

Alexis Christoforides

Somerville, MA USA

[email](#) - [Github](#) - [Google Scholar](#) - [LinkedIn](#)

Expert software engineer offering more than 15 years of professional software development experience and leadership. I've been a senior engineer and project leader for successful scientific software, programming language runtimes, Web API projects and IoT.

Very comfortable driving LLMs for powering through code faster than ever.

Career & Highlights

2020 - Present

OS Team Engineering Lead at [Wilderness Labs](#)

I lead the [Meadow.OS](#) project: the system software for the Meadow IoT single-board computer, which lets developers use C# and .NET for complex IoT applications.

- Ported the Mono .NET runtime to run on an STM32F7 MCU, NuttX RTOS, <32MB of RAM and <32MB of flash
- Integrated mbedTLS to serve as a new MCU-friendly TLS provider for Mono
- Designed and implemented full-system (firmware + app), assured and secure over-the-air (OTA) update machinery, spanning from custom bootloader to reliable network messaging using C# + MQTT + Azure
- Co-designed our IoT app lifecycle for resilience, live monitoring, crash recovery, and OTA update and rollback support
- Co-designed low-level I/O API for .NET (GPIO, SPI, I2C, interrupt processing)
- Ported TensorFlow Lite Micro to the Meadow and wrote bindings for .NET
- Maintained our CI jobs and Azure Pipelines-based OS release process
- Guided the team through developing OS features and resolving user issues

2014 - 2020

Mono Runtime Engineer at [Xamarin](#) & [Microsoft](#)

I was part of the [Mono](#) runtime engine team, an open-source and cross-platform .NET implementation used for C# and F#-based apps on iOS, Android, video game consoles, and other small devices. Xamarin was acquired by Microsoft in 2016 where my work continued.

- Improved the "SGen" generational garbage collector, e.g. reducing memory allocation for the string type, adding "canary" diagnostics to the heap and fixing bugs
- Improved capabilities of Mono's native crash report machinery ("MERP")
- Ported the file and network I/O subsystem from Microsoft's CoreFX library to Mono
- Maintained and improved the CI and Release packaging software for the Mono MacOS SDK, a >1GB installable archive.
- Collaborated with the product teams (in rotations) to integrate the latest Mono development into the Xamarin Android/iOS products

2009 - 2014

Bioinformatician & Software Engineer at [TGen](#)

I wrote research and medical-use analysis software and methods for whole-genome sequencing data (using Java, C++, Python, shell scripts, R, etc.). Specialized in cancer genomics and sequencing analysis.

- Developed a method for comparing DNA/RNA between tumor and normal samples in patients with solid cancers. Wrote and maintained the software implementation and published a paper (see Publications)
- Was a small part of the [1000 Genomes](#) pilot project, which created the most comprehensive variant map of the human genome at the time and created a public dataset used as reference in hundreds of subsequent studies (see Publications)
- Helped design, maintain, run and troubleshoot TGen's HPC cancer genomics analysis pipeline and genomic data store
- Created a custom web portal for collaborative version-tracked data entry and report generation of confidential cancer patient data
- Provided whole-genome data analysis and internal software support to PIs and studies throughout the institute

Higher Education

**Computer Science BSc
at Arizona State University, Tempe AZ**

**Biomedical Informatics Ph. D. (abandoned)
at Arizona State University/Mayo Clinic**

Completed all coursework and published one first-author paper before withdrawing to move to Boston for the Xamarin opportunity

Most Important Publications

[Christoforides, A., Carpten, J. D., Weiss, G. J., Demeure, M. J., Hoff, D. D. V., & Craig, D. W. \(2013\). **Identification of somatic mutations in cancer through Bayesian-based analysis of sequenced genome pairs.** *BMC Genomics*, 14\(1\), 302. doi:10.1186/1471-2164-14-302](#)

[\(2010\). **A map of human genome variation from population-scale sequencing.** *Nature*, 467\(7319\), 1061–1073. doi:10.1038/nature09534](#)