

# TASEP in presence of a localised dynamical constraint



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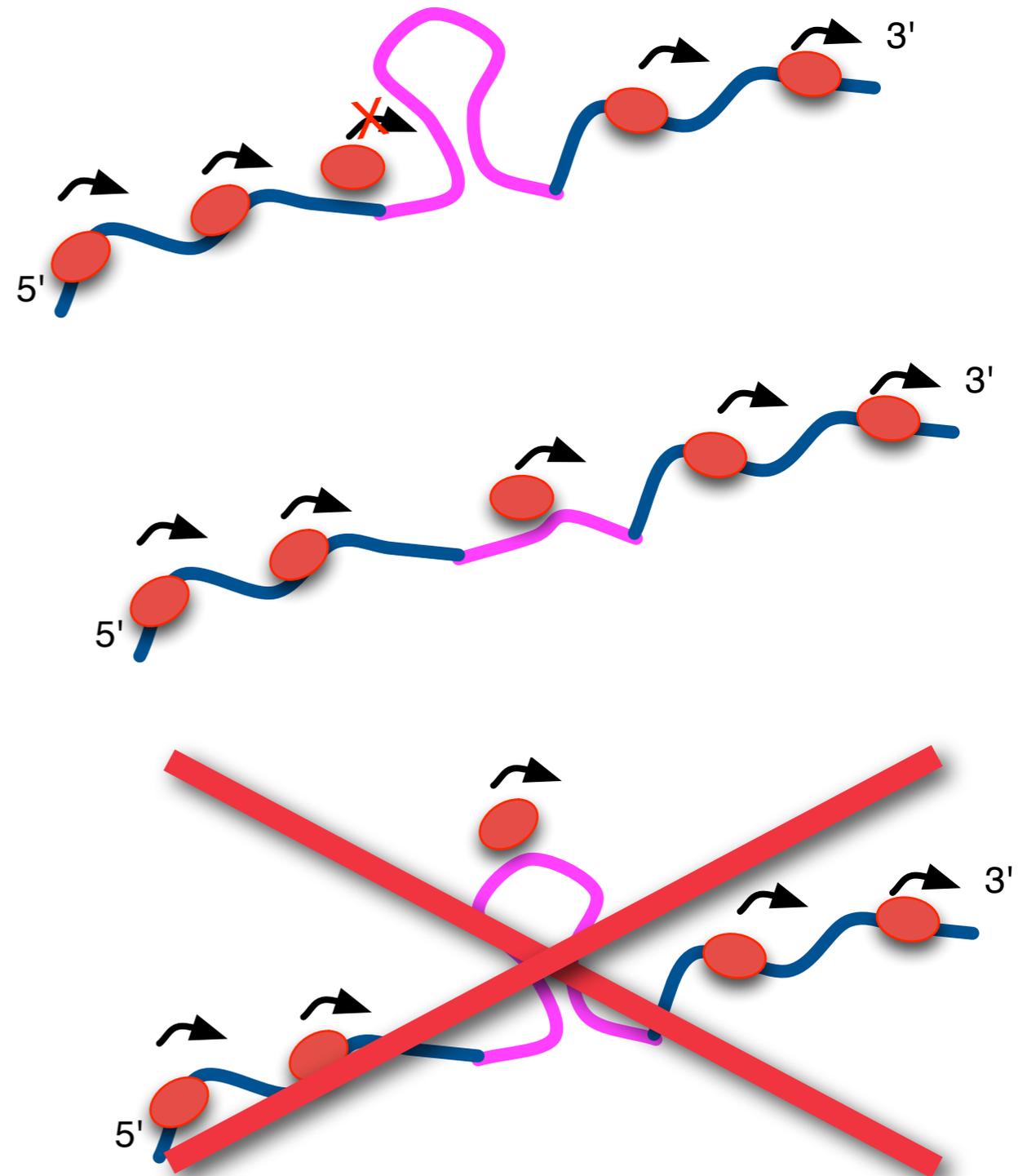
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# Outline

- Biological motivation
- The model
- Mean Field analysis and results

# TASEP and Translation

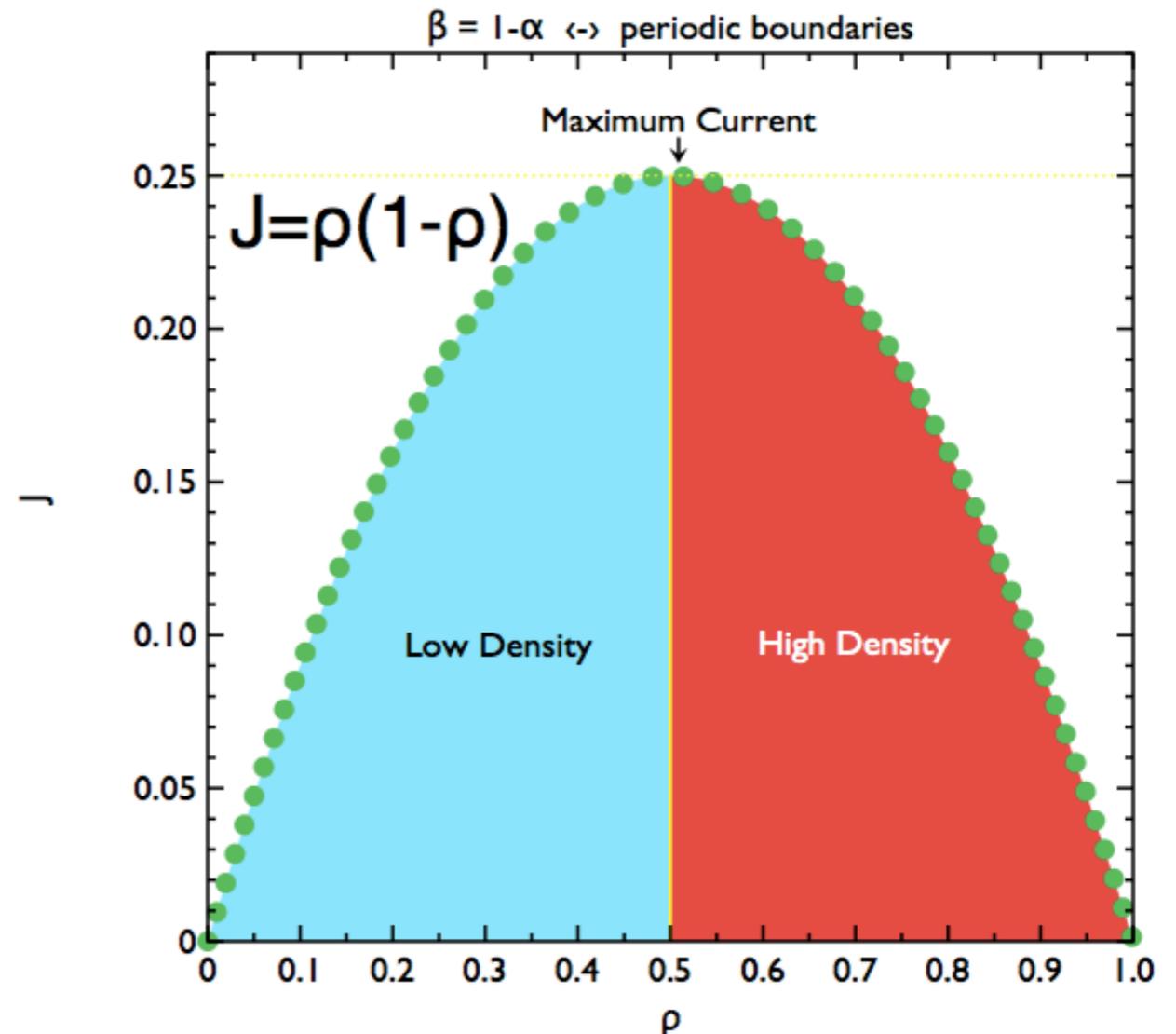
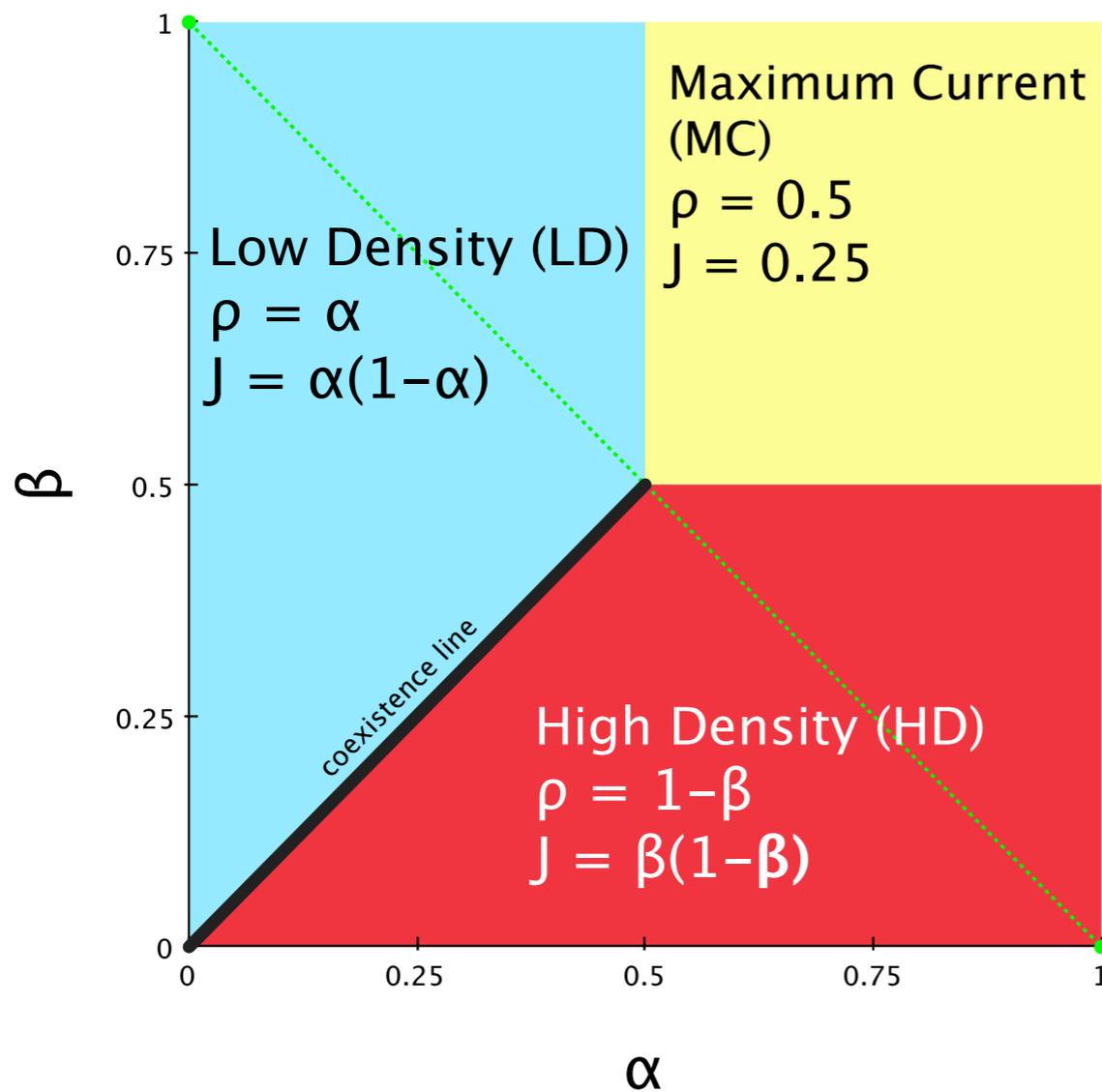
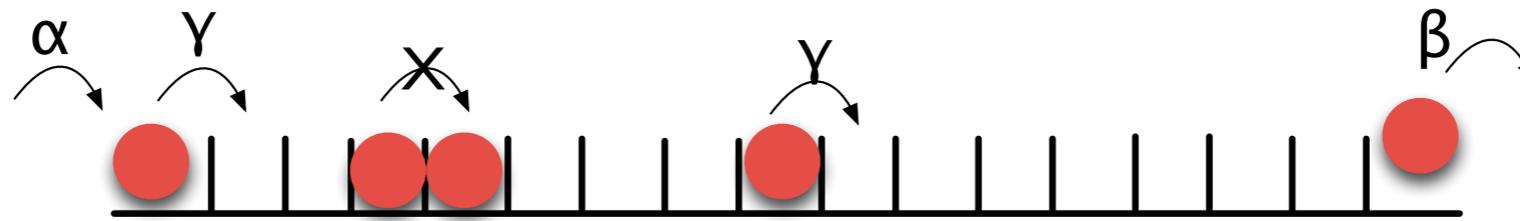
- **TASEP** has been originally proposed for mRNA translation.[1]
- mRNA is complex : **secondary structures exists** regulating the translation.
- Such regions can be active or not, depending on their **folding status**.
  - **folded** -> **inhibited** translation.
  - **unfolded** -> translation is **allowed**.
  - if a **ribosome** is **initiating** the translation, the **secondary structure** stays **unfolded**.



