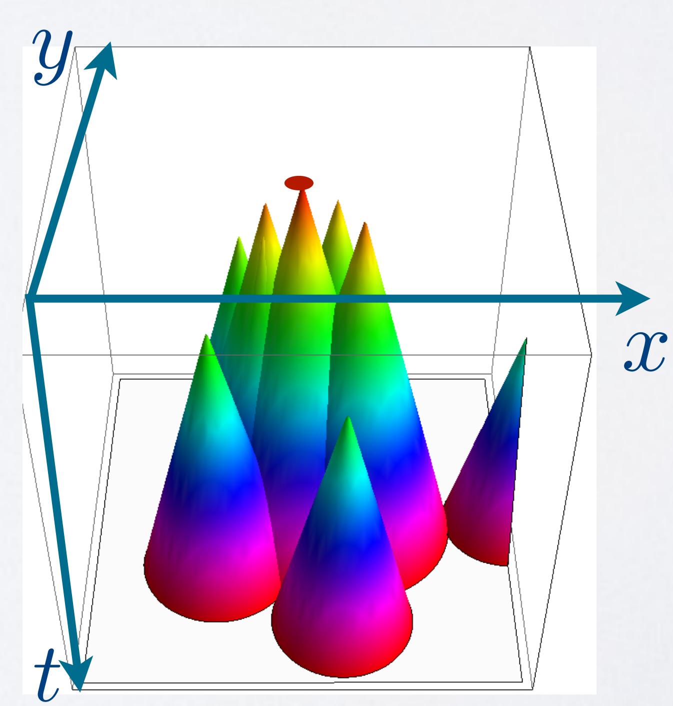
inconsistent with simulations, see below

SIMULATIONS

- Start with one 'seed' on a d={1,2} lattice.
- New seeds due to long range jumps from established populations.

$$G(\vec{z}) \sim \epsilon |\vec{z}|^{-(\mu+d)}$$

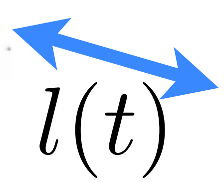


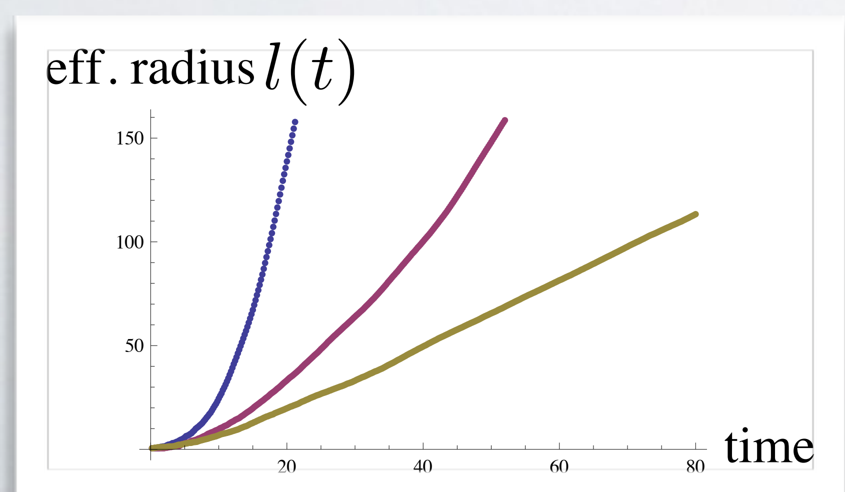


MOVIES

$\mu = 3.5$

Finite speed

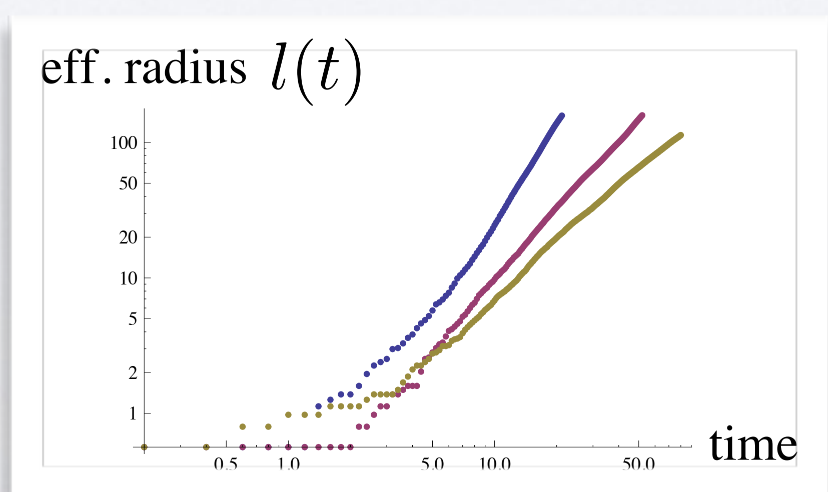




$\mu = 2.5$

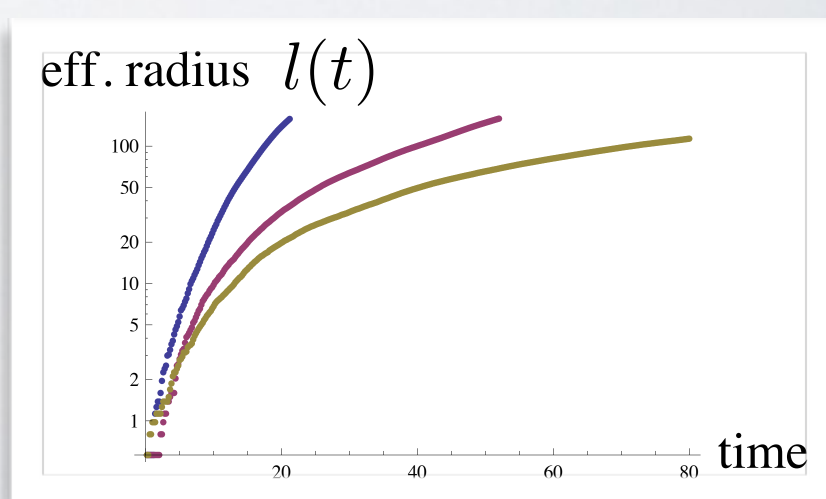
Power law

(even though variance of jump sizes is finite)

