

# 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), Italian (Basic proficiency)

## 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**<sup>\*</sup>, Tsementzi D<sup>\*</sup>, 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 chronoserries.   

**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**<sup>\*</sup>, Tsementzi D<sup>\*</sup>, 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**<sup>\*</sup>, Gunturu S<sup>\*</sup>, 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**, 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.  
- 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**, Barazesh JM, Anderson BE, Beyersdorf AJ, Ziemba LD, Bergin M, Nenes A, Konstantinidis KT. 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, **Rodriguez-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, **Rodriguez-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, **Rodriguez 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. 

## 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 chronoserries 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**, 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 chronoserries 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**, 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.

### 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**, Overholt WA, Lin X, Delgadio 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.

### 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

**Rodriguez LM**, Mantilla JR, Falquet L, Reguero Reza MT, Barreto-Hernández E. Design and implementation of a bioinformatics system for the storage and classification of beta-lactamases: BLA.id. Oral presentation.