Rodriguez-R, Luis Miguel

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PROFILE

MICROBIAL ECOLOGY AND EVOLUTION

My main research interest is the understanding of eco-evolutionary principles governing microbial communities, including primary evolutionary and ecologic forces shaping populations and their metabolic potential, their interactions with other microbial species, their hosts, and the environment, and the role of stochasticity

MICROBIOME ANALYSIS

In the pursuit of these questions, I've garnered ample experience on genomic and metagenomic analyses in environmental, clinical, agricultural, and engineered settings, including the description, characterization, modeling, and simulation of microbial communities and populations. I've explored and discussed both theoretical and practical problems on microbiome analysis including the development and application of methods on phylogenetics and phylogenomics, taxonomy of prokaryotes, metabolic modeling, statistical techniques, and sequence analyses. I've authored over three dozen papers and book chapters (about a third as first author) with over a thousand citations and an h-index of 18, presented multiple workshops, seminars, and talks on microbiome analysis for researchers and undergraduate educators, and served as reviewer for several international journals

BIOINFORMATIC SOFTWARE DEVELOPMENT

New ideas need implementation, and throughout my research I've made it a point to implement those ideas in efficient, high-quality, well-documented, and user-friendly software with as general purpose as possible. I've developed tens of bioinformatic tools and web interfaces in a variety of programming languages (Ruby, Perl, R, C++, etc) such as the Enveomics Collection (~70 citations, >5,000 online queries/month), enveomics.R (>300 downloads/month), Nonpareil (>100 citations, >100 downloads and online queries/month), and MiGA (>200 registered users, >500 online queries/month), among others available at http://enve-omics.ce.gatech.edu/ and http://microbial-genomes.org/

EXPERIENCE

GEORGIA INSTITUTE OF TECHNOLOGY

Postdoctoral Fellow, Konstantinidis lab	Atlanta, USA, 2017-2018
Research Assistant, Konstantinidis lab (2012-2016); Teaching Assistant, Biological Principles, Biology 1510 (2011-2012)	Atlanta, USA, 2011-2016

INSTITUT DE RECHERCHE POUR LE DÉVELOPPEMENT (IRD)

Intern, Laboratory of Plant Resistance to Bio-aggressors (RPB)	Montpellier, France, 2011
Temporal Researcher, Laboratory of Plant Genomics and Development (LGDP)	Montpellier, France, 2010

COLOMBIAN CENTER FOR GENOMICS AND BIOINFORMATICS OF EXTREME ENVIRONMENTS (GEBIX)

Researcher, Bioinformatics team	Bogotá, Colombia, 2009-2010

UNIVERSIDAD DE LOS ANDES, DEPARTMENT OF BIOLOGICAL SCIENCES

Teaching Assistant, Cell Biology (2009, two terms); Researcher, Laboratory of Mycology and Plant Pathology (LAMFU)	Bogotá, Colombia, 2009-2010
Researcher, Laboratory of Mycology and Plant Pathology (LAMFU)	Bogotá, Colombia, 2008

UNIVERSIDAD NACIONAL DE COLOMBIA, BIOTECHNOLOGY INSTITUTE

Researcher, Centre for Bioinformatics of the Biotechnology Institute (CBIB)	Bogotá, Colombia, 2006-2008
Undergraduate Teaching Assistant, Bioinformatics	Bogotá, Colombia, 2006

AWARDS AND DISTINCTIONS

SIGMA XI, GEORGIA TECH CHAPTER

Sigma Xi 2017 Best Ph.D. Thesis Award — Atlanta, USA, 2017

INTERNATIONAL SOCIETY FOR MICROBIAL ECOLOGY – ISME

ISME Travel Award, ISME 16, Montréal, Canada — Montréal, Canada, 2016

GEORGIA INSTITUTE OF TECHNOLOGY, SCHOOL OF BIOLOGY

School of Biology Graduate Excellence Award 2015 — Atlanta, USA, 2015

RÉGION LANGUEDOC ROUSSILLON (NOW OCCITANIE), FRANCE

Fellowship granted by the region to outstanding international students — Montpellier, France, 2010-2011

EVALUATION-ORIENTATION OF SCIENTIFIC COOPERATION (ECOS) PROGRAM

Scientific mission to the *Institut de Recherche pour le Développement* (IRD) — Montpellier, France, 2009

UNIVERSIDAD NACIONAL DE COLOMBIA, COLLEGE OF SCIENCE

Award *Matrícula de Honor* — Bogotá, Colombia, 2004

PUBLICATIONS

CURRENTLY IN PREPARATION OR UNDER REVIEW

Rodriguez-R LM*, Tsementzi D*, Luo C, Hatt JK, Konstantinidis KT. Biogeography and seasonal variation disentangled in microbial meta-communities of five connected lakes. * Equal contribution.

