Héctor García Martín

Curriculum vitae

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PERSONAL INFORMATION

Address:
EmeryStation East
5885 Hollis St., 4th Floor
Emeryville, CA 94608
USA

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Status: Green card holder

EDUCATION

Ph. D. in Physics — October 2004
University of Illinois at Urbana-Champaign — Urbana, IL USA

Licenciado en Ciencias Fisicas, — Spring 1999
University of the Basque Country (UPV/EHU) — Bilbao, SPAIN
(Corresponds to five years of study in Physics)

PRESENT POSITION

Deputy Vice President, Biofuels and Bioproducts Division (BBD)
Director, Quantitative Metabolic Modeling
Joint BioEnergy Institute (JBEI)

Computational Biologist Research Scientist Engineer
Lawrence Berkeley National Laboratory

External Scientific Member
Basque Center for Applied Mathematics (BCAM)

RESEARCH EXPERIENCE

Deputy Vice President, — 2018-Present
Joint BioEnergy Institute
Biofuels and Bioproducts Division

Director, Quantitative Metabolic Modeling — 2011-Present
Joint BioEnergy Institute
Fuel Synthesis Division
Responsibilities:

- Develop mathematical models to improve biofuel production.
- Develop a standardized online database for data produced at JBEI.
- Develop online visualization tools for transcriptomics, proteomics, metabolomics and fluxomics data.

Computational Biologist Research Scientist Engineer — 2009-Present
Lawrence Berkeley National Laboratory
Responsibilities:

- Develop infrastructure for quantitative metabolic modeling efforts.
- Raise funds for research from governmental and private sources.
- Research functions as per Project Scientist.

Deputy Director, Host Engineering — 2008-2011
Joint BioEnergy Institute

Fuel Synthesis Division
Responsibilities:

- Develop and deploy quantitative models of microbial metabolism to guide metabolic engineering in order to improve biofuel production.
- Lead with the director the technical activities of the Host Engineering directorate.

Computer Project Scientist 2007-2009
Lawrence Berkeley National Laboratory
Responsibilities:

- Develop quantitative predictive models for microbial metabolism.
- Develop methods to measure metabolic fluxes using ^{13}C tracing experiments and nonlinear optimization.
- Develop methods to measure metabolic fluxes for microbial communities using ^{13}C tracing experiments and nonlinear optimization.

Computational Biologist Post Doctoral Fellow 2005-2007
DOE Joint Genome Institute
Lawrence Berkeley National Laboratory
Advisor: Philip Hugenholtz
Research:

- Metagenomics of phosphorus removing communities.
- Metagenomics of termite gut microbial communities.

Graduate Research Assistant 2000-2004
Department of Physics
University of Illinois at Urbana-Champaign
Advisor: Nigel Goldenfeld
Research:

- Scaling laws in ecology.
- Microbial ecology in the context of pattern formation of travertine terraces.
- Path Integral Monte Carlo simulations of Bose Einstein Condensates.

TEACHING EXPERIENCE

Graduate Teaching Assistant 1999-2000
Department of Physics
University of Illinois at Urbana-Champaign

Physics 336 Fall 1999
Electromagnetic Fields and Sources, II

Physics 112 Spring 2000
General Physics (Electricity and Magnetism)

INVITED TALKS

Agile BioFoundry (ABF) Annual Meeting September 2018
Talk title: A New Approach to Flux Analysis Berkeley, USA

Machine Learning for Science Workshop September 2018
Talk title: Towards a Predictive Synthetic Biology Enabled by Machine Learning and Automation Berkeley, USA

Joint BioEnergy Institute (JBEI) Annual Meeting August 2018
Talk title: Opportunities in the Intersection of Synthetic Biology, Sonoma, USA

Machine Learning and Automation

10th International Workshop on Bio-Design and Automation August 2018
Talk title: Towards a Predictive Synthetic Biology Enabled by Berkeley, USA
Machine Learning and Automation

