Dr Andrew Phillips

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INNOVATOR AND LEADER IN MOLECULAR AND GENETIC PROGRAMMING

Innovator with the ambition to make genetically programming cells a reality in the true sense of the word *programming*, by precisely predicting how changes to the genetic code of a cell will affect its behaviour. Pioneer in the development of programming languages for molecular and genetic circuits, which automatically generate computational models of behaviour from annotated DNA sequences.

Leader in Synthetic Biology with experience leading high-performing multidisciplinary teams at the intersection of computational modelling, lab automation and machine learning. Led research on learning computational models of cell dynamics from experimental data and on predicting interactions between DNA molecules from sequence.

Inspired by the potential of combining machine learning methods with domain knowledge in the form of automatically generated computational models, to predict the behaviour of a cell from changes to its genetic code.

AWARDS AND RECOGNITION

- Winner of the Rozenberg Tulip Award for outstanding contribution to DNA computing, to be announced 2022.
- Co-chair of the International Conference on DNA Computing and Molecular Programming 2020, 2021.
- Led the creation of a Microsoft Research partnership with Novartis Cell & Gene therapy, which was a key component of a broader Microsoft-Novartis partnership, announced as "one of the most expansive tie-ups between big pharma and big tech", in [Financial Times 2019].
- Feature article on the Station B initiative at Microsoft Research, in [Nature Biotechnology 2019].
- Led the creation and launch of Station B at Microsoft Research, reported in [Financial Times 2019b].
- Golden Jubilee Award for service to Barbados in the United Kingdom, 2016.
- Led the creation of the first molecular biology lab at Microsoft, reported in [Fast Company 2016].
- Proposed the concept for a Microsoft Office Envisioning video on a future version of Office that enables programming yeast cells to biomanufacture therapeutics, 2M views, [Office Envisioning 2015].
- Programme co-chair of the International Conference on DNA Computing and Molecular Programming, 2015.
- Led research on a programming language for DNA circuits, highlighted in [The Economist 2012].
- MIT Technology Review TR35 award for computer-assisted genetic engineering, [Technology Review 2011].
- Led the creation of programming languages for DNA and genetic circuits, reported in [Science 2011].
- Co-editor and contributing author of the 2020 Science report. "That report inspired this week's focus on computing in Nature", including the cover, in [Nature 2006].

PROFESSIONAL EXPERIENCE

HEAD OF BIOLOGICAL COMPUTATION, MICROSOFT RESEARCH CAMBRIDGE   2010 - 2021

Led research in Biological Computation at Microsoft, developing methods for understanding and programming information processing in biological systems. Responsible for setting the research direction of the team, creating academic and industrial partnerships, presenting to senior leadership, and securing internal funding to ensure the continued operation and growth of the team.

Scientific Research

- Jointly led scientific research with Dave Zhang on predicting DNA interactions from sequence. Developed a model that predicts both DNA sequencing depth and DNA kinetics from sequence with high accuracy, by incorporating domain knowledge in the form of free energy calculations with a deep learning recurrent neural network [Nature Communications 2021]. Generalises previous joint work on a feature-based model [Nature Chemistry 2018]. Contributed joint leadership of the project and expertise in computational modelling.
- Jointly led scientific research with Paul Grant on programming cell populations. Programmed a mutual inhibition genetic circuit in cell populations and showed that mutual inhibition is sufficient to produce stable domains of gene expression in response to dynamic morphogen gradients. This addressed important

questions on the mechanisms of organism development. Computational models of synthetic circuits provided a theoretical and experimental framework for programming spatial patterning in cell populations [Nature Communications 2020b]. Main experiments performed at Microsoft in the Station B wet lab. Contributed joint leadership of the project and expertise in computational modelling.

- Led the development of the Visual DSD programming language [Bioinformatics 2011] for designing molecular circuits. Developed new computational methods and incorporated them into the language [DNA 2011, 2011b, 2013, 2013b, 2014 , 2014b, 2017], [ACS Synthetic Biology 2014b, 2015, 2019], [Royal Society Interface 2012, 2012b], [Theoretical Computer Science 2012, 2012b, 2016, 2016b]. Worked closely with academic collaborators to use this language to make scientific advances in programming molecular circuits, including a distributed consensus algorithm, scalable logic circuits and DNA-based communication in synthetic protocells [Nature Nanotechnology 2013, 2017, 2019].