Rodriguez-R LM, Tsementzi D, Dam P, Luo C, Voit E, Konstantinidis KT. Characterization of microbial interactions and detection of microbial guilds in a six-years freshwater metagenomic chronoseries.

Rodriguez-R LM, Gunturu S, Harvey WT, Roselló-Mora R, Tiedje JM, Cole J, Konstantinidis KT. The Microbial Genomes Atlas (MiGA) webserver: Taxonomic and gene content diversity analysis of *Archaea* and *Bacteria* at the whole genome level.

Rodriguez-R LM, Pena-Gonzalez A, Gee JE, Marston CK, Hoffmaster A, Konstantinidis KT. Accurate typing of *Bacillus anthracis* in hundreds of genomes using Average Nucleotide Identity.

Rodriguez-R LM*, Tsementzi D*, Konstantinidis KT. A novel method for the quantification of *in situ* intra-population genetic diversity from metagenomes. * Equal contribution.

PUBLISHED RESEARCH WORKS

Rodriguez-R LM, Gunturu S, Tiedje JM, Cole J, Konstantinidis KT. 2018. Nonpareil 3: Fast estimation of metagenomic coverage and sequence diversity. *mSystems* 3(3):e00039-18.

Rodriguez-R LM, Castro JC, Kyrpides NC, Cole JR, Tiedje JM, Konstantinidis KT. 2018. How much do rRNA gene surveys underestimate extant bacterial diversity? *Applied and Environmental Microbiology* 84(6):e00014-18.

Pena-Gonzalez A, Marston CK, **Rodriguez-R LM**, Kolton CB, Garcia-Diaz J, Theppote A, Frace M, Konstantinidis KT, Hoffmaster AR. 2017. Draft genome sequence of *Bacillus cereus* LA2007, a human-pathogenic isolate harboring anthrax-like plasmids. *Genome announcements* 5(16):e00181-17.

Wang Y, Hatt JK, Tsementzi D, **Rodriguez-R LM**, Ruiz-Pérez CA, Weigand MR, Kizer H, Maresca G, Krishnan R, Poretsky R, Spain JC, Konstantinidis KT. 2017. Quantifying the importance of the rare biosphere for microbial community response to organic pollutants in a freshwater ecosystem. *Applied and Environmental Microbiology* 83(8):e03321-16.

Orellana LH*, **Rodriguez-R LM***, Konstantinidis KT. 2017. ROCker: accurate detection and quantification of target genes in short-read metagenomic data sets by modeling sliding-window bitscores. *Nucleic Acids Research* 45(3): e14. * Equal contribution.

Tsementzi D, Wu J, Deutsch S, Nath S, **Rodriguez-R LM**, Burns AS, Ranjan P, Sarode N, Malmstrom RR, Padilla CC, Stone BK, Bristow LA, Larsen M, Glass JB, Thamdrup B, Woyke T, Konstantinidis KT, Stewart FJ. 2016. SAR11 bacteria linked to ocean anoxia and nitrogen loss. *Nature* 536(7615): 179-183.

Soto-Giron MJ, **Rodriguez-R LM**, Luo C, Elk M, Ryu H, Hoelle J, Santo Domingo J, Konstantinidis KT. 2016. Biofilms on hospital shower hoses: Characterization and implications for nosocomial infections. *Applied and Environmental Microbiology* 82(9): 2872-2883.

Rodriguez-R LM, Konstantinidis KT. 2016. The enveomics collection: a toolbox for specialized analyses of microbial genomes and metagenomes. *PeerJ Preprints*: e1900v1.

