Dr. Kevin **Rue-Albrecht**

Dipl. Ing., Ph.D.

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WORK EXPERIENCE

Dr. Stephen Sansom *(University of Oxford)* · *Oxford, UK*
POSTDOCTORAL RESEARCHER – COMPUTATIONAL BIOLOGIST · *Sep. 2017 - PRESENT*
- Molecular pathogenesis of inflammatory bowel disease, in collaboration with the group of Prof. Fiona Powrie
- Role of thymic epithelial cells in T-cell development, in collaboration with Prof. Georg Holländer and Prof. Chris Ponting.
- Development and maintainenance of software pipelines and programs for data analysis:
  - 10x Genomics analysis pipeline (🐙 sansomlab/tenx).
  - Configurable Shiny application for SummarizedExperiment objects (📙 iSEE).
  - Functions for post-processing ChIP-seq data (🐙 kevinrue/deeperTools).

Prof. David Mole *(University of Oxford)* · *Oxford, UK*
POSTDOCTORAL RESEARCHER – COMPUTATIONAL BIOLOGIST · *Dec. 2016 – Sep. 2017*
- Management, quality control, and coordination of genomics data for integrative 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).

Prof. Martin Wilkins *(Imperial College London)* · *London, UK*
RESEARCHER ASSOCIATE – BIOINFORMATICS / BIOSTATISTICS · *Sep. 2015 – Dec. 2016*
- Integration of genetic variation, proteomic and metabolomics data and associated deep phenotype data, in collaboration with the *Computational Genome Biology and Medicine* team led by Dr. Stefan Gräf (University of Cambridge).
- Bioconductor package: tools for genetic variants (📙 TVTB).

Dr. Stewart Adcock *(MEDIT S.A.)* · *Palaiseau, France*
SOFTWARE DEVELOPER (INTERN) · *Apr. 2012 – Jul. 2012*
- Implementation of structurally-constrained multiple alignment of protein sequences for the commercial software MED-SuMo.

Dr. Nora Khaldi, Prof. Denis Shields *(University College Dublin)* · *Dublin, Ireland*
RESEARCH ASSISTANT – BIOINFORMATICS (INTERN) · *Jun. 2010 – Sep. 2010*
- Analysis of structural disorder in *Saccharomyces cerevisiae* interacting proteins.

Dr. Henri De La Salle *(Établissement Français du Sang)* · *Strasbourg, France*
RESEARCH ASSISTANT (INTERN) · *Jul. 2009 – Aug. 2009*
- Recombinant protein expression in HeLa cells.

EDUCATION

Prof. David MacHugh, Prof. Stephen Gordon *(University College Dublin)*   *Dublin, Ireland*
PHD CANDIDATE   *2011 – 2015*
- **Thesis**: Comparative systems biology analyses of the bovine transcriptional response to species of the *Mycobacterium* genus.
  - o Functions for Gene Ontology analysis of gene expression data using (⬛ GOexpress).
- **Rotation year projects:**
  - o In silico structure-based prediction of *Mycobacterium bovis* epitopes in cattle (Dr. Anthony Chubb).
  - o Expression and purication of a Hepatitis B protein construct for experimental screening of interacting drug fragments (Dr. Neil Ferguson).
  - o Evaluation of a gene candidate underlying *Staphylococcus aureus* antibiotic resistance by Sanger sequencing and biofilm assay (Prof. James O'Gara).

École Polytechnique Universitaire Polytech Nice-Sophia   *Sophia-Antipolis, France*
INGÉNIEUR DIPLÔMÉ   *2008 – 2011*
- Biological engineering; Pharmacology, Biotechnology, Toxicology, Human and Environmental Health.
- **Major**: Bioinformatics and Modelling for Biology.

