

KEVIN RUE-ALBRECHT

Computational Biologist (Dipl. Ing., Ph.D.)





I am a computational biologist at the [University of Oxford](#).

My research interests in computational biology include software engineering best practices, DevOps, single-cell genomics, and interactive data visualization. I particularly enjoy using and contributing R packages part of the [Bioconductor project](#). A list of software packages that I maintain or contributed to is available on the "Software" page of my [website](#).


My academic research primarily explores the host immune response to infectious diseases, inflammation, and self-antigens.



EDUCATION

- 2015 • **University College Dublin**
Ph.D. in Computational Infection Biology  Dublin, Ireland
- Thesis:** Comparative systems biology analyses of the bovine transcriptional response to species of the *Mycobacterium* genus.
- [Bioconductor](#) package for [Gene Ontology \(GO\)](#) analysis of gene expression data ( [GOexpress](#)).
- 2011 • **École Polytechnique Universitaire Polytech Nice-Sophia**
Ingénieur diplômé, MSc  Sophia Antipolis
- Pharmacology
 - Environmental Safety
 - Biotechnology
 - Bioinformatics
 - Toxicology
- Major:** Bioinformatics and Modelling for Biology
- 2008 • **CPGE BCPST Vêto - Lycée Jean Rostand**
Class Préparatoire aux Grandes Écoles  Strasbourg, France
- Biology
 - Earth Sciences
 - Chemistry
 - Mathematics
 - Physics
 - Programming

RESEARCH EXPERIENCE

- 2020-present • **Postdoctoral Researcher - Computational Biologist**
[Sims Group](#), [MRC WIMM Centre for Computational Biology](#), [University of Oxford](#)  Oxford, UK
- Development and delivery of training materials to cohorts of trainees as part of the [Oxford Biomedical Data Science Training Programme](#).
 - Development of novel bioinformatics tools and pipelines following software engineering best practices.
 - Contribution to scientific reports and publications.

CONTACT INFO

 kevinrue67@gmail.com

 github.com/kevinrue

For more information, please contact me via email.

SKILLS

Experienced in statistical analysis, genomics, and software engineering.

Full experience with next generation sequencing data analysis.

Highly skilled in R, Bash, Python, with experience in C#, JavaScript, HTML, SQL, PHP, CSS, LaTeX, Perl, and Matlab.

This resume was made with the R package [pagedown](#).

A PDF version is available [here](#).

Last updated on 2020-08-06.

2017- 2020	<ul style="list-style-type: none"> Postdoctoral Researcher - Computational Biologist Sansom Group, Kennedy Institute of Rheumatology, University of Oxford <div> Oxford, UK </div> <ul style="list-style-type: none"> Molecular pathogenesis of inflammatory bowel disease, in collaboration with the Powrie Group. Role of thymic epithelial cells in T-cell development, in collaboration with the Holländer Group and Ponting Group. Contribution to software pipelines for single-cell genomics data analysis (sansomlab/tenx). Bioconductor package for interactive exploration of SummarizedExperiment objects (iSEE). R package for the analysis of ChIP-seq data (kevinrue/deeperTools).
2016 2017	<ul style="list-style-type: none"> Postdoctoral Researcher - Computational Biologist Ratcliffe group, Target Discovery Institute, University of Oxford <div> Oxford, UK </div> <ul style="list-style-type: none"> Management and quality control of genomics data for analyses of DNA targeted resequencing, ChIP-seq, RNA-seq in the context of oxygen sensing and renal cancer. Prototype of MeteorJS application to manage sequencing data (kevinrue/Seqbook).
2015 2016	<ul style="list-style-type: none"> Research associate - Bioinformatics & Biostatistics Prof. Martin Wilkins's Group, Imperial Centre for Translational and Experimental Medicine, Imperial College London <div> London, UK </div> <ul style="list-style-type: none"> Integration of genetic variation, proteomic and metabolomics data and associated deep phenotype data, in collaboration with the Morrell Group. Bioconductor package for the analysis of genetic variants (TVTB).
Apr. 2012 Jul. 2012	<ul style="list-style-type: none"> Ph.D. student - Computational Infection Biology, rotation 3 Prof. James O'Gara's Group, UCD Science Centre North <div> Dublin, Ireland </div> <ul style="list-style-type: none"> Evaluation of a gene candidate underlying <i>Staphylococcus aureus</i> antibiotic resistance by Sanger sequencing and biofilm assay
Jan. 2012 Apr. 2012	<ul style="list-style-type: none"> Ph.D. student - Computational Infection Biology, rotation 2 Dr Neil Ferguson's Group, UCD Conway Institute <div> Dublin, Ireland </div> <ul style="list-style-type: none"> Expression and purification of a Hepatitis B protein construct for experimental screening of interacting drug fragments.
Sep. 2011 Jan. 2012	<ul style="list-style-type: none"> Ph.D. student - Computational Infection Biology, rotation 1 Shields Lab, UCD Complex and Adaptive Systems Laboratory (CASL) <div> Dublin, Ireland </div> <ul style="list-style-type: none"> <i>In silico</i> structure-based prediction of <i>Mycobacterium bovis</i> epitopes in cattle (supervisor: Dr. Anthony Chubb).
Jun. 2010 Sep. 2010	<ul style="list-style-type: none"> Research Assistant - Computational Biology, intern Shields Lab, University College Dublin <div> Dublin, Ireland </div> <ul style="list-style-type: none"> Computational analysis of structural disorder in <i>Saccharomyces cerevisiae</i> interacting proteins.

