UNIVERSITY OF AMSTERDAM

Computational Science

Cellular blood flow simulations for HPC

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CompBioMed
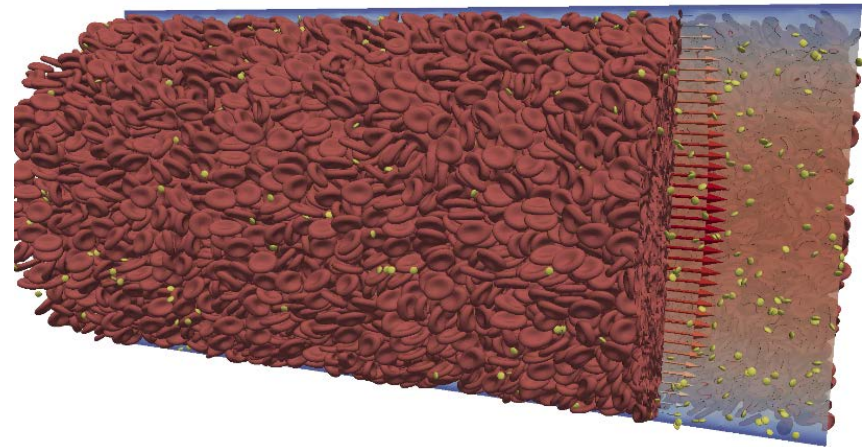
HemoCell

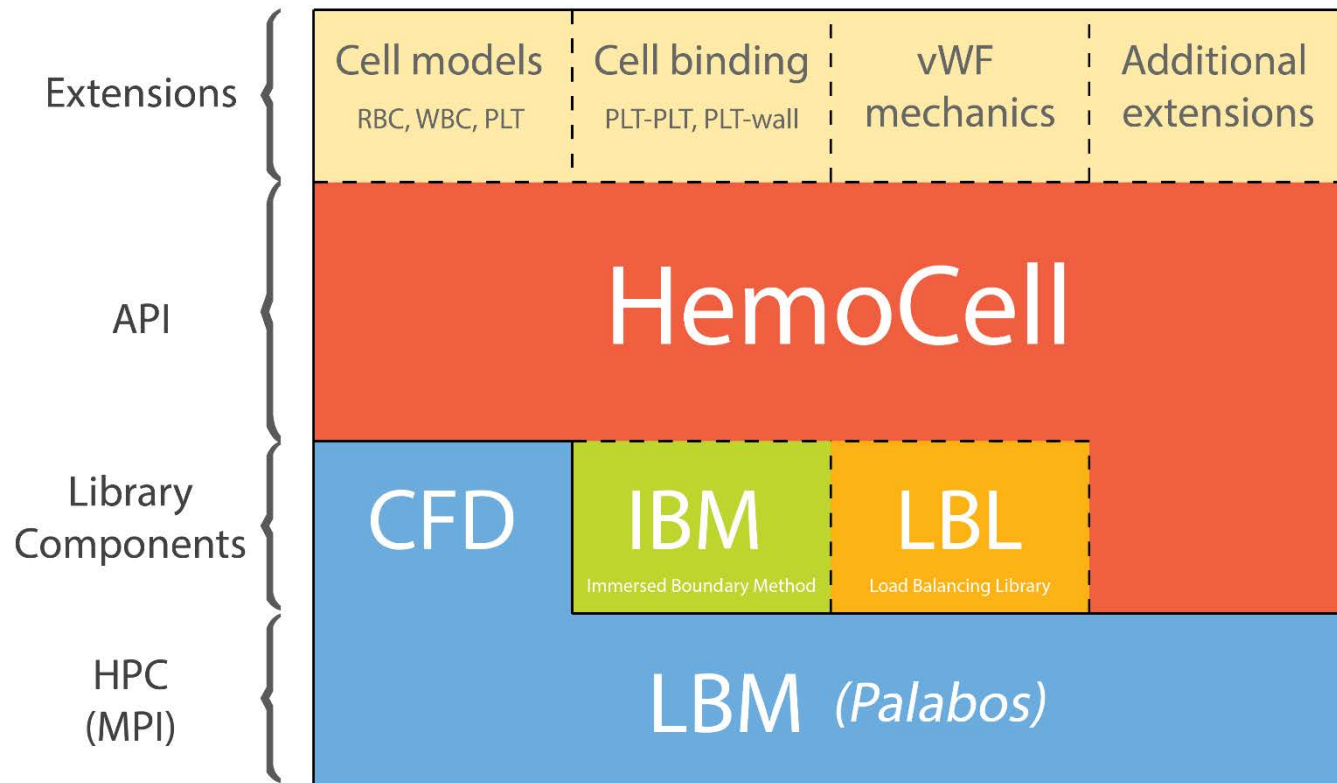Lattice Boltzmann method (LBM) ←→ Immersed boundary method (IBM) ←→ Discrete particle method (DEM)