Johnston ER, **Rodriguez-R LM**, Luo C, Yuan MM, Wu L, He Z, Schuur EAG, Luo Y, Tiedje JM, Zhou J, Konstantinidis KT. 2016. Metagenomics reveals pervasive bacterial populations and reduced community diversity across the Alaska tundra ecosystem. *Frontiers in Microbiology* 7:579.

Rodriguez-R LM, Overholt WA, Hagan C, Huettel M, Kostka JE, Konstantinidis KT. 2015. Microbial community successional patterns in beach sands impacted by the Deepwater Horizon oil spill. *The ISME Journal* 9(9): 1928-1940.

Poulin L, Grygiel P, Magne M, Gagnevin L, **Rodriguez-R LM**, Forero Serna N, Zhao S, El Rafii M, Dao S, Tekete C, Wonni I, Koita O, Pruvost O, Verdier V, Vernière C, Koebnik R. 2015. New Multilocus Variable-Number Tandem-Repeat analysis tool for surveillance and local epidemiology of bacterial leaf blight and bacterial leaf streak of rice caused by *Xanthomonas oryzae*. *Applied and Environmental Microbiology* 81(2): 688-698.

Tsementzi D, Poretsky R, **Rodriguez-R LM**, Luo C, Konstantinidis KT. 2014. Evaluation of metatranscriptomic protocols and application to the study of freshwater microbial communities. *Environmental Microbiology Reports* 6(6): 640-655.

Luo C, **Rodriguez-R LM**, Konstantinidis KT. 2014. MyTaxa: an advanced taxonomic classifier for genomic and metagenomic sequences. *Nucleic Acids Research* 42(8): e73.

Rodriguez-R LM, Konstantinidis KT. 2014. Nonpareil: a redundancy-based approach to assess the level of coverage in metagenomic datasets. *Bioinformatics* 30(5): 629-635.

Luo C, **Rodriguez-R LM**, Johnston ER, Wu L, Cheng L, Xue K, Tu Q, Deng Y, He Z, Zhou Shi J, Yuan MM, Sherry RA, Li D, Luo Y, Schuur EAG, Chain P, Tiedje JM, Zhou J, Konstantinidis KT. 2014. Soil microbial community responses to a decade of warming as revealed by comparative metagenomics. *Applied and Environmental Microbiology* 80(5): 1777-1786.

Orellana LH, **Rodriguez-R LM**, Higgins S, Chee-Sanford JC, Sanford RA, Ritalahti KM, Löfler FE, Konstantinidis KT. 2014. Detecting nitrous oxide reductase (*nosZ*) genes in soil metagenomes: method development and implications for the nitrogen cycle. *mBio* 5(3): e01193-14.

Poretsky R, **Rodriguez-R LM**, Luo C, Tsementzi D, Konstantinidis KT. 2014. Strengths and limitations of 16S rRNA gene amplicon sequencing in revealing temporal microbial community dynamics. *PLoS ONE* 9(4): e93827.

DeLeon-Rodriguez N, Lathem TL, **Rodriguez-R LM**, Barazesh JM, Anderson BE, Beyersdorf AJ, Ziemba LD, Bergin M, Nenes A, Konstantinidis KT. 2013. *PNAS* 110(7): 2575-2580.

Pérez-Quintero AL, **Rodriguez-R LM**, Dereeper A, López C, Koebnik R, Szurek B. 2013. An improved method for TAL effectors DNA-binding sites prediction reveals functional convergence in TAL repertoires of *Xanthomonas oryzae* strains. *PLoS ONE* 8(7): e68464.

Arrieta-Ortiz ML, **Rodriguez-R LM**, Pérez-Quintero AL, Poulin L, Díaz AC, Arias Rojas N, […], Koebnik R, Bernal A. Genomic survey of pathogenicity determinants and VNTR markers in the cassava bacterial pathogen *Xanthomonas axonopodis* pv. *manihotis* strain CIO151. *PLoS ONE* 8(11): e79704.

Zhao S, Poulin L, **Rodriguez-R LM**, Forero Serna N, Liu S-Y, Wonni I, Szurek B, Verdier V, Leach JE, He Y-Q, Feng J-X, Koebnik R. 2012. Development of a Variable Number of Tandem Repeats typing scheme for the bacterial rice pathogen *Xanthomonas oryzae* pv. *oryzicola*. *Phytopathology* 102(10): 948-956.

