

## CURRICULUM VITAE

MIKE STEEL

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Biomathematics Research Centre  
University of Canterbury  
Christchurch, New Zealand

Phone: +64-3-366 7001

Fax: +64-3-364 2587

Email: [mike.steel@canterbury.ac.nz](mailto:mike.steel@canterbury.ac.nz)

<http://www.math.canterbury.ac.nz/~m.steel>

### Current position

Director, Biomathematics Research Centre, University of Canterbury (1998-present).

Professor of Mathematics, University of Canterbury (since 2002).

### Education

PhD in Mathematics Massey University (1989).

Dip. Journalism, University of Canterbury (1985).

MSc (Distinction) in Mathematics, University of Canterbury (1983).

B.Sc.(Hons I) in Mathematics, University of Canterbury (1982).

### Honors, Awards and Distinctions

2017 Marsden Fund grant (2017-2019: NZ\$650,000)

2014 Promoted to Distinguished Professor

2014 Awarded University of Canterbury annual Research Award

2014 3-year NSF research grant (jointly with Michael Sanderson and Alexis Stammatakis).

2012 Marsden Fund grant (also grants in 1994, 1997, 2000, 2003, 2006, 2009)

2010 Awarded James Cook Fellowship by the Royal Society of New Zealand

2009-2015 Deputy Director of the Allan Wilson Centre (a NZ- government funded Centre of Research Excellence)

2008 Awarded annual Research Award College of Engineering, University of Canterbury

2007 Isaac Newton Institute for Mathematical Sciences program co-organiser

2004 Awarded Maclaurin Fellowship (NZIMA)

2003 Elected Fellow of the Royal Society of New Zealand.

2002 Founding PI of the Allan Wilson Centre for Molecular Ecology and Evolution.

2001 Re-appointed for three years as a programme associate of the Canadian Institute for Advanced Research (Evolutionary Biology)

2000 Appointed as Associate Editor for *Systematic Biology* (-2006).

## **Publication Record**

Refereed Journal Articles: 245  
Books (edited and co-authored): 3  
Book chapters: 6  
h-index (Google Scholar, 23/11/2017): 61  
Citations (Google Scholar, 23/11/2017): >14,000

## **Research Interests**

Mathematical biology, particularly phylogenetics, molecular evolution, origin of life, speciation and extinction and biodiversity conservation. Applications of probability theory and discrete mathematics in biology, philosophy of science, and systems chemistry.

## **Professional Service:**

Associate editor *Bulletin of Mathematical Biology* (since 2012-present)  
Elected to the council of the *Society for Systematic Biology* (2012-2015)  
Editorial board member of *Algorithms in Molecular Biology*, and *Evolutionary Bioinformatics*  
Co-organiser of numerous international workshops and conferences, including a 2017 meeting in BIRS institute in Banff, a 2014 conference on computational models in evolution at the *Simons Institute* (UC Berkeley) and a 4-month phylogenetics programme at the *Isaac Newton Institute* in Cambridge UK (Sept-Dec. 2007).  
Keynote speaker at numerous meetings, including a phylogenetics summer school and conference in Barcelona (June-July 2017), and in Leipzig (August 2013), principal lecturer at the NSF-CBMS phylogenetics lecture series at Winthrop (USA) in July 2014, and at phylogenetic meetings in Singapore and Australia in 2015.  
Panelist for the NZ Marsden Fund (2002, 2004, 2005) and PBRF panel (equivalent of RAE/NSF panel) in 2006. Panelist for Royal Society of NZ awards and new fellows.  
Reviewer for ~15 papers each year.

## Research Statement

I am an applied mathematician, with a leading international reputation in mathematical biology (particularly molecular genetics and evolution), statistical modelling in biology and some foundational work in applied probability.

My research develops and applies new approaches to fundamental questions in evolutionary biology, based on combinatorial, stochastic and algorithmic techniques, and other approaches (e.g. differential equation or algebraic methods). I publish technical papers in the mainstream mathematics statistics and computer science literature, as well as applied papers in biology journals, and in other disciplines (e.g. philosophy of science).

