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**: evolutionary and ecologic forces shaping **populations** and their **metabolic potential**, their **interactions** with other 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 fifty papers and book chapters** (about a third as first author) with **more than six thousand citations** and an **h-index of 29**, frequently present **workshops**, **seminars**, and **symposia** on microbiome analysis for researchers and undergraduate educators, and serve 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 10,000 downloads or online queries per month, available at **https://rodriguez-r.com/software**.

PROFESSIONAL EXPERIENCE

Leopold-Franzens Universität Innsbruck; Innsbruck, Austria

2021-	Assistant Professor, Department of Microbiology and Digital Science Center (DiSC)
2020	Research Scientist, Department of Microbiology and Digital Science Center (DiSC)

Georgia Institute of Technology; Atlanta, USA

2018-2020	Research Engineer (Research Faculty)
2017-2018	Postdoctoral Fellow (Advisor: Dr. K. T. Konstantinidis)
2012-2016	Research Assistant, (Advisor: Dr. K. T. Konstantinidis)
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.
Advisor: Dr. Konstantinos T. Konstantinidis

M.Sc. Applied Informatics (Skills integration, Bioinformatics)

2010-2011 Université de Montpellier 2, Montpellier, France
Advisor: Dr. Ralf Koebnik

M.Sc. Biological Sciences (Microbiology)

2009-2010 Universidad de Los Andes, Bogotá, Colombia
Co-Advisors: Dr. Adriana Bernal and Dr. Silvia Restrepo

B.Sc. Biology

2004-2009 Universidad Nacional de Colombia, Bogotá, Colombia
Co-Advisors: Mr. Emiliano Barreto and Dr. María Teresa Reguero Reza

Languages

Spanish (mother tongue), English (fluent, ten year immersion), French (intermediate proficiency, one year immersion), Italian (basic proficiency) and German (basic proficiency)

PERSONAL INTERESTS

Dancing (Zouk, Salsa, Bachata, Tango, Blues, Ballet), Social Justice (ethics and 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**.

Published Works

Heritier-Robbins P, Karthikeyan S, Hatt JK, Kim M, Huettel M, Kostka JE, Konstantinidis KT & **Rodriguez-R LM** (2021). Beach sand oil spills select for generalist microbial populations. *The ISME Journal* 15:3418-3422. 🍃

Rodriguez-R LM, Jain C, Conrad RE, Aluru S & Konstantinidis KT (2021). Reply to: "Re-evaluating the evidence for a universal genetic boundary among microbial species". *Nature Comm.* 12. 🧰 🍃 🌲

Rodriguez-R LM, Rossello-Mora R, & Konstantinidis KT (2021). Chapter 13: Identification and Classification of Prokaryotes Using Whole Genome Sequences. In Stackebrandt E, Bridge P & Smith D (Eds.), Reconciling microbial systematics. CABI. ❝ 🍃 🌲

Rodriguez-R LM, Harvey W, Rossello-Mora R, Tiedje JM, Cole JR & Konstantinidis KT (2020). Classifying Prokaryotic Genomes Using the Microbial Genomes Atlas (MiGA) Webserver. In Bergey's Manual of Systematics of Archaea and Bacteria. Wiley. </> 🌲

Rodriguez-R LM, Tsementzi D, Luo C, Konstantinidis KT. 2020. Iterative Subtractive Binning of Freshwater Chronoseries Metagenomes Identifies over 400 Novel Species and their Ecologic Preferences. *Environmental Microbiology* 22(8):3394-3412. </> 🍃 🌲

Tsementzi D•, **Rodriguez-R LM•**, *et al*. 2019. Ecogenomic characterization of widespread, closely-related SAR11 clades of the freshwater genus "*Candidatus* Fonsibacter" and proposal of *Ca.* Fonsibacter lacus sp. nov. *Sys. App. Microbiology* 42(4):495-505. • Equal contribution. 🍃 🌲

Meziti A•, Tsementzi D•, **Rodriguez-R LM•**, *et al*. 2019. Quantifying the changes in genetic diversity within sequence-discrete bacterial populations across a spatial and temporal riverine gradient. *The ISME Journal* 13:767-779. • Equal contribution. 🍃 🌲

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. *Nucl. Acids Res.* 46(W1). </> 🌲

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). • Equal contrib. </> 🍃

Rodriguez-R LM, Castro JC, Kyrpides NC, Cole JR, Tiedje JM, Konstantinidis KT. 2018. How much do rRNA gene surveys underestimate extant bacterial diversity? *Appl. Env. Microbiol.* 84(6). 🧰 🍃 🌲

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**, *et al*. 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**, *et al*. 2016. Metagenomics reveals pervasive bacterial populations and reduced community diversity across the Alaska tundra ecosystem. *Front. Microbiol.* 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. </> 🧰 ❝

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. 🌲

SELECT CONFERENCES

International Society for Microbial Ecology (ISME) Latin America, Colombia, 2021

Rodriguez-R LM. Indexing the genomic diversity of Archaea and Bacteria with MiGA, the Microbial Genomes Atlas. Invited talk.

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.