

JAMES (JAMIE) T. MORTON

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RESEARCH INTERESTS

Machine learning and applied statistical modeling with applications to microbial ecology and evolution with special interests in microbial metabolism and functional genomics.

WORK EXPERIENCE

Tenure-track Investigator	NICHD, MD, Jan 2022 - Present
Associate Research Scientist	Simons Foundation, NY, March 2021 - Jan 2022
Research Fellow	Simons Foundation, NY, 2019-2021
Founder	Gutz Analytics, NY, Jan. 2019 - Jan 2022
Chief Scientist	Esoterica, NY, Apr. 2019 Jan 2022
Consultant	Native Microbials, CA, Jan. 2019 - Jan 2022
Teaching Assistant	University of California San Diego, CA, Fall 2018
Graduate Researcher	University of California San Diego, CA, 2015-2018
Graduate Researcher	University of Colorado Boulder, CO, 2014-2015
Undergraduate Researcher	Johns Hopkins University, MD, Summer 2013
Undergraduate Researcher	Cold Spring Harbor Laboratories, NY, Summer 2012
Undergraduate Researcher	Miami University, OH, 2010-2014

EDUCATION

Ph.D.	(2018)	Computer Science, University of California, San Diego, CA
B.S.	(2014)	Computer Science (Cum Laude), Miami University, Oxford, OH
B.S.	(2014)	Electrical Engineering (Cum Laude), Miami University, Oxford, OH
B.S.	(2014)	Mathematics and Statistics, Miami University, Oxford, OH
B.S.	(2014)	Engineering Physics, Miami University, Oxford, OH

SELECT LEAD AUTHOR PUBLICATIONS

1. **Morton J. T.**, Bonneau, R., Taroncher, G., and the SFARI consortium (2022). Multi-omic analysis along the gut-brain axis points to a functional architecture of autism. *Nature Medicine* (in review)
2. **Morton J. T.**, Silverman, J., Tikhonov, G., Lhdesmki, H., and Bonneau, R. (2021). Multinomial Variational Autoencoders can infer microbial co-occurrences across tens of thousands of samples and dimensions. Learning Meaningful Representations of Life, Neurips Workshop
3. **Morton, James T**, Strauss, C., Blackwell, R., Gligorijevic, V., Berenberg, D., and Bonneau, R. (2020). Protein structural alignments from sequence. Learning Meaningful Representations of Life, Neurips Workshop
4. **Morton, James T**, Aksenov, A. A., Nothias, L. F., Foulds, J. R., Quinn, R. A., Badri, u., Swenson, T. L., Van Goethem, M. W., Northen, T. R., Vazquez-Baeza, Y., et al. (2019). Learning representations of microbe-metabolite interactions. *Nature methods*, 16(12):1306–1314
5. **Morton, James T**, Marotz, C., Washburne, A., Silverman, J., Zaramela, L. S., Edlund, A., Zengler, K., and Knight, R. (2019). Establishing microbial composition measurement standards with reference frames. *Nature communications*, 10(1):2719
6. Martino, Cameron, **Morton, James T**, Marotz, C. A., Thompson, L. R., Tripathi, A., Knight, R., and Zengler, K. (2019). A Novel Sparse Compositional Technique Reveals Microbial Perturbations. *MSystems*, 4(1):e00016–19

7. Washburne, A. D., **Morton, James T**, Sanders, J., McDonald, D., Zhu, Q., Oliverio, A. M., and Knight, R. (2018). Methods for phylogenetic analysis of microbiome data. *Nature microbiology*, 3(6):652–661
8. **Morton, James T**, Sanders, J., Quinn, R. A., McDonald, D., Gonzalez, A., Vázquez-Baeza, Y., Navas-Molina, J. A., Song, S. J., Metcalf, J. L., Hyde, E. R., et al. (2017). Balance trees reveal microbial niche differentiation. *MSystems*, 2(1):e00162–16
9. **Morton, James T**, Toran, L., Edlund, A., Metcalf, J. L., Lauber, C., and Knight, R. (2017). Uncovering the horseshoe effect in microbial analyses. *MSystems*, 2(1):e00166–16
10. **Morton, James 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
11. **Morton, James T**, Abrudan, P., Figueroa, N., Liang, C., and Karro, J. E. (2014). SCOPE++: Sequence Classification Of homoPolymer Emissions. *Genomics*, 104(3):157–162