[1] MacDonald CT, Gibbs JH, Pipkin AC. Biopolymers. 1968;6:1-25.

# Totally Asymmetric Simple Exclusion Process

- If the folding/unfolding process is not present, we can model the process as a TASEP:



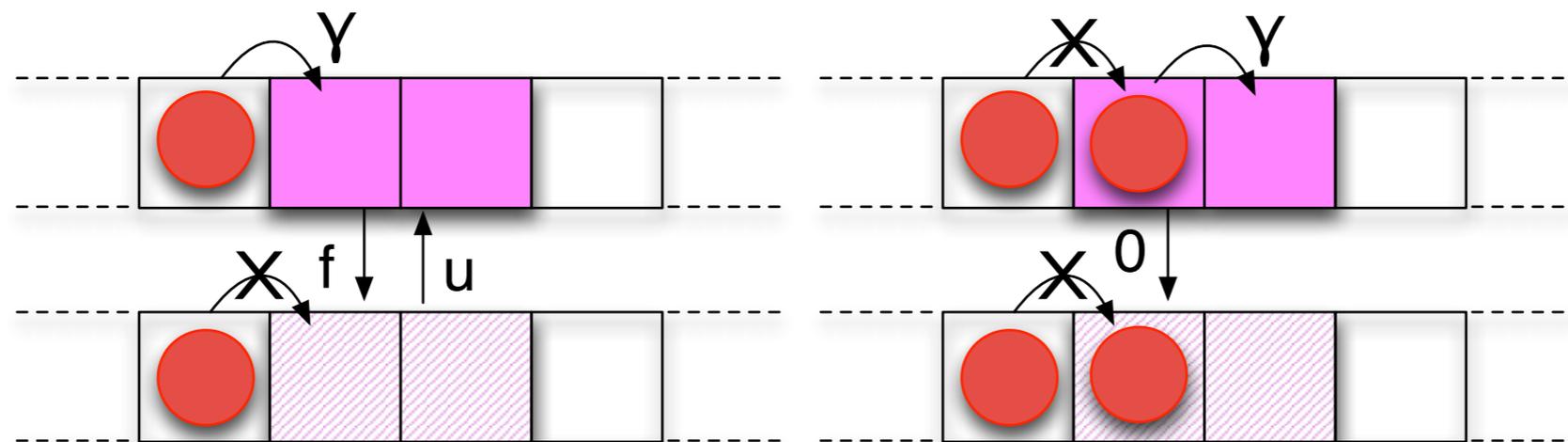
- exact results [1]
- paradigm for non equilibrium physics and biological processes [2]

[1] For instance B Derrida et al. Journal of Physics A (1993) vol. 26 pp. 1493

[2] Chou et al. Reports on Progress in Physics (2011) vol. 74 pp. 116601

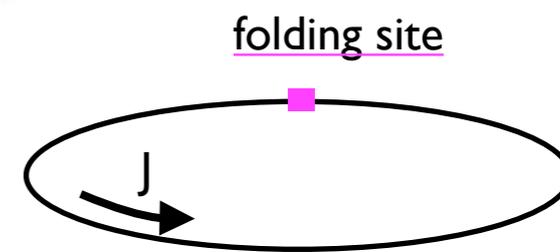
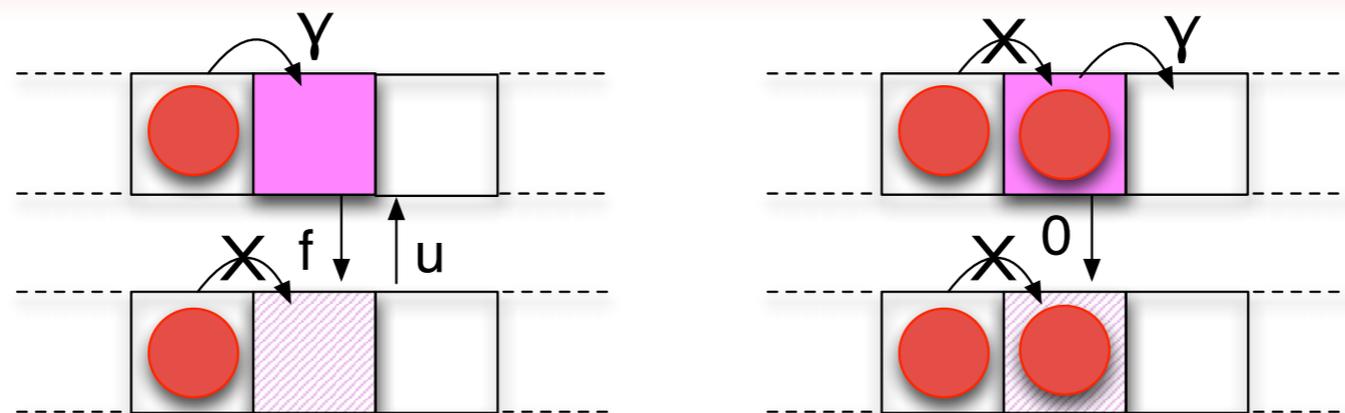
# Introducing a *folding region*