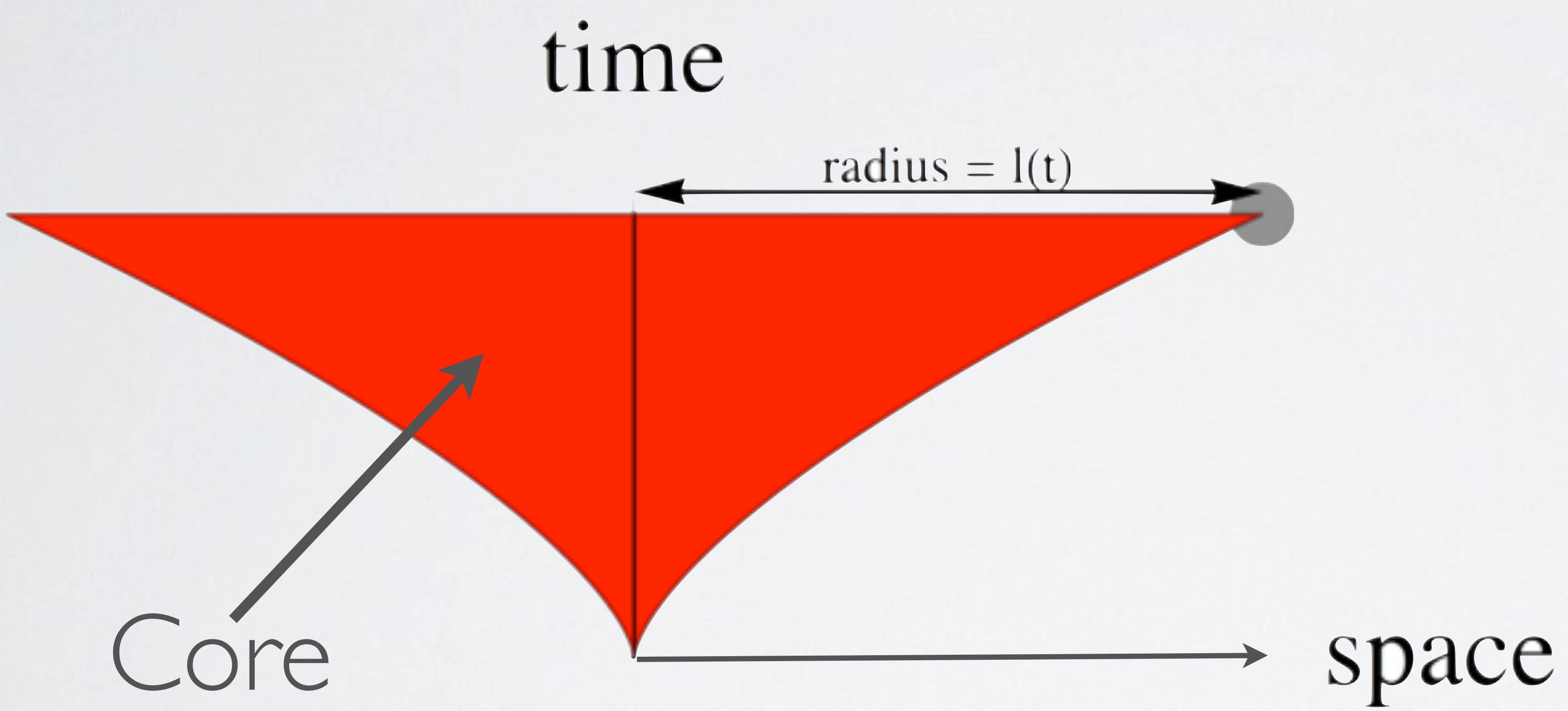


$\mu = 1.5$

Stretched exponential



SELF-CONSISTENCY ARGUMENT



O. H., D. S. Fisher, 2014, arXiv:1403.4639

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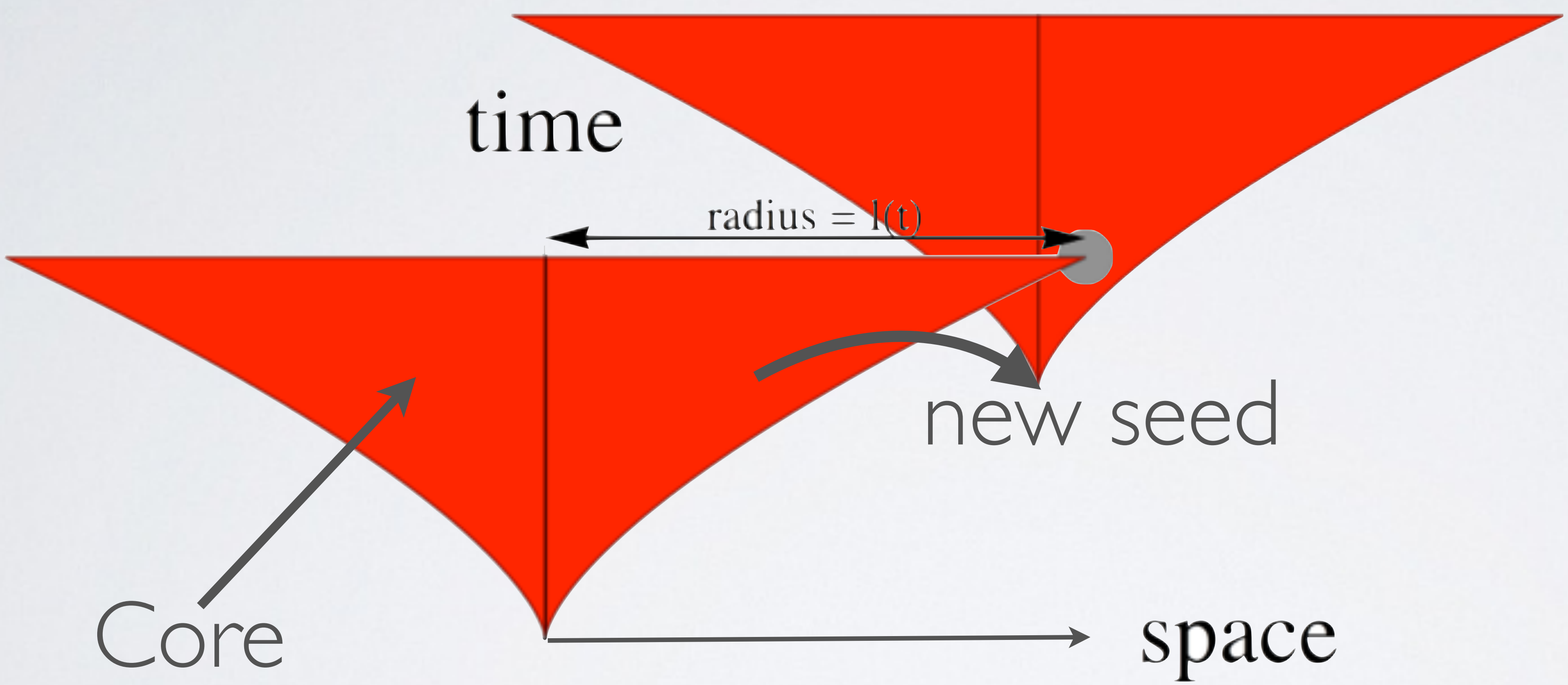

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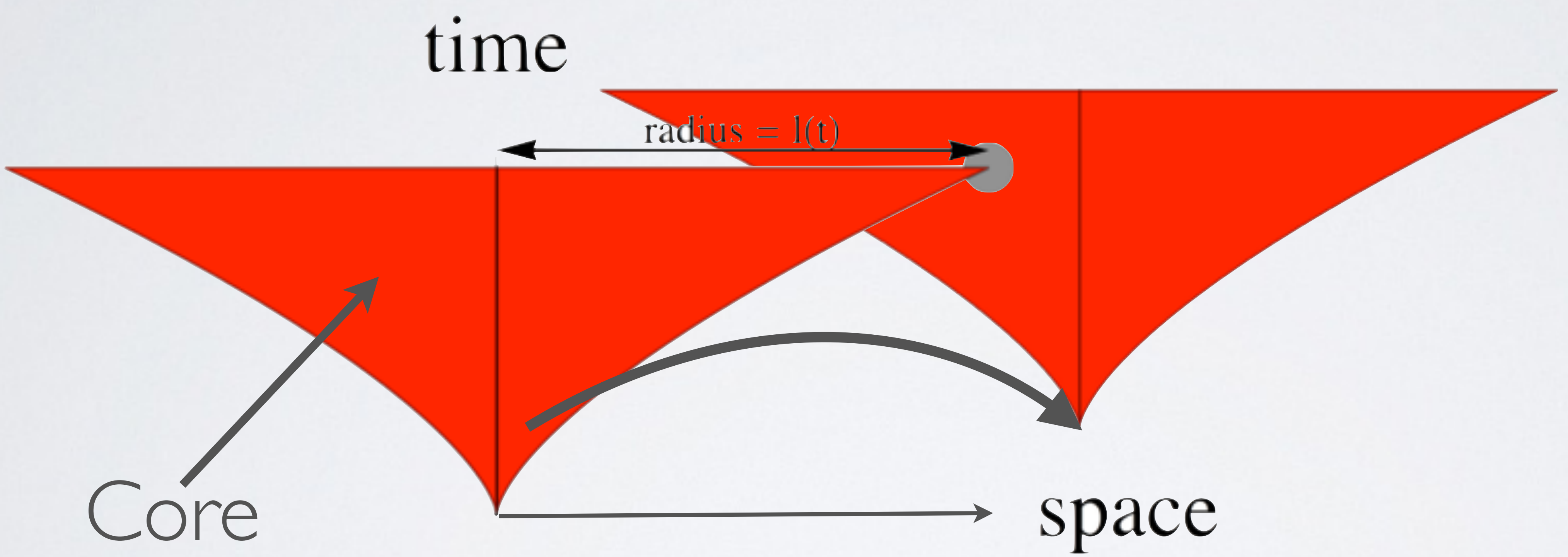