- Validated [1]
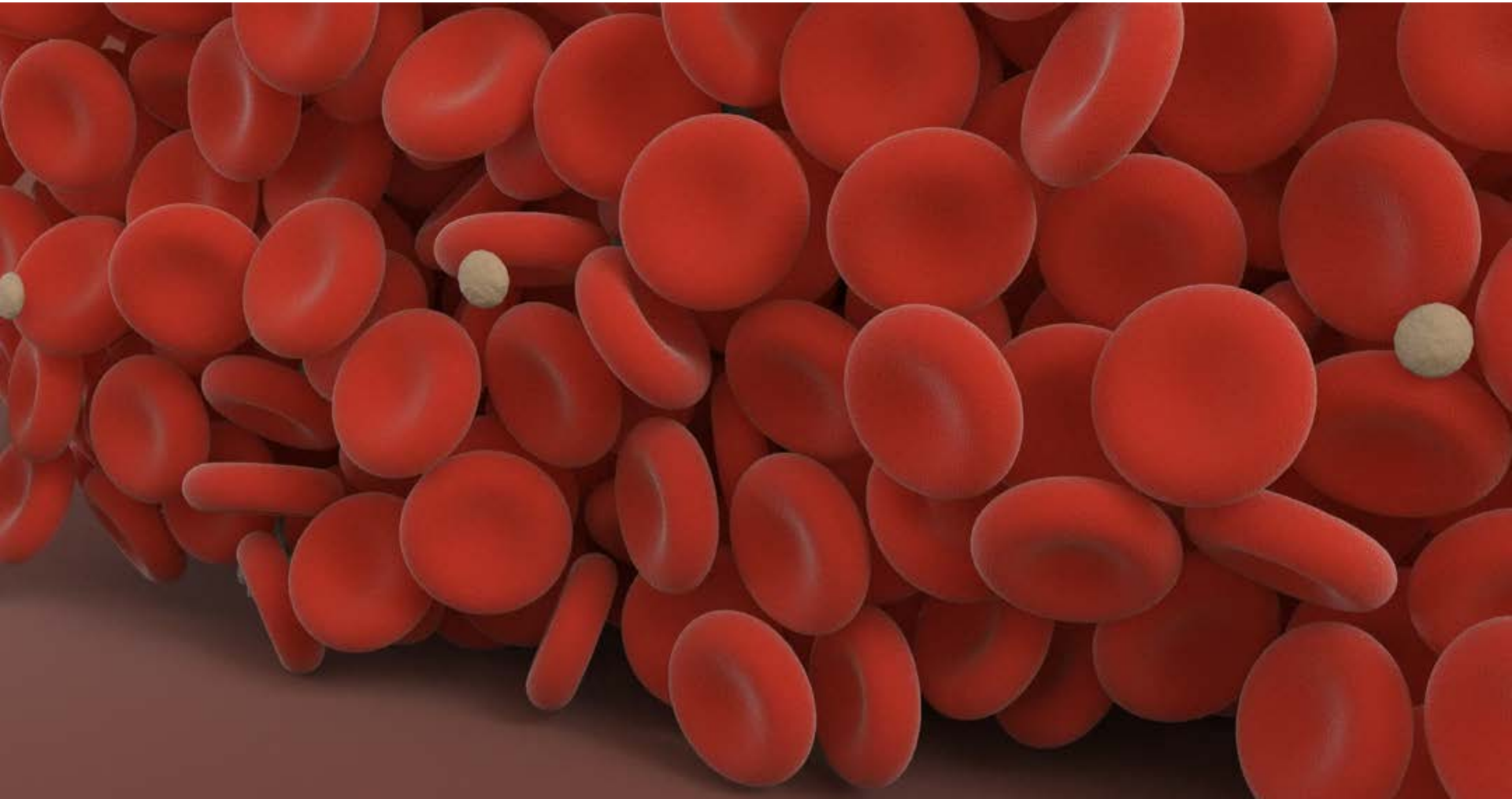- Fully parallelized
- Physiological hematocrit
- High shear rates

