When algebra meets biology

Professor Andrew Francis, from the Centre for Research in Mathematics within the School of Computing, Engineering and Mathematics, is leading an investigation into how algebra might be used to better explain the progress of evolution in bacteria. The project, which is supported by the Australian Research Council Discovery Project, aims to develop new algorithms for the modelling of evolutionary processes. His fellow chief investigator is Associate Professor Volker Gebhardt.

'Mathematics is the language of science. Mathematical approaches to biological processes date back at least as far as Fibonacci eight centuries ago,' says Professor Francis. 'A fundamental evolutionary challenge is to understand how different species are related; what sequence of changes to the molecular fundamentals of life have led to the diverse landscape of organisms that we can currently observe? To understand the relatedness of forms of life at a molecular level, one must understand the mechanisms by which evolution occurs.'

Bacteria are hugely important in our Earth's evolutionary context. Not only are they among the first life forms, but they are believed to constitute a larger biomass than plants and animals combined. Their ability to transfer genetic material across species (lateral gene transfer), as well as their numerous mechanisms for change within a single organism, make their evolutionary histories complex and challenging to infer. While lateral gene transfer is thought to explain the rapid acquisition of entire genetic pathways, such as drug resistance, local mutations are more frequent, facilitated by enzymes that reside within the bacterial cell. Of these local mutation events, inversion (excising a segment and reinserting it with the opposite orientation) is most common.
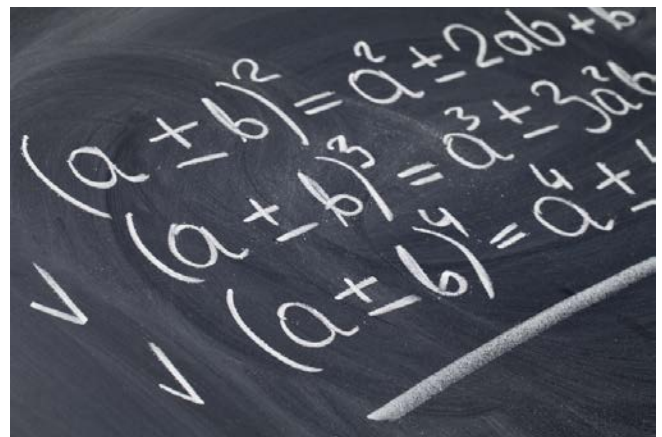
Professor Francis's project applies algebraic concepts to understand problems in bacterial evolution. It will establish methods for determining the evolutionary distance between two genomes by building computational models based on the inversion process. This will allow the reconstruction of an evolutionary history, or a phylogeny, of a set of bacterial genomes.

Understanding evolutionary processes and the way organisms are related is a fundamental objective of the biological sciences. This project develops new ways of understanding them and new tools to address them: the outcomes will be new methods for evolutionary biology, and new results and algorithms in computational, combinatorial and geometric group theory. Another significant outcome will be the building of a bridge between two disciplines as new ideas from computational algebra are brought into the realm of theoretical biology.