- Localisation of an extended defect
  - internal dynamics
  - coupling with particles presence.
- Effects on the dynamics
  - periodic boundaries
  - open boundaries



# Periodic Boundaries

# 1 site long folding region

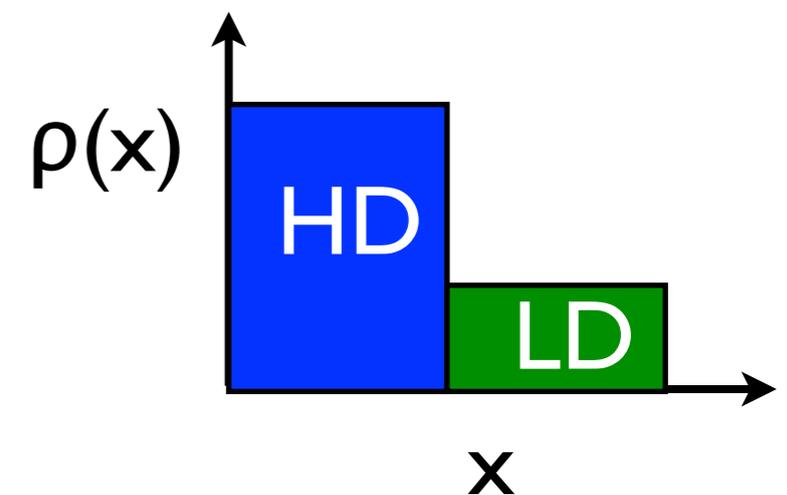


- Ring of **L sites**;
- **N particles** fixing the density  $\rho=N/L$
- **1 site** with internal dynamics
- Simulations performed using the **Gillespie Algorithm**.

# Finite-Segment Mean Field approach

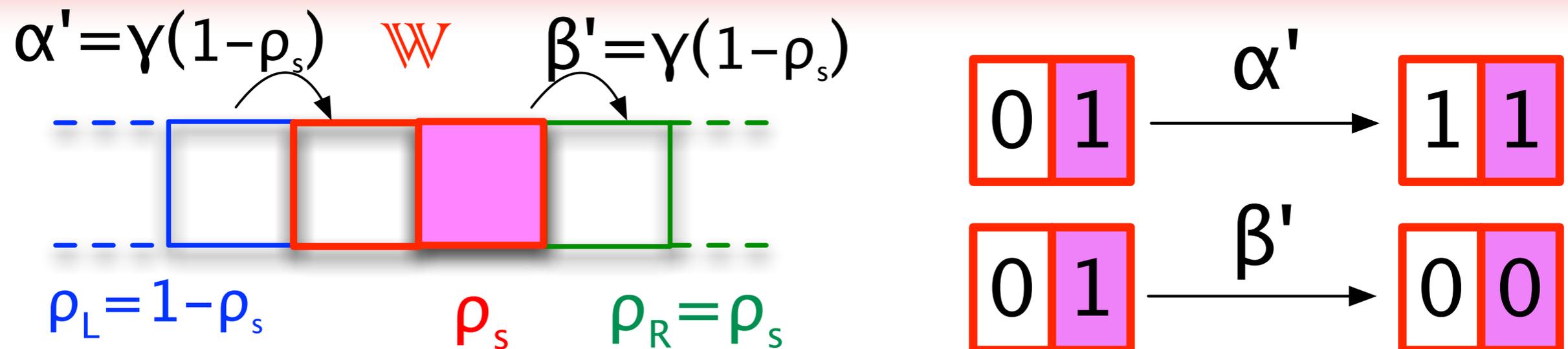
- The folding region is a defect:

- slows down the dynamics
- the system is split in two phases
  - High density  $\rho_{\text{HD}}$  before the defect
  - Low density  $\rho_{\text{LD}}$  after
- by spatial continuity of the current through the boundary  $\rho_{\text{HD}} (1 - \rho_{\text{HD}}) = \rho_{\text{LD}} (1 - \rho_{\text{LD}})$
- if we have a splitting  $\rightarrow \rho_{\text{H}} = 1 - \rho_{\text{LD}}$



similar to Janowsky et Lebowitz Physical Review A (1992) vol. 45 (2) pp. 618

# Finite-Segment Mean Field approach



- The folding site  $s$  has density  $\rho_s$  and makes incoming particles wait before it.
- the system is analysed in three parts, conserving the current spatial continuity:
  - high density  $1 - \rho_s$  (LEFT)
  - the **folding region + one site before** it (MIDDLE): decoupling the folding process and the injection of particles.
  - low density  $\rho_s$  (RIGHT)
- The **MIDDLE** region is governed by an exact transition matrix  $\mathbb{W}$  for the Probability  $P(\{n_{s-1}, n_s\})$ .  $\mathbb{W}$  depends  $\rho_s, f, u, \gamma$ .

\*J J Dong et al 2009 J. Phys.A: Math.Theor. 42 015002

# Finite-Segment Mean Field approach

- 2 sites  $\rightarrow$  6 possible states :  $\{\text{empty, full}\} \times \{\text{empty \& open, full \& open, closed}\}$

$$\hat{\rho}_s = 1 - \rho_s$$

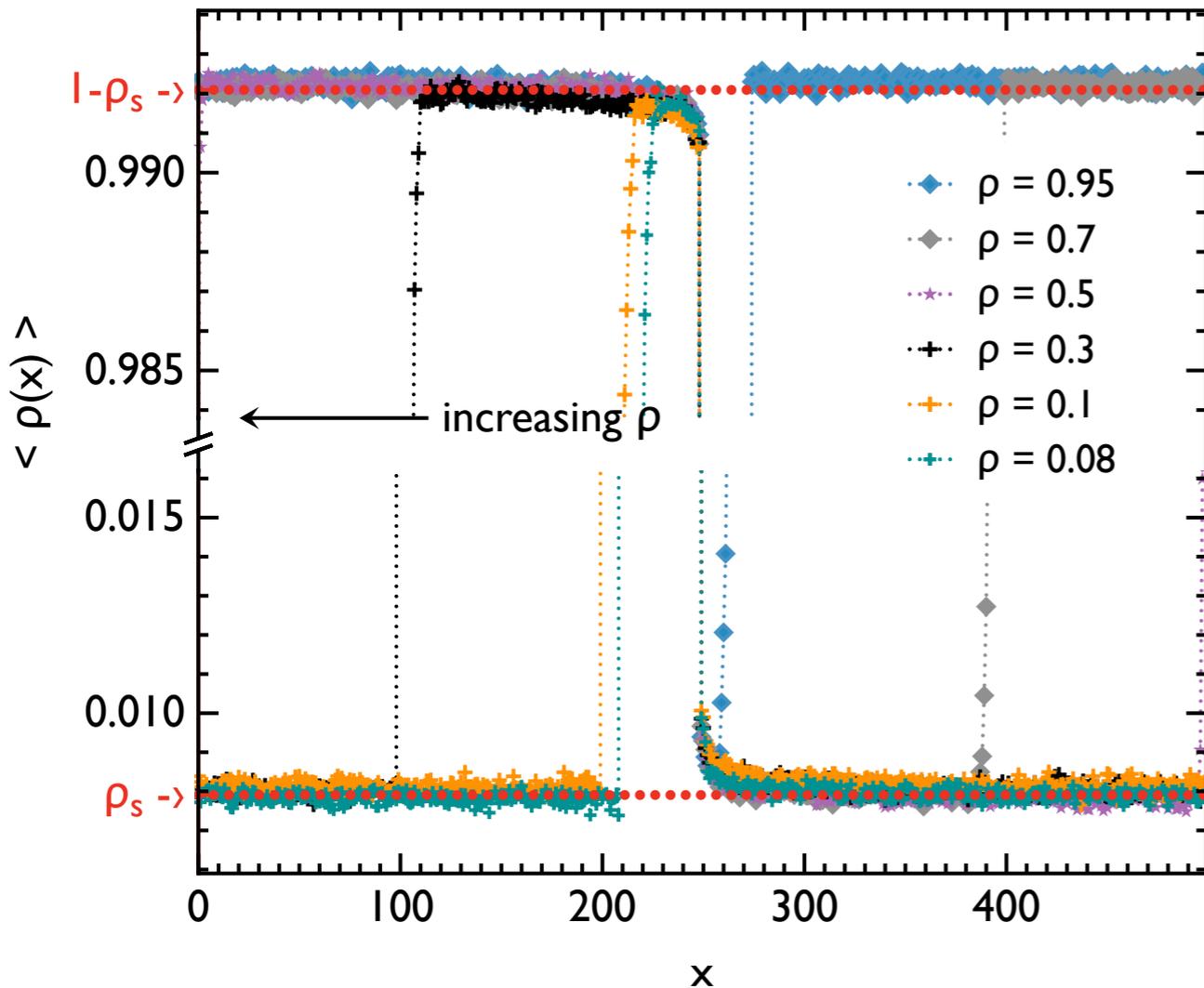
$$\mathbb{W} = \begin{pmatrix} -f - \gamma\hat{\rho}_s & u & 0 & 0 & \gamma\hat{\rho}_s & 0 \\ f & -u - \gamma\hat{\rho}_s & 0 & 0 & 0 & 0 \\ \gamma\hat{\rho}_s & 0 & -f - \gamma & u & 0 & \gamma\hat{\rho}_s \\ 0 & \gamma\hat{\rho}_s & f & -u & 0 & 0 \\ 0 & 0 & \gamma & 0 & -2\gamma\hat{\rho}_s & 0 \\ 0 & 0 & 0 & 0 & \gamma\hat{\rho}_s & -\gamma\hat{\rho}_s \end{pmatrix}$$