OTHER PUBLICATIONS

12. Dallago, C., Schütze, K., Heinzinger, M., Olenyi, T., Littmann, M., Lu, A. X., Yang, K. K., Min, S., Yoon, S., Morton, J. T., et al. (2021). Learned embeddings from deep learning to visualize and predict protein sets. *Current Protocols*, 1(5):e113
13. Liu, J., Zhang, X., Chen, T., Wu, T., Lin, T., Jiang, L., Lang, S., Liu, L., Natarajan, L., Tu, J., et al. (2021). A semiparametric model for between-subject attributes: Applications to beta-diversity of microbiome data. *Biometrics*
14. Dillon, M. R., Bolyen, E., Adamov, A., Belk, A., Borsom, E., Burcham, Z., Debelius, J. W., Deel, H., Emmons, A., Estaki, M., et al. (2021). Experiences and lessons learned from two virtual, hands-on microbiome bioinformatics workshops. *PLoS computational biology*, 17(6):e1009056
15. Marotz, C., Morton, J. T., Navarro, P., Coker, J., Belda-Ferre, P., Knight, R., and Zengler, K. (2021). Quantifying Live Microbial Load in Human Saliva Samples over Time Reveals Stable Composition and Dynamic Load. *Msystems*, 6(1):e01182–20
16. Fedarko, M. W., Martino, Cameron, **Morton, James T**, González, A., Rahman, G., Marotz, C. A., Minich, J. J., Allen, E. E., and Knight, R. (2020). Visualizingomic feature rankings and log-ratios using Qurro. *NAR Genomics and Bioinformatics*, 2(2):lqaa023
17. Aksenov, A. e. a. (2020). Algorithmic Learning for Auto-deconvolution of GC-MS Data to Enable Molecular Networking within GNPS. *Nature Biotechnology*
18. Martino, Cameron, Shenhav, L., Marotz, C. A., Armstrong, G., McDonald, D., Vázquez-Baeza, Y., **Morton, James T**, Jiang, L., Dominguez-Bello, M. G., Swofford, A. D., et al. (2020). Context-aware dimensionality reduction deconvolutes gut microbial community dynamics. *Nature biotechnology*, pages 1–4
19. J. Tsay, J.-C., G. Wu, B., Sulaiman, I., Gershner, K., Schluger, R., Li, Y., Yie, T.-A., Meyn, P., Olsen, E., Perez, L., Franca, B., El-ashmawy, M., Bardi, M., **Morton , James T.**, Shen, N., He, L., Michaud, G., Rafeq, S., Bessich, J., L. Smith, R., Sauthoff, H., Felner, K., Moreira, A., Moore, W., Tsirigos, A., Heguy, A., N. Rom, W., H. Sterman, D., Pass, H., C. Clemente, J., Li, H., Bonneau, R., Wong, K.-k., Papagiannakopoulos, T., and N. Segal, L. (2019). Lower airway dysbiosis affects lung cancer progression. *Nature Medicine (submitted)*,
20. Gulino, K., Rahman, J., Badri, M, **Morton, James T**, Bonneau, R., and Ghedin, E. (2020). Initial Mapping of the New York City Wastewater Virome. *mSystems*,

