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

2008

CPGE BCPST Véto - Lycée Jean Rostand
Class Préparatoire aux Grandes Écoles   📍 Strasbourg, France

- Biology
- Chemistry
- Physics
- Earth Sciences
- Mathematics
- Programming

2011

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

- Pharmacology
- Biotechnology
- Toxicology
- Environmental Safety
- Bioinformatics

Major: Bioinformatics and Modelling for Biology

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.

🖥 RESEARCH EXPERIENCE

2017-2020

Postdoctoral Researcher - Computational Biologist
Sansom Group, Kennedy Institute of Rheumatology   📍 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 (sansomlab/tenx)
- Creation of a *Bioconductor* package for interactive exploration of `SummarizedExperiment` objects (iSEE).
- R package for the analysis of ChIP-seq data (kevinrue/deeperTools).

2016

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 2020-03-30.

2017 ● **Postdoctoral Researcher - Computational Biologist**
Ratcliffe group, Target Discovery Institute   📍 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 (⌾ kevin-rue/Seqbook).

2011 ● **Graduate Research Assistant**
| Beijing Institute of Genomics, Chinese Academy of Sciences
2014   📍 Beijing, China
- Performed computational biology research towards understanding regulation of alternative splicing in human and mouse transcriptome.
- Found EGFR pathway related mutations, aimed to understand the impacts of cancer mutations on EGFR signaling pathway.

2015 ● **Bioinformatican**
| My Health Gene Technology Co., Ltd.   📍 Beijing, China
2016
- Investigated how cancer cells spread to other parts of the body at the single cell level.

2016 ● **Visiting Scientist**
| University of Alabama at Birmingham   📍 AL, USA
2018
- Investigated the role of mitochondria in development of cancer.
- Investigated the evolution of genome architecture and its role in important evolutionary events.
- Detected thrombotic thrombocytopenic purpura related mutations in mutiple patients' blood genome.

🖳 TEACHING EXPERIENCE

2014 ● **Introduction to R Language for Beginners.**
Instructor of R and Data Mining Training Courses at SupStat Inc.
📍 Beijing, China

2016 ● **Computational Biology and Bioinformatics.**
| Teaching assistant of GBS CB2-201 courses at UAB   📍 AL, USA
2017

📄 SELECTED PUBLICATIONS AND POSTERS

2014 ● **Genetic and epigenetic signals are found predictive to the distribution of intra-individual divergence of alternative splicing.**
Poster for 2013 International Conference of Genomics
📍 Qingdao, China

Yu L, Chen B, Zhang Z.

2016 ● **ESCRT-0 complex modulates Rbf mutant cell survival by regulating Rhomboid endosomal trafficking and EGFR signaling.**
J Cell Sci. 2016 May 15;129(10):2075-84.

Sheng Z, **Yu L**, Zhang T, Pei X, Li X, Zhang Z and Du W.