

May 11th, 2022

Dear Search Committee,

I am writing to apply for the position of Assistant Professor in Forest Genetics and Genomics. I think I would be a good fit for the position because my research experience and personal outlook closely match the description of the desired candidate. I am an evolutionary biologist working on the genomics of conifers. My research draws on population genetics, genomics, bioinformatics and statistics and I have extensive experience teaching on these topics. I am a Bioinformatics Postdoctoral Fellow in the Biodiversity Research Centre at UBC and part of the multidisciplinary CoAdapTree project. I received my PhD from the University of Edinburgh in 2018.

Understanding natural selection is central to the study of evolution and conservation of biodiversity. However, despite more than 100 years of research in evolutionary genetics, we still know little about the strength of natural selection and the genetic variation upon which it acts in nature. Recently, I have been developing methods to identify the genetic basis of local adaptation and to assess the extent of convergent evolution. I am currently applying these methods to several economically important conifer species. My work has been published in well respected, high-impact journals (*Conservation Biology*, *Molecular Biology and Evolution*, *Molecular Ecology*).

With my experience and expertise in modern techniques for studying evolutionary genetics, I would complement existing expertise in the Department of Forest & Conservation Sciences at UBC. My research program would tackle empirical and theoretical questions at the heart of evolution and conservation genetics. I plan to harness powerful developments in population genetics and DNA sequencing technology to characterise the genetics of local adaptation of forest trees. As well as working towards a predictive model of the genetics of local adaptation based on species ranges. UBC is a world leader in the field of forest genetics and would be the ideal place to develop my research group.

I work at the interface of theoretical and empirical population genetics, which has given me the ability to communicate and teach complex topics. I currently lead a graduate course on bioinformatics at UBC (BIOL525D) and would be keen to incorporate similar material into the undergraduate forest genetics course. I use complex evolutionary simulations to generate datasets for teaching. Comparing simulated and empirical datasets helps demonstrate important bioinformatic and genetic concepts, while providing an opportunity for active learning where a ground truth is known. Incorporating active learning with bioinformatics into genetics courses would help students develop transferable skills that provide options for their careers.

I am committed to Equity, Diversity and Inclusion in academia and currently serve on the EDI committee in the Department of Zoology. I would want to continue to serve in a similar role in the Department of Forestry & Conservation Science. I firmly believe in treating everyone with friendliness and collegiality and strive to act in a way that engenders an inclusive and respectful environment with the aim of building a research community based on mutual respect.

I am a permanent resident of Canada, eligible to apply for citizenship in August of this year.

Thank you for your consideration.

Sincerely,

Tom Booker

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Phone: 778-751 4586

Tom R. Booker

CONTACT INFORMATION University of British Columbia, Vancouver +1 778-751-4586 (Cell)
booker@zoology.ubc.ca <https://tbooker.github.io/>

EMPLOYMENT **University of British Columbia**, Vancouver, Canada
- Bioinformatics Postdoctoral Fellow (Oct 2021 - October 2023)
University of Calgary, Calgary, Canada
- Postdoctoral Research Fellow (March - October 2021)
- Supervised by Professor Michael Whitlock and Associate Professor Sam Yeaman
University of British Columbia, Vancouver, Canada
- Postdoctoral Research Fellow (Sept 2018 - March 2021)
- Supervised by Professor Michael Whitlock and Associate Professor Sam Yeaman

EDUCATION **University of Edinburgh**, Edinburgh, Scotland
PhD., [Evolutionary Genetics](#), October 2014 - October 2018
- Thesis Title: UNDERSTANDING PATTERNS OF GENETIC DIVERSITY IN THE HOUSE MOUSE GENOME
- Supervisors: Professor Peter Keightley and Professor Brian Charlesworth
- Spring 2018: Visiting student at UBC hosted by Professor Sarah Otto
MSc., [Evolutionary Genetics](#), 2013 - 2014 (Distinction)
- Thesis Title: SEARCHING FOR BALANCING SELECTION ON A MIMICRY SUPERGENE IN THE BATESIAN MIMIC *Papilio polytes*
- Supervisors: Professor Deborah Charlesworth and Rob W. Ness (Now Assistant Professor at University of Toronto - Mississauga)
University of Stirling, Stirling, Scotland
BSc Hons, [Ecology](#), 2009 - 2013 (First Class)
- Dissertation Title: AN INVESTIGATION INTO THE FITNESS AND DISTRIBUTION OF A NEWLY DISCOVERED ALLOPOLYPLOID SPECIES, *Mimulus peregrinus*
- Supervisor: Dr Mario Vallejo-Marin
- 2011-2012: Study abroad at Simon Fraser University, Vancouver, Canada.