BioEPIC workshop August 2018
Talk title: Modeling from Molecules to Ecosystems: Berkeley, USA
Opportunities, Challenges and Vision

Society for Industrial Microbiology (SIMB) Annual Meeting August 2018
Talk title: Towards a Predictive Synthetic Biology Enabled by Chicago, USA
Machine Learning and Automation

Artificial Intelligence for Synthetic Biology July 2018
Talk title: Machine Learning to Predict Metabolic Pathway Stockholm, Sweden
Dynamics from Multiomics Data

Basque Center for Applied Mathematics (BCAM) July 2018
Talk title: Towards a Predictive Synthetic Biology Enabled by BCAM
Machine Learning and Automation Bilbao, Spain

Biocruces July 2018
Talk title: Towards a Predictive Synthetic Biology Enabled by Biocruces
Machine Learning and Automation Bilbao, Spain

Madison Microbiome Meeting April 2018
Talk title: A Machine Learning Approach to Predict Madison, USA
Metabolic Pathway Dynamics from Time Series Multiomics Data

LEARN summit at Argonne National Lab March 2018
Talk title: EDD as a data warehouse and Learn facilitator Lemont, USA

Bayer February 2018
Talk title: Metabolic Modeling of –omics Data for Sacramento, USA
Biofuel Production

Environmental Genomics and Systems Biology retreat January 2018
Talk title: Machine Learning and Mechanistic Models to Predict Berkeley, USA
Biological Outcomes using ‘omics Data

Washington University EECE Department Seminar October 2017
Talk title: Modeling of –omics Data for Biofuel Production St. Louis, USA
through Synthetic Biology

Hellenic Bioinformatics 10 September 2017
Talk title: Modeling of –omics Data for Biofuel Production Heraklion, Greece
through Synthetic Biology

Multi-omics for Microbiomes conference July 2017
Talk title: Predicting Metabolic Pathway Dynamics by Combining Pasco, USA
Multiomics Data with Machine Learning and Kinetic Modeling

LBNL ecology monthly meeting July 2017
Talk title: Modeling of –omics Data for Biofuel Production Berkeley, USA
through Synthetic Biology

Second encounter of Spanish scientists in USA June 2017
Talk title: Mathematical Modeling of –omics Data for Biofuel Cambridge, USA
Production through Synthetic Biology

Zymergen April 2017
Talk title: Mathematical Modeling of –omics Data for Biofuel Emeryville, USA
Production through Synthetic Biology

REDBIO 2016 conference June 2016
Talk title: Quantitative metabolic modeling for biofuel synthesis Lima, Peru

Biogune May 2016
Talk title: Mathematical Modeling of –omics Data for Biofuel Bilbao, Spain
Production

Basque Center for Applied Mathematics (BCAM) May 2016
Talk title: Mathematical Modeling of –omics Data for Biofuel Bilbao, Spain
Production

BSE Division Seminar February 2016
Talk title: Mathematical Modeling of –omics Data for Biofuel Berkeley, USA
Production

Multiomics conference September 2015
Talk title: Mathematical Modeling of –omics Data for Biofuel Richland, USA
Production

Society for Industrial Microbiology (SIMB) Annual Meeting August 2015
Talk title: Principal component analysis of proteomics (PCAP) Philadelphia, USA
as a tool to direct metabolic engineering

2015 UK Metabolomics Symposium July 2015
Talk title: Metabolic engineering tools for biofuel production Lexington, USA

Cell factories and sustainability May 2015
Talk title: Quantitative metabolic modeling for biofuel Hillerod, Denmark
Synthesis

Genomatica March 2015
Talk title: Quantitative metabolic modeling for biofuel San Diego, USA
Synthesis

Joint Genome Institute January 2015
Talk title: Quantitative metabolic modeling for biofuel Walnut Creek, USA
Synthesis