Cárdenas A, **Rodriguez-R LM**, Pizarro V, Cadavid LF, Arévalo-Ferro C. 2012. Shifts in bacterial communities of two caribbean reef-building coral species affected by white plague disease. *The ISME Journal* 6: 502-512.

Rodriguez-R LM, Grajales A, Arrieta-Ortiz ML, Salazar C, Restrepo S, Bernal A. 2012. Genomes-based phylogeny of the genus *Xanthomonas*. *BMC Microbiology* 12:43.

Pinzón A, **Rodriguez-R LM**, González A, Bernal A, Restrepo S. 2011. Targeted Metabolic Reconstruction: a novel approach for the characterization of plant pathogen interactions. *Briefings in Bioinformatics* 12(2): 151-62.

Gorrón E, Rodríguez F, Bernal D, **Rodriguez-Rojas LM**, Bernal A, Restrepo S, Tohme J. 2010. A new method for designing degenerate primers and its use in the identification of sequences in *Brachiaria* showing similarity to apomixis-associated genes. *Bioinformatics* 26(16): 2053-2054.

Méndez-Ortega MC, Restrepo S, **Rodríguez-R LM**, Pérez I, Mendoza JC, Martínez AP, Sierra R, Rey-Benito GJ. 2010. An RNAi *in silico* approach to find an optimal shRNA cocktail against HIV-1. *Journal of Virology* 7:369.

Sierra R*, **Rodriguez-R LM***, Chaves D, Pinzon A, Grajales A, Rojas A, Mutis G, Cárdenas M, Burbano D, Jiménez P, Bernal A, Restrepo S. 2010. Discovery of *Phytophthora infestans* genes expressed in planta through mining of cDNA libraries. *PLoS ONE* 5(3): e9847. * Equal contribution.

Cháves D, Sandoval A, **Rodríguez L**, Garcia JC, Restrepo S, Zambrano MM. 2010. Análisis comparativo de seis genomas del complejo *Mycobacterium tuberculosis* [Comparative analysis of six genomes of the complex *Mycobacterium tuberculosis*]. *Biomédica* 30(1).

Burbano Sefair DA, Castro Barrera HE, Pérez Cabarcas MA, Restrepo Restrepo S, **Rodríguez LM**. 2009. Grid-enabled HMMER (G-HMMER): A Uniandes contribution to the biology community. In: Mayo R, Hoeger H, Ciuffo LN, Barrera R, Dutra I, Gavillet P, Marechal B (eds.). 2009. Proceedings of the second EELA-2 Conference. Ed. CIEMAT. Madrid. ISBN: 978-84-7834-627-1.

Buitrago F, Sierra R, Grajales A, **Rodríguez-R LM**, Jiménez P, Bernal A, Restrepo S. 2009. Comparative study of Chalcone synthase promoters across plant families. *Revista Colombiana de Biotecnología*, 11(2):136-142.

PUBLISHED REVIEWS AND COMMENTARIES

Rodriguez-R LM, Konstantinidis KT. 2014. Estimating coverage in metagenomic data sets and why it matters. *The ISME Journal* 8: 2349-2351.

Rodriguez-R LM, Konstantinidis KT. 2014. Bypassing cultivation to identify bacterial species. *Microbe* 9(3): 111-118.

Luo C*, **Rodriguez-R LM***, Konstantinidis KT. 2013. Chapter 23: A user's guide to quantitative and comparative analysis of metagenomic datasets. In: DeLong EF (ed.). 2013. Microbial metagenomics, metatranscriptomics, and metaproteomics. *Methods in enzymology* 531. * Equal contribution.

Restrepo S, Pinzón A, **Rodríguez-R LM**, Sierra R, Grajales A, Bernal A, Barreto E, Moreno P, Zambrano MM, Cristancho M, González A, Castro H. 2009. Computational Biology in Colombia. *PLoS Computational Biology* 5(10): e1000535.

Rodríguez LM., Reguero Reza MT. 2007. Toxicómica: una aproximación racional para ensayos toxicológicos [Toxicomics: a rational approach for toxicologic assays]. *Revista Colombiana de Biotecnología* ISSN 1909-8758, 9(2):79-81.

