

## PROFILE

### David Bryant



Professor **David James Bryant** is the Director of Computational Modelling (COMO) at University of Otago. He is also the new NZMS president (2020—2022).

Born 1972 in Christchurch, David spent much of his early life in this city. His father, Peter, joined the University of Canterbury in the late 1960s, where he became Reader/Associate Professor in applied mathematics. It might be assumed, therefore, that David developed an early love for mathematical study; however, he insists that his real joy was playing piano, and, at a certain point, he would have been just as keen to have carved out a career as a pianist. Indeed, he won a music competition at school in Year 12, featuring on TV. Years later, I recall watching David on piano, accompanied by a saxophonist, as he entertained a large conference dinner hosted by the Institute Henri Poincaré.

David studied mathematics at the University of Canterbury. Straight after getting his BSc Hons with first class, David asked me about a possible PhD thesis on mathematical phylogenetics. I mentioned various questions concerning the combinatorics of trees, and he later told me he was convinced he could quickly solve them all using matroid theory! It turned out that matroid structures are few and far between in phylogenetics, so some of the questions required more elaborate arguments. Despite this, David did solve many of the problems posed (and those that weren't became conjectures that prompted later work). Indeed, his thesis ended up having considerable impact – it has been cited over 200 times, and results from it led to David being awarded “Best paper by a young scientist” at the International Conference in Computational Molecular Biology (RECOMB'99).

David was a delightful and easy student to supervise – he just went off and came back with a new theorem every few weeks! Sadly, however, only months into his thesis, he lost his father (and we lost a colleague) when Peter Bryant passed away suddenly.

After finishing his PhD, David was invited to the Centre de Recherches Mathématiques at Université de Montréal, Canada, for a postdoc (1998—2000) with David Sankoff, one of the pioneers of mathematical genomics and one of David's PhD examiners. David recalls being a little underprepared for this Canadian postdoc – arriving just before a major ice storm with insufficient clothing and unaware that French was the main language in Québec. From there, he moved to France for a second postdoc with Olivier Gascuel in Montpellier (2000—2001) before returning to Montreal in 2001 to take up an Assistant Professor position in Computer Science, Mathematics and Statistics at McGill University. He later obtained tenure as Associate Professor before leaving Canada in 2005.

David's experiences in Canada also extended to its wildlife. Those of us who attended a workshop at the Banff Research Station a few years ago will never forget the moment when David and a couple of other colleagues stumbled upon a grizzly bear during a hike. One of the party had the steady nerve to turn their phone video on,

and David could later be heard in the video whispering to hiking buddies Tanja Stadler and Du Vinh the priceless line: “Don’t run; it can run faster.” Fortunately, all survived unscathed.

In 2005, David returned to New Zealand to join the new bioinformatics institute set up by Allen Rodrigo at Auckland University. Five years later, David moved south to take up an associate professor position in Dunedin, becoming professor a few years later. He lives there with wife Melanie and their sons Max and Jim (currently aged 12 and 10).

David’s life was temporarily upended around 2009 when he was diagnosed with a rare bone tumour deep inside his hip. The initial prognosis did not look promising, and even obtaining a biopsy required a tricky 3 hours of surgery because of the inaccessible location of the tumour. Labs in NZ were unable to determine if it was malignant, so it was eventually sent to the US for expert opinion; as David puts it: “My tumour went to Harvard!” Fortunately, the tumour turned out to be benign. Although the resulting surgery to remove it left David in crutches for some months, he made a full recovery: “I was in the lucky 5%”.

David has worked on a range of problem in mathematical phylogenetics – from genome rearrangement, to tree reconstruction using characters and quartet trees, and to phylogenetic networks. He has supervised 11 PhD and 8 MSc students. While most of David’s research has been applied mathematics, some of it has led him more recently into areas of pure mathematics, including geometry, analysis and symbolic logic. These projects over the last 5 years have involved joint work with Paul Tupper, Andre Nies and others. David also publishes in high-ranking science journals, including a letter and article in *Nature* and a letter to PNAS entitled “Statistical Flaws undermine pre-Columbian chicken debate.”

David’s highest-impact discovery sprang from a collaboration with another mathematician (Vincent Moulton, a mathematics professor in Norwich). The pair developed a novel mathematical way for biologists to represent evolutionary signal using networks (rather than just trees). The method is called NeighborNet and it is widely used for representing and visualising evolution on many scales – from resolving difficult questions about how animals arose at the Cambrian explosion, to the classification of present-day infectious bacteria and viruses (including SARS-CoV-2), the evolution of languages, and applications far beyond biology (including an amusing paper published in PLoS One that used NeighborNet to classify the many different versions of the fairytale “Little Red Riding Hood”). David said the hardest part of the NeighborNet project was formally proving that the method does what it should (i.e. establish combinatorial consistency), which took several years. The 2004 paper that described NeighborNet has been cited 1800 times, and a more general paper with Daniel Huson on phylogenetic networks 2 years later has been cited 6880 times.

In 2019, David was elected fellow of the Royal Society/Te Apārangi. He is also director of the company Bayesian Demography Ltd together with his brother John, and has started working on improved computational techniques and algorithms for large-scale demographic analysis.

David’s list of other ongoing and up-and-coming projects includes: convex geometry and diversities, tensor decomposition and diffusion approximations for efficient inference under multi-population models, evolutionary genetic modelling for micorrhizal fungi, and improved algorithms for evaluating the likelihood of a phylogeny.

On top of this is his role as the new NZMS president, for which David is looking at spending a year planning and then a year making some changes, promising that “I’ll be throwing myself into the role.”

*Mike Steel*