Agilent August 2014
Talk title: Quantitative metabolic modeling for biofuel Santa Clara, USA
synthesis

EMSL May 2014
Talk title: Metabolic Flux Analysis Richland, USA

Metabolomics 2014 conference June 2014
Talk title: Quantitative metabolic modeling for biofuel Tsuruoka, Japan
synthesis

COBRA 2014 conference
Talk title: Quantitative metabolic modeling for biofuel synthesis
May 2014
Wintergreen, USA

EMSL
Talk title: Quantitative metabolic modeling for biofuel synthesis
May 2014
Richland, USA

“Bioenergy and Biosynthesis of Specialty Chemicals” invited lecture
Talk title: Metabolic flux analysis
February 2014
UC Berkeley, USA

RECOMB ISCB Conference on Regulatory and Systems Genomics with DREAM Challenges
Talk title: A ^{13}C-based method for metabolic flux measurement and prediction in genome-scale models
November 2013
Toronto, Canada

Lawrence Livermore National Laboratory
Talk title: Quantitative metabolic modeling for biofuel synthesis
November 2013
Livermore, USA

EMSL Biosciences Theme Advisory Panel
Talk title: Quantitative metabolic modeling for biofuel synthesis at JBEI
May 2013
Richland, USA

Conference on Predicting Cellular Metabolism and Phenotypes
Talk title: Quantitative metabolic modeling for biofuel synthesis
May 2013
Menlo Park,USA

Frontiers in Large Scale Organism and Pathway Engineering Conference
Talk title: Quantitative metabolic modeling for biofuel synthesis
April 2013
Walnut Creek, USA

“Bioenergy and Biosynthesis of Specialty Chemicals” invited lecture
Talk title: Metabolic flux analysis
March 2013
UC Berkeley, USA

SRI
Talk title: Quantitative metabolic modeling for biofuel synthesis
March 2013
Menlo Park, USA

AIChE annual meeting
Talk title: A two-scale ^{13}C-based method for metabolic flux measurement and prediction in genome-scale models
November 2012
Pittsburgh, USA

2nd International conference on COBRA
Talk title: A two-scale ^{13}C-based method for metabolic flux measurement and prediction in genome-scale models
October 2012
Elsinore, Denmark

Abengoa
Talk title: Quantitative metabolic modeling for biofuel synthesis
October 2012
Seville, Spain

Taxon Biosciences
Talk title: Measuring and predicting fluxes through ^{13}C carbon labeling experiments
May 2012
Tiburon, USA

Industrial Biotechnology conference
Talk title: Measuring and predicting fluxes through ^{13}C carbon labeling experiments
April 2012
Xian, China

"Bioenergy and Biosynthesis of Specialty Chemicals" invited lecture March 2012
Talk title: Metabolic flux analysis UC Berkeley
Berkeley, USA

Joint Genome Institute February 2012
Talk title: Measuring and predicting fluxes through Walnut Creek, USA
^{13}C carbon labeling experiments

Codexis December 2011
Talk title: Measuring and predicting fluxes through Redwood City, USA
^{13}C carbon labeling experiments

Amyris December 2011
Talk title: Measuring and predicting fluxes through ^{13}C carbon Emeryville, USA
labeling experiments

Statistics and Genomics seminar November 2011
Talk title: Measuring and predicting fluxes through UC Berkeley, USA
^{13}C carbon labeling experiments

Bay Area Bioinformatics Forum (BAYBIFX) June 2011
Talk title: Metabolic flux analysis of biodiesel UC Berkeley, USA
producing *E. coli*

Energy Biosciences Institute May 2011
Talk title: Metabolic flux analysis of biodiesel producing *E. coli* Berkeley, USA

Basque Center for Applied Mathematics (BCAM) September 2010
Talk title: Combining synthetic biology and modeling of bacterial Bilbao, Spain
metabolism to increase biofuel production from lignocellulosic
biomass