FUNDING & AWARDS

- **Conference travel grant**: Bioconductor 2019 conference (New York, USA).
- **Winner of the 1st RStudio Shiny Contest**: "Most technically impressive" app.
- **Conference travel grant**: Bioconductor 2017 conference (Boston, USA).
- **Conference fee waiver**: ISMB conference 2015 (Dublin, Ireland); Bioinformatics Open Source Conference (BOSC) Special Interest Group.
- **Conference travel grant**: FEMS Young Scientist Meeting Grant (YSMG); FEMS 2014 conference "Microbiology in the New Genomics Era" (Paris, France).
- **Best oral presentation**: Computational Biology and Innovation PhD Symposium 2014 (Dublin, Ireland).
- **Wellcome Trust Four-year PhD Programme:** Computational Infection Biology.

CONFERENCE PRESENTATIONS

- **Workshop:** Bioconductor 2019 conference (New York, USA).
- **Special Interest Group:** Bioconductor 2019 conference (New York, USA).
- **Poster:** Genome Informatics 2018 (Cambridge, UK).
- **Short talk:** Bioconductor 2017 conference (Boston, USA).
- **Talk:** NGS-SIG Single-cell RNAseq (Oxford, UK).
- **Poster :** Quantitative Genomics 2015 (London, UK).
- **Longer talk:** Bioinformatics Open Source Conference (BOSC) 2015 (Dublin, Ireland).
- **Poster:** Wellcome Trust Final Year PhD Students' Meeting 2014 (London, UK).
- **Poster:** UCD Conway Festival of Research & Innovation 2014 (Dublin, Ireland).
- **Talk:** The Acid Fast Club, Summer Meeting 2014 (Berlin, Germany).
- **Poster:** EMBO conference 2014 (Paris, France).
- **Talk:** Virtual Institute of Bioinformatics & Evolution (VIBE) 2014 (Carlow, Ireland).
- **Poster:** Society for General Microbiology (SGM) 2014 (Dublin, Ireland).

Conference presentations (Continued)

- **Poster:** Dublin Academy of Pathogenomics & Infection Biology (DAPI) 2013 (Ireland).
- **Poster:** Computational Biology & Innovation Symposium 2013 (Dublin, Ireland).
- **Talk:** Virtual Institute of Bioinformatics and Evolution (VIBE) 2013 (Galway, Ireland)
- **Poster:** Animal Health Ireland Workshop & Conference 2013 (Cork, Ireland).
- **Talk:** Association of Veterinary Teachers and Research Workers (AVTRW) 2013 (Hillsborough, Ireland)

Organizer & Chair

- **Coordinator**: Genomics Forum, Kennedy Institute of Rheumatology (2018-present).
- **Co-organiser:** Computational Biology and Innovation PhD Symposium (2012).

Teaching

- **Demonstrator**: Agricultural Microbiology (2014).
- **Demonstrator:** Molecular Genetics and Biotech (2014).

Training & Courses

- **Machine Learning** (Coursera, Stanford University, 2016).
- **Python for Genomic Data Science** (Coursera, Johns Hopkins University, 2015).
- **Command Line Tools for Genomic Data Science** (Coursera, JHU, 2015).
- **Bioconductor for Genomic Data Science** (Coursera, Johns Hopkins University, 2015).
- **Statistics for Genomic Data Science** (Coursera, Johns Hopkins University, 2015).
- **Teaching in Higher Education** (2014).
- **Network Analysis in Systems Biology** (Coursera, 2013)
- **Sequence Data Analysis Training** (Wageningen Institute of Animal Sciences, 2013).
- **Hot Topics in Food and Nutrition Research** (University College Dublin, 2013)
- **Genomics – Principles and Practical Applications** (University College Dublin, 2012).
- **Bioinformatics Research Seminars** (University College Dublin , 2012).
- **Advances in Infection Biology** (University College Dublin , 2012).
- **Online Research Skills for Computational Biologists** (University College Dublin, 2012).
- **Python Programming for Computational Biologists** (University College Dublin, 2012).
- **Introductory Statistics using R for computational biologists** (UCD, 2012).

Professional memberships

- **International Society for Computational Biology (ISCB):** 2012-present.

Peer review

- **OUP Bioinformatics**: 1 article
- **Journal of Open Source Software**: 1 article

SKILLS & EXPERIENCE

Programming
(alphabetical)

C#, Java, JavaScript, Matlab, PHP, Python, R, SQL, Unix, XHTML.