- Stationary state :  $\mathbb{W}P = 0$ 
  - one obtains the probability  $P(\mathbf{n}_s = \mathbf{l})$  as a function of  $\rho_s, \gamma, u, f$ .
  - solve  $P(\mathbf{n}_s = \mathbf{l}) = \rho_s$
  - get  $\rho_s(\gamma, u, f)$ .
  - The corresponding value for the current is  $J_{\max} = \rho_s(1 - \rho_s)$

# Periodic Boundaries Results

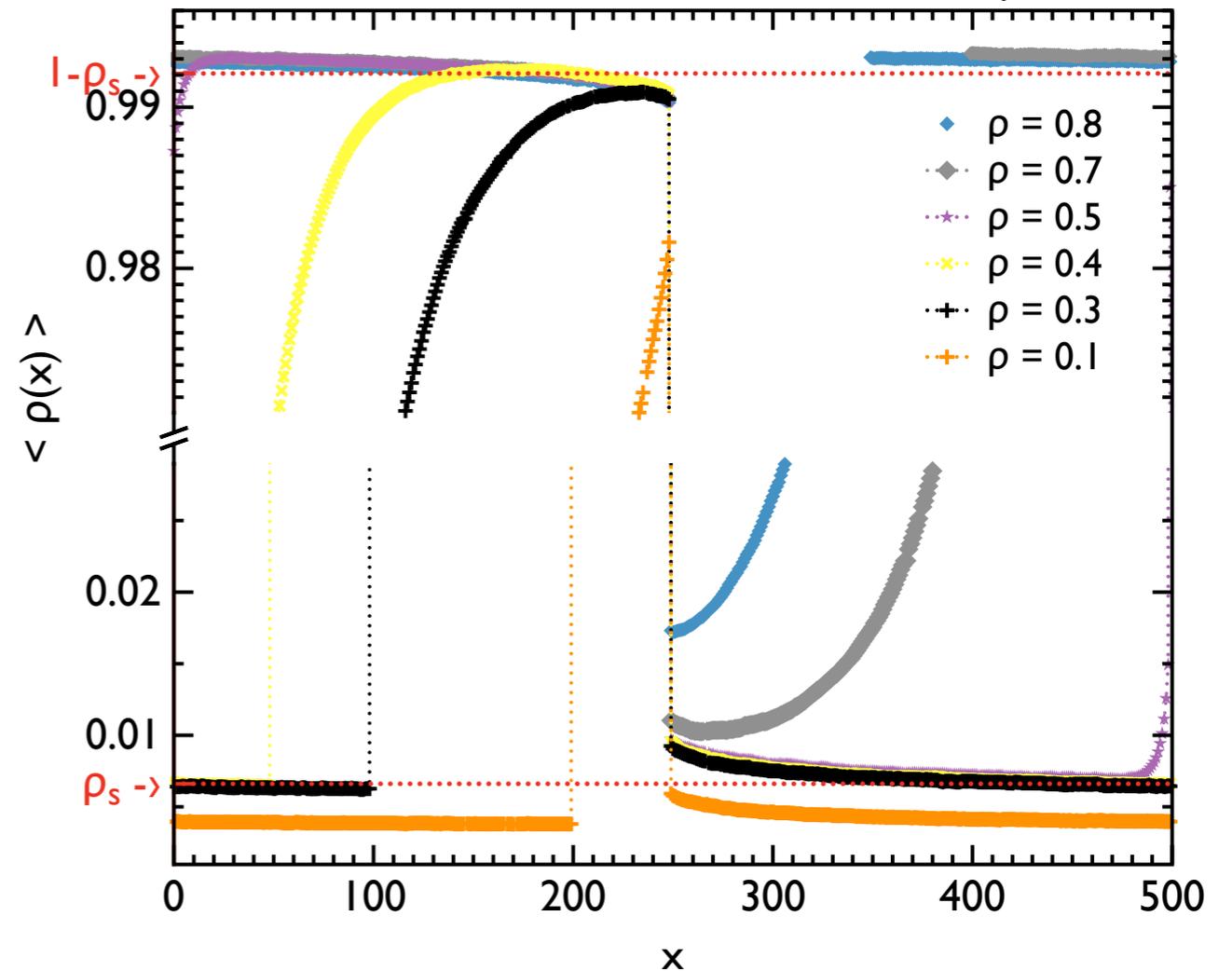
# Mean field and simulation comparison

$d = 1$  at  $x = 250$ ,  $L = 500$ ,  $f = 1$ ,  $u = 0.01$ ,  $\gamma = 1$



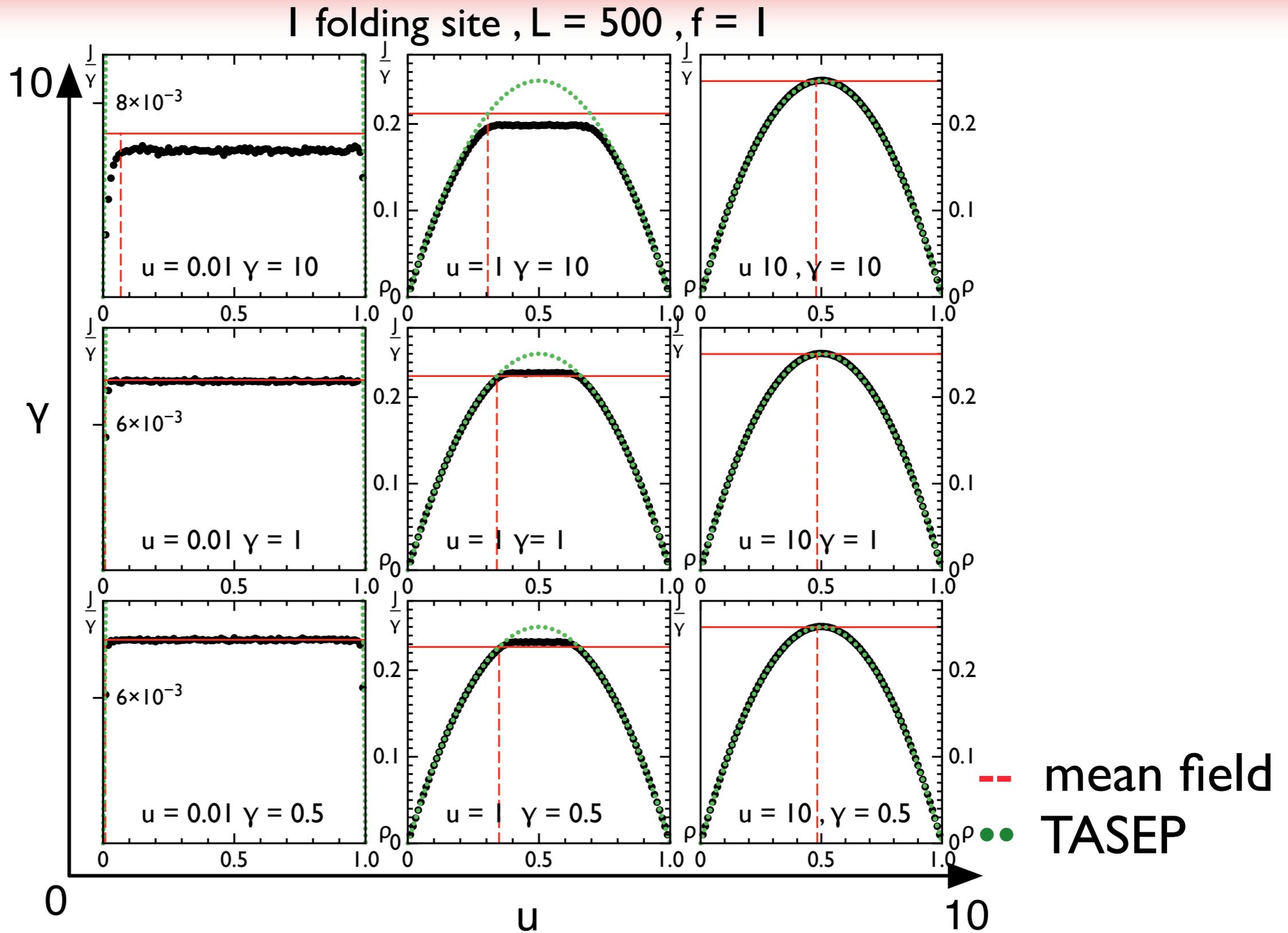
the system is split in two phases  
(= MF hypothesis)

