**University of Pittsburgh**

**School of Medicine**

**BIOGRAPHICAL**

**Name:** Erik S. Wright

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 Pittsburgh, PA 15219

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**EDUCATION and TRAINING**

**UNDERGRADUATE:**

2003 - 2007 Cornell University B.S. 2007 Electrical and Computer

Ithaca, NY Engineering

**GRADUATE:**

2010 - 2012 University of Wisconsin M.S. 2012 Civil and Environmental

Madison, WI Engineering

 Advisor: Dr. Daniel Noguera

2012 – 2016 University of Wisconsin Ph.D., 2016 Microbiology

 Madison, WI Advisor: Dr. Kalin Vetsigian

# APPOINTMENTS and POSITIONS

**ACADEMIC:**

2010 – 2016 University of Wisconsin, Madison, WI Research Assistant, Microbiology

2015 – 2016 University of Wisconsin, Madison, WI Lecturer, Computer Sciences

2017 – present University of Pittsburgh, Pittsburgh, PA Assistant Professor, Biomedical Informatics

**NON‐ACADEMIC:**

2007-2008 Apple, Inc., Cupertino, CA Reliability Engineer

**CERTIFICATION and LICENSURE**

**SPECIALTY CERTIFICATION:**

Not applicable

**MEDICAL or OTHER PROFESSIONAL LICENSURE:**

Not applicable

# MEMBERSHIP in PROFESSIONAL and SCIENTIFIC SOCIETIES

American Society for Microbiology 2012 – present

## American Society for Mass Spectrometry 2021 – present

## American Medical Informatics Association 2017 – 2020

# HONORS

Becker Travel Supplements Award 2011, 2012, 2013

BACTER (Bringing Advanced Computational Techniques to Energy Research) Award 2011

