

# Morgan Conrad

Software Developer  
and Consultant



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NEXTQ.INFO

## CAREER SKILLS

- Thirty years experience in a wide range of biotech instrumentation, on all aspects of data collection, analysis, algorithms, storage and user interface.
- Proven excellence in Java, Swing, Multi-Threading and Object-Oriented Design.
- Knowledge of JavaScript, HTML5, CSS3, node.js, Express and mongoDB. Some experience with Python, PHP, RDBs, C/C++, agile and test-driven-development.
- Ability to develop, integrate and modify high performance algorithms.
- Strong scientific background to interact with in-house scientists and end users.

## CLIENTS

### LEUKOBYTE INC.

2010-2015

For their Java / Swing based CytoPaint software, I developed:

- Robust statistics, using medians and percentiles instead of standard deviations.
- Parallel code exploited multi-core architectures, running nearly 4x faster.
- Paginated printing with flexible headers and footers. PDF export using iText.
- A parallelized Parks/Roederer/Moore "biexponential" transform.
- A parallelized Automatic Compensation algorithm with a novel, simple UI.
- Swing based contextual menus, and interactive "cropping" of data space.

### SAN FRANCISCO GIANTS BASEBALL TEAM

2014

- Helped integrate their data systems with the 2014 Amateur Player Draft.
- Wrote several node.js command line apps to authenticate using OAuth, query MLB's REST APIs, and convert JSON data into database friendlier formats.

### COMPLETE GENOMICS

2012-2013

Worked with their Business Process Automation Software, a distributed JEE web app using JBoss, JMS, Servlets, .Net, SQL and XML. I implemented:

- A new table and JDBC to capture imaging issues by slide and lane.
- Numerous feature requests, bug fixes, and support issues.
- Improvements on their C# / .NET interface and functionality.

### CYTEK DEVELOPMENT

2009-2010

Lead developer for the multi-level hierarchical live gating component of their Java / Swing based FlowJo Collector's Edition software.

- Developed extensible Java models, views, actions and controllers for typical flow cytometry gates. All important settings could be persisted as XML.
- Integrated gate code with existing data collection UI and underlying C++ code.
- Developed a Java queue for commands ("command pattern") to solve multiple issues caused by the underlying C++ code which was not thread-safe.
- Developed Swing and SwingX trees and tables for a hierarchical statistics UI.

## RECENT INDEPENDENT WORK

- Developed [nextq.info](http://nextq.info), a node.js web site to find upcoming Dog Agility Trials.
- Two time presenter at the BayNode "Meetup" group, specializing in node.js.
- Wrote the NPM module "FCS" to read FCS format Flow Cytometry Data.
- More (mainly Java) on my GitHub page, <https://github.com/MorganConrad>

## PREVIOUS EXPERIENCE

### **APPLIED BIOSYSTEMS (NOW THERMO-FISCHER) 1990-2009**

Staff Software Engineer. Developed numerous software applications, mainly in Java, to acquire, analyze, store, and display data from high-throughput genetic analysis instrumentation. Developed highly interactive GUIs using Swing.

### **BECTON DICKINSON BIOSYSTEMS 1984-1990**

Senior Research Scientist. Developed software, mainly in Pascal and C, to support R&D and commercial applications for flow cytometry.

## EDUCATION

Ph.D, Physical Chemistry, University of California, Berkeley, CA

B.A., Chemistry, Dartmouth College, Hanover, NH

## PATENTS AND PUBLICATIONS

US Patents numbers 4,845,653 6,379,957 6,531,588 6,804,046.

Selected publications available at <http://flyingspaniel.com/patentsandpapers.html>