

Graduate Engineer · Computational Biologist

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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 maintenance 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: functions for analysing 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.
 - Functions for Gene Ontology analysis of gene expression data using ([GOexpress](#)).
- **Rotation year projects:**
 - In silico structure-based prediction of *Mycobacterium bovis* epitopes in cattle (Dr. Anthony Chubb).
 - Expression and purification of a Hepatitis B protein construct for experimental screening of interacting drug fragments (Dr. Neil Ferguson).
 - 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 <i>(alphabetical)</i>	C#, Java, JavaScript, Matlab, PHP, Python, R, SQL, Unix, XHTML.
Software <i>(alphabetical)</i>	Bioconductor, cgat-core, cgat-apps, cgat-flow, conda, Django, Eclipse, git, GitHub, MongoDB, MeteorJS, NodeJS, PyCharm, Rstudio, Ruffus, Subversion, Visual Studio.
Creativity <i>(release date)</i>	Bioconductor packages (deeperTools, iSEE, TVTB, GOexpress).
Languages <i>(fluency)</i>	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. Amezcua, 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". Nature Methods

2019

Schulthess, J., S. Pandey, M. Capitani, **K. C. Rue-Albrecht**, I. Arnold, F. Franchini, A. Chomka, N. E. Iltis, 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." Immunity **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." Nat Commun **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." Sci Rep **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. Aebbersold, 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." Microb Genom.

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." Sci Rep **8**(1): 894.

Rue-Albrecht, K., F. Marini, C. Soneson and A. T. L. Lun (2018). "iSEE: Interactive SummarizedExperiment Explorer." F1000Res **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)." Front Genet **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.