Physical modeling of active bacterial DNA segregation
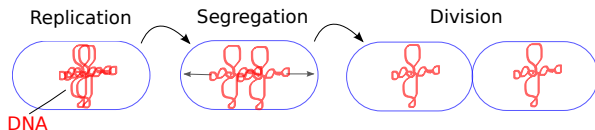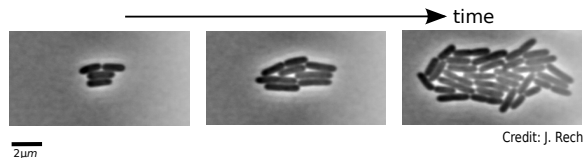
Jean-Charles Walter

Laboratoire Charles Coulomb,
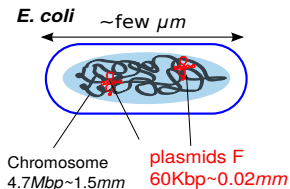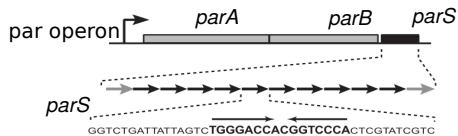CNRS & Université de Montpellier, France

iPoLS 2017
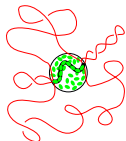Institut Pierre-Gilles de Gennes
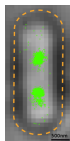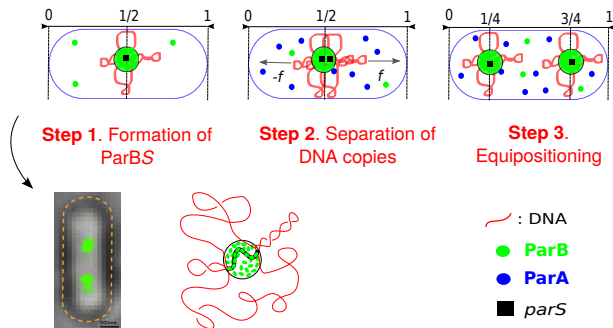June 29

Bacterial DNA segregation

time

Credit: J. Rech

2μm

Replication   Segregation   Division

DNA

How is the bacterial genome segregated ?

The ParAB*S* operon
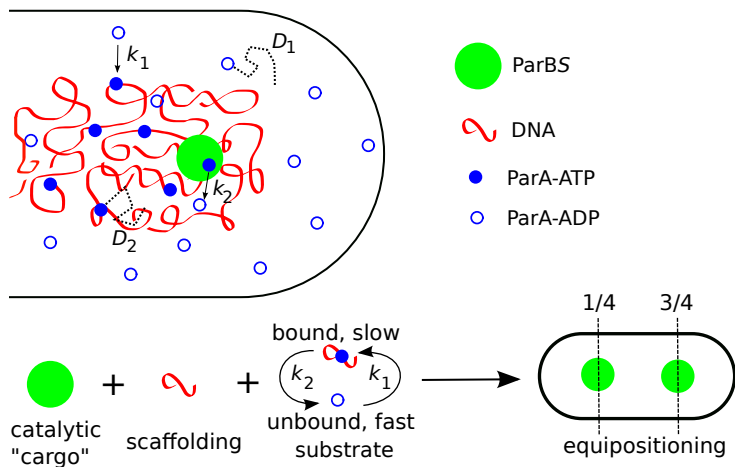

- ParA: "motor" protein (ATPase, Walker-type)

- ParB: binding protein (specific or non-specific binding)

- *parS*: centromere-like DNA sequence

How does ParAB*S* work ?

Step 1. Formation of ParB*S*

Step 2. Separation of DNA copies

Step 3. Equipositioning

⌢ : DNA

● **ParB**

● **ParA**

■ *parS*

Cell Systems 2015

Interactions between ParAB*S* components

Self-consistent non-linear system

ParA-ADP:
$$\frac{\partial u}{\partial t} = D_1 \, \Delta u - k_1 \, u(\mathbf{r}, t) + k_2 \, v(\mathbf{r}, t) \sum_i S(\mathbf{r} - \mathbf{r}_i(t))$$

ParA-ATP:
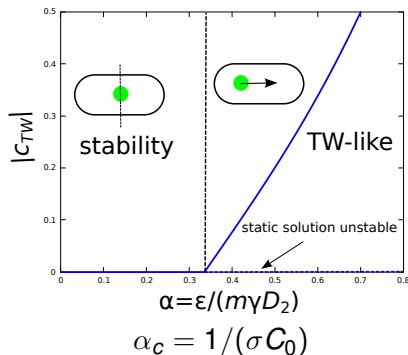$$\frac{\partial v}{\partial t} = D_2 \, \Delta v + k_1 \, u(\mathbf{r}, t) - k_2 \, v(\mathbf{r}, t) \sum_i S(\mathbf{r} - \mathbf{r}_i(t))$$

