

# Virus Mechanics: Designing a Physical Model for STEAM Learning

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## Abstract

An understanding of viral mechanics is crucial in enabling informed decisions about the role of vaccinations and antivirals in the control of disease. This paper reports on the development of a 3D prototype model as an educational tool to communicate the mechanics of viral infection to a general audience.

## Introduction

The communication of virus structure and mechanics is key in raising public awareness about the role of vaccinations and antivirals in the control of disease, thus supporting health education and vaccine acceptance. Representational models are essential tools in this respect, to help describe, explain and reason abstract scientific ideas, aiding in the understanding of phenomena that cannot always be seen.

Most viruses consist of viral genomic material encapsulated inside a protective protein “capsid” shell. Viral capsids are a fascinating example of symmetry in nature, as capsid proteins often self-assemble into icosahedral structures, with a quasi-equivalent arrangement of subunits. The icosahedral structure of the capsid readily lends itself to representational modeling and is particularly appropriate for analogical reasoning across disciplines. Mathematics, in particular geometry, plays a crucial role in the description and modeling of these biological structures.

Using poliomyelitis (commonly known as polio) as an exemplar of virus anatomy and behavior, this project aimed to develop a dynamic physical model that learners can see, touch and manipulate as part of a “hands-on, minds-on” educational approach [6]. The project builds on previous work that has visualized mathematical predictions of capsid thickness [5] and conformation changes [1] through digital and physical artistic representations. This paper reports on the design of a 3D mechanical prototype model for use as an educational tool to demonstrate virus structure and the mechanisms by which infection can be prevented.

## Virus Structure

The poliovirus capsid is a dynamic structure composed of 60 copies of four repeating structural proteins—VP1, VP2, VP3, and VP4—arranged with icosahedral symmetry. VP1, VP2 and VP3 form the surface of the capsid and VP4 is an internal protein that stabilizes the capsid structure. VP1 forms a prominent star-shaped plateau or “mesa” at the fivefold axis of symmetry, which is surrounded by a deep depression or “canyon”. Another protrusion—the “propeller”—is formed by VP2 and VP3 at the threefold axis of symmetry [2, 3, 4].

Poliovirus undergoes a conformational change when it interacts with a living cell, resulting in symmetry breaking of the capsid. This change involves the movement of proteins on the virus surface, whereby internal components of VP1 and VP4 become externalized. VP4 forms a pore through which the viral genome is released to infect the living cell [3, 4]. This change in state can only occur when a particular region of the viral capsid interacts with a particular protein on the surface of a living cell (the poliovirus receptor).

## Design Process

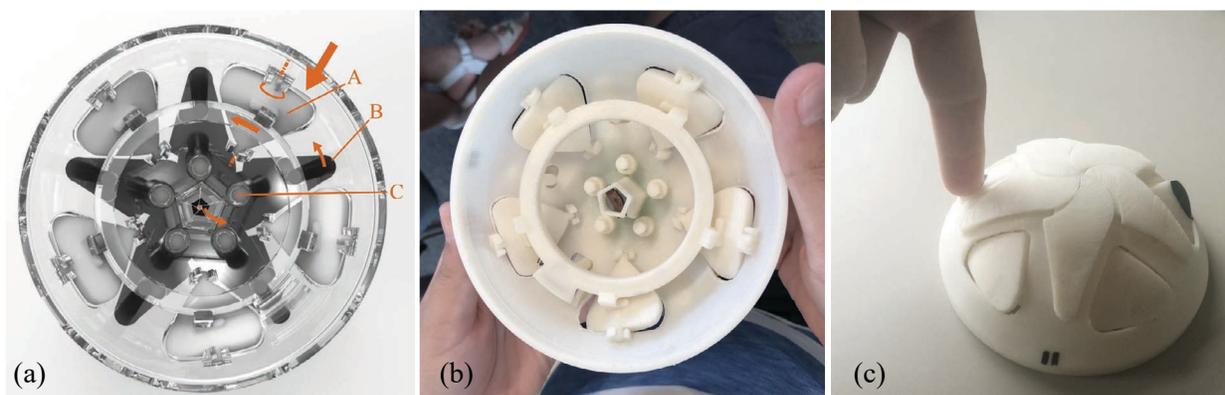
The majority of current poliovirus models present the virus as fixed in one of its two states, either before or after conformational change. The challenge was to translate its microscopic mechanical features into a dynamic model that demonstrates the capsid transformation through this conformational change, in what we model as its inactive and active states (before and after conformational change). Using a “research through design” approach, poliovirus structure and infection mechanisms were explored, in order to develop exploratory prototypes. A key area for exploration was the multicomponent nature of the viral capsid and the conformational change that occurs in its proteins at the early stage of infection.

