



Quantitative assessment of lipid bilayer-cytoskeleton coupling in red blood cell membrane

V. Puthumana, Paul G. Chen, Marc Leonetti, R. Lasserre, Marc Jaeger

► To cite this version:

V. Puthumana, Paul G. Chen, Marc Leonetti, R. Lasserre, Marc Jaeger. Quantitative assessment of lipid bilayer-cytoskeleton coupling in red blood cell membrane. Biomembrane Days 2022, Sep 2022, Berlin, Germany. 2022. hal-03781115

HAL Id: hal-03781115

<https://hal.science/hal-03781115>

Submitted on 20 Sep 2022

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Quantitative assessment of lipid bilayer-cytoskeleton coupling in red blood cell membrane

V. Puthumana¹, P. G. Chen¹, M. Leonetti², R. Lasserre³, and M. Jaeger¹

¹Aix Marseille Univ, CNRS, Centrale Marseille, M2P2, Turing Centre for Living Systems, France

²Aix Marseille Univ, CNRS, CINaM, Turing Centre for Living Systems, Marseille, France

³Aix Marseille Univ, INSERM, CNRS, CIML, Turing Centre for Living Systems, Marseille, France



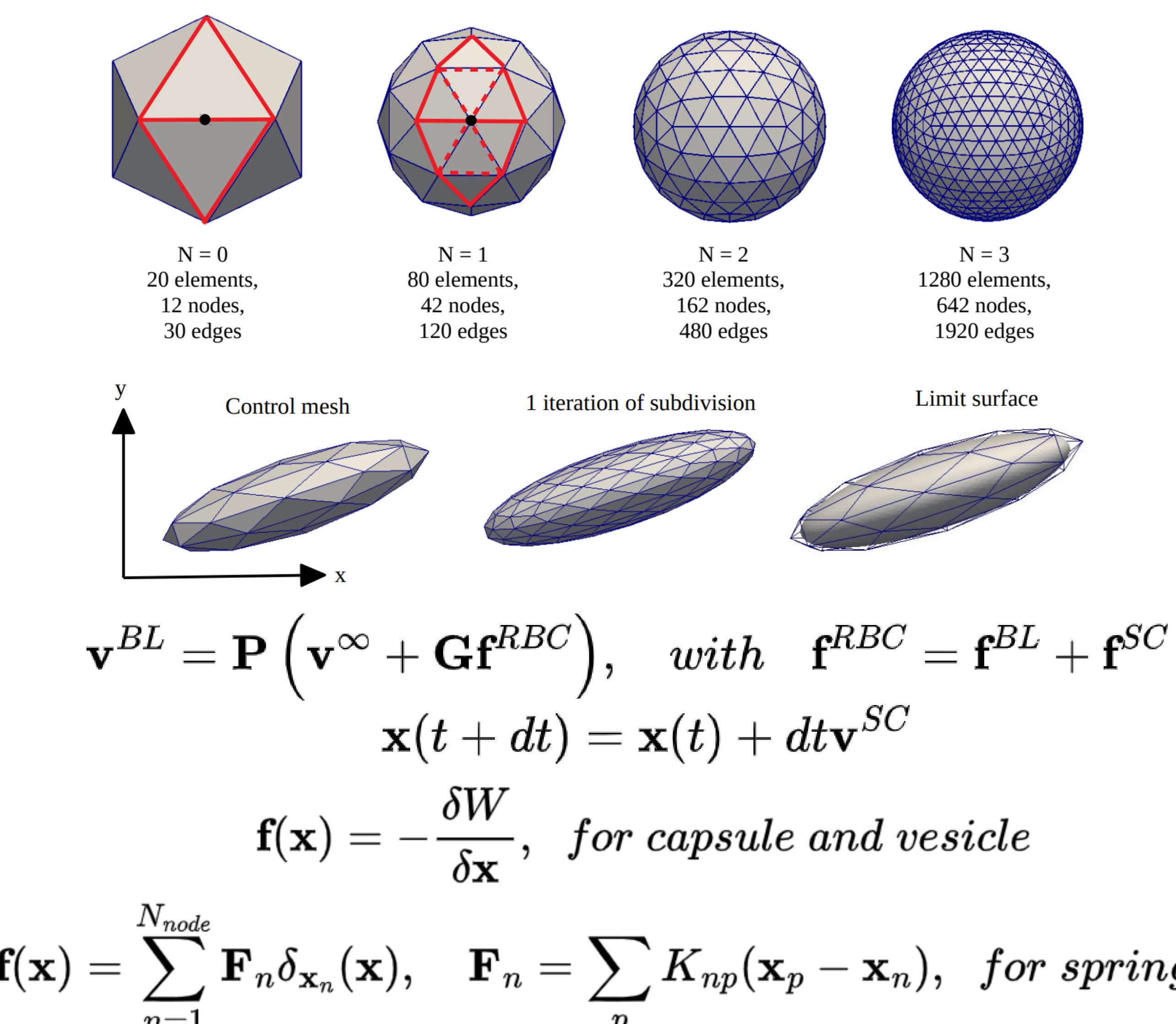
Scan for
full article

Overview

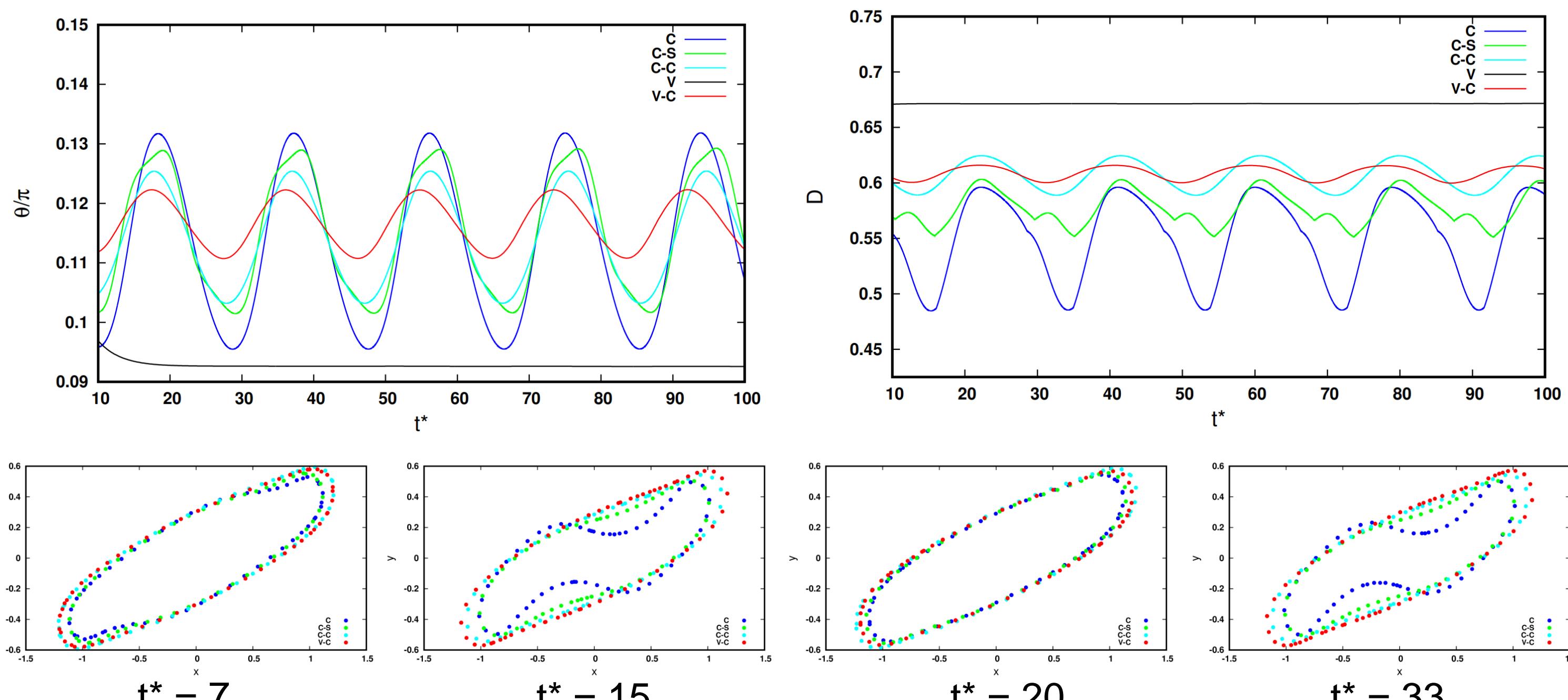
Like other cells, the RBC membrane is composed of a lipid bilayer (BL) supported by a cytoskeleton (SC). The BL provides fluidity, area incompressibility and slight resistance to bending. The SC provides shear elasticity. The coupling of the SC to the BL is provided by protein junction complexes, with possible sliding. Despite this biological reality, the most commonly adopted modelling strategy is of the capsule type^[1], representing the SC and the BL in only one solid layer. To quantify the consequences of this simplification, we compare Capsule (C) and Vesicle (V) models with models that distinguish the bilayer from cytoskeleton by a combination of Capsule-Capsule (C-C) and Vesicle-Capsule (V-C), as well as Capsule-Spring (C-S) and Vesicle-Spring (V-S) on the typical dynamic regimes (Ca , λ) observed for shear flow.