21. Raghuvanshi, R., Vasco, K., Vasquez-Baeza, Y., Jiang, L., **Morton , James**, Li, D., Gonzlez, A., DeRight-Goldasich, L., Humphrey, G., Ackermann, G., Swafford, A., Conrad, D., Knight, R., Dorrestein, P., and Quinn, R. (2020). High-resolution Longitudinal Dynamics of the Cystic Fibrosis Sputum Microbiome and Metabolome Through Antibiotic Therapys. *mSystems*,
22. Aksenov, A. e. a. (2020). Algorithmic Learning for Auto-deconvolution of GC-MS Data to Enable Molecular Networking within GNPS. *Nature Biotechnology*
23. Mu, A., Carter, G. P., Li, L., Isles, N. S., Vrbanc, A. F., **Morton, James T**, De Souza, D. P., Narayana, V. K., Kanojia, K., Nijagal, B., et al. (202). Microbe-metabolite associations linked to the rebounding murine gut microbiome post-colonization with vancomycin resistant *Enterococcus faecium*. *MSystems*
24. Zhu, Q. et al. (2019). Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. *Nature communications*, 10(1):1–14
25. Gauglitz, J. M., **Morton, James T**, Tripathi, A., Hansen, S., Gaffney, M., Carpenter, C., Weldon, K. C., Shah, R., Parampil, A., Fidgett, A., et al. (2020). Metabolome-informed microbiome analysis refines metadata classifications and reveals unexpected medication transfer in captive cheetahs. *MSystems*
26. Baker, J. L., **Morton, James T**, Dinis, M., Alvarez, R., Tran, N. C., Knight, R., and Edlund, A. (2019). Deep metagenomics examines the oral microbiome during dental caries, revealing novel taxa and co-occurrences with host molecules. *bioRxiv (submitted to Nature Microbiology)*, page 804443
27. Amato, K. R., Sanders, J. G., Song, S. J., Nute, M., Metcalf, J. L., Thompson, L. R., **Morton, James T**, Amir, A., McKenzie, V. J., Humphrey, G., et al. (2019). Evolutionary trends in host physiology outweigh dietary niche in structuring primate gut microbiomes. *The ISME journal*, 13(3):576
28. Xu, Z. Z., Amir, A., Sanders, J., Zhu, Q., **Morton, James T**, Bletz, M. C., Tripathi, A., Huang, S., McDonald, D., Jiang, L., et al. (2019). Calour: an Interactive, Microbe-Centric Analysis Tool. *MSystems*, 4(1):e00269–18
29. Washburne, A. D., Silverman, J. D., **Morton, James T**, Becker, D. J., Crowley, D., Mukherjee, S., David, L. A., and Plowright, R. K. (2019). Phylofactorization: a graph partitioning algorithm to identify phylogenetic scales of ecological data. *Ecological Monographs*, 89(2):e01353
30. Thompson, L. R., Haroon, M. F., Shibl, A. A., Cahill, M. J., Ngugi, D. K., Williams, G. J., **Morton, James T**, Knight, R., Goodwin, K. D., and Stingl, U. (2019). Red Sea SAR11 and *Prochlorococcus* Single-cell Genomes Reflect Globally Distributed Pangenomes. *Applied and environmental microbiology*, 85(13):e00369–19
31. Bolyen, E. et al. (2019). Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature biotechnology*, 37(8):852–857
32. Cao, L. et al. (2019). MetaMiner: A Scalable Peptidogenomics Approach for Discovery of Ribosomal Peptide Natural Products with Blind Modifications from Microbial Communities. *Cell Systems*, 9(6):600–608
33. Lavrinienko, A., Mappes, T., Tukalenko, E., Mousseau, T. A., Møller, A. P., Knight, R., **Morton, James T**, Thompson, L. R., and Watts, P. C. (2018). Environmental radiation alters the gut microbiome of the bank vole *Myodes glareolus*. *The ISME journal*, 12(11):2801
34. Kapono, C. A., **Morton, James T**, Bouslimani, A., Melnik, A. V., Orlinsky, Kayla, Knaan, T. L., Garg, N., Vázquez-Baeza, Y., Protsyuk, I., Janssen, S., et al. (2018). Creating a 3D microbial and chemical snapshot of a human habitat. *Scientific reports*, 8(1):3669

