Rodriguez-R Luis Miguel

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PROFILE AT A GLANCE

Microbial Ecology & Evolution

My main research interest is the understanding of **eco-evolutionary principles governing microbial communities**: 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 **phylogenomics**, **taxonomy** of prokaryotes, **metabolic modeling**, **statistical techniques**, and **sequence analyses**.

Scientific Production

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 19**, presented multiple **workshops**, **seminars**, and **symposia** on microbiome analysis for researchers and undergraduate educators, and served as **reviewer** for several international journals.

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**. I've developed tens of **bioinformatic tools** and **web interfaces** including **grid** and **cloud computing** in a variety of programming languages and frameworks (**Ruby**, **Rails**, **Perl**, **R**, **C++**, etc) with over 6,000 downloads or online queries per month, available at **https://lmrodriguezr.github.io/software**.

PROFESSIONAL EXPERIENCE

Georgia Institute of Technology; Atlanta, USA

2017-2018	Postdoctoral Fellow, Konstantinidis Lab
2012-2016	Research Assistant, Konstantinidis Lab
2011-2012	Teaching Assistant, Biological Principles, Biology 1510

Institut de Recherche pour le Développement (IRD); Montpellier, France

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

Center for Genomics and Bioinformatics of Extreme Environments (GeBiX); Bogotá, Colombia

2009-2010	Researcher, Bioinformatics team

Universidad de Los Andes, Department of Biological Sciences; Bogotá, Colombia

2008-2010	Research Assistant, Laboratory of Mycology and Plant Pathology (LAMFU)
2009	Teaching Assistant, Cell Biology

Universidad Nacional de Colombia, Biotechnology Institute (IBUN); Bogotá, Colombia

2006-2008	Research Assistant, Centre for Bioinformatics of the Biotechnology Institute (CBIB)
2006	Teaching Assistant, Bioinformatics

AWARDS & DISTINCTIONS

Sigma Xi, Georgia Tech Chapter
2017, Atlanta, USA   2017 Best Ph.D. Thesis Award

International Society for Microbial Ecology (ISME)
2016, Montréal, Canada   ISME Travel Award, ISME 16

Georgia Institute of Technology, School of Biology
2015, Atlanta, USA   School of Biology Graduate Excellence Award 2015

Région Languedoc Roussillon (now Occitanie), France
2010, Montpellier, France   Fellowship granted by the region to outstanding international students

Evaluation-Orientation of Scientific Cooperation Program (ECOS)
2009, Montpellier, France   Scientific Mission to *Institut de Recherche pour le Développement* (IRD)

Universidad Nacional de Colombia
2004, Bogotá, Colombia   Award *Matrícula de Honor*

EDUCATION

Ph.D. Bioinformatics (Minor: Biomedical Engineering)
2011-2016   Georgia Institute of Technology. Atlanta, USA.

M.Sc. Applied Informatics (Skills integration, Bioinformatics)
2010-2011   Université de Montpellier 2, Montpellier, France

M.Sc. Biological Sciences (Microbiology)
2009-2010   Universidad de Los Andes, Bogotá, Colombia

B.Sc. Biology
2004-2009   Universidad Nacional de Colombia, Bogotá, Colombia

Languages
Spanish (mother tongue), English (fluent, seven year immersion), French (Intermediate proficiency, one year immersion), and Italian (basic proficiency)

PERSONAL INTERESTS

Dancing (Zouk, Salsa, Bachata, Tango, Blues, Ballet), Social Justice (intersectional feminism), Theater, and World Religions

PUBLICATIONS

This list only includes **select publications** reporting </> new software and algorithms, 🏛 method evaluations, 📖 reviews and commentaries, or primary research on 🌿 microbial ecology, 🌲 evolution, or 🦠 clinical microbiology. For the full updated list, visit **https://rodriguez-r.com/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, 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 Works

Rodriguez-R LM, Gunturu S, Harvey WT, Rosselló-Mora R, Cole JR, Tiedje JM, Konstantinidis KT. 2018. The Microbial Genomes Atlas (MiGA) webserver: taxonomic and gene diversity analysis of *Archaea* and *Bacteria* at the whole genome level. *Nucleic Acids Research* 46(W1):W282-W288. </> 🌲

Rodriguez-R LM•, Gunturu S•, Cole JR, Tiedje JM, Konstantinidis KT. 2018. Nonpareil 3: Fast estimation of metagenomic coverage and sequence diversity. *mSystems* 3(3):e00039-18. • Equal contribution. ‹/›

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.

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**, *et al*. 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.

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

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.

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

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

DeLeon-Rodriguez N, Lathem TL, **Rodriguez-R LM**, *et al*. 2013. Microbiome of the upper troposphere: species composition, effects of tropical storms, and atmospheric implications. *PNAS* 110(7): 2575-2580.

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. ‹/›

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.

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.

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, *et al* (eds.). 2009. Proceedings of EELA-2. Ed. CIEMAT. Madrid. ISBN: 978-84-7834-627-1. ‹/›

SELECT CONFERENCES

American Society for Microbiology (ASM) 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. Symposium.

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, *et al*. 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 (ASM) 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, *et al*. 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.

CDC, 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.

IUMS XIV International Congress of Bacteriology & 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.

American Society for Microbiology General Meeting; Boston (MA), USA, 2014

Rodriguez-R LM, *et al*. Metagenomics insights into the effects of the Deepwater Horizon oil spill on indigenous communities in beach sands. Oral presentation.

ASM 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.

European Conference in Computational Biology 2010; 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. Design and implementation of a bioinformatics system for the storage and classification of betalactamases: BLA.id. Oral presentation.