More information: www.hemocell.eu

HemoCell structure
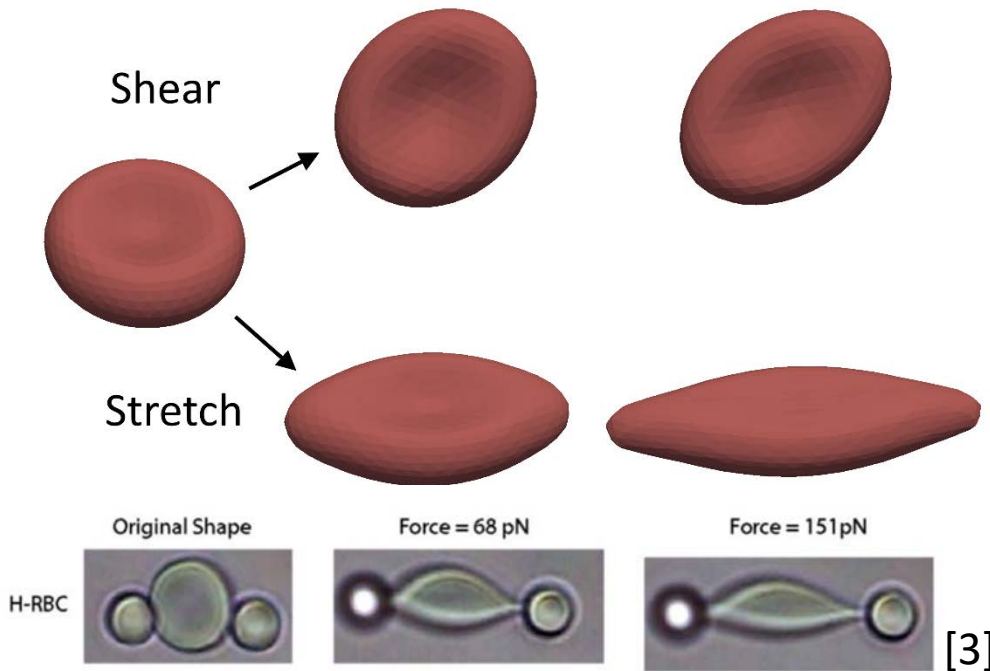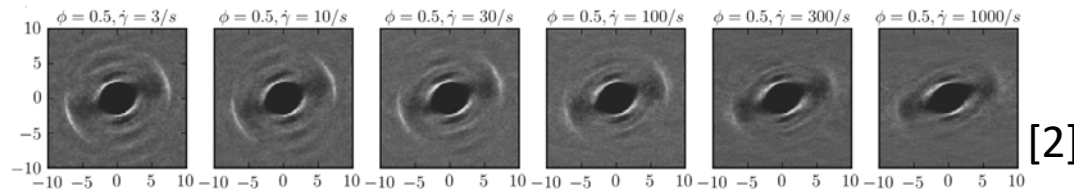
HemoCell movie

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# Single cell validations

[2]

Shear

Stretch

[3]