**Table 1:** *Prioritized design requirements.*

Requirement	Importance
Model demonstrates virus structure and capsid conformational changes.	Crucial
Clear and accurate representation: simplified elements have a geometry allowing similar movements as those occurring in nature.	Crucial
Interactive: engages the user to manipulate the model and helps to visualize microscopic structure and workings.	Crucial
Self-explanatory and intuitive operation: does not require special skills or great dexterity.	Important
Robust and hard-wearing: moving components designed for frequent use, therefore hard-wearing and sturdy construction.	Important
Suitable for 3D printing: single part size should not exceed printer capabilities, appropriate wall thickness for strength and within printing budget.	Important
Foolproof: minimum parts that should assemble only in a correct way.	Minor
Mechanical parts should work smoothly and have prominent and robust end limits.	Minor

Low-fidelity prototypes were created in order to evaluate function and suitability against the design requirements shown in Table 1. A testing prototype comprising of one star-shaped mesa region, was digitally fabricated to assess usability with a focus group of potential users, providing valuable feedback for the final design. During the focus group, users engaged with exploratory design sketches and the testing prototype, in order to gain an understanding of the infection process. Mechanical aspects, as shown in Figure 1, were also explored through assembly and disassembly of the prototype by the group.

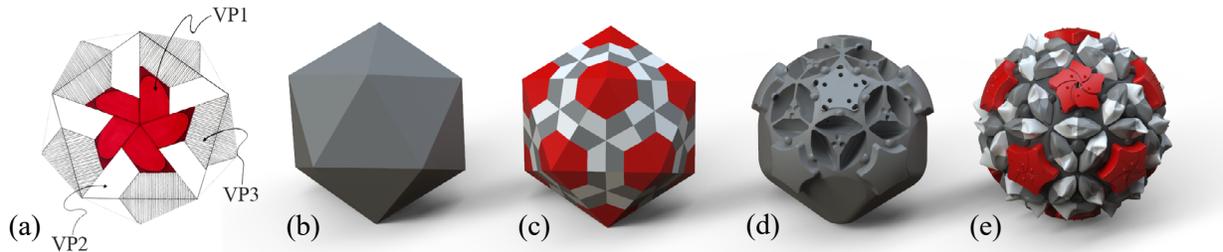
The dome-shaped testing prototype is based on a mechanical iris, similar to a camera lens aperture. Applying pressure to the tilting element “A” results in an oscillatory movement around its central axis of symmetry. This motion is transferred to the movement of the ring and element “B”, through a link and slot mechanism. This turning motion rotates element “B” around mounting point “C”, resulting in a movement away from the center of the iris, thus widening the opening. The ring ensures that all five units are synchronized, and a spring allows the iris to return to its initial state.



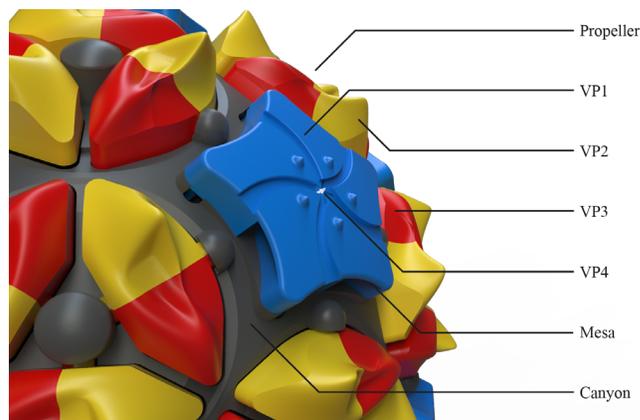
**Figure 1:** *The testing prototype (a) structure and mechanism; (b) and (c) 3D printed for user testing.*