O. H., D. S. Fisher, 2014, arXiv:1403.4639

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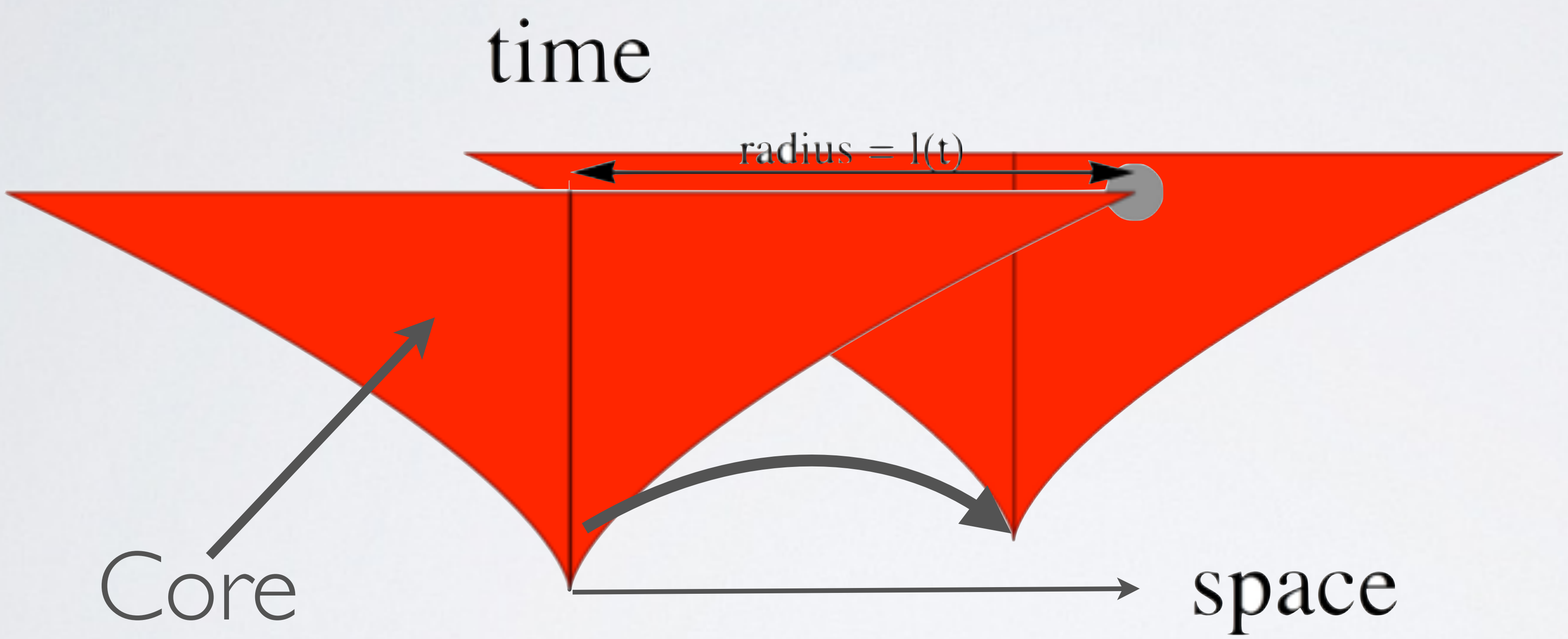

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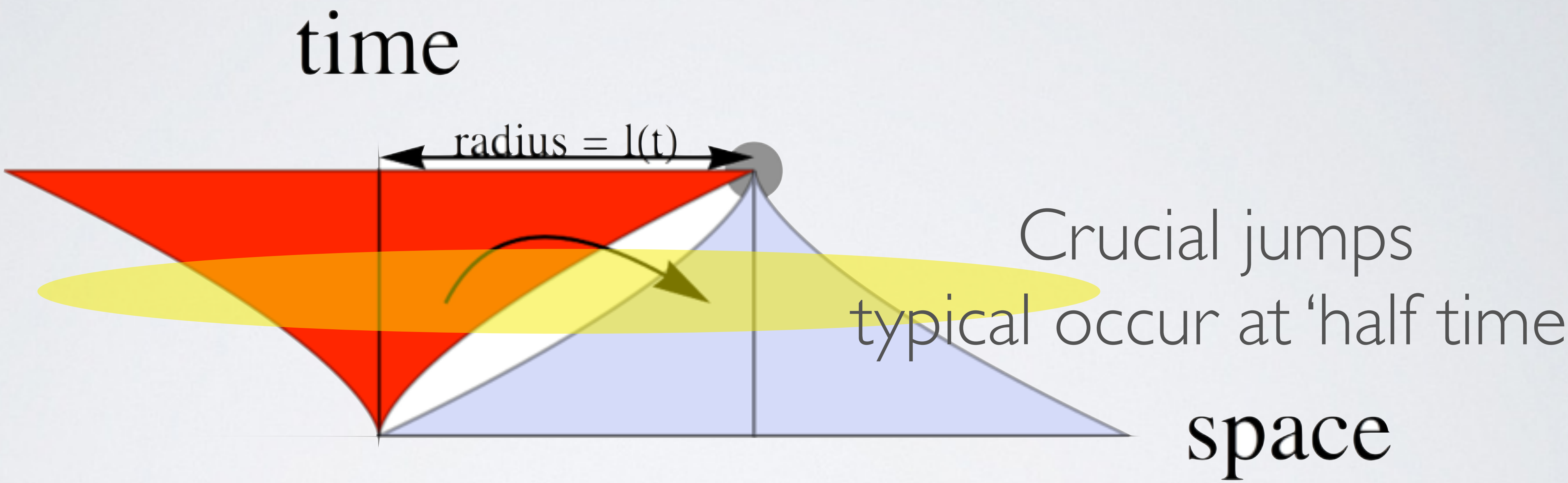
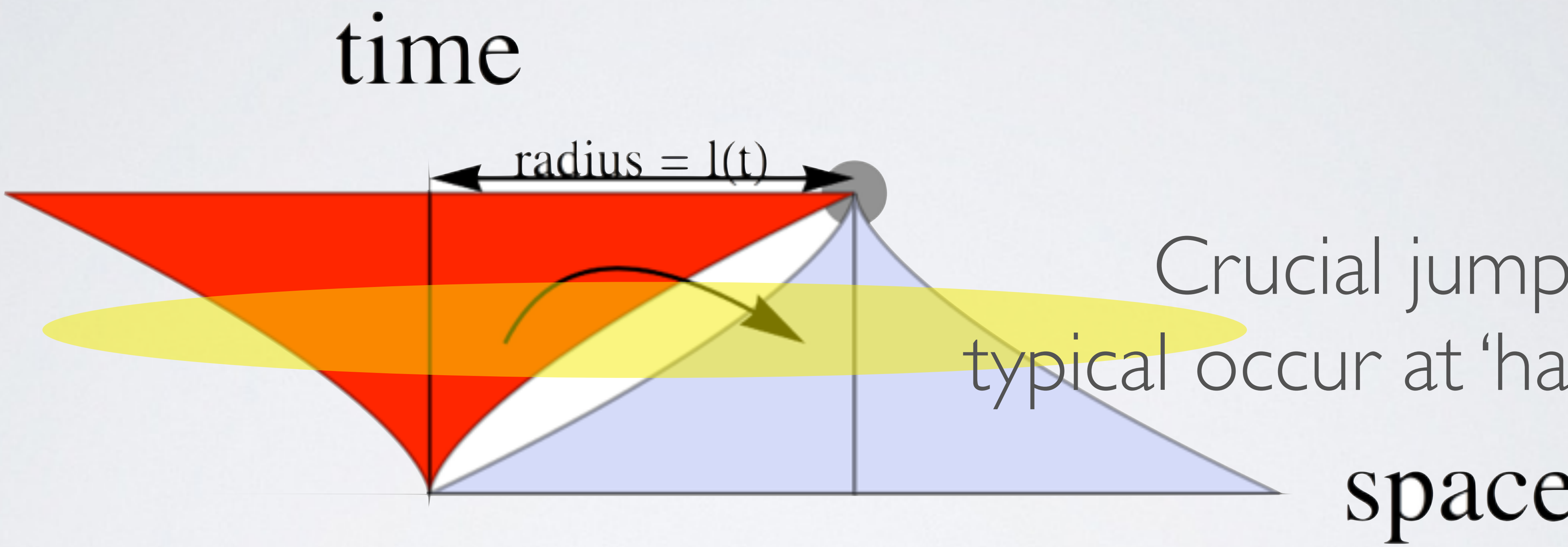


