# 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**

CPGE BCPST Véto - Lycée Jean Rostand 2008

Class Préparatoire aux Grandes Écoles

Strasbourg, France

Biology

 Earth Sciences Mathematics

Chemistry

Physics

Programming

École Polytechnique Universitaire Polytech Nice-Sophia 2011 Ingénieur diplômé, MSc Sophia Antipolis

- Pharmacology
- · Environmental Safety
- Biotechnology
- Bioinformatics

- Toxicology
- Major: Bioinformatics and Modelling for Biology

2015

**University College Dublin** 

Ph.D. in Computational Infection Biology

Oublin, 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).

# RESEARCH EXPERIENCE

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.

Jun. 2010 Sep. 2010 Research Assistant - Computational Biology, intern Shields Lab, University College Dublin Oublin, Ireland

· Computational analysis of structural disorder in Saccharomyces cerevisiae interacting proteins.

### 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 2020-04-02.

Ph.D. student - Computational Infection Biology, rotation 1 Sep. 2011 Shields Lab, UCD Complex and Adaptive Systems Laboratory Jan. 2012 (CASL) Oublin, Ireland • In silico structure-based prediction of Mycobacterium bovis epitopes in cattle (supervisor: Dr. Anthony Chubb). Ph.D. student - Computational Infection Biology, rotation 2 Jan. 2012 Dr Neil Ferguson's Group, UCD Conway Institute Oublin, Ireland Apr. 2012 · Expression and purication of a Hepatitis B protein construct for experimental screening of interacting drug fragments. Ph.D. student - Computational Infection Biology, rotation 3 Apr. 2012 Prof. James O'Gara's Group, UCD Science Centre North Jul. 2012 Oublin, Ireland • Evaluation of a gene candidate underlying Staphylococcus aureus antibiotic resistance by Sanger sequencing and biofilm assay Research associate - Bioinformatics & Biostatistics 2015 Prof. Martin Wilkins's Group, Imperial Centre for Translational and 2016 Experimental Medicine, Imperial College London O London, UK · 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). Postdoctoral Researcher - Computational Biologist 2016 Ratcliffe group, Target Discovery Institute, University of Oxford 2017 Oxford, UK · 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). Postdoctoral Researcher - Computational Biologist 2017-2020 Sansom Group, Kennedy Institute of Rheumatology, University of Oxford Oxford, UK • 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

# PROFESSIONAL EXPERIENCE

Apr. 2011 | Jul. 2011 Software developer, intern

( sansomlab/tenx).

MEDIT S.A.

periment objects ( isee).

 Implementation of structurally-constrained multiple alignment of protein sequences for the commercial software MED-SuMo.

Palaiseau, France

• Bioconductor package for interactive exploration of SummarizedEx-

• R package for the analysis of ChIP-seq data ( kevinrue/deeperTools).

# **TEACHING EXPERIENCE**

2014 • Agricultural Microbiology

University College Dublin Dublin, Ireland

Teaching assistant of MICR20010 at University College Dublin.

2014 • Molecular Genetics and Biotech

Teaching assistant of BMOL20090 at University College Dublin.

2019 • iSEE: Interactive visualization of SummarizedExperiment

Co-instructor of a 2-hour workshop at the Bioconductor conference 2019.

2019 • R Code Clinic

present

2015

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

# **6** FUNDING AND AWARDS

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.

5th Annual PhD Symposium in Computational Biology & Innovation

Best oral presentation

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).

2017 • Bioconductor 2017 conference

Conference fee waiver and travel grant for BioC 2017. 

◆ Boston, USA

- Flash presentation for TVTB.
- Flash presentation for **☑** GOexpress.

2019 Bioconductor 2019 conference
Conference fee waiver and travel grant for BioC 2019.

New York, USA

Oublin, Ireland

- 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.

2019 • RStudio Shiny Contest

Winner of the "Most technically impressive" prize.

	##	ORGANISER AND CHAIR
2012	•	Computational Biology and Innovation PhD Symposium University College Dublin Co-organiser in charge of sponsorships and the abstract book.
2013   2014		Bioinformatics Seminar University College Dublin Co-organiser of a weekly meeting to present and discuss ongoing projects in the university.  Output  Dublin, Ireland
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.
2019		Special Interest Group Bioconductor conference 2019.
		TRAINING AND COURSES
2012	•	Introductory Statistics using R for Computational Biologists University College Dublin  P Dublin, Ireland
2012	•	Python Programming for Computational Biologists University College Dublin  Public Publ
2012	•	Online Research Skills for Computational Biologists University College Dublin Public P
2012		Advances in Infection Biology University College Dublin
2012	•	Bioinformatics Research Seminars University College Dublin
2012		Genomics – Principles and Practical Applications University College Dublin
2013	•	Hot Topics in Food and Nutrition Research University College Dublin
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
2014		Teaching in Higher Education University College Dublin
2015		Statistics for Genomic Data Science Coursera, Johns Hopkins University This course is part of the Genomic Data Science Specialization.

**Bioconductor for Genomic Data Science** 

2015

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.
2016	•	Machine Learning Coursera, Stanford University
	١	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
2018		iSEE: Interactive SummarizedExperiment Explorer. F1000Res. Rue-Albrecht, K., F. Marini, C. Soneson and A. T. L. Lun
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. Ilott, D. G. W. Johnston, E. Pires, J. McCullagh, S. N. Sansom, C. V. Arancibia-Carcamo, H. H. Uhlig and F. Powrie
	P	CONFERENCE PRESENTATIONS
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

**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

**Title:** Microarray analysis of the bovine macrophage response to *Mycobacterium bovis*, *M. bovis* Bacille Calmette-Guérin (BCG) and *M. avium* subspecies *paratuberculosis*.

# Dublin Academy of Pathogenomics & Infection Biology (DAPI)

**Title:** Microarray analysis of the bovine macrophage response to *Mycobacterium bovis*, *M. bovis* Bacille Calmette-Guérin (BCG) and *M. avium* subspecies *paratuberculosis*.

# 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)

Title: The quest for meaningful visualisation of genome-wide expression data

# EMBO conference: Microbiology after the genomics revolution - Genomes 2014

**Title:** Transcriptome analysis reveals differential innate immune response to members of the *Mycobacterium tuberculosis* complex.

### 2014 • The Acid Fast Club, Summer Meeting

**Title:** Transcriptome analysis reveals differential innate immune response of bovine macrophages to strains of the *Mycobacterium tuberculosis* complex.

### **UCD Conway Festival of Research & Innovation**

Poster. 

• Dublin, Ireland.

**Title:** Transcriptome analysis reveals differential innate immune response to members of the *Mycobacterium tuberculosis* complex.

**Title:** Transcriptome analysis reveals differential innate immune response to members of the *Mycobacterium tuberculosis* complex.

### 2015 • Quantitative Genomics

Poster. Q 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.

Oublin, 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.

### 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.

Soston, USA

- GOexpress: Visualise and summarise gene expression data using Gene Ontology
- TVTB: The VCF Tool Box: an effort to summarise and visualise variants

### 2018 • Genome Informatics

Poster.

Oambridge, UK

Title: Promiscuous expression of lincRNAs in medullary thymic epithelial cells

# 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.

# A LANGUAGE

French

Native.

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**English** Fluent. TOEIC score 970.

### Italian

Working knowledge.

# Spanish

Limited. Used to be fluent though ②.

### German

Limited. Haven't practiced in a long time.