Microbial Data Integration Workshop August 2010
Talk title: Metafluxomics, measuring metabolic flux Berkeley, USA
distributions for microbial communities

Contra Costa College April 2010
Talk title: Developing predictive models of microbial San Pablo, USA
metabolism for biofuel production and microbial ecology

Jornada Metagenomica December 2006
Talk title: Wastewater sludge metagenomics Valencia, Spain

AWARDS AND HONORS

MIT's "Innovators under 35" competition jury 2017 and 2018
Berkeley, USA

Member of Pacific Northwest National Lab's (PNNL) advisory 2015-2017
committee for the "Microbes in Transition" initiative Richland, USA

Selected to participate in NSF's Innovation Corps (I-Corps) 2015
competitive entrepreneurship program Berkeley, USA
Lawrence Berkeley National Laboratory/JBEI

US permanent resident as Oustanding Researcher (EB-12) 2012
Lawrence Berkeley National Laboratory/JBEI Berkeley, USA

Member of Congresswoman Lee’s biotech advisory committee 2011
Lawrence Berkeley National Laboratory/JBEI Berkeley, USA

Renato Bobone Award to the Outstanding 2002
European Grad Student in Physics Urbana-Champaign, USA
Department of Physics
University of Illinois at Urbana-Champaign

Excellence in Teaching award 2000
Department of Physics Urbana-Champaign, USA
University of Illinois at Urbana-Champaign

Incomplete List of Teachers Ranked as Excellent 2000
by Their Students Urbana-Champaign, USA
University of Illinois at Urbana-Champaign

Phi Kappa Phi Honors Society 2002
University of Illinois at Urbana-Champaign Chapter Urbana-Champaign, USA

TASSEP exchange program 1998
University of Texas at Austin Austin, USA

BBK scholarship for TASSEP exchange program 1998
University of the Basque Country (UPV/EHU) Bilbao, Spain

PUBLICATIONS

Costello, Z., and *Garcia Martin H*. "A machine learning approach to predict metabolic pathway dynamics from time-series multiomics data." **Nature pj Systems Biology & Applications 4.1: 19 (2018).**

Oyetunde, T., Bao, F. S., Chen, J. W., *Garcia Martin, H.*, Tang, Y. J. "Leveraging knowledge engineering and machine learning for microbial biomanufacturing." **Biotechnology Advances 36(4):1308 (2018).**

Iwai, K., Ando, D., Kim, P. W., Gach, P. C., Raje, M., Duncomb, T. A., Heinemann, J., Northen, T., *Garcia Martin, H.*, Hillson, N., Adams, P. D., Singh. A. “Automated flow-based/digital microfluidic platform integrated with onsite electroporation process for multiplex genetic engineering applications.”
Micro Electro Mechanical Systems (MEMS): IEEE (pp. 1229-1232) (2018).

Denby C.M., Li R.A., Vu V.T., Costello Z., Lin W., Chan L.J., Williams J., Donaldson B., Bamforth C.W., Petzold C.J., Scheller H.V., *Garcia Martin H.* and Keasling, J.D. “Industrial brewing yeast engineered for the production of primary flavor determinants in hopped beer.”
Nature Communications, 9(1): 965 (2018).

Backman, T.W., Ando, D., Singh, J., Keasling, J.D. and *García Martín, H*. “Constraining Genome-Scale Models to Represent the Bow Tie Structure of Metabolism for 13C Metabolic Flux Analysis.”
Metabolites, 8(1), p.3 (2018).

Ando, D., and *Garcia Martin, H*. "Two-Scale 13C Metabolic Flux Analysis for Metabolic Engineering."

Synthetic Metabolic Pathways. Humana Press, NY, 2018. 333-352 (2018).