Some of my recent discoveries, over the last decade have included:

- Developing new techniques for extracting evolutionary relationships from species under more realistic models of DNA evolution. A recent paper provides an explanation of why evolutionary rates appear to ‘slow down’ with time and lead to estimated ancestral dates that disagree with fossils (published in *Molecular Biology and Evolution*).
- A series of papers that have developed a new mathematical treatment of autocatalysis, which is relevant to the unsolved ‘Origin of Life’ problem. This work involved extensive use of super computing and is now being cited and applied by leaders in the origin-of-life field (such as W. Martin, E. Szathmary, S. Kauffman, N. Lehman and others).
- Developing new techniques for dealing with patchy taxon coverage and lateral gene transfer (with Michael Sanderson’s group in Arizona) including in a recent paper published in *Science*.
- Unexpected new results concerning ancestral state reconstruction (with Olivier Gascuel), published in the *Systematic Biology*.
- Results that overturned a much-cited *Science* paper by showing that the expected biodiversity loss due to current extinction is likely to be much higher than previously suggested.
- A detailed mathematical analysis of speciation and extinction models (with Mooers, Stadler and Lambert). One surprise of this work is that the expected length of edges under most models turns out to be around 50% of what had previously been supposed.
- Development of new algorithms for analysing phylogenetic networks, including the first exact analysis of a model of lateral gene transfers, published in 2014. A related project led to a published paper in the high-impact journal *Proc. Natl. Acad. Sci. USA* in 2012.
- A novel mathematical analysis of the ‘Noah's Ark’ optimization problem in biodiversity conservation. Our published algorithms have been developed further by others and included in biodiversity software (e.g. the *Tuatara* software developed at UBC, Vancouver Canada).
- Foundational new work on the nature of causality and information loss (with Elliott Sober) published in the prestigious *British Journal for the Philosophy of Science* (2013) and *Philosophy of Science* in 2014.

Highlights in my earlier work (more than 10 years ago) including developing new methods that explained why molecular genetic data was at variance with the fossil record (in a paper that has been cited 960 times), and establishing deep and unexpected links between apparently very different methods for inferring evolutionary trees (a result that the noted philosopher of biology, Prof. Elliott Sober described as having ‘great significance’ (*Monist*, 85(1))).

**Research Output:** I have more than 240 refereed publications, in peer-reviewed international journals (mostly A or A\* rated by the Australian Research Council) and as book chapters, and which range across a range of disciplines: mathematics, systematic and molecular biology, theoretical biology, systems chemistry, and philosophy of science. I also publish periodically in high-impact science journals, including in the last few years: *Science*, *Proceedings of the National Academy of Sciences USA*, and a 'news and views' article in *Nature*. I have co-authored two academic books, both published by Oxford University Press, one of which has been cited >1000 times in other publications.

**Research Impact:** My current h-index is currently 61, with >12,000 citations in total (>5000 since 2012) [Google Scholar, 23 Nov. 2017]. For each of the last 12 years I have had between 720 and 960 citations per year to my work.

**Research grants:** My research has attracted considerable external funding from the Marsden Fund, the NZ Government's CoRE program, and other agencies (e.g. NSF). I have been successful in 8 out of 10 Marsden Fund applications (thereby securing almost continuous funding since this fund was established 23 years ago), the most recent being the 'Combinatorics of Reticulate Evolution' project (\$650,000; 2017—2019). This grant was in addition to 12 years of funding from the *Allan Wilson Centre*, which attracts 0.3 FTE to UC each year (plus research funds for projects and students) in my dual role as a principal investigator (PI) and (since 2008) Deputy Director. The *Allan Wilson Centre* (AWC) was a government-funded "Centre of Research Excellence" (CoRE). I also was awarded a RSNZ James Cook Fellowship and an NZIMA 'McLaurin Fellowship' in the last decade.

In 2014, I was one of four PIs in a successful 3-year research project, *Terraces, Large Trees and Trait Evolution*, funded by the US-based National Science Foundation (NSF), worth \$US695,000 over three years. The NSF panel summary recognized the significance of this work for systematic biology by stating that "there is a potentially huge impact on the field."

My recent work on mathematical modeling in origin of life research has led to invitations to present my work at numerous conferences and institutions, including College de France (2013), UC Berkeley (2014), Simons Institute (2014), and the Max Planck Institute for Mathematics in the Sciences (July 2017).

