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Education

Ph.D., May 2009

Dissertation title: *Extracting signal from noise in biological data: Evaluations and applications of text mining and sequence coevolution.*

Mentor: Lawrence Hunter, Ph.D.

Program in Biophysics and Structural Biology

Department of Biochemistry and Molecular Genetics

University of Colorado Denver, Aurora, CO (Formerly U of C Health Sciences Center.)

Bachelor of Arts in Biochemistry, Minor in Chemistry, August 2004

University of Colorado at Boulder, College of Arts and Sciences, Boulder, CO

Bachelor of Science in Computer Science, May 2001

University of Colorado at Boulder, College of Engineering and Applied Science, Boulder, CO

Current Positions

Assistant Professor, 2011 – Present

Department of Biological Sciences, Northern Arizona University, Flagstaff, AZ, USA.

Department of Computer Science, Northern Arizona University, Flagstaff, AZ, USA.

Assistant Professor, 2012 – Present

Institute for Genomics and Systems Biology, Argonne National Laboratory, Argonne, IL, USA.

Research Affiliate, 2012 – Present

Microbial Genetics and Genomics Center, Northern Arizona University, Flagstaff, AZ, USA.

Grant funding

PI: Alfred P. Sloan Foundation; Funding period: October 2012 – September 2014

Microbial succession on common office surfaces across three climates

Co-PIs: Rob Knight, Jeffrey Siegel, Scott Kelley

\$249,876

Co-PI: NSF Dimensions of Biodiversity; Funding period: January 2013-December 2017

The taxonomic, genomic, and functional diversity of soil carbon dynamics

PI: Bruce Hungate; Co-PIs: Jane Marks, Egbert Schwartz, Paul Dijkstra, Lance Price

\$1,487,750

PI: Northern Arizona University Parent Leadership Council Microgrant; Funding period: January 2013-December 2013

Bringing the Cloud to the Classroom: Preparing our Students for Careers in Scientific Computing

\$1,750 for use of cloud computing resource in NAU courses and independent studies.

Co-PI: Northern Arizona University Research Investment Fund

Development of an automated method for signature discovery to increase taxonomic resolution and increase quantification accuracy in studies of microbial communities

PI: Talima Pearson (Dr. Pearson and I will co-mentor this post-doctoral scholar)

Two years salary and benefits support for post-doctoral scholar

Co-PI: Northern Arizona University Technology and Research Investment Fund Support for Post-doctoral Associates Program

PI: David Wagner (Dr. Wagner and I will co-mentor this post-doctoral scholar)

Two years salary and benefits support for post-doctoral scholar

PI: Amazon Web Services Research Grant; Funding period: January 2011, June 2011

Deploying Bioinformatics Software on the Amazon Elastic Compute Cloud

Co-PI: Rob Knight

\$62,500 in credit (total for initial grant and two renewals)

PI: Lewis and Clark Fund for Exploration and Field Research in Astrobiology; Funding period: May, 2011

Microbial Community Characterization of the Atacama Desert Soils

\$5000 for travel

PI: Amazon Web Services Education Grant; July 2011; August 2012; December 2012.

Approximately \$7000 in credit over multiple awards to support course work on the Amazon Web Services Elastic Compute Cloud.

National Library of Medicine Informatics Pre-Doctoral Training Fellowship

Funding period: July 2007 - July 2009; Grant number: T15LM009451.

Provided full funding, including tuition and stipend, for the final two years of my doctoral training.

Travel award for Argonne Soils Workshop

Provided registration and travel costs to attend the 2010 Argonne National Labs Soils Workshop, Sept. 2010.

NSF Travel Fellowship, Dec. 2008

Provided registration and travel costs to attend the 2008 Rocky Mountain Bioinformatics Conference.

Awards and Honors

Outstanding Dissertation Award Finalist

University of Colorado Denver, May 2009.

Outstanding Research Award, 23rd Annual Student Research Forum, University of Colorado Denver

Sequence co-occurrence and covariation suggest a model of the Type VI Secretion System, Jan. 2009.

Outstanding Research Award, 22nd Annual Student Research Forum, University of Colorado Denver

A Comparison of Coevolution Detection Methods on Protein Alpha Helices, Jan. 2008.

Best Presentation, Rocky Mountain Bioinformatics Conference

A Sentence Recognizer for Mutant Protein Structure Studies: Toward Intelligent Systems for the Management of Structural Biology Data, Dec. 2005.