Morrell, W., Birkel, G., Forrer, M., Lopez, T., Backman, T., Dussault, M., Petzold, C.J., Baidoo, E.E.K., Costello, Z., Ando, D., Alonso-Gutierrez, J., George, K., Mukhopadhyay, A., Vaino, I., Keasling, J.D., Adams, P.D., Hillson, N.J., *Garcia Martin, H.* ”The Experiment Data Depot: a web-based software tool for biological experimental data storage, sharing, and visualization”
ACS Synthetic Biology DOI: 10.1021/acssynbio.7b00204 (2017).

D’Espaux, L., Gosh, A., Runguphan, W., Wehrs, M., Xu, F., Konzock, O., Dev, I., Nhan, M., Gin, J., Reider Apel, A., Petzold, C. J., Singh, S., Simmons, B. A., Mukhopadhyay, A., *Garcia Martin, H***.**, Keasling, J.D. "Engineering high-level production of fatty alcohols by Saccharomyces cerevisiae from lignocellulosic feedstocks."
Metabolic Engineering 42: 115-125 (2017).

Birkel, G. W., Ghosh, A., Kumar, V.S., Weaver, D., Ando, D., Backman, T.W.H.B., Arkin, A.P., Keasling, J.D., *Garcia Martin, H.* "The JBEI quantitative metabolic modeling library (jQMM): a python library for modeling microbial metabolism.”
BMC bioinformatics 18 (1): 205 (2017).

Shymansky, C., Wang, G., Baidoo, E.E.K., Gin, J., Reider Apel, A., Mukhopadhyay, A., *Garcia Martin, H.,* Keasling, J.D. "Flux-Enabled Exploration of the Role of Sip1 in Galactose Yeast Metabolism."
Frontiers in Bioengineering and Biotechnology 5 (2017).

Ghosh, A., Ando, D., Gin, J., Runguphan, W., Denby, C., Wang, G., Baidoo, E.E.K., Shymansky, C., Keasling, J.D., *Garcia Martin, H.* "^{13}C Metabolic Flux Analysis for Systematic Metabolic Engineering of S. cerevisiae for Overproduction of Fatty Acids."
Frontiers in Bioengineering and Biotechnology 4 (2016).

Hollinshead, W. D., Rodriguez, S., *Garcia Martin, H.*, Wang, G., Baidoo, E.E.K., Sale, K.L., Keasling, J.D., Mukhopadhyay, A., Tang, Y. J. "Examining Escherichia coli glycolytic pathways, catabolite repression, and metabolite channeling using Δ pfk mutants."
Biotechnology for Biofuels 9 (1): 212 (2016).

Brunk, E., George, K.W., Alonso-Gutierrez, J., Thompson, M., Baidoo, E.E.K., Wang, G., Petzold, C.J., McCloskey, D., Monk, J., Yang, L., O'Brien, E.J., Batth, T.S., *Garcia Martin, H.*, Feist, A., Adams, P.D., Keasling, J.D., Palsson, B.O., Lee, T.S. "Characterizing Strain Variation in Engineered *E. coli* Using a Multi-Omics-Based Workflow."
Cell Systems 2 (5): 335-346 (2016).

Chubukov, V., Mukhopadhyay, A., Petzold, C.J., Keasling, J.D., *Garcia Martin, H.*
“Synthetic and systems biology for microbial production of commodity chemicals”
Nature pj Systems Biology & Applications 2: 16009 (2016).

Garcia Martin, H., Kumar, V.S., Weaver, D., Ghosh, A., Chubukov, V., Mukhopadhyay, A., Arkin, A., Keasling, J.D.
“A method to constrain genome-scale models with ^{13}C labeling data”
PLOS Computational Biology 11(9): e1004363 (2015).

Alonso-Gutierrez, J., Kim E.M., Bath, T.S., Cho, N., Hu, Q., Chan, L.J., Petzold, C.J., Hillson, N.J., Adams, P.D., Keasling, J.D., *Garcia Martin, H.*, Lee, T.S.
“Principal component analysis of proteomics (PCAP) as a tool to direct metabolic

engineering"
Metabolic Engineering 28: 123-133 (2015).