Many of my graduate students and postdocs are now established researchers in the field of phylogenetics; these include: Professor David Bryant (Otago), Professor Tanja Stadler (KTH Zurich), Professor Mareike Fischer (Greifswald University), Professor Leo van Iersel (Delft University), Dr Erick Matson (Fred Hutchinson research Centre).

**Proposing challenges for the field:** I actively put forth 'conjectures' as challenges for the international community. In 2009, leading probability theorists from UC Berkeley and MIT solved a particular difficult one (described as a "striking" conjecture by Roch *et al* 2010) in a 41-page paper titled "Evolutionary trees and the Ising model on the Bethe lattice: a proof of Steel's conjecture". It stated "Steel's insightful conjecture suggests that there are deep connections between the reconstruction problem and phylogenetic reconstruction." This result alone has led to many new (and ongoing) developments.

## Publications: Mike Steel

Steel, M. and Kauffman, S. (2018). A note on random catalytic branching processes. *Journal of Theoretical Biology*, 437, 222-224.

Francis, A., Semple, C. and Steel, M. (2018). New characterisations of tree-based networks and proximity measures. *Adv. Appl. Math.* 93: 93-107.

Gabora, L. and Steel, M. (2017), Autocatalytic networks in cognition and the origin of culture. *J. Theor. Biol.* 431: 87-95.

Bryant, D., Francis, A. and Steel, M. (2017). Can we "future-proof" consensus trees? *Syst. Biol.* 66(4): 611-619.

Casanellas, M. and Steel, M. (2017), Phylogenetic mixtures and linear invariants for equal input models *J. Math. Biol.*, 74(5): 1107-1138.

Huson, D. H., Steel, M., El-Hadidia, M., Mitrac, S., Silke, P. and Willmann, M. (2017). A simple statistical test of taxonomic or functional homogeneity using replicated microbiome sequencing samples. *Journal of Biotechnology*, 250: 45-50.

Steel, M. and Leuenberger, C. (2017). The optimal rate for resolving a near-polytomy in a phylogeny. *J. Theor. Biol.*, 420: 174-179.

Hordijk, W. and Steel, M. (2017). Chasing the tail: The emergence of autocatalytic networks. *Biosystems*, 152:1-10.

Matschiner, M., Musilová, Z., Barth, J. M. I., Starostová, Z., Salzburger, W., Steel, M. and Bouckaert, R. (2017). Bayesian phylogenetic estimation of clade ages supports trans-atlantic dispersal of cichlid fishes, *Systematic Biology*, 66 (1): 3-22.

Sober, E. and Steel, M. (2017). Similarities as Evidence for Common Ancestry — A Likelihood Epistemology. *British J. Phil. Sci.* 68(3): 617-638.

J. V. De Jong, J. C. McLeod, and M. Steel. (2016). Neighbourhoods of phylogenetic trees: exact and asymptotic counts. *SIAM Journal on Discrete Mathematics*, 30(4): 2265-2287.

Casanellas, M. and Steel, M. (2016), Phylogenetic mixtures and linear invariants for equal input models *J. Math. Biol.* (in press).

Matschiner, M., Musilová, Z., Barth, J. M. I., Starostová, Z., Salzburger, W., Steel, M. and Bouckaert, R. (2016). Bayesian node dating based on probabilities of fossil sampling supports trans-atlantic dispersal of cichlid fishes, *Proc. Natl. Acad. Sci. USA* (in press).

Huson, D. H., Steel, M., El-Hadidi, M., Willmann, M. (2016). A statistical test for detecting taxonomic or functional inhomogeneity using replicated metagenomic samples (submitted).

Steel, M. (2016). *Phylogeny: Discrete and random processes in evolution* (Book), CBMS-NSF Regional conference series in Applied Mathematics (SIAM) (in press for publication in September 2016), 303 pages.

Hordijk, W. and Steel, M. (2016). Autocatalytic sets in polymer networks with variable catalysis distributions, *J. Math. Chem.*, 54(10): 1997-2021.

Mark, S., McLeod, J.C., and Steel, M. (2016). A navigation system for tree space. *Journal of Graph Algorithms and Applications*, 20(2): 247-268.

Huber, K. T., Moulton, V., Steel, M. and Wu, T. (2016). Folding and unfolding phylogenetic trees and networks. *J. Math. Biol.* 73(6): 1761-1780.