Previous Positions

Research associate, March 2009 – July 2011

Rob Knight Laboratory, Department of Chemistry and Biochemistry, University of Colorado at Boulder, Boulder, CO.

Research assistant, February 2005 - 2009

Lawrence Hunter Laboratory, Computational Bioscience Program, Department of Pharmacology, University of Colorado Denver, Aurora, CO.

Research assistant (as rotation student), December 2004 - February 2005.

Mark Duncan Laboratory, Biomolecular Structure Program, University of Colorado Health Sciences Center, Aurora, CO.

Research assistant (as rotation student), August 2004 - November 2004.

Robert Garcea Laboratory, Biomolecular Structure Program, University of Colorado Health Sciences Center, Aurora, CO.

Research assistant, January 2003 - August 2004.

Michael Yarus and Rob Knight Laboratories, Department of Molecular, Cellular and Developmental Biology, University of Colorado at Boulder, Boulder, CO.

Contract Web Developer, 1999 - 2002.

American Business English Internet School, Boulder, CO.

Software Engineer, 2001 - 2002.

Freshwater Software (acquired by Mercury Interactive), Boulder, CO.

Student Intern, 2000 - 2001.

Freshwater Software, Boulder, CO.

Web Developer, System Administrator, 1998 - 2000.

Web Communications, University of Colorado at Boulder, Boulder, CO.

Teaching (all course materials available at <http://caporaso.us/teaching/>)

CS299/BIO299: Introduction to Bioinformatics, Northern Arizona University, Fall 2011; Spring 2013.

Designed and taught an undergraduate bioinformatics course for computer science and biology majors.

BIO599: Computational Biology. Designed and taught a graduate bioinformatics course for biology masters and doctoral students, Fall 2012.

CS486: Senior Capstone, Spring 2012. Mentored a team of five Computer Science seniors as they developed a software package for the biogeographical analysis of microbial communities. These tools were contributed to the QIIME software package in May of 2012 under an open source license.

CS399/BIO399: Introduction to Bioinformatics, Northern Arizona University, Spring 2012.

Designed and taught an undergraduate bioinformatics course for computer science and biology majors.

ISME 14 Bioinformatics Workshop: Using QIIME and MG-RAST to study microbial communities (I planned and organized this workshop; <http://www.isme-microbes.org/isme14/workshop>)

August, 2012, Copenhagen University, Copenhagen, Denmark. (Eight-hour course, including keynotes)

Using QIIME for the Analysis of Viral Communities

Environmental Virology Workshop, Tucson, AZ, USA. (Three-hour course)

Quantitative Insights Into Microbial Ecology (QIIME) Workshop

Swiss Microbial Ecology Satellite Symposium, February 2013, Neuchâtel, Switzerland (Four-hour course)

Argonne Soil Metagenomics Meeting, October 2012, Chicago, IL, USA. (Three-hour course)

Microbiology of the Built Environment Meeting, October 2012, Boulder, CO (Two-hour course)
International Geobiology Course, July 2012, Catalina Island, CA, USA. (Seven-day course)
University of Arizona, May 2012, Tucson, AZ, USA. (Eight-hour course.)
Northern Arizona University, January 2012, Flagstaff, AZ, USA. (Five-hour course)
International Geobiology Course, July 2011, Catalina Island, CA, USA. (Seven-day course)

Workshop on Comparative Genomics, July 2011.
Co-taught for two days on the PyCogent and QIIME software packages.

Extracting ecological signal from noise workshop. September 2010.
Co-taught a three-day course on computational tools for microbial ecology.
Molecular and Computational Biology Research School, Bergen, Norway.

Guest Lecturer, Fall semester, 2010; Fall semester 2009; Spring 2007.
Bioinformatics 7711/2, University of Colorado Denver, Aurora, CO.

Guest Lecturer, Spring semester, 2009.
CHEM/MCDB 4621/5621; CSCI 4317/5317, University of Colorado at Boulder, Boulder, CO.

High School Mathematics Tutor (IMP Program), December 2008 - June 2009.
Boulder, CO.

Curriculum Development: Mathematics assignments for undergraduate Biology students, 2003 - 2004.
Department of Human Resources, University of Colorado at Boulder, Boulder, CO.

Students Mentored

John Chase, Biology post-baccalaureate student, Northern Arizona University, Fall 2012 – Present. One co-publication.

Giorgio Casaburi, Biology Ph.D. student, Università di Napoli (visiting NAU), Fall 2012 – Present.