$d = 1$  at  $x = 250$ ,  $L = 500$ ,  $f = 1$ ,  $u = 0.01$ ,  $\gamma = 100$

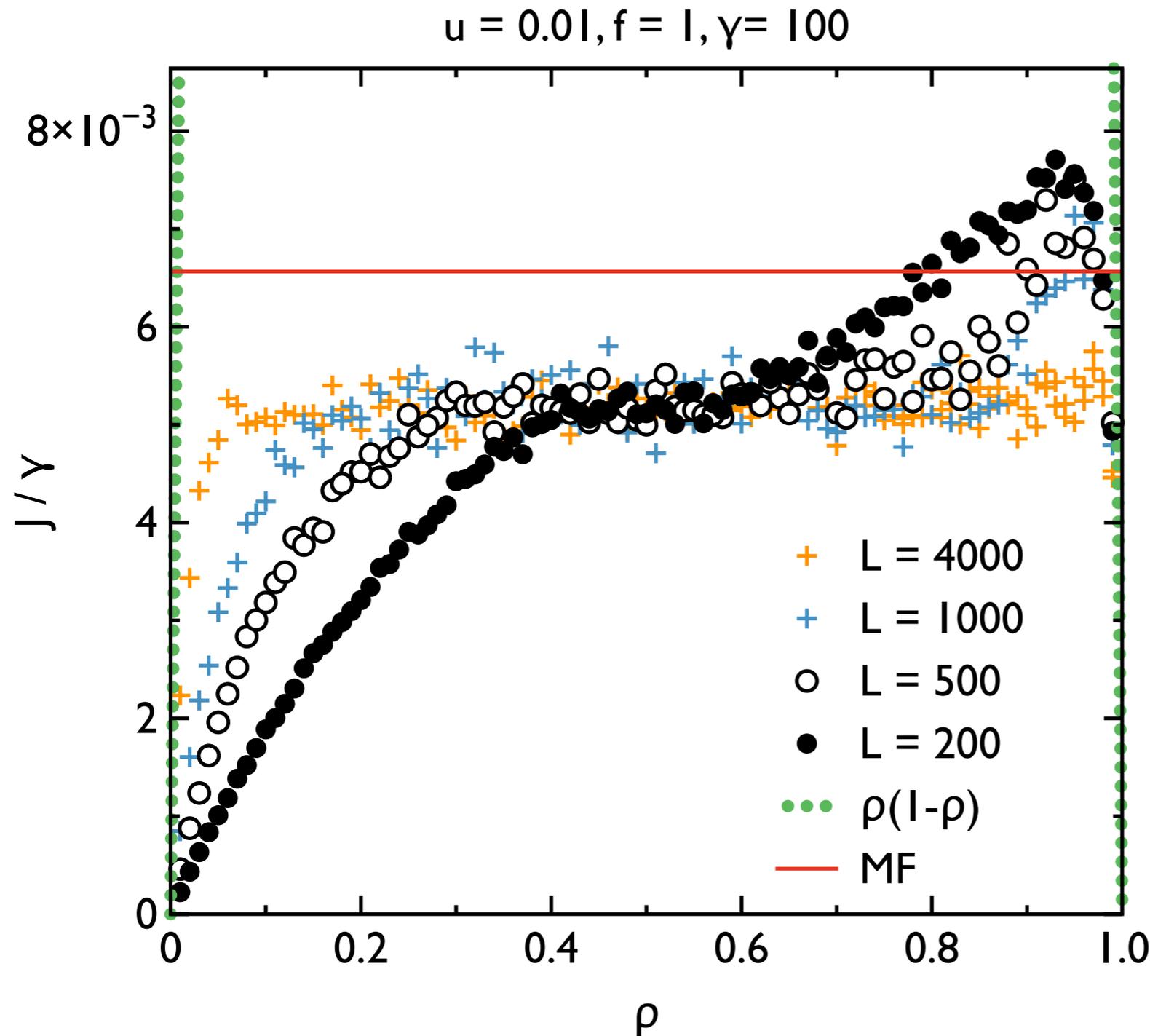


non flat profiles, non diffusive shocks dynamics  
( $\neq$  MF hypothesis)

# Results



# L-dependent $J(\rho)$ at very large $\gamma/u$

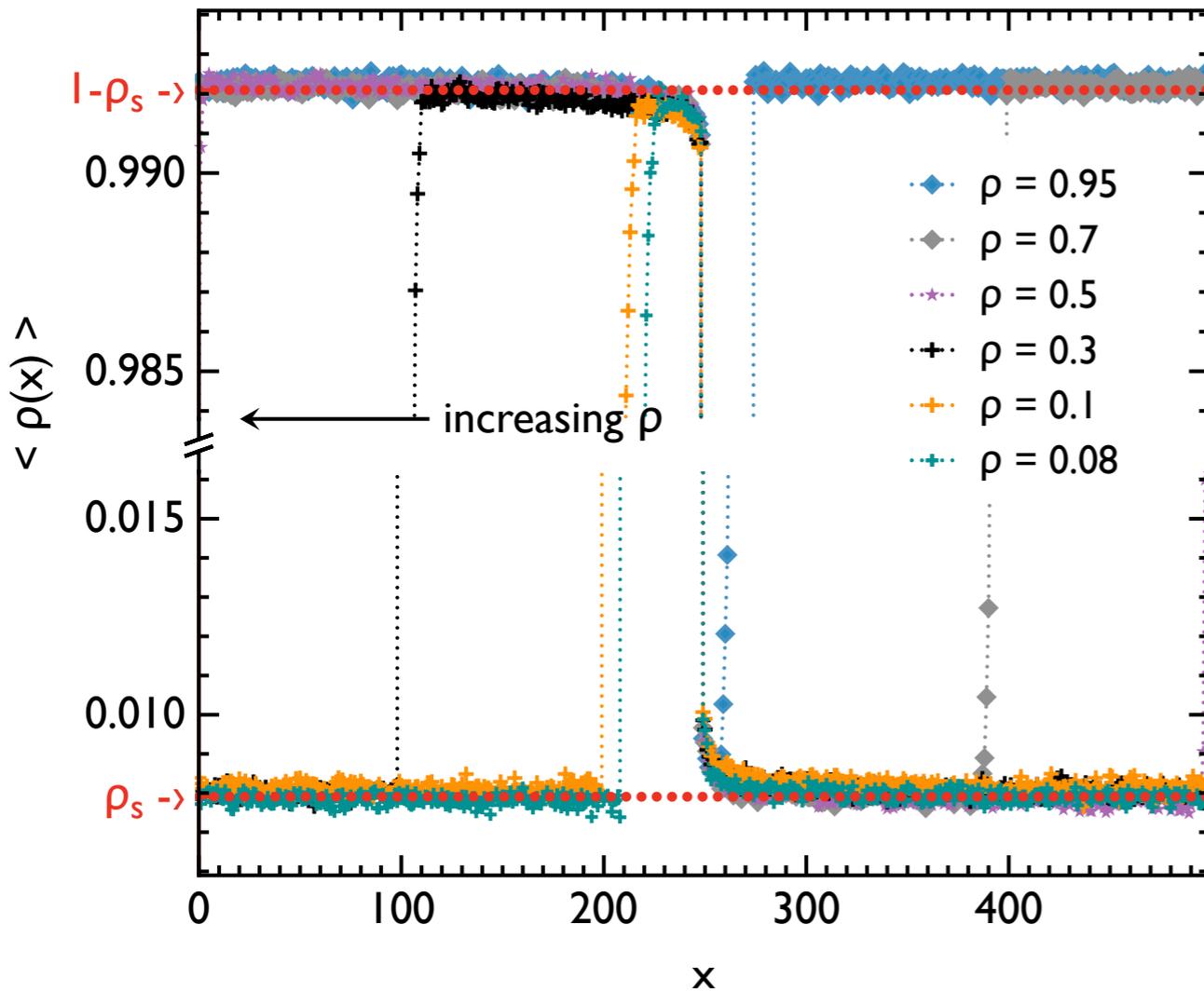


- strong correlations
- **enhanced** particles flow at high density ( $>0.5$ )
- **reduced** particle flow at low density ( $<0.5$ )
- **slow** convergence to  $L \rightarrow \infty$  plateaux