[1] Závodszky et al., *Frontiers in Physiology*, 2017, **8**, 563
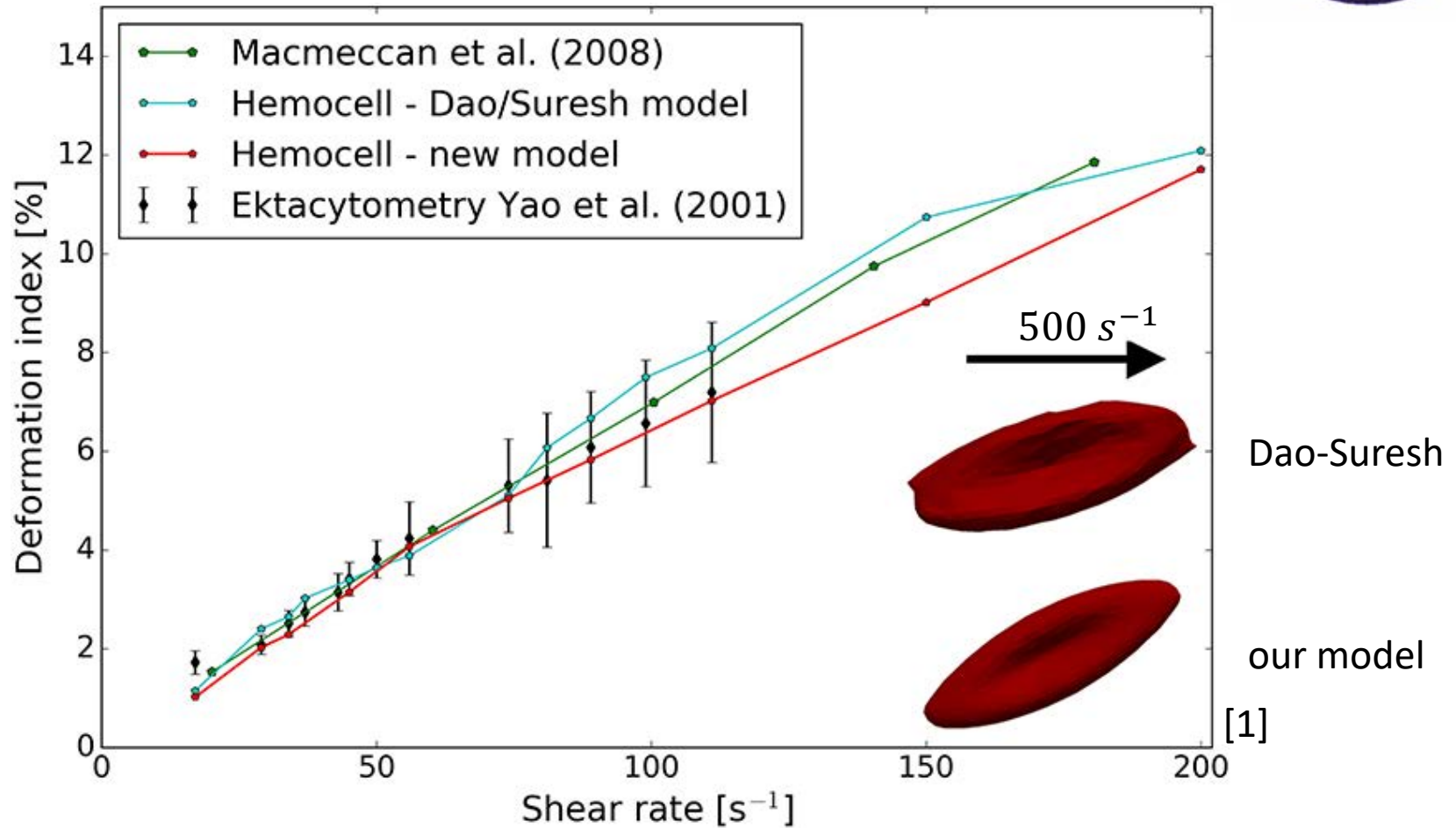[2] Yao et al., *Journal of Biomechanics*, 2001, **34**(11), 1501-1509
[3] Suresh et al., *Acta Biomater.*, 2005, **1**(1), 15-30

Stretching

Original Shape   Force = 68 pN   Force = 151pN

H-RBC

[3]

[1]

[1] Závodszky et al., *Frontiers in Physiology*, 2017, **8**, 563
[3] Suresh et al., *Acta Biomater.*, 2005, **1**(1), 15-30

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Shearing

$500\ s^{-1}$

Dao-Suresh

our model

[1]