### Mechanical Model

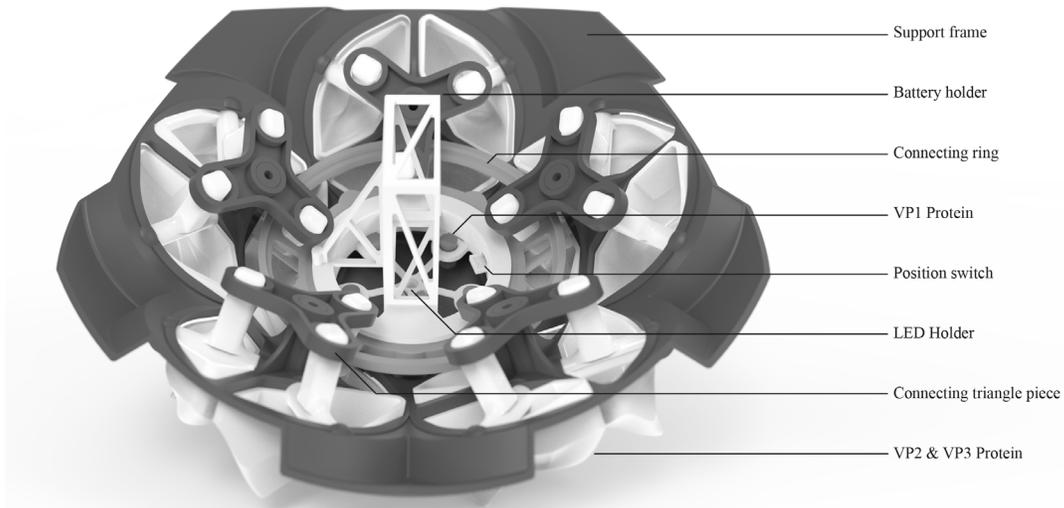
Following the user testing and feedback from the focus group, the prototype mechanisms were revised and developed into a final prototype model. The development of the geometric structure of the final prototype, from an initial sketch of the protein arrangement to the interior and exterior design configuration, is shown in Figure 2. The topology of the final prototype is shown in Figure 3, which indicates both the mathematical and biological structure of the poliovirus capsid.



**Figure 2:** Development of the mechanical model. (a) A sketch of the virus proteins arranged around the fivefold axis of symmetry; (b) the icosahedral capsid shape and (c) arrangement of proteins; (d) the internal mechanism of the model and (e) the exterior design, showing surface proteins VP1–VP3.

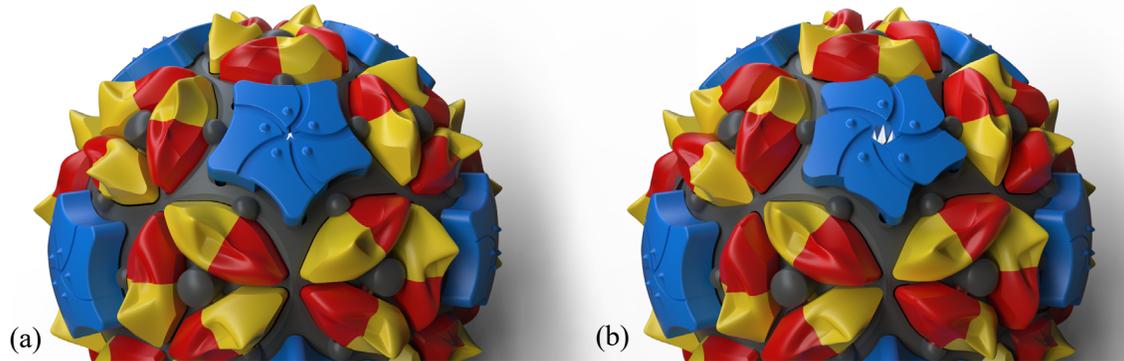


**Figure 3:** The topography of the final prototype model indicating biological structure.



**Figure 4:** The internal structure and mechanics of the final prototype model.

The design of the final prototype enables several changes to the topology of the capsid model as it transforms between states. Figure 4 shows the internal mechanisms of the model. Figures 5 illustrates the model exterior in inactive and active states. In its inactive state, the shape of the mesa resembles a star. Transformation into an active state causes arms of the star to move, opening a hole at the center of the mesa. The widening of the mesa is achieved through the same iris mechanism used in the testing prototype. The VP4 proteins, located directly below the top surface of the mesa, slide on a spherical surface and are tied up with an elastic band at one end. This configuration allows the VP4 “claw” to expand as the mesa opens.



**Figure 5:** *The final prototype model in (a) inactive and (b) active states.*

### Summary

This paper presents ongoing work in the design of a 3D mechanical prototype model for use as an educational tool to demonstrate the dynamics of virus structure. The next stage of the design is to develop supplementary parts to show that certain antibodies can bind to the capsid and prevent conformational change, thereby blocking the ability of the virus to infect a cell. The authors also intend to develop supporting materials to convey these concepts in a variety of representational modes e.g. digital animation. The final prototype model will be evaluated during public engagement activities and through classroom activities.

### Acknowledgements

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