- mean field
- TASEP

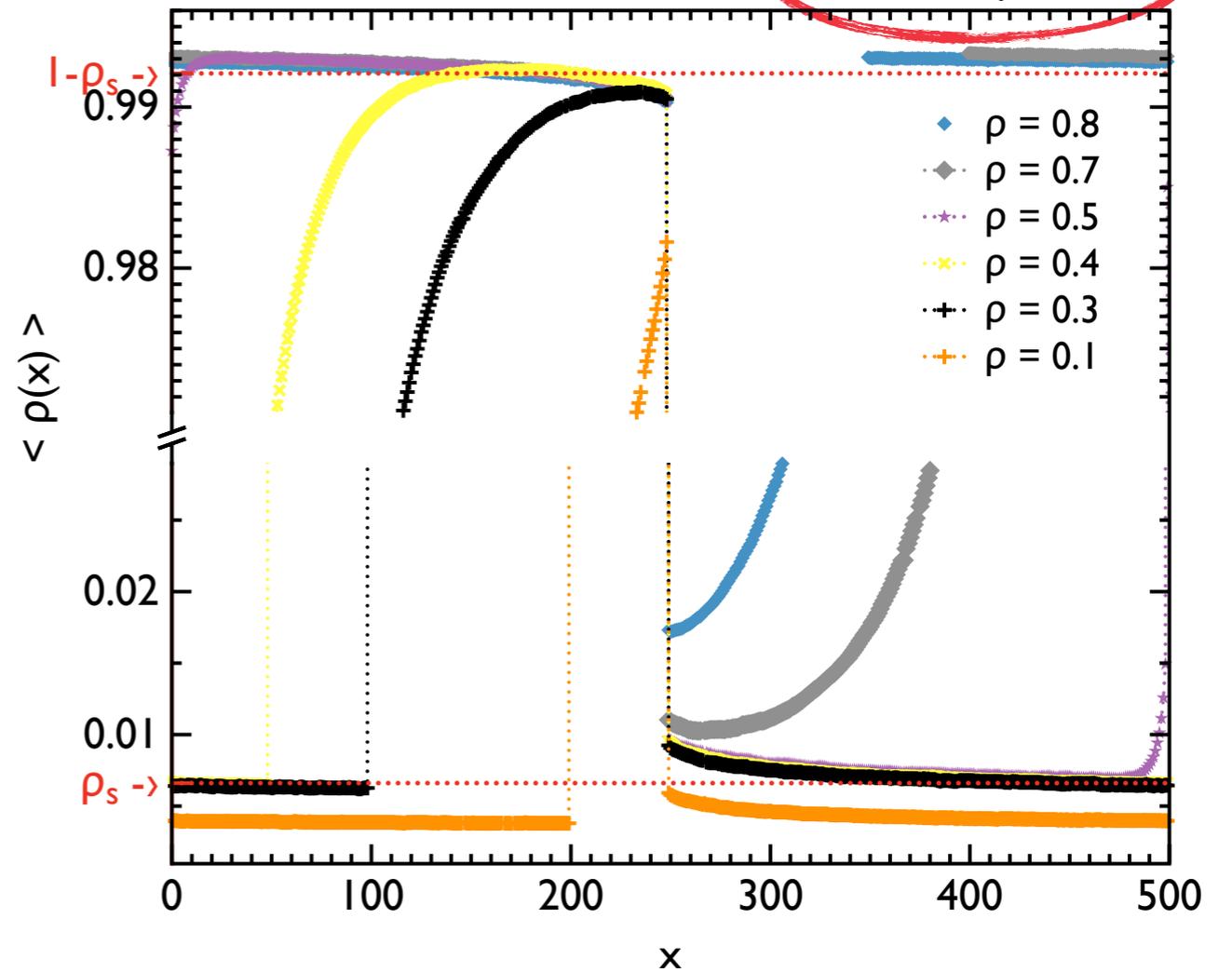
# Mean field failure for highly correlated density profiles

$d = 1$  at  $x = 250$ ,  $L = 500$ ,  $f = 1$ ,  $u = 0.01$ ,  $\gamma = 1$



the system is split in two phases  
(= MF hypothesis)

$d = 1$  at  $x = 250$ ,  $L = 500$ ,  $f = 1$ ,  $u = 0.01$ ,  $\gamma = 100$



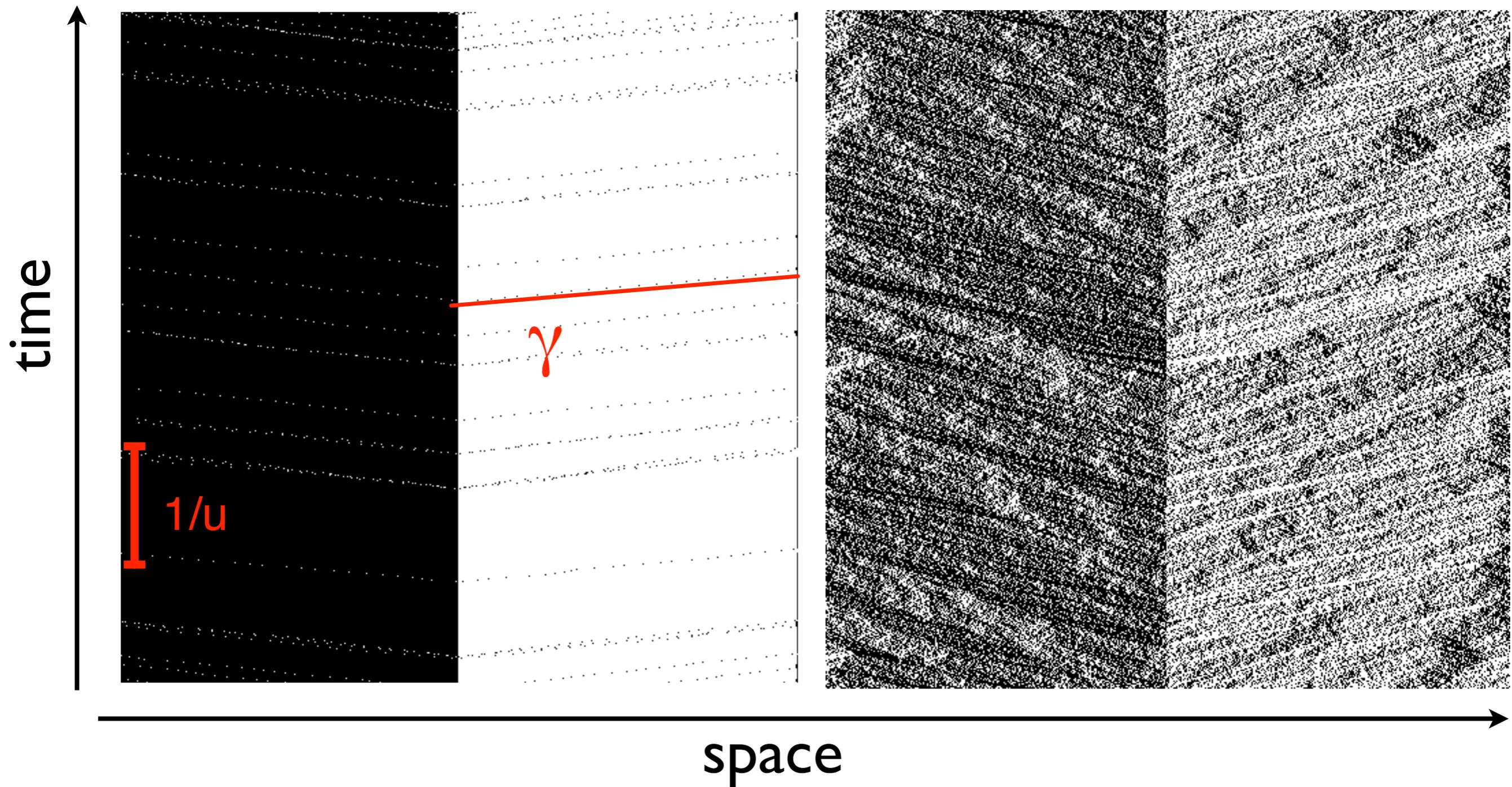
non flat profiles, non diffusive shocks dynamics  
( $\neq$  MF hypothesis)