35. McDonald, D., Hyde, E., Debelius, J. W., **Morton, James T**, Gonzalez, A., Ackermann, G., Aksenov, A. A., Behsaz, B., Brennan, C., Chen, Y., et al. (2018). American gut: an open platform for citizen science microbiome research. *mSystems*, 3(3):e00031–18
36. Quinn, R. A., Comstock, W., Zhang, T., **Morton, James T**, da Silva, R., Tran, A., Aksenov, A., Nothias, L.-F., Wangpraseurt, D., Melnik, A. V., et al. (2018). Niche partitioning of a pathogenic microbiome driven by chemical gradients. *Science advances*, 4(9):eaau1908
37. Knight, R. et al. (2018). Best practices for analysing microbiomes. *Nature Reviews Microbiology*, 16(7):410–422
38. McCall, L.-I., **Morton, James T**, Bernatchez, J. A., de Siqueira-Neto, J. L., Knight, R., Dorrestein, P. C., and McKerrow, J. H. (2017). Mass spectrometry-based chemical cartography of a cardiac parasitic infection. *Analytical chemistry*, 89(19):10414–10421
39. Thompson, L. R. et al. (2017). A communal catalogue reveals Earths multiscale microbial diversity. *Nature*, 551(7681):457
40. Mohimani, H. e. a. (2017). Metarippquest: a peptidogenomics approach for the discovery of ribosomally synthesized and post-translationally modified peptides. *bioRxiv*, page 227504
41. Jiang, L., Amir, A., **Morton, James T**, Heller, R., Arias-Castro, E., and Knight, R. (2017). Discrete false-discovery rate improves identification of differentially abundant microbes. *MSystems*, 2(6):e00092–17
42. Vázquez-Baeza, Y., Gonzalez, A., Smarr, L., McDonald, D., **Morton, James T**, Navas-Molina, J. A., and Knight, R. (2017). Bringing the dynamic microbiome to life with animations. *Cell host & microbe*, 21(1):7–10
43. Vrbanc, A., Debelius, J. W., Jiang, L., **Morton, James T**, Dorrestein, P., and Knight, R. (2017). An Elegan (t) Screen for Drug-Microbe Interactions. *Cell host & microbe*, 21(5):555–556
44. Metcalf, J. L., Song, S. J., **Morton, James T**, Weiss, S., Seguin-Orlando, A., Joly, F., Feh, C., Taberlet, P., Coissac, E., Amir, A., et al. (2017). Evaluating the impact of domestication and captivity on the horse gut microbiome. *Scientific reports*, 7(1):15497
45. Maier, T. V. et al. (2017). Impact of dietary resistant starch on the human gut microbiome, metaproteome, and metabolome. *MBio*, 8(5):e01343–17
46. Amir, A., McDonald, D., Navas-Molina, J. A., Debelius, J., **Morton, James T**, Hyde, E., Robbins-Pianka, A., and Knight, R. (2017). Correcting for microbial blooms in fecal samples during room-temperature shipping. *MSystems*, 2(2):e00199–16
47. Amir, A., McDonald, D., Navas-Molina, J. A., Kopylova, E., **Morton, James T**, Xu, Z. Z., Kightley, E. P., Thompson, L. R., Hyde, E. R., Gonzalez, A., et al. (2017). Deblur rapidly resolves single-nucleotide community sequence patterns. *MSystems*, 2(2):e00191–16
48. Vázquez-Baeza, Y., Gonzalez, A., Smarr, L., McDonald, D., **Morton, James T**, Navas-Molina, J. A., and Knight, R. (2017). Bringing the dynamic microbiome to life with animations. *Cell host & microbe*, 21(1):7–10
49. Vrbanc, A., Debelius, J. W., Jiang, L., **Morton, James T**, Dorrestein, P., and Knight, R. (2017). An Elegan (t) Screen for Drug-Microbe Interactions. *Cell host & microbe*, 21(5):555–556
50. Hill-Burns, E. M., Debelius, J. W., **Morton, James T**, Wissemann, W. T., Lewis, M. R., Wallen, Z. D., Peddada, S. D., Factor, S. A., Molho, E., Zabetian, C. P., et al. (2017). Parkinson’s disease and Parkinson’s disease medications have distinct signatures of the gut microbiome. *Movement Disorders*, 32(5):739–749

51. 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, James T**, et al. (2017). The microbiome in posttraumatic stress disorder and trauma-exposed controls: an exploratory study. *Psychosomatic medicine*, 79(8):936
52. Reber, S. O., Siebler, P. H., Donner, N. C., **Morton, James T**, Smith, D. G., Kopelman, J. M., Lowe, K. R., Wheeler, K. J., Fox, J. H., Hassell, J. E., et al. (2016). Immunization with a heat-killed preparation of the environmental bacterium *Mycobacterium vaccae* promotes stress resilience in mice. *Proceedings of the National Academy of Sciences*, 113(22):E3130–E3139
53. Gilbert, J. A., Quinn, R. A., Debelius, J., Xu, Z. Z., **Morton, James**, 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
54. Nellore, A., Collado-Torres, L., Jaffe, A. E., Alquicira-Hernández, J., Wilks, C., Pritt, J., **Morton, James**, Leek, J. T., and Langmead, B. (2016). Rail-RNA: scalable analysis of RNA-seq splicing and coverage. *Bioinformatics*, 33(24):4033–4040
55. Petras, D. et al. (2016). Mass Spectrometry-Based 3D Cartography Displays the Chemistry Associated with Modern Human Habitats. *Analytical chemistry*, 88(22):10775
56. Barberán, A., Dunn, R. R., Reich, B. J., Pacifici, K., Laber, E. B., Menninger, H. L., **Morton, James M**, Henley, J. B., Leff, J. W., Miller, S. L., et al. (2015). The ecology of microscopic life in household dust. *Proceedings of the Royal Society B: Biological Sciences*, 282(1814):20151139