Software
(alphabetical)

Bioconductor, cgat-core, cgat-apps, cgat-flow, conda, Django, Eclipse, git, GitHub, MongoDB, MeteorJS, NodeJS, PyCharm, Rstudio, Ruffus, Subversion, Visual Studio.

Creativity
(release date)

Bioconductor packages (deeperTools, iSEE, TVTB, GOexpress).

Languages
(fluency)

French (native), English (fluent, TOEIC 970), Italian (working), Spanish (limited), German (limited).

PUBLICATIONS

Publications: 18	h-index: 11	Total citations: 540

Manuscripts awaiting publication

Robert A. Amezquita, Vince J. Carey, Lindsay N. Carpp, Ludwig Geistlinger, Aaron T. L. Lun, Federico Marini, **Kevin Rue-Albrecht**, Davide Risso, Charlotte Soneson, Levi Waldron, Hervé Pagès, Mike Smith, Wolfgang Huber, Martin Morgan, Raphael Gottardo, Stephanie C. Hicks (2020). "Orchestrating Single-Cell Analysis with Bioconductor". <u>Nature Methods</u>

2019

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 (2019). "The Short Chain Fatty Acid Butyrate Imprints an Antimicrobial Program in Macrophages." <u>Immunity</u> **50**(2): 432-445 e437.

2018

Aulicino, A., **K. C. Rue-Albrecht**, L. Preciado-Llanes, G. Napolitani, N. Ashley, A. Cribbs, J. Koth, B. C. Lagerholm, T. Ambrose, M. A. Gordon, D. Sims and A. Simmons (2018). "Invasive Salmonella exploits divergent immune evasion strategies in infected and bystander dendritic cell subsets." <u>Nat Commun</u> **9**(1): 4883.

O'Doherty, A. M., **K. C. Rue-Albrecht**, D. A. Magee, S. Ahting, R. E. Irwin, T. J. Hall, J. A. Browne, N. C. Nalpas, C. P. Walsh, S. V. Gordon, M. W. Wojewodzic and D. E. MacHugh (2019). "The bovine alveolar macrophage DNA methylome is resilient to infection with Mycobacterium bovis." <u>Sci Rep</u> **9**(1): 1510.

Malone, K. M., **K. Rue-Albrecht**, D. A. Magee, K. Conlon, O. T. Schubert, N. C. Nalpas, J. A. Browne, A. Smyth, E. Gormley, R. Aebersold, D. E. MacHugh and S. V. Gordon (2018). "Comparative 'omics analyses differentiate Mycobacterium tuberculosis and Mycobacterium bovis and reveal distinct macrophage responses to infection with the human and bovine tubercle bacilli." <u>Microb Genom</u>.

Villarreal-Ramos, B., S. Berg, A. Whelan, S. Holbert, F. Carreras, F. J. Salguero, B. L. Khatri, K. Malone, **K. Rue-Albrecht**, R. Shaughnessy, A. Smyth, G. Ameni, A. Aseffa, P. Sarradin, N. Winter, M. Vordermeier and S. V. Gordon (2018). "Experimental infection of cattle with Mycobacterium tuberculosis isolates shows the attenuation of the human tubercle bacillus for cattle." <u>Sci Rep</u> **8**(1): 894.

Rue-Albrecht, K., F. Marini, C. Soneson and A. T. L. Lun (2018). "iSEE: Interactive SummarizedExperiment Explorer." <u>F1000Res</u> **7**: 741.

Correia, C. N., K. E. McLoughlin, N. C. Nalpas, D. A. Magee, J. A. Browne, **K. Rue-Albrecht**, S. V. Gordon and D. E. MacHugh (2018). "RNA Sequencing (RNA-Seq) Reveals Extremely Low Levels of Reticulocyte-Derived Globin Gene Transcripts in Peripheral Blood From Horses (Equus caballus) and Cattle (Bos taurus)." <u>Front Genet</u> **9**: 278.