Gascuel, O. and Steel, M. (2016). A 'stochastic safety radius' for distance-based tree reconstruction. *Algorithmica*. 74: 1386-1403.

Hordijk, W. and Steel, M. (2016). Comment on "Tibor Gánti and Robert Rosen" by Athel Cornish-Bowden. *J. Theor. Biol.* 392: 122-123.

Bernstein, D.I., Ho, L.S.T, Long, C., Steel, M. St John, K. and Sullivant, S. (2015). Bounds on the expected size of the maximum agreement subtree. *SIAM J Discr. Math.* 29(4): 2065-2074.

McTavish, E.J., Steel, M. and Holder, M.T. (2015). Twisted trees and inconsistency of tree estimation when gaps are treated as missing data — the impact of model misspecification in distance corrections. *Mol. Phyl. Evol.* 93:289-295.

Francis, A. and Steel, M. (2015). Which phylogenetic networks are merely trees with additional arcs? *Syst. Biol.* 64 (5): 768-777.

Steel, M. (2015). Self-sustaining autocatalytic networks within open-ended reaction systems. *Journal of Mathematical Chemistry*, 53(8): 1687-1701.

Sober, E. and Steel, M. (2015). Similarities as Evidence for Common Ancestry — A Likelihood Epistemology. *British J. Phil. Sci.* (in press).

Sanderson, M.J., Steel, M., Zwickl, D., McMahon, M., and Stamatakis, A. (2015). Impacts of terraces on phylogenetic inference. *Systematic Biology* 64 (5): 709-726

Hordijk, W., Smith, J. and Steel, M. (2015). Algorithms for detecting and analysing autocatalytic sets. *Algorithms in Molecular Biology* 10: 15.

Chor, B. and Steel, M. (2015). Do tree split probabilities determine the branch lengths? *J. Theor. Biol.* 374: 54-59

Steel, M. (2015). Reflections on the extinction-explosion dichotomy. *Theor. Pop. Biol.* 101: 61-66.

Sober, E. and Steel, M. (2015). How probable is common ancestry according to different evolutionary processes? *J. Theor. Biol.* 373: 111-116.

Gravel, S. and Steel, M. (2015). The existence and abundance of 'ghost' ancestors in biparental populations. *Theor. Pop. Biol.* 101: 47-53.

Scotland, R.W. and Steel, M. (2015). Circumstances in which parsimony but not compatibility will be provably misleading. *Systematic Biology* 64 (3): 492-504

Francis, A.R. and Steel, M. (2015). Tree-like reticulation networks -- When do tree-like distances also support reticulation evolution? *Math. Biosci.* 259: 12-19.

Hagen, O., Hartmann, K., Steel, M. and Stadler, T. (2015). Age-dependent speciation explains empirical tree shape distribution. *Syst. Biol.* 64 (3): 432-440