Daniel Domogala, Biology Master's student, Northern Arizona University, Spring 2012 – Present.

Jai Rideout, Computer Science Bachelor's student, Northern Arizona University, Fall 2011-Spring 2012.
Recipient of the *Most Promising Undergraduate Researcher* award at NAU in Spring of 2012. This was the first time this was awarded to a Computer Science student at NAU. Two co-publications.

William A. Walters, Molecular Biology Ph.D. student, University of Colorado at Boulder (graduate student in Rob Knight's laboratory), Spring 2009-Fall 2011. Four co-publications.

Anna Lindemann, Computer Science Bachelor's student, University of Colorado Health Science Center, Summer 2006. Two co-publications.

Conference Presentations

Ultra-high-throughput microbial ecology: software, sequencing and practice for studying tens of thousands of environments.

Swiss Microbial Ecology Meeting, February 2013, Neuchâtel, Switzerland.

American Society for Microbiology (Arizona regional meeting), Tempe, AZ, USA, April, 2012.

Genomics Standards Consortium 13, March 2012, Shenzhen, China.

American Society for Microbiology (Colorado regional meeting), Boulder, CO, USA, April, 2011.

QIIME and the art of fungal community analysis
Sloan Foundation Fungal Workshop, October 2012, Boulder, CO, USA.

Procrustes Analysis to Compare Biological Conclusions in Studies of the Human Microbiome
Cloud Computing for the Microbiome, April 2012, Boulder, CO, USA.

Earth Microbiome Project Data Analysis Update
Earth Microbiome Project/National Ecological Observatory Joint Meeting, November 2011, Boulder, CO.

Argonne Soil Metagenomics Meeting Wrap-up Talk
3rd Argonne Soil Metagenomics Meeting, October 2011, Chicago, IL, USA.

Moving Pictures of the Human Microbiome
Infectious Disease Research Network: Microbial Community Profiling Workshop, June 2011, London, UK.

Quantitative Insights Into Microbial Ecology
Infectious Disease Research Network: Microbial Community Profiling Workshop, June 2011, London, UK.

Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample.
Genomics Automation Congress, May 2010, Boston, MA, USA.
13th International Symposium on Microbial Ecology (poster presentation), Seattle, WA, USA, August, 2010.

Recovery of biological soil crust-like microbial communities in previously submerged soils of Glen Canyon.
11th Biennial Conference of Research on the Colorado Plateau, Flagstaff, AZ, USA, September, 2011.

Intermolecular Coevolution Suggests Interactions Between Type VI Secretion System Proteins
Rocky Mountain Bioinformatics Conference (oral and poster presentation), December, 2008.

Rapid Pattern Development for Concept Recognition Systems.
DMAP meeting, April, 2008, Aurora, CO.

Intrinsic Evaluation of Text Mining Tools May Not Predict Performance on Realistic Tasks
Pacific Symposium on Biocomputing (oral presentation), January, 2008.

A Comparison of Coevolution Detection Methods on Protein Alpha Helices
Pacific Symposium on Biocomputing (poster presentation), January, 2008.
Rocky Mountain Bioinformatics Conference (oral and poster presentation), December, 2007.

Recognizing Point Mutations in Text: Techniques and Applications in Biomedical Text Mining
Pacific Symposium on Biocomputing (poster presentation), January, 2007.

Concept Recognition, Information Retrieval, and Machine Learning in Genomics Question Answering
Rocky Mountain Bioinformatics Conference (oral and poster presentation), December, 2006.
Text REtrieval Conference (TREC) 2006 (poster presentation), November, 2006.

A Sentence Recognizer for Mutant Protein Structure Studies: Toward Intelligent Systems for the Management of Structural Biology Data.
Rocky Mountain Bioinformatics Conference (oral and poster presentation), December, 2005.

Concept Recognition and the TREC Genomics Tasks
Text REtrieval Conference (TREC) 2005 (poster presentation), November, 2005.

Stereochemical and Adaptive Factors in Genetic Code Evolution
Evolution 2004 (poster presentation), July, 2004.

Invited Presentations

From the swab to the cloud: advances toward understanding our microbial world
Science on Tap, February 2013, Flagstaff, AZ, USA.
National Cancer Institute, January 2013, Bethesda, Maryland, USA.