SELECT CONFERENCES

AMERICAN SOCIETY FOR MICROBIOLOGY MICROBE 2018; ATLANTA, USA, 2018

Rodriguez-R LM, Tsementzi D, Luo C, Konstantinidis KT. Iterative subtractive binning of freshwater chronoseries metagenomes recovers nearly complete genomes from over four hundred novel species. Oral presentation.

Rodriguez-R LM, Gunturu S, Jain C, Tiedje JM, Cole JR, Konstantinidis KT. MiGA – The Microbial Genomes Atlas: Expanding the catalogued diversity of *Archaea* and *Bacteria*. Poster presentation and Poster Talk.

11TH INTERNATIONAL CONFERENCE IN BIOINFORMATICS; ATLANTA, USA, 2017

Rodriguez-R LM, Pena-Gonzalez A, Marston CK, Beesle C, Gee JE, Hoffmaster A, Konstantinidis KT. Accurate typing of hundreds of genomes using the Microbial Genomes Atlas (MiGA) webserver. Poster.

Rodriguez-R LM, Tsementzi D, Luo C, Konstantinidis KT. Iterative subtractive binning of freshwater chronoseries metagenomes recovers nearly complete genomes from over four hundred novel species. Poster.

AMERICAN SOCIETY FOR MICROBIOLOGY MICROBE 2016; BOSTON, USA, 2016

Rodriguez-R LM, Gunturu S, Luo C, Tiedje JM, Cole JR, Konstantinidis KT. Microbial Genomes Atlas: Standardizing Genome-based Taxonomic Analyses for *Archaea* and *Bacteria*. Oral presentation.

16TH INTERNATIONAL SYMPOSIUM ON MICROBIAL ECOLOGY – ISME16; MONTRÉAL, CANADA, 2016

Rodriguez-R LM, Tsementzi D, Luo C, Hatt JK, Konstantinidis KT. Biogeography and seasonal variation disentangled in microbial meta-communities of five connected lakes. Oral presentation.

Rodriguez-R LM, Gunturu S, Luo C, Tiedje JM, Cole JR, Konstantinidis KT. Microbial Genomes Atlas (MiGA): Standardized diversity and taxonomic analyses of archaeal and bacterial genomes and metagenomes at the whole-genome level. Poster.

10TH INTERNATIONAL CONFERENCE IN BIOINFORMATICS; ATLANTA, USA, 2015

Rodriguez-R LM, Tsementzi D, Konstantinidis KT. A novel method to measure genetic diversity within natural bacterial populations. Poster.

Rodriguez-R LM, Pena-Gonzalez A, Marston CK, Gee JE, Beesley CA, Saile E, Frace M, Weigand MR, Konstantinidis KT, Hoffmaster A. A bioinformatics pipeline for the comparative analysis of 100s of *Bacillus anthracis* genome sequences. Poster.

Rodriguez-R LM, Luo C, Konstantinidis KT. Expanding the bioinformatics toolbox for the analysis of genomes and metagenomes. Poster.

CENTER FOR DISEASE CONTROL AND PREVENTION, DIVISION OF HIGH-CONSEQUENCE PATHOGENS AND PATHOLOGY SCIENCE SEMINAR; ATLANTA, USA, 2015

Rodriguez-R LM, Pena-Gonzalez A, Gee J, Konstantinidis K, Hoffmaster A. Increased utilization of WGS for molecular epidemiology investigations of anthrax and melioidosis. Invited talk.

AMERICAN SOCIETY FOR MICROBIOLOGY GENERAL MEETING; NEW ORLEANS, USA, 2015

Rodriguez-R LM, Orellana LH, Konstantinidis KT. Accurate detection and quantification of functional genes in complex short-read metagenomic datasets: methods development and application to nitrogen cycle genes. Poster.

INTERNATIONAL UNION OF MICROBIOLOGICAL SOCIETIES (IUMS) - XIV INTERNATIONAL CONGRESS OF BACTERIOLOGY AND APPLIED MICROBIOLOGY; MONTRÉAL, CANADA, 2014

Rodriguez-R LM, Luo C, Konstantinidis KT. Expanding the bioinformatics toolbox for the analysis of genomes and metagenomes. Oral presentation.

