Alex Popinga

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"All models are wrong but some are useful."
-George E. P. Box

WORK EXPERIENCE

POSTDOCTORAL RESEARCH FELLOW, *March 2024 – Present*
Colorado State University, Fort Collins, Colorado, USA
I am developing computational models to handle noise and uncertainty in single-cell experiments measured by fluorescence imaging. I am furthering Bayesian sequential experimental design.

POSTDOCTORAL RESEARCH FELLOW, *April 2019 – August 2021*
School of Biological Sciences, University of Auckland, Auckland, New Zealand
I performed molecular dynamics simulations on protein crystal structures to sample additional conformations for the measurement of uncertainty in deep phylogenetics.

INSTRUCTOR, WORKSHOP FOR THE INSTITUTE OF ENVIRONMENTAL SCIENCE AND RESEARCH (ESR) AND THE MINISTRY FOR PRIMARY INDUSTRIES (MPI), *March 2019*
Animal Health Laboratory, Wallaceville, Wellington, New Zealand
I instructed scientists from ESR and MPI on the use and development of the Bayesian inference software package BEAST2 (Bayesian Evolutionary Analysis by Sampling Trees).

ASSISTANT, *TAMING THE BEAST* WORKSHOP, *June 2018*
Computational Evolution Group, ETH Zurich, Oberägeri, Switzerland
I assisted in data analyses using the Bayesian inference software package BEAST2.

PART-TIME DATA ANALYST (DURING PHD), *June 2017 – July 2018*
Bioinformatics Institute, University of Auckland, Auckland, New Zealand
I performed Bayesian inference on biological data as requested by Scion (New Zealand Forest Research Institute Limited) and the Ministry of Primary Industries (MPI).

ORIGINS OF LIFE INTERNSHIP, *May 2015 – July 2015*
Department of Statistics, University of Oxford, Oxford, England
I performed stochastic simulations of reaction-diffusion processes in an autocatalytic system of molecules carrying a minimal amount of information for self-replication.

AWC SUMMER INTERNSHIP, *December 2012 – January 2013*
Allan Wilson Centre for Molecular Ecology and Evolution, New Zealand
I developed a Bayesian inference package for modelling the spread and evolution of influenza viruses, which was published in the journal *Bioinformatics*.

NASA STUDENT AIRBORNE RESEARCH PROGRAM INTERNSHIP, *June 2012 – August 2012*
NASA Airborne Science Program, Dryden Aircraft Operations Facility and the University of California Irvine, California, United States of America
I investigated the impact of the hydrocarbon composition of liquefied petroleum gas on air quality in the Los Angeles Basin and presented my findings to NASA.

LAB MANAGER, *August 2011 – December 2011*
Coevolution Laboratory, University of Northern Iowa, Iowa, United States of America
I studied co-evolution of mitochondrial cytochrome oxidase I genes between hosts and their parasites and trained undergraduate students in DNA lab techniques.

INTERNSHIP IN NEURODEGENERATION, *July 2011 – August 2011*
National Chengchi University, Taipei, Taiwan
I studied the effects of calorie restriction on metabolic pathways and longevity in *Drosophila* and presented my results to the neurodegeneration scientists at National Chengchi.

INTERNSHIP IN GLYCOCHEMISTRY, *June 2012 – August 2012*
L'École Nationale Supérieure de Chimie de Rennes (ENSCR), Bretagne, France
I investigated biosynthetic pathways to per-O-acetyl furanoses.

EDUCATION

PH.D. COMPUTER SCIENCE   09 December 2019
University of Auckland
From the Origins of Life to Epidemics: Bayesian Inference, Stochastic Simulation, and Dynamics of Bioinformatic Systems

B.SC. BIOINFORMATICS, HONORS RESEARCH IN BIOLOGY   05 May 2013
University of Northern Iowa
Cophylogeny of Geomydoecus *Chewing Lice and* Cratogeomys *Pocket Gophers of the Trans-Mexican Volcanic Belt*

PUBLICATIONS LIST

C. W. Carter Jr. and A. Popinga and R. Bouckaert and P. R. Wills, (2022). "Multidimensional phylogenetic metrics identify Class I aminoacyl-tRNA synthetase evolutionary mosaicity and inter-modular coupling." *International Journal of Molecular Sciences*, 23(1520). https://doi.org/10.3390/ijms23031520.