SELECTED PRESENTATIONS

- **Morton, J. T.** (2021). Compositional frameworks for microbiome research. 8th International Human Microbiome Conference (invited)
- **Morton, J. T.** (2020). Protein Structure Alignment From Sequence. Learning Meaningful Representation of Life, Neurips Workshop (invited)
- **Morton, J. T.** (2020). Differential Dynamic Programming for Protein Structural Alignment. Flatiron Internal Conference: Flatiron-wide Algorithms and Mathematics (invited)
- **Morton, J. T.**, Marotz, C., Washburne, A., Silverman, J., Zaramela, L. S., Edlund, A., Zengler, K., and Knight, R. (2019). Establishing microbial composition measurement standards with reference frames. Illumina Boston Meetup (invited)
- **Morton J. T.**, Marotz, C., Washburne, A., Silverman, J., Zaramela, L. S., Edlund, A., Zengler, K., Aksenov, A. A., Felix Nothias, L., Foulds, J. R., Quinn, R. A., Badri, M. H., Swenson, T. L., Van Goethem, M. W., Northen, T. R., Vazquez-Baeza, Y., Wang, M., Bokulich, N. A., Watters, A., Song, S. J., Bonneau, R., Dorrestein, P. C., and Knight, R. (2019). Statistical caveats behind microbiome compositional data analysis. Penn State (invited)
- **Morton J. T.**, Aksenov, A. A., Felix Nothias, L., Foulds, J. R., Quinn, R. A., Badri, M. H., Swenson, T. L., Van Goethem, M. W., Northen, T. R., Vazquez-Baeza, Y., Wang, M., Bokulich, N. A., Watters, A., Song, S. J., Bonneau, R., Dorrestein, P. C., and Knight, R. (2019). Learning representations of microbe-metabolite interactions. Broad Institute (invited)
- **Morton J. T.**, Aksenov, A. A., Felix Nothias, L., Foulds, J. R., Quinn, R. A., Badri, M. H., Swenson, T. L., Van Goethem, M. W., Northen, T. R., Vazquez-Baeza, Y., Wang, M., Bokulich, N. A., Watters, A., Song, S. J., Bonneau, R., Dorrestein, P. C., and Knight, R. (2019). Learning representations of microbe-metabolite interactions. Multiomics for Microbiomes
- **Morton J. T.**, Aksenov, A. A., Felix Nothias, L., Foulds, J. R., Quinn, R. A., Badri, M. H., Swenson, T. L., Van Goethem, M. W., Northen, T. R., Vazquez-Baeza, Y., Wang, M., Bokulich,

