

RECONFIGURABLE MATERIALS

Algorithm for architectural origami

An algorithm has been developed allowing the rational design of origami-inspired materials that can be rearranged to change their properties. This might open the way to strategies for making reconfigurable robots. [SEE ARTICLE P.347](#)

JAMIE PAIK

The properties of most materials depend on their composition, but when a material's crystal structure changes, its properties also change drastically. Such behaviour often occurs in smart materials and polymers, the properties of which alter in response to external stimuli such as temperature or pH. Architected materials, also known as metamaterials, can mimic this behaviour by containing engineered structures. Many automated technologies would benefit from the use of reconfigurable architected materials. On page 347, Overvelde *et al.*¹ report an algorithm that allows one class of these materials to be designed and their deformation properties to be investigated.

Advances in manufacturing technologies have enabled the production of architected materials that would be laborious or impossible to make using conventional methods, at multiple scales. These technologies can fabricate complex mechanical components of materials, print 3D scanned objects and prepare structures that can even 'program' the stiffness of a material.

Such advances have diverse applications, but have been particularly useful in robotics. To build adaptable robots that interact easily with their environments, designs are needed that enable transformation of machine assemblies and shapes. Such reconfigurable robots have been made using hardware components that reshape according to the task in hand or the environment^{2–4}. The greatest challenge in designing such robots is determining the geometric and mechanical parameters of both the machines and their components needed for various tasks and environments.

One of the principles that can be used to address this issue is origami-based design^{5–10}, in which architected materials are made by folding sheets into shapes along pre-defined creases. However, practical difficulties arise because not all origami-based structures can be reconfigured, and it is not obvious which ones can. Overvelde and colleagues use an algorithm to work out some of the reconfigurable configurations that can be achieved for origami-based modules of architected materials. The work focuses on prismatic origami

structures and their 3D-array patterns, which are relevant not only to the design of modules for origami robots, but potentially also to metre-scale architecture for buildings, and for understanding the behaviour of many chemical reactions and materials.

The concept of reconfigurable and controllable origami-based architected materials is not new^{11,12}. Indeed, Overvelde *et al.* previously reported¹³ an algorithm that allowed them to design and prepare a highly reconfigurable architected material inspired by snapology (a form of origami). The authors now use that algorithm to further explore the achievable degrees of freedom of origami-based architected materials, by considering prismatic geometry configurations of their snapology structure.

To understand the process involved, imagine extruding all the faces of a polyhedron to form prismatic pillars of equal length (Fig. 1). The resulting shape can be combined with other extruded prismatic structures by matching up prisms that have the same cross-section, thus forming the basic unit — a cell — of an architected material. The cells can then be tessellated to form the material itself. The authors find that the deformation modes of the architected materials predictably depend on the tessellated patterns of the cells and on the shapes of the extruded prisms. Overvelde and colleagues also provide an algorithm to determine the geometric parameters of cardboard prototypes that can be constructed as models. These structures include systems of triangular and hexagonal prisms, of octahedra and cuboctahedra, and of triangular prisms alone (see Figure 1 of the paper¹).

The researchers go on to show that not all the faces of the original polyhedra need to be extruded to be part of a cell, and that the deformation modes and mobility of the architected materials change depending on which faces are extruded. This offers a means of reconfiguring the cells to alter the materials' properties. The authors clearly demonstrate that the geometric parameters of the cells dictate the overall motion, functionality and physical space occupied by the materials. Indeed, the authors' algorithm can determine the mobility

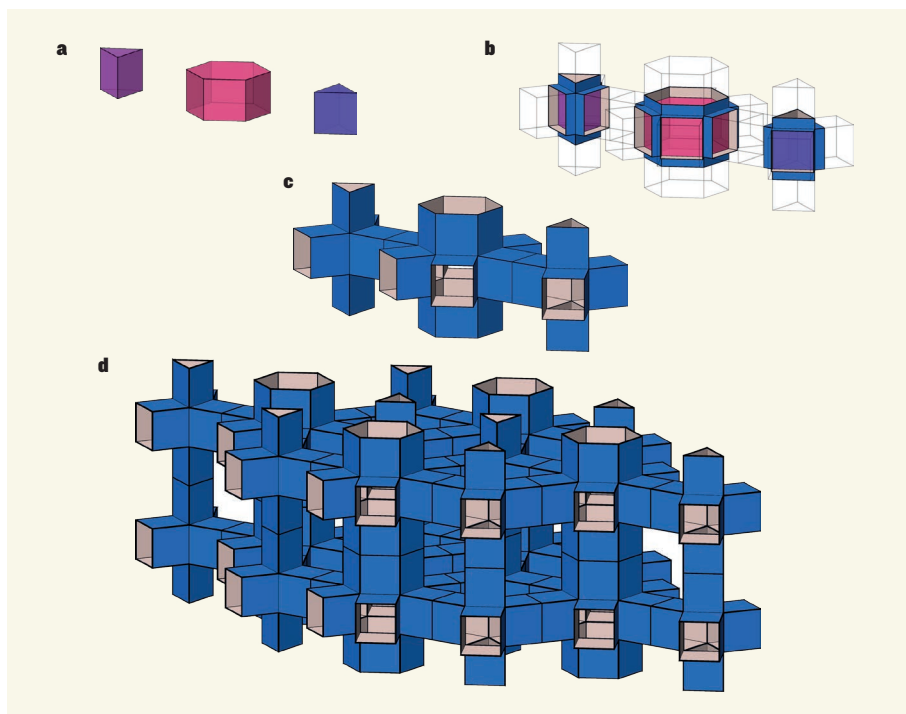


Figure 1 | Designing prismatic architected materials based on origami. Architected materials contain specially engineered structural elements. **a**, Designs for origami-inspired architected materials can begin by identifying a repeating unit composed of polyhedra. **b**, Prismatic pillars of equal length are extruded from the faces of the polyhedra. **c**, The resulting shapes are combined into the basic unit — a cell — of the material by aligning prisms that have the same cross-section. **d**, Many of the cells are then tessellated to form the architected material. Overvelde *et al.*¹ report an algorithm that allows the rational design of reconfigurable prismatic architected materials and determines their modes of deformation.

and deformation modes of the prismatic architected materials.

