Numerical modeling of microfossils

Nature's Algorithm

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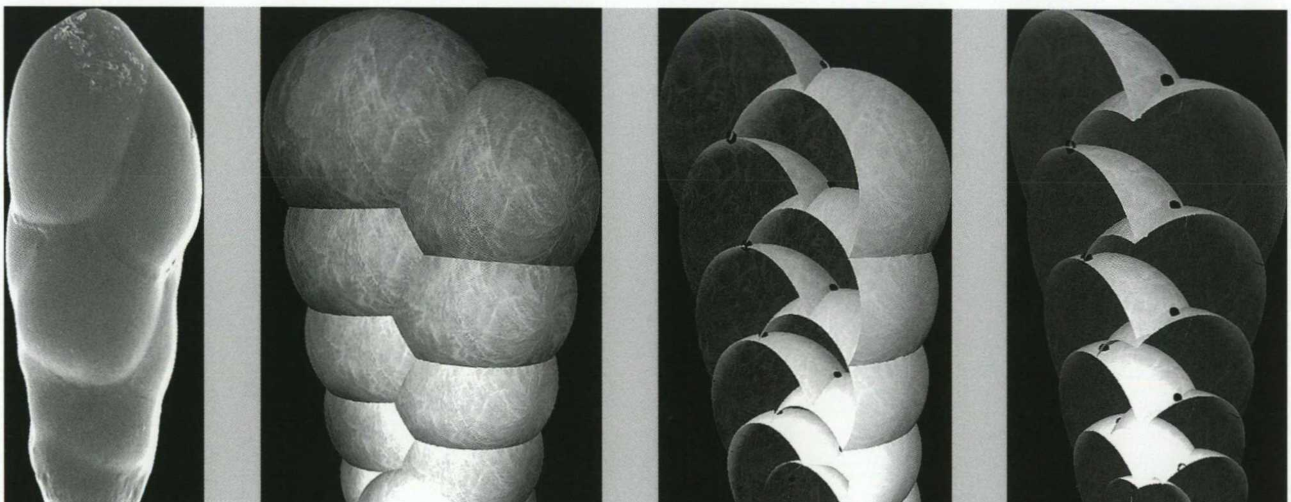
The beautiful, intricate shells produced by foraminifera with astounding complexity turn out to be governed by simple mathematic rules. Once the underlying principles are discovered, foraminifera shapes can be "grown" on a computer screen

Dinosaur and mammoth bones, trilobite imprints, ammonite shells... while we are fascinated by the fossils of such large organisms, we generally overlook a multitude of microscopic treasures. Foraminifera, for instance, are single-celled organisms classified as Protozoa. Though some specimens may grow to 20 centimeters, most do not exceed a tenth of a millimeter. They are the typical microfossils found in fine-grained sea sediments, both ancient and modern. Foraminifera have existed for over 600 million years and they occur in all climate zones, in seas and oceans of every depth - ranging from lagoons and estuaries to the abyssal waters. A small, one cubic centimeter sample of sediment may contain tens, hundreds or even thousands of their shells.

In over 200 years of studying modern and fossil foraminifera, researchers have collected descriptive data on approx. 3600 genera and over 60 thousand species. This amazing variety of forms, characteristic for specific periods and regions, makes analyzing the foraminifera in a given sediment a reliable source of information about its geological age and environmental conditions. It is now difficult to imagine paleoceanographic research or prospecting for oil and gas without such techniques based on foraminifera.

The key to the shell

Micropaleontologists and biologists have tried to classify this wealth of types by establishing systematic groups based on similarities of shell composition and morphology. In recent years it has become possible to verify these classifications using molecular biology techniques. This has shown that many groupings and hypotheses relying solely on shell structure are false and the relation between morphology and genetically



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The eForams program acts like a virtual foraminiferal farm. It can accurately generate the structure of foraminiferal skeletons by following mathematical dependencies encoded information remains unknown. In fact, we do not know which genes are responsible for the shape of foraminiferal shells. Discovering the processes governing the development of skeletal forms is a key objective of research on these organisms.