$$1 \approx \int_0^t dt' \int_{\mathcal{B}_{l(t')}} d^d r \int_{\mathcal{B}_{l(t-t')}} d^d r' \; G\left[l(t)\hat{e} + \vec{r} - \vec{r}'\right]$$

(jump kernel)

O. H., D. S. Fisher, 2014, arXiv:1403.4639

SELF-CONSISTENCY ARGUMENT



Crucial jumps typical occur at 'half time'

Saddle Point Approximation

$$1 \approx t\, l(t/2)^{2d}\, G[l(t)]$$

$$\Rightarrow \quad l(t)^{\mu+d} \approx t\, l(t/2)^{2d}$$

O. H., D. S. Fisher, 2014, arXiv:1403.4639

ASYMPTOTICS

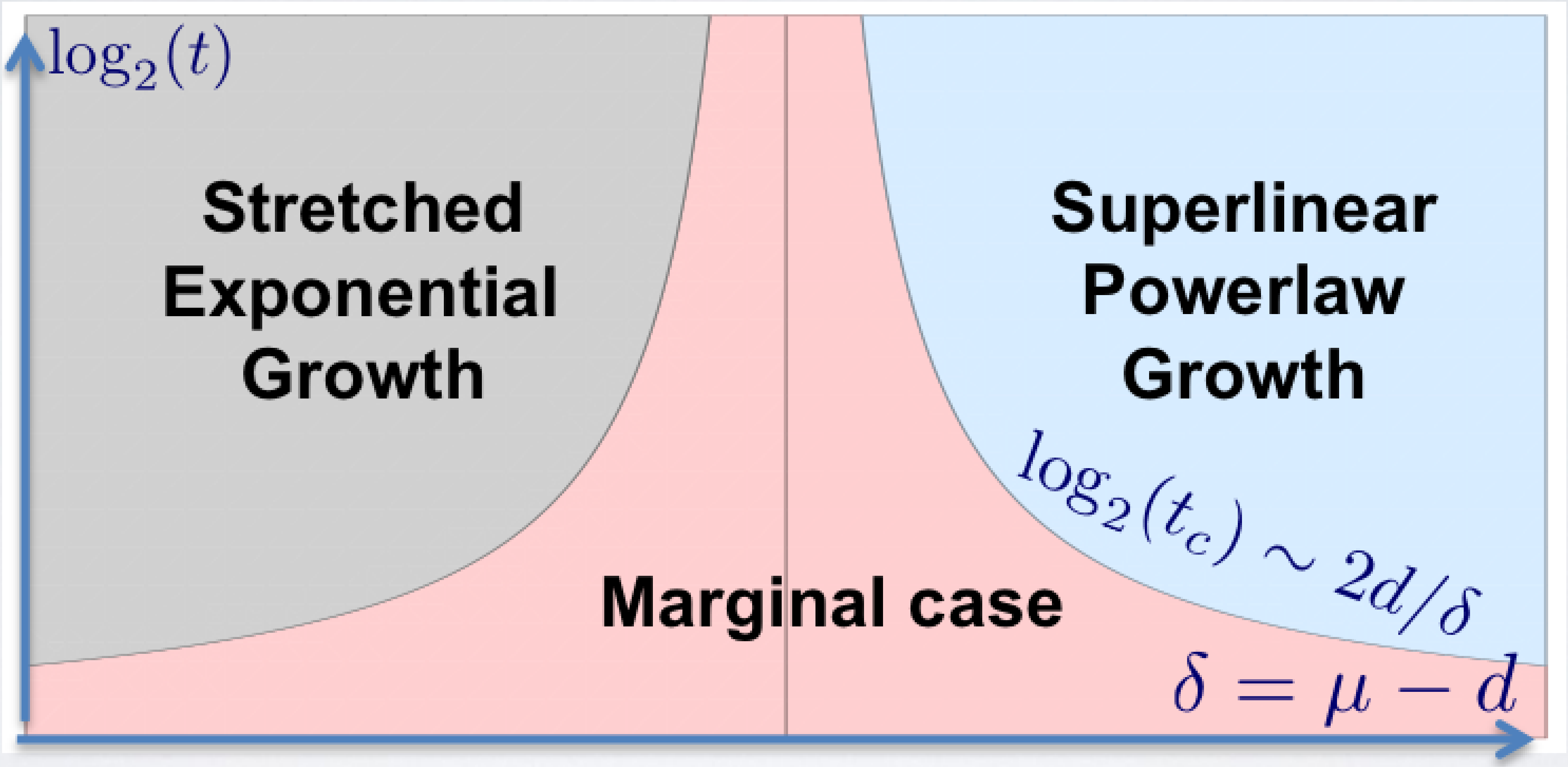
Supposing: $G(\vec{z}) \sim \epsilon|\vec{z}|^{-(\mu+d)}$

$\mu < d$	$\log l(t) \sim B_\mu t^\eta$ $\quad \eta = \frac{\log[2d/(d+\mu)]}{\log 2}$
$\mu = d$	$\log l(t) \sim C_d \log^2(t)$
$d+1 > \mu > d$	$l(t) \sim A_\mu t^\beta$ $\quad \beta = (\mu - d)^{-1}$
$\mu = d+1$	$l(t) \sim t \log(t)$
$\mu > d+1$	short-range dispersal dominates; linear spread

[1] Supercritical long-range percolation:
M. Biskup, The Annals of Applied Probability 32, 2938 (2004).

