

Neil Kindlon

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Sr. Bioinformatics Engineer w/ M.S. in Bioinformatics, B.S. Comp Sci, 13 years in industry, 12 years of C++

KEY SKILLS

Bioinformatics: HTS and microarray data analysis, SV and SNP detection, cancer genomics, DNA & cDNA mapping and de novo assembly, **bedtools co-author**

Programming: **C++** (STL/Boost), Matlab. Some R, Perl, and Java.

OS/DB/SCM/IDE: **Linux**, Github, Eclipse, VS, and VMS. Some SQL, Oracle, and SVN

BIOINFORMATICS EXPERIENCE

Sr. Biostatistician, University of Virginia, Charlottesville, VA (10/12 – 06/15)

- Recreated **bedtools**, a fast, flexible, **linux** command line toolset for genomic arithmetic, written in **C++**. **60x faster** than previous versions in key benchmarking cases
- Used templating and polymorphism to handle ten bioinformatics file format types, four compression types, and four file/stdin input types. Refactored code base for modularity, allowing vastly easier maintenance and rapid future development
- Provided support for bugs and enhancements to over 30,000 users on open source github site

Software Developer III, 454 Life Sciences, a member of Roche, Branford, CT (12/06 – 07/12)

- Engineered **C++** software in Linux environment for genomic and cDNA reference-guided assembly
- Awarded permanent position after initial 3 month contract augmenting pairwise aligner for split reads
- Promoted from Bioinformatics Developer II in March 2009 for outstanding performance
- Created **structural variation detection** application to locate nearly undetectable gene fusions, critical to cancer research. Used signal processing algorithms to find consistent deviation patterns in NGS data
- Advanced **structural variation** detection with a challenging and rarely done **categorization** tool
- Assisted mechanical engineering team by re-writing **Matlab** script for sequencer camera quality test

Graduate Student, M.S. in Bioinformatics, Rensselaer Polytechnic Institute, Troy, NY (8/03-7/04)

- Successfully completed aggressively paced 30 credit Master of Science program in a single year
- Professional Master's Project - Created a suite of C++ programs in Linux for modified BLAST search of genomic databases
- Soft computing - Programmed a genetic algorithm in Matlab 6.5 for multiple protein sequence alignment, and other scripts for fuzzy clustering, neural nets, and case-based reasoning
- Additional coursework in data mining, sequence analysis, molecular biology, and probability theory

OTHER HIGHLIGHTED SOFTWARE EXPERIENCE

Software Engineer, Susquehanna International Group, Bala Cynwyd PA (2/16 – 9/16)

- Developed **C++** application w/ Boost library for network traffic and outage monitoring
- Added concurrency scheduling to prevent data loss or high system load

Staff Software Engineer, Lockheed Martin, King of Prussia, PA (10/15 – 2/16)

- Appointed lead architect for 9-man team modelling satellite, ground, naval, and cyber war game
- Rescued first project by finding and fixing a critical design flaw in a large C++ codebase during first month on job

Systems Programmer, Cendant Internet Engineering, Cambridge, MA (6/98 – 10/98)

- Wrote C++ programs with Oracle APIs for data mining of customer transaction logs
- Educated the engineering staff in awareness and usage of the Standard Template Library

Software Engineer, FactSet Research Systems, Greenwich, CT (7/96 – 6/98)

- Wrote C++ programs for database management and updates of in-house database system
- Worked with marketing and client support to develop application specifications and address enhancement requests
- Trained new engineers in in-house development environment and procedures

EDUCATION

M.S. Applied Science (Computational Biology). August 2004, Rensselaer Polytechnic Institute, Troy, NY. B.S. Computer Science. December 1996, Rensselaer Polytechnic Institute, Troy, NY