INTERNATIONAL SOLVAY INSTITUTES BRUSSELS

Solvay Colloquium

Professor Sauro Succi

IAC-CNR, Rome, Italy and IACS Harvard, Cambridge, USA

Computational Explorations of Flowing Matter at the Physics-Biology Interface

Boltzmann kinetic theory is the fundamental cornerstone of statististical mechanics, the branch of theoretical physics which endeavours to unravel the subtle connections between the microscopic world of the "things we cannot see", molecules, atoms and below, and the macroscopic world, as we perceive it through our common senses. Its mathematical cornerstone, the Boltzmann equation, describes the way how microscopic motion organizes into the flow of mass, momentum and energy, which feeds and sustains virtually all natural and industrial processes around us.

Yet, the Boltzmann equation is all but an easy piece; a non-linear integral-differential equation living in seven-dimensional phase-space time, and thus setting a formidable computational challenge even to the most advanced numerical methods, let alone analytical ones. In recent times, the Boltzmann equation has made proof of yet one more precious virtue: it (often) lends itself to minimal formulations which manage to relinquish most of the math complexity, without surrendering the essential physics at hand.

In particular, over the last three decades, the Lattice Boltzmann (LB) method has gained a prominent role as an efficient and versatile scheme for the computational exploration of complex states of flowing matter across a broad range of scales. From fully-developed turbulence in real-life geometries, to multiphase flows, all the way down to microfluidics and biopolymer translocation in nanopores. Lately, even quantum-relativistic matter, such as electron flows in graphene and subnuclear quark-gluon plasmas.

After a brief introduction to Boltzmann's kinetic theory and to the main ideas behind the LB method, in this Colloquium we shall illustrate a selected list of recent applications from the above, along with prospects for future explorations at the interface between physics and biology, such as protein folding and aggregation in the cell and the direct simulation of biological organelles on extreme-computing (Exascale) platforms.

Tuesday 30 May 2017 at 4.00 P.M.

COFFEE AND TEA WILL BE SERVED AT 3.45 P.M. IN FRONT OF THE SOLVAY ROOM

SOLVAY ROOM

Université Libre de Bruxelles

Campus Plaine - Boulevard du Triomphe - Access 2 - 1050 Brussels

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