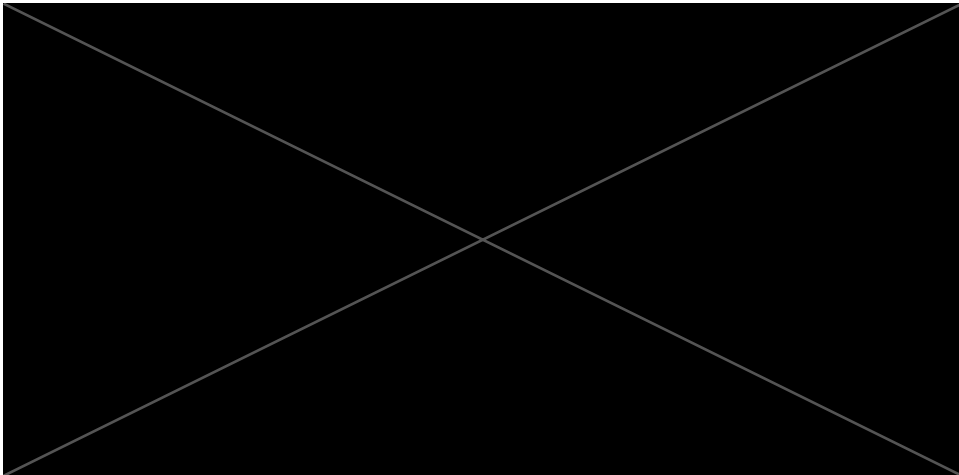
PUBLICATIONS **Preprints**
Booker, T. R., Yeaman, S., & Whitlock, M. C. (*Submitted*). "Using genome scans to identify genes used repeatedly for adaptation."
Preprint online at: <https://www.biorxiv.org/content/10.1101/2022.03.24.485690v1>
Booker, T. R., Payseur, B. A., & Tigano, A. (*In revision at Proc. Roy. Soc. B*). "Background selection under evolving recombination rates".
Preprint online at: <https://doi.org/10.1101/2021.12.20.473549>
Booker, T. R., Jackson, B., Craig, R., Charlesworth, B. & Keightley, P. D. (*In revision at Molecular Biology and Evolution*) "Patterns of genetic diversity around protein-coding exons and conserved non-coding elements are explained by strong selective sweeps in mice".
Preprint online at: <https://doi.org/10.1101/2021.06.10.447924>

Booker, T. R., Yeaman, S. & Whitlock, M. C. (*In revision at Molecular Ecology Resources*)
 “The WZA: A window-based method for characterizing genotype-environment association”.
 Preprint online at: <https://doi.org/10.1101/2021.06.25.449972>

Exposito-Alonso, M., **Booker, T. R.**, Czech, L., Fukami, T., Gillespie, L., Hateley, S.,
 ... & Zess, E. (*In revision at Science*). “Quantifying the scale of genetic diversity
 extinction in the Anthropocene.”
 Preprint online at: <https://doi.org/10.1101/2021.10.13.464000>

Published Papers

11. Grummer, J. A.* , **Booker, T. R.***, Matthey-Doret, R.* , Nietlisbach, P.* , Thomaz, A. T.* ,
 & Whitlock, M. C. (2022). “The immediate costs and long-term benefits of assisted
 gene flow in large populations”. *Conservation Biology*, e13911.
 * Joint first author
10. Lind, B. M., Lu, M., Vidakovic, D., Singh, P., **Booker, T. R.**, Yeaman, S., & Aitken, S.
 (2022). “Haploid, diploid, and pooled exome capture recapitulate features of biology
 and paralogy in two non-model tree species”. *Molecular Ecology Resources*, 22:
 225238.
9. **Booker, T. R.**, Yeaman S. & Whitlock M. C. (2021). “Global adaptation complicates
 the search for local adaptation”. *Evolution Letters*, 5: 4-15.
8. **Booker, T. R.**, Yeaman S. & Whitlock M. C. (2020) “Variation in recombination rate
 affects detection of outliers in genome scans under neutrality”. *Molecular Ecology*,
 29: 42744279.
Highlighted on the cover and with a perspective piece
7. Byers K.A., **Booker T. R.**, Combs M., Himsworth C.G., Munshi-South J., Patrick
 D.M., Whitlock M.C.. (2020) “Using genetic relatedness to understand heterogeneous
 distributions of urban rat-associated pathogens”. *Evolutionary Applications* 00: 112.
6. **Booker, T. R.** (2020) “Inferring parameters of the distribution of fitness effects of new
 mutations when beneficial mutations are strongly advantageous and rare”.
G3: Genes, Genomes, Genetics, 10(7) 2317-2326
5. **Booker, T. R.**, & Keightley, P. D. (2018). “Understanding the factors that shape
 patterns of nucleotide diversity in the house mouse genome”. *Molecular Biology and
 Evolution*, 35(12) 2971-2988
4. **Booker, T. R.**, Jackson, B. C., & Keightley, P. D. (2017). “Detecting positive selection
 in the genome”. *BMC Biology*, 15:98.
3. **Booker, T. R.**, Ness, R. W., & Keightley, P. D. (2017). “The recombination landscape
 in wild house mice inferred using population genomic data”. *Genetics*, 207(1) 297-309
2. Keightley, P. D., Campos, J. L., **Booker, T. R.**, & Charlesworth, B. (2016). “Inferring
 the frequency spectrum of derived variants to quantify adaptive molecular evolution in
 protein-coding genes of *Drosophila melanogaster*”. *Genetics*, 203(2), 975-984.
1. **Booker, T.**, Ness, R. W., & Charlesworth, D. (2015). “Molecular evolution: breakthroughs
 and mysteries in Batesian mimicry”. *Current Biology*, 25(12), R506-R508.

