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| OMB No. 0925-0001/0002 (Rev. 08/12 Approved Through 8/31/2015) | | | | |
| BIOGRAPHICAL SKETCH Provide the following information for the Senior/key personnel and other significant contributors.  Follow this format for each person. DO NOT EXCEED FOUR PAGES. | | | | |
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| NAME  Matthew D. MacManes | | POSITION TITLE  Assistant Professor of Genome Enabled Biology | | |
| eRA COMMONS USER NAME (credential, e.g., agency login)  MMACMANES | |
| EDUCATION/TRAINING | | | | |
| INSTITUTION AND LOCATION | DEGREE  *(if applicable)* | | MM/YY | FIELD OF STUDY |
| Broome Community College | AAS | | 1999 | Nursing |
| University of Michigan | BS | | 2005 | Biology |
| University of California, Berkeley  University of California, Berkeley | PhD  Post-doc | | 2011  2013 | Biology  Genomics |
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# Personal Statement

Broadly defined, my career goal is to understand how natural selection shapes phenotypic variation, and, further, how genes underlie this variation. Stemming from my experience as a bedside RN in an ICU setting, I aim to apply my interest in evolutionary biology towards medically relevant problems in an attempt to improve health and wellness. To this end, my PhD research focused on better understanding how a behavioral phenotype (sexual behavior) modified the selective landscape (e.g. pathogen load), and, thus, the action of natural selection. My post-doctoral training, supported by a NIH F32, enabled me to receive training in computational genomics. This training, in combination with my PhD, has allowed me to develop a unique skill set – that of a researcher competent in field, molecular, and computational biology.

Currently, the MacManes lab has two complementary major research foci – biology and bioinformatics. This proposal aims to understand the genomic underpinnings of complex phenotypes and adaptation, and in particular, understand how desert animals survive intense heat and aridity without drinking water. We aim to collect the relevant behavior, physiological, metabolic and genomic data to gain a deep understanding of the links between genotype and phenotype in the context of desert biology.

Related to the collection of genomic data, the lab has recognized authority on the genome and transcriptome assembly as a developer of the Trinity and Trinotate software packages and co-author of the recent Assemblathon 2 paper. In addition, the lab has expertise in the quality control and pre-processing of high-throughput sequencing data with both published manuscripts and software packages.

# B. Positions and Honors

**Positions and Employment**

1999-2001 Registered Nurse: Emergency Department. Cayuga Medical Center

2001-2005 Registered Nurse: Emergency Department. University of Michigan Medical Center

2005-2011 Registered Nurse: Neuro-trauma ICU. Stanford University Medical Center

2011-2013 NIH NRSA Postdoctoral Fellow, Department of FILL IN, University of California, Berkeley

2013-present Assistant Professor, Department of Molecular, Cellular, and Biomedical Sciences,

University of New Hampshire, Durham

**Honors**

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| --- | --- |
| 2005 | UC Berkeley Edge Fellowship |
|  | MVZ Martens Research Award |
|  | UCB Chancellor's Fellowship for Graduate Studies |
| 2006 | California Desert Research Fund Award |
|  | NSF Pre-Doctoral Fellowship |
| 2007 | NSF Doctoral Dissertation Improvement Grant |
| 2010 | MVZ Fellowship |
| 2011 | NIH NRSA Postdoctoral Fellowship |

# C. Publications

**Most relevant to the current application**

1. Bradnam, K.R., Fass J.N., Alexandrov, A., Baranay, P., Bechner, M., Birol, I., Boisvert, S., **MacManes**, M.D., et al. (2013). Assemblathon 2: Evaluating *De Novo* Methods of Genome Assembly in Three Vertebrate Species. *GigaScience,* 2(1). DOI: 10.1186/2047-217X-2-10
2. Haas, B. J., Papanicolaou, A., Yassour, M., Grabherr, M., Blood, P.D., Bowden, J., M.B., **MacManes**, M.D., et al. (2013). *De Novo* Transcript Sequence Reconstruction From RNA-Seq Using the Trinity Platform for Reference Generation and Analysis. *Nature Protocols,* 8(8):1494–1512.

DOI: 10.1038/nprot.2013.084

1. **MacManes**, M.D., & Eisen, M.B. (2013). Improving Transcriptome Assembly Through Error Correction of High-Throughput Sequence Reads. *PeerJ,* 1: e113. DOI: 10.7717/peerj.113
2. **MacManes**, M.D. & Lacey, E.A. (2013). The Social Brain: Transcriptome Assembly and Characterization of the Hippocampus From a Social Subterranean Rodent, the Colonial Tuco-Tuco (*Ctenomys sociabilis*). *PLOS ONE,* 7(9): e45524. DOI: 10.1371/journal.pone.0045524.t001
3. **MacManes**, M.D. (2014). On the Optimal Trimming of High-Throughput mRNA Sequence Data. *Frontiers in Genetics*. **5**:13. DOI: 10.3389/fgene.2014.00013

**Other Publications and Products**

1. Quan, Y.F., **MacManes**, M.D., Ebensperger, L.A., Lacey, E.A., & Hayes, L.D. (2009). Isolation and Characterization of Polymorphic Microsatellite Loci From *Octodon degus*. *Molecular Ecology Resources*, 9(3): 999–1001. DOI: 10.1111/j.1755-0998.2009.02536.x
2. Benedict, L, Bowie, R.C.K., Fuchs J., & **MacManes**, M.D. (2010). When Non-Coding Is Non-Neutral: the Role of CHD1 Gene Polymorphism in Sexing, in Phylogenetics and as a Correlate of Fitness in Birds. *Ibis,* 152(2): 223–225. DOI: 10.1111/j.1474-919X.2010.01015.x
3. **MacManes**, M.D. (2011). Promiscuity in Mice Is Associated with Increased Vaginal Bacterial Diversity. *Naturwissenschaften*, 98(11): 951–960. DOI: 10.1007/s00114-011-0848-2
4. Rowe, K.C., Singhal, S., **MacManes**, M.D., Ayroles, J.F., Morelli, T.L., Rubidge, E., Bi, K., & Moritz, C. (2011). Museum Genomics: Low-Cost and High-Accuracy Genetic Data From Historical Specimens. *Molecular Ecology Resources*, 11(6): 1082–1092. DOI: 10.1111/j.1755-0998.2011.03052.x
5. **MacManes**, M., & Lacey, E.A. (2012). Is Promiscuity Associated with Enhanced Selection on MHC-DQα in Mice (Genus Peromyscus)? *PLOS ONE*, 7(5): e37562. DOI: 10.1371/journal.pone.0037562

# D. Research Support

**Ongoing Research Support**  
n/a

**Completed Research Support**

n/a