C → Blue C-S → Green C-C → Cyan V → Black V-S → Orange V-C → Red

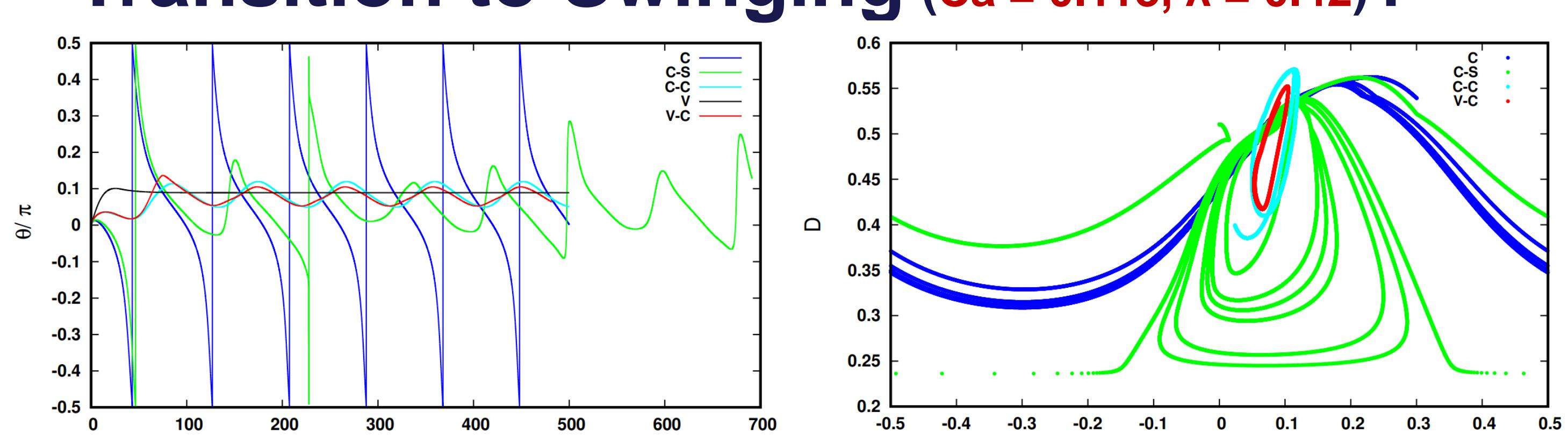
Modelling strategy^[2,3]