EQUITY, DIVERSITY & INCLUSION ACTIVITIES	Panellist - Parenting in Academia <i>Discussion group in the Biodiversity Research Centre at UBC</i>	2022
	Member of Zoology Equity, Diversity and Inclusion (ZEDI) Committee at UBC	2022-Present
	Participant - Indigenous Awareness <i>Organised by Indigenous Corporate Training inc.</i>	2021
	Participant - pgEd Webinar Series: History of Eugenics <i>Organised by the GSA</i>	2021
TEACHING EXPERIENCE	Course Coordination	
	BIOL525D: Bioinformatics for Evolutionary Genetics <i>Upper division course at UBC on bioinformatics.</i> <i>Website and course materials at: (https://ubc-biol525d.github.io/)</i>	2020-2023
	Teaching Assistance	
	Statistics and Data Analysis, MSc course <i>Upper division course, part of the MSc QGGA program at the University of Edinburgh</i>	2014-2017
	Population and Quantitative Genetics, MSc course <i>Upper division course, part of the MSc QGGA program at the University of Edinburgh</i>	2015-2017
	Ecology and Evolutionary Genetics, BSc course <i>Undergraduate course, offered at the University of Edinburgh</i>	2014-2015
STUDENT SUPERVISION		2022-Present
		2019-2020
		2018-2020
		2018
		2017
		2016-2017
ACADEMIC HONOURS AND AWARDS	<i>Runner up Harry Smith Prize - Molecular Ecology</i>	2020
	<i>University of British Columbia - Bioinformatics Research Fellowship</i>	2020
	<i>Registration Award - Society of Molecular Biology and Evolution</i>	2019
	<i>Runner up Best student talk at Population Genetics Group 51</i>	2018
	<i>Runner up Best student poster at Population Genetics Group 50</i>	2017
	<i>Environment Yes! Won regional heat - runner up at the national final</i>	2016

EASTBIO Doctoral Training Partnership Studentship	2014-2018
Genetics Society, Sir Kenneth Mather Memorial Prize	2013/2014
University of Edinburgh, Douglas Falconer Award, best MSc dissertation	2013/2014
Undergraduate Project Funding - Botanic Society of Scotland	2012
Undergraduate Project Funding - Society of Biology	2012
<i>Nominated</i> , Simon Fraser University Student Conservation Prize	2012

SERVICE & OUTREACH

Reviewing

Science, PLoS Genetics, Molecular Biology and Evolution, Evolution, Molecular Ecology, Proceedings of the Royal Society B, New Phytologist, Genome Biology and Evolution, Ecology and Evolution, Frontiers in Zoology, Frontiers in Ecology and Evolution, Peer Community in Evolutionary Biology, G3, BMC Biology

Academic Service

Member of the Molecular Ecology Junior Editorial Board	2021 - <i>Present</i>
Undergraduate Student Mentor <i>Society for Molecular Biology and Evolution</i>	2019 & 2021

Departmental Service

Postdoc representative on search committee for head of the BRC at UBC	2021
I organise Δ -tea, an evolutionary genetics discussion group at UBC	2021- <i>Present</i>
I hold bioinformatics office hours in the BRC at UBC	2020- <i>Present</i>
I ran virtual trivia nights for the BRC at UBC during the COVID-19 pandemic	2020-2021
Postdoc representative on expansion committee for the BRC at UBC	2020
Co-organiser of the Vancouver Evolution Group (VEG) <i>I stopped due to childcare out of work hours</i>	2019 - 2020
Organised the Classic Theory Journal Club at the University of Edinburgh	2017

Outreach

Skype a Scientist participant	2021
Essay judge for Canadian Undergraduate Research Competition (CURC)	2020-2021
Teen Nerd Nite High School Student Mentor	2020
Poster Judge BIOL 310 Animal Behaviour	2019
Poster and talk judge EcoEvo Retreat	2018-2019

INVITED	2022	University of British Columbia, Biodiversity Research Centre, Canada
PRESENTATIONS	2021	Universidad del Rosario, Faculty of Natural Sciences, Columbia
	2021	Monash University, School of Biological Sciences, Australia
	2021	Virtual SMBE 2021
	2021	Mooers lab group at Simon Fraser University, Canada
	2020	Introgression Discussion Group, UC Berkeley
	2015	Population Genetics Group 49, UK
CONTRIBUTED	2021	EvoTree, Switzerland (Poster - Virtual)
PRESENTATIONS	2021	BLISS, UBC, Vancouver, Canada (Talk)
	2021	Virtual EcoEvo Retreat, Canada (Talk - Virtual)
	2020	BLISS, UBC, Vancouver, Canada (Talk)
	2020	American Society of Naturalists (Talk)
	2019	EcoEvo Retreat, Canada (Talk)
	2019	BLISS, UBC, Vancouver, Canada (Talk)
	2019	SMBE, Manchester, UK (Poster)
	2018	EcoEvo Retreat, Canada (Talk)
	2018	Population Genetics Group 51, UK (Talk)
	2017	ESEB 2017, Netherlands (Poster)
	2017	Population Genetics Group 50, UK (Poster)
	2016	SMBE, Gold Coast, Australia (Talk)
	2015	SMBE, 2015, Vienna, Austria (Poster)
	2015	Quantitative Genomics, 2015, UK (Talk)

