JAMES (JAMIE) T. MORTON

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EDUCATION

Graduate	University of California, San Diego, CA
2015 - Present	PhD student in Computer Science
	Expected Graduation Date: August 2018
Graduate	University of Colorado, Boulder, CO
2014 - 2015	PhD student in Computer Science
	Integrative Quantitative Biology Program
Undergraduate	Miami University, Oxford, OH
2010 - 2014	B.S. Computer Science (Cum Laude)
	B.S. Electrical Engineering (Cum Laude)
	B.S. Mathematics and Statistics
	B.S. Engineering Physics
Study Abroad	Hong Kong University of Science and Technology, Hong Kong
Spring 2012	

HONORS

- **NSF Graduate Fellow**, 2014 - present
- **Integrated Quantitative Biology Fellowship**, University of Colorado Boulder, 2014 - 2015
- **National Barry Goldwater Scholar**, 2013
- **Benjamin Harrison Scholar**, Miami University, 2010-2014
- **First place**, Institute of Navigation (ION) Autonomous Snowplow Competition, 2014
- **NSF REU**, Cold Spring Harbor Laboratories, Summer 2012
- **Provost Academic Achievement Award**, Miami University, 2012
- **Ohio Space Grant Scholar Award**, NASA, 2012 - 2014
- **Dean's List**, Miami University, 2010-13
- **R.L. Edwards Scholarship**, Department of Physics, Miami University, 2011, 2013
- **Mary Jeannette and Clifford Harvey Scholarship**, Department of Mathetmatics, Miami U., 2013
- **Mary Jean and Joseph R. Priest Scholarship**, Department of Physics, Miami University, 2012
- **President List**, Miami University, 2010-11
- **Nestle Scholar**, Computer Sci. and Software Eng. Dept, Miami University, 2011
- **Faculty Prize**, Department of Mathematics, Miami University, 2011
- **Joseph A. Culler** Award, Department of Physics, Miami University, 2010,2011
- **NSF Travel Grant**, Coupling, Energetics, & Dynamics of Atmospheric Regions workshop, 2010
- **Wright Scholar**, Air Force Research Laboratory, Wright Patterson Air Force Base, 2009

RESEARCH INTERESTS

High dimensional statistics, compositional data analysis, multi-omics data fusion and machine learning techniques with applications to microbial ecology with special interests in functional genomics, microbial metabolism and microbial niche differentiation.

PUBLICATIONS

1. **Morton, J. T.**, Sanders, J., Quinn, R. A., McDonald, D., Gonzalez, A., Vázquez-Baeza, Y., Navas-Molina, J. A., Song, S. J., Metcalf, J. L., and Hyde, E. R. (2017a). Balance trees reveal microbial niche differentiation. *mSystems*, 2(1):e00162–16

2. **Morton, J. T.**, Toran, L., Edlund, A., Metcalf, J. L., Lauber, C., and Knight, R. (2017b). Uncovering the horseshoe effect in microbial analyses. *mSystems*, 2(1):e00166–16

3. Amir, A., McDonald, D., Navas-Molina, J. A., Debelius, J., **Morton, J. T.**, Hyde, E., Robbins-Pianka, A., and Knight, R. (2017a). Correcting for microbial blooms in fecal samples during room-temperature shipping. *mSystems*, 2(2):e00199–16

4. Amir, A., McDonald, D., Navas-Molina, J. A., Kopylova, E., **Morton, J. T.**, Zech Xu, Z., Kightley, E. P., Thompson, L. R., Hyde, E. R., Gonzalez, A., and Knight, R. (2017b). Deblur rapidly resolves single-nucleotide community sequence patterns. *mSystems*, 2(2)

5. Vázquez-Baeza, Y., Gonzalez, A., Smarr, L., McDonald, D., **Morton, J. T.**, Navas-Molina, J. A., and Knight, R. (2017). Bringing the dynamic microbiome to life with animations. *Cell Host & Microbe*, 21(1):7–10

6. Vrbanac, A., Debelius, J. W., Jiang, L., **Morton, J. T.**, Dorrestein, P., and Knight, R. (2017a). An elegan (t) screen for drug-microbe interactions. *Cell Host & Microbe*, 21(5):555–556

7. Hill-Burns, E. M., Debelius, J. W., **Morton, J. T.**, Wissemann, W. T., Lewis, M. R., Wallen, Z. D., Peddada, S. D., Factor, S. A., Molho, E., Zabetian, C. P., Knight, R., and Payami, H. (2017). Parkinson's disease and parkinson's disease medications have distinct signatures of the gut microbiome. *Movement Disorders*, 32(5):739–749

