Benjamin L. Moore

Bioinformatics PhD and data scientist

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Currently

I'm a Bioinformatics Scientist at Illumina, based at their R&D site near Cambridge, UK. Here I develop software and use data science, machine learning and statistical programming to analyse large volumes of high-throughput sequencing data.

Employment

2015– **Illumina, Inc.** Bioinformatics scientist (data scientist and statistical programmer)

Education

2012–15 **University of Edinburgh** Bioinformatics PhD (supervisors: Colin Semple and Stuart Aitken). My thesis was titled Unravelling higher order chromatin organisation through statistical analysis and is available through the Edinburgh Research Archive.

2011–12 **Imperial College London** MSc Bioinformatics and Theoretical Systems Biology (Distinction)

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

Presentations

Tutorials 2014 WikiProject Computational Biology half-day tutorial (ISMB, Boston, USA)

Talks 2015 EdinbR: The Edinburgh R usergroup (various)
MRC IGMM research seminars and section meetings (various)

2014 Unravelling higher order chromatin structure (4th Edinburgh Bioinformatics meeting, Edinburgh, UK)
blogR: pop data analysis and R for the web (Psychology R-users, Edinburgh, UK)

Posters 2015 Keystone Epigenomics (Keystone CO, USA)

2014 ISMB (Boston MA, USA)
Genome informatics (Cambridge, UK)
Chromatin: From nucleosomes to chromosomes (Cambridge, UK)

2013 Genome informatics (CSHL NY, USA)
EpiGeneSys (Cambridge, UK)

Publications

2017 Peluso S, Douglas A, Hill A, De Angelis C, **Moore BL** et al. Fibroblast growth factors (FGFs) prime the limb specific Shh enhancer for chromatin changes that balance histone acetylation mediated by E26 transformation-specific (ETS) factors. eLife, 6: e28590.

Eberle MA, Fritzilas E, Krusche P, Källberg M, **Moore BL** et al. A reference data set of 5.4 million phased human variants validated by genetic inheritance from sequencing a three-generation 17-member pedigree. Genome Research, 27:157-164.

2016 Yu N, Nützmann H-W, MacDonald JT, **Moore B** et al. Delineation of metabolic gene clusters in plant genomes by chromatin signatures. Nucleic Acids Research,

44(5):2255-2265.

2015 **Moore BL** et al. Integrative modeling reveals the principles of multi-scale chromatin boundary formation in human nuclear organization. Genome Biology, 16:110.

Fraser J, Ferrai C, Chiariello AM, Schueler M, Rito T, Laudanno G, Barbieri M, **Moore BL** et al. Hierarchical folding and reorganization of chromosomes are linked to transcriptional changes in cellular differentiation. Molecular systems biology, 11:852.

2013 **Moore BL** et al. High–quality protein backbone reconstruction from alpha carbons using Gaussian mixture models. Journal of computational chemisty, 34(22):1881-9.

2011 Gardner PP, Daub J, Tate J, **Moore BL** et al. Rfam: Wikipedia, clans and the "decimal" release. Nucleic acids research, 39(S1):D141-5.

Non-academic

2014 Pieces in The Huffington Post (US): Here Are the Most Overrated and Underrated Movies of All Time; Celebrity Twitter Followers, by Gender (huffingtonpost.com/benjamin-moore)

2006– Articles for English Wikipedia: European Nucleotide Archive, RNA thermometer, Toxin-antitoxin system and more (en.wikipedia.org/wiki/User:Ben_Moore).

Technical skills

R	HTML and CSS	Cluster computing
Python	LaTeX	Docker
Javascript (incl. Typescript, Angular)	Bash	AWS
Go	Git / Mercurial	
	UNIX	

Areas of expertise

Bioinformatics	Machine learning	Software development
Statistics	Data visualisation	NGS and variant calling

Projects

github My personal github account hosts my hobby development projects as well as listing contributions to open source tools. Examples include: shiny apps blackspot and shinybrot, as well as an R package hosted by CRAN (mandelbrot).

blog I write a data science blog at blm.io where I apply R and Python to open datasets and write-up the results. My posts have been featured by sites including FiveThirtyEight, BuzzFeed, AVclub, io9 and more, and also led to being an invited blogger at the Huffington Post. My original wordpress blog (benjaminlmoore.wordpress.com) has received over 150,000 unique visitors from 180 countries.

EdinbR I co-founded a usergroup for the R programming language in Edinburgh called EdinbR. I helped to organise our monthly meetings and built 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. We're sponsored by Revolution Analytics and have an organisational github account at github.com/EdinbR.

datarea 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. My entry can be seen at blm.io/datarea and the code is shared on my github account.

Awards

MRC Capacity building scholarship (PhD fees + enhanced stipend)
MRC Full postgraduate scholarship (MSc fees + stipend)
ISCB computational biology Wikipedia competition 2013
(doi:10.1371/journal.pcbi.1003242; 2nd place)
Imperial Create Lab's "Summer data challenge" (summerdatachallenge.com; 3rd place)
Individual engagement grant from the Wikimedia Foundation to attend ISMB 2014
Training accreditation for Wikimedia UK, the national chapter of the Wikimedia Foundation
Front cover design selected for J. Comp. Chem. (34:22) (doi:10.1002/jcc.23388)

Placements

2010–11 **Wellcome Trust Sanger Institute** (Cambridge, UK) Worked for two summers on the Rfam database (rfam.xfam.org) in the Bateman group

Links

✉ ben@blm.io	in LinkedIn	ᵍ Google scholar
⌂ blmoore	StackOverflow	ⓘ ORCiD
🐦 benjaminlmoore	W Wikipedia Userpage	◎ figshare

References

Available on request.