[1] Závodszky et al., *Frontiers in Physiology*, 2017, **8**, 563
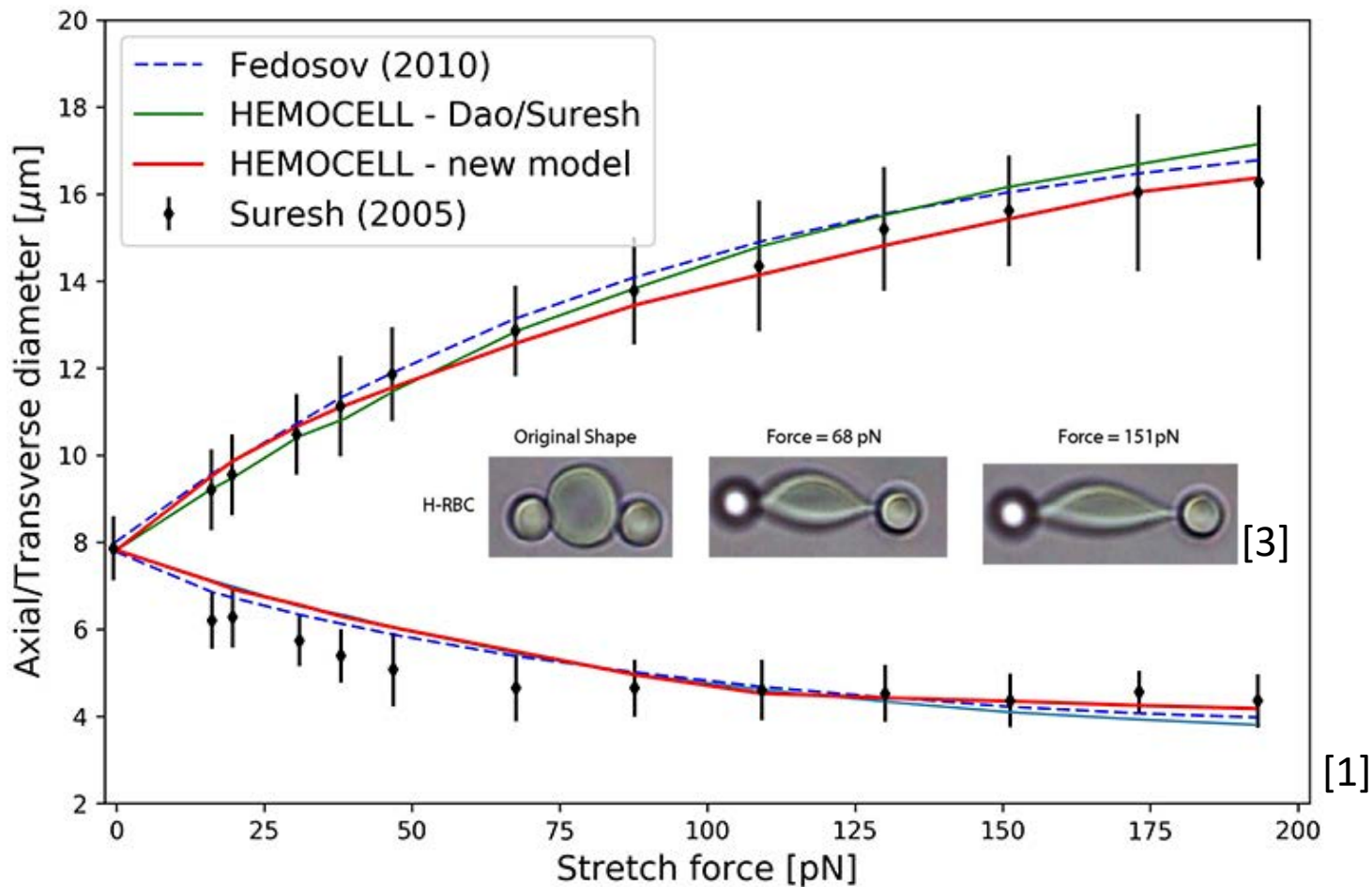