8. Hemmings, S. M., Malan-Muller, S., van den Heuvel, L. L., Demmitt, B. A., Stanislawski, M. A., Smith, D. G., Bohr, A. D., Stamper, C. E., Hyde, E. R., **Morton, J. T.**, Marotz, C. A., Siebler, P. H., Braspenning, Maarten Irand Van Criekinge, W. I. H. A. J., Brenner, L. A., Postolache, T. T., McQueen, M. B., Krauter, K. S., Knight, R., Seedat, S., and Lowry, C. A. (2017). The microbiome in posttraumatic stress disorder and trauma-exposed controls: An exploratory study. *Psychosomatic Medicine*

9. Reber, S. O., Siebler, P. H., Donner, N. C., **Morton, J. T.**, Smith, D. G., Kopelman, J. M., Lowe, K. R., Wheeler, K. J., Fox, J. H., Jr., J. E. H., Greenwood, B. N., Jansch, C., Lechner, A., Schmidt, D., Uschold-Schmidt, N., Fchsl, A. M., Langgartner, D., Walker, F. R., Hale, M. W., Perez, G. L., Treuren, W. V., Gonzlez, A., Halweg-Edwards, A. L., Fleshner, M., Raison, C. L., Rook, G. A., Peddada, S. D., Knight, R., , and Lowry, C. A. Immunization with a heat-killed preparation of the environmental bacterium mycobacterium vaccae promotes stress resilience in mice

10. Gilbert, J. A., Quinn, R. A., Debelius, J., Xu, Z. Z., **Morton, J**, Garg, N., Jansson, J. K., Dorrestein, P. C., and Knight, R. (2016). Microbiome-wide association studies link dynamic microbial consortia to disease. *Nature*, 535(7610):94–103

11. Nellore, A., Collado-Torres, L., Jaffe, A. E., Alquicira-Hernández, J., Wilks, C., Pritt, J., **Morton, J**, Leek, J. T., and Langmead, B. (2016). Rail-rna: Scalable analysis of rna-seq splicing and coverage. *Bioinformatics*, page btw575

12. Petras, D., Nothias, L.-F., Quinn, R. A., Alexandrov, T., Bandeira, N., Bouslimani, A., Castro-Falcn, G., Chen, L., Dang, T., Floros, D. J., Hook, V., Garg, N., Hoffner, N., Jiang, Y., Kapono, C. A., Koester, I., Knight, R., Leber, C. A., Ling, T.-J., Luzzatto-Knaan, T., McCall, L.-I., McGrath, A. P., Meehan, M. J., Merritt, J. K., Mills, R. H., **Morton, J. T.**, Podvin, S., Protsyuk, I., Purdy, T., Satterfield, K., Searles, S., Shah, S., Shires, S., Steffen, D., White, M., Todoric, J., Tuttle, R., Wojnicz, A., Sapp, V., Vargas, F., Yang, J., Zhang, C., and Dorrestein, P. C. (2016). Mass spectrometry-based visualization of molecules associated with human habitats. *Analytical Chemistry*, 88(22):10775–10784. PMID: 27732780

13. Barberán, A., Dunn, R. R., Reich, B. J., Pacifici, K., Laber, E. B., Menninger, H. L., **Morton, J. T.**, Henley, J. B., Leff, J. W., Miller, S. L., and Fierer, N. (2015). The ecology of microscopic life in household dust. *Proceedings of the Royal Society of London B: Biological Sciences*, 282(1814)

14. **Morton, J. T.**, Freed, S. D., Lee, S. W., and Friedberg, I. (2015). A large scale prediction of bacteriocin gene blocks suggests a wide functional spectrum for bacteriocins. *BMC bioinformatics*, 16(1):381

15. **Morton, J. T.**, Abrudan, P., Figueroa, N., Liang, C., and Karro, J. E. (2014). Scope++: Sequence classification of homopolymer emissions. *Genomics*, 104(3):157–162

PUBLICATIONS IN REVIEW

1. Washburne, A., **Morton, J. T.**, Sanders, J., McDonald, D., Zhu, Q., Oliverio, AM, and Knight, R. (2017). Phylogenetic analysis of microbiome data: making sense of microbiomes in light of evolution. *Nature Microbiology*

2. McCall, L.-I., **Morton, J. T.**, Bernatchez, J. A., de Siqueira-Neto, J. L., Knight, R., C., D. P., and McKerrow, J. H. (2017). Molecular cartography of experimental cardiac infection by the parasite trypanosoma cruzi. *Analytical Chemistry*

3. Jiang, L., Amir, A., **Morton, J. T.**, Heller, R., Arias-Castro, E., and Knight, R. (2017). Discrete false discovery rate improves identification of differentially abundant microbes. *mSystems*

