Computational Fluid Dynamics with the Lattice Boltzmann Method

Overview, computational issues and biomedical applications

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Abstract

After two decades of intensive research the Lattice Boltzmann Method¹ (LBM) emerged as a powerful alternative model to study fluid dynamics. Applications are plentiful² and range from e.g. flow in porous media³ to suspension flows⁴ or blood flows^{5, 6}. Originally LBM was valid for incompressible (athermal) Newtonian flows, but now the method has been extended to allow for e.g. non-Newtonian rheology⁷.

The LBM is a large collection of models, but they all share the property that they numerically solve the Boltzmann Equation using a fixed regular lattice and a small set of discrete velocities. The discrete velocities are such that they match the underlying lattice, thereby transforming the advection operator to a streaming from one lattice node to a neighbouring lattice node. The LBM algorithm becomes a very clean streaming from lattice node to lattice node, followed by a collision operator that is local to lattice nodes. This computational structure allows for highly efficient parallel implementations of the LBM⁸. However, if the fluid domain becomes very irregular, like in any other parallel computation, special care must be taken to get well balanced computations⁹.

LBM has found applications in many domains. As an example I will discuss biomedical applications, and most specifically blood flow simulations^{5, 6, 10, 11}.

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