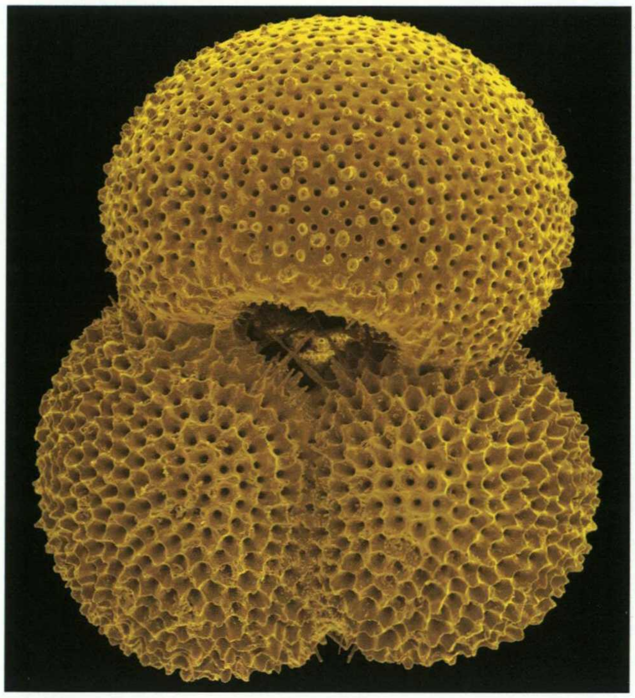
For most organisms, ontogenetic growth simply means increasing in size - but that is not so easy for organisms with a stiff, mineral skeleton. Foraminifera cope with this problem by adding successive chambers to their existing skeleton or by further elongating existing oblong chambers, akin to the shells of snails or crustaceans. This growing process may proceed in diverse ways. In multi-chambered foraminifera, for instance, specific chambers may grow spirally, in a single, double, or triple linear series, or they might suddenly change their growth strategy, e.g. switching from a triple linear series to a double linear series. What governs this process? The answer to this mystery could be unlocked by a theoretical model developed on the basis of empirical observations.

The first model of foraminiferal growth was described by Wolfgang H. Berger in 1969. His virtual, two-dimensional shells grew by adding successive circles in a repeated manner. As growth proceeded, the chambers were rotated, enlarged, and shifted according to specific parameters around a stable reference point: the "foraminiferal center." This generated two-dimensional, and subsequently three-dimensional virtual foraminifera of regular shapes similar to the spiral forms of real foraminifera. However, this model, like later ones developed by many other authors, cannot simulate forms with changing growth patterns. The reason for this is quite trivial: they fail to account for the location of a basic element of the foraminiferal shell - i.e. its aperture.

From opening to opening

The aperture (an opening or series of openings in a foraminiferal skeleton) is in fact inscribed in the Latin name of this group of organisms, *Foraminiferida* - the Latin *foramen* meaning "opening." These apertures appeared to us to be a crucial element in chamber growth, as successive foraminiferal chambers develop in places where apertures are located. Most foraminifera, both calcareous and agglutinated, try to minimize the distance between successive apertures. This group is the first target of our research.

Altering the reference system made it possible to account for these apertures in theoretical terms. Instead of a stable reference for all chambers, i.e. a central axis or point, we instead employed a moving system, in which the aperture of the previous chamber automatically becomes the reference point for the next. This system is more consistent with the principles observed in nature. Designating each successive aperture is quite simple geometrically and involves finding the shortest distance between an old aperture and the surface of a new chamber.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Foraminifera are microscopic single-celled organisms that develop extremely complex and diverse skeletons

Computer software which implements this principle can generate geometric forms that imitate the shape and growing process of foraminiferal skeletons. A number of such programs have been developed, modeling the whole range of morphotypes of multi-chambered foraminifera. Most significantly, this software can simulate forms which regularly or irregularly change their manner of growth, and it allows many parameters to be altered interactively. Foraminiferal simulations can be rotated in three-dimensional space and cross-sections can be created for viewing their interior structure.

Although our model rests on biological foundations, it is still a geometrical model with parameters defined in terms of angles and coefficients. The ultimate aim of our research is to develop a third-generation model taking account of the fact that the form of a foraminiferal skeleton depends on the cytoskeletal self-organization of the cell controlled by genotype and environmental influences. The most intriguing discoveries, therefore, still lie ahead. ■

Further reading:

Tyszka J. (2006). Morphospace of foraminiferal shells: results from the moving reference model. *Lethaia, 39 (1)*, 1-12.

Tyszka J., Topa P. (2005). A new approach to modeling of foraminiferal shells. *Paleobiology, 31 (3)*, 526-541.

eForams - VirtuaLab of Foraminiferal Morphogenesis: http://eforams.icsr.agh.edu.pl/index.php/VirtuaLab.