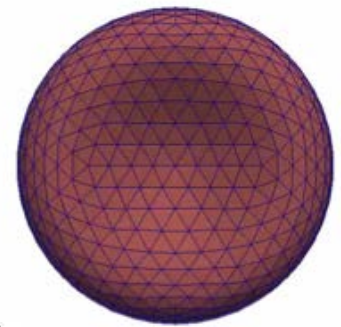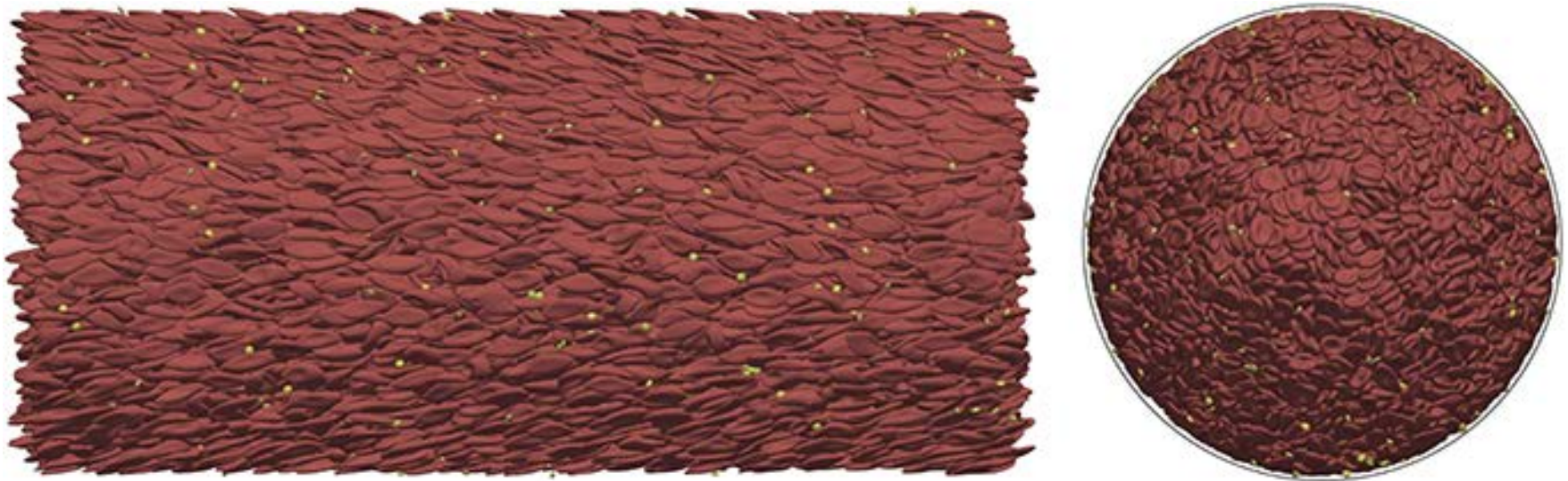
Pipeflow