Sigrid Leirmo Memorial Award 2014

Advanced Computing Infrastructure Fellow 2014 – 2015

MDTP (Microbiology Doctoral Training Program) Travel Award 2016

## Graduate School Student Research Travel Grant Award 2016

BioC 2018 Travel Award 2018

NIH Director's New Innovator Award 2018

BioC 2022 Travel Award 2022

# PUBLICATIONS

Original peer reviewed articles

1. **Wright ES**, Yilmaz LS, Noguera DR\*. DECIPHER, a search-based approach to chimera identification for 16S rRNA sequences. *Applied and Environmental Microbiology*. 2012 Feb;78(3):717-25. PMID: 22101057
2. Yilmaz LS, Loy A, **Wright ES**, Wagner M, Noguera DR\*. Modeling Formamide Denaturation of Probe-Target Hybrids for Improved Microarray Probe Design in Microbial Diagnostics. *PLoS ONE*. 2012;7(8):e43862. PMID: 22952791
3. Noguera DR\*, **Wright ES**, Camejo P, Yilmaz LS. Mathematical tools to optimize the design of oligonucleotide probes and primers. *Applied Microbiology Biotechnology*. 2014 Dec;98(23):9595–608. PMID: 25359473
4. **Wright ES\***. DECIPHER: harnessing local sequence context to improve protein multiple sequence alignment. *BMC Bioinformatics*. 2015 Oct;16:322. PMID: 26445311
5. **Wright ES**, Vetsigian KH\*. Inhibitory interactions promote frequent bistability among competing bacteria. *Nature Communications*. 2016 Apr;7:11274. PMID: 27097658
6. **Wright ES**, Vetsigian KH\*. DesignSignatures: a tool for designing primers that yields amplicons with distinct signatures. *Bioinformatics*. 2016 May;32(10):1565–7. PMID: 26803162
7. **Wright ES**\*, Yilmaz LS, Corcoran AM, Okten HE, Noguera DR. Automated design of probes for rRNA-targeted fluorescence in situ hybridization reveals the advantages of using dual probes for accurate identification. *Applied and Environmental Microbiology*. 2014 Aug;80(16):5124–33. PMID: 24928876
8. **Wright ES**, Yilmaz LS, Ram S, Gasser JM, Harrington GW, Noguera DR\*. Exploiting extension bias in polymerase chain reaction to improve primer specificity in ensembles of nearly identical DNA templates. *Environmental Microbiology*. 2014 May;16(5):1354–65. PMID: 24750536
9. **Wright ES**, Vetsigian KH\*. Quality filtering of Illumina index reads mitigates sample cross-talk. *BMC Genomics*. 2016 Nov;17(1):876. PMID: 27814679
10. Murali A, Bhargava A, **Wright ES**\*. IDTAXA: a novel approach for accurate taxonomic classification of microbiome sequences. *Microbiome*. 2018 Sep;6:140. PMID: 30092815
11. **Wright ES**\*, Baum DA. Exclusivity offers a sound yet practical species criterion for bacteria despite abundant gene flow. *BMC Genomics*. 2018 Oct;19(1):724. PMID: 30285620
12. Birer C, **Wright ES**\*. Capturing the complex interplay between drugs and the intestinal microbiome. *Clinical Pharmacology & Therapeutics*. 2019 Aug;106(3):501-504. PMID: 31102465
13. **Wright ES**, & Vetsigian KH\*. Stochastic exits from dormancy give rise to heavy-tailed distributions of descendants in bacterial populations. *Molecular Ecology*. 2019 Oct;28(17):3915-3928. PMID: 31355980
14. Korandla DR, Wozniak JM, Campeau A, Gonzalez DJ, **Wright ES**\*. AssessORF: combining evolutionary conservation and proteomics to assess prokaryotic gene predictions. *Bioinformatics*. 2020 Feb;36(4):1022-1029. PMID: 31532487
15. **Wright ES**\*. RNAconTest: Comparing tools for non-coding RNA multiple sequence alignment based on structural consistency. *RNA*. 2020 May;26(5):531-540. PMID: 32005745
16. Rost LM, Nguyen MH, Clancy CJ, Shields RK, **Wright ES**\*. Discordance among antibiotic prescription guidelines reflects a lack of clear best practices. *Open Forum Infectious Diseases*. 2021 Jan, 8(1):ofaa571. PMID: 33447636.
17. Morgan WR, **Wright ES**\*. Ten simple rules for hitting a home run with your elevator pitch. *PLoS Computational Biology*. 2021 Mar;(17)3:e1008756. PID: 33735178.
18. **Wright ES**, Gupta R, Vetsigian KH\*. Multi-stable bacterial communities exhibit extreme sensitivity to initial conditions. FEMS Microbiology Ecology. 2021 Jun;97(6):fiab073. PMID: 34021563.
19. Beckley AE, **Wright ES\***. Identification of antibiotic pairs that evade concurrent resistance via a retrospective analysis of antimicrobial susceptibility test results. *The Lancet Microbe*. 2021 Jul;2(10):e545-e554.
20. Birer-Williams CMC, Chu RK, Anderton CR, **Wright ES\***. SubTap, a Versatile 3D Printed Platform for Eavesdropping on Extracellular Interactions. *Msystems*. 2021 Aug;6(4):e00902-21. PMID: 34427520
21. Jones JE, Le Sage V, Padovani GH, Calderon M, **Wright ES\***, Lakdawala S\*. Parallel evolution between genomic segments of seasonal human influenza viruses reveals RNA-RNA relationships. *eLife*. 2021 Aug;10:e66525. PMID: 34448455.
22. Cooley NP, **Wright ES\***. Accurate annotation of protein coding sequences with IDTAXA. *NAR Genomics and Bioinformatics*. 2021 Sep;3(3):lqab080. PMID: 34541527.
23. **Wright ES\***. FindNonCoding: rapid and simple detection of non-coding RNAs in genomes. Bioinformatics. 2022 Feb; btab708. PMID: 34636849.
24. Brennan J, Jain L, Garman S, Donnelly AE, **Wright ES**, Jamieson K\*. Sample-efficient identification of high-dimensional antibiotic synergy with a normalized diagonal sampling design. *PLoS Computational Biology*. 2022 Jul;18(7):e1010311. PMID: 35849634.
25. Donnelly AE, Narayanan N, Birer-Williams CM, DeWolfe TJ, Chu RK, Anderton CR, **Wright ES**\*. Balancing Trade-Offs Imposed by Growth Media and Mass Spectrometry for Bacterial Exometabolomics. *Applied Environmental Microbiology*. 2022 Oct;88(30):e0092222. PMID: 36197102.
26. De Wolfe TJ, **Wright ES**\*. Multi-factorial examination of amplicon sequencing workflows from sample preparation to bioinformatic analysis. *BMC Microbiology*. 2023 Apr;23(1):107. PMID: 37076812.
27. Way A, Bond M, Nanna B, **Wright ES\***. Evaluating the long-term portrayal of antibiotic resistance in major U.S. newspapers. BMC Public Health. 2023 Jul;23(1343). PMID: 37438767.