- Led the development of the Visual GEC programming language for designing genetic circuits, which underpinned the computational modelling of experiments performed in the Station B wet lab. Developed new computational methods and integrated them with the language [Royal Society Interface 2012c], [ACS Synthetic Biology 2012, 2014, 2016]. Worked with academic collaborators to make scientific advances using the underlying methods developed [Molecular Systems Biology 2016], [Nature Communications 2018, 2020].

Partnerships and Funding

- Microsoft lead for the creation of a research partnership between Station B and the Novartis Cell & Gene therapy division, as a key component of a broader Microsoft - Novartis partnership [Microsoft News 2019], reported as "one of the most expansive tie-ups between big pharma and big tech" [Financial Times 2019]. This enabled Microsoft access to the world's largest repository of CAR-T therapy patient data. Secured Microsoft funding to hire two senior Machine Learning researchers in Station B.

- Microsoft lead for the creation of a research partnership between Station B and Oxford Biomedica, to investigate how the Station B platform can accelerate the production of life-saving therapies and vaccines [Wall Street Journal 2019, Bloomberg 2019].

- Microsoft lead for the creation of a research partnership between Station B and Princeton University. Presented the Station B vision to the Princeton University President and Leadership Team to obtain strategic buy-in. Co-authored a research proposal with Prof Bonnie Bassler, head of the Molecular Biology Department at Princeton, and Prof. Ned Wingreen. Secured funding from Microsoft President Brad Smith to hire 4 postdoctoral researchers for a 3-year period.

- Led the creation and launch of the Station B project, with the aim of developing a platform for genetically programming cells [Microsoft Research 2019]. Feature article on Station B highlighted role as a thought leader in programming biology [Nature Biotechnology 2019]. Secured Microsoft funding to grow Station B to a 10-person team.

- Led the creation of the first molecular biology laboratory at Microsoft [Fast Company 2016]. Secured Microsoft funding to hire two computational biology researchers, an experimental biologist, and a flow cytometry laboratory expert.

- Proposed the concept for a Microsoft Office Envisioning video on a future version of Office that enables programming yeast cells to biomanufacture therapeutics using kelp as an energy source. Collaborated extensively with the team as a domain expert. 2M views, [Office Envisioning 2015].

Strategy and Communication

- Strategic presentations to Microsoft senior leadership to obtain buy-in and financial support for Synthetic Biology research over a 10-year period. Includes presentations to CEO Satya Nadella, president Brad Smith, co-founder Bill Gates, the Senior Leadership Team and the Board of Directors.
- Worked extensively with Business Development and Corporate Strategy to create a strategic vision for Synthetic Biology at Microsoft, which was instrumental in obtaining sustained investment and growth.

RESEARCHER, MICROSOFT RESEARCH CAMBRIDGE   2007 - 2010

- Led the creation of the Visual DSD programming language for designing DNA circuits [Royal Society Interface 2009b] and jointly created the Visual GEC programming language for designing genetic circuits [Royal Society Interface 2009].

- Led the development of the Stochastic Pi Machine (SPiM) programming language and used it to model key biological processes, including gene regulatory networks [HFSP Journal 2008], the polymerisation of actin filaments [ENTCS 2009b], rho GTP binding proteins [Theoretical Computer Science 2009], Epidermal Growth Factor Receptor networks [BMC Systems Biology 2009] and antigen presentation to T-cells [PLoS Computational Biology 2011].

POSTDOCTORAL RESEARCHER, MICROSOFT RESEARCH CAMBRIDGE 2005 - 2007

- Supervised by Luca Cardelli and Stephen Emmott. Led the creation of the Stochastic Pi Machine (SPiM) programming language for computational modelling of biological systems. The language is based on a formal model of concurrency known as the pi-calculus, and the simulation algorithm is based on stochastic kinetics of physical chemistry.

- Developed a formal specification of the language syntax and semantics [CMSB 2007], together with a corresponding graphical formalism for representing computational models [TCSB 2006b] and their execution traces [ENTCS 2008]. Used the language for compositional modelling of synthetic gene circuits [TCSB 2006].

INTERN, MICROSOFT RESEARCH CAMBRIDGE 2004

Internship on *Simulating Biological Systems in the Stochastic Pi-calculus*. Supervised by Luca Cardelli (3 months).

RESEARCH ASSISTANT, DEPARTMENT OF COMPUTING, IMPERIAL COLLEGE 2000-2004

Lectured in Java Programming and Declarative Programming in Haskell.

SOFTWARE DEVELOPER, CNES FRENCH SPACE AGENCY 1999

Deployed a quality management application on the web for monitoring satellites in orbit (3 months).