One of the appealing aspects of Overvelde and colleagues' algorithm is that it describes architected materials defined by simple structural and physical rules: the entire deformable architecture is made up of a single type of cell. The idea of using tessellated and repeated cell components resonates with the design principles of origami and of modular robots.

The controllability of the architected materials could be increased by introducing 'lockable' joints that can be made either rigid or flexible, rather than using passive elastic hinges as in the current work. The authors manually handled their prototypes to demonstrate the deformation modes (see Supplementary Information for the paper¹), but the size and direction of the applied loading stresses are constrained by the flexibility of the hinges. Having actively lockable joints could further validate the effects of reconfigurable modes under various loadings. It would also allow the robotics community to discover origami platforms that have controllable degrees of freedom dictated only by the geometric constraints of a repeating cell module.

Building interactive, versatile hardware that has a high degree of freedom and mobility remains a key design challenge for many automated instruments and robots. Overvelde *et al.* introduce a robust strategy for designing reconfigurable modes for architected materials. Potentially, many more designs for architected materials will be made possible by using different assemblies of convex polyhedra. The authors' algorithm might well translate into strategies for designing automated systems, including diverse origami robotic systems. ■

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MICROBIOLOGY

Mind the gaps in cellular evolution

Eukaryotic cells, with complex features such as membrane-bound nuclei, evolved from prokaryotic cells that lack these components. A newly identified prokaryotic group reveals intermediate steps in eukaryotic-cell evolution. SEE ARTICLE P.353

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Eukaryotic cells contain membrane-bound organelles such as a nucleus, and complex cellular components, including protein-based transport systems that move molecules around the cell. About 1.8 billion years ago¹, eukaryotic cells arose from cells that lack these features, known as prokaryotic cells. However, there are gaps in the cellular family tree, specifically between prokaryotes and eukaryotes. There is limited evidence for how some eukaryote-specific features arose in the evolution of eukaryotic cells. On page 353, Zaremba-Niedzwiedzka *et al.*² identify a superphylum branch of the prokaryotic family tree that contains some genes previously thought to be eukaryote-specific.

On the basis of their gene content and aspects of their cellular physiology, prokaryotes are classified into two domains: Bacteria and Archaea. Their common ancestor is known as the 'last universal common ancestor'. Eukaryotes are thought to be derived from a merger that occurred when an archaeal cell engulfed a bacterial cell related to modern alphaproteobacteria³. It has been proposed⁴ that, within these early eukaryotic cells, the internalized proteobacterium eventually evolved to form the membrane-bound organelles known as mitochondria that provide energy for the cell. However, early events in eukaryotic evolution have remained poorly understood. Few species have been identified whose genome content could provide insight into steps in the transition between prokaryotic and eukaryotic cells.

Until now, the archaea that have been identified as the most closely related ancestors of eukaryotic cells come from the group known as Lokiarchaeota⁵; these were identified by genome sequencing of organisms found in deep-sea sediments. Lokiarchaeota contain features that were previously thought to be eukaryote-specific, including several genes distantly related to those involved in eukaryotic protein transport. However, to understand the transition from prokaryotic to eukaryotic cellular life, a more complete picture is needed of the genes present in the archaeal cells that gave rise to eukaryotes.

DNA encoding 16S ribosomal RNA sequences is often used to determine the genetic relationships (phylogeny) between species. Twenty-five years ago, a study⁶ of such DNA, obtained from seawater organisms, revealed the presence of archaeal groups related only distantly to the known archaea cultured in laboratories. This work hinted that cultured prokaryotes capture just a small fraction of global prokaryotic diversity. Zaremba-Niedzwiedzka *et al.* also investigated samples of underwater organisms, and their results reveal that major groups of life can still be discovered.

The authors obtained samples of aquatic sediments from seven locations worldwide. They extracted short fragments of DNA, representing a mixture of the species present, and sequenced more than 644 billion nucleotides. The short fragments of sequence were assembled into longer pieces, and sequences containing at least six genes from an evolutionarily conserved ribosomal-protein gene cluster were identified. These were analysed to determine the taxonomic relationships of the sampled genomes. The researchers identified the sequences that were most similar to the previously sequenced Lokiarchaeota⁵ and Thorarchaeota⁷ (another archaeal species related to eukaryotes).

Zaremba-Niedzwiedzka *et al.* used a statistical method⁸ to classify the ribosomal sequences on the basis of similarities in the patterns of nucleotides used. From this analysis, they identified a superphylum of Archaea containing four major lineages of genetic material: Lokiarchaeota, Thorarchaeota and the newly found groupings of Odiarchaeota and Heimdallarchaeota. The authors named this superphylum Asgard. The exact family-tree relationships between the groupings within the Asgard superphylum are difficult to ascertain, because of statistical uncertainty in the phylogenetic trees that were constructed. But the analyses support the existence of the superphylum as a whole.

The position of the Asgard group in the family tree of cellular life suggests that its members form the closest known archaeal sister lineage to eukaryotes (Fig. 1). This finding is consistent with the view³ that the