Modelling non-equilibrium polysome dynamics with TASEP

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ABSTRACT

In bacteria transcription and translation are closely related and consists of a complex system of mechanical and chemical interactions that lead to gene expression Fig. 1. A common approach to model translation is trough ordinary differential equations (ODE), but in order to consider the complexity of this phenomenon has been modelled in terms of totally asymmetric simple exclusion process (TASEP) that came from non-equilibrium statistical physics Fig.1. This model has interesting properties like the formation of three regimes: low density (LD), high density (HD) and maximum current (MC). Also has two transitions: from LD or HD to MC is lineal and from LD to HD is non-lineal. We write a python code that modelled translation like a TASEP and test the impact of opposing initial condition when the RNA start being translated, empty or full of ribosomes and found that the flux in HD regime with full start is similar to the flux in LD regime with empty start and the flux in LD regime with full start is similar to the flux in HD regime with empty start. Since the initial condition change the behaviour of translation, we modelled the coupling of transcription and translation with a two particles TASEP, ribosomes and an RNA polymerase (RNAP), we found that transcription and in special the RNAP hoping rate and pauses sets the initial conditions and can influence translation. Such a cooperative mechanism can improve RNA stability and open new ways to tune gene expression.

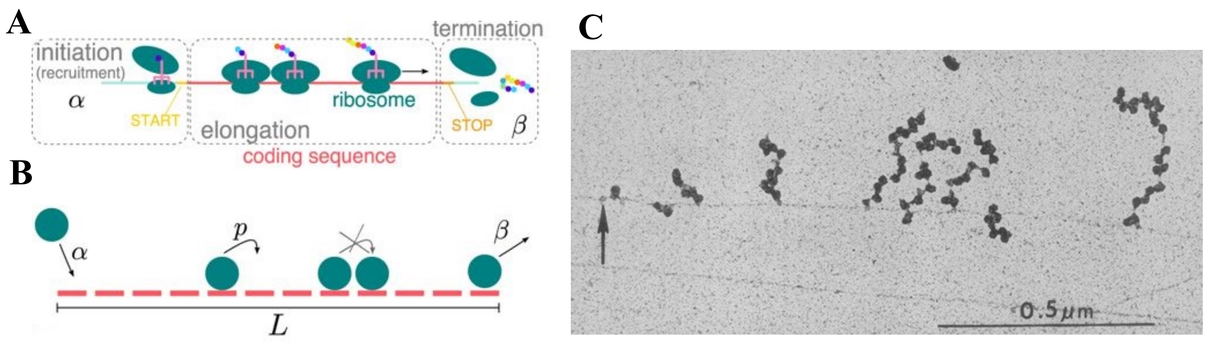

Figure 1. TASEP model . **A**, TASEP translation model. **B**, TASEP model parts **C**, Electron micrograph showing polysomes extension in *E. coli* chromosome that exhibit imperfect gradients of increasing lengths.

METHODS

We code in Python a computational TASEP approach to translation based on relevant biological numbers from E.coli. We run a Montecarlo simulation and analyze it with statistical physics.

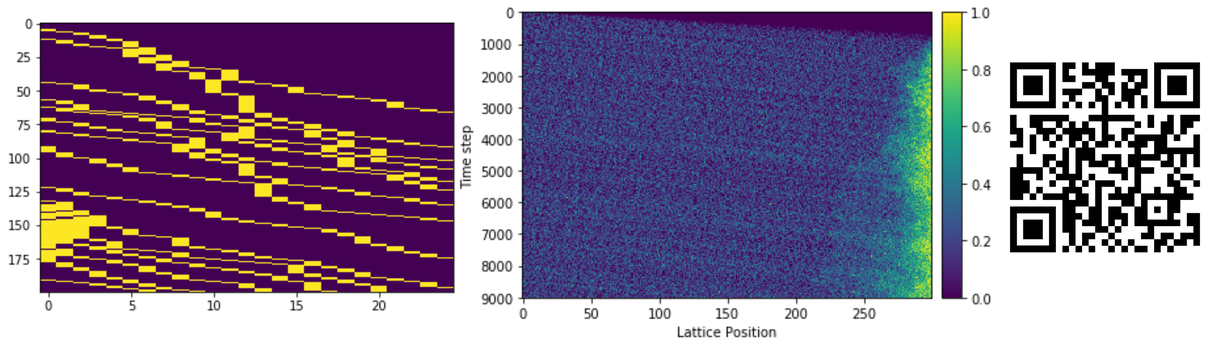

Figure 2. Python code TASEP model . **A**, Result array from a simple TASEP **B**, Result array from a Montecarlo simulation of TASEP **C**, QR code to the repository and data https://github.com/Gonza10V/TASEP.

AGRADECIMIENTOS

Thanks to the SynBio Lab for your support and good disposition. Fondecyt Iniciación 11161046.

RESULTS AND CONCLUSIONS

To test the impact of the initial conditions we set the extreme cases full and empty of ribosomes. The change to empty to full increase the flux (J) in the LD regime and decreased it in HD regime Fig.3. We test the symmetry J change running 25 representative points and ordering it like a TASEP phase diagram Fig. 4. J was calculated using the formula Pρ(1ρ) where ρ is the average occupation for each site and P is the hopping rate.