Jul. 2009
|
Aug. 2009

● **Research Assistant, intern**

INSERM, Unité Mixte de Recherche S725, Biologie des Cellules
Dendritiques Humaines

📍 Strasbourg, France

- Recombinant protein expression of MHC class II molecules in HeLa cells.



PROFESSIONAL EXPERIENCE

Apr. 2011
|
Jul. 2011

● **Software developer, intern**

[MEDIT S.A.](#)

📍 Palaiseau, France

- Implementation of structurally-constrained multiple alignment of protein sequences for the commercial software [MED-SuMo](#).



TEACHING EXPERIENCE

2020

● **Intuitive interactive data exploration with iSEE**

[Swiss Institute of Bioinformatics](#)

📍 Zoom (online)

Co-organizer of a [2h30 workshop](#) at the [SIB Days 2020](#).

2019

|
present

● **R Code Clinic**

[Big Data Institute](#), [University of Oxford](#)

📍 Oxford, UK

Volunteer to sit with individuals and assist them with any R problems they need help with. Website: <https://bdioclub.netlify.com/>.

2019

● **Interactive visualisation of SummarizedExperiment objects using iSEE**

[Bioconductor conference 2019](#)

📍 New York, USA

Co-instructor of a [2-hour workshop](#) at the [Bioconductor conference 2019](#).

2014

● **Molecular Genetics and Biotech**

[University College Dublin](#)

📍 Dublin, Ireland

Teaching assistant of [BMOL20090](#) at [University College Dublin](#).

2014

● **Agricultural Microbiology**

[University College Dublin](#)

📍 Dublin, Ireland

Teaching assistant of [MICR20010](#) at [University College Dublin](#).



FUNDING AND AWARDS

2019

● **RStudio Shiny Contest**

[Winner](#) of the “Most technically impressive” prize.

2019

● **Bioconductor 2019 conference**

Conference fee waiver and travel grant for [BioC 2019](#).

📍 New York, USA

- Instructor of a [2-hour workshop](#) at the [Bioconductor conference 2019](#).
- Co-organiser of the Special Interest Group (SIG) [Extending gene set and signature representations](#).

- 2017 ● **Bioconductor 2017 conference**
Conference fee waiver and travel grant for [BioC 2017](#). 📍 Boston, USA
 - Flash presentation for [TVTB](#).
 - Flash presentation for [GOexpress](#).
- 2015 ● **ISMB/ECCB conference**
Conference fee waiver 📍 Dublin, Ireland
[23rd Annual International Conference on Intelligent Systems for Molecular Biology \(ISMB\) and 14th European Conference on Computational Biology \(ECCB\)](#). Special Interest Group (SIG) [Bioinformatics Open Source Conference \(BOSC\)](#).
- 2014 ● **5th Annual PhD Symposium in Computational Biology & Innovation**
Best oral presentation 📍 Dublin, Ireland
- 2011 ● **Wellcome Trust Four-year PhD Programme**
Computational Infection Biology 📍 Dublin, Ireland
Title: Transcriptome analysis of the bovine macrophage response to *Mycobacterium tuberculosis* complex strains.