# Small unfolding rates lead to intermittency

$$L = 500, \rho = 0.5, f = 1, \gamma = 1$$

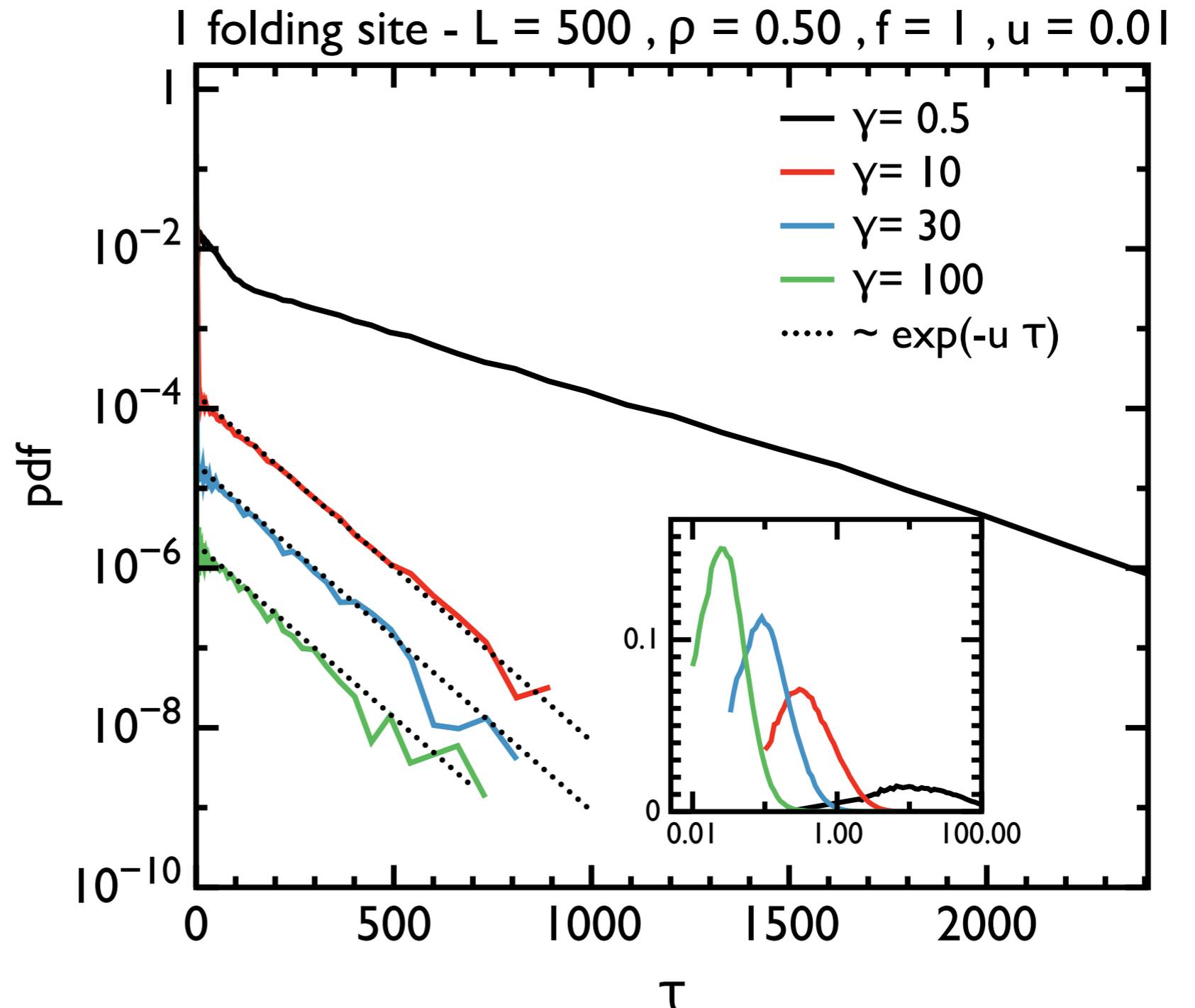
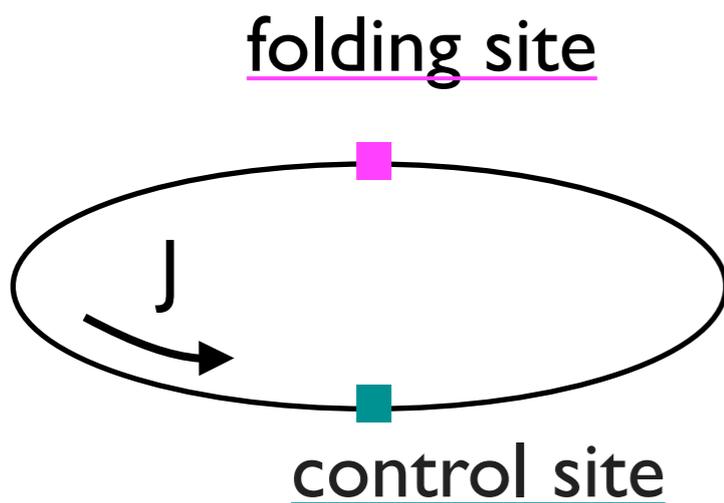
$u = 0.01$

$u = 1$

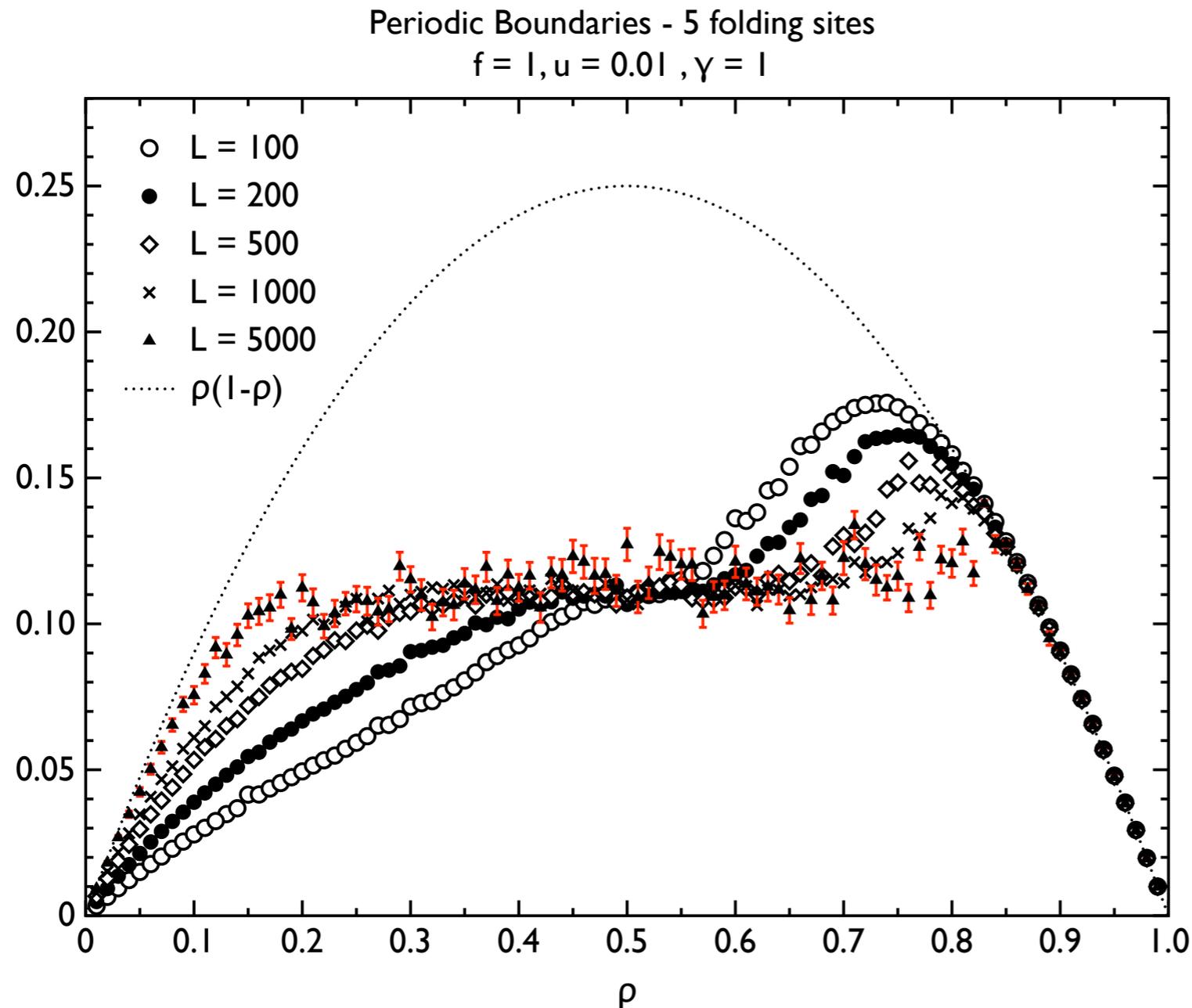


# Passage times distributions

- Distr. of the time lag between two successive particles passing through a **control site**
  - two typical times
  - high  $\gamma/u$  increase the time separation



