

# ROBERT M. HUBLEY

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**PROFESSIONAL STATEMENT:** I have been fortunate to spend the past 20+ years developing and applying technology to a wide-variety of fascinating and challenging problem domains. Through these experiences, I have honed a diverse set of skills ranging from systems architecture/management to algorithm design, data analysis, and full stack web development. I seek challenges that diversify my knowledge, tackle compelling problems, and present opportunities to collaborate with creative individuals.

## TECHNICAL SKILLS

Languages: C/C++, Perl, Java, Javascript, and SQL programming languages.

Technologies: Node, Sequelize, DBIx::Class, Swagger, Angular, GWT, Mysql, MongoDB, GIT/CVS/SVN

Operating Systems and Environments: UNIX, Windows, Beowolf clusters, AWS

Circuit Design, Embedded Systems: KiCad, Arduino, Tattletale, Raspberry-Pi

## EXPERIENCE

**Institute for Systems Biology, Seattle, WA**

*Senior Software Engineer, Computational Biology*

Sep. 2014 - Present

- Develop algorithms and tools for the analysis of genomic sequences.
- Prepare manuscripts, grant reports and contribute to the submission of new research grants.
- Developed the first complete database of Transposable Element profile hidden Markov models for Human in collaboration with the Xfam consortium – ([www.dfam.org](http://www.dfam.org)).
- Extended the Dfam database and web services to include four additional model organisms.
- Developed a new Transposable Element visualization track for the UCSC genome browser in collaboration with Jim Kent and UCSC genome browser staff.
- Developed several external websites ([www.dfam.org](http://www.dfam.org), [www.repeatmasker.org](http://www.repeatmasker.org), [www.repeatasker.org/Dfam\\_consensus](http://www.repeatasker.org/Dfam_consensus)), and internal-use full stack single-page applications (HTML/Javascript, GWT, Angular, REST-API, Node, Mysql).
- Scaled and extended the RepeatScout algorithm for the analysis of complete genomes and improve the sensitivity of the approach.

**Institute for Systems Biology, Seattle, WA**

*Software Engineer, Computational Biology*

Mar. 2000 – Sep. 2014

- Developed sequence annotation software for the 27K CPU Paracel Genematcher.
- Refactored and enhanced the RepeatMasker interspersed repeat analysis program and managed its continued development.
- Created web services to support RepeatMasker job submission on a custom-built Beowolf compute cluster.
- Developed the RepeatModeler de-novo repeat identification program (<https://github.com/rmhubley/RepeatModeler>).
- Developed the DupMasker program - A tool for annotating primate segmental duplications (<http://www.repeatmasker.org/DupMaskerDownload.html>).
- Developed an algorithm for picking SNP assays using an evolutionary multi-objective approach (<http://snp-magma.sourceforge.net>).
- Wrote the RMBlast matrix-based sequence search program which is now part of the NCBI Blast Toolkit.
- Contributed code and genome sequence analysis to the Miller Syndrome project – the first nuclear family quartet to have their genomes fully sequenced.
- Contributed to the development of proteomic tools (comet), converters and data standards development at ISB and collaborating institutions.

**University of Washington, Seattle, WA**  
*Consultant*

Int. 2004-2015

- Developed two generations of an embedded control system for the School of Oceanography ORCA project. The first was based on the BitsyX platform and the follow up was based on the Raspberry-Pi board. The second generation also involved the development of two support boards to provide I/O, ADC, power regulation, communications, and real-time clock functions.
- Developed code to run the ORCA buoy's winch, power systems, and sensor package. In collaboration with the ORCA lab I developed systems to communicate with the buoys over long-distances using WIFI and cellular technologies.
- Developed Arduino code and a touch screen visual interface for a ventricular shunt prototype at the School of Genome Sciences.
- Extended and maintained Tattletale code and assisted with testing of a custom-built oxygen sensor calibration system for the Emerson lab at the School of Oceanography.

**University of Washington Genome Center, Seattle, WA**  
*Senior Systems Programmer*

Jan. 1998 - Mar. 2000

- Responsible for the computing architecture, system and data management in a research lab working on the Human Genome Project.
- Designed and built a laboratory information system using Visual Basic, ADO and MS SQL Server technologies to support large-scale DNA sequencing projects.
- Wrote web-based Java and Visual Basic programs to support database access through the center's web server.
- Built a system for assembling the genome of the bacteria *Pseudomonas Aeruginosa* – the largest single assembly created directly from reads at that time.
- Supervised the center's computing support staff.

**University of Washington Tacoma, Tacoma, WA**  
*Manager of Computer Services*

Sep. 1995 - Jan. 1998

- Managed a department supporting 200 campus systems including IBM PC, Macintosh, X-Terminals and UNIX workstations.
- Responsible for all aspects of the Tacoma branch computer purchasing, specification, support and operations.
- Responsible for the design and construction of the campus academic computing labs.
- Developed a web-based problem tracking system written in CGI conformant Perl and Java.
- Migrated the UWT server environment from Novell 4.x server to Windows NT 4.0 servers.
- Wrote conversion software for importing data between two student records databases.
- Developed installation standards and procedures for workstation installation process.

**Yale University Computer Science Department, New Haven, CT**  
*Systems Programmer II*

Nov. 1992 - Sep. 1995

- Implemented a successful, campus-wide support program for UNIX workstations.
- Responsible for porting and maintaining public domain software including, GNU, MIT X11, TeX, e-mail, and news reading utilities.
- Individually responsible for the design and implementation of complex e-mail, news, and printing systems for several large work groups.
- Ported a complex database package written in C from an obsolete IBM platform to a scalable SUN platform.
- Enhanced the department's problem reporting system and created WWW/HTML servers for the CUSP program, Speleology Information Service, and the 1995 Special Olympics World Games.

**Maine Yankee Atomic Power Co., Wiscasset, ME**  
*Computer Engineer/Analyst*

Jan. - Aug. 1990, Jan. - Nov. 1992

- Wrote and maintained safety-related software on the real-time plant monitoring system.
- Assisted in the installation of a dedicated Internet link through UUNET.
- Maintained a DECNET/PATHWORKS/TCP-IP local area network.
- Aided in the implementation of a computerized maintenance, inventory, purchasing, and payables system.
- Gained valuable experience in network management and UNIX (Ultrix) system administration.

**Tuck School of Business**, Dartmouth College, Hanover, NH

*Full-time Research Assistant*

Jun. - Aug. 1991

- Developed application to simulate machine scheduling scenarios.
- Designed graphical user interface in SunOS and X-Windows for bond calculation programs.
- Gained valuable experience with Client/Server and RPC programming.

## **SELECTED PUBLICATIONS**

Robert Hubley; Robert D. Finn; Jody Clements; Sean R. Eddy; Thomas A. Jones; Weidong Bao; Arian F.A. Smit; Travis J. Wheeler

The Dfam database of repetitive DNA families

Nucleic Acids Research (2016) Database Issue 44:D89-89. Doi 10.1093/nar/gkv1272

Jared C. Roach, Gustavo Glusman, Arian F. A. Smit, Chad D. Huff, Robert Hubley, Paul T. Shannon, Lee Rowen, Krishna P. Pant, Nathan Goodman, Michael Bamshad, Jay Shendure, Radoje Drmanac, Lynn B. Jorde, Leroy Hood, David J. Galas

Analysis of Genetic Inheritance in a Family Quartet by Whole-Genome Sequencing Science March 10, 2010, [DOI: 10.1126/science.1186802]

Heidi J. T. Pagan, Jeremy D. Smith, Robert M. Hubley and David A. Ray

PiggyBac-ing on a primate genome: Novel elements, recent activity and horizontal transfer

Genome Biology and Evolution, May 2010, [doi:10.1093/gbe/evq021]

Jiang Z., Hubley R, Smit A.F.A, and Eichler E.

DupMasker: A tool for annotating primate segmental duplications

Genome Research May 23, 2008, 10.1101/gr.078477.108

Robert M Hubley, Eckart Zitzler and Jared C Roach

Evolutionary Algorithms for the Selection of Single Nucleotide Polymorphisms,

BMC Bioinformatics 2003 PDF

International Human Genome Sequencing Consortium.

Initial sequencing and analysis of the human genome

Nature 409, 860-921 (2001) The Human Genome Project

## **PROFESSIONAL ACTIVITIES**

Ad hoc reviewer for PLOS One, PLOS Computational Biology, and Bioinformatics

## **EDUCATION**

CLARKSON UNIVERSITY, Potsdam, NY.

Bachelor of Science in Computer Engineering, December 1991