Contribution ID: **20** Type: **not specified**

Hands-on Mechanobiology of Cell Motility

Wednesday, December 10, 2025 4:00 PM (2 hours)

This contribution reviews recent advancements in mechanobiology at the University of Brescia (UNIBS), with particular emphasis on the development of advanced computational models—built on the deal.II finite element library—for investigating cell motility.
Controlling cell motility remains a major scientific challenge, as it underpins key biological processes such as metastasis, embryogenesis, angiogenesis, and hemostasis. These phenomena depend on the dynamics of sometimes transient, force-bearing cytoskeletal networks, regulated and activated by the molecular activity of adhesive proteins (receptors) on the cell membrane.
Accordingly, our research focuses on two central aspects:
(i) the role of actin cytoskeleton dynamics in the mechanobiology of cell motility, and
(ii) the role of cell mechanics in receptor activity.
For (i), we propose a multiphysics model extending the Larché–Cahn framework for chemo-mechanical coupling. It captures the interaction between actin transport, polymerization, and mechanical forces driving membrane protrusion and cell migration.
For (ii), we introduce a model exploring how cell mechanics influences the chemo-diffusive behavior of adhesive receptors and their interactions with extracellular molecules called ligands. In this context, the cell membrane is idealized as the boundary of a deformable body, with its morphology governed by intracellular dynamics.
Simulations for both models (i) and (ii) are obtained using a Lagrangian perspective.
Numerical studies based on model (i) demonstrate the code's ability to generate force-bearing domains through monomer polymerization—an approach particularly suited for simulating fibrin network formation in hemostasis. In silico experiments relying on model (ii) provide insights into the mechanobiology of adhesive protein relocation in advecting cells.
We conclude by outlining future developments and offering hands-on sessions, where participants will have the opportunity to run mechanobiological simulations using our computational tools.

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Session Classification: HANDS-ON TUTORIAL