SOFTWARE DEVELOPER, LAAS SYSTEMS LABORATORY 1997

Developed an application to test the dispersion characteristics of high-frequency transistors for telecommunications satellites (6 weeks).

EDUCATION

PhD in Computer Science 2000-2004

Department of Computing, Imperial College. Department Scholarship. Overseas Research Scholarship. Winner in the Imperial College Ideas Challenge 2001. Thesis title: *Specifying and Implementing Secure Mobile Applications in the Channel Ambient System*. Supervised by Susan Eisenbach, Nobuko Yoshida and Bashar Nuseibeh.

Master's in Computer Science (Distinction) 1999-2000

Computer Laboratory, University of Cambridge. Award for outstanding dissertation. Scholarship for outstanding examination results. Dissertation title: *Implementation of a Mobile Agent Language based on Pi-Calculus*. Supervised by Peter Sewell and Paweł Wojciechowski.

Master's in Electrical and Computer Engineering (First class honours) 1997-2000

Institut National des Sciences Appliquées (INSA), Toulouse, France. Final year spent at the University of Cambridge as part of a joint honours programme.

Undergraduate Degree in Electrical Engineering (First class honours) 1995-1997

Université Paul Sabatier, Toulouse, France. Award for best examination results.

Secondary Education 1988-1995

Harrison College, Barbados. National scholarship for A-level results. National award for best O-level results.

PERSONAL INTERESTS

Sports: kitesurfing, snowboarding, calisthenics, Thai boxing, kickboxing (black belt, qualified UK instructor).

Ballroom Dancing: Imperial Society of Teachers of Dancing gold* medal, awarded with honours. Member of Imperial College Dance Team, competed on the UK university circuit 2001-2003, qualified UK instructor.

Chess: Regional junior champion, Haute Garonne, France 1996. National champion by age group, Barbados 1988-1995. World junior championships by age group, Puerto Rico 1986 (5th), 1987 (8th).

PRESS

1. [Microsoft Research Podcast 2019] Programming biology with Dr. Andrew Phillips.
2. [Microsoft News 2019] Novartis and Microsoft announce collaboration to transform medicine with artificial intelligence.
3. [Financial Times 2019] Novartis and Microsoft join forces to develop drugs using AI.
4. [Nature Biotechnology 2019] Microsoft makes splash in AI-enabled lab solutions.
5. [Financial Times 2019b] Microsoft moves into biological computing with Station B.

6. [Wall Street Journal 2019] Oxford BioMedica Looks to Cut Costs of Gene Therapies With Microsoft Collaboration.

7. [Fierce Biotech 2019] Microsoft partners with biotech on 'biological computing' and cell DNA programming.

8. [Bloomberg 2019] Microsoft Brings AI to U.K. Gene-Therapy Firm.

9. [Microsoft Research 2019] With lessons learned from computers, a new platform could help boost production of lifesaving biological therapies.

10. [Microsoft Research 2019b] Researchers build nanoscale distributed DNA computing systems from artificial protocells.

11. [Microsoft Research 2019c] Scientists discover how bacteria use noise to survive stress.

12. [Microsoft Research 2017] Scientists use machine learning to predict DNA binding rates from sequence.

13. [Nature Nanotechnology 2017b] DNA computing: Spatially localized DNA domino.

14. [IEEE Spectrum 2017] DNA Logic Gets Much Faster.

15. [Microsoft Research 2017b] Researchers build nanoscale computational circuit boards with DNA.

16. [Fast Company 2016] Microsoft's "Biological Computing" lab aims to fight diseases by reprogramming cells.

17. [Microsoft Research 2016] How Microsoft computer scientists and researchers are working to 'solve' cancer.

18. [Office Envisioning 2015] Productivity Future Vision.

19. [Chemistry World 2015] DNA gets with the program.

20. [O'Reilly Radar 2014] The revolution in biology is here, now.

21. [Microsoft Research 2014] Creating tools and algorithms that unlock the power of living cells.

22. [Nature Nanotechnology 2013b] DNA computing: Molecules reach consensus.

23. [The Economist 2012] Computing with soup.

24. [Technology Review 2011] Computer-assisted genetic engineering.

25. [Science 2011] Coming Soon to a Lab Near You: Drag-and-Drop Virtual Worlds.

26. [Microsoft Channel 9 2010] Coding 4 DNA.

27. [Nature 2006] Steering the Future of Computing.

