Benjamin L. Moore
Bioinformatics PhD

ben@blm.io
+44 (0)7854 212484

Education

PhD Bioinformatics (2012-15) *University of Edinburgh*, Supervised by Colin Semple and Stuart Aitken

During my PhD I analysed a diverse array of publicly-available biological datasets to uncover new insights into the epigenetics underlying higher-order chromatin stucture. I integrated Hi-C and other chromosome conformation capture experimental results with...

MSc Bioinformatics and theoretical systems biology (2011-12) *Imperial College London*, Distinction

My MSc included both taught (statistics, programming and biology) components, as well as three research projects. These included a software engineering project where I helped develop a stochastic Petri net library in Python with Prof. Michael Stumpf (Sputnik), and another project (since published) in which I applied Guassian mixture modelling to a long-standing problem in structural bioinformatics.

BSc Biology (2008-11) *University of York*, First class honours

My undergradute provided a broad education in biological sciences. My dissertation was a bioinformatics project in Prof. Peter Young's lab, looking at the evolution of toxin-antitoxin systems in *Rhizobia* genomes.

Publications

Integrative modelling reveals the principles of multi-scale chromatin boundary formation in human nuclear organization. (2015) **Moore, BL** *et al.* (Submitted).

High–quality protein backbone reconstruction from alpha carbons using Gaussian mixture models. (2013) **Moore, BL** *et al.* Journal of Computational Chemistry 34 (22), 1881-1889. doi:10.1002/jcc.23330

Rfam: Wikipedia, clans and the "decimal" release. (2011) PP Gardner, J Daub, J Tate, **Moore, BL** *et al.* Nucleic acids research 39 (S1), D141-D145. doi:10.1093/nar/gkq1129

Placements

Wellcome Trust Sanger Institute, Cambridge.

During my undergraduate degree I spent two summers working in Alex Bateman's group on the Rfam database and supporting materials.

Presentations

Talks   **Posters**   **Tutorials**

4th Edinburgh bioinformatics meeting
EdinbR: The Edinburgh R usergroup (various)
Edinburgh Psychology R-users
Several research talks within the institute

Integrative modelling of higher order chromatin structure. *Genome Informatics* 2013 CSHL, NY, USA; *Keystone Epigenomics* 2015 Colorado, USA.
Unravelling higher order chromatin structure. *EpiGeneSys* 2013, Cambridge, UK.

WikiProject Computational Biology, ISMB 2014, Boston USA with Daniel Mietchen (half day), with grant support from the Wikimedia Foundation and ISCB.

Technical

R and Bioconductor	Python and Biopython	LaTeX
Git / Mercurial	UNIX	Bash
Emacs	Inkscape	Mediawiki
Grid computing (SGE / PBS)	HTML / CSS / Javascript	

Projects

EdinbR

I co-founded a usergroup for the R programming language in Edinburgh called EdinbR. I help to organise our monthly meetings and run our website: edinbr.org. Our meetings attract 30-50 statisticians, data scientists and developers for talks and discussion about the R language and its applications.

Summer Data Challenge

I entered Imperial College's Summer Data Challenge competition, where entrants analysed a given dataset and then proposed a startup idea based on their results. I developed a modelling technique to select housing areas for investment and was awarded third place: £2,000 and startup support from Imperial Create Lab.

Blog

I author a data science blog at blm.io where I apply R and Python to open datasets and write-up any interesting results. My posts have been picked up by sites including FiveThirtyEight, BuzzFeed, AVclub, io9 and more, and also led to being an invited blogger at the Huffington Post.

Awards

MRC Capacity building scholarship (fees + enhanced stipend) for my PhD
MRC Full postgraduate scholarship (fees + stipend) for MSc
ISCB computational biology Wikipedia competition: second place prizewinner
Summer data challenge: third place prizewinner

User profiles

Github: blmoore	Twitter: @benjaminlmoore	Wikipedia: Ben Moore
Domains: blm.io, edinbr.org	Biostars: Ben	StackOverflow: blmoore

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References

Available on request.