ORGANISER AND CHAIR

- 2019 ● **Special Interest Group**
[Bioconductor conference 2019](#). 📍 New York, USA
Topic: [Extending gene set and signature representations](#).
- 2018-2020 ● **Genomics Forum**
[Kennedy Institute of Rheumatology, University of Oxford](#) 📍 Oxford, UK
Coordinator of a weekly meeting to present and discuss ongoing projects in the institute.
- 2013 | 2014 ● **Bioinformatics Seminar**
[University College Dublin](#) 📍 Dublin, Ireland
Co-organiser of a weekly meeting to present and discuss ongoing projects in the university.
- 2012 ● **Computational Biology and Innovation PhD Symposium**
[University College Dublin](#) 📍 Dublin, Ireland
Co-organiser in charge of sponsorships and the abstract book.



TRAINING AND COURSES

- 2016 ● **Machine Learning**
[Coursera](#), [Stanford University](#)
- 2015 ● **Bioconductor for Genomic Data Science**
[Coursera](#), [Johns Hopkins University](#)
This course is part of the [Genomic Data Science Specialization](#).

- 2015 ● **Command Line Tools for Genomic Data Science**
[Coursera, Johns Hopkins University](#)
 This course is part of the [Genomic Data Science Specialization](#).
- 2015 ● **Python for Genomic Data Science**
[Coursera, Johns Hopkins University](#)
 This course is part of the [Genomic Data Science Specialization](#).
- 2015 ● **Statistics for Genomic Data Science**
[Coursera, Johns Hopkins University](#)
 This course is part of the [Genomic Data Science Specialization](#).
- 2014 ● **Teaching in Higher Education**
[University College Dublin](#) 📍 Dublin, Ireland
- 2013 ● **Hot Topics in Food and Nutrition Research**
[University College Dublin](#) 📍 Dublin, Ireland
- 2013 ● **Sequence Data Analysis Training**
 Wageningen Institute of Animal Sciences 📍 Wageningen, Netherlands
- 2013 ● **Network Analysis in Systems Biology**
[Coursera, Icahn School of Medicine at Mount Sinai](#)
- 2012 ● **Introductory Statistics using R for Computational Biologists**
[University College Dublin](#) 📍 Dublin, Ireland
- 2012 ● **Python Programming for Computational Biologists**
[University College Dublin](#) 📍 Dublin, Ireland
- 2012 ● **Online Research Skills for Computational Biologists**
[University College Dublin](#) 📍 Dublin, Ireland
- 2012 ● **Advances in Infection Biology**
[University College Dublin](#) 📍 Dublin, Ireland
- 2012 ● **Bioinformatics Research Seminars**
[University College Dublin](#) 📍 Dublin, Ireland
- 2012 ● **Genomics – Principles and Practical Applications**
[University College Dublin](#) 📍 Dublin, Ireland



PROFESSIONAL MEMBERSHIPS

- 2012 | present ● **International Society for Computational Biology (ISCB)**
<https://www.iscb.org/>



PEER REVIEW

- 2019 ● **OUP Bioinformatics**
<https://academic.oup.com/bioinformatics>
 1 article
- 2019 ● **Journal of Open Source Software**
<https://joss.theoj.org/>
 1 article



SELECTED PUBLICATIONS AND POSTERS

- 2019 • **Orchestrating single-cell analysis with Bioconductor.**
Nat Methods.
Amezquita, R. A., A. T. L. Lun, E. Becht, V. J. Carey, L. N. Carpp, L. Geistlinger, F. Marini, **K. Rue-Albrecht**, D. Risso, C. Soneson, L. Waldron, H. Pages, M. L. Smith, W. Huber, M. Morgan, R. Gottardo and S. C. Hicks
- 2019 • **The Short Chain Fatty Acid Butyrate Imprints an Antimicrobial Program in Macrophages**
Immunity.
Schulthess, J., S. Pandey, M. Capitani, **K. C. Rue-Albrecht**, I. Arnold, F. Franchini, A. Chomka, N. E. Iltott, D. G. W. Johnston, E. Pires, J. McCullagh, S. N. Sansom, C. V. Arancibia-Carcamo, H. H. Uhlig and F. Powrie
- 2018 • **iSEE: Interactive SummarizedExperiment Explorer.**
F1000Res.
Rue-Albrecht, K., F. Marini, C. Soneson and A. T. L. Lun



