

Advanced Computational Framework for Simulating Multiple Myeloma Proliferation Dynamics: Development, Calibration and Experimental Validation

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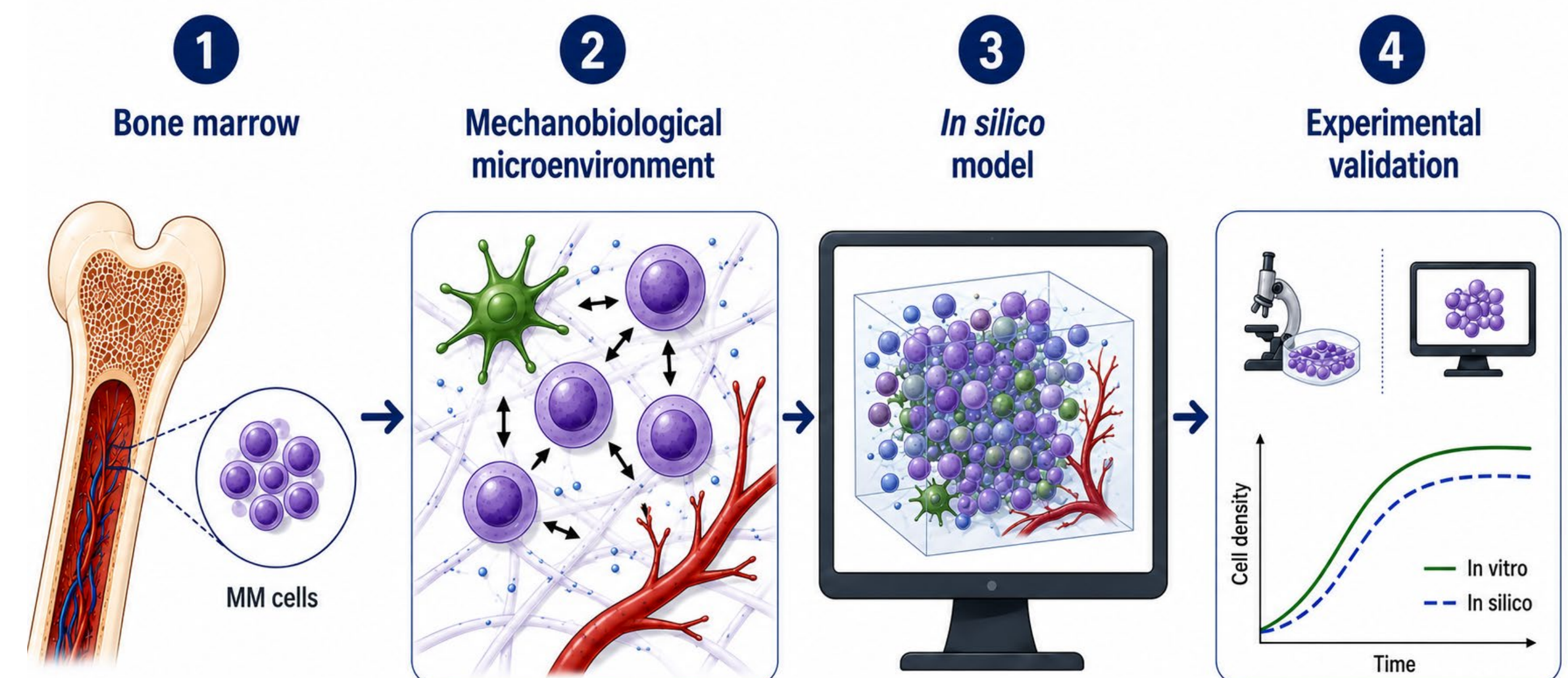
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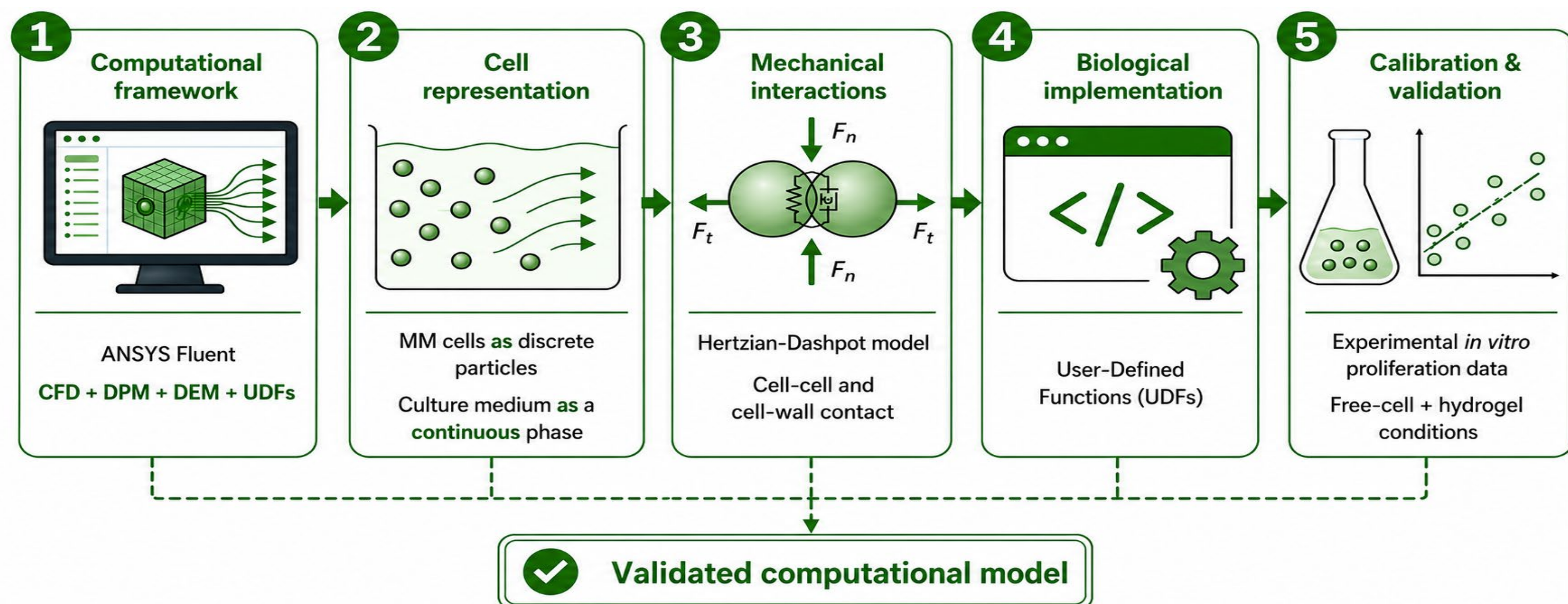
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Introduction

