

CAMERON MARTINO

cameronmartino@gmail.com ◊ <https://cameronmartino.github.io/>

EMPLOYMENT

Native Microbials

Interim Chief Scientific Officer

September 2020 - March 2021

Microbial Community Data Scientist

2016 - 2018

General Automation Lab Technologies

Data Scientist

2016 - 2017

NanoConversion Technologies

Engineer

2012 - 2014

EDUCATION

PhD, University of California, San Diego

2018 - Present

PhD in Bioinformatics and Systems Biology

Mentor: Rob Knight

Bachelors of Science, University of California, San Diego

2014 - 2017

B.S. Bioengineering

PUBLICATIONS

1. **Zaramela, Livia S, Martino, Cameron, Alisson-Silva, Frederico**, Rees, S. D., Diaz, S. L., Chuzel, L., Ganatra, M. B., Taron, C. H., Secrest, P., Zuñiga, C., et al. (2019). Gut bacteria responding to dietary change encode sialidases that exhibit preference for red meat-associated carbohydrates. *Nature microbiology*, pages 1–8, Bold authors contributed equally
2. **Martino, Cameron**, Morton, J. 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
3. **Martino, Cameron**, Shenhav, L., Marotz, C., Armstrong, G., McDonald, D., Vázquez-Baeza, Y., Morton, J. T., Jiang, L., Dominguez-Bello, M. G., Swafford, A. D., Halperin, E., and Knight, R. (2020). Context-Aware Dimensionality Reduction Deconvolutes Dynamics of Gut Microbial Community Development. *Nature Biotechnology*, pages 165–168
4. **Martino, Cameron**, Kellman, B. P., Sandoval, D. R., Clausen, T. M., Marotz, C. A., Song, S. J., Wandro, S., Zaramela, L. S., Salido Bentez, R. A., Zhu, Q., Armingol, E., Vázquez-Baeza, Y., McDonald, D., Sorrentino, J. T., Taylor, B., Belda-Ferre, P., Liang, C., Zhang, Y., Schifanella, L., Klatt, N. R., Havulinna, A. S., Jousilahti, P., Huang, S., Haiminen, N., Parida, L., Kim, H.-C., Swafford, A. D., Zengler, K., Cheng, S., Inouye, M., Niiranen, T., Jain, M., Salomaa, V., Esko, J. D., Lewis, N. E., and Knight, R. (2020). Bacterial modification of the host glycosaminoglycan heparan sulfate modulates SARS-CoV-2 infectivity. *bioRxiv : the preprint server for biology*
5. **Song, Se Jin Song, Wang, Jincheng, Martino, Cameron**, Jiang, L., Thompson, W. K., Shenhav, L., McDonald, D., Harris, P. R., Hernandez, C., Henderson, N., Ackley, E., Nardella, D., Gillihan, C., Montacuti, V., Schweizer, W., Jay, M., Combellick, J., Garcia-Mantrana, I., Gil Raga, F., Collado, M. C., Rivera-Viñas, J. I., Campos-Rivera, M., Ruiz-Calderon, J. F., Knight, R., and Dominguez-Bello, M. G. (2021). Restoration of the microbiome trajectory by vaginal seeding of C-section born infants. *Cell Reports Medicine* Bold authors contributed equally

