Alexander Holloway

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✈ Nationality: Australian (current Swiss B permit)

EDUCATION

ÉCOLE POLYTECHNIQUE FÉDÉRALE DE LAUSANNE   2016–2019
Master of Computer Science
Coursework included: Database Systems, Distributed Algorithms, Performance Evaluation
Thesis title: Visualisation and classification of large-scale consumer device data

QUEENSLAND UNIVERSITY OF TECHNOLOGY   2011–2014
Bachelor of Information Technology (First Class Honours)
Coursework included: Software Development, Professional Practice in IT, Scalable Systems Development
Thesis title: k-mer methods for the inference of bacterial gene origins

EXPERIENCE

GENEDATA AG   NOVEMBER 2022–PRESENT
Software Engineer
- Lead development of an interactive logfile processing and visualisation tool for in-house analytics
- Developed Java tools to customise product functionality for "Top 25" pharmaceutical companies
- Built and delivered code and database configuration packages on a quarterly basis
- Established and maintained team-wide standards for version control conventions

UNIVERSITÄT BERN   DECEMBER 2020–OCTOBER 2022
Software Engineer, Institute of Social and Preventive Medicine
- Implemented a data collection and processing toolchain for a crowdsourcing-based living systematic review
- Designed and implemented visualisations of the processed dataset using D3
- Performed routine sysadmin and web server maintenance tasks, supporting the entire lab
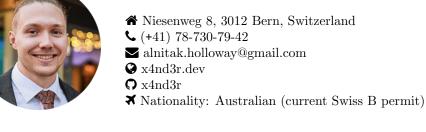
UNIVERSITÉ DE LAUSANNE   DECEMBER 2019–NOVEMBER 2020
Software Engineer, Department of Computational Biology
Implemented large-scale, highly parallel data processing workflows for analysis of human genetic data.

LOGITECH   AUGUST 2018–MARCH 2019
Intern
- Developed big data processing pipeline using Spark on Amazon's Elastic Map Reduce platform
- Designed and implemented novel data visualisations with Javascript's D3 library
- Implemented a web application to present visualisations using Angular framework

Queensland Brain Institute

March 2014–June 2016

Research Technician

- Curated and analysed large genomic datasets for an international consortium, leading to multiple high-impact publications
- Designed and developed online data browsing application for published consortium findings
- Built new, and improved existing end-to-end shell pipelines for processing large datasets reliably
- Designed and implemented multiple web pages for communicating research findings to the public

Technical Skills

Language	Full-time experience	Libraries/Frameworks
R	6 years	`shiny`, `dplyr`, `ggplot2`, `knitr`, Bioconductor
HTML & CSS	5 years	HTML5, CSS3, Sass
Java	4 years	Gradle, Maven, Ant, Hadoop, Spring Boot
JavaScript	3 years	D3, jQuery, Node.js, Meteor, Webpack
Python	2 years	`pandas`, `numpy`, Flask, PySpark, Keras
TypeScript	1 year	Angular
C++	1 year	MPI, OpenMP, Eigen, Boost

Daily tools

`vim`, `git`, `bash`, `nginx`, Docker, Jenkins, Adobe Creative Suite (Illustrator, Photoshop, InDesign)

Languages

English	Mother tongue
German	B1
French	A2

Selected Publications

Salanti, G.[†], Peter, N.[†], Tonia, T.[†], **Holloway, A.**[†], White, I. R., Darwish, L., ... Leucht, S. (2022). The impact of the COVID-19 pandemic and associated control measures on the mental health of the general population: A systematic review and dose-response meta-analysis. *Annals of Internal Medicine*.

Lloyd-Jones, L. R.[†], **Holloway, A.**[†], McRae, A., Yang, J., Small, K., Zeng, B., ... Powell, J. E. (2017). The genetic architecture of gene expression in peripheral blood. *The American Journal of Human Genetics*.

Lukowski, S. W., Lloyd-Jones, L. R., **Holloway, A.**, Holger, K., Hemani, G., Yang, J., ... Powell, J. E. (2017). Genetic correlations reveal the shared genetic architecture of transcription in human peripheral blood. *Nature Communications*.

Kassam, I., Lloyd-Jones, L., **Holloway, A.**, Small, K. S., Zeng, B., Bakshi, A., ... McRae, A. F. (2016). Autosomal genetic control of human gene expression does not differ across the sexes. *Genome Biology*, *17*(1), 248.

Hogan, J., Holland, P., **Holloway, A.**, Petit III, R., & Read, T. (2013). Read classification for next generation sequencing. In *Proceedings of ESANN 2013: European Symposium on Artificial Neural Networks*.

[†] denotes equal contribution.