Ultra-high-throughput microbial ecology: software, sequencing and practice for studying tens of thousands of environments.
Fred Hutchinson Cancer Research Center, November 2012, Seattle, Washington, USA.
Lawrence Berkeley National Laboratory, June 2012, Berkeley, CA, USA.
Arizona State University, April 2012, Tempe, Arizona, USA.
University of Arizona, February 2012, Tucson, Arizona, USA.
University of Montana, April 2011, Bozeman, Montana, USA.

Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample.
Los Alamos National Laboratories, September 2010, Los Alamos, NM, USA.

Detecting Coevolution by Disregarding Evolution? Tree-Ignorant Metrics of Coevolution Perform As Well As Tree-Aware Metrics.
Genome Biology Seminars, Australian National University, November 2009, Canberra, Australia.

Invited Interdepartmental Seminars

Intermolecular Coevolution Suggests Interactions Between Type VI Secretion System Proteins.
Bioinformatics Supergroup, University of Colorado at Boulder, April, 2009.

Detecting Coevolution by Disregarding Evolution?
Bioinformatics Supergroup, University of Colorado at Boulder, April, 2008.

Peer-reviewed publications

Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing.
Bokulich NA, Subramanian S, Faith JJ, Gevers D, Gordon JI, Knight R, Mills DA, **Caporaso JG**.
Nature Methods, 2013.

Phylogenetic stratigraphy in the Guerrero Negro hypersaline microbial mat
Harris JK*, **Caporaso JG***, Walker JJ, Spear, JR, Gold NJ, Robertson CE, Hugenholtz P, Goodrich J, McDonald D, Knights D, Marshall P, Tufo H, Knight R, Pace NR (*contributed equally).
International Society for Microbial Ecology Journal, 2013.

Cross-biome metagenomic analyses of soil microbial communities and their functional attributes.
Fierer N, Leff JW, Adams BJ, Nielsen UN, Bates ST, Lauber CL, Owens S, Gilbert JA, Wall DH, **Caporaso JG**.
Proceedings of the National Academy of Science, 2012.

Human gut microbiome viewed across age and geography
Yatsunenko T, Rey FE, Manary MJ, Trehan I, Dominguez-Bello MG, Contreras M, Magris M, Hidalgo G, Baldassano RN, Anokhin AP, Heath AC, Warner B, Reeder J, Kuczynski J, **Caporaso JG**, Lozupone CA, Lauber C, Clemente JC, Knights D, Knight R, Gordon JI.
Nature, 2012.

Collaborative cloud-enabled tools allow rapid, reproducible biological insights.
Ragan-Kelley B, Walters WA, McDonald D, Riley J, Granger BE, Gonzalez A, Knight R, Perez F, **Caporaso JG**.
International Society for Microbial Ecology Journal, 2012

The Biological Observation Matrix (BIOM) Format or: How I Learned To Stop Worrying and Love the Ome-
ome

McDonald D, Clemente JC, Kuczynski J, Rideout JR, Stombaugh J, Wendel D, Wilke A, Huse S, Hufnagle J, Meyer F, Knight R, **Caporaso JG**.
GigaScience, 2012.

Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms.

Caporaso JG, Lauber C, Walters WA, Berg-Lyons D, Huntley J, Fierer N, Betley J, Fraser L, Bauer M, Gormley N, Smith G and Knight R.

International Society for Microbial Ecology Journal, 2012.

**ISME Journal Top Ten download articles list from April 2012-Present. Selected for review by Faculty of 1000.*

The interpersonal and intrapersonal diversity of human-associated microbiota in key body sites.

Ursell LK, Clemente JC, Rideout JR, Gevers D, **Caporaso JG**, Knight R.

Journal of Allergy and Clinical Immunology, 2012.

Diversity, distribution and sources of bacteria in residential kitchens.

Flores GE, Bates ST, **Caporaso JG**, Lauber CL, Leff JW, Knight R, Fierer N.

Environmental Microbiology, 2012.

Sequencing our way towards understanding global eukaryotic biodiversity.

Bik HM, Porazinska DL, Creer S, **Caporaso JG**, Knight R, Thomas WK.

Trends in Ecology and Evolution, 2012.

The under-recognized dominance of Verrucomicrobia in soil bacterial communities.

Bergmann GT, Bates ST, Eilers KG, Lauber CL, **Caporaso JG**, Walters WA, Knight R, Fierer N.

Soil Biology and Biochemistry, 2011.

Using QIIME to analyze 16S rRNA gene sequences from microbial communities.

