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# Kinetic equations and inverse problems: an application to chemotaxis

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When modeling phenomena in nature, the choice of scaling is important. The microscopic level, where single particles are traced, typically is computationally not feasible, whereas the macroscopic level, where information is reduced to the population density in space and time, might be too coarse for the problem at hand. There are cases where one considers the mesoscopic kinetic level in-between. Here the information on the direction of travel of individual particles is maintained in the population density. A well-known example is the kinetic Boltzmann equation and its corresponding macroscopic parabolic Navier-Stokes equations in the limit of the Knudsen number going to zero.
We will consider such a kinetic description in the phase space with a velocity jump process in the collision term

$$\partial_t f(x,t,v) + v \cdot \nabla_x f(x,t,v) = \int_V K(x,t,v,v') f(x,t,v') - K(x,t,v',v) f(x,t,v)\, dv'. \tag{1}$$

In this notation, $f(x,t,v)$ denotes the density of particles with velocity $v \in V \subset \mathbb{R}^d$ at point $x \in \mathbb{R}^d$ in space at time $t \geq 0$. The particle motion is driven by the velocity jump kernel $K(x,t,v,v')$ that describes the probability of particles changing from velocity $v'$ to $v$ at point $(x,t)$ in space-time.

In our work we are interested in recovering this kernel $K$. For the reconstruction, experimental data is used. These data are macroscopic measurements, namely velocity averaged particle density $\int_V f(x,t,v)\, dv$. We don't use mesoscopic velocity dependent measurements, since they are difficult to obtain for experimentalists. This recovery of the collision kernel from data constitutes an inverse problem in the kinetic regime.

We study this inverse problem in the framework of chemotaxis: Since certain bacteria move by running along a straight line until they stop and choose a new direction, their movement is a velocity jump process. When the movement is directed, e.g. induced by a gradient in the concentration of an attracting chemical substance, this phenomenon is called chemotaxis. On the population level, this „run-and-tumble" process if often modeled by a kinetic chemotaxis equation of the form of (1). The influence of the chemical attractant is then encoded in the velocity jump kernel $K$. In the scaling limit, these models are typically linked to macroscopic PDEs, e.g. the Keller-Segel equation, describing the bacteria density in space and time. Biologists and practitioners are interested in recovering the velocity jump kernel $K$ in order to study and control the bacterial movement e.g. in bioreactors.

For this inverse problem, typical questions arising from a theoretical point of view are:

- is the reconstruction of the collision kernel possible? Is it unique?
- is it stable w.r.t. small perturbations of the measurements?
- is the kinetic inverse problem also asymptotically equivalent to the macroscopic inverse problem in the scaling limit?

We shall report on results [1] in this direction.

This is joint work with Christian Klingenberg (Würzburg, Germany), Qin Li (Madison, Wisc., USA) and Min Tang (Shanghai, China).

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## References

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