HUGH CROSS

I am a computational biologist with a background in ecology and evolutionary genetics. I work on projects across the tree of life, utilising many kinds of data and multiple approaches. With biodiversity studies as a centerpoint, I have naturally come to specialise in metagenomics research. To study any environment is to study a community of genes engaged in molecular dialogues—both within and between species, and this requires a community of researchers working together. I hope to find this team.

EDUCATION

2003 • Ph.D., Ecology and Evolutionary Biology

Columbia University

New York, NY

M.Sc., Plant Breeding and Genetics

Colorado State University

♥ Fort Collins, CO

1993 • B.A., Anthropology

1998

2017

2013

2008

2020

2020

University of Colorado

♀ Boulder, CO

♠ SELECTED POSITIONS

Present • Bioinformatician

Department of Anatomy, University of Otago

- Conducting bioinformatic analyses on several projects in the department, including on genome and transcriptome assembly and annotation, gene expression, population and phylogenetic research
- · Training staff and students in basic and advanced data analysis methods

2017 • Scientist

Department of Forest Health, Norwegian Institute for Bioeconomy Research (NIBIO)

• Primary responsibility was conducting bioinformatic analyses on several projects in the department of Forest Health at the institute, including genome and transcriptome assembly, gene expression, population and phylogenetic research of plants, animals, and fungus, and metagenomics

2013 • Molecular Botanist

State Herbarium of South Australia

- Conducted research in all areas of plant and fungal genomics, including genomic, transcriptomic, and bioinformatic applications for biodiversity and ecology
- · Main coordinator for DNA Barcoding projects
- Trained and consulted with staff for next generation sequencing research

SELECTED PUBLICATIONS

Molecular underpinnings of long-term methyl jasmonate-induced resistance in Norway spruce

Plant Cell & Environment 43: 1827-1843.

· Magerøy, M., Wilkinson, S., Tengs, T., **Cross, H.B.**, Almvik, M., Petriacq, P., Vivian-Smith, A., Zhao, T., Fossdal, C.G., Krokene, P.

Stress, novel sex genes and epigenetic reprogramming orchestrate sociallycontrolled sex change

Science Advances 7 eaaw 7006

· Todd, E.V., Ortega-Recalde, O., Liu, H., Lamm, M.S., Rutherford, K.M., **Cross, H.B.**, Black, M.A., Kardailsky, O., Marshall Graves, J.A., Hore, T.A., Godwin, J.R., Gemmell, N.J.

CONTACT

- hughbcross@gmail.com
- github.com/hughcross
- hughcross.github.io/
- **J** +64 (0) 21 980 027

PROGRAMMING SKILLS

Python

Jupyter

Bash

R

SQL

HTML/CSS

FIELDWORK

Australia Costa Rica Mexico USA: Colorado and Hawaii

FOREIGN LANGUAGE

Fluent in Spanish

MORE INFO

See full CV at hughcross.github.io/cv for more complete list of positions and publications.

Publications Overview:

Citations: 1400

h-index: 14

Google Scholar profile

Made w/ pagedown. Source code: github.com/hughcross/cv. Last updated on 2021-10-13.

2017	•	Fungal diversity and seasonal succession in ash leaves infected by the invasive ascomycete <i>Hymenoscyphus fraxineus</i>
		New Phytologist, 213(3): 1405-1417
		· Cross, H.B., Sønstebø, J.H., Nagy, N.E., Timmermann, V., Solheim, H., Børja, I., Kauserud, H., Carlsen, T., Rzepka, B., Wasak, K., Vivian-Smith, A., Hietala, A.M.
2016		Effective application of next generation sequencing (NGS) approaches in systematics and population genetics - case studies in <i>Eucalyptus</i> and <i>Acacia</i>
		Australian Systematic Botany 29(3): 235-246
		· Cross, H.B., Biffin, E., van Dijk, K., Lowe, A., Waycott, M.
2010		Distribution and abundance of the introduced ectomycorrhizal fungus, <i>Amanita phalloides</i> , in North America
		New Phytologist 185: 803-816
		· Wolfe B.E., Richard, F., Cross, H.B. , and Pringle A.
2009	•	The ectomycorrhizal fungus <i>Amanita phalloides</i> was introduced and is expanding its range on the west coast of North America
		Molecular Ecology 18: 817-833
		· Pringle, A., Rachel I. Adams, R. I., Cross, H.B. , Bruns, T.D.
2008	•	The ecological implications of a Yakutian mammoth's last meal
		Quaternary Research 69: 361-376
		· van Geel, B., Aptroot, A., Baittinger, C., Birks, H.H., Bull, I.D., Kompanje, E.J.O., Cross, H.B. , Evershed, R.P., Gravendeel, B., Kuperus, P., Nierop, K.G.J., Mol, D., Pals, J.P., Tikhonov, A. N., van Reenen, G., and van Tienderen, P.H.
	*	SELECTED TEACHING AND PRESENTATIONS
Present	•	Instructor, Workshop in Environmental DNA
 2019		University of Otago © Dunedin & Auckland, NZ
		 Designed from bottom up course to teach methods & concepts for eDNA metabarcoding
Present	•	Instructor, Software/Data Carpentry
 2018		University of Otago ♥ Dunedin, NZ
		 Teaching basic and advanced bioinformatic skills using live coding in a team- teaching environment
2013		Exploring plant genomic biodiversity in South Australia
		Presented at the CBA Biodiversity Genomics Conference, Canberra, Australia
		· Cross, H.B., Biffin, E., van Dijk, K. Waycott, M.
2011		Tales from the cryptogams, fungal DNA from museum collections
		Plenary speaker at the Fourth International Barcode of Life Conference, Adelaide, Australia
		· Cross, H.B., Pringle, A.
2011	•	Utilizing Grass DNA barcodes to Explore Australian Ecosystems
		Presented at the International Botanical Congress, Melbourne, Australia
		· Cross, H.B., Murphy, D., Brown, A., Gardner, S., Syme, A., Jardine, D., Cantrill, D., Lowe, A.J.

Certified Software Carpentry Instructor

link to environmental DNA workshop

I also run a biweekly bioinformatics help session