Kuczynski J, Stombaugh J, Walters WA, González A, **Caporaso JG**, Knight R.

Current Protocols in Bioinformatics. 2012

The Western English Channel contains a persistent microbial seed bank.

Caporaso JG, Paszkiewicz K, Field D, Knight R, Gilbert JA.

International Society for Microbial Ecology Journal, 2012.

Comparison of Illumina paired-end and single-direction sequencing for microbial 16S rRNA gene
amplicon surveys.

Werner JJ, Zhou D, **Caporaso JG**, Knight R, Angenent LT.

International Society for Microbial Ecology Journal, 2011.

TopiaryExplorer: visualizing large phylogenetic trees with environmental metadata.

Pirrung M, Kennedy R, **Caporaso JG**, Stombaugh J, Wendel D, Knight R.

Bioinformatics, 2011

Defining seasonal marine microbial community dynamics.

Gilbert JA, Steele JA, **Caporaso JG**, Steinbrück L, Reeder J, Temperton B, Huse S, McHardy AC, Knight R, Joint I, Somerfield P, Fuhrman JA, Field D.

International Society for Microbial Ecology Journal, 2011.

Impact of training sets on classification of high-throughput bacterial 16s rRNA gene surveys.

Werner JJ, Koren O, Hugenholtz P, Desantis TZ, Walters WA, **Caporaso JG**, Angenent LT, Knight R, Ley RE.

International Society for Microbial Ecology Journal, 2011.

Moving Pictures of the Human Microbiome

Caporaso JG, Lauber CL, Costello EK, Berg-Lyons D, Gonzalez A, Stombaugh J, Knights D, Gajer P, Ravel J, Fierer N, Gordon JI, Knight R
Genome Biol. 2011 May 30;12(5):R50.

** Selected for review by Faculty of 1000.*

New insight into the diversity of life's building blocks: evenness, not variance.

Caporaso JG, Knight R.

Astrobiology. 2011 Apr;11(3):197-8

PrimerProspector: de novo design and taxonomic analysis of barcoded PCR primers

Walters WA*, **Caporaso JG***, Lauber CL, Berg-Lyons D, Fierer N Knight R (*contributed equally)

Bioinformatics. 2011 Apr 15;27(8):1159-61.

Host-Associated and Free-Living Phage Communities Differ Profoundly in Phylogenetic Composition

Caporaso JG, Knight R, Kelley ST

PLoS One. 2011 Feb 24;6(2):e16900.

Bacterial communities associated with the lichen symbiosis

Bates ST, Cropsey GW, **Caporaso JG**, Knight R, Fierer N

Appl Environ Microbiol. 2011 Feb;77(4):1309-14

Examining the global distribution of dominant archaeal populations in soil

Bates ST, Berg-Lyons D, **Caporaso JG**, Walters WA, Knight R, Fierer N

International Society for Microbial Ecology Journal 2010

Soil bacterial diversity in the Arctic is not fundamentally different from that found in other biomes

Chu H, Fierer N, Lauber CL, **Caporaso JG**, Knight R, Grogan P

Environmental Microbiology, 2010 Nov;12(11):2998-3006.

Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample

Caporaso JG, Lauber CL, Walters WA, Berg-Lyons D, Lozupone CA, Turnbaugh PJ, Fierer N, Knight R

Proceedings of the National Academy of Science, 2010.

Soil bacterial and fungal communities across a pH gradient in an arable soil

Rousk J, Baath E, Brookes PC, Lauber CL, Lozupone C, **Caporaso JG**, Knight R, Fierer N

International Society for Microbial Ecology Journal, 2010 May.

QIIME allows analysis of high-throughput community sequencing data

Caporaso JG*, Kuczynski J*, Stombaugh J*, Bittinger K, Bushman FD, Costello EK, Fierer N, Peña AG, Goodrich JK, Gordon JI, Huttley GA, Kelley ST, Knights D, Koenig JE, Ley RE, Lozupone CA, McDonald D, Muegge BD, Pirrung M, Reeder J, Sevinsky JR, Turnbaugh PJ, Walters WA, Widmann J, Yatsunenko T, Zaneveld J, Knight R (*contributed equally).

Nature Methods 2010 May, 7(5):335-6.

PyNASt: a flexible tool for aligning sequences to a template alignment

Caporaso JG, Bittinger K, Bushman FD, DeSantis TZ, Andersen GL, Knight R

Bioinformatics 2010, 26(2):266-7.