References

Professor Michael C. Whitlock
Postdoctoral Supervisor
Department of Zoology
University of British Columbia



Professor Peter Keightley
PhD Supervisor
Institute of Evolutionary Biology
University of Edinburgh



Assistant Professor Sam Yeaman
Postdoctoral Supervisor
Department of Biological Sciences
University of Calgary



Representative Publications - *PDFs Included With Application*

Booker, T. R., Yeaman S. & Whitlock M. C. (2020) "Variation in recombination rate affects detection of outliers in genome scans under neutrality". *Molecular Ecology*, 29: 4274-4279.

Grummer, J. A.* , **Booker, T. R.***, Matthey-Doret, R.* , Nietlisbach, P.* , Thomaz, A. T.* , & Whitlock, M. C. (2022). "The immediate costs and long-term benefits of assisted gene flow in large populations". *Conservation Biology*, e13911.

* *Joint first author*

Booker, T. R., Yeaman, S. & Whitlock, M. C. (*In revision at Molecular Ecology Resources*) "The WZA: A window-based method for characterizing genotype-environment association". Preprint online at: <https://doi.org/10.1101/2021.06.25.449972>

I am an evolutionary biologist, and **my research draws on population genetics, forestry, conservation, statistics, and bioinformatics**. I am currently working on the population genomics of ecologically and economically important conifer species as part of the CoAdapTree project. A constant theme in my research is the combination of theoretical and empirical evolutionary genetics. Being a bridge between these domains helps me as a collaborative scientist work towards **answering fundamental questions in evolutionary biology and conservation genetics**.

1. The genetic architecture of local adaptation and conservation of biodiversity

A major focus of mine has been characterising **the genetic architecture of local adaptation**. The mutations that generate variation in survival and reproduction and ultimately lead to adaptation can have highly variable effects. Some molecular changes have very weak effects on fitness individually, but in aggregate many such changes could have large effects on functional traits. On the other hand, some mutations may have large effects on fitness, and a comparatively small number of them could lead to adaptation. For species that are adapted to highly heterogeneous environments, the genetic architecture of adaptation, the effect sizes and number of genetic changes that underpin adaptive traits, is not well understood. In the face of climate change, **characterising the architecture of adaptation is important for ecologically and economically important species**, such as conifers in British Columbia.

In the Anthropocene, virtually all species on earth have experienced habitat loss and in response the UN Environment Programme's Post-2020 Biodiversity Framework seeks to prevent the loss of more than 10% of all species' genetic diversity. **Losing genetic diversity, particularly that which gives rise to variation in fitness, will make species less able to adapt to changing conditions**. Recently, I contributed to a population genetic analysis of genetic diversity as a function of habitat loss that showed that many species, particularly those already vulnerable to human activity, are on their way to losing more than the 10% specified by the UN ([Exposito-Alonso, Booker, et al. 2022, bioRxiv; in revision at Science](#)). If we are to preserve genetic diversity, particularly the variation that will help species adapt to changing climates, **we need to understand how genetic diversity is distributed in space**.

Aim 1A. Characterising the architecture of local adaptation

Identifying the genetic basis of local adaptation has been the focus of intense research for the past 20 years. A powerful method for identifying locally adaptive genetic variation is the **genotype-environment association (GEA) analysis**, where correlations between environmental variation and allele frequencies are assessed at many sites across the genome. As a post-doc, I developed a novel approach for performing GEA that can identify genomic regions involved in local adaptation ([Booker et al. 2021 bioRxiv; in revision at Mol. Ecol. Res.](#)). The method I developed, called the WZA (<https://github.com/CoAdapTree/WZA>), is more powerful than commonly used GEA tools as it makes use of information across genetically linked sites. However, **distinct evolutionary processes can give rise to similar patterns of genetic variation**, which makes interpretation of population genomic data difficult ([Booker et al. 2021, Evolution Letters](#)). Furthermore, features of the genome such as recombination rate variation can affect the statistical properties of tests for adaptive genetic variation ([Booker et al. 2020, Mol. Ecol.](#)). Building these sources of uncertainty into methods for analysing the genetic architecture of local adaptation is a major frontier in population genetics.