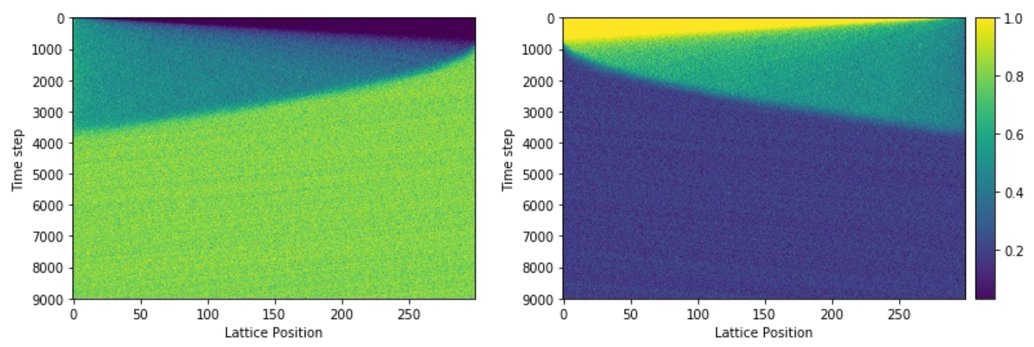

Figure 3. TASEP simulation result array. **A**, HD point with empty initial conditions α=0.32, β=0.08, P=0,4, J=0.086. **B**, LD point with full initial conditions α=0,08, β=0.32, P=0.4, J=0.087.

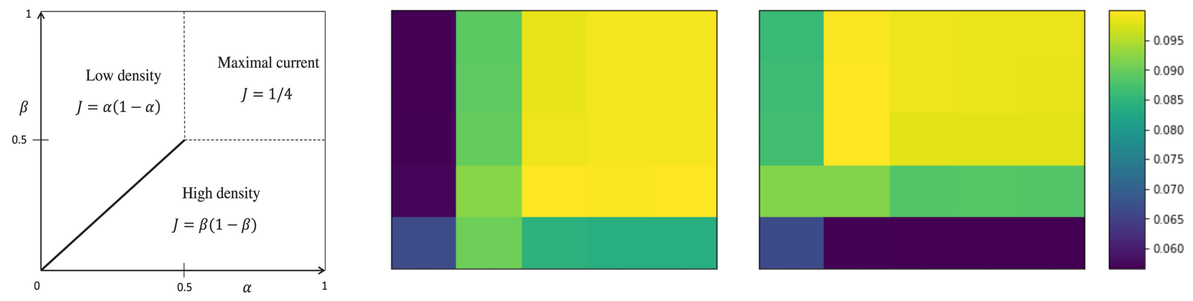

Figure 4. Symmetrical change of regime. **A**, Mean field phase diagram for TASEP, with the simple equation to calculate J in each regime P=1. **B and C**, Empty and full initial conditions respectively of a 2D array with J values ordered like TASEP phase diagram α and β take values from the list (0.08, 0.16, 0.24, 0.32, 0.4) and P=0,4

DISCUSION

In polysome the initial conditions for translation are settled during transcription Fig.5. This can be a new approach to modify gene expression with elongation factors or codogenic use for example.

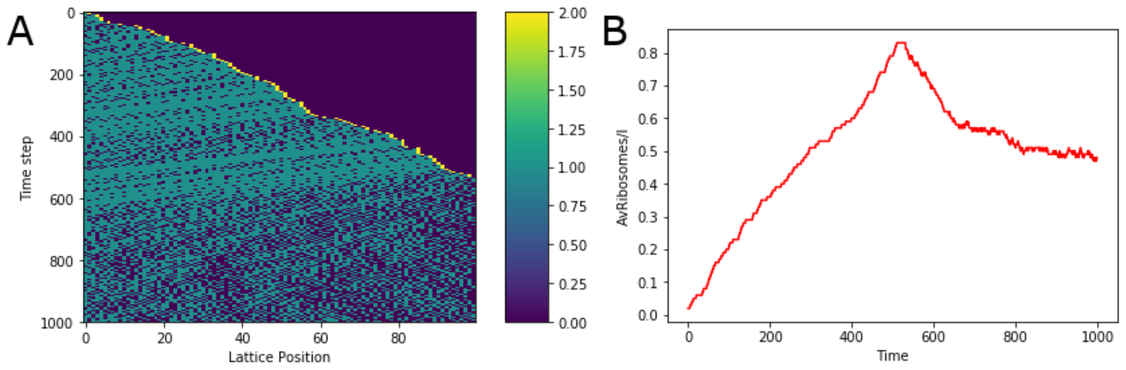

Figure 5. dr-TASEP two particles approach. **A**, Result array image where 2 is RNAP, 1 is ribosome and 0 is an empty space. **B**, Average ribosomes in lattice over timesteps, there is a peak in this value due to the difference in hopping rate between RNAP and ribosomes make ribosomes stack behind RNAP and it matches the RNAP leaving the lattice or the transcription end.

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