Tom R. Booker

CONTACT INFORMATION

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Institute of Evolutionary Biology
Ashworth Laboratories
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RESEARCH INTERESTS

Theoretical and empirical population genetics, evolution, genomics, bioinformatics, statistical analysis

EDUCATION

University of Edinburgh, Edinburgh, Scotland

Ph.D., Evolutionary Genetics, *Expected:* Autumn 2018

- Thesis Title: *Understanding patterns of genetic diversity in the house mouse genome*
- Supervisors: Professor Peter Keightley and Professor Brian Charlesworth
- As part of my EASTBIO scholarship, I spent 3 months learning bioinformatic approaches and techniques at Fusion Genomics, Vancouver, Canada

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 Dr Rob W. Ness
- In addition to the thesis component, the MSc program consisted of courses on statistical analysis, population genetics, molecular evolution and phylogenetics, as well as linkage analysis.

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
- I undertook a Summer research project on *Mimulus spp.* in Southern and Central Scotland in 2012 with Dr Vallejo-Marin. Courses taken on ecology, conservation biology and genetics. Spent a year on exchange at Simon Fraser University, Vancouver, Canada.

EXPERIENCE & SKILLS

Population genetics

Including: theory, simulations (both forward-time and coalescent), genome scans, demographic analyses, detecting natural selection

Bioinformatics:

Including: Handling high-throughput sequence data, read-mapping, variant calling, *de novo* assembly
Attended "*GATK Best practices for variant discovery*", Edinburgh, UK (2015).

Statistical Analysis:

Including: Linear and non-linear regression, parametric and non-parametric statistics, maximium likelihood estimation.

Computer skills

Scripting: Highly competent in Python, R and Bash, experience with C and Perl
OS: Ubuntu, Windows, Mac OSX
Miscellaneous: Grid Engine clustering systems, git, emacs, ssh/scp, tmux, Microsoft Office

Science communication: Written and verbal

ACADEMIC SERVICE

I have reviewed articles for the following journals:

Ecology and Evolution, *Molecular Biology and Evolution*

Published papers

1. **Booker, T. R.**, Jackson, B. C., & Keightley, P. D. (2017). "Detecting positive selection in the genome." *BMC Biology*, 15:98.
2. **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
3. 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.
4. **Booker, T.**, Ness, R. W., & Charlesworth, D. (2015). "Molecular evolution: breakthroughs and mysteries in Batesian mimicry". *Current Biology*, 25(12), R506-R508.

Papers in preparation

1. **Booker, T. R.**, Charlesworth, B. & Keightley, P. D. (*In preparation*). "Estimating parameters of strong positive selection from patterns of genetic diversity in house mice"
2. **Booker, T. R.**, & Keightley, P. D. (*In preparation*). "Understanding the forces that shape patterns of genetic diversity in the house mouse genome"

Selected Presentations

Estimating the parameters of selective sweeps from patterns of diversity around functional elements in wild house mice Mus musculus castaneus (Oral Presentation)
Population Genetics Group 51 , Bristol, UK — January 2018

Selective sweeps and background selection in the genome of wild house mice, Mus musculus castaneus
ESEB 2017, Groningen, Netherlands — August 2017
Population Genetics Group 50, Cambridge, UK — Jan 2017

Hill-Robertson Interference in wild mice, Mus musculus castaneus (Oral Presentation)
SMBE, Gold Coast, Australia — July 2016
Population Genetics Group 49, Edinburgh, UK — December 2015

Selective sweeps and background selection in the genome of wild house mice, Mus musculus castaneus (Poster)
SMBE, Vienna, Austria — July 2015

Simulating genome evolution in the house mouse: understanding the contribution of Hill-Robertson interference to patterns of genetic diversity (Oral Presentation)
Quantitative Genomics London, UK — May 2015

Academic Honours and Awards

- *Runner up* Best student poster at Population Genetics Group 50 — 2017
- Environment Yes! *Won regional heat - runner up at the final* — Sept 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
- Funding for Undergraduate Summer Project:
  Botanic Society of Scotland and the Society of Biology — Summer 2012
- *Nominated*, Simon Fraser University Student Conservation Prize — May 2012

Teaching

Supervision
Carolina Barata - Master's project - *Now PhD student at the University of St. Andrews*
Brice Lecher - Honour's project - *Now MSc student at Universit Claude Bernard*

Statistics and Data Analysis, MSc course — 2014-2017
Demonstrated in computer practical sessions, ran tutorials on probability theory and statistical analysis and marked term papers

Population and Quantitative Genetics, MSc course 2015-2017
Ran tutorial sessions on population genetic theory

Ecology and Evolutionary Genetics, BSc course 2014-2015
Demonstrated in computer practical sessions on evolutionary biology

Interests

Aside from evolutionary biology I have several hobbies that I try and find time for. I enjoy playing guitar, woodworking (particularly woodturning), helping out around my parents' farm and hill-walking.