\* Corresponding author

Other peer reviewed publications

1. **Wright ES**, Strait JM, Yilmaz LS, Harrington GW, Noguera DR. Identiﬁcation of Bacterial and Archaeal Communities from Source to Tap, Water Research Foundation, 2013, 1–76.

Other non-peer reviewed publications

1. **Wright ES**. Getting my feet wet. Science. 2017 Apr 7;356(6333). PMID: 28386014

# PROFESSIONAL ACTIVITIES

**TEACHING:**

Graduate Student Teaching

2014 Teaching Assistant, Microbiology 304: “Biology of Microorganisms laboratory.” University of Wisconsin – Madison.

2015 – 2016 Instructor, Computer Science 368: “Introduction to R Programming for Scientiﬁc Research.” University of Wisconsin – Madison.

2018 – 2021 Instructor, BIOINF 2018, “Introduction to R Programming for Scientific Research”, University of Pittsburgh

2018 – present Lecturer, ISB 2020, “Systems Biology I”, University of Pittsburgh

2020 – present Lecturer, ISB 2075, “Evolutionary Biology of Human Disease”, University of Pittsburgh

2023 – present Lecturer, MSMI 2480, “Mechanisms of Viral Persistence and Pathogenesis”, University of Pittsburgh

**MENTORING:**

Post-doctoral scholar mentoring/advising:

2018 – 2020 Caroline Birer

2018 – 2020 Travis De Wolfe

2021 – 2023 Gaby Sycz

2017 – 2023 Nicholas Cooley

Graduate student mentoring/advising**:**

2017 – 2018 Deepank Korandla

2017 – 2019 Lauren Rost

2018 – 2021 Andrew Beckley

2021 – present Aidan Laskshman

2021 – present Nishant Panicker

2021 – present Shu-Ting Cho

2022 – present Samuel Blechman

Undergraduate student mentoring/advising:

2011 – 2012 Jacqueline Strait

2011 – 2012 Jeremy Gasser

2012 – 2013 Brian Bauer

2014 Ryan Przybylski

2014 – 2015 Amelia Remiarz

2014 – 2015 Hannah Haight

2015 – 2016 Raveena Gupta

2016 – 2018 Adithya Murali

2018 Vibha Reddy

2019 – 2020 Aidan Lakshman

2019 – 2020 Nithya Narayanan

2022 Jordan Pater

2020 – 2022 Shania Khatri

High School student mentoring/advising:

2011 Alexander Bastian

2012 Rowan Meara

2012 – 2014 Gabe Kruse

2020 Adelle Fernando

2021 Amish Sethi

2021 Alina Ahmad

**RESEARCH**

**Current Grant Support:**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Grant Number | Grant Title | Role in Project | Years Inclusive | Source/$ Amount |
| EMSL 60302 | Illuminating emergent properties underlying complex carbon degradation within communities of soil microorganisms | PI | 2022 – 2024 | PNNL$80,000 (in-kind support) |
| 1U01AI176418-01 | Connecting the universe of proteins to address annotation inequality in the microbial proteome | PI75% effort Year 18 calendar months47% effort Year 25.64 calendar months34% effort Year 34.08 calendar months | 2023 – 2026 | NIH (NIAID)Direct: $899,995Indirect: $472,641 |

**Pending Grant Support:**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| R01AI180324-01A1(A0 scored 33rd percentile)SRG Meeting 02/24 | Optimizing antibiotic combination therapies for multi-drug resistant organisms with adaptive machine learning | PI 35% effort4.2 calendar months | 2024-2029 | NIHDirect: $2,317,423Indirect: $699,720Pending SRG Review |

**Prior Grant Support:**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Grant Number | Grant Title | Role in Project | Years Inclusive | Source/$ Amount |
| 1DP2AI145058 | Uncovering synergistic antibiotic cocktails with comparative genomics | PI50% effort3.0 calendar months | 2018 – 2023 | NIH (NIAID)Direct: $1,500,000Indirect: $847.50 |
| 1R21AI144769-01A1 | Overcoming Antibiotics of Last Resort: Determining the Role of Compensatory Mutations in Promoting Vancomycin Resistance in *Staphylococcus Aureus* | PI25% effort3.0 calendar months | 2020 – 2021 | NIH (NIAID)Direct: $275,000Indirect: $155,375 |
| EMSL 50808 | Decrypting inter-cellular communication within the soil microbiome by eavesdropping on pairwise signaling between bacteria | PI | 2019 – 2021 | PNNL$74,103 (in-kind support) |

**Current Research Interests:**

Dr. Wright's research integrates experimental evolution and computational approaches to tackle the problem of antibiotic resistance. Although antibiotics have been used by microorganisms for eons, it remains unclear how these organisms have mitigated the rise of antibiotic resistance in their competitors. Dr. Wright studies the strategies that naturally antibiotic-producing bacteria have evolved to discourage the build-up of resistance, and how some bacteria have adapted to overcome antibiotics while paying a minimal price for resistance. The goal of this research is to develop new strategies for treating pathogens in the clinic, ultimately turning the tide against increasing antibiotic resistance.

**Invited seminars and lectureships:**

Local Presentations

2017 “Jackpots Skew the Distribution of Descendants Arising from Individual Bacteria”, Biological Sciences, Duquesne University, Pittsburgh, PA

2017 "Improving the Accuracy of Taxonomic Classification for Microbiome Studies", Computational and Systems Biology, University of Pittsburgh, Pittsburgh, PA

2017 “Invasion and Interaction Networks in Microbial Communities Composed of Antibiotic Producers”, Science 2017, Pittsburgh, PA

2017 “Improving the accuracy of taxonomic classification for microbiome studies”, Center for Medicine and the Microbiome, Pittsburgh, PA

2018 “What do patterns of gene flow among thousands of genomes reveal about bacterial species?”, Microbiology and Molecular Genetics, University of Pittsburgh, Pittsburgh, PA

2018 “First-step mutations reveal a multitude of evolutionary pathways to antibiotic resistance”, Science 2018, University of Pittsburgh, Pittsburgh, PA

2018 “First-step mutations reveal a multitude of evolutionary pathways to antibiotic resistance”, Biomedical Informatics, University of Pittsburgh, Pittsburgh, PA

2019 “Piecing together the puzzle of antibiotic resistance through the lens of big data”, Senior Vice Chancellor Seminar Series, University of Pittsburgh, Pittsburgh, PA

2019 “Can Cycling between Different Antibiotics Cure the Rise of Antibiotic Resistance?”, Science 2019, University of Pittsburgh, Pittsburgh, PA

