

Surfing on protein waves: proteophoresis as a mechanism for bacterial genome partitioning

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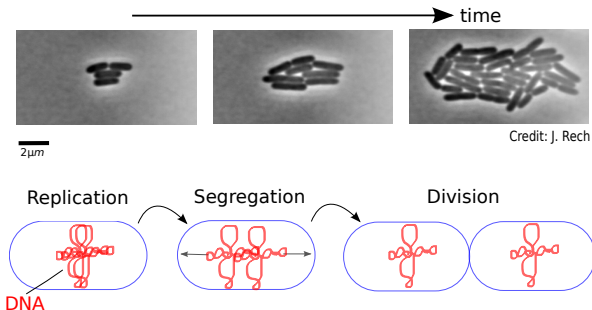
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Outline

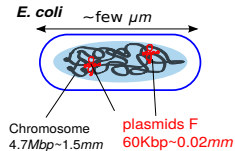
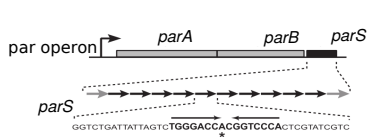
- 1 Bacterial DNA segregation: the ParABS system
- 2 Dynamics: complexes surfing on protein waves

Segregation of bacterial DNA



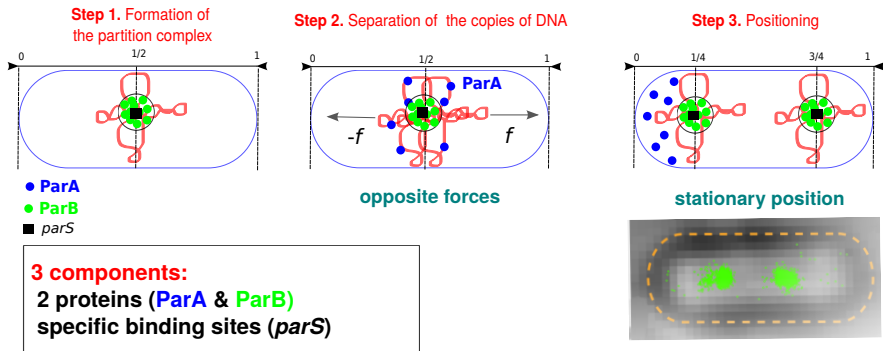
How is the bacterial genome segregated ?

The ParABS operon



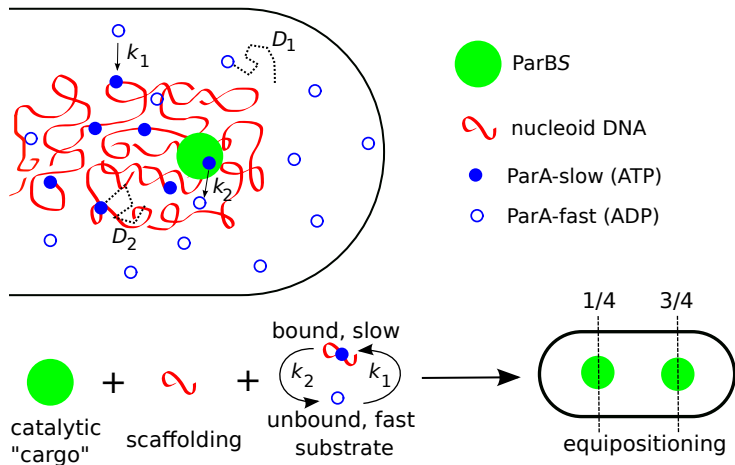
- ParA: “motor” protein (ATPase, Walker-type)
- ParB: binding protein (specific or non-specific binding)
- *parS*: centromere-like DNA sequence

The ParABS segregation system: molecular actors



How to describe both segregation and positioning of macromolecular assembly in a fluid phase ?

Molecular interactions and diffusion



Reaction-Diffusion equations (ParA) coupled to Brownian motion (ParBS)

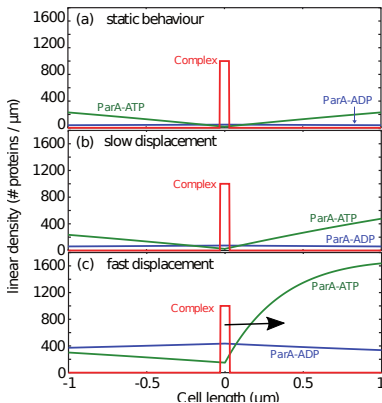
$$\text{ParA-fast : } \frac{\partial u}{\partial t} = D_1 \Delta u - k_1 u(\mathbf{r}, t) + k_2 v(\mathbf{r}, t) \sum_i S(\mathbf{r} - \mathbf{r}_i(t))$$

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

$$\text{ParBS: } m\gamma \frac{d\mathbf{r}_i}{dt}(t) = \varepsilon \int_V \nabla v(\mathbf{r}', t) S(\mathbf{r}' - \mathbf{r}_i(t)) d^3\mathbf{r}'$$

- **Feedback** between the partition complexes and ParA densities
→ Non-linear system with **dynamical instability**

