# VARIOUS MATHEMATICAL APPROACHES TO MODELLING MECHANICAL STRAIN STATE IN VIRUS PARTICLE

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# **OBJECTIVES**

The main objective of my research is to find a mathematical model that will fit viral shell's **hyperelasticity** (the most common example of hyperelastic material is rubber) and **anisotropic** properties (different properties in different directions), that appears in nonempty viral capsids.

In order to that, the main methods of modelling viral capsids were compared to investigate how mechanical properties and parameters, such as Young's modulus, Poisson's ration can change along different symmetry axes.

## Introduction

With modern experimental introductions it has become possible to probe the elastic and mechanical properties of living matter on the single cell and molecular level.

Viral capsids are self-assembled nanostructures consisting of a protein shell to protect the genetic material inside. Spherical viruses display **icosahedral symmetry** in their protein shell (capsid), and many high-resolution structures of capsids have been determined. These spherical capsids typically consist of 60T copies of a single protein subunit arranged in an icosahedral lattice, where T is the triangulation number that describes the architecture of the capsid. T can take on only a select set of integer values according to  $T = h^2 + k^2 + hk$ , where  $\mathbf{h}$  and  $\mathbf{k}$  are nonnegative integers.

A new route to probe elastic properties was opened by *atomic-force microscopy* (AFM) measurements. Recent modeling studies of the indentation of the cowpea chlorotic mottle virus predict that the mechanical response may show orientation dependence at large indentations where nonlinear effects are pronounced, so anisotropy should be considered.

# MATERIALS & METHODS

#### Finite-element simulations

The capsid deformation can be modeled by **finite-deformation continuum hyperelasticity**, with a neo-Hookean constitutive law. The strain energy density function is

$$W(C) = \frac{\mu}{2}(I_1 - 3) + \frac{\lambda}{2}(\ln J)^2 - \mu \ln J$$

where  $I_1 = \operatorname{tr} C$  and  $J = \det C$  are invariants of the Right Cauchy-Green deformation tensor  $C = F^T F$ , the metric associated with the gradient F of the deformation mapping, and  $\lambda$  and  $\mu$  are the linearized Lame constants, which can be related to the Young's modulus E and Poisson's ration  $\nu$  as  $\lambda = E\nu/[(1-2\nu)(1+\nu)]$  and  $\mu = E/2(1+\nu)$ .

#### Thin-shell simulations

The thin-shell simulations model the capsid as an icosahedral shell surface with elastic energy described by **Föppl-von Kármán** (FvK) thin-shell elasticity as

$$F = \int \left[rac{k}{2}(2H)^2 + rac{\lambda}{2}(E_{ii})^2 + \mu(E_{ij}E_{ij})
ight]dA$$

where k is bending modulus, and  $\lambda$  and  $\mu$  are the 2D Lamé constants. The stress-free reference shell surface is discretized with triangular subdivision-surface FEs and the energy is relaxed by numerical optimization using the **Broyden-Fletcher-Goldfarb-Shanno** (BFGS) method to determine a prestressed equilibrium shape.

# Molecular dynamics simulations

**Coarse-grained models** are attractive because they potentially can capture the essential physics and allow for loading rates closer to experimental timescales. The SBCG beads interact with each other through **Lennard-Jones** (LJ) and **Coulomb** potentials, and harmonic potentials are introduced for all bonds, as well as for angles formed by triples of bonded beads. The bonded potentials (bonds and angles) are parameterized to reproduce the protein stiffness observed in an allatom simulation of a monomer. The dynamics of the SBCG system is described by the **Langevin equation**, with a damping constant of  $2ps^{-1}$ .

# RESULTS

Indentation of T=3 (a) and T=4 (b) capsids along their two- and threefold symmetry axes.

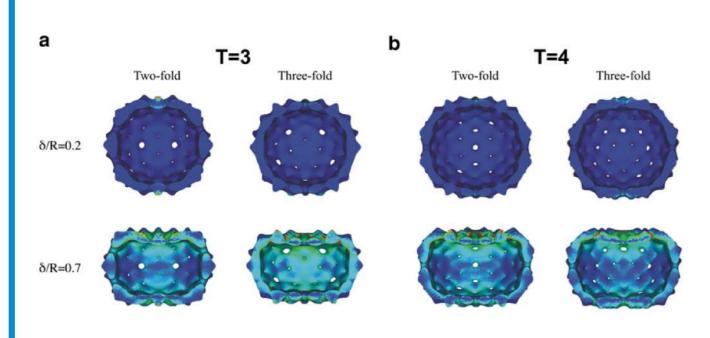


Figure 1: FE simulation

Whereas for small deformations the *von Mises* stresses are mainly apparent at the contact points with the tip and the surface (top and bottom).

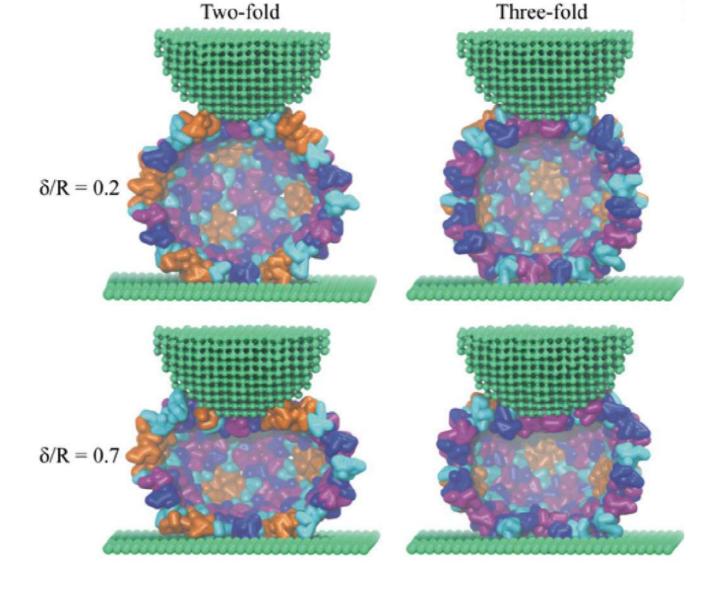


Figure 2: MD simulation

**SBCG MD** representation of an AFM tip indenting a T=4 capsid at the same relative indentations and along the same pushing directions as those shown in **Fig. 1 b** for the FE model.

The agreement between the CG MD results and the experimental data is especially satisfying considering that the MD model was parameterized without any knowledge of its deformation or interaction with the AFM tip or substrate. Thinshell modelling shows acceptable result only on small deformations, when response is close to linear and make different of orientation dependence, continuum models can describe not only quantitatively linear features, but also key nonlinear features. Thus, FE simulation is a suitable method for modelling an anisotropic elastic body.

# REFERENCES

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# FUTURE RESEARCH

Simulate viral capsid as linear orthotropic (material properties differ only along two(three) mutually-orthogonal twofold axes of rotational symmetry) sphere with internal and external pressure. This model will be first step to hyperelastic anisotropic model.

# ACKNOWLEDGEMENT

I would like to thank teachers from my home institution, especially N. Vaysfeld and V. Reut ,as well as Dr Dmitry Nerukh for their overall help in development this research. And also I'm very thankful for Erasmus+ programme for giving me this great opportunity to be here.