Multiple myeloma (MM) is a hematological malignancy characterized by the uncontrolled proliferation of plasma cells within the bone marrow [1]. Its progression is strongly influenced by the surrounding mechanobiological microenvironment [2], [3]. This work presents a computational framework to simulate MM cell proliferation under free-cell and hydrogel conditions, providing an *in silico* complement to *in vitro* experiments for studying complex mechanobiological phenomena.



Methods



CFD: Computational Fluid Dynamics,

DPM: Discrete Phase Modeling,

DEM: Discrete Element Method.

Results and conclusions

Free-cell condition

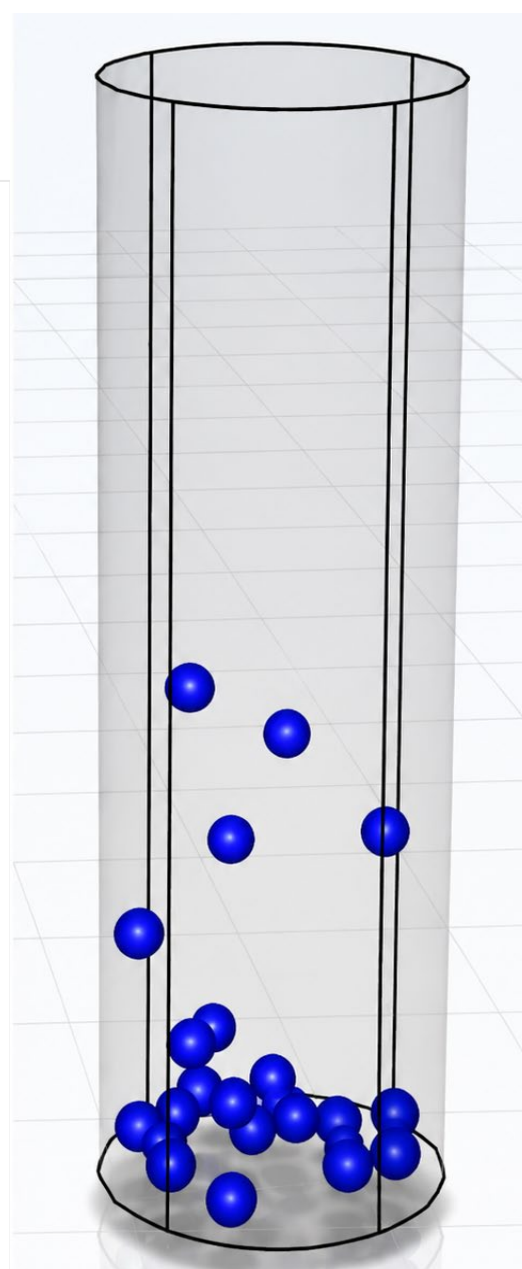
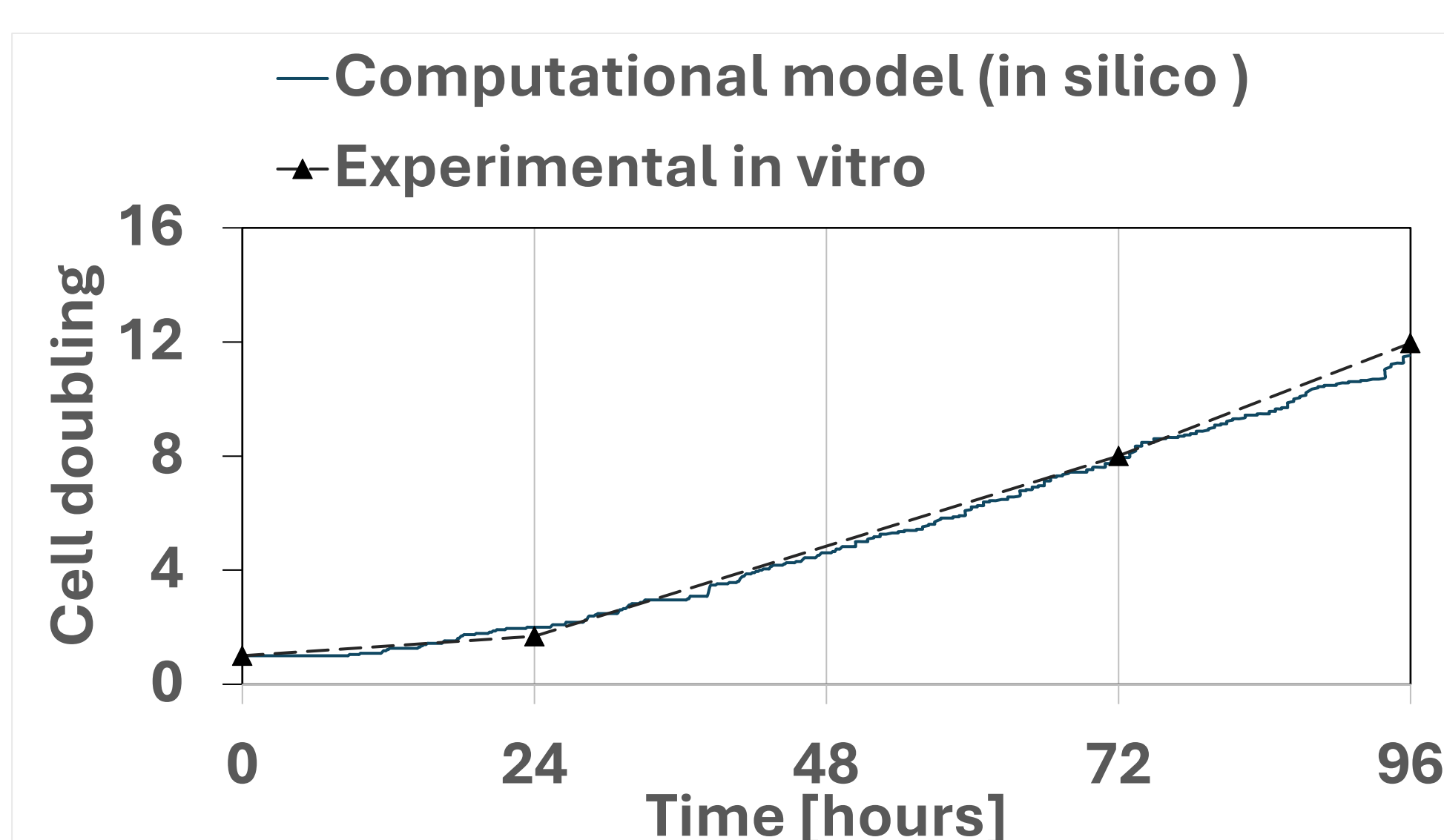