PUBLICATIONS

1. [Nature Communications 2021] *A deep learning model for predicting next-generation sequencing depth from DNA sequence*. JX Zhang, B Yordanov, A Gaunt, MX Wang, P Dai, YJ Chen, K Zhang, JZ Fang, N Dalchau, J Li, A Phillips, DY Zhang.

2. [Nature Communications 2020b] *Interpretation of morphogen gradients by a synthetic bistable circuit*. PK Grant, G Szep, O Patange, J Halatek, V Coppard, A Csikász-Nagy, J Haseloff, JCW Locke, N Dalchau, A Phillips.

3. [ACS Synthetic Biology 2020] *Domain-Specific Programming Languages for Computational Nucleic Acid Systems*. MR Lakin, A Phillips.

4. [Nature Communications 2020] *Stochastic pulsing of gene expression enables the generation of spatial patterns in Bacillus subtilis biofilms*. E Nadezhdin, N Murphy, N Dalchau, A Phillips, JCW Locke.

5. [CMSB 2019] *Fast enumeration of non-isomorphic chemical reaction networks*. C Spaccasassi, B Yordanov, A Phillips, N Dalchau. International Conference on Computational Methods in Systems Biology.

6. [ICML 2019] *Efficient Amortised Bayesian Inference for Hierarchical and Nonlinear Dynamical Systems*. G Roeder, P Grant, A Phillips, N Dalchau, T Meeds. International Conference on Machine Learning.

7. [Nature Nanotechnology 2019] *DNA-based communication in populations of synthetic protocells*. A Joesaar, S Yang, B Bögels, A van der Linden, P Pieters, BVVSP Kumar, N Dalchau, A Phillips, S Mann, TFA de Greef.

8. [ACS Synthetic Biology 2019] *A Logic Programming Language for Computational Nucleic Acid Devices*. C Spaccasassi, MR Lakin, A Phillips.

9. [Nature Communications 2018] Escherichia coli can survive stress by noisy growth modulation. O Patange, C Schwall, M Jones, C Villava, DA Griffith, A Phillips, JCW Locke.

10. [Royal Society Interface 2018] *Synthesizing and tuning stochastic chemical reaction networks with specified behaviours*. N Murphy, R Petersen, A Phillips, B Yordanov, N Dalchau.

11. [Frontiers in Immunology 2018] *A Mechanistic Model for Predicting Cell Surface Presentation of Competing Peptides by MHC Class I Molecules*. DSM Boulanger, RC Eccleston, A Phillips, PV Coveney, T Elliott, N Dalchau.

12. [Nature Chemistry 2018] *Predicting DNA hybridization kinetics from sequence*. JX Zhang, JZ Fang, W Duan, LR Wu, AW Zhang, N Dalchau, B Yordanov, R Petersen, A Phillips, DY Zhang.

13. [DNA 2017] *Automated, Constraint-Based Analysis of Tethered DNA Nanostructures*. MR Lakin, A Phillips. International Conference on DNA Computing and Molecular Programming.

14. [Nature Nanotechnology 2017] *A spatially localized architecture for fast and modular DNA computing*. G Chatterjee, N Dalchau, RA Muscat, A Phillips, G Seelig.

15. [Theoretical Computer Science 2016b] *A strand graph semantics for DNA-based computation*. RL Petersen, MR Lakin, A Phillips.

16. [Theoretical Computer Science 2016] *Modular verification of chemical reaction network encodings via serializability analysis*. MR Lakin, D Stefanovic, A Phillips.

17. [ACS Synthetic Biology 2016] *Characterization of intrinsic properties of promoters*. TJ Rudge, JR Brown, F Federici, N Dalchau, A Phillips, JW Ajioka, J Haseloff.

18. [Molecular Systems Biology 2016] *Orthogonal intercellular signaling for programmed spatial behavior*. PK Grant, N Dalchau, JR Brown, F Federici, TJ Rudge, B Yordanov, O Patange, A Phillips, J Haseloff.

19. [Scientific Reports 2015] *Selector function of MHC I molecules is determined by protein plasticity*. A Bailey, N Dalchau, R Carter, S Emmott, A Phillips, JM Werner, T Elliott.

20. [ACS Synthetic Biology 2015] *Probabilistic analysis of localized DNA hybridization circuits*. N Dalchau, H Chandran, N Gopalkrishnan, A Phillips, J Reif.

21. [PLoS One 2015] *A high-level language for rule-based modelling*. M Pedersen, A Phillips, GD Plotkin.