Ghosh, A., Nilmeier, J., Weaver, D., Adams, P.D., Keasling, J.D., Mukhopadhyay, A., Petzold, C.J., *Garcia Martin, H.*
"A Peptide-Based Method for ^{13}C Metabolic Flux Analysis in Microbial Communities"
PLOS Computational Biology 10(9): e1003827 (2014).

Sarria, S., Wong, B., *Garcia Martin, H.*, Keasling, J.D., Peralta-Yahya, P.
"Microbial Synthesis of Pinene"
ACS Synthetic Biology 3(7): 466-75 (2014).

Bokinsky, G. Baidoo, E.E.K., Akella, S., Burd, H., Weaver, D., Alonso-Gutierrez, J., *Garcia Martin, H.*, Lee, T.S., Keasling, J.D.
"HipA-Triggered Growth Arrest and beta-Lactam Tolerance in Escherichia coli are Mediated by RelA-Dependent ppGpp Synthesis"
Journal of Bacteriology 195(14): 3173-82 (2013).

Garcia Martin, H., Veysey, J., Bonheyo, G.T., Frias-Lopez, J., Goldenfeld, N. and Fouke, B.W.
"Statistical Evaluation of Bacterial 16S rRNA Gene Sequences in Relation to Travertine Mineral Precipitation and Water Chemistry at Mammoth Hot Springs, Yellowstone National Park, USA"
In **Geomicrobiology: molecular and environmental perspective, 11: 239-249 (2010).**

Shaikh, A.S., Tang, Y.J., Mukhopadhyay, A., *Garcia Martin, H.*, Gin, J. Benke, P., Keasling, J.D.
"Study of stationary phase metabolism via isotopomer analysis of amino acids from an isolated protein"
Biotechnology Progress 26(1):52-6 (2010).

He, S., Kunin, V., Haynes, M., *Garcia Martin, H.*, Ivanova, N., Rohwer, F., McMahon, H., Hugenholtz, P.
"Metratranscriptomic array analysis of 'Candidatus Accumulibacter phosphatis'-enriched enhanced biological phosphorus removal sludge".
Environmental Microbiology 12(5):1205-17 (2010).

Tang, Y.J., *Garcia Martin, H.*, Deutschbauer, A., Feng, X., Huang, R., Llora, X., Arkin, A., Keasling, J.D.
"Invariability of central metabolic flux distribution in Shewanella oneidensis MR-1 under environmental or genetic perturbations"
Biotechnology Progress 25(5): 1254-1259 (2009).

Tang, Y.J.*, *Garcia Martin, H.**, Myers, S., Rodriguez, S., Baidoo, E.E.K., Keasling, J.D.
"Advances in analysis of microbial metabolic fluxes via ^{13}C isotopic labeling"
Mass Spectrometry Reviews, 28(2): 362-375 (2009).
* Contributed equally to this study.

Tang, Y.J.*, *Garcia Martin, H.**, Dehal, P.S., Deutschbauer, A., Llora, X., Meadows, A., Arkin, A., Keasling, J.D.
"Metabolic flux analysis of *Shewanella* spp. Reveals evolutionary robustness in central carbon metabolism"
Biotechnology Bioengineering, 102: 1161-1169 (2009).
* Contributed equally to this study.

Kunin, V., He, S., Warnecke, F., Peterson, S.B., *García Martín, H.*, Haynes, M., Ivanova, N., Blackall, L.L., Breitbart, M., Rohwer, F., McMahon, K.D., Hugenholtz, P.
¨A bacterial metapopulation adapts locally to phage predation despite global dispersal¨
Genome Research, 18:293-7 (2008).