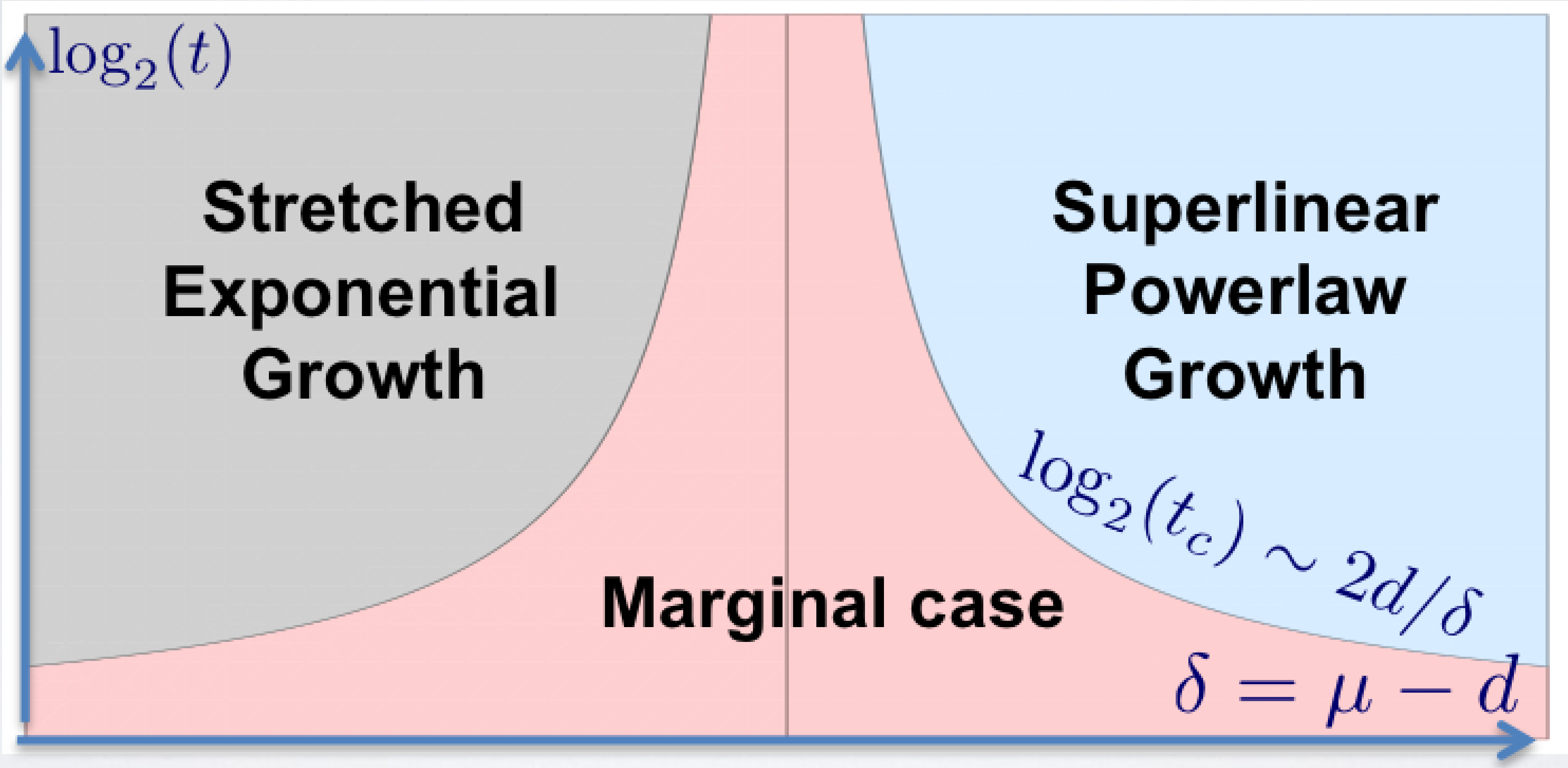
[2] Long-Range First Passage Percolation:
S. Chatterjee, P. S. Dey. arXiv:1309.5757 (2013).

BEYOND ASYMPTOPIA



Full cross-over form is needed for comparison with simulations and nature.

BEYOND ASYMPTOPIA



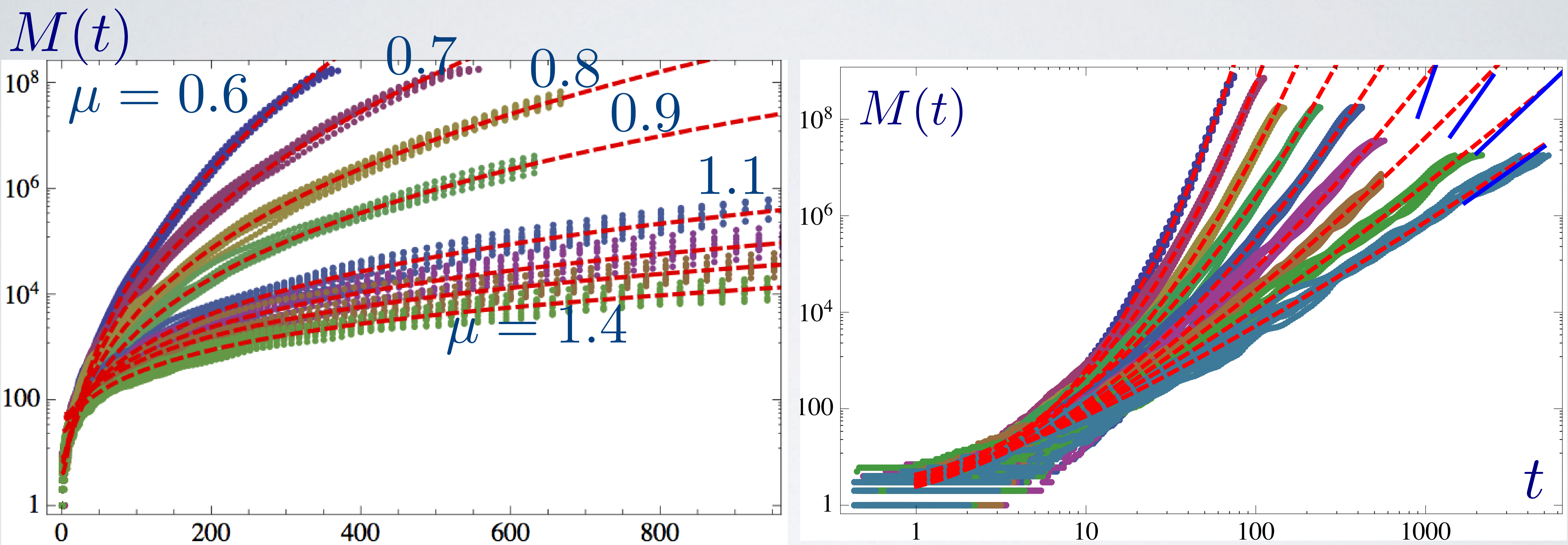
$\varphi = \log_2(l)$ 'log-size'

$z = \log_2(t)$ 'log-time'

$\delta = \mu - d$ distance to marginal case

$$\frac{\delta^2}{2d}\varphi(z) = \frac{\delta z}{2d} + \left(1 + \frac{\delta}{2d}\right)^{-z} - 1$$

THEORY VS. SIMULATIONS - 1D



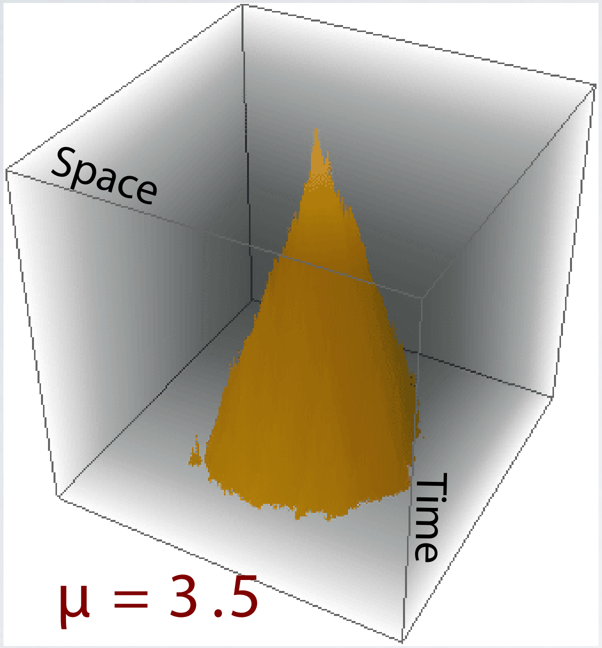
$\varphi = \log_2(l)$
'log-size'