Current work: I am currently in the process of **applying the WZA to population genomic datasets for 8 species of conifers** from North America and Europe (including Douglas fir, Western larch and lodgepole pine). Using these results, I will compare the genetic architecture of local adaptation across the various conifers using a statistical test I have recently developed that can identify genes with evidence for convergent adaptation ([Booker et al. 2022 bioRxiv; in review at Evolution](#)). By applying this method, which I call *PicMin*, to the WZA results for conifers, I may identify genes that have undergone

convergent adaptation among species that began to diverge approximately 200 million years ago. Finding any such genes would indicate fundamental aspects of climate adaptation in conifers and provide foresters with *a priori* gene candidates for breeding programmes. Additionally, *PicMin* is currently being used to look for repeated adaptation by researchers at the University of Calgary (with whom I am collaborating), Charles University, the University of Connecticut and Monash University.

Future work: In population genomics, we use patterns of allele frequency to study evolutionary history in the knowledge that **there is a genealogical process that connects all the individuals we sequence**. The *WZA* represents a step forward for performing GEA, but it is still not the most efficient use of genomic data. Recently, population genetic methods have been developed to estimate “tree-sequences” the genealogical history of a sample at each site in the genome (e.g. *tsinfer*, *ARGweaver*, *Relate*). With these tree-sequences, one could perform GEA analysis directly on the genealogy of a sample. Development of a genealogy based GEA method would be an ideal project for a post-doc as it would require simulation-based analysis for benchmarking (e.g. using *SLiM*), which would involve programming and statistical analysis. Inferring tree-sequences requires phased genomes for numerous individuals. Given the extensive genomic resources of black-cottonwood (*Populus trichocarpa*) it would be an ideal system to apply our method. At ~500Mbp, the *P. trichocarpa* genome is small enough that sequencing many individual genomes is feasible. Generating such datasets would require collaboration between my lab and existing expertise at UBC. This large project that would form the basis of a PhD.

Aim 1B. Incorporating the genetics of local adaptation into conservation

Climate change is progressing rapidly, and large-scale human interventions have been suggested for some species that are particularly at risk. For example, efforts are already underway to incorporate climate change predictions into reforestation policy in Canada (see BC’s [Assisted Migration Adaptation Trial](#)). The central idea is that genetic variation that helps a species thrive in one area of its range could be introduced to other parts that are predicted to face similar climates in the future. However, in a paper that I jointly first-authored, we showed that the long-term success of such initiatives is dependent on the genetic architecture of local adaptation ([Grummer, Booker, et al. 2022, Cons. Biol.](#)). Specifically, that if the architecture of local adaptation is dominated by genetic changes with small effects, the movement of individuals around a species range may only have modest effects on fitness in the long-term. If, however, local adaptation is predominantly caused by genetic changes of large effects, such human interventions may be highly effective. Thus, understanding **the genetic architecture of local adaptation is important for planning conservation interventions**.

Current work: I am contributing to a project that is benchmarking statistical and machine learning tools to identify populations particularly vulnerable to climate change and am on the committee for an MSc student at Simon Fraser University who is studying how understanding the genetics of local adaptation can potentially help conservation decision making for vulnerable species.

Future work: Do selection gradients that vary evenly across a species range (e.g. day length from North to South) lead to the same architectures of local adaptation as selection gradients that are more clustered in space (e.g. regions of high altitude)? This question could be tested using simulations, and would not require the generation of data. It would be suitable for an MSc student or as a chapter of a PhD thesis, or even a working group involving researchers from across Canada. This work would potentially lead to a model of how a species’ range may predict the both the strength and architecture of local adaptation. Furthermore, the ecological community that a species exists in likely contains information that could be used to predict the strength of local adaptation. Developing machine learning methods to analyse community data to identify populations that are vulnerable to climate change would be suitable for a post-doc project.

2. Patterns of genetic diversity and linked selection

A second theme in my work has been to study the effects that natural selection has on patterns of neutral genetic variation. Natural selection can increase or decrease the frequency of genetic variants that affect their carriers' fitness, but also influences evolution at genetically linked sites. Recombination during meiosis breaks apart associations between selected and neutral sites. The effect that the interplay between natural selection and recombination has on neutral genetic variability—**linked selection**—is a major factor shaping patterns of diversity across the genome (Booker *et al.* 2017, *BMC Biol.*). Understanding the origins and maintenance of genetic diversity is a central goal of biology, so developing a full understanding of linked selection is a major aspect of that.

Aim 2A: Extending the standard models of linked selection

There is a sophisticated theoretical literature on the expectations of linked selection. **Connecting theory to the analysis of real data**, however, makes assumptions and requires estimates of important population genetic parameters such as mutation and recombination rates. For example, theoretical models of linked selection assume that such parameters are static—that they do not evolve. However, this assumption has been challenged by recent findings in evolutionary biology.

Current Work: Mounting evidence shows that recombination rates evolve rapidly in some lineages. Recently, in collaboration with Anna Tigano (UBC – Okanagan) and Bret Payseur (University of Wisconsin, Madison), I have examined how **patterns of linked selection change under evolving recombination rates** (Booker *et al.* 2022, *bioRxiv*; in revision at *Proc. B*). I show that the effects of linked selection may be underestimated in lineages that have undergone recent recombination rate evolution.