Detecting Coevolution by Disregarding Evolution? Tree-Ignorant Metrics of Coevolution Perform As Well As Tree-Aware Metrics

Caporaso JG, Smit S, Easton BC, Hunter L, Huttley GA, Knight R

BMC Evolutionary Biology 2008, 8:327.

An Integrated Approach to Concept Recognition in Biomedical Text

Baumgartner WA Jr., Lu Z, Johnson HL, **Caporaso JG**, Paquette J, Lindemann A, White EK, Medvedeva O, Cohen KB, Hunter L
Genome Biology, 2008, Suppl 2:S9.

Intrinsic Evaluation of Text Mining Tools May Not Predict Performance on Realistic Tasks

Caporaso JG, Deshpande N, Fink JL, Bourne PE, Cohen KB, Hunter L
Pacific Symposium on Biocomputing 13:640-651(2008).

Rapid Pattern Development for Concept Recognition Systems: Application to Point Mutations

Caporaso JG, Baumgartner WA Jr., Randolph DA, Cohen KB, Hunter L
Journal of Bioinformatics and Computational Biology, 2007 Dec;5(6):1233-59.

PyCogent: A Toolkit for Making Sense from Sequence

Knight R, Maxwell P, Birmingham A, Carnes J, **Caporaso JG**, Easton BC, Eaton M, Hamady M, Lindsay H, Liu Z, Lozupone C, McDonald D, Robeson M, Sammut R, Smit S, Wakefield MJ, Widmann J, Wikman S, Wilson S, Ying H, Huttley GA
Genome Biology 2007, 8:R171.

MutationFinder: A High-Performance System for Extracting Point Mutation Mentions from Text

Caporaso JG, Baumgartner WA Jr, Randolph DA, Cohen KB, Hunter L
Bioinformatics, 2007 23(14):1862-1865.

Error Minimization and Coding Triplet/Binding Site Associations are Independent Features of the Canonical Genetic Code

Caporaso JG, Yarus M, and Knight R
Journal of Molecular Evolution, 2005.

Origins of the Genetic Code: The Escaped Triplet Theory

Yarus,M, **Caporaso JG**, and Knight R
Annual Review of Biochemistry, 2005.

Invited Publications

Concept Recognition, Information Retrieval, and Machine Learning in Genomics Question Answering

Caporaso JG, Baumgartner WA Jr., Kim H, Lu Z, Johnson HL, Medvedeva O, Lindemann A, Fox LM, White EK, Cohen KB, and Hunter L
TREC 2006 Conference Proceedings, January, 2007.

Concept recognition and the TREC Genomics tasks

Caporaso JG, Baumgartner WA Jr, Cohen KB, Johnson HL, Paquette J, Hunter L
TREC 2005 Conference Proceedings, January, 2006.

Open-source Software Projects

Lead developer, QIIME (Quantitative Insights Into Microbial Ecology)

<http://www.qiime.org>

Developer, PyCogent (Python Comparative GENomics Toolkit)

<http://www.pycogent.org>

Developer, PICRUSt (Phylogenetic Investigation of Communities by Reconstruction of Unobserved States)

<http://picrust.github.com>

Developer, BIOM (BIological Observation Matrix) project and file format

<http://biom-format.org>

**A candidate project of the Genomics Standards Consortium, and an Earth Microbiome Project standard.*

Lead developer, PyNAST (Python Nearest Alignment Space Termination tool)

<http://qiime.github.com/pynast>

Developer, PrimerProspector

<http://pprospector.sourceforge.net>

Lead developer, MutationFinder (no longer under active development)

<http://mutationfinder.sourceforge.net>

Professional Society Memberships

International Society for Microbial Ecology, since 2010.

American Society for Microbiology, since 2011.

International Society for Computational Biology, 2005-2009.

American Association for the Advancement of Science, 2006-2009.

References

Rob Knight, Associate Professor

Howard Hughes Medical Institute

Department of Chemistry and Biochemistry, University of Colorado at Boulder.

rob.knight@colorado.edu; (303) 492-1984

Lawrence Hunter, Professor

Computational Bioscience Program, University of Colorado Denver.

Department of Pharmacology, University of Colorado Denver.

larry.hunter@ucdenver.edu; (303) 724-3574

Noah Fierer, Assistant Professor

Department of Ecology & Evolutionary Biology, University of Colorado at Boulder

Cooperative Institute for Research in Environmental Sciences

noah.fierer@colorado.edu; (303) 492-5615