OMB No. 0925-0001 and 0925-0002 (Rev. 11/16 Approved Through 10/31/2018)

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@pitt.edu

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 Date  MM/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**

**Dr. Erik Wright is an Assistant Professor of Biomedical Informatics at the University of Pittsburgh. His research involves the use of bioinformatics, comparative genomics, and experimental evolution to address problems related to the rise of antibiotic resistance in pathogens. He is currently involved in projects related to understanding the evolution of biosynthetic gene clusters, the role of compensatory mutations in antibiotic resistance, evolution in spatially structured environments, and developing bioinformatics tools for deciphering large-scale biological sequence data.**

**B. Positions and Honors**

Professional Experience

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

**C. Contributions to Science**

1. **Development of software 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 software 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 tools for PCR primer, FISH probe, and microarray probe design. Dr. Wright's Master's thesis focused on analysis of the drinking water microbiome through custom-designed microarrays. He also created an algorithm for detecting PCR artifacts that is widely cited. Recently, he introduced an approach for detecting and eliminating errors that occur during Illumina sequencing.
2. Wright, E. S., et al. (2012). DECIPHER, a search-based approach to chimera identification for 16S rRNA sequences. Applied and Environmental Microbiology, 78(3), 717–725. http://doi.org/10.1128/AEM.06516-11
3. Wright, E. S., 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.
4. Wright, E. S., 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
5. Wright, E. S., & Vetsigian, K. H. (2016). Quality filtering of Illumina index reads mitigates sample cross-talk. BMC Genomics, 17(876), 1–7. http://doi.org/10.1186/s12864-016-3217-x
6. **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*. In particular, he discovered that inhibitory interactions contribute to multi-stability in competition among *Streptomyces* isolates. Dr. Wright is now studying how *Streptomyces* have evolved to mitigate the rise of antibiotic resistance in their competitors.
7. Wright, E., & Vetsigian, K. (2016). Inhibitory interactions promote frequent bistability among competing bacteria. Nature Communications, 7, 11274. http://doi.org/10.1038/ncomms11274
8. Wright, E. S. (2016). Population and community ecology of bacteria from the genus Streptomyces. Thesis.
9. Wright, E. S., & Baum, D. A.. Exclusivity offers a sound yet practical species criterion for bacteria. *In Review.*
10. Wright, E. S., & Vetsigian, K. H. Jackpots skew the distribution of descendants arising from individual bacteria. *In Review.*
11. **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 under active development by Dr. Wright and others in his lab.
12. Wright, E. S. (2015). DECIPHER: harnessing local sequence context to improve protein multiple sequence alignment. BMC Bioinformatics, 16, 322. http://doi.org/10.1186/s12859-015-0749-z
13. Wright, E. S. (2016). Using DECIPHER v2.0 to Analyze Big Biological Sequence Data in R. The R Journal, 8(1), 352–359.
14. Wright, E. S., & Vetsigian, K. H. (2016). DesignSignatures: a tool for designing primers that yields amplicons with distinct signatures. Bioinformatics, 32(10), 1565–1567.

**D. Additional Information: Research Support and/or Scholastic Performance**

**Dr. Wright is currently support by a start-up grant from the University of Pittsburgh.**