Future Work: When modelling the contribution of adaptation to patterns of linked selection, it is often assumed that that adaptation only ever acts on *de novo* mutations. However, there is mounting evidence suggesting that adaptation often acts on standing genetic variation or alleles that are introduced via gene flow. By relaxing the assumption of adaptation on *de novo* mutations my lab will examine a) how patterns of diversity vary when a species experiences recurrent adaptation from different sources and b) whether different modes of adaptation are equally likely to occur in different regions of the genome. These projects would be suitable for MSc students or as part of a PhD thesis.

Aim 2B: Estimating the strength of natural selection

A long-standing question in evolutionary biology is how much molecular change in protein-coding versus gene regulatory regions of the genome contributes to adaptation. By **fitting models of linked selection to genetic diversity patterns** we can estimate the history of natural selection that a species experienced. With estimates of the strength of selection we can work towards understanding how phenotypic evolution is influenced by adaptation in different parts of the genome.

Current work: I have been working on an analysis of linked selection in the house mouse. In this work, I show **that positive selection is required to fully explain patterns of linked selection**. Furthermore, that the structure of the genome – e.g. the distribution of protein-coding genes - is a vital parameter when estimating the strength of selection (Booker *et al.*, 2021 *bioRxiv*; in revision at *MBE*).

Future work: In my lab, we will develop maximum-likelihood and/or machine learning approaches to model the genome-wide effects of linked selection that incorporate genome structure. These methods could be used to obtain estimates for the fitness effects of new mutations and would represent a substantial contribution to the field. Developing and applying this method to publicly-available datasets for species such as *Capsella grandiflora* and *Picea abies* would be a full PhD project, or suitable for a post-doc.

Core Values

- To understand and value diverse experiences and learning styles
- To create a collaborative environment for research and learning that is safe and inspirational for all
- To uphold the integrity and excellence of research in evolutionary genetics
- To emphasise skill-building and reproducible research methods
- To grow and improve through reflection and an openness to feedback

My career so far has given me a solid grounding in population and quantitative genetics, statistics and data science. **My main areas of teaching interest are in population and quantitative genetics, statistics and data analysis, bioinformatics and data science.**

Developing a course to teach the fundamentals of forest genetics is very exciting to me. In this course I would teach by comparing simulated datasets, generated using a software tool I have developed (<https://github.com/TBooker/Chinook>), to real DNA sequence data for conifers. The simulations help students build intuition and a deep understanding of the analyses they conduct, while the empirical data analysis allow students to tackle meaningful questions in forestry genetics. I would demonstrate core principles when going from sequence data to biological inference such as genome assembly and read mapping, variant calling and quality control, QTL analysis and GWAS, population structure and population genetic inference. As I mention in my EDI statement, I would incorporate First Peoples Principles of Learning (<http://www.fnesc.ca/first-peoples-principles-of-learning/>) into classes I develop and teach.

Teaching philosophy

There are as many learning styles and preferences as there are students. Furthermore, it is difficult to foresee all of the possible exceptionalities that students may possess. For those reasons, I would attempt to design courses with accessibility and flexibility in mind from the outset. My aim is to provide space for each student to learn the appropriate subject matter in ways that are effective and constructive for them by remaining flexible to a diverse array of learners. Emphasizing learning outcomes is an excellent way to structure classes and courses, but there is a balance to be struck between discrete learning outcomes and an emphasis on critical thinking. Overemphasising learning outcomes may lead to a kind of “learning by rote” style of pedagogy, while a more diffuse self-directed structure may result in some learners being left without a clear idea of how to proceed. **Finding the balance between inquiry-based and learning-outcome directed study is critical** for teaching in the 21st century.

I believe in ground-up teaching, by which I mean that it is important to fully understand the fundamental components of a topic before applying them. By way of illustration, when teaching statistics, I think that it is important for students to understand probability theory and distributions before they perform hypothesis tests.

I emphasize developing transferable skills. Over the last few decades, research in genetics and genomics has become increasingly reliant on skills in computation, coding and statistics. Research tools and software such as the *UNIX* command line environment, *Python* and *R* are increasingly required and are also valuable on the job market. Designing courses that use such tools to communicate and teach scientific concepts **gives students experience with valuable transferable skills which can be applied to a diverse range of careers.**

Teaching experience

I currently co-organise and lead a workshop in Bioinformatics for Evolutionary Biology at UBC (BIOL525D; <https://ubc-biol525d.github.io/>) on an ongoing basis. I developed a pipeline to generate datasets for this workshop using simulations (<https://github.com/TBooker/Chinook>). The simulations allow students to explore bioinformatics and compare their results to a ground truth. BIOL525D is typically offered in-person for graduate students at UBC in Vancouver. During the COVID-19 pandemic, we offered the course online so I have experience with online teaching. **BIOL525D provides an introduction to working at the UNIX command line, high performance computing, bioinformatics and population genomic analysis.**

Throughout the course of my PhD I was heavily involved with the MSc in Quantitative Genetics and Genome Analysis (QGGA) at the University of Edinburgh both as a supervisor and a teacher. For the four years of my PhD, my involvement in QGGA involved tutoring and demonstrating on a graduate level course in probability theory and statistics (<http://www.drps.ed.ac.uk/20-21/dpt/cxpgbi11003.htm>) as well as population and quantitative genetics. I organised and ran exam revision sessions and guest lectures as well as marking term papers. I have also tutored on an undergraduate course in ecology and evolutionary genetics.