2021 “Can Cycling between Different Antibiotics Abate Antibiotic Resistance?”, CEBaM Seminar Series, University of Pittsburgh, Pittsburgh, PA

National Presentations

2011 “DNA Tools for Identifying Microbes in Drinking Water”, Wisconsin Water Association Annual Conference, Wisconsin Dells, WI

2013 “Design of a 16S rRNA High-Density Microarray and Application to Studying the Microbiome of Drinking Water Distribution Systems”, Microbial Ecology in Water Engineering International Conference, Ann Arbor, MI

2015 “Multiple Genome Alignment”, IPAM: Workshop on Multiple Sequence Alignment, Los Angeles, CA

2016 “Invasion and Interaction Networks in Microbial Communities Composed of Antibiotic Producers”, ASM General Meeting, Boston MA

2016 “Managing big biological sequence data with Biostrings and DECIPHER”, BioC 2016, Palo Alto, CA

2016 “Analysis of big biological sequence datasets using the DECIPHER package”, useR! 2016, Palo Alto, CA

2016 “Survival of the Common is Nearly as Widespread as Survival of the Fittest among Antibiotic Producing Bacteria”, Workshop on Evolutionary Systems Biology & Modeling, Madison, WI

2018 “Jackpots Skew the Distribution of Descendants Arising from Individual Bacteria”, Biological Sciences, Florida State University, Tallahassee, FL

2018 “What do patterns of gene flow among thousands of genomes reveal about bacterial species?”, Supercomputing Life Sciences Symposium, University of Nebraska–Lincoln, Lincoln, NE

2020 “Can Cycling between Different Antibiotics Cure the Rise of Antibiotic Resistance?”, Wake Forest School of Medicine, Winston-Salem, NC (virtual)

2021 “Can Cycling between Different Antibiotics Cure the Rise of Antibiotic Resistance?”, Department of Biomedical Informatics, Vanderbilt University, Nashville, TN (virtual)

2022 “Evolution of the DECIPHER package for comparative genomics”, BioC 2022, Seattle, WA

International Presentations

2018 Murali, A., Bhargava, A., and Wright, E. S. “Improving the accuracy of taxonomic classification for identifying taxa in microbiome samples”, BioC 2018, Toronto, Canada

2022 “Multi-stable bacterial communities exhibit extreme sensitivity to initial conditions”, FEMS Microbial Life Strategies, The Netherlands (virtual)

2023 “Clustering enormous numbers of sequences with Clusterize”, ISMB/ECCB 2023, Lyon, France

Poster Presentations

2011 “DECIPHER: A Search-Based Approach to Chimera Identiﬁcation for 16S rRNA Sequences”, MathBio3, Madison, WI

2012 “Improving Speciﬁcity in qPCR with Primer Design Utilizing Taq’s Terminal Mismatch Bias”, ASM General Meeting, San Francisco, CA

2016 “Survival of the common nearly as widespread as survival of the ﬁttest among competing bacteria”, Population, Evolution, and Physics, Aspen, CO

2018 “Improving the accuracy of taxonomic classification for identifying taxa in microbiome samples”, ASM General Meeting, Atlanta, GA

2022 “Strategies to sustainably evade antibiotic resistance in the clinic”, Gordon Research Conference, Smithfield, RI

**SERVICE**

University

2020 – present Member, Biomedical Informatics Comprehensive Exam Committee

2017 – present Member, Biomedical Informatics Training Program Core Faculty

2017 – present Executive Committee member, Center for Evolutionary Biology and Medicine (CEBaM)

2018, 2021 Member, Biomedical Informatics Training Program Admissions Committee

2019 Member, Integrative Systems Biology Training Program Admissions Committee

2018 – present Member, Master's and PhD thesis committees at University of Pittsburgh

National

2017 Member, National Science Foundation, Advances in Biological Information (ABI) Innovation Review Panel