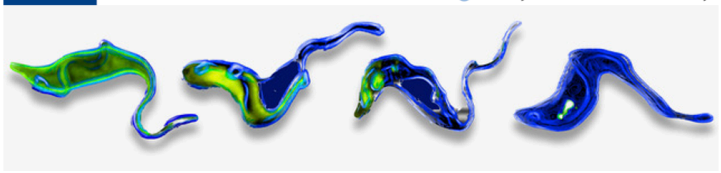

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Bacterial chemotaxis considering memory effects

The ability of motile microorganisms to sense and migrate along due to a chemical or ligand gradient is known as Chemotaxis. This process is a key ingredient in some biological performances, like the acting of immune systems or tumoral migration in metastasis. This mechanism is used also for bacteria to find places to proliferate. The first relevant theoretical model to describe this phenomenon at a macroscopic scale came at the hands of the Keller and Segel article **[1]**. They introduce a macroscopic equation that couples a diffusion-drift equation for bacterial density with a reaction-diffusion equation for the chemoattractant concentration. Over the years, chemotaxis has been increasingly understood. For example, a bacterium like *E. coli*,
orients itself through run-and-tumble movements, altering its tumble rate when moving in the direction of the ligand gradient. The variation of this magnitude depends on fluctuations in the concentration of phosphorylated CheY protein (CheY-P) **[2]**. Tracking *E. coli* bacteria,it was found that these fluctuations have large amplitude and present long memory times (tens of seconds) **[3]**. These new performances are not taken into account in the Keller-Segel model and fails to predict some experimental results. The objective of this work is to obtain new macroscopic equations that can perform the phenomena precisely. Considering a stochastic differential model for CheY-P concentration with memory effects **[4]**, we use a kinetic equation that presents the memory relaxation time and changes in tumble rate **[5]**. By identifying different scales of memory time, we derive a Keller–Segel type chemotaxis model by applying the Chapman-Enskog method in each case. For short memory times, we can only consider the bacteria's density as a conserved field. We deduce the equation, which allows us to obtain the diffusion coefficient and mobility. The results are in agreement with Keller-Segel's predictions for the memoryless time limit. When we consider long memory times, the density of CheY-P protein is a quasi-conserved field. In this case, macroscopic equations of bacteria's density and CheY-P density are derived, together with the associated transport coefficients. In this case, macroscopic equations of bacteria's density and CheY-P density are derived, together with the
associated transport coefficients. An Onsager's relation is obtained for the transport coefficients. We validate these equations by analyzing the stationary regime and linear response to a spatiotemporal signal and compare them with simulations.

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