2017

Rhodes, C. J., P. Ghataorhe, J. Wharton, **K. C. Rue-Albrecht**, C. Hadinnapola, G. Watson, M. Bleda, M. Haimel, G. Coghlan, P. A. Corris, L. S. Howard, D. G. Kiely, A. J. Peacock, J. Pepke-Zaba, M. R. Toshner, S. J. Wort, J. S. Gibbs, A. Lawrie, S. Graf, N. W. Morrell and M. R. Wilkins (2017). "Plasma Metabolomics Implicates Modified Transfer RNAs and Altered Bioenergetics in the Outcomes of Pulmonary Arterial Hypertension." Circulation **135**(5): 460-475.

2016

Rue-Albrecht, K., P. A. McGettigan, B. Hernandez, N. C. Nalpas, D. A. Magee, A. C. Parnell, S. V. Gordon and D. E. MacHugh (2016). "GOexpress: an R/Bioconductor package for the identification and visualisation of robust gene ontology signatures through supervised learning of gene expression data." BMC Bioinformatics **17**: 126.

Farrell, D., G. Jones, C. Pirson, K. Malone, **K. Rue-Albrecht**, A. J. Chubb, M. Vordermeier and S. V. Gordon (2016). "Integrated computational prediction and experimental validation identifies promiscuous T cell epitopes in the proteome of Mycobacterium bovis." Microb Genom **2**(8): e000071.

2015

Nalpas, N. C., D. A. Magee, K. M. Conlon, J. A. Browne, C. Healy, K. E. McLoughlin, **K. Rue-Albrecht**, P. A. McGettigan, K. E. Killick, E. Gormley, S. V. Gordon and D. E. MacHugh (2015). "RNA sequencing provides exquisite insight into the manipulation of the alveolar macrophage by tubercle bacilli." Sci Rep **5**: 13629.

Park, S. D., D. A. Magee, P. A. McGettigan, M. D. Teasdale, C. J. Edwards, A. J. Lohan, A. Murphy, M. Braud, M. T. Donoghue, Y. Liu, A. T. Chamberlain, **K. Rue-Albrecht**, S. Schroeder, C. Spillane, S. Tai, D. G. Bradley, T. S. Sonstegard, B. J. Loftus and D. E. MacHugh (2015). "Genome sequencing of the extinct Eurasian wild aurochs, Bos primigenius, illuminates the phylogeography and evolution of cattle." Genome Biol **16**: 234.

Aulicino, A., A. M. Dinan, A. A. Miranda-CasoLuengo, J. A. Browne, **K. Rue-Albrecht**, D. E. MacHugh and B. J. Loftus (2015). "High-throughput transcriptomics reveals common and strain-specific responses of human macrophages to infection with Mycobacterium abscessus Smooth and Rough variants." BMC Genomics **16**: 1046.

2014

Rue-Albrecht, K., D. A. Magee, K. E. Killick, N. C. Nalpas, S. V. Gordon and D. E. MacHugh (2014). "Comparative functional genomics and the bovine macrophage response to strains of the mycobacterium genus." Front Immunol **5**: 536.

McLoughlin, K. E., N. C. Nalpas, **K. Rue-Albrecht**, J. A. Browne, D. A. Magee, K. E. Killick, S. D. Park, K. Hokamp, K. G. Meade, C. O'Farrelly, E. Gormley, S. V. Gordon and D. E. MacHugh (2014). "RNA-seq Transcriptional Profiling of Peripheral Blood Leukocytes from Cattle Infected with Mycobacterium bovis." Front Immunol **5**: 396.

2013

Nalpas, N. C., S. D. Park, D. A. Magee, M. Taraktsoglou, J. A. Browne, K. M. Conlon, **K. Rue-Albrecht**, K. E. Killick, K. Hokamp, A. J. Lohan, B. J. Loftus, E. Gormley, S. V. Gordon and D. E. MacHugh (2013). "Whole-transcriptome, high-throughput RNA sequence analysis of the bovine macrophage response to Mycobacterium bovis infection in vitro." BMC Genomics **14**: 230.

2012

Rue-Albrecht, K., D. C. Shields and N. Khaldi (2012). "Correlation of disorder between S. cerevisiae interacting proteins." Mol Biosyst **8**(1): 417-425.