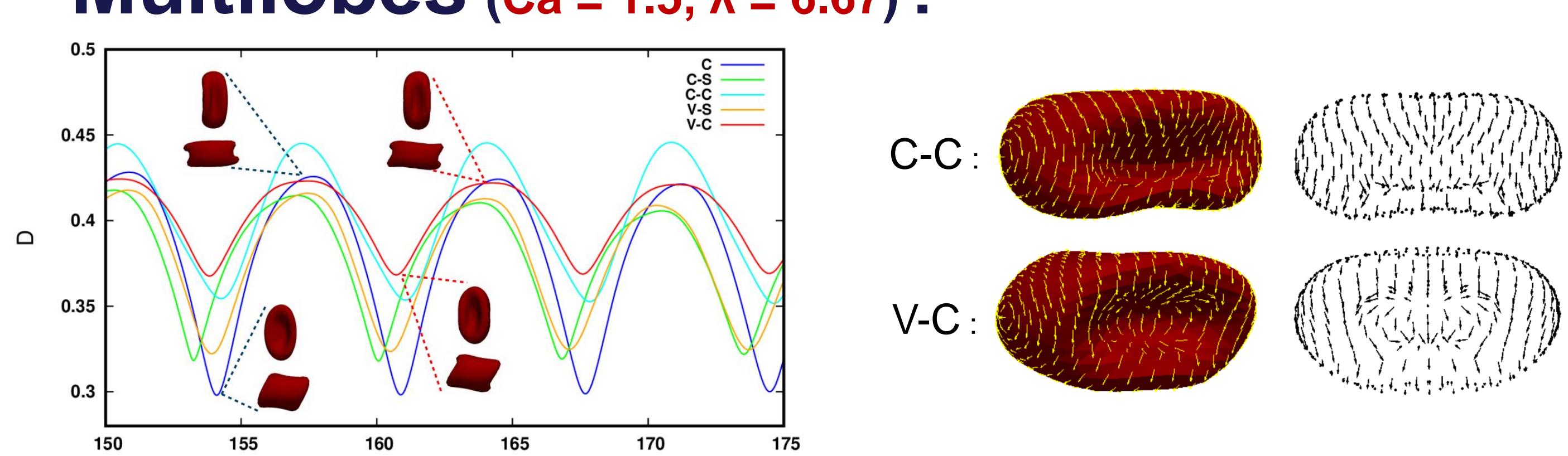
Swinging (Ca = 0.5, λ = 0.4) :



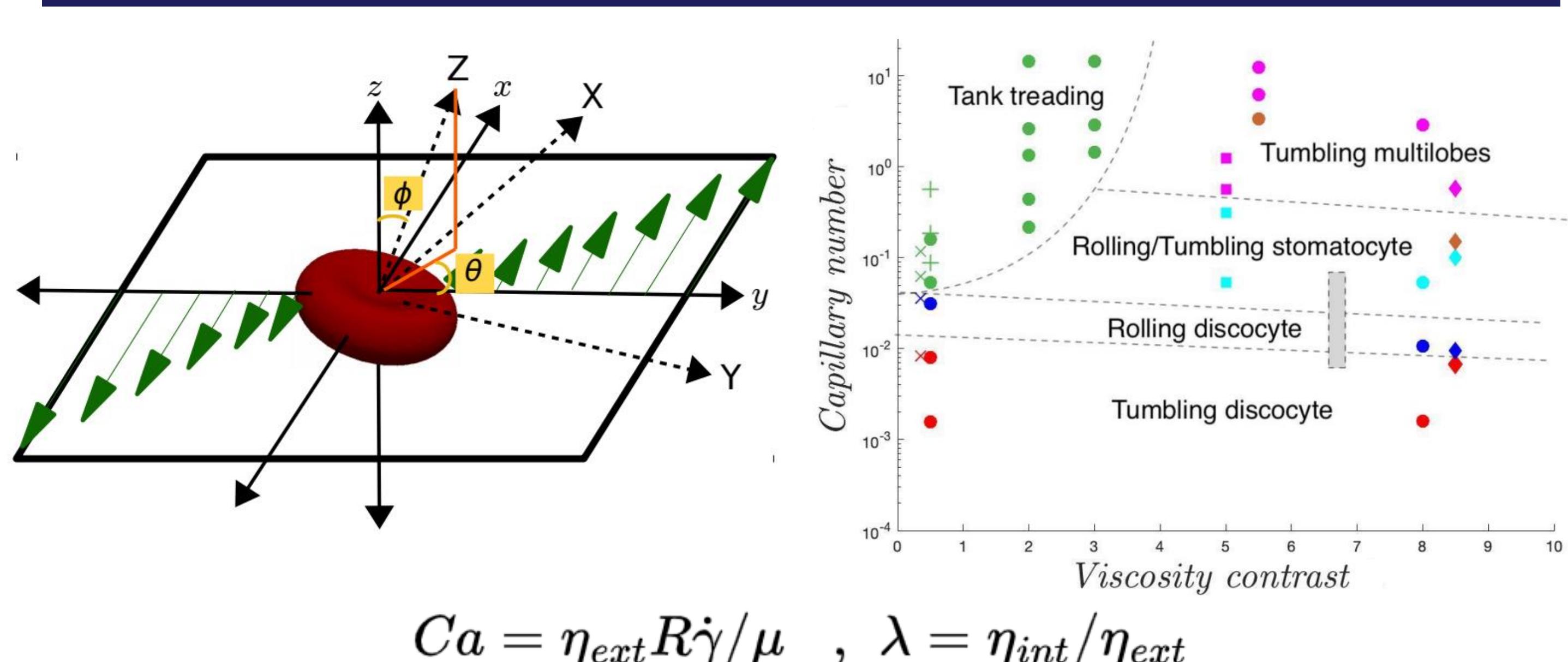
Transition to Swinging (Ca = 0.113, λ = 0.42) :