A. J. Drummond and A. Popinga, (2021). "Bayesian inference of the climbing grade scale." *arXiv*. https://doi.org/10.48550/arXiv.2111.08140.

A. Popinga and J. W. Demastes and T. A. Spradling and D. J. Hafner and M. S. Hafner, (2019). "Host-parasite associations of the *Cratogeomys fumosus* species group and their chewing lice, *Geomydoecus*." *Therya*, 10(2). https://www.doi.org/10.12933/therya-19-739.

A. Popinga and R. Bouckaert and P. Wills, (2019). "Aminoacyl-tRNA synthetases: Protein structures and the dawn of the genetic code." *Quantitative and Computational Chemistry Student Conference*, Kioloa.

A. Popinga and R. Bouckaert and P. Wills, (2018). "A new model of amino acid substitution using iteratively added exchangeability rates to improve phylogenetic inference of aminoacyl-tRNA synthetases." *Te Ao Marama (Centre for Fundamental Inquiry) Meeting*, Auckland.

A. Popinga and P. Wills, (2016). "The search for simple systems: Minimal genetic information and autocatalytic sets." *New Zealand Astrobiology Workshop*, Kaikoura.

S. Wasef and S. Subramanian and R. O'Rorke and L. Huynen and S. El-Marghani and C. Curtis and A. Popinga and B. Holland and S. Ikram and C. Millar and E. Willerslev and D. Lambert, (2019). "Mitogenomic diversity in sacred ibis mummies sheds light on early Egyptian practices." *PLoS One*, 14(11). https://www.doi.org/10.1371/journal.pone.0223964.

R. Bouckaert and T. G. Vaughan and J. Barido-Sottani and S. Duchne and M. Fourment and A. Gavryushkina and J. Heled and G. Jones and D. Kühnert and N. De Maio and M. Matschiner and N. F. Müller and H. Ogilvie and L. du Plessis and A. Popinga and A. Rambaut and D. Rasmussen and I. Siveroni and M. A. Suchard and C-H. Wu and D. Xie and C. Zhang and T. Stadler and A. J. Drummond, (2019). "BEAST 2.5: An Advanced Software Platform for Bayesian Evolutionary Analysis." *PLoS Computational Biology*, 15(4). https://www.doi.org/10.1371/journal.pcbi.1006650.

A. Popinga and Ant Poole and Ashar Malik and Fábio Mendes and Jane Allison, (2019). "Resolving protein families using structural phylogenetics." *AMMA Molecular Modelling Conference*, Bintan.

A. Popinga and T. Vaughan and T. Stadler and A. J. Drummond, (2015). "Inferring epidemiological dynamics with Bayesian coalescent inference: The merits of deterministic and stochastic models." *Genetics*, 199(2):595–607. https://www.doi.org/10.1534/genetics.114.172791.

A. Popinga and Carter, Jr., C. W. and R. Bouckaert and P. Wills, (2015). "Complex phylogeny of aminoacyl-tRNA synthetases." *European Society for Evolutionary Biology Congress*, Lausanne.

A. Popinga and T. Vaughan and D. Welch and A. J. Drummond, (2015). "Stochastic population dynamics in Bayesian epidemic parameter inference with the coalescent Susceptible-Infected-Removed (SIR) model." *Annual Meeting of the Society for Molecular Biology and Evolution*, Vienna.

T. Vaughan and D. Kühnert and A. Popinga and D. Welch and A. J. Drummond, (2014). "Efficient Bayesian phylogenetic inference under the structured coalescent." *Bioinformatics*, 30(16):2272–2279. https://www.doi.org/10.1093/bioinformatics/btu201.