22. [ACS Synthetic Biology 2014b] *Computational design of nucleic acid feedback control circuits*. B Yordanov, J Kim, RL Petersen, A Shudy, VV Kulkarni, A Phillips.

23. [Bioinformatics 2014] *Bio Simulators: a web UI for biological simulation*. M Pedersen, N Oury, C Gravill, A Phillips.

24. [ACS Synthetic Biology 2014] *A Computational Method for Automated Characterization of Genetic Components*. B Yordanov, N Dalchau, PK Grant, M Pedersen, S Emmott, J Haseloff, A Phillips.

25. [DNA 2014b] *Abstract Modelling of Tethered DNA Circuits*. MR Lakin, R Petersen, KE Gray, A Phillips. International Conference on DNA Computing and Molecular Programming.

26. [DNA 2014] *Computational design of reaction-diffusion patterns using DNA-based chemical reaction networks*. N Dalchau, G Seelig, A Phillips. International Conference on DNA Computing and Molecular Programming.

27. [Nature Nanotechnology 2013] *Programmable chemical controllers made from DNA*. YJ Chen, N Dalchau, N Srinivas, A Phillips, L Cardelli, D Soloveichik, G Seelig.

28. [DNA 2013b] *Functional analysis of large-scale DNA strand displacement circuits*. B Yordanov, CM Wintersteiger, Y Hamadi, A Phillips, H Kugler. International Conference on DNA Computing and Molecular Programming.

29. [DNA 2013] *Modular verification of DNA strand displacement networks via serializability analysis*. MR Lakin, A Phillips, D Stefanovic. International Conference on DNA Computing and Molecular Programming.

30. [Royal Society Interface 2012c] *Towards the rational design of synthetic cells with prescribed population dynamics*. N Dalchau, MJ Smith, S Martin, JR Brown, S Emmott, A Phillips.

31. [ACS Synthetic Biology 2012] Computational modeling of synthetic microbial biofilms. TJ Rudge, PJ Steiner, A Phillips, J Haseloff.

32. [Royal Society Interface 2012b] *Design and analysis of DNA strand displacement devices using probabilistic model checking*. MR Lakin, D Parker, L Cardelli, M Kwiatkowska, A Phillips.

33. [Theoretical Computer Science 2012] *Stochastic simulation of multiple process calculi for biology*. MR Lakin, L Paulevé, A Phillips.

34. [Royal Society Interface 2012] *Abstractions for DNA circuit design*. MR Lakin, S Youssef, L Cardelli, A Phillips.

35. [Bioinformatics 2011] *Visual DSD: a design and analysis tool for DNA strand displacement systems*. MR Lakin, S Youssef, F Polo, S Emmott, A Phillips.

36. [PLoS Computational Biology 2011] *A Peptide Filtering Relation Quantifies MHC Class I Peptide Optimization*. N Dalchau, A Phillips, LD Goldstein, M Howarth, L Cardelli, S Emmott, T Elliott, JM Werner.

37. [DNA 2011] *Localized hybridization circuits*. H Chandran, N Gopalkrishnan, A Phillips, J Reif. International Conference on DNA Computing and Molecular Programming.

38. [DNA 2011b] *Modelling, simulating and verifying turing-powerful strand displacement systems*. M Lakin, A Phillips. International Conference on DNA Computing and Molecular Programming.

39. [Tissue antigens 2010] *The cell biology of major histocompatibility complex class I assembly: towards a molecular understanding*. A Van Hateren, E James, A Bailey, A Phillips, N Dalchau, T Elliott.

40. [CMSB 2010] *A generic abstract machine for stochastic process calculi*. L Paulevé, S Youssef, MR Lakin, A Phillips. International Conference on Computational Methods in Systems Biology.

41. [BMC Systems Biology 2009] *Computational modeling of the EGFR network elucidates control mechanisms regulating signal dynamics*. DYQ Wang, L Cardelli, A Phillips, N Piterman, J Fisher.

42. [Theoretical Computer Science 2009] *A process model of Rho GTP-binding proteins*. L Cardelli, E Caron, P Gardner, O Kahramanoğulları, A Phillips.

43. [Royal Society Interface 2009b] *A programming language for composable DNA circuits*. A Phillips, L Cardelli.

44. [Royal Society Interface 2009] *Towards programming languages for genetic engineering of living cells*. M Pedersen, A Phillips.

45. [ENTCS 2009b] *A process model of actin polymerisation*. L Cardelli, E Caron, P Gardner, O Kahramanoğulları, A Phillips. Electronic Notes in Theoretical Computer Science.