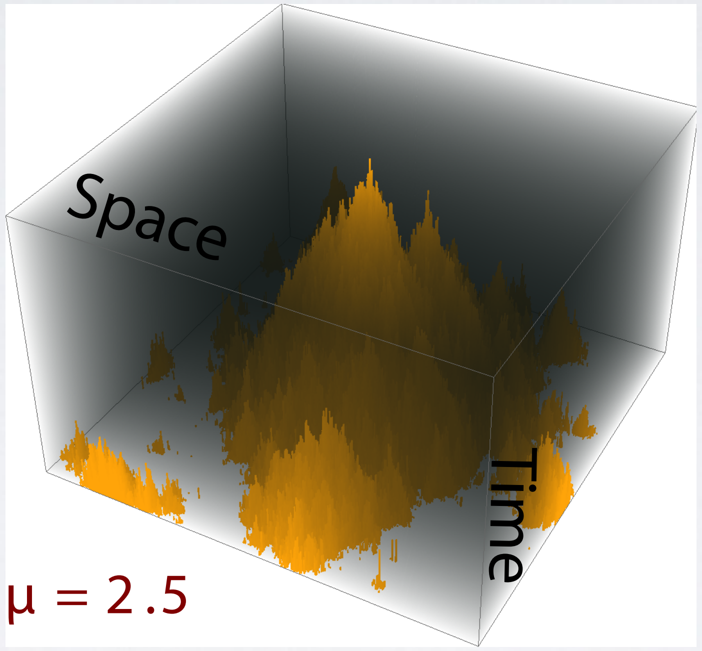
$z = \log_2(t)$
'log-time'

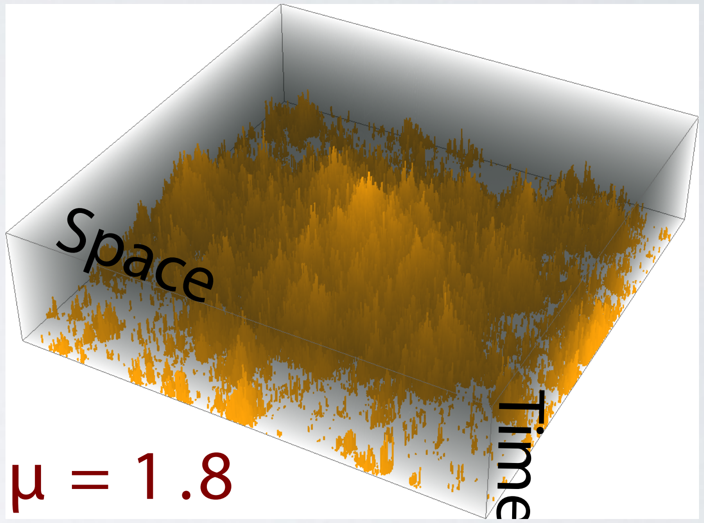
$\delta = \mu - d$
distance to marginal case

$$\frac{\delta^2}{2d}\varphi(z) = \frac{\delta z}{2d} + \left(1 + \frac{\delta}{2d}\right)^{-z} - 1$$

SUMMARY OF SPREADING ANALYSIS

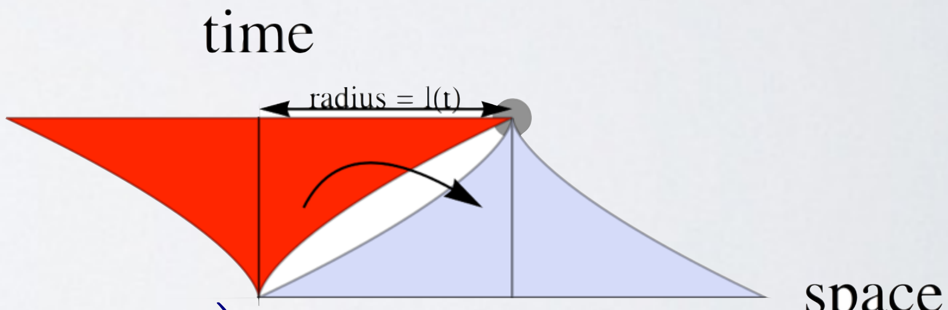






- Mean-field theories fail because they neglect discreteness of long-range jumps.

- Self-consistency constrains the leading order dynamics



- Indirect seeding: mean occupancy @ x :

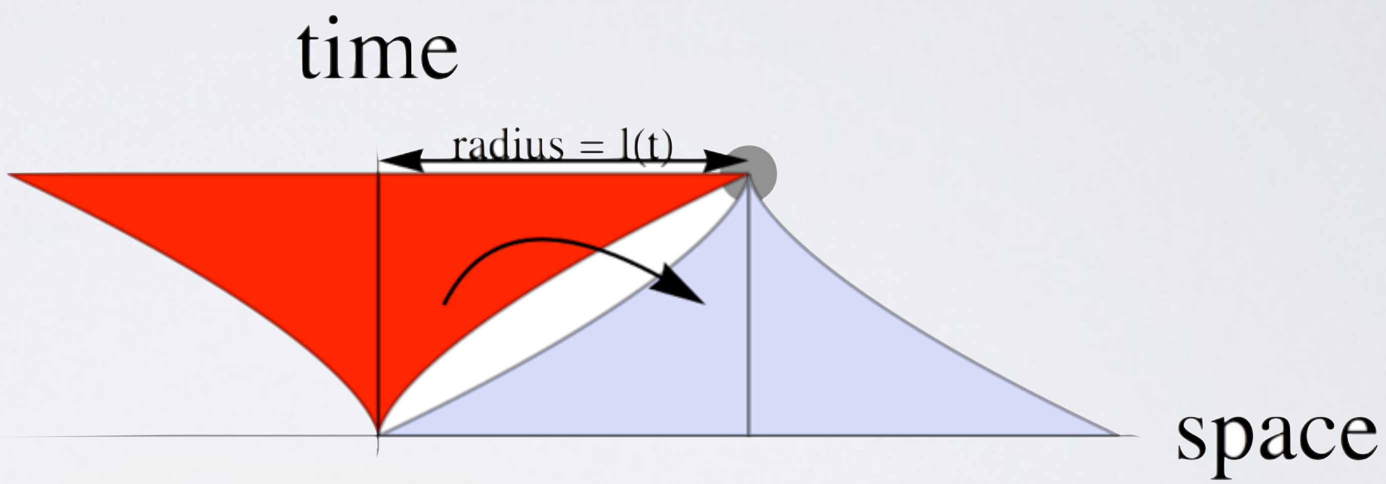
$$\langle c(x)\rangle = 1 - \exp\left(|x/l(t)|^{-(d+\mu)}\right)$$

- *Sub-exponential* growth laws for l(t):
  Power law, stretched exponentials and a crucial marginal case in between.

MORE COMPLEX EPIDEMIC MODELS

SI model

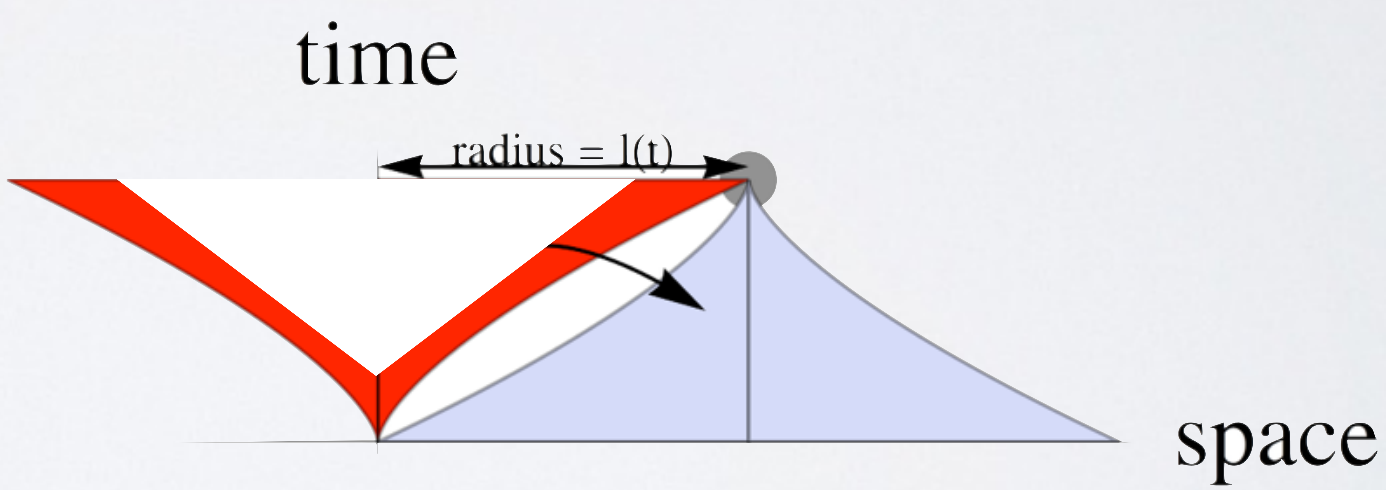
$$S + I \to 2I$$



SIR model

$$S + I \to 2I$$

$$I \to R$$

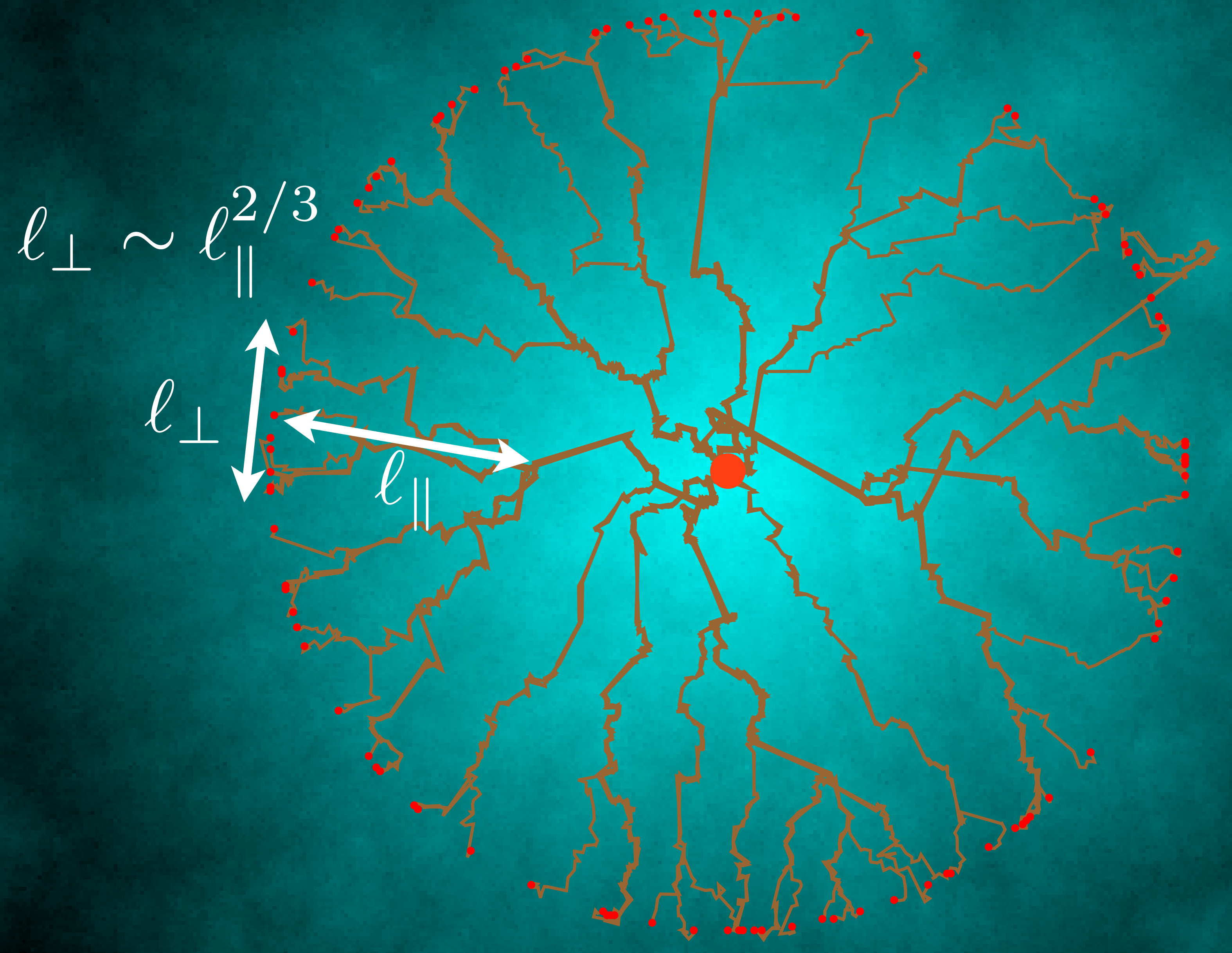


symmetry breaking

SIR → *Supercritical long-range percolation*

[1] M. Biskup, The Annals of Applied Probability 32, 2938 (2004).
[2] P. Grassberger, J. Stat. Mech. 2013, P04004 (2013).

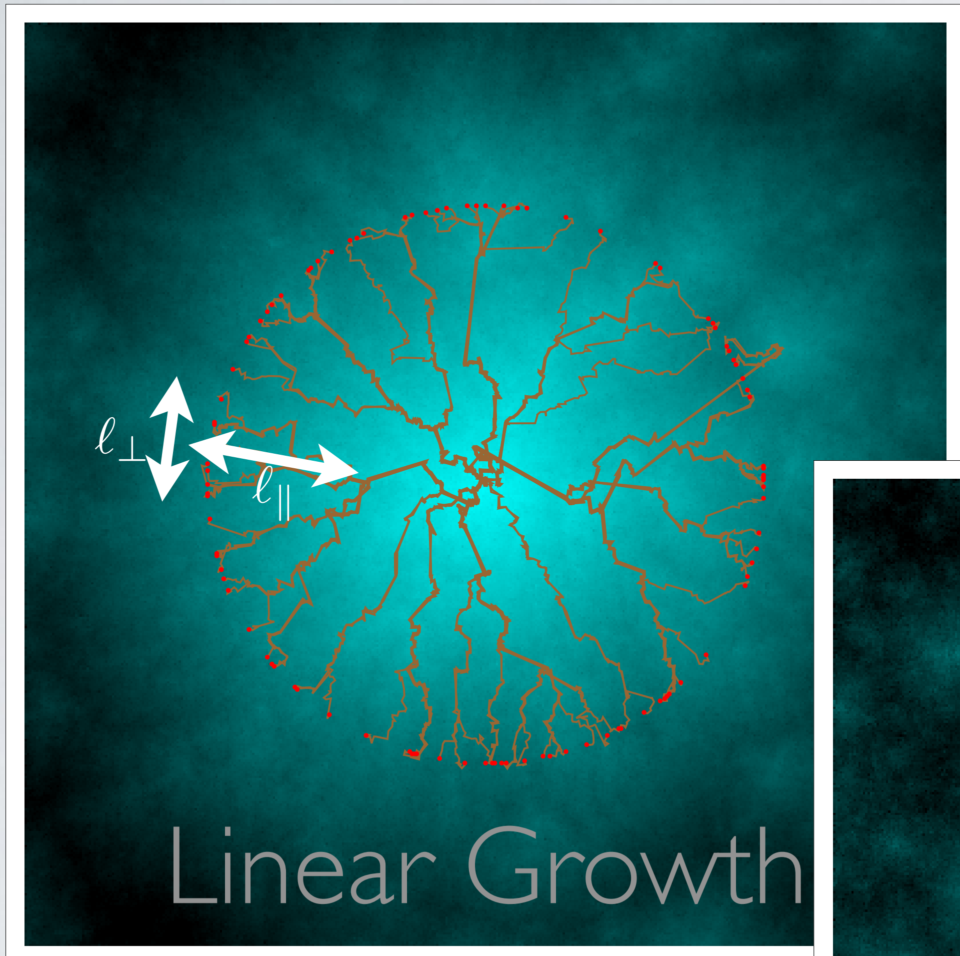
INFECTION TREES



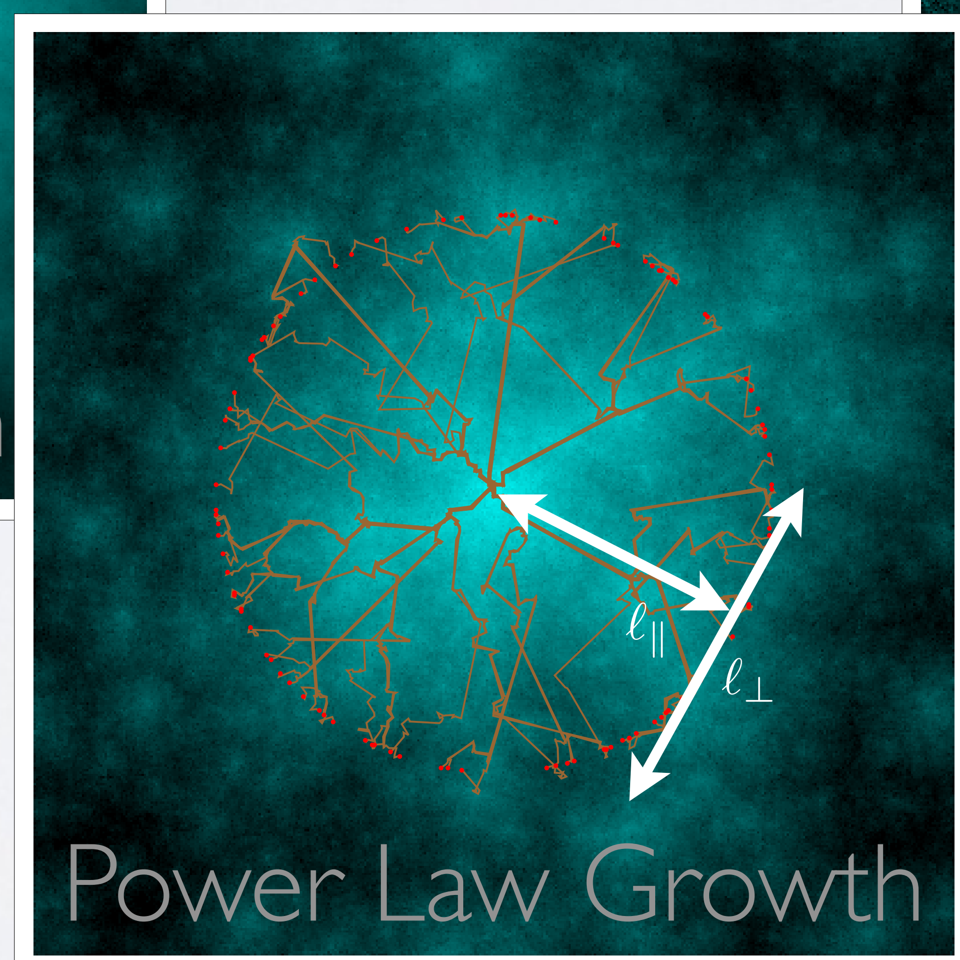
Linear Growth
$\mu = 3.5$

INFECTION TREES

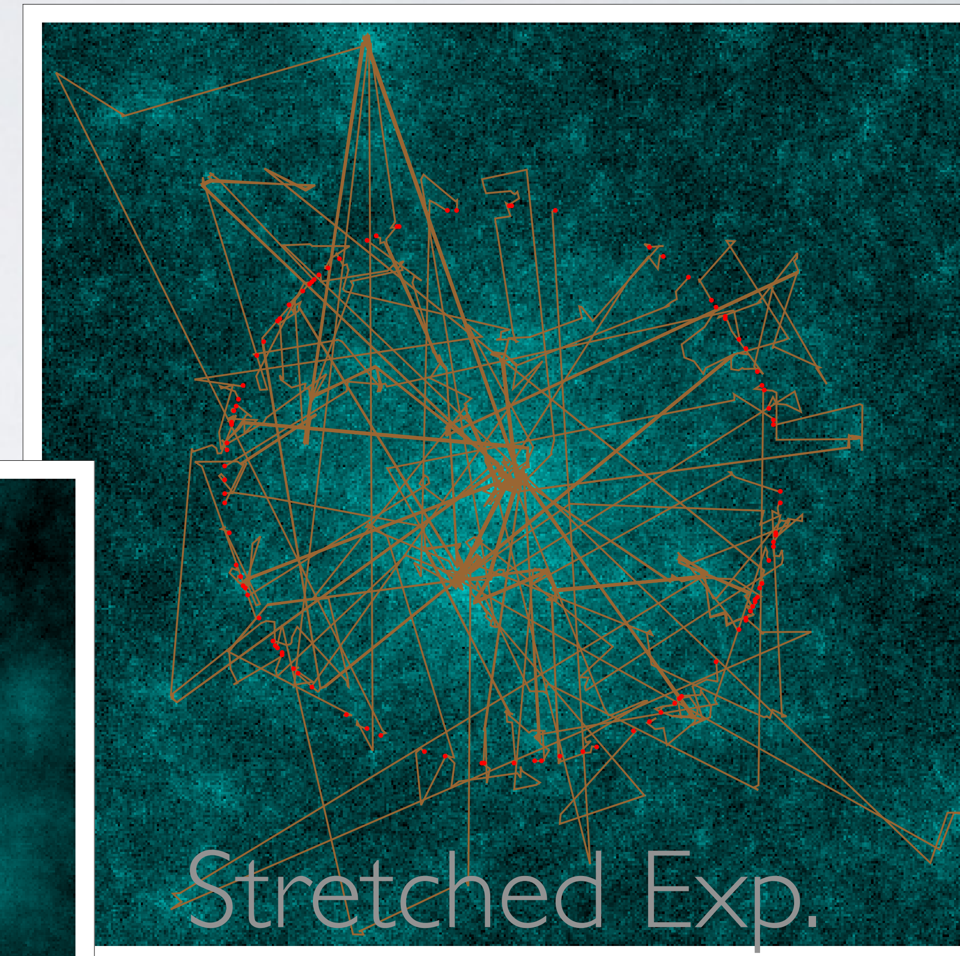
How are Genealogies embedded in space?



$\mu = 3.5$



$\mu = 2.5$



$\mu = 1.5$

OTHER THINGS ON THE HORIZON:

- **Hitchhiking**
- **Soft sweeps**
- **Clonal interference**
- **Data?**

Preprint:

O. H., and D. S. Fisher, 2014, arXiv:1403.4639

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