- N. A., Watters, A., Song, S. J., Bonneau, R., Dorrestein, P. C., and Knight, R. (2019). Learning accurate representations of microbe-metabolite interactions. International Society of Molecular Biology
- **Morton J. T.**, Aksenov, A. A., Felix Nothias, L., Foulds, J. R., Quinn, R. A., Badri, M. H., Swenson, T. L., Van Goethem, M. W., Northen, T. R., Vazquez-Baeza, Y., Wang, M., Bokulich, N. A., Watters, A., Song, S. J., Bonneau, R., Dorrestein, P. C., and Knight, R. (2019). Learning accurate representations of microbe-metabolite interactions. CoDaWork2019
 - **Morton J. T.**, Aksenov, A. A., Felix Nothias, L., Foulds, J. R., Quinn, R. A., Badri, M. H., Swenson, T. L., Van Goethem, M. W., Northen, T. R., Vazquez-Baeza, Y., Wang, M., Bokulich, N. A., Watters, A., Song, S. J., Bonneau, R., Dorrestein, P. C., and Knight, R. (2019). Learning representations of microbe-metabolite interactions. Probabilistic Microbial Modeling Symposium
 - **Morton J. T.** (2017). The microbiome and sex differences. Sex and the Kidneys: Sex Differences in Renal Disease Workshop in Bethesda, MD
 - **Morton, J. T.**, Sanders, J., Quinn, R. A., McDonald, D., Gonzalez, A., Vazquez-Baeza, Y., Navas-Molina, J. A., Song, S. J., Metcalf, J. L., and Hyde, E. R. (2017). Balances reveal microbial niche differentiation. CODAwork in Abbadia San Salvatore, Siena, Italy
 - **Morton, J. T.**, Freed, S., Lee, S., and Friedberg, I. (2014). Prediction of Bacteriocin Associated Operons. Rocky Mountain Bioinformatics Conference, Aspen, CO
 - **Morton, J. T.**, Richard, M., and Robert, C. (2013). Redblade Miami University's autonomous vehicle. Institute of Navigation (ION) Autonomous Snowplow Competition, St. Paul, MN

HONORS

- **NSF Graduate Research Fellowship**, 2014 - 2018
- **Integrated Quantitative Biology Fellowship**, University of Colorado Boulder, 2014 - 2015
- **National Barry Goldwater Scholar**, 2013
- **Benjamin Harrison Scholar**, Miami University, 2010-2014
- **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 & Clifford Harvey Scholarship**, Mathematics Department, Miami U., 2013
- **Mary Jean & Joseph R. Priest Scholarship**, Physics Department, Miami U., 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

SELECTED POSTER PRESENTATIONS

- **Morton J. T.**, Aksenov, A. A., Felix Nothias, L., Foulds, J. R., Quinn, R. A., Badri, M. H., Swenson, T. L., Van Goethem, M. W., Northen, T. R., Vazquez-Baeza, Y., Wang, M., Bokulich, N. A., Watters, A., Song, S. J., Bonneau, R., Dorrestein, P. C., and Knight, R. (2019). Learning representations of microbe-metabolite interactions. Genome Informatics
- **Morton, J. T.**, Sanders, J., Quinn, R. A., McDonald, D., Gonzalez, A., Vazquez-Baeza, Y., Navas-Molina, J. A., Song, S. J., Metcalf, J. L., and Hyde, E. R. (2017). From probabilities to

balances: an alternative approach. Information Theory and Applications Workshop in San Diego, CA

- **Morton, J. T.**, Sanders, J., Quinn, R. A., McDonald, D., Gonzalez, A., Vazquez-Baeza, Y., Navas-Molina, J. A., Song, S. J., Metcalf, J. L., and Hyde, E. R. (2017). From probabilities to balances: an alternative approach. Random Processes and Time Series: Theory and Applications in San Diego, CA
- 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. (2016). An immunization strategy for prevention of post-traumatic stress disorder (PTSD) promotes stress resilience in mice. University California San Diego Pediatrics Symposium in San Diego, CA
- **Morton, J. T.**, Lladser, M., and Knight, R. (2015). Uncovering the Unknown: a new approach in analyzing microbiome data. NSF Data Science Workshop in University of Washington, Seattle, WA
- **Morton, J. T.**, Freed, S., and Lee, S. Friedberg, I. (2014). Discovering the next antibiotic. Ohio Space Grant Consortium in Cleveland, OH
- **Morton, J. T.**, Abrudan, P., Karro, J., and Liang, C. (2013). Sequence classification of homopolymer emissions (SCOPE). Great Lakes Bioinformatics Conference, Pittsburgh, PA
- **Morton, J. T.**, Abrudan, P., Karro, J., and Liang, C. (2012). Sequence classification of homopolymer emissions (SCOPE). IEEE 2nd International Conference on Computational Advances in Bio and Medical Sciences, ICCABS , Las Vegas, NV
- **Morton, J. T.**, Karro, J., and Liang, C. (2011). A novel approach for identifying poly(A) tails in raw cDNA sequence data using Hidden Markov Models. Genome Informatics in Cold Spring Harbor, NY
- Santana, J., **Morton J. T.**, and Zhou, Q. (2010). A fuzzy logic approach to extract plasma line frequencies from Arecibo incoherent scatter radar measurements. Coupling, Energetics, and Dynamics of Atmospheric Regions Workshop, Boulder, CO