Density profiles obtained with biological parameters



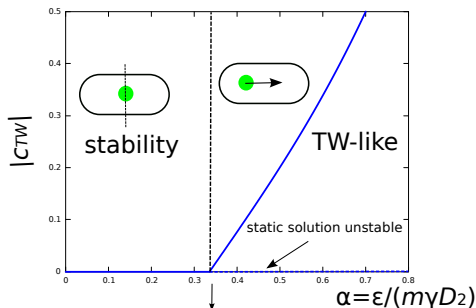
$$\alpha < \alpha_c$$

$$\alpha = \alpha_c$$

$$\alpha > \alpha_c$$

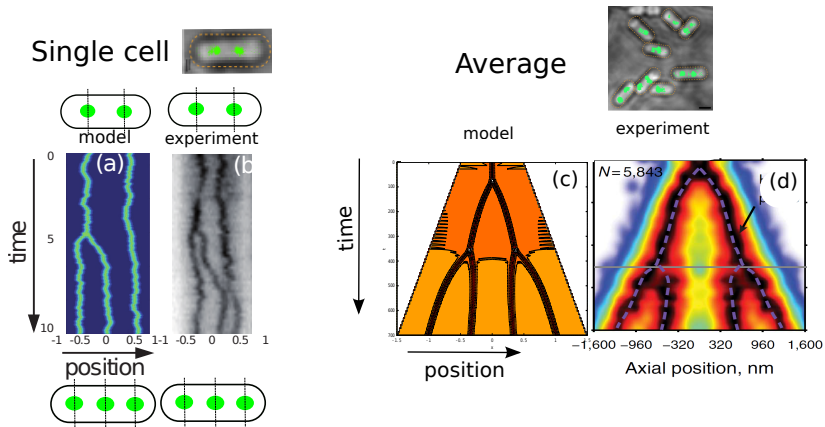
Dynamical instability: supercritical pitchfork bifurcation

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



$$\alpha_c = N_{ParA \in C}^{-1}$$

Comparison with experiments



Summary

- **Minimal reaction-diffusion** system:
→ sufficient to explain segregation and positioning in ParABS
- Non-linear coupling between ParBS and ParA densities:
→ **Self-consistent description of the 3 protein species**
- Analytical analysis:
→ **dynamical transition (stable/unstable regime)**

JCW, 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*, *Phys. Rev. Lett.* **119**, 028101.

arXiv:1702.07372 [q-bio.SC]

Physical modeling

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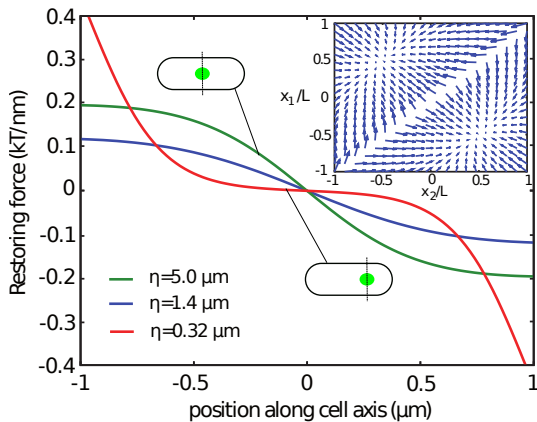


Super-resolution microscopy

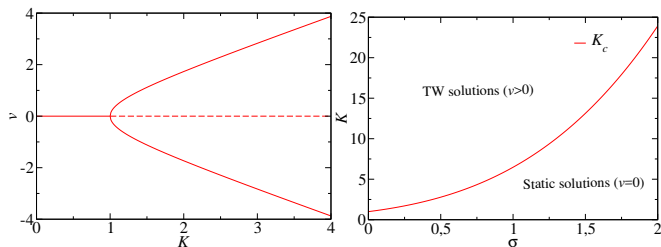
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Screening length



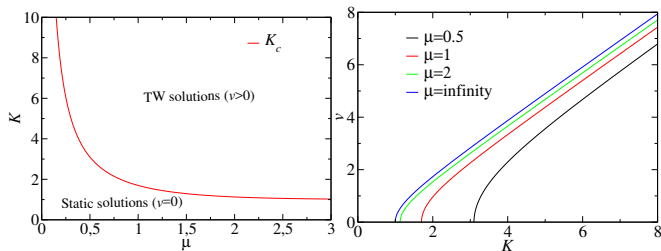
Supercritical pitchfork bifurcation



Infinite system (left) Supercritical pitchfork bifurcation diagram of reduced system in the (K, v) space.

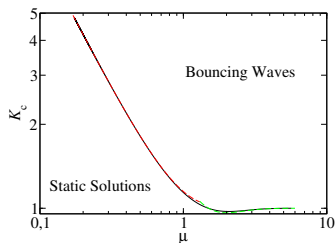
(right) Dynamical phase diagram in the plane (K, σ) where $K = \alpha m_0 / (4D\ell)$ and σ is the dimensionless width of a gaussian source. The red curve represents the boundary (critical value K_c vs. σ).

Supercritical pitchfork bifurcation



Periodic Boundary Conditions (left) Dynamical phase diagram in the plane (K, μ) where $K = \alpha m_0 / (4D\ell)$ and $\mu = L/\ell$ is the dimensionless ratio between L (size domain $2L$) and the screening length $\ell = \sqrt{D/k}$. (right) TW dimensionless velocity v (positive) vs. parameter $K = \alpha m_0 / (4D\ell)$ for different values of $\mu = L/\ell$ from 0.5 to 2 and for $\mu \rightarrow \infty$. The blue curve is the same as the upper part for infinite system, thus the right limit is recovered.

Supercritical pitchfork bifurcation



No-Flux Boundary Conditions (Log-log plot of the instability threshold $K_c(\mu)$ versus the system size to screening length ratio $\mu = L/\ell$ for a Dirac source.