Mentorship


I have supervised students at both undergraduate and graduate levels, during my PhD and at UBC during my postdoc. **Here I give testimonials from three former mentees** (reproduced with permission):

"As a mentor, Dr. Booker was patient and attentive, meeting with me weekly as well as at other times when I needed guidance. Dr. Booker was able to explain complex content to me in a way that was clear, and he made sure I had the tools to explore these methods on my own and build from them. But above all, Dr. Booker was a supportive mentor. He was enthusiastic about my project, encouraged me to present my findings in the Department and at local and international conferences, and spent time providing feedback at all stages and on all forms of my work. I am extremely grateful to him for his mentorship and hope to channel many of these admirable qualities as I supervise my own students in the future."

"I met Tom whilst doing my MSc at the University of Edinburgh. He supervised me during my summer research project on the genomics of adaptation of the house mouse. What was most striking about Tom was his passion for his work, and how he was always able to help keep me curious and motivated. Tom was the sort of supervisor who was always available. He would provide valuable insight into whatever questions I might have had, as well as point me in the direction of the most appropriate resources. Tom's patience and kindness made all the difference to me when I was feeling the most overwhelmed. He was a brilliant supervisor. I have no doubt he would be a fantastic asset to your institution."

"I received Tom's thoughtful and compassionate guidance on the design, execution, and reporting of my Directed Studies work. He has by far been the most generous and reliable mentor I have had. Tom

demonstrated his genuine investment in my learning and the success of my project by enthusiastically engaging with all my questions and issues, reliably making time to help me, and explicitly encouraging me on a daily basis. When he helped by writing code that was beyond my abilities, he explained it to me line by line as a learning opportunity. When I completed drafts of my final report, Tom gave me multiple rounds of thoughtful line edits and consultation. In addition to inspiring me personally, Tom's passion and investment in his work makes him an excellent teacher and mentor. Along with providing me immense help with my learning and project, Tom has the sort of personality that makes these experiences really fun and meaningful. His humour, openness, and warmth made me comfortable and our relationship truly generative. As a woman in science, I recognised Tom's efforts to ensure I felt belonging, support, and a sense that I had something to offer. This is invaluable to any early-career scientist in a potentially intimidating environment. In my opinion, Tom has an exceptional balance of professional and interpersonal skills."



The learning environment and community

Throughout my academic career I have been based in excellent research institutions and remain dedicated to excellence within my field. My career goal is to run a research group that follows a program of my own design. To that end, thinking carefully about how one can be the best mentor for individual trainees is critically important. **I would make it clear to all trainees that I work for them and that I am dedicated to helping them succeed in their careers**, whichever direction they choose to take. As leader of a research group, I would build an environment where all members understand what they can expect of me. I would start by writing a "*lab manual*" where we could collaboratively build our group's philosophy, vision and approach to research. This would make me accountable to the members of my research group. I would set aside at least an hour per week for personal meetings with each member of my group. In addition, I would run labgroup meetings where we can discuss each other's work, research papers and practice talks.

There is an increasingly open and frank discussion about mental health and work-life balance in academics. It is important to create a healthy work environment for individuals at all career stages, allowing them to manage their workloads and stress in personally appropriate ways. Everyone handles stress differently, so I think that it is important to give people the freedom to develop strategies that work for them. Furthermore, **it is vital to embrace the fact that there are many different paths that students may take** once they finish their undergraduate or postgraduate degrees. From personal experience, I have perceived a stigma around non-academic careers for graduate students and believe that by openly discussing career paths with my labgroup I can help establish an environment where every member feels able to discuss where they want their careers to go.

I believe that a respectful and collegial working environment is paramount for the success of researchers at all levels. I conduct myself in a way that puts people at ease and allows them to voice their ideas while building a sense of community. For example, during the COVID-19 pandemic, I organised and ran trivia evenings for the Biodiversity Research Centre at UBC to maintain community while we all worked remotely. During my PhD and postdoc I have organised journal clubs and meeting groups, providing a way for me and my colleagues to learn from each other in an interactive way. I think I am a valued member of my department. Faculty at UBC have invited me to be the postdoc representative on multiple committees. I would want to continue to organise and be involved with similar activities in the Department of Forestry & Conservation Science at UBC.