- Roch, S. and Steel, M. (2015). Likelihood-based tree reconstruction on a concatenation of aligned sequence data sets can be statistically inconsistent. *Theoretical Population Biology*, 100: 56-62.
- Sousa, F.L., Hordijk, W., Steel, M. and Martin, W. (2015). Autocatalytic sets in the metabolic network of *E. coli*. *J. Syst. Chem.* 6: 4.
- Hordijk, W. and Steel, M. (2015). Autocatalytic sets and boundaries. *J. Syst. Chem.* 6: 1 DOI 10.1186/s13322-014-0006-2.
- Hordijk, W. and Steel, M. (2015). Conditions for evolvability of autocatalytic sets: a formal example and analysis. *Origins of Life and Evolution of Biospheres* 44(2): 111-124.
- Molitor, D., Steel, M. and Taylor, A. (2015). The structure of symmetric n-player games when influence and independence collide. *Adv. Appl. Math.* 62: 15-40.
- Steel, M. (2015). Capturing a phylogenetic tree when the number of character states varies with the number of leaves. (ArXiv).
- Steel, M. (2015). A consistency lemma in statistical phylogenetics. (ArXiv).
- Mossel, E. and Steel, M. (2014). Majority rule has transition ratio 4 on Yule trees under a 2-state symmetric model. *Journal of Theoretical Biology* 360: 315-318.
- Fischer, M., Galla, M., Herbst, L. and Steel, M. (2014). The most parsimonious tree for random data. *Molecular Phylogenetics and Evolution* 80: 165-168.
- Dress, A., Huber, K. and Steel, M. (2014). A matroid associated with a phylogenetic tree. *Discrete Mathematics and Theoretical Computer Science* 16(2): 41-56.
- Steel, M. and Velasco, J. (2014). Axiomatic opportunities and obstacles for inferring a species tree from gene trees. *Syst. Biol.* 63(5): 772-778.
- Steel, M. (2014). Tracing evolutionary links between species. *American Mathematical Monthly* 121(9): 771-792.
- Sober, E. and Steel, M. (2014). Time and knowability in evolutionary processes. *Philosophy of Science* 81(4): 558-579
- Huber, K. and Steel, M. (2014). Reconstructing fully-resolved trees from triplet cover distances. *Electronic Journal of Combinatorics* 2: 15
- Smith, J., Steel, M. and Hordijk, W. (2014). Autocatalytic sets in a partitioned biochemical network. *Journal of Systems Chemistry* 5: 2
- Gascuel, O. and Steel, M. (2014). Predicting the ancestral character changes in a tree is typically easier than predicting the root state. *Systematic Biology*. 63(3): 421-435
- Hordijk, W., Wills, P. and Steel, M. (2014). Autocatalytic Sets and Biological Specificity. *Bulletin of Mathematical Biology* 76(1): 201-224.
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- Hordijk, W., Steel, M. and Kauffman. (2013). The origin of life, evolution, and functional organization. pp. 49-60 in *Evolutionary Biology: Exobiology and Evolutionary Mechanisms* Pierre Pontarotti (Editor), Springer.
- Steel, M. (2013). Consistency of Bayesian inference of resolved phylogenetic trees. *Journal of Theoretical Biology*. 336: 246-249.
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- Lambert, A. and Steel, M. (2013). Predicting the loss of phylogenetic diversity under non-stationary diversification models. *Journal of Theoretical Biology*. 337: 111-124.
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- Steel, M., Hordijk, W., and Smith, J. (2013). Minimal autocatalytic networks. *Journal of Theoretical Biology* 332: 96-107.
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- Martyn, I. and Steel, M. (2012). The impact and interplay of long and short branches on phylogenetic information content. *Journal of Theoretical Biology* 314: 157-163.
- Hordijk, W., Steel, M. and Kauffman, S. (2012). The Structure of Autocatalytic Sets: Evolvability, Enablement, and Emergence. *Acta Biotheoretica*, 60: 379-392.
- Hordijk, W. and Steel, M. (2012). Autocatalytic Sets Extended: Dynamics, Inhibition, and a Generalization. *Journal of Systems Chemistry*, 3:5 (12 pp.).
- Steel M. (2012). Root location in random trees: A polarity property of all sampling consistent phylogenetic models except one. *Molecular Phylogenetics and Evolution* 65: 345-348.
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- sites on the time dependence of molecular rates. *Molecular Biology and Evolution* 29(11): 3345-3358.
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- Bryant, D. and Steel, M. (2012). 'Bureaucratic' set systems, and their role in phylogenetics. *Applied Mathematics Letters* 25: 1148-1152.
- Hordijk, W. and Steel, M. (2012). Predicting template-based catalysis rates in a simple catalytic reaction model. *Journal of Theoretical Biology* 295: 132-138.
- Stadler, T. and Steel, M. (2012). Distribution of branch lengths and phylogenetic diversity under homogeneous speciation models. *Journal of Theoretical Biology*. 297: 33-40.
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- Moulton, V. and Steel, M. (2012). The 'Butterfly effect' in Cayley graphs with applications to genomics. *Journal of Mathematical Biology*, 65(6-7): 1267-1284.
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- Hordijk, W., Kauffman, S., and Steel, M. (2011). Required levels of catalysis for the emergence of autocatalytic sets in models of chemical reaction systems. *International Journal of Molecular Sciences (Special issue: Origin of Life 2011)* 12: 3085-3101.
- Steel, M. (2011). Can maths help us glimpse the future? *NZ Science Teacher* 126: 6-7(non-peer reviewed).
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