4. Thompson, L. R., Sanders, J. G., McDonald, D., Ladau, J., Locey, K. J., Navas-Molina, J. A., Prill, R. J., Gibbons, S. M., Gonzalez, A., Amir, A., Tripathi, A., Song, S. J., Vzquez-Baeza, Y., Kopylova, E., **J T. Morton**, Mirarab, S., Haroon, M. F., Kosciolek, T., Xu, Z. Z., Bokulich, N. A., Humphrey, G. C., Ackermann, G., Owens, S. M., Janssen, S., BrislawnK, C. J., Lefler, J., Hampton-Marcell, J., Zhu, Q., Kanbar, J., Berg-Lyons, D., Fierer, N., Shade, A., Pollard, K. S., Goodwin, K. D., JanssonK, J. K., Gilbert, J. A., Knight, R., and the Earth Microbiome Project Consortium (2017). The earth microbiome project. *Nature*

5. Vazquez-Baeza, Y., Callewaert, C., Debelius, J., Hyde, E., Marotz, C., **Morton, J. T.**, Swafford, A., Vrbanac, A., Dorrestein, P. C., and Knight, R. (2017). Impacts of the human gut microbiome on therapeutics. *Annual Reviews*

6. Metcalf, J. L., Song, S. J., **Morton, J. T.**, Weiss, S., Seguin-Orlando, A., Joly, F., Feh, C., Taberlet, P., Coissac, E., Amir, A., Willerslev, E., Knight, R., McKenzie, V., and Orlando, L. (2017). Domestication and captivity shape the horse gut microbiome. *Scientific Reports*

7. Vrbanac, A., Taylor, B. C., Aksenov, A., Callewaert, C., Debelius, J., Gonzalez, A., McCall, L.-I., McDonald, D., Melnik, A. V., **Morton, J. T.**, Navas, J., Quinn, R., Sanders, J. G., Swafford, A. D., Thompson, L. R., Tripathi, A., Vazquez-Baeza, Y., Xu, Z. Z., Zaneveld, J., Zhu, Q., Caporaso, J. G., C., D. P., and Knight, R. (2017b). Best practices for analyzing microbiomes. *Nature Reviews Microbiology*

8. Debelius, J. W., McDonald, D., Hyde, E., Ackermann, G., Aksenov, A., Chen, Y., Dorrestein, P. C., Dunn, R. R., Fahimpour, A. K., Gaffney, J., Gilbert, J. A., Gogul, G., Gonzalez, A., Green, J. L., Hugenholtz, P., Humphrey, G., Huttenhower, C., Jackson, M. A., Kelley, S. T., Knights, D., JoshuaLadau, Leach, J., Melnik, A., Metcalf, J. L., Montassier, E., **J T. Morton**, Navas-Molina, J., Peddada, S., Pollard, K. S., Rahnavard, G., Robbins-Pianka, A., Sangwan, N., Shorenstein, J., Spector, T., Thackray, V. G., Thompson, L. R., Vazquez-Baeza, Y., Wischmeyer, P., Wolfe, E., Consortium, T. A. G., and Knight, R. (2017). American gut: an open platform for citizen-science microbiome research. *Science*

9. Quinn, R. A., Comstock, W., Zhang, T., **Morton, J. T.**, Silva, R. d., Tran, A., Aksenov, A., Nothias-Scaglia1, L.-F., Wangpraseurt, D., Melnik, A. V., Ackerman, G., Conrad, D., Klapper, I., Knight, R., and Dorrestein, P. C. (2017). Niche partitioning of a polymicrobial infection driven by chemical gradients. *Nature*

PUBLICATIONS IN PREPARATION

1. Kapono, C. A., **Morton, J. T.**, Bouslimani, A., Orlinsky, K., Melnik, A. V., Knaan, T. L., Garg, N., Vzquez-Baeza, Y., Alexandrov, T., Protsyuk, I., Smarr, L., Knight, R., and Dorrestein, P. C. (2017). 3d chemical tracking of a human habitat and its human and microbial occupants. *Scientific Reports*

2. Martino, C., **Morton, J. T.**, Knight, R., and Zengler, K. (2017). Extrapolations across the vast unobserved microbial space with matrix completion. *mSystems*

3. Lavrinienko, A., Mappes, T., Tukalenko, E., Mousseau, T. A., Mller, A. P., Knight, R., **Morton, J. T.**, Thompson, L. R., and Watts, P. C. (2017). Environmental radiation alters the gut microbiome of the bank vole myodes glareolus. *Nature*

PRESENTATIONS

- Morton J. T. et al. The Microbiome and Sex Differences. Sex and the Kidneys: Sex Differences in Renal Disease Workshop in Bethesda, MD (2017)