Multilobes (Ca = 1.5, λ = 6.67) :

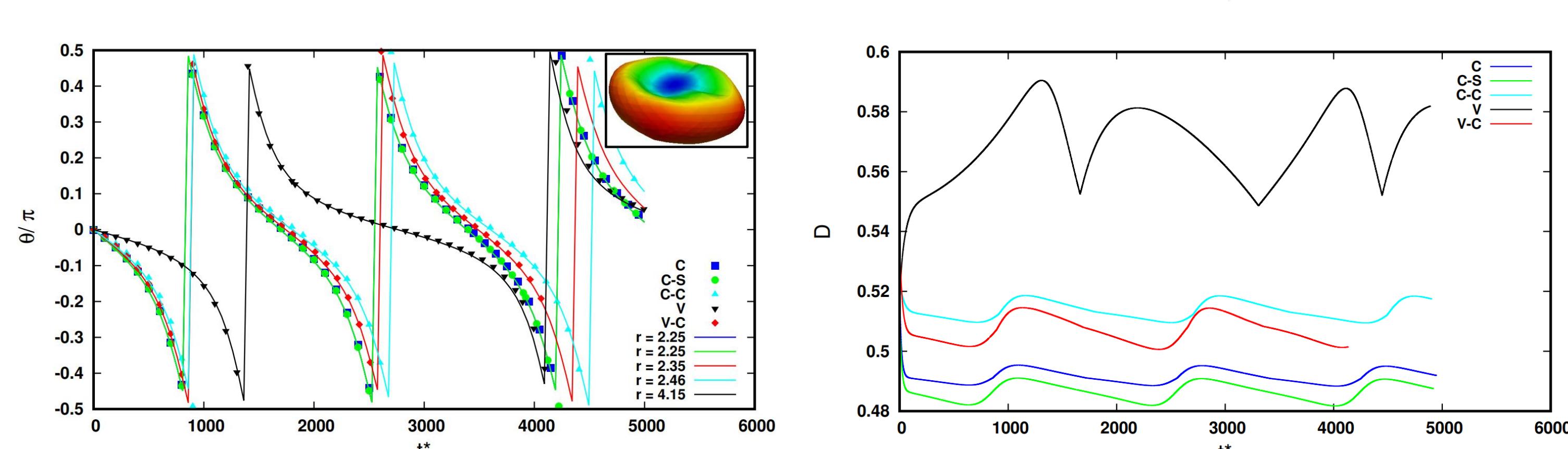


Comparison in shear flow^[3,4,5,6]



Tumbling (Ca = 0.005, λ = 6.67) :

From Jeffery's theory, $r \tan \theta = \tan \frac{\dot{\gamma} t}{r + r^{-1}}$



❖ Different models follows different Jeffery's orbits.

Conclusion^[3]

- Precise quantification shows that the deviation of modelling RBC as a Capsule is not so negligible.
- Accurate modelling strategy is at least as important as the choice of the stress free shape.
- Along with accurate mechanical membrane properties, the way they combine is also important as well.
- The anisotropy developed by the spring network made the V-S model unstable.

References

- Barthès-Biesel, D. et al. J. Fluid Mech. 113:251–267, 1981
- Boedec, G. et al. J. Comp. Phy. 342:117-138, 2017
- Puthumana, V. et al. arXiv:2209.02328 [physics.flu-dyn]
- Minetti, C. et al. J. Fluid Mech. 864:408-448, 2019
- Mauer, J. et al. Phys. Rev. Lett. 121, 118103, 2018
- Agarwal, D. et al. arXiv:2111.14206 [cond-mat.soft]