

# Matthew D. MacManes, PhD

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## Expertise related to proposed research

The primary goal of the MacManes lab is to understand the genomic underpinnings of complex phenotypes and adaptation. This work integrates the power of novel sequencing technologies with ecology, physiology, and behavior. The lab has recognized authority in 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.

## Professional Preparation

- 1996 - 1999 **Associate of Science.** Broome Community College. Binghamton, NY. Major: Nursing
- 2002 - 2005 **Bachelor of Science.** The University of Michigan - Ann Arbor. Major: Natural Resources Minor: Ecology and Evolutionary Biology
- 2005 - 2011 **Doctor of Philosophy.** The University of California - Berkeley. Integrative Biology.
- 2011 - 2013 **Postdoctoral Training.** The University of California, Berkeley. California Institute for Quantitative Biosciences

## Appointments

- 2013 - **Assistant Professor** The University of New Hampshire. Department of Molecular, Cellular & Biomedical Sciences.
- 2013 - **Faculty Member** Hubbard Center for Genome Studies

## Five publications related to the proposed project

- 2014 **Matthew. D. MacManes** and Michael B. Eisen Characterization of the transcriptome, nucleotide sequence polymorphism, and natural selection in the desert adapted mouse *Peromyscus eremicus* submitted PeerJ. <http://dx.doi.org/10.1101/009134>.
- 2014 **Matthew D. MacManes** On optimal trimming of high-throughput sequence data. *Frontiers in Genetics*. 5:13. <http://dx.doi.org/10.3389/fgene.2014.00013>.
- 2013 Haas, Brian J., Papanicolaou, Alexie, Yassour, Moran, Grabherr, Manfred, Blood, Philip D., Bowden, Joshua, Couger, Matthew Brian, Eccles, David, Li, Bo, Lieber, Matthias, **MacManes, Matthew D.**, Ott, Michael, Orvis, Joshua, Pochet, Nathalie, Strozzi, Francesco, Weeks, Nathan, Westerman, Rick, William, Thomas, Dewey, Colin N., Henschel, Robert, Leduc, Richard D., Friedman, Nir, Regev, Aviv *De novo* transcript sequence reconstruction from RNA-Seq: reference generation and analysis with Trinity. *Nature Protocols*. 8, 1494 - 1512 <http://dx.doi.org/10.1038/nprot.2013.084>.
- 2013 **Matthew. D. MacManes** and Michael .B. Eisen. Improving transcriptome assembly through error correction of high-throughput sequence reads. *PeerJ*. 1:e113 <http://dx.doi.org/10.7717/peerj.113>.

- 2013 Bradnam, Keith R., Fass, Joseph N., Alexandrov, Anton, Baranay, Paul, Bechner, Michael, Birol, Inanç, Boisvert, Sébastien, Chapman, Jarrod A., Chapuis, Guillaume, Chikhi, Rayan, Chitsaz, Hamidreza, Chou, Wen-Chi, Corbeil, Jacques, Del Fabbro, Cristian, Docking, T Roderick, Durbin, Richard, Earl, Dent, Emrich, Scott, Fedotov, Pavel, Fonseca, Nuno A., Ganapathy, Ganeshkumar, Gibbs, Richard A., Gnerre, Sante, Godzaridis, Elénie, Goldstein, Steve, Haimel, Matthias, Hall, Giles, Haussler, David, Hiatt, Joseph B., Ho, Isaac Y., Howard, Jason, Hunt, Martin, Jackman, Shaun D., Jaffe, David B., Jarvis, Erich, Jiang, Huaiyang, Kazakov, Sergey, Kersey, Paul J., Kitzman, Jacob O., Knight, James R., Koren, Sergey, Lam, Tak-Wah, Lavenier, Dominique, Laviolette, François, Li, Yingrui, Li, Zhenyu, Liu, Binghang, Liu, Yue, Luo, Ruibang, Maccallum, Iain, **MacManes, Matthew D.**, Maillet, Nicolas, Melnikov, Sergey, Naquin, Delphine, Ning, Zemin, Otto, Thomas D., Paten, Benedict, Paulo, Octávio S., Phillippy, Adam M., Pina-Martins, Francisco, Place, Michael, Przybylski, Dariusz, Qin, Xiang, Qu, Carson, Ribeiro, Filipe J., Richards, Stephen, Rokhsar, Daniel S., Ruby, J Graham, Scalabrin, Simone, Schatz, Michael C., Schwartz, David C., Sergushichev, Alexey, Sharpe, Ted, Shaw, Timothy I., Shendure, Jay, Shi, Yujian, Simpson, Jared T., Song, Henry, Tsarev, Fedor, Vezzi, Francesco, Vicedomini, Riccardo, Vieira, Bruno M., Wang, Jun, Worley, Kim C., Yin, Shuangye, Yiu, Siu-Ming, Yuan, Jianying, Zhang, Guojie, Zhang, Hao, Zhou, Shiguo, Korf, Ian F. Assemblathon 2: genome assembly in three vertebrate species. *GigaScience*. 2:10 <http://dx.doi.org/10.1186/2047-217X-2-10>.

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## Other publications

- 2012 **Matthew D. MacManes** and Eileen A. Lacey. The social brain: Transcriptome assembly and characterization of the hippocampus from a social subterranean rodent, the tuco-tuco (*Ctenomys sociabilis*). *PLOS ONE*. 7(9): e45524 <http://dx.plos.org/10.1371/journal.pone.0045524>.
- 2011 Kevin C Rowe, Singhal, Sonal, **MacManes, Matthew D.**, Ayroles, Julien F., Morelli, Toni Lyn, Rubidge, Emily M., Bi Ke, Craig C Moritz Museum genomics: low cost and high accuracy genetic data from historical specimens *Molecular Ecology Resources*. 11(6): 1082-1092.

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## Collaborators

Kelley Thomas, Enrique Lessa, Becca Calisi, Dustin Rubenstein, Kyle Summers, Rasmus Nielsen.

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## Advisors

Eileen Lacey (PhD supervisor), Michael Eisen (post-doctoral advisor).

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## Advisees

Lauren Kordonowy, Lindsay Havens, Jennifer Dickson, Kae Lombardo, Kathy Antosca.