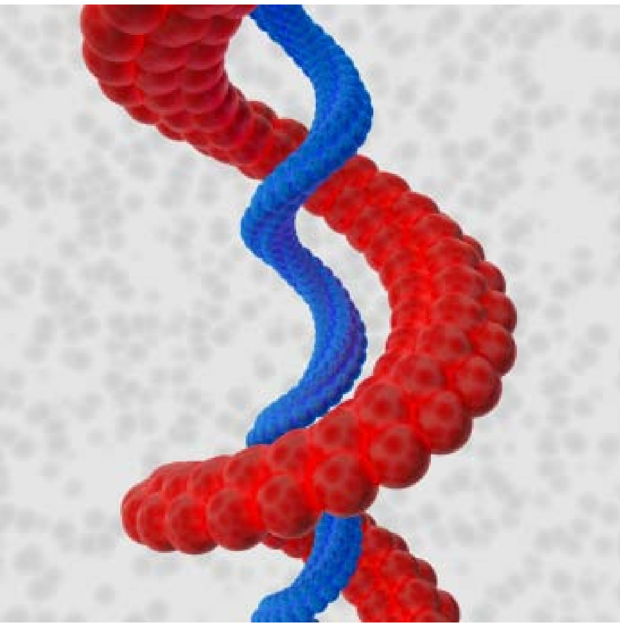
Knotty Problems

Australian Research Council Future Fellow, Associate Professor Andrew Francis from the School of Computing and Mathematics is using mathematical modelling to explore biological systems. This research is funded by the Australian Research Council.

'Mathematics has made numerous significant contributions to our understanding of the evolution of biological systems,' says Associate Professor Francis. 'Both algebra and biology have developed at an unprecedented pace over the last 30 years. The structural approach at the core of algebra has long found applications in sciences such as physics and analytical chemistry but only in a limited way, so far, in biology. I will be modelling DNA cutting and rejoining as operations in an algebraic setting. The goal is to enable scientists to address certain specific biological problems in new ways, provide new tools and ways of thinking for biologists, and bring new problems in algebra to the mathematical community. In turn, this could lead to a better understanding of such problems as cross-species infections, and the development and proliferation of antibiotic resistant bacteria.'

The research will use algebraic methods such as knot theory and group theory to develop models of evolution in bacteria, the dominant form of life on our planet. These models will allow scientists to understand the evolutionary processes giving rise to the richly diverse genetic structures we observe today. Such processes cannot be studied directly in the laboratory because the time scales are too long. Mathematical methods using the latest genetic data provide a way to address these questions. Developing accurate models that explain the present diversity may also help to predict the consequences of specific genetic changes in bacteria, and has the potential to affect the way we do both algebra and biology.



This research will demonstrate new ways in which computational and mathematical power can be applied to novel questions in living systems. Algebraic methods can give biologists novel ways to deal with large amounts of data in the study of evolution due to genetic mutations.

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