OMB No. 0925-0001 and 0925-0002 (Rev. 10/2021 Approved Through 09/30/2024)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Erik S. Wright

eRA COMMONS USER NAME (credential, e.g., agency login): eswright

POSITION TITLE: Assistant Professor of Biomedical Informatics

EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)

| INSTITUTION AND LOCATION | DEGREE(if applicable) | Completion DateMM/YYYY | FIELD OF STUDY |
| --- | --- | --- | --- |
| Cornell University | B.S. | 01/2007 | Electrical and Computer Engineering |
| University of Wisconsin-Madison | M.S. | 08/2012 | Civil and Environmental Engineering |
| University of Wisconsin-Madison | Ph.D. | 12/2016 | Microbiology |

**A. Personal Statement**

**My mission is to develop innovative solutions to the problem of antimicrobial resistance. I am approaching this mission from multiple angles, including comparative genomics, electronic health record mining, mass spectrometry, and experimental evolution. My diversity of research interests reflect my hybrid wet and dry lab background. I am currently an Assistant Professor of Biomedical Informatics at the University of Pittsburgh and mentor four graduate students. Although originally trained as an electrical and computer engineer, I pivoted to microbiology in graduate school. During this time, I worked on natural products and developed my current interest in antibiotics and antibiotic resistance. My lab focuses on addressing the problem of antibiotic resistance from both the antibiotic discovery and antibiotic resistance sides of the problem. We are presently developing genomics and mass spectrometry methods to identify biosynthetic gene clusters that may harbor the information for discovering new antibiotics. We are simultaneously researching clinical strategies for extending the lifetime of our existing antibiotics arsenal against pathogens. To date, our focus has been on elucidating the mechanisms that make some antibiotics durable to resistance evolution in specific pathogens. We are also working on finding novel approaches for treating patients that evade resistance, which is the focus of the current proposal. I have been continuously funded by several grants from the NIAID since 2018.**

**B. Positions and Honors**

Professional Experience

|  |  |
| --- | --- |
| 2017 - | Assistant Professor, University of Pittsburgh |
| 2015 - 2016 | Lecturer, Computer Sciences, University of Wisconsin-Madison |
| 2010 - 2016 | Research Assistant, University of Wisconsin-Madison |
| 2007 - 2008 | Reliability Engineer, Reliability Engineering Department, Apple, Inc. |
| 2006 | Intern, Reliability Engineering Department, Apple, Inc. |

**C. Contributions to Science**

1. **Development of software for large-scale biological sequence analysis**. The amount of biological sequence data is currently growing at a remarkable pace, necessitating tools that can handle and derive insights from copious sequences. Dr. Wright has developed a software, named DECIPHER, that is used by thousands of researchers around the world to maintain, analyze, and manipulate their biological sequences. DECIPHER is based on a scalable database foundation that enables large-scale analyses of sequences, such as comparative genomics. This software continues to be actively developed by Dr. Wright and others in his lab.
2. Wright, E. (2016). Using DECIPHER v2.0 to Analyze Big Biological Sequence Data in R. The R Journal, 8(1), 352–359.
3. Wright, E. S. (2020). RNAconTest: Comparing tools for non-coding RNA multiple sequence alignment based on structural consistency. RNA, 26:531-40.
4. Cooley, N. & Wright, E. (2021). Accurate annotation of protein coding sequences with IDTAXA. NAR Genom Bioinform., 3(3):lqab080.
5. Wright, E. (2022). FindNonCoding: rapid and simple detection of non-coding RNAs in genomes. Bioinformatics, 38(3):841-843.
6. **Development of tools for microbiome analyses**. Microbiome studies are increasingly common as we begin to better understand the importance and role of the microbiome in human and ecosystem health. Dr. Wright has created a number of tools that are regularly used by the microbiology community to design and analyze microbiome experiments. In particular, his previous research has focused on the development of programs for oligonucleotide design, taxonomic classification, sequence alignment, and comparative genomics.
7. Wright, E., et al. (2014). Exploiting extension bias in polymerase chain reaction to improve primer specificity in ensembles of nearly identical DNA templates. Environmental Microbiology, 16(5), 1354–1365.
8. Wright, E., et al. (2014). 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, 80(16), 5124–5133. http://doi.org/10.1128/AEM.01685-14
9. Murali, A., Bhargava, A., Wright, E. (2018). IDTAXA: a novel approach for accurate taxonomic classification of microbiome sequences. Microbiome, 6(1):140.
10. **Birer-Williams, C., Chu, R., Anderton, C., Wright, E.. (2021). SubTap, a Versatile 3D Printed Platform for Eavesdropping on Extracellular Interactions. mSystems. 6(4):e0090221.**
11. **Optimizing treatment strategies for sustainable use of antibiotics in the clinic**. Antibiotic resistance is currently a significant clinical challenge for the treatment of patients. Dr. Wright's research in this area focuses on improving the stewardship of our existing antibiotics. He is approaching this by analyzing clinical data stored in electronic health records, and applying this information to experimentally test alternative strategies for antibiotic treatment.
12. Beckley, A., & Wright, E. (2021). Identification of antibiotic pairs that evade concurrent resistance via a retrospective analysis of antimicrobial susceptibility test results. The Lancet Microbe, 2(10), e545–e554.
13. Rost, L., Nguyen, M.H., Clancy, C., Shields, R., & Wright, E**. (2021). Discordance Among Antibiotic Prescription Guidelines Reflects a Lack of Clear Best Practices. Open Forum Infectious Diseases, 8(1):ofaa571.**
14. **Brennan, J., Jain, L., Garman, S., Donnelly, A., Wright, E., & Jamieson, K. (2022). Sample-efficient identification of high-dimensional antibiotic synergy with a normalized diagonal sampling design. PLoS Comput Biol 18, e1010311.**
15. **Ecology and evolution of naturally antibiotic producing microorganisms**. Over half of antibiotics used in the clinic were derived from molecules produced by members of the bacteria genus *Streptomyces*. Despite their contribution to our antibiotic arsenal, we know relatively little about their ecology and evolution. Dr. Wright's doctoral dissertation dealt with understanding the role of natural antibiotic production in shaping the ecology of bacteria belonging to the genus *Streptomyces*. Dr. Wright is now studying how *Streptomyces* have evolved to mitigate the rise of antibiotic resistance in their competitors.
16. Wright, E., & Vetsigian, K. (2016). Inhibitory interactions promote frequent bistability among competing bacteria. Nature Communications, 7, 11274.
17. Wright, E., & Baum, D. (2018). Exclusivity offers a sound yet practical species criterion for bacteria despite abundant gene flow. BMC Genomics, 19(1):724.
18. Wright, E. & Vetsigian, K. (2019). Stochastic exits from dormancy give rise to heavy-tailed distributions of descendants in bacterial populations. Molecular Ecology, 28(17):3915-28.
19. Wright, E., Gupta, R., & Vetsigian, K. (2021). Multi-stable bacterial communities exhibit extreme sensitivity to initial conditions. FEMS Microbiol Ecology, 97(6).