CONFERENCE ORGANIZATIONS

- Co-organizer, 2019, Simons Foundation, NY, 3rd Workshop on Statistical and Algorithmic Challenges in Microbiome Data Analysis, over 150 participants.
- Organizer, 2018, UCSD, Probabilistic Microbial Modeling Symposium, over 120 participants.
- Coordinator, UCSE CSE 2018 Visit Day

TECHNICAL REVIEWS

- Reviewer for Nature Biofilms journal, 2020
- Reviewer for Msystems, 2020
- Reviewer for Molecular Ecology Resources, 2020
- Reviewer for NAR Genomics and Bioinformatics, 2020
- Reviewer for Microbiome, 2020
- Reviewer for GigaScience, 2020
- Reviewer for ISME journal, 2020
- Reviewer for Nature Biofilms journal, 2019
- Reviewer for Microbiome journal, 2019
- Reviewer for PLOS One journal, 2019
- Reviewer for BMC microbiome journal, 2018

PROFESSIONAL MEMBERSHIPS

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

TEACHING

- Instructor. Online Compositional Data Analysis workshop. March 2021
- Instructor. Online Qiime2 workshop. January 2021
- Instructor. Online Qiime2 workshop. October 2020
- Instructor. Multiomics Qiime2 workshop. Penn State University, Fall 2019
- Teaching Assistant. A Practical Introduction to Probability and Statistics, Fall 2018
- Instructor. Qiime2 workshop. Colorado State University, November 20-21, 2017
- Instructor. Qiime2 workshop. UBC Vancouver, August 23-25, 2017
- Instructor. Qiime2 workshop. UBC Kelowna, August 21-22, 2017
- Teaching Assistant. Qiime2 workshop. Las Vegas, NV, June 21-23, 2017
- Teaching Assistant. STAMPS, Woodshole, MA, August 2-13, 2016
- Instructor. Qiime workshop. Scripps Institute of Oceanography, CA, June 29, 2016
- Instructor. MED 263 invited speaker. UCSD Medical School, CA, March 9, 2016

MENTORING

- Aashna Shah, Simons Foundation intern, 2020-present
- Michelle Badri, NYU PhD student, 2019-present
- Danxun Li, Simons Foundation programmer, 2019-present
- Kalen Cantrell, UCSD undergraduate student, 2017-2018
- Thant Htoo Zaw, UCSD undergraduate student, 2017-2018
- Yimeng Yang, UCSD undergraduate student, 2017-2018
- Andrew Nyugen, UCSD undergraduate student, 2017-2018
- Jue Wang, UCSD undergraduate student, Summer 2017
- Cameron Martino, UCSD undergraduate student, Spring 2017
- Josh Lefler, UCSD undergraduate student, Fall 2016
- Liam Toran, UCSD masters student, Summer 2016
- Kayla Orlinsky, UCSD undergraduate student, Spring 2016

SKILLS

Foreign Language Skills

- Chinese – Competent in Mandarin and in written Chinese

Highly skilled in the following languages and computational platforms

- Python • Pytorch • Tensorflow • Stan • CUDA • C/C++ • Javascript • AWS

OPEN SOURCE CONTRIBUTIONS

- [DeepBLAST](#) (Lead Developer)
- [Gneiss](#) (Lead Developer)
- [scikit-bio](#) (Developer)
- [Deblur](#) (Developer)
- [Scipy](#) (Contributor)
- [mmvec](#) (Lead Developer)
- [BOA](#) (Lead Developer)
- [Emperor](#) (Developer)
- [Rail-RNA](#) (Contributor)
- [Biopython](#) (Contributor)
- [Songbird](#) (Lead Developer)
- [SCOPE](#) (Lead Developer)
- [Qiime2](#) (Developer)
- [Statsmodels](#) (Contributor)

PERSONAL INTERESTS

- Music: Piano, Cello, Guitar, and Voice (bass).
- Sports: Surfing, Scuba Diving, Skiing, Biking and Hiking