

*Biomedical Computation Review*

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seeing science

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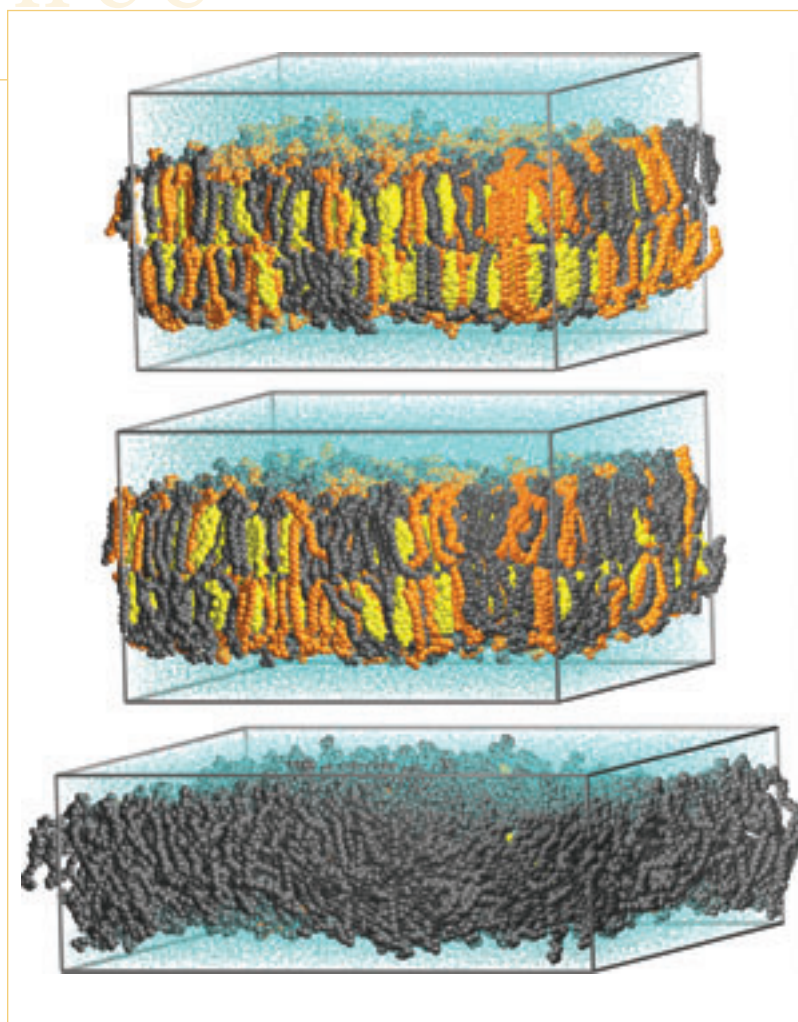
## Simulated Lipid Rafts

According to traditional theory, lipid membranes consist of a “fluid-mosaic” in which molecular components, including membrane proteins, are randomly distributed and move freely against a fluid background.

In recent years, however, this idea has been challenged by experimental results suggesting membranes may contain nano-sized rigid patches known as lipid rafts. Some have suggested that these rafts are involved in membrane trafficking, signal transduction, and regulation of membrane proteins.

But it’s nearly impossible to observe rafts in action. So **Perttu Niemala**, a graduate student at Helsinki Institute of Technology, and his colleagues decided to simulate lipid rafts on a computer. They compared the structures of three different mixtures of a background lipid, cholesterol and sphingomyelin—with ratios of 1:1:1 (top); 2:1:1 (middle); 62:1:1 (bottom). Cholesterol and sphingomyelin are believed to induce raft formation.

The researchers found that at higher cholesterol and sphingomyelin concentrations, the membrane becomes thicker (as shown here) as well as more rigid. Moreover, the measured lateral pressure profiles within the studied membranes were considerably different, which is suggested to be an important factor for regulating the action of membrane proteins.



*Image provided courtesy of Perttu Niemala. It was published as part of a paper titled “Assessing the Nature of Lipid Raft Membranes” in PLOS Computational Biology in February 2007.*