Blood flow simulation in a straight vessel section of D = 128 μ m diameter with a hematocrit value of 45% at an average velocity of 1.5 cm/s using our new material model. **(Left)** side view; **(Right)** 2D-projected axial view (the black outline shows the location of the vessel wall). The simulation of this case consists of ~2 × 10^4 cells and it was computed on 512 cores

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Validations of transport properties
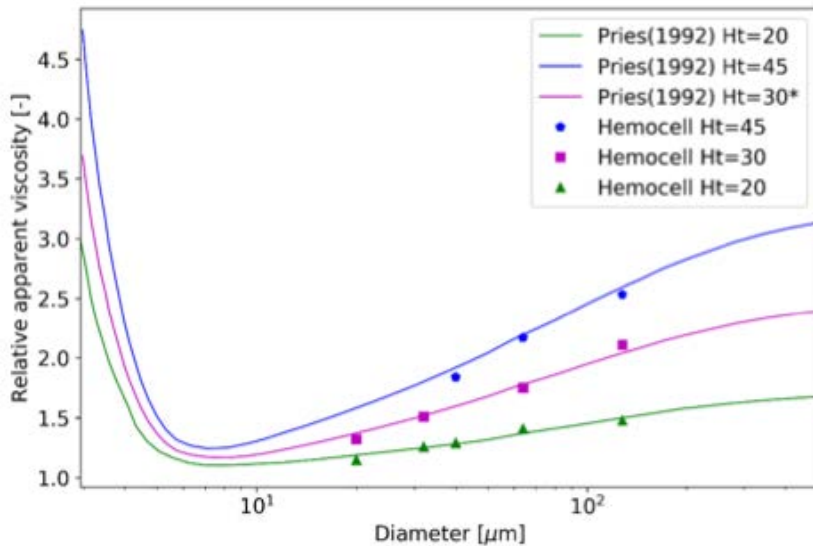
Relative apparent viscosity as a function of diameter at the hematocrit levels of 20, 30, and 45%.
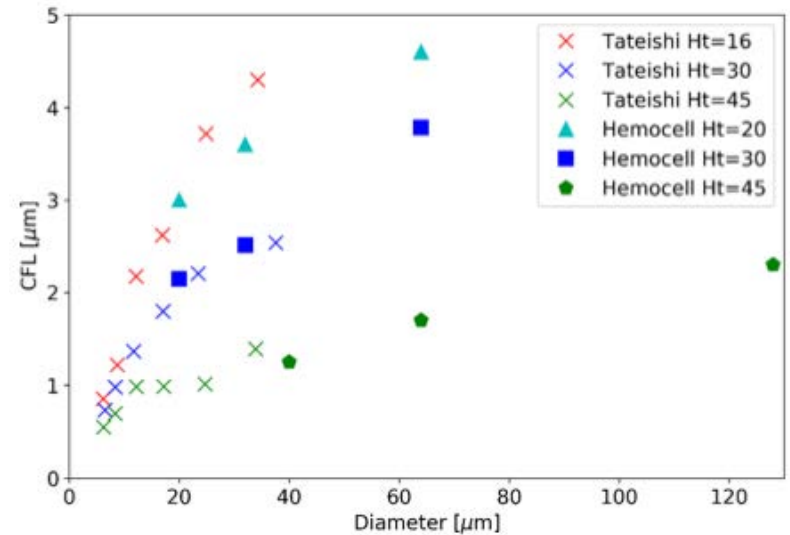
The width of the cell-free layer as a function of vessel diameter in a straight section. Hemocell results are compared to experiments of Tateishi et al. (1994).
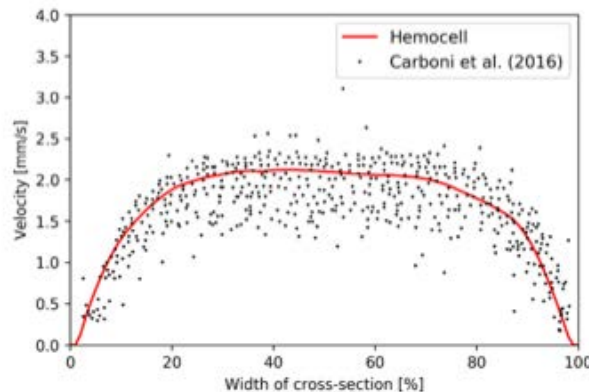
Velocity profile arising in Hemocell simulation (red line) and the particle tracking results of Carboni et al. (2016) (black dots).

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Hemocell deployments
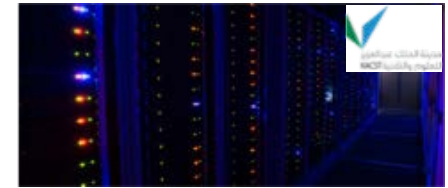
Superman (BME, Budapest)

Marenostrum (BSC, Barcelona)

Sanam (KACST)

Supermuc (LRZ, Munich)

Cartesius and Lisa (SurfSara, Amsterdam)

Aspire I (NSCC, Singapore)

Lomonosov (MSU, Moscow)

Eagle (PSNC, Poznan)

Demo: working with HemoCell

- Download HemoCell (hemocell.eu or git-repository)
- Compile HemoCell
- Run ShearCell test case
- Visualize results (Paraview)

Time to try it out!

Download HemoCell

- https://www.hemocell.eu/
- https://github.com/UvaCsl/HemoCell

Setup and Compile HemoCell
- https://www.hemocell.eu/user_guide/QuickStart.html

Follow along with ascii cinema
- https://asciinema.org/~bczaja

- Get Paraview
- https://www.paraview.org/

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Post processing and Paraview

- https://www.paraview.org/

- Generate .xmf files by running /hemocell/scripts/batchPostProcess.sh in the case directory.

- Open .xmf files with XDMF reader (NOT XDMF3!!) option in Paraview.

- a HemoCell case produces multiple types of output. The simplest is the csv output which consists of all the information about cells in csv files. To merge the csv files into a single one per timestep you can use the script /hemocell/scripts/CellIntoMergeCSV.sh in the *tmp* directory.

- More detailed output is stored in hdf5 format

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Thank you!

Are there any questions?

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