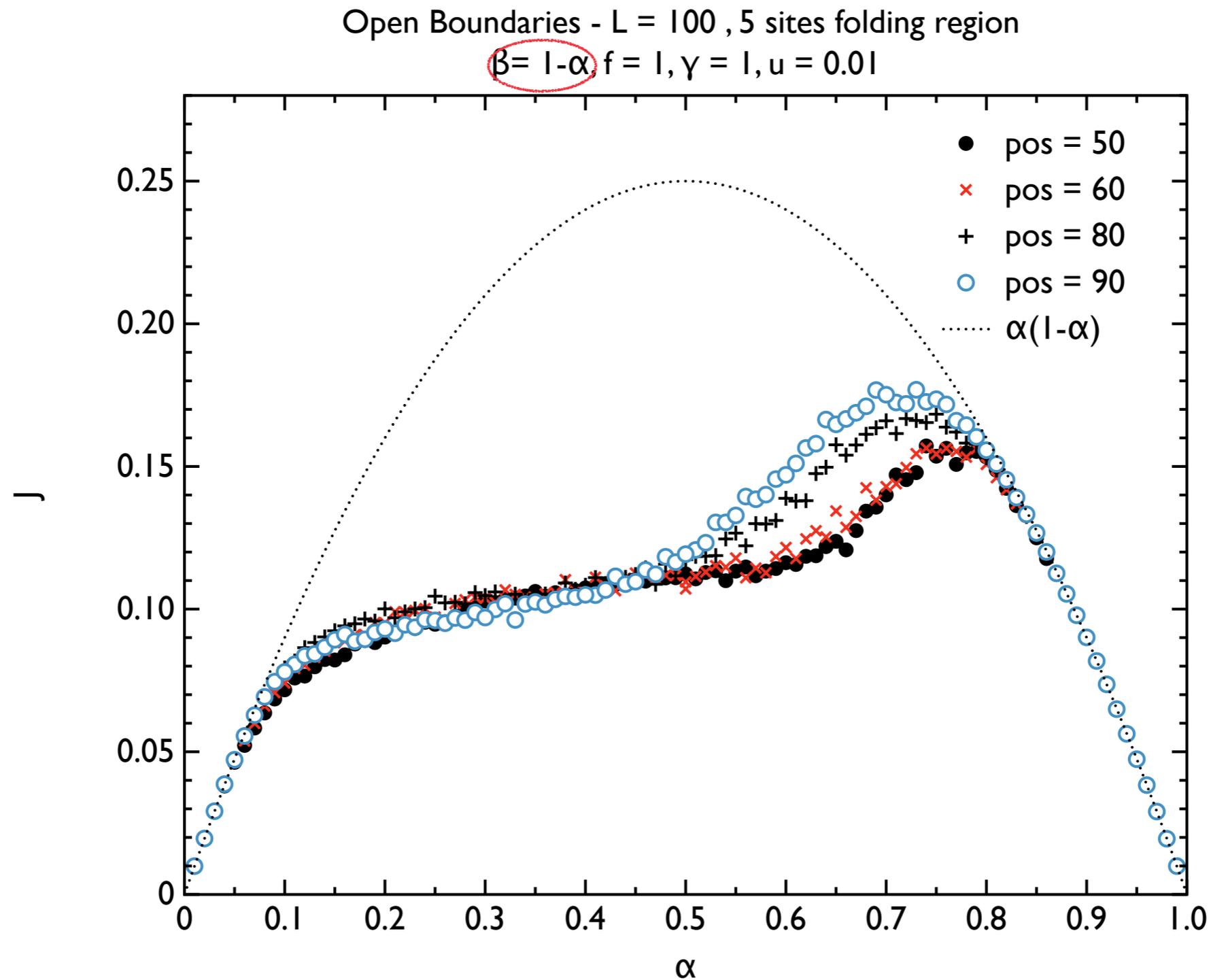
# Large folding regions have stronger effects



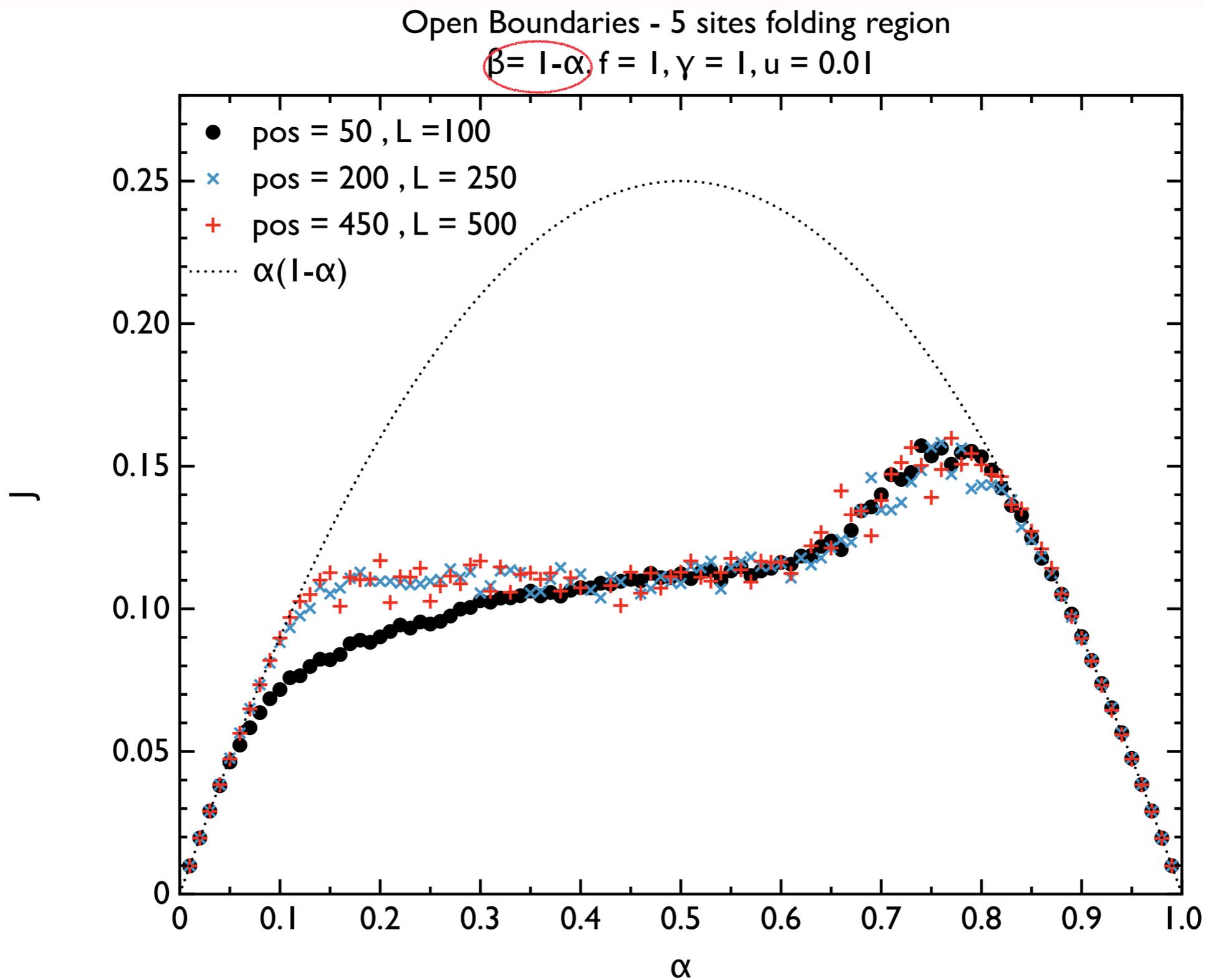
- $d > 1, L \rightarrow \infty$ 
  - more particles configurations leading to an open folding region
    - higher currents for a given set  $\{u, f, \gamma\}$
- $d > 1, \text{finite } L$ 
  - strong correlations
    - **enhanced** particles flow at high density ( $>0.5$ )
    - **reduced** particle flow at low density ( $<0.5$ )
    - **slow** convergence to  $L \rightarrow \infty$  plateaux
    - complex domain wall diffusion within the lattice

# Some Open Boundaries Results

## Finite size effects depend on the size of the LD part



## Finite size effects depend on the size of the LD part



# Conclusions

- MF description of the homogeneous flow regime.
- Intermittent dynamics at high  $\gamma/u$  :
  - 2 typical waiting times  $\rightarrow$  2 typical microscopic currents
- Current enhancement/reduction depending on the extension of the LD phase.
  - strong size effects;
  - relevant for biology : mRNA length  $10^2 - 10^3$  bases  $\sim 10^2$  of codons.
  - long range density profiles tails