- Morton J. T. et al. Balances Reveal Microbial Niche Differentiation. CODAwork (2017)

- Morton J. T. et al. From Probabilities to Balances: An Alternative Approach. Information Theory and Applications Workshop (2016)

- Morton J. T. et al. From Probabilities to Balances: An Alternative Approach Random Processes and Time Series: Theory and Applications (2016)

- Reber et al. An immunization strategy for prevention of post-traumatic stress disorder (PTSD) promotes stress resilience in mice. University California San Diego Pediatrics Symposium (2016)

- Reber et al. Immunization with a heat-killed preparation of the environmental bacterium Mycobacterium vaccae promotes stress resilience in mice. DNA Day (2015)

- Morton, J. T, Lladser M., Knight R., Uncovering the Unknown: A New Approach in Analyzing Microbiome Data NSF Data Science Workshop, 2015

- Morton, J. T, Freed, S. Lee, S. Friedberg, I. Prediction of Bacteriocin Associated Operons Rocky Mountain Bioinformatics Conference, 2014

- Morton, J. T, Freed, S. Lee, S. Friedberg, I. A pipeline for Identifying Bacteriocin-Associated Gene Clusters. ISMB Boston, 2014

- Morton, J. T, Freed, S. Lee, S. Friedberg, I. Discovering the Next Antibiotic Ohio Space Grant Consortium, Cleveland OH, 2014

- Morton, J. T, P., Abrudan, J. Karro, C. Liang , Sequence classification of homopolymer emissions (SCOPE), Great Lakes Bioinformatics Conference, Pittsburgh, PA, 2013

- Morton, J. T, P., Abrudan, J. Karro, C. Liang , Sequence classification of homopolymer emissions (SCOPE), Ohio Space Grant Consortium, Cleveland OH, 2013

- Morton, J. T, P., Abrudan, J. Karro, C. Liang , Sequence classification of homopolymer emissions (SCOPE), IEEE 2nd International Conference on Computational Advances in Bio and Medical Sciences, ICCABS 2012, Las Vegas, NV, February 2012

- Morton, J. T, J. Karro, C. Liang, A novel approach for identifying poly(A) tails in raw cDNA sequence data using General Hidden Markov Models, Genome Informatics Cold Spring Harbor, NY, November 2011.

PROFESSIONAL MEMBERSHIPS

- International Society of Computational Biology Student member, Summer 2014-Present
- Association for Computing Machinery Student member, 2011-Present
- Sigma Pi Sigma,Tau Beta Pi,Eta Kappa Nu, 2014
- National Society of Collegiate Scholars, 2012 - 2013
- Institute of Electrical and Electronics Engineers Student member, 2011-2016
- IEEE Miami Student Chapter Treasurer, 2011 - 2012

PROFESSIONAL SERVICES

- Poster Reviewer for ISMB 2015 2014-2016

WORKSHOPS

- Teaching Assistant. Qiime2 workshop. Las Vegas, NV June 21-23, 2017
- Teaching Assistant. STAMPS, Woodshole, MA, August2-13, 2016

TEACHING

- Instructor. Qiime2 workshop. UBC Vancouver August 23-25, 2017
- Instructor. Qiime2 workshop. UBC Kelowna August 21-22, 2017

Student Mentoring

- Jue Wang (undergraduate student Summer 2017)
- Cameron Martino (undergraduate student Spring 2017)
- Liam Toran (masters student Summer 2016)
- Kayla Orlinsky (undergraduate student Spring 2016)

SKILLS

Foreign Language Skills
- Chinese – Fluent in Mandarin and competent in written Chinese

Highly skilled in the following languages and computational platforms
- Python
- C/C++
- Java
- Javascript
- LaTeX
- ROS
- Hadoop
- Matlab
- R
- Unix
- SQL
- OpenCL
- CUDA
- git

OPEN SOURCE CONTRIBUTIONS

- Gneiss (Core Maintainer)
- Sci-kit Bio (Developer)
- Emperor (Developer)
- Qiime2 (Contributor)
- Deblur (Contributor)
- Micronota (Developer)
- BOA: Bacteriocin Operon Associator (Lead Developer)
- SCOPE++: Sequence Classification Of homoPolymer Emissions (Lead Developer)
- Rail-RNA (Contributor)
- Statsmodels (Contributor)
- Scipy (Contributor)
- Biopython (Contributor)

PERSONAL INTERESTS

- Music: Piano, Cello, Guitar, and Voice (base).
- Sports: Surfing, Scuba Diving, Ice Hockey, Skiing, Hiking, Biking, Kung Fu
- Others: Traveling, Cooking