15TH INTERNATIONAL SYMPOSIUM ON MICROBIAL ECOLOGY – ISME15; SEOUL, SOUTH-KOREA, 2014

Rodriguez-R LM, Luo C, Konstantinidis KT. Expanding the bioinformatics toolbox for the analysis of genomes and metagenomes. Poster.

AMERICAN SOCIETY FOR MICROBIOLOGY GENERAL MEETING; BOSTON (MA), USA, 2014

Rodriguez-R LM, Overholt WA, Lin X, Delgardio J, Huettel M, Kostka JE, Konstantinidis KT. Metagenomics insights into the effects of the Deepwater Horizon oil spill on indigenous communities in beach sands. Oral presentation.

AMERICAN SOCIETY FOR MICROBIOLOGY CONFERENCE FOR UNDERGRADUATE EDUCATORS (ASMCUE); DANVERS (MA), USA, 2014

Course Integrated Research by J Tiedje, KT Konstantinidis, J Cole, and **LM Rodriguez-R**. Hands-on bioinformatics exercises for the analysis of complex microbiomes in the classroom. Workshop.

9TH INTERNATIONAL CONFERENCE IN BIOINFORMATICS; ATLANTA, USA, 2013

Rodriguez-R LM, Luo C, Konstantinidis KT. From theory to practice: new approaches and accompanying bioinformatics tools in environmental genomics. Poster.

14TH INTERNATIONAL SYMPOSIUM ON MICROBIAL ECOLOGY – ISME14; COPENHAGEN, DENMARK, 2012

Rodriguez-R LM, Tsementzi D, Luo C, Konstantinidis KT. Spatial and temporal characterization of bacterial metapopulations reveal dispersal and habitat limitations in interconnected freshwater ecosystems. Poster.

FIRST COLOMBIAN MEETING IN COMPUTATIONAL BIOLOGY; BOGOTÁ, COLOMBIA, 2011

Rodriguez-R LM, Perlaza L, Grajales A, Arrieta M, Salazar C, Koebnik R, Restrepo S, Bernal A. Genomes-based phylogeny of the genus *Xanthomonas*. Oral presentation (Perlaza L).

EUROPEAN CONFERENCE IN COMPUTATIONAL BIOLOGY 2010, SATELLITE MEETING OF THE EUROPEAN STUDENTS COUNCIL; GHENT, BELGIUM, 2010

Rodriguez-R LM, Grajales A, Arrieta M, Salazar C, Szurek B, Verdier V, Koebnik R, Restrepo S, Bernal A. Bacterial phylogenomics revisited: A case study for the *Xanthomonas* genus. Poster.

3RD COLOMBIAN MEETING ON BIOTECHNOLOGY; BOGOTÁ, COLOMBIA, 2008

Rodríguez LM, Mantilla JR, Falquet L, Reguero Reza MT, Barreto-Hernández E. Diseño e implementación de un sistema bioinformático para el almacenamiento y clasificación de beta-lactamasas: BLA.id [Design and implementation of a bioinformatics system for the storage and classification of beta-lactamases: BLA.id]. Oral presentation.

EDUCATION

PH.D. BIOINFORMATICS (MINOR: BIOMEDICAL ENGINEERING)

Georgia Institute of Technology. Dissertation: Bioinformatic tools for testing microbial ecology theory in natural environments through metagenomics Atlanta, USA, 2011-2016

M.SC. APPLIED INFORMATICS (SKILLS INTEGRATION, BIOINFORMATICS)

Université de Montpellier 2. Thesis: Polloc – A Perl library for polymorphic loci analyses in bacterial molecular typing studies Montpellier, France, 2010-2011

M.SC. BIOLOGICAL SCIENCES (MICROBIOLOGY)

Universidad de Los Andes. Thesis: Genomes-based phylogeny of the genus *Xanthomonas* Bogotá, Colombia, 2009-2011

B.SC. BIOLOGY (5 YEAR PROGRAM)

Universidad Nacional de Colombia. Thesis: Diseño e implementación de un sistema de información en β-lactamasas [Design and implementation of an information system in β-lactamases] Bogotá, Colombia, 2004-2009

LANGUAGES

Spanish Mother tongue; fluent

English Reading, writing, speaking; fluent, seven years immersion

French Reading, speaking; intermediate proficiency, one year immersion

Italian Reading, writing, speaking; intermediate proficiency