"Education holds the key to reconciliation. It is where our country will heal itself"

Murray Sinclair

There is no doubt that I have benefited from enormous privilege in my life, and while acknowledging this is an important first step, it is not sufficient. **I believe that I have a responsibility to continually reflect on how I have benefited and unwittingly perpetuate an unfair system.** In my current position at UBC, I work, live and raise my family on the traditional, ancestral and unceded territories of the Musqueam, Squamish and Tseil-Waututh First Nations. As a representative of the education system, it is important for me to recognise that this system has been central to a history of abuse and erasure of the Indigenous peoples of Canada. Understanding this history and conducting ourselves in light of it is critical as we work towards reconciliation. I currently serve on the Zoology Equity Diversity and Inclusion (ZEDI) committee at UBC. In ZEDI, we are currently working on a proposal to incorporate EDI concerns into fieldwork planning at UBC. As a member of the faculty in Forestry & Conservation Science I would devote time and energy to similar initiatives.

The aims of a public university are to educate and to expand human knowledge through research. A lack of diversity negatively impacts those aims. Faculties across Canada have fewer researchers who self-identify as female, Indigenous or as members of visible minorities than one would expect based on demography [1]. To create an education system that includes everyone, we need systemic change in the academy. Having role models contributes to whether students from underrepresented groups remain committed to a career in science [2]. Furthermore, a recent study demonstrated that researchers from gender and racial minorities a) produce innovative research at higher rates than the respective majorities and b) that their contributions are frequently undervalued [3]. These results highlight how a diverse research community that draws from many different perspective helps universities achieve their aims and that the contributions of those from underrepresented minorities (URMs) should be amplified. **Addressing the lack of diversity in academia will require coordinated action at all levels of the university system: in hiring and recruitment, in how we teach and in workplace culture.** I will take steps to highlight the contributions of diverse scientists in my teaching materials and approach to hiring and when seeking collaborators or visitors to the department.

It is important to consider how a person's background and identity can influence their success in academia. As the head of a research group, I would be providing mentorship for students and postdocs navigating **a complex and largely unwritten set of rules that underpin academia.** This "hidden curriculum" represents a barrier that needs to be removed. By clearly communicating my expectations for lab members and what lab members can expect of me, I will work towards removing this barrier. It is also important to keep in mind that students may come from a variety of socio-economic backgrounds; first-generation university students are under-represented in academia and often face financial hardship during their studies [4]. By obtaining a lab credit card that lab members could use for research purchases, lab members would not have to make potentially large out-of-pocket expenses. Financial hardship may also mean that students from URMs are less able to obtain early career research experience, which is often obtained via unpaid positions. Furthermore, in biomedical science, female postdocs and URM postdocs have fewer publications than well-represented postdocs [5]. Thus, when recruiting lab members, it is important to prioritize potential over experience.

As a teacher, I would strive to make a learning environment that encourages, engages, and celebrates everyone. **By structuring courses and assignments in ways that incorporate the First Peoples Principles of Learning (FPPL; 6)**, we would benefit all learners. For example, the FPPLs state that *“Learning is holistic, reflexive, reflective, experiential, and relational”*. Making classes experiential by emphasizing active learning benefits everyone and reduces the discrepancy in performance between underrepresented minorities and students belonging to the majority [7]. When teaching genetics and statistics, we necessarily invoke prominent researchers from the early history of the field (e.g. Fisher, Galton and Pearson) who were influential advocates for eugenics, a pseudoscientific movement from the late 19th and 20th centuries with explicitly racist, classist and ableist aims. In many nations around world, eugenic ideas were used to justify hugely damaging policies. In Canada, for example, policies of forced sterilization of Indigenous women, informed by eugenic thinking, were in place as recently as the 1970s [8]. The consequences of such policies are still very much evident today. If we are to teach genetics and statistics, we must do so in the full understanding of how these disciplines have been abused in the past and how they are misused in the present. **I would acknowledge this history in the classroom, rather than sweeping it under the rug or venerating those who perpetuated eugenics.** I would create space for conversation within the classroom that integrates the complexities of how science and identity intersect.

Toxic work habits in academia and university departments are self-perpetuating and act against diversity. There is a general feeling that success in academia is tied to working extremely long hours as summarised in the following quote from a professor at Yale, *“I tell my graduate students and post-docs that if they're working 60 hours per week, they're working less than the full professors”* [9]. Research and teaching are obviously very time-demanding and long hours are often unavoidable, but such working conditions should be considered the exception, not the rule. The COVID-19 pandemic has demonstrated how this particular issue disproportionately affects female researchers [10]. There are many reasons why someone might not be able to commit to more than a typical work week and it seems clear to me that such reasons intersect with diversity. **Working against the notion that academic success depends on extremely long hours would foster a more inclusive environment.**

As we work towards a more equitable future, **actively listening and soliciting feedback on how we are doing as supervisors, teachers and members of the community on an ongoing basis is critical.** I take mentoring seriously. As a supervisor and mentor, I want to contribute to a workplace community that is safe and welcoming for all. When mentoring students, I actively reflect on how I can best serve each individual. In my teaching statement, I include testimonials from students that demonstrate the success I've had, particularly when mentoring women in STEM. I have undertaken EDI training courses, will continue to do so and expect my lab members to do the same. I would actively encourage lab members (including myself) to undertake outreach activities, particularly focussing on high schools, and would emphasize that this is an important part of scholarship.

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