Figure 1. Computational and experimental *in vitro* cell doubling under free-cell conditions after 96 h. Right: ANSYS snapshot at 19 h.

Hydrogel condition

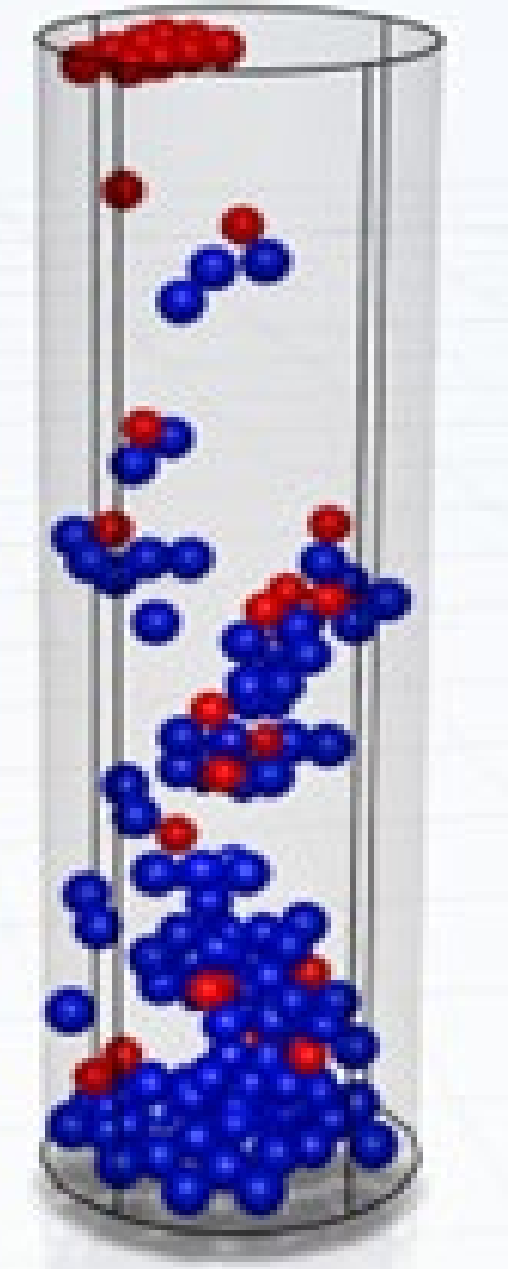
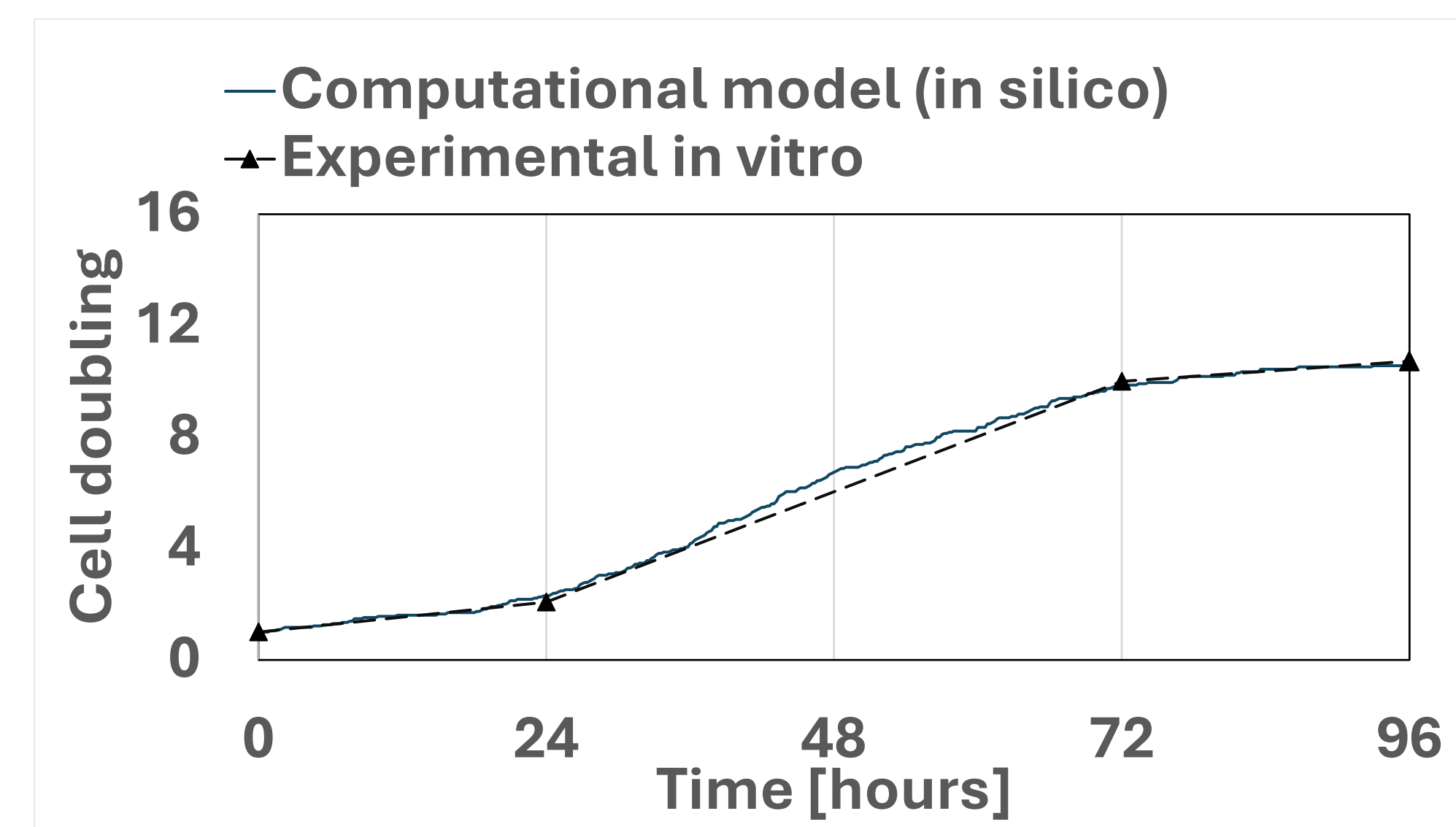


Figure 2. Computational and experimental *in vitro* cell doubling under hydrogel conditions after 96 h. Right: ANSYS snapshot at 19 h (blue: cells; red: hydrogel).

Key findings

- ✓ **Successful calibration and validation** under both free-cell (Figure 1) and hydrogel conditions (Figure 2).
- ✓ The model reproduced the characteristic lag, exponential, and saturation phases observed experimentally.
- ✓ Hydrogel simulations captured proliferation under mechanically constrained conditions, highlighting the influence of mechanical interactions on cell growth.

Future outlook: Predictive studies in vascular-inspired environments.

Acknowledgements

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References

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