Warnecke, F., Luginbühl, P., Ivanova, N., Ghassemian, M., Richardson, T.H., Stege, J.T., Cayouette, M., McHardy, A.C., Djordjevic, G., Aboushadi, N., Sorek, R., Tringe, S.G., Podar, M., *García Martín, H.*, Kunin, V., Dalevi, D., Madejska, J., Kirton, E., Platt, D., Szeto, E., Salamov, A., Barry, K., Mikhailova, N., Kyrpides, N.C., Matson, E.G., Ottesen, E.A., Zhang, X., Hernández, M., Murillo, C., Acosta, L.G., Rigoutsos, I., Tamayo, G., Green, B.D., Chang, C., Rubin, E.M., Mathur, E.J., Robertson, D.E., Hugenholtz, P., Leadbetter, J.R.
"Metagenomic and functional analysis of hindgut microbiota of a wood feeding higher termite"
Nature, 450(7169):560-5 (2007).

McMahon, K.D., *García Martín, H.*, Hugenholtz, P.
"Integrating ecology into biotechnology"
Current Opinion in Biotechnology 18(3):287-92 (2007).

Marcy, Y., Ouverney, C., Bik, E.M., Lösekann, T., Ivanova, N., *García Martín, H.*, Szeto, E., Platt, D., Hugenholtz, P., Relman, D.A., Quake, S.R.
"Dissecting biological 'dark matter' with single-cell genetic analysis of rare and uncultivated TM7 microbes from the human mouth."
Proceedings of the National Academy of Sciences 104(29): 11889-94 (2007).

Tang, Y.J., Chakraborty, R., *Garcia Martin, H.*, Chu, J., Hazen, T.C., Keasling, J.D.
"Flux analysis of central metabolic pathways in Geobacter metallireducens during reduction of soluble Fe(III)-nitrilotriacetic acid"
Applied Environmental Microbiology, 73(12):3859-64 (2007).

McHardy, A. C., *García Martín, H.*, Tsirigos, A., Hugenholtz, P. and Rigoutsos, I.
"Accurate Phylogenetic Classification of variable-length DNA fragments"
Nature Methods, 4(1):63-72 (2006).

García Martín, H., Ivanova, N., Kunin, V., Warnecke, F., Barry, K., McHardy, A.C., Yeates, C., He, S., Salamov, A., Szeto, E., Dalin, E., Putnam, N., Shapiro, H.J., Pangilinan, J.L., Rigoutsos, I., Kyrpides, N.C., Blackall, L.L., McMahon, K.D. and Hugenholtz, P.
"Metagenomic analysis of phosphorus removing sludge communities"
Nature Biotechnology, 24: 1263-9 (2006).

Markowitz, V.M., Ivanova, N., Palaniappan, K., Szeto, E., Korzeniewski, F., Lykidis, A., Anderston, I., Mavromattis, K., Kunin, V., *Garcia Martin, H.*, Dubchack, I., Hugenholtz, P. and Kyrpides, N.C.
"An experimental metagenome data management and analysis system"
Bioinformatics 22(14): e359-67 (2006).

García Martín, H. and Goldenfeld, N.
"On the origin and robustness of power-law species-area relationships in ecology"
Proceedings of the National Academy of Sciences 103(27):10310-5 (2006).

García Martín, H. and Goldenfeld, N.
"Estimation of microbial cover distributions at Mammoth Hot Springs using a

multiple clone library resampling method”
Environmental Microbiology 8(7):1145-54 (2006).

García Martín, H. and Goldenfeld, N.
“Linearity and scaling of a statistical model for the species abundance distribution”
Physical Review E 65 032901 (2002).

(Updated citation numbers in https://scholar.google.com/citations?user=_1ubJ4AAAAAJ&hl=en)

SKILLS

Python, FORTRAN, C/C++, Perl
Matlab, Mathematica
UNIX, Linux
Spanish native speaker
Knowledge of Basque and German

ACTIVITIES

UIUC Graduate Students Advisory Council:
Recruiting Officer (2001-2002)
Member of the Social Events Committee (2002-2003)