6. Fedarko, M. W., **Martino, Cameron**, Morton, J. T., Gonzlez, A., Rahman, G., Marotz, C. A., Minich, J. J., Allen, E. E., and Knight, R. (2020). Visualizing'omic feature rankings and log-ratios using Qurro. *NAR genomics and bioinformatics*, 2(2):lqaa023
7. Clausen, T. M., Sandoval, D. R., Spliid, C. B., Pihl, J., Perrett, H. R., Painter, C. D., Narayanan, A., Majowicz, S. A., Kwong, E. M., McVicar, R. N., Thacker, B. E., Glass, C. A., Yang, Z., Torres, J. L., Golden, G. J., Bartels, P. L., Porell, R. N., Garretson, A. F., Laubach, L., Feldman, J., Yin, X., Pu, Y., Hauser, B. M., Caradonna, T. M., Kellman, B. P., **Martino, Cameron**, Gordts, P. L. S. M., Chanda, S. K., Schmidt, A. G., Godula, K., Leibel, S. L., Jose, J., Corbett, K. D., Ward, A. B., Carlin, A. F., and Esko, J. D. (2020). SARS-CoV-2 Infection Depends on Cellular Heparan Sulfate and ACE2. *Cell*, 183(4):1043–1057.e15
8. Mu, A., McDonald, D., Jarmusch, A. K., **Martino, Cameron**, Brennan, C., Bryant, M., Humphrey, G. C., Toronczak, J., Schwartz, T., Nguyen, D., Ackermann, G., D'Onofrio, A., Strathdee, S. A., Schooley, R. T., Dorrestein, P. C., Knight, R., and Aslam, S. (2021). Assessment of the microbiome during bacteriophage therapy in combination with systemic antibiotics to treat a case of staphylococcal device infection. *Microbiome*, 9(1):92
9. Huey, S. L., Jiang, L., Fedarko, M. W., McDonald, D., **Martino, Cameron**, Ali, F., Russell, D. G., Udipi, S. A., Thorat, A., Thakker, V., Ghugre, P., Potdar, R. D., Chopra, H., Rajagopalan, K., Haas, J. D., Finkelstein, J. L., Knight, R., and Mehta, S. (2020). Nutrition and the Gut Microbiota in 10- to 18-Month-Old Children Living in Urban Slums of Mumbai, India. *mSphere*, 5(5)
10. Estaki, M., Jiang, L., Bokulich, N. A., McDonald, D., Gonzlez, A., Kosciolk, T., **Martino, Cameron**, Zhu, Q., Birmingham, A., VazquezBaeza, Y., Dillon, M. R., Bolyen, E., Caporaso, J. G., and Knight, R. (2020). QIIME 2 Enables Comprehensive EndtoEnd Analysis of Diverse Microbiome Data and Comparative Studies with Publicly Available Data. *Current protocols in bioinformatics / editorial board, Andreas D. Baxevanis ... [et al.]*, 70(1):e00010
11. Taylor, B. C., Lejzerowicz, F., Poirel, M., Shaffer, J. P., Jiang, L., Aksenov, A., Litwin, N., Humphrey, G., **Martino, Cameron**, Miller-Montgomery, S., Dorrestein, P. C., Veiga, P., Song, S. J., McDonald, D., Derrien, M., and Knight, R. (2020). Consumption of Fermented Foods Is Associated with Systematic Differences in the Gut Microbiome and Metabolome. *mSystems*, 5(2)
12. Litwin, N., Taylor, B., Lejzerowicz, F., Poirel, M., Shaffer, J., Jiang, L., Aksenov, A., Humphrey, G., **Martino, Cameron**, Miller-Montgomery, S., Dorrestein, P., Veiga, P., Song, S. J., McDonald, D., Derrien, M., and Knight, R. (2020). Consumption of Fermented Plant Foods Is Associated with Systematic Differences in the Human Gut Microbiome and Metabolome. *Current Developments in Nutrition*, 4(Supplement_2):1573–1573
13. Xue, J., Allaband, C., Zhou, D., Poulsen, O., **Martino, Cameron**, Jiang, L., Tripathi, A., Elijah, E., Dorrestein, P. C., Knight, R., Zarrinpar, A., and Haddad, G. G. (2021). Influence of Intermittent Hypoxia/Hypercapnia on Atherosclerosis, Gut Microbiome, and Metabolome. *Frontiers in physiology*, 12:663950
14. Shaffer, J. P., Marotz, C., Belda-Ferre, P., **Martino, Cameron**, Wandro, S., Estaki, M., Salido, R. A., Carpenter, C. S., Zaramela, L. S., Minich, J. J., Bryant, M., Sanders, K., Fraraccio, S., Ackermann, G., Humphrey, G., Swafford, A. D., Miller-Montgomery, S., and Knight, R. (2021). A comparison of DNA/RNA extraction protocols for high-throughput sequencing of microbial communities. *BioTechniques*, 70(3):149–159
15. Cantrell, K., Fedarko, M. W., Rahman, G., McDonald, D., Yang, Y., Zaw, T., Gonzalez, A., Janssen, S., Estaki, M., Haiminen, N., Beck, K. L., Zhu, Q., Sayyari, E., Morton, J. T., Armstrong, G., Tripathi, A., Gauglitz, J. M., Marotz, C., Matteson, N. L., **Martino, Cameron**, Sanders, J. G., Carrieri, A. P., Song, S. J., Swafford, A. D., Dorrestein, P. C., Andersen, K. G., Parida, L.,

- Kim, H.-C., Vazquez-Baeza, Y., and Knight, R. (2021). EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets
16. Gauglitz, J. M., Bittremieux, W., Williams, C. L., Weldon, K. C., Panitchpakdi, M., Di Ottavio, F., Aceves, C. M., Brown, E., