

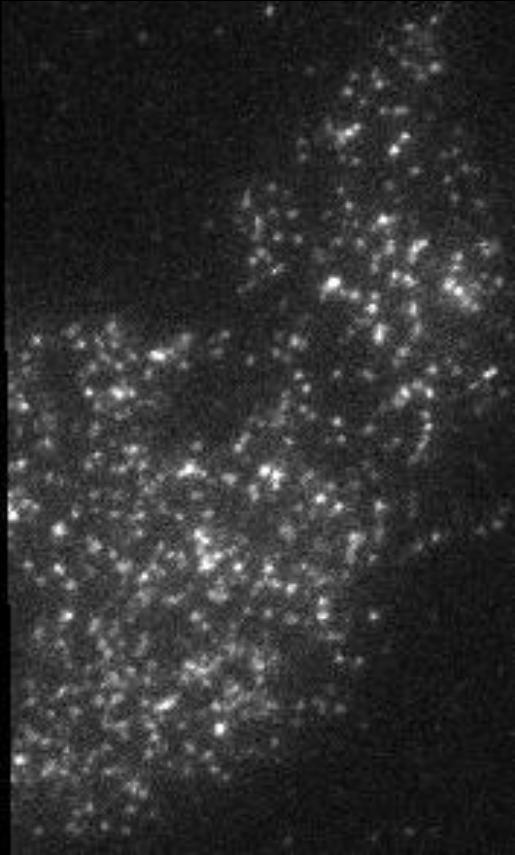
# SAMPLE-DEPENDENT FIRST-PASSAGE TIME DISTRIBUTION IN A DISORDERED MEDIUM

Liang Luo and Lei-Han Tang  
Beijing Computational Science Research Center

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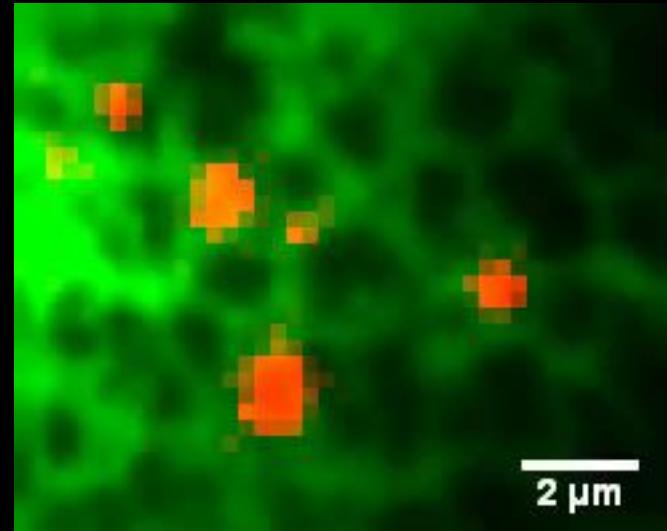
# (Sub-)Diffusion in the cell

*In vivo* imaging experiments offer not only the **particle trajectories** but also the **large structure** of the environment.



G protein-coupled receptor  
on cell membrane

Yongfang Zhao *et al.* private communication

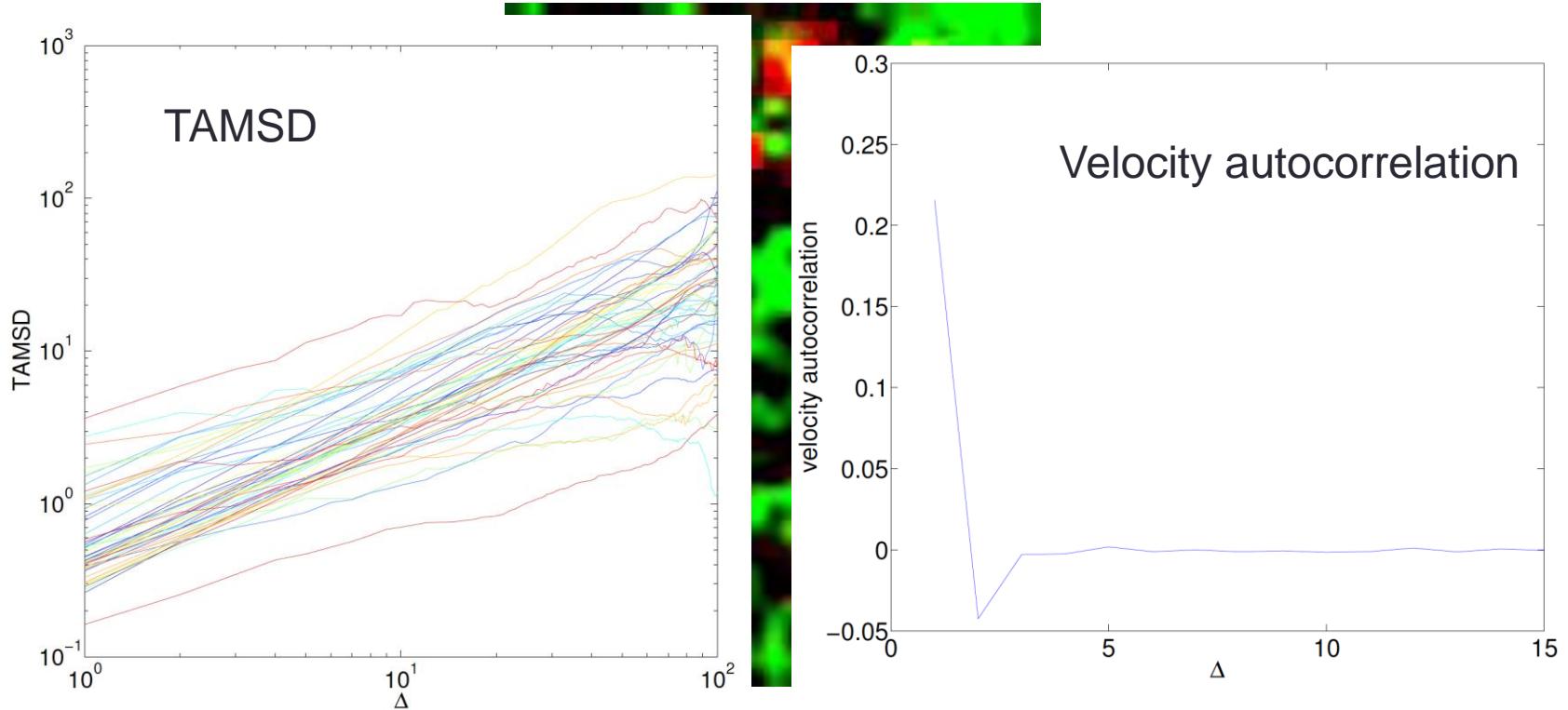


(red) Quantum Dots (QD) in  
cytoplasm  
(green) *endoplasmic reticulum*  
(ER)

Hui Li *et al.* JACS (2015)

# Sub-diffusion observed in experiments

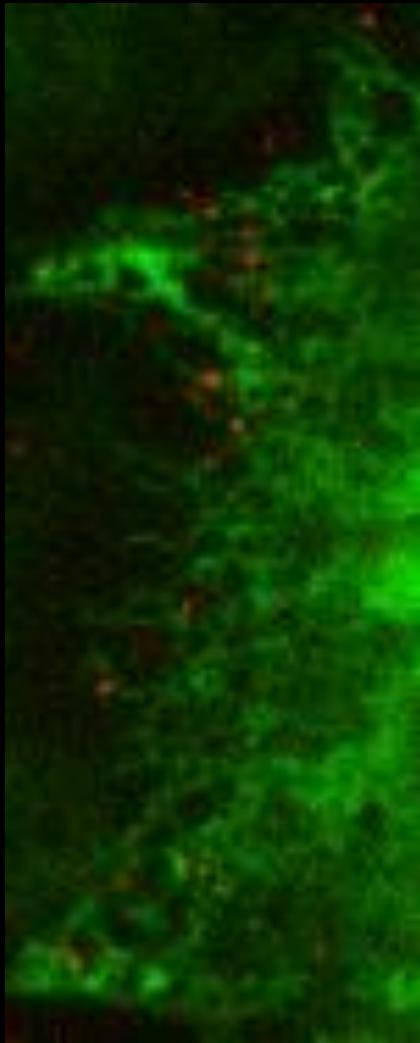
## QD in cytoplasm



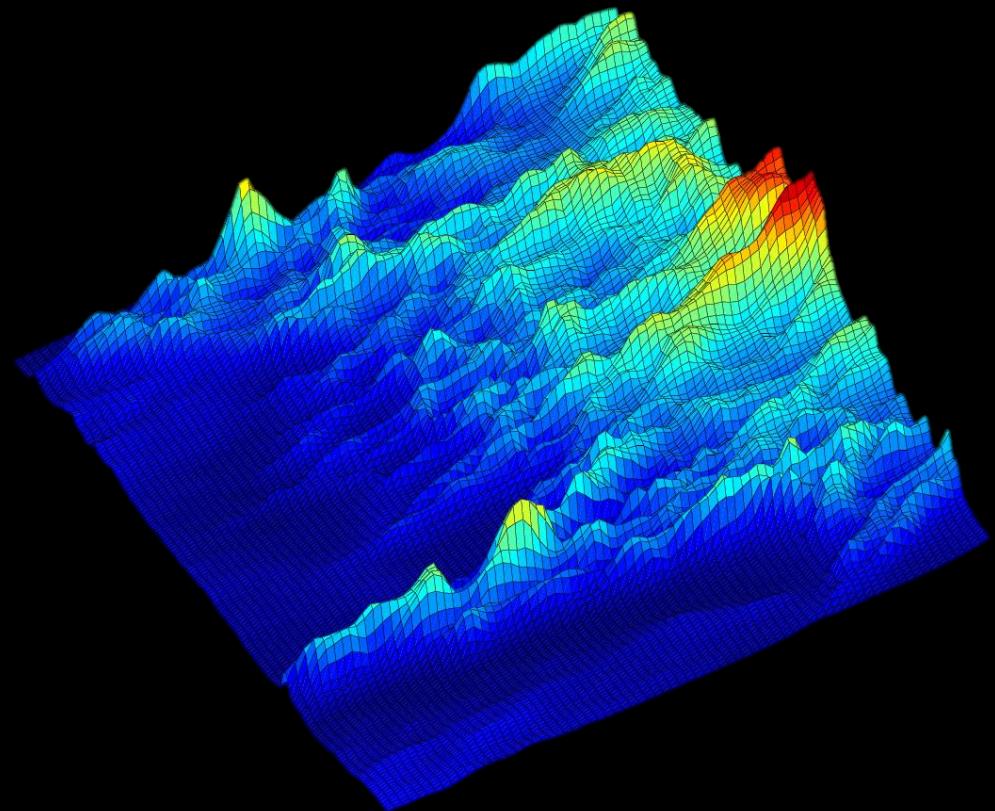
Analysis is still in progress...  
Collaborating with Hui Li

# *endoplasmic reticulum (ER) structure as a quasi-static landscape*

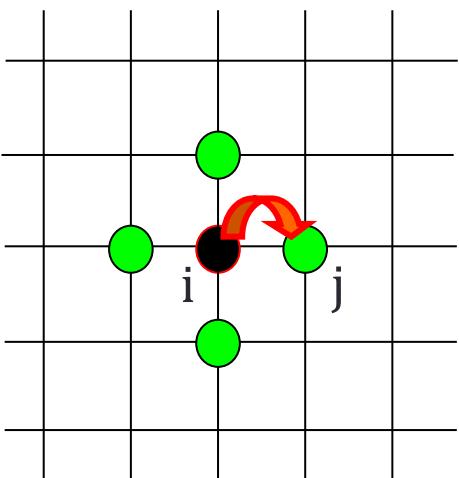
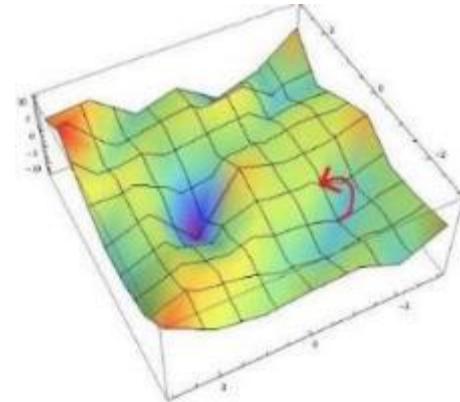
A slice of the ER structure



The dynamics on the static disordered samples!



# Quenched trap model (QTM)



Hopping rate:

$$W_{i \rightarrow j} = \frac{\omega_0}{2d} \exp(V_i/T)$$

$\{V_i\}$ : static random potential

Special case with anomalous diffusion:

$$P(V) = T_g^{-1} \exp(V/T_g), V < 0$$

The mean waiting time distribution:

$$P(\tau) = \mu \omega_0^{-\mu} \tau^{-(1+\mu)}, \mu \equiv T/T_g$$

## Continuous Time Random Walk (CTRW):

NO static potential.

The waiting time is independently generated for each hopping.

$$\text{QTM} \longleftrightarrow \text{CTRW}, d > 2$$

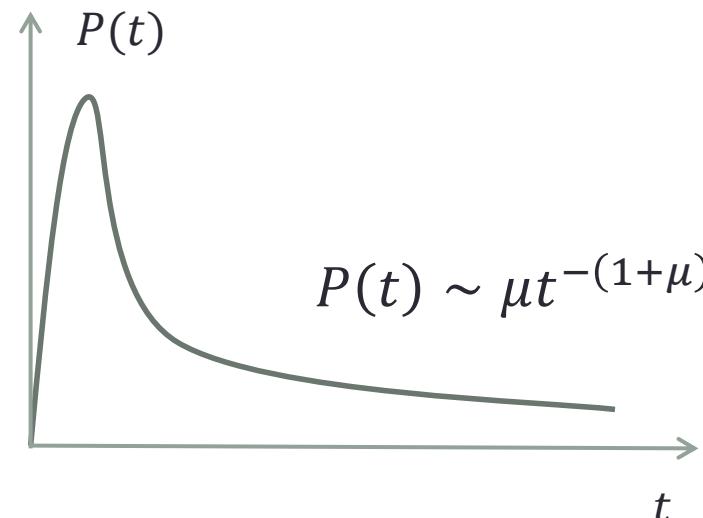
RG in real-space, Machta, J. Phys. A, (1985)

Arguments, Bouchaud and George, Phys. Rep. (1990)

# The CTRW time scale

The total walking time of a  $N$ -step walk

$$t_N = \sum_{i=1}^N t_i$$



A fat tail case:  $P(t_i = t) \sim \mu t^{-(1+\mu)}$ ,  $\mu < 1$

$$\langle t_N \rangle / N = \int_1^\infty dt t P(t) \rightarrow \infty$$

$P(t_N/N)$ : one-side Levy stable distribution

See e.g. Bouchaud and George 1990.

$$t_{typ} \equiv \exp(\langle \ln t_N \rangle) \sim N^{1/\mu}$$

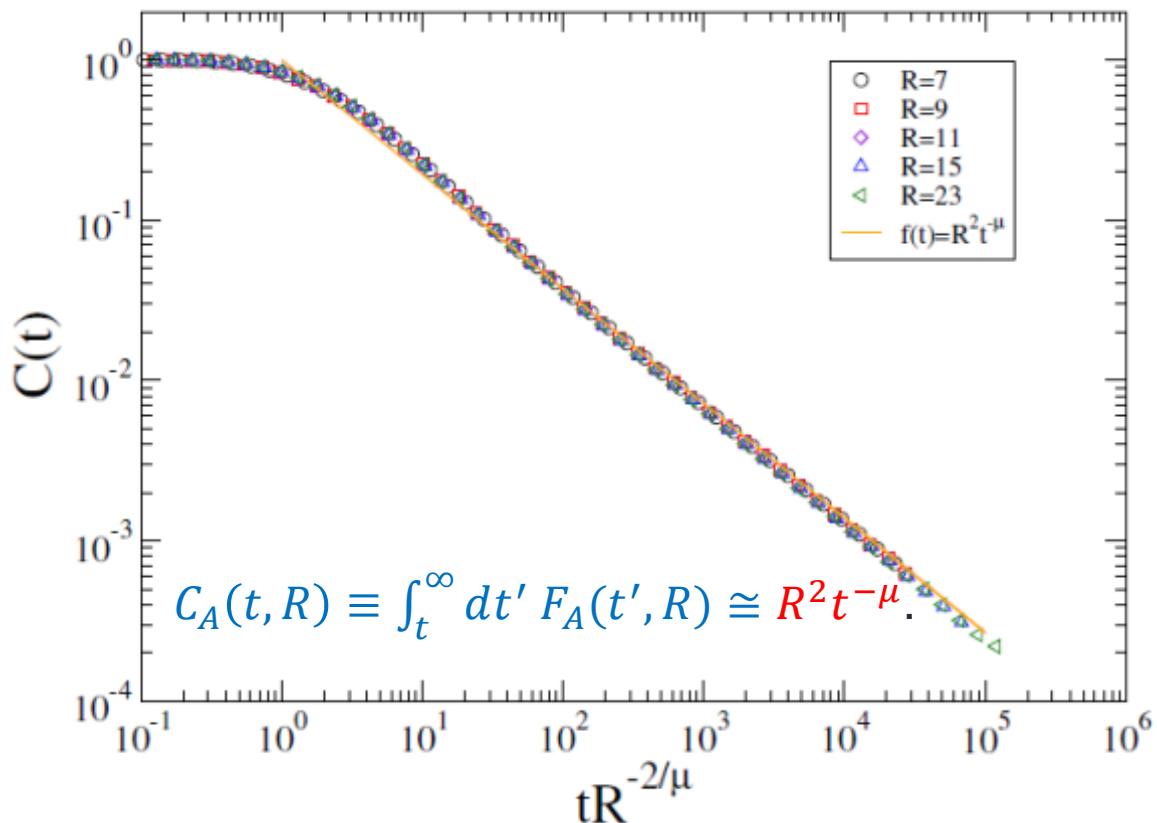
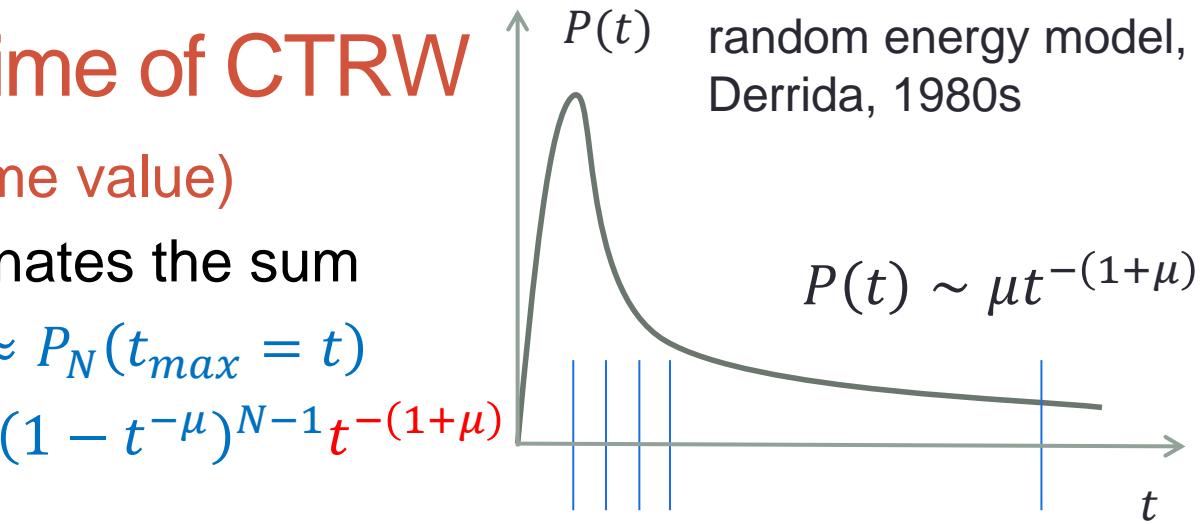
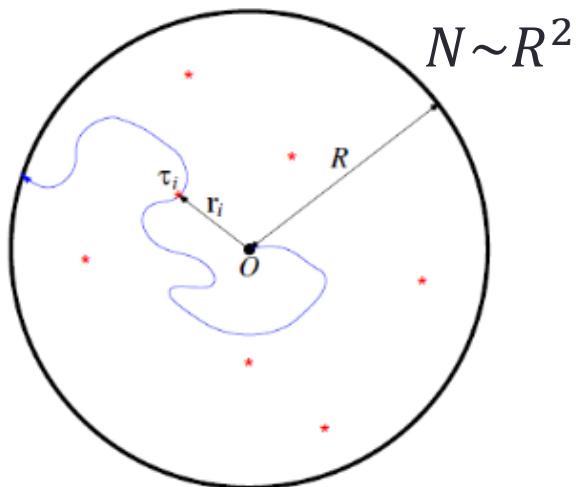
# The first-passage time of CTRW

Another approach (Extreme value)

the maximum value dominates the sum

$$t_N = \sum_{i=1}^N t_i$$

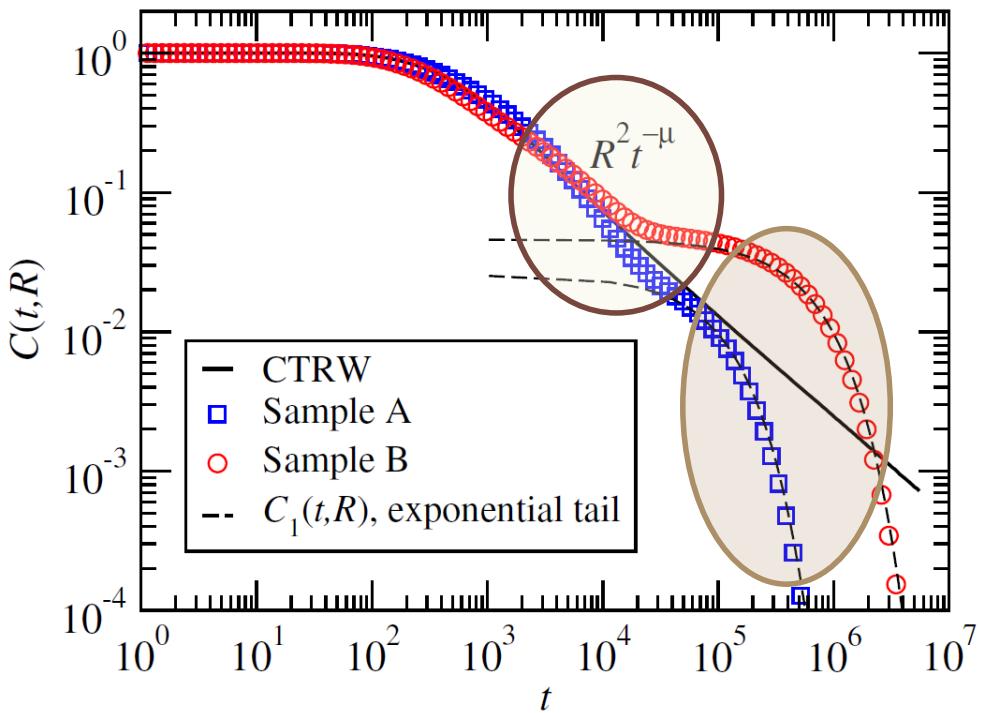
$$\begin{aligned} P(t_N = t) &\approx P_N(t_{max} = t) \\ &= N\mu(1 - t^{-\mu})^{N-1} t^{-(1+\mu)} \end{aligned}$$



# The time scales in quenched potential

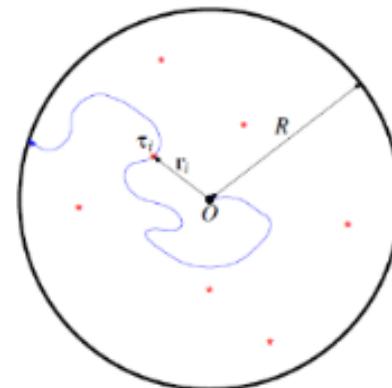
The CTRW time scale  
(irrelevant to the disorder sample)

$$\tau_{CTRW} \sim R^{2/\mu}$$



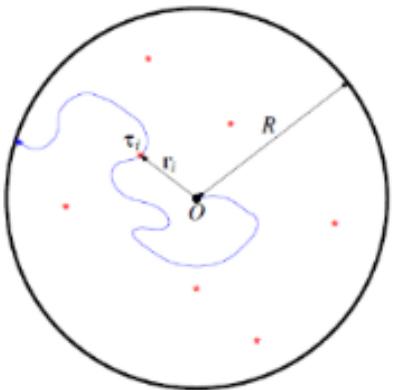
The mean waiting time of a jump out of the deepest trap of the given sample

$$\tau_{QTM} \sim R^{d/\mu}$$



Cumulative distribution of waiting time for a jump out of the deepest trap:  
 $C_1(t, R | \tau_Q, r) \simeq w(r, R) \exp(-e_d t / \tau_Q)$

# Counting strong traps



A filtered landscape only with deep traps  $\tau_i > \tau_c$ .

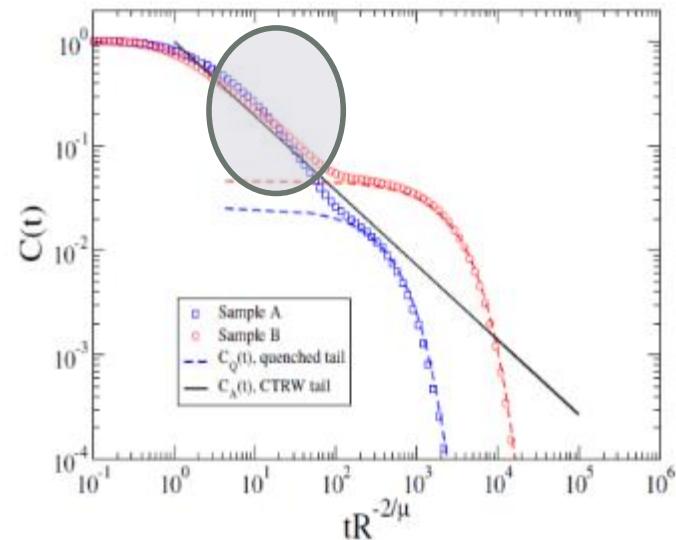
$$\begin{aligned} C(t, R) &= \sum_{\Gamma} W_{\Gamma} C_{\Gamma}(t) \\ &= \sum_{\text{trap } i} \sum_{\Gamma \in \Lambda_i} W_{\Gamma} C_{\Gamma}(t) \end{aligned}$$

$$\approx \sum_{\text{trap } i} C_1(t, R | \tau_i, r_i)$$

$\Gamma$ : path

$W_{\Gamma}$ : the probability for path  $\Gamma$ ,  $\sum_{\Gamma} W_{\Gamma} = 1$

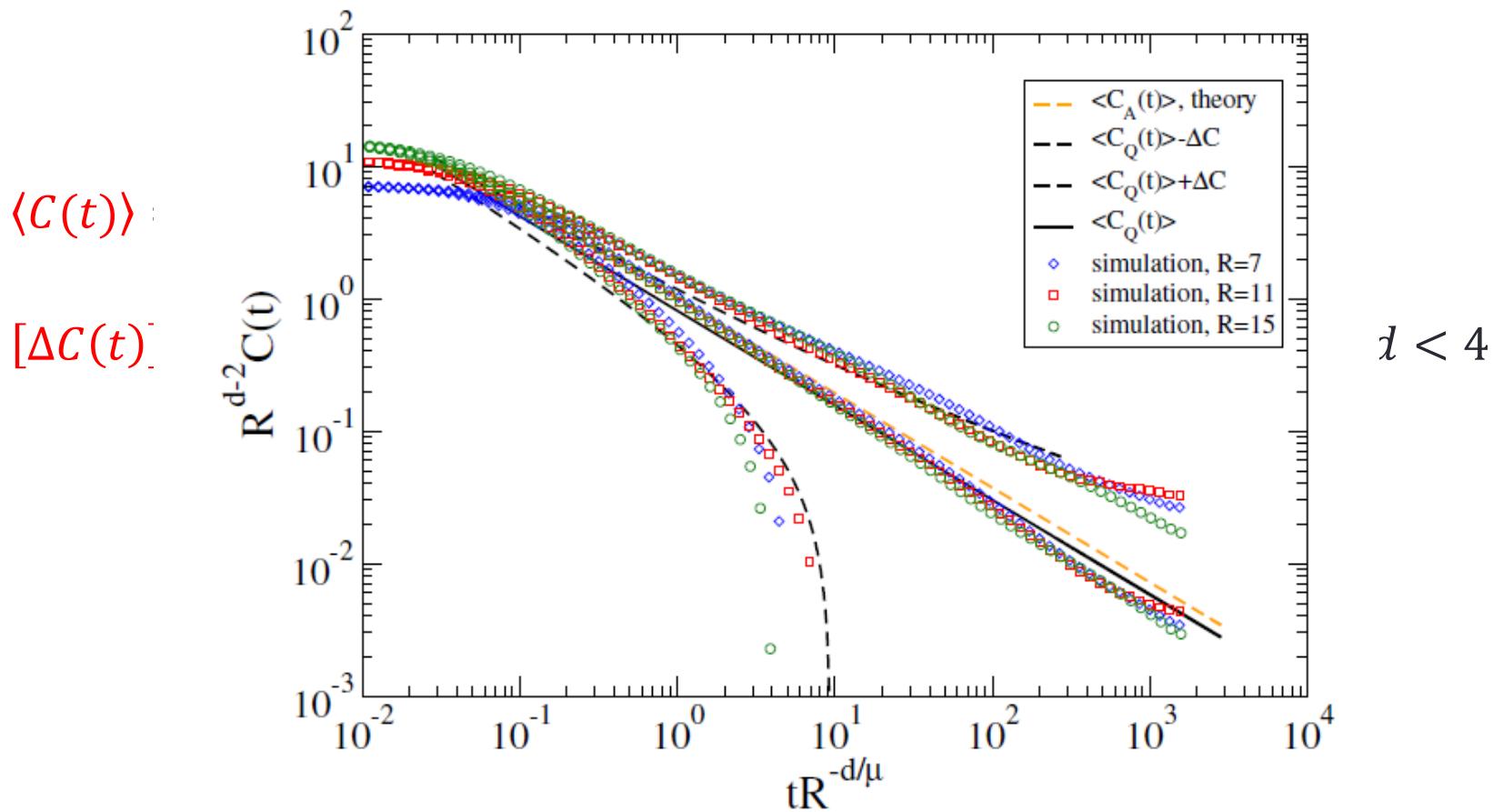
$\Lambda_i$ : the set of all the paths visit trap  $i$



$$C_1(t, R | \tau, r) \approx w(r, R) \exp(-e_d t / \tau)$$

# Statics over disorder ensemble

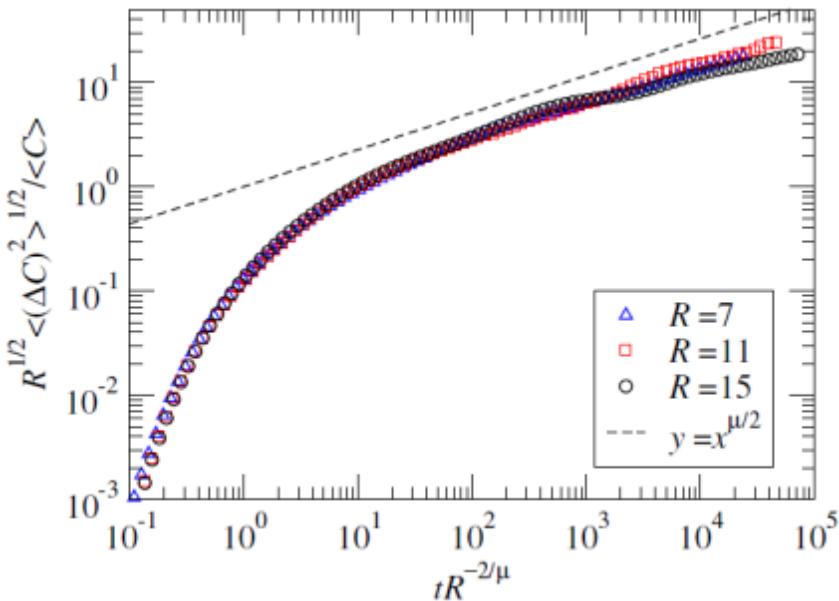
$$C(t, R | \{\tau_i, r_i\}) \approx \sum_{trap i} C_1(t, R | \tau_i, r_i)$$



$$\lambda < 4$$

$$\langle C(t, R) \rangle \propto R^2 t^{-\mu},$$
$$\Delta C(t, R) \propto R^{2-d/2} t^{-\mu/2}.$$

# Sample-dependent FPT distribution



CTRW

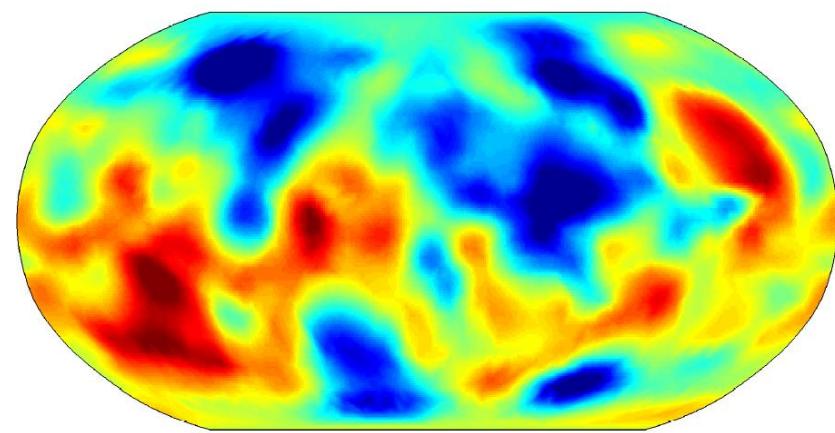
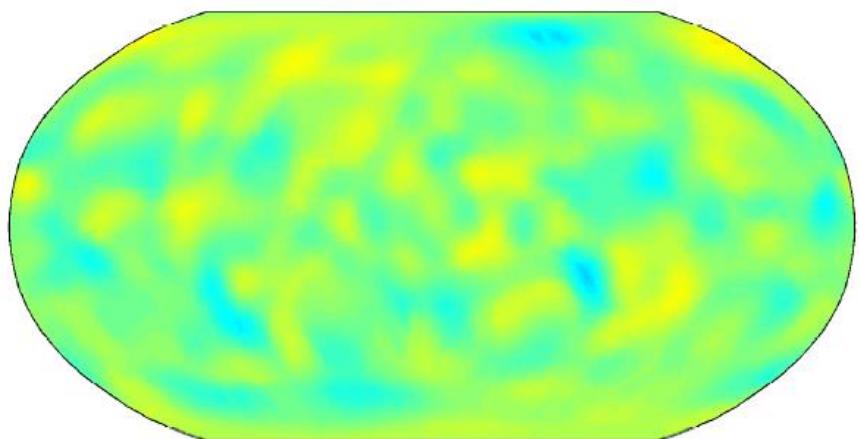
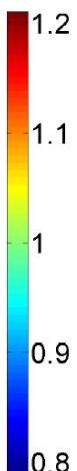
Sample-to-sample fluctuation  
overwhelms the mean distribution !

$$\frac{\langle [\Delta C(t, R)]^2 \rangle^{1/2}}{\langle C(t, R) \rangle} = R^{(\alpha_d - 2)/2} f(tR^{-2/\mu}),$$

$$f(z) \sim z^{\mu/2} \text{ for } z \gg 1.$$

Earth plot of the hit map

QTM



The hit map of sites on the absorbing surface

# Summary

More details in arXiv:1507.07409

- Quasi-static structures in living cell largely determine the passive transport of macro-molecules.
- We propose an analytic approach to estimate the FPT distribution in given quenched samples.
- The FPT distribution in a sub-diffusive quenched trap model is sample-dependent for finite-size systems. (even for  $d > 2$  !)
- The earth map is proposed as a novel technique to detect the inner structures of the cell.

Thank you!