CONFERENCE PRESENTATIONS

- 2019 • **Bioconductor**
Oral presentations. New York, USA
• [Talk](#): Interactive and reproducible visualization of SummarizedExperiment objects.
• [Workshop](#): Interactive visualization of SummarizedExperiment objects with iSEE.
• [Special Interest Group](#): Extending gene set and signature representations.
- 2018 • **Genome Informatics**
Poster. Cambridge, UK
Title: Promiscuous expression of lincRNAs in medullary thymic epithelial cells
- 2017 • **NGS-SIG - Single-cell RNA-seq**
Oral presentation. Oxford, UK
Title: Variability of human dendritic cells responses to differentially invasive Salmonella strains at single-cell level.
- 2017 • **Bioconductor**
Oral presentations. Boston, USA
• [GOexpress](#): Visualise and summarise gene expression data using Gene Ontology
• [TVTB](#): The VCF Tool Box: an effort to summarise and visualise variants

- 2015 ● **Quantitative Genomics**
Poster.  London, UK
Title: GOexpress: A R/Bioconductor package for the identification and visualisation of robust gene ontology signatures through supervised learning of gene expression data.
- 2015 ● **BOSC - ISMB/ECCB conference**
Oral presentation and poster.  Dublin, Ireland
• [Talk](#) GOexpress: A R/Bioconductor package for the identification and visualisation of robust gene ontology signatures through supervised learning of gene expression data.
• [Poster](#) GOexpress: Identify and visualise gene expression using supervised learning and Gene Ontology.
- 2014 ● **Society for General Microbiology (SGM)**
Poster.  Dublin, Ireland
Title: Microarray analysis of the bovine macrophage response to *Mycobacterium bovis*, *M. bovis* Bacille Calmette-Guérin (BCG) and *M. avium* subspecies *paratuberculosis*.
- 2014 ● **Virtual Institute of Bioinformatics & Evolution (VIBE)**
Oral presentation.  Carlow, Ireland
Title: The quest for meaningful visualisation of genome-wide expression data.
- 2014 ● **EMBO conference: Microbiology after the genomics revolution - Genomes 2014**
Poster.  Paris, France
Title: Transcriptome analysis reveals differential innate immune response to members of the *Mycobacterium tuberculosis* complex.
- 2014 ● **The Acid Fast Club, Summer Meeting**
Oral presentation.  Berlin, Germany
Title: Transcriptome analysis reveals differential innate immune response of bovine macrophages to strains of the *Mycobacterium tuberculosis* complex.
- 2014 ● **UCD Conway Festival of Research & Innovation**
Poster.  Dublin, Ireland.
Title: Transcriptome analysis reveals differential innate immune response to members of the *Mycobacterium tuberculosis* complex.
- 2014 ● **Wellcome Trust Final Year PhD Students' Meeting**
Poster.  London, UK
Title: Transcriptome analysis reveals differential innate immune response to members of the *Mycobacterium tuberculosis* complex.
- 2013 ● **Association of Veterinary Teachers and Research Workers (AVTRW)**
Oral presentation.  Hillsborough, Ireland
Title: Systems Biology of Host-Pathogen Interactions and Bovine Tuberculosis - Differential transcriptional response of bovine monocyte-derived macrophages following different mycobacterial infections

- 2013 ● **Animal Health Ireland Workshop & Conference**
Poster. 📍 Rochestown Park Hotel, Cork
Title: Microarray analysis of the bovine macrophage response to *Mycobacterium bovis*, *M. bovis* Bacille Calmette-Guérin (BCG) and *M. avium* subspecies *paratuberculosis*.
- 2013 ● **Virtual Institute of Bioinformatics and Evolution (VIBE)**
Oral presentation. 📍 Galway, Ireland
Title: Systems Biology of Host-Pathogen Interactions and Bovine Tuberculosis - Differential transcriptional response of bovine monocyte-derived macrophages following different mycobacterial infections.
- 2013 ● **Computational Biology & Innovation Symposium**
Poster. 📍 Dublin, Ireland
Title: Microarray analysis of the bovine macrophage response to *Mycobacterium bovis*, *M. bovis* Bacille Calmette-Guérin (BCG) and *M. avium* subspecies *paratuberculosis*.
- 2013 ● **Dublin Academy of Pathogenomics & Infection Biology (DAPI)**
Poster. 📍 Dublin, Ireland
Title: Microarray analysis of the bovine macrophage response to *Mycobacterium bovis*, *M. bovis* Bacille Calmette-Guérin (BCG) and *M. avium* subspecies *paratuberculosis*.

🗣️ LANGUAGE

- **French**
Native.
- **English**
Fluent. TOEIC score 970.
- **Italian**
Working knowledge.
- **Spanish**
Limited. Used to be fluent though 😊.
- **German**
Limited. Haven't practiced in a long time.