46. [ENTCS 2009] *An abstract machine for the stochastic bioambient calculus*. A Phillips. Electronic Notes in Theoretical Computer Science.

47. [HFSP Journal 2008] *Compositionality, stochasticity, and cooperativity in dynamic models of gene regulation*. R Blossey, L Cardelli, A Phillips. 2 (1), 17-28, 2008.

48. [ENTCS 2008] *A chart semantics for the pi-calculus*. J Borgström, AD Gordon, A Phillips. Electronic Notes in Theoretical Computer Science.

49. [CMSB 2007] *Efficient, correct simulation of biological processes in the stochastic pi-calculus*. A Phillips, L Cardelli. International Conference on Computational Methods in Systems Biology.

50. [TCSB 2006b] *A graphical representation for biological processes in the stochastic pi-calculus*. A Phillips, L Cardelli, G Castagna. Transactions on Computational Systems Biology.

51. [TCSB 2006] *A compositional approach to the stochastic dynamics of gene networks*. R Blossey, L Cardelli, A Phillips. Transactions on Computational Systems Biology.

52. [ESOP 2004] *A distributed abstract machine for boxed ambient calculi*. A Phillips, N Yoshida, S Eisenbach. European Symposium on Programming.

BOOKS AND CHAPTERS

1. DNA 21 Collection. Editors: A Phillips. ACS Synthetic Biology 5 (8), 877-877, 2016.

2. Toward Programmable Biology. Editors: H Fellermann, O Markovitch, O Gilfellon, C Madsen, A Phillips. ACS Synthetic Biology 5 (8), 793-794, 2016.

3. DNA Computing and Molecular Programming: 21st International Conference, DNA 21, Boston and Cambridge, MA, USA, August 17-21, 2015. Proceedings. Editors: A Phillips, P Yin. Springer, 2015.

4. High-Level Programming Languages for Biomolecular Systems. J Beal, A Phillips, D Densmore, Y Cai. Design and Analysis of Biomolecular Circuits: Engineering Approaches to Systems and Synthetic Biology, Springer, 2011.
5. A Visual Process Calculus for Biology. A Phillips. Symbolic Systems Biology: Theory and Methods, Jones and Bartlett Publishers, 2009.
6. Specifying and Implementing Secure Mobile Applications. A Phillips. Process Algebra for Parallel and Distributed Processing, Chapman & Hall/CRC, 2008.
7. Towards 2020 Science. Editors: S Emmott, E Shapiro, S Rison, A Phillips, A Herbert. Microsoft, 2006.
8. Specifying and Implementing Secure Mobile Applications in the Channel Ambient System. A Phillips. Ph.D. Thesis, 2006.

PEER REVIEW

Journals
Nature. Nature Biotechnology. Nature Nanotechnology. Science Advances. Journal of the American Chemical Society. ACS Nano. ACS Synthetic Biology. Cell Systems. PLoS Computational Biology. Methods. Journal of the Royal Society Interface. BMC Systems Biology. Natural Computing. Theoretical Computer Science. Information and Computation. Science of Computer Programming. Transactions on Software Engineering.

Conferences
International Conference on DNA Computing and Molecular Programming (DNA). Computational Methods in Systems Biology (CMSB). International Workshop on Biodesign Automation (IWBDA). European Symposium on Programming (ESOP). Foundations of Software Science and Computation Structures (FoSSaCS), International Conference on Concurrency Theory (CONCUR). Asian Symposium on Programming Languages and Systems (APLAS).

SUPERVISION

Jointly obtained internal funding to support and co-supervise 9 Microsoft PhD scholars. Obtained internal funding to hire and supervise 13 Microsoft Research Interns for 12-week internships. Obtained internal funding to hire and supervise 13 postdocs and 8 senior researchers over a 12-year period.

TEACHING

- Taught Functional Programming to undergraduate students, Imperial College (2003), and Java Programming to Master of Science students, Imperial College (2004).
- Guest lectures on applications of concurrency theory to biological modelling, for the Imperial College concurrency theory course in the Department of Computing (2005-2006, 2008, 2010-2012).
- Tutorials on programming languages for biological modelling at international summer schools (Mexico City 2006, Tangier 2006, Cape Town 2007).
- Tutorials on a programming language for genetic circuits at the international Genetically Engineered Machines (iGEM) summer school, University of Cambridge (2009-2013).
- Tutorials on a programing language for nucleic acid circuits at international conferences (DNA 2013, VEMDP 2014, UCNC 2021).