

Traffic jams on networks of biological molecular highways

Living cells heavily rely on cytoskeletal transport driven by motor proteins for efficient delivery of biochemical cargoes within the cytoplasm. We recently provided a general theoretical framework to acquire a throughout understanding of nonequilibrium, collective, stochastic transport of motor proteins on simple and complex network topologies mimicking the cell skeleton, with emergent properties which can be directly observed in experiments..

Biological cells require active fluxes of matter to control their internal organization and operate multiple tasks to live. Freight of intracellular cargoes assures cell viability, whereas transport anomalies and perturbations lead to diseases.

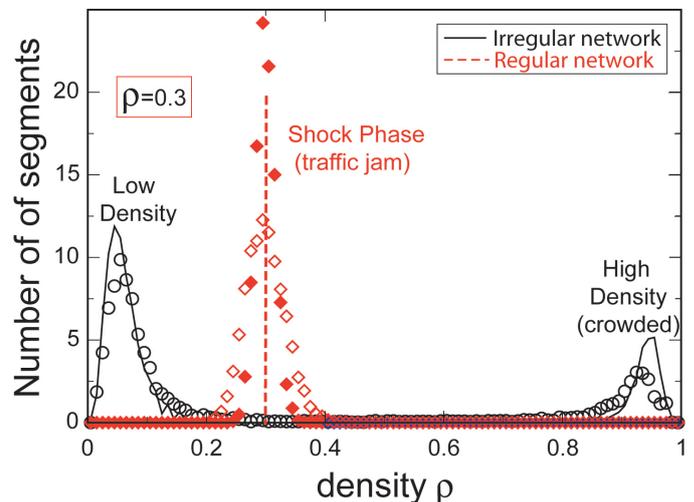
In eukaryotic cells, living matter transport occurs via molecular ATP driven engines called motor proteins that transport cargoes along filamentous protein assemblies forming the cytoskeleton. On this very large “highway” network, motors alternate processive runs to Brownian motion in the cytoplasm, spanning the structurally complex intracellular medium for delivery and logistics.

Experimental progress has opened the door to quantitative studies on transport phenomena down to the molecular scales of single proteins. These processes and their regulation however are so far not well understood. They involve multiple stochastic, nonequilibrium and nonlinear phenomena, challenging intuition and general understanding of fundamental physics. This aspects get even more puzzling when these processes take place along the whole network. To make an analogy, the difficulty in computing and understanding motor transport on the whole cell scale is comparable to mastering the whole road car traffic of a big nation like France!

To get adequate theoretical knowledge, we use nonequilibrium lattice gas models called Exclusion Processes (EP) [1,2]. They mimic the collective stepping of motors along filaments (with excluded volume interactions, including molecular features like processivity) providing also predictions for experiments.

We have advanced considerably in understanding the multiscale properties of motor transport by applying EP on small and very large networks. We showed that motors can develop new stationary regimes of transport, leading to density heterogeneities of matter such as molecular traffic jams.

These nonequilibrium phenomena not only rely on molecular properties (such as stepping cycle, processivity, or kinetics at junctions), but also on global ones such as the filament network connectivity: a random network with a disordered connectivity induces a new phase separation phenomenon between crowded and empty filaments. To follow the road analogy, we showed that



Distribution of segment states as a function of the overall density for large networks (~104 junctions). Irregularly connected networks are organized in low (almost empty) and high (crowded) density segments, while regular networks always present jam configurations (figure modified from [1])

traffic in road systems with regular crossings like Manhattan’s streets produces jams almost systematically and at every crossing. This is not the case for old cities like Montpellier where the urban structural “disorder” allows one to find almost systematically a way to escape from jams.

We thus identified new general laws controlling living matter organization. Recent in-vitro studies concretely suggest the possibility of experimental tests of our predictions.

Understanding these processes is also very valuable for other fundamental systems, like ribosomal protein synthesis in biology, urban and data traffic, physics of reactive media as well as for technological and biomedical use.

References

- [1] I. Neri, N. Kern, A. Parmeggiani, Phys. Rev. Lett. 107 (2011), 068702
- [2] I. Neri, N. Kern, A. Parmeggiani, Phys. Rev. Lett. 110 (2013), 098102.

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