ParBS :
$$m\gamma \frac{d\mathbf{r}_i}{dt}(t) = \varepsilon \int_V \nabla v(\mathbf{r}', t) \, S(\mathbf{r}' - \mathbf{r}_i(t)) \, d^3\mathbf{r}'$$
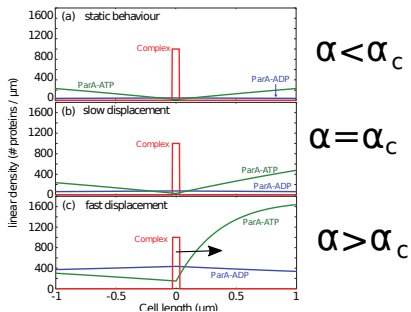
- Feedback between the partition complexes and ParA densities
  $\rightarrow$ Non-linear system with dynamical instability
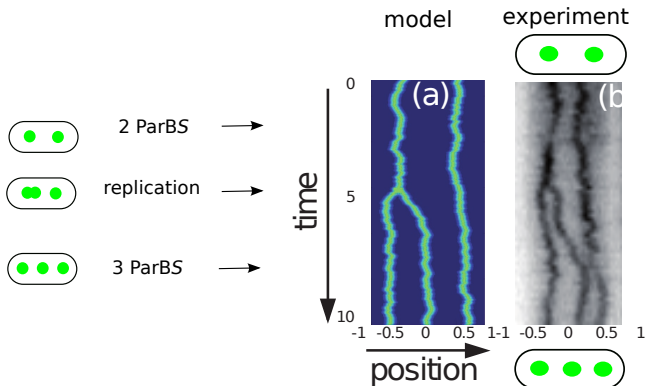
Stable and unstable (TW) dynamical regimes

Threshold of dynamical stability obtained with Traveling Waves (TW) *ansatz*: $u(x, t) = u(\xi)$; $v(x, t) = v(\xi)$, where $\xi = x - c_{TW} t$

$$\alpha_c = 1/(\sigma C_0)$$

Density profiles

Modeling versus microscopy experiments

Summary

- Minimal reaction-diffusion system without extra mechanism:
  $\rightarrow$ sufficient to explain segregation and positioning of bacterial genome

- Self-consistent non-linear system of the components
  $\rightarrow$ transient regime
  $\rightarrow$ global dynamical picture

  $\rightarrow$ Published on ArXiv/1702.07372 – to appear in Phys. Rev. Lett.
  Walter J.-C., Dorignac J., Lorman V., Rech J., Bouet J.-Y., Nollmann M.,
  Palmeri J., Parmeggiani A. & Geniet F. *Surfing on protein waves: proteophoresis as a mechanism for bacterial genome partitioning*

Physical modeling

G. David
J. Dorignac
F. Geniet
V. Lorman
J. Palmeri
A. Parmeggiani

Molecular biology
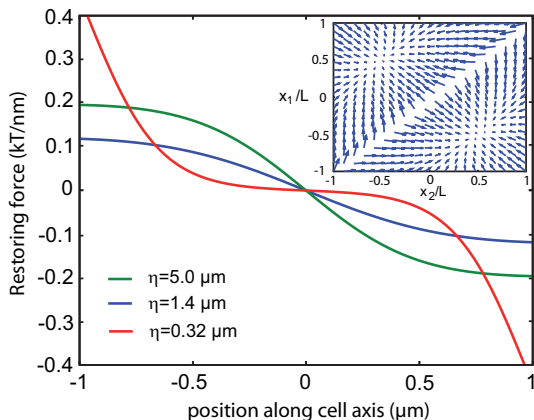
R. Diaz
A. Sanchez
J. Rech
J-Y. Bouet

Super-resolution microscopy

D. Cattoni
A. Le Gall
M. Nollmann

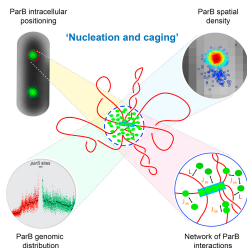# The screening length is in charge of equipositioning in the stable regime

How does ParAB*S* work ?

- Partition complexes: diameter $\sigma \approx 50 - 75nm$ containing ≈ 300 proteins
  - $\rightarrow$ porous particle with volumetric interactions