


ALASTAIR MAXWELL

 [helloabunai.github.io](https://github.com/helloabunai)

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Basics

Residence: Pirkanmaa,
Finland 

Dual Nationality

 Scottish (UK)

 Irish (EU)

E-Mail

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Interests

Cars & Motorsports
Dogs & Nature Walks
Competitive Badminton
Video Games
Cooking
Music

I'm a down-to-Earth and motivated **Software Developer and Bioinformatician**, and Bioinformatics, Polyomics and Systems Biology MRes graduate from **Glasgow, Scotland**. I have **proven communication skills**, a strong interest in the interface between web technologies, computing, big-data and biology, and **excellent technical skills**. Currently, I am a Full-Stack Software Developer at Futurice Oy, where I write clean and responsive frontends, efficient backends and manage cloud infrastructure, for client projects. I have broad professional experience, which allows me to contribute within any area of software development. I have **9 years of software development and bioinformatics experience**, having worked on many projects, from command line analysis pipelines to full-stack web applications – for both academic and industrial applications.

Technical Skills



Extensive knowledge and experience in software development, independently and as part of a team.

System Administrator



Experienced with x86 hardware; configuring maintaining and developing high performance compute clusters.


Soft Skills Capable






Sociable, excellent presentation skills and clear communication, alongside a very keen eye for design and attention to detail.


Work Experience



- 2022- **Software Developer (Full Stack)** (Hybrid) Futurice Oy
Responsible for developing, testing and maintaining high-quality web applications using a robust stack including React, TypeScript, GoLang and Python. Demonstrated consistent capability in delivering both frontend and backend solutions, ensuring seamless user experiences. Implemented multiple microservice architectures, via gRPC or GoLang based REST APIs. Administered and deployed applications on leading cloud platforms such as AWS and Azure; leverage of cloud-native services to maximise application reliability, scalability and security. Worked in diverse teams to drive project success from concept to completion via code reviews, mentoring junior developers and following agile development practices. Established and maintained CI/CD pipelines to ensure for rapid and reliable code deployments.
Key clients: Supercell, Microsoft.
- 2020-2022 **Bioinformatician & Systems Administrator** (Remote) Genevia Technologies Oy, Finland
Carrying out bioinformatic analyses on client projects of varying sizes (from RNASeq to Whole Genome analysis); I am tasked with writing analysis scripts to automate common tasks, command-line based analysis pipelines, or coding full-stack web applications, to meet our client's demands, both academic and industrial.
I also lead development of an in-house distributed computing infrastructure, forecasting compute and storage demand from client work. Administration of server clusters, organising data management and backups, analysis queuing systems, software compilation/support and networking tools to aid remotely working staff. Imple-


 Select Tech


Software Development (Agile)
~10 years 

Sys Admin ~5 yrs.  **Full Stack** ~4 yrs. 

Containerisation & Cloud Services
~5 yrs. 

Version Control ~8 yrs.  **SQL** ~5 yrs. 

Bioinformatics Analyses
~10 yrs. 

Data Science
~8 yrs. 

 Select Languages

Python ~8 yrs. **JS** ~5 yrs.

HTML & CSS
~5 yrs.

Bash ~10 yrs. **R** ~5 yrs.

C++ ~2 yrs. **Java** ~5 yrs.

mented systems for critical compute resource monitoring, providing alerts to company workspaces via webhook-based Applications.

2016-2020 **Bioinformatician** [University of Glasgow, Scotland](#)
Continued lead development on ScaleHD; wrote a novel, performant Digital Signal Processing module to determine literal amplicon sequence structures of patient alleles; implemented machine learning classifiers to reduce genotyping complexity and drive a parallel genotyping platform. Configured, built and administered local UNIX-based server node to enable Huntington Disease genotyping service for CHDI Foundation.
Collaboration with international Huntington Disease colleagues to generate and verify large datasets, uncovering more detailed understanding of how genetic mutations alter Huntington Disease pathology, leading to numerous publications. Developed HTML5 based interactive interface for ScaleHD, enabling users to share detailed analysis results from extremely large datasets, in an instant.

2016-2016 **Visiting Technical Expert** [EMBL-EBI, England](#)
Working as a visiting technical expert at EMBL-EBI in Cambridge, to assist with deployment of my genotyping software onto numerous clusters; feedback and collaboration enabled improvement of the codebase, genotyping precision and accuracy. Developed, in tandem with EMBL-EBI colleagues, a Bayesian based approach to Huntington Disease genotyping, to act as a further quality metric for heuristically driven automated confidence scores. Distributed multiple software packages to the open source community via Git and Pypi.

2014-2016 **Bioinformatician** [University of Glasgow, Scotland](#)
Led design and development of a custom Python-based pipeline (ScaleHD) to genotype Huntington Disease data in an automated manner, accounting for complex real-world phenomena which typically bottlenecks attempts at automation. Implemented this command-line based analysis pipeline to incorporate all required third-party binaries, allowing end-users to run all analyses easily.
Wrote supporting code for other diseases being researched within the group, to automate common tasks such as genome quality control and alignment. Optimised workflows within our research group and implemented robust data archive standards.

Academic Qualifications

2013-2014 **MRes: Bioinformatics, Polyomics and Systems Biology** [Keio University, Japan](#)
Awarded Project Merit
Extensive postgraduate research project at Keio University, Japan. Designed and developed a Python and R based Carbon-13 atom transition mapping package, to aid in generation of more energy efficient yeast. Collaborated between colleagues across locations in Japan, in order to improve functionality of developed software. Numerous presentations at conferences within Japan, communicating clear and concise information across language barriers.

2013-2014 **MRes: Bioinformatics, Polyomics and Systems Biology** [University of Glasgow, Scotland](#)
Awarded First class, with Distinction
Research based postgraduate degree, centered around real-world based classes to provide experience with academic and industrial applications of the technology field.

Protein structure informatics; Next-Generation Sequencing technologies (Illumina, Roche-454, IonTorrent, Oxford Nanopore); Machine learning, Support Vector Machine classification and hyper-dimensionality complexity reduction; Object oriented programming (Java, Python); command line scripting (Bash); statistical modelling and programming (R); Relational database design and implementation (MySQL & similar).

2009-2013 **BSc (Hons): Immunology and Microbiology** [University of Strathclyde, Scotland](#)
Awarded First class

Studied mucosal vaccines under Dr. Val Ferro. Large data set analysis and statistical interpretation, writing software to utilise genomic analysis web-services such as BLAST, to uncover statistically significant mutations and targets for further research. Developed knowledge and interest of computational biology analysis pipelines.