

## Tom R. Booker

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CONTACT INFORMATION	<p>t.r.booker@sms.ed.ac.uk mrtombooker@gmail.com</p> <p>Institute of Evolutionary Biology Ashworth Laboratories Edinburgh, EH9 3FL</p>	Tel. +447858896621
RESEARCH INTERESTS	Theoretical and empirical population genetics, biodiversity, evolution, genomics, bioinformatics, statistical analysis	
EDUCATION	<p><b>University of Edinburgh</b>, Edinburgh, Scotland</p> <p>PhD., <a href="#">Evolutionary Genetics</a>, October 2014 - September 2018</p> <ul style="list-style-type: none"><li>- Thesis Title: UNDERSTANDING PATTERNS OF GENETIC DIVERSITY IN THE HOUSE MOUSE GENOME</li><li>- Supervisors: Professor Peter Keightley and Professor Brian Charlesworth</li></ul> <p>MSc., <a href="#">Evolutionary Genetics</a>, 2013 - 2014 (Distinction)</p> <ul style="list-style-type: none"><li>- Thesis Title: SEARCHING FOR BALANCING SELECTION ON A MIMICRY SUPERGENE IN THE BATESIAN MIMIC <i>Papilio polytes</i></li><li>- Supervisors: Professor Deborah Charlesworth and Dr Rob W. Ness</li></ul> <p><b>University of Stirling</b>, Stirling, Scotland</p> <p>BSc Hons, <a href="#">Ecology</a>, 2009 - 2013 (First Class)</p> <ul style="list-style-type: none"><li>- Dissertation Title: AN INVESTIGATION INTO THE FITNESS AND DISTRIBUTION OF A NEWLY DISCOVERED ALLOPOLYPLOID SPECIES, <i>Mimulus peregrinus</i></li><li>- Supervisor: Dr Mario Vallejo-Marin</li></ul>	
EXPERIENCE & SKILLS	<p>Population genetics</p> <p>Including: theory, simulations (both forward-time and coalescent), genome scans, demographic analyses, detecting natural selection</p> <p>Bioinformatics:</p> <p>Including: Handling high-throughput sequence data, read-mapping, variant calling, <i>de novo</i> assembly</p> <p>Attended “<i>GATK Best practices for variant discovery</i>”, Edinburgh, UK (2015).</p> <p>Statistical Analysis:</p> <p>Including: Linear, non-linear and mixed models, parametric and non-parametric statistics and maximum likelihood estimation.</p> <p>Computer skills</p> <p>Scripting: Highly competent in Python, R and Bash, experience with C and Perl</p> <p>OS: Ubuntu, Windows, Mac OSX</p> <p>Miscellaneous: Grid Engine clustering systems, git, emacs, ssh/scp, tmux, Microsoft Office</p> <p>Science communication: Written and verbal</p>	
ACADEMIC SERVICE	<p>I have reviewed articles for the following journals:</p> <p><i>Ecology and Evolution</i>, <i>Molecular Biology and Evolution</i></p> <p>I started and organised a journal club on classic population genetic papers at the University of Edinburgh in 2017</p>	

PUBLISHED PAPERS	<ol style="list-style-type: none"> <li>1. <b>Booker, T. R.</b>, &amp; Keightley, P. D. (<i>Accepted</i>). “Understanding the factors that shape patterns of nucleotide diversity in the house mouse genome”. <i>Molecular Biology and Evolution</i></li> <li>2. <b>Booker, T. R.</b>, Jackson, B. C., &amp; Keightley, P. D. (2017). “Detecting positive selection in the genome.” <i>BMC Biology</i>, 15:98.</li> <li>3. <b>Booker, T. R.</b>, Ness, R. W., &amp; Keightley, P. D. (2017). “The recombination landscape in wild house mice inferred using population genomic data”. <i>Genetics</i>, 207(1) 297-309</li> <li>4. Keightley, P. D., Campos, J. L., <b>Booker, T. R.</b>, &amp; Charlesworth, B. (2016). “Inferring the frequency spectrum of derived variants to quantify adaptive molecular evolution in protein-coding genes of <i>Drosophila melanogaster</i>.” <i>Genetics</i>, 203(2), 975-984.</li> <li>5. <b>Booker, T.</b>, Ness, R. W., &amp; Charlesworth, D. (2015). “Molecular evolution: breakthroughs and mysteries in Batesian mimicry”. <i>Current Biology</i>, 25(12), R506-R508.</li> </ol>
PAPERS IN PREPARATION	<ul style="list-style-type: none"> <li>• <b>Booker, T. R.</b>, Jackson, B. Craig, R. Charlesworth, B. &amp; Keightley, P. D. (<i>In preparation</i>). “Estimating parameters of strong positive selection from patterns of genetic diversity in house mice”</li> </ul>
ACADEMIC HONOURS AND AWARDS	<ul style="list-style-type: none"> <li>• <i>Runner up</i> Best student talk at Population Genetics Group 51 2018</li> <li>• <i>Runner up</i> Best student poster at Population Genetics Group 50 2017</li> <li>• Environment Yes! <i>Won regional heat - runner up at the final</i> Sept 2016</li> <li>• EASTBIO Doctoral Training Partnership Studentship 2014-2018</li> <li>• Genetics Society, Sir Kenneth Mather Memorial Prize 2013/2014</li> <li>• University of Edinburgh, Douglas Falconer Award, best MSc dissertation 2013/2014</li> <li>• Funding for Undergraduate Summer Project: Botanic Society of Scotland and the Society of Biology Summer 2012</li> <li>• <i>Nominated</i>, Simon Fraser University Student Conservation Prize May 2012</li> </ul>
TEACHING	<p>Supervision:</p> <p>S-A. Xerri - Master’s project - <i>Now PhD student at the Max Planck Institute</i></p> <p>C. Barata - Master’s project - <i>Now PhD student at the University of St. Andrews</i></p> <p>B. Lecher - Honour’s project - <i>Now MSc student at Universit Claude Bernard</i></p> <p>Tutoring and Demonstrating</p> <p>Statistics and Data Analysis, MSc course 2014-2017  <i>Demonstrated in computer practical sessions, ran tutorials on probability theory and statistical analysis and marked term papers</i></p> <p>Population and Quantitative Genetics, MSc course 2015-2017  <i>Ran tutorial sessions on population genetic theory</i></p> <p>Ecology and Evolutionary Genetics, BSc course 2014-2015  <i>Demonstrated in computer practical sessions on evolutionary biology</i></p>
SELECTED PRESENTATIONS	<p><b>January 2018</b> - Population Genetics Group 51, Bristol, UK (Oral Presentation)  <i>Estimating the parameters of selective sweeps from patterns of diversity around functional elements in wild house mice</i> <i>Mus musculus castaneus</i></p> <p><b>August 2017</b> - ESEB 2017, Groningen, Netherlands (Poster)  <i>Selective sweeps and background selection in the genome of wild house mice</i>, <i>Mus musculus castaneus</i></p> <p><b>January 2017</b> - Population Genetics Group 50, 2017, Cambridge, UK (Poster)  <i>Selective sweeps and background selection in the genome of wild house mice</i>, <i>Mus musculus castaneus</i></p>

**July 2016** - SMBE, Gold Coast, Australia (Oral Presentation)  
*Hill-Robertson Interference in wild mice, Mus musculus castaneus*

**December 2015** - Population Genetics Group 49, Edinburgh, UK (Oral Presentation - Invited)  
*Hill-Robertson Interference in wild mice, Mus musculus castaneus*

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

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

#### 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.