

Randy Heiland

WORK EXPERIENCE

2003 – PRESENT

Senior Software Analyst/Programmer

Indiana University, Bloomington IN

Scientific software developer for bioinformatics, computational biology, and computational neuroscience. HPC manager. Cybersecurity analyst/programmer. Adjunct faculty in Mathematics Dept.

2005 – 2010

President

Acquired Science LLC

Consulting and scientific software development.

1997 – 2003

Senior Research Scientist

*National Center for Supercomputing Applications (NCSA),
University of Illinois, Urbana IL*

Scientific visualization software developer, including virtual reality (CAVE) and haptics. Taught course in OpenGL.

1993 – 1997

Computer Scientist

Pacific Northwest National Lab, Richland WA

Scientific visualization software developer for computational chemistry and image analysis.

JULY 1992 – DEC 1992

Graduate Research Associate

Los Alamos National Lab, Los Alamos NM

Software developer for data visualization and analysis on HPC.

1985 – 1987

Computer Programmer

Center for Industrial Research, Oslo Norway

Software developer for computer-aided geometric design.

EDUCATION

1992 **M.A., Mathematics**
(dynamical systems)
Arizona State University, Tempe

1985 **M.S., Computer Science**
(computer graphics, CAGD)
University of Utah, Salt Lake City

1979 **B.S., Computational Math**
Eastern Illinois University, Charleston

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🌐 [scholar.google.com/...](https://scholar.google.com/)
🌐 github.com/rheiland?tab=repositories

SAMPLE OF PROJECTS

CompuCell3D (compucell3d.org)

Modeling environment for multi-cell behavior

LifeScienceWeb

Web services for bioinformatics

VisBench/VisPort

Remote data visualization and analysis

ECCE (ecce.pnl.gov)

Extensible Computational Chemistry Environment

SOFTWARE SKILLS

GOOD LEVEL	C/C++, Python(+numerous pkgs), OpenGL, VTK, CMake, ParaView, MATLAB, git, \LaTeX , Eclipse, gdb, Linux, OSX
INTERMEDIATE	Fortran, Java, R, CUDA, OpenCL, OpenMP, ITK, HTML, Xcode, CAVE, cybersecurity
BASIC LEVEL	MySQL, MPI, Boost, Django, Mathematica, Javascript, Blender, Windows

SELECTED PUBLICATIONS & PRESENTATIONS

The Cell Behavior Ontology: Describing the intrinsic biological behaviors of real and model cells seen as active agents

J. P. Sluka, A. Shirinifard, M. Swat, A. Cosmanescu, R. W. Heiland, J. A. Glazier
Bioinformatics (2014) doi:10.1093/bioinformatics/btu210

Toward a Research Software Security Maturity Model

R Heiland, B Thomas, V Welch, C Jackson
Working Towards Sustainable Software for Science, SC13, Denver, CO, Nov 2013

Visualizing Cells and their Connectivity Graphs for CompuCell3D

R Heiland, M Swat, J Sluka, B Zaitlen, A Shirinifard, G Thomas, A Lumsdaine, and J Glazier
IEEE BioVis Symposium, Seattle, WA, Oct 2012

Introduction to Modeling and Computational Neuroscience using Python

R Heiland, J Champlin, S Ito, A Litke, A Lumsdaine, and J Beggs
Presentation at Society for Mathematical Biology Annual Meeting and Conference, July 2012

Extending transfer entropy improves identification of effective connectivity in a spiking cortical network model

S Ito, ME Hansen, R Heiland, A Lumsdaine, AM Litke, JM Beggs. *PloS one* 6 (11), e27431

Multicell simulations of development and disease using the CompuCell3D simulation environment

MH Swat, SD Hester, AI Balter, RW Heiland, BL Zaitlen, JA Glazier. *Systems Biology*, 361-428

VisPort: Web-Based Access to Community-Based Visualization Functionality

MP Baker, R Heiland, E Bachta, and M Das. *TeraGrid Conference, Madison, WI, June 2007*

Python for Scientific Gateways Development

R Heiland, S Mooney, J Boverhof, K Jackson, M Swat, A Balter, M Christie, J Insley
International Workshop on Grid Computing Environments, Reno, NV, Nov 2007

Web service infrastructure for chemoinformatics

X Dong, KE Gilbert, R Guha, R Heiland, J Kim, ME Pierce, GC Fox, DJ Wild
Journal of chemical information and modeling 47 (4), 1303-1307

Visual methods for interpreting optical nonlinearity at the molecular level

RD Wampler, AJ Moad, CW Moad, R Heiland, GJ Simpson
Accounts of chemical research 40 (10), 953-960

MutDB services: interactive structural analysis of mutation data

J Dantzer, C Moad, R Heiland, S Mooney. *Nucleic acids research* 33 (suppl 2), W311-W314

Identification of similar regions of protein structures using integrated sequence and structure analysis tools

B Peters, C Moad, E Youn, K Buffington, R Heiland, S Mooney
BMC structural biology 6 (1), 4

VisBench: A framework for remote data visualization and analysis

RW Heiland, MP Baker, DK Tafti. *Computational Science-ICCS 2001*, 718-727

Towards analyzing the dynamics of flames

D Armbruster, E Stone, R Heiland. *Fields Institute Communications* 5, 1-17

Phase-space analysis of bursting behavior in Kolmogorov flow

D Armbruster, R Heiland, EJ Kostelich, B Nicolaenko
Physica D: Nonlinear Phenomena 58 (1), 392-401

KLTOOL: a tool to analyze spatiotemporal complexity

D Armbruster, R Heiland, EJ Kostelich
Chaos: An Interdisciplinary Journal of Nonlinear Science 4 (2), 421-424