

Bacterial movement by run and tumble: models, patterns,  
pathways, scales

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**Abstract :** At the individual scale, bacteria as *E. coli* move by performing so-called run-and-tumble movements. This means that they alternate a jump (run phase) followed by fast re-organization phase (tumble) in which they decide of a new direction for run. For this reason, the population is described by a kinetic-Boltzmann equation of scattering type. Nonlinearity occurs when one takes into account chemotaxis, the release by the individual cells of a chemical in the environment and response by the population.

These models can explain experimental observations, fit precise measurements and sustain various scales. They also allow to derive, in the diffusion limit, macroscopic models (at the population scale), as the Flux-Limited-Keller-Segel system, in opposition to the traditional Keller-Segel system, this model can sustain robust traveling bands as observed in Adler's famous experiment.

Furthermore, the modulation of the tumbles, can be understood using intracellular molecular pathways. Then, the kinetic-Boltzmann equation can be derived with a fast reaction scale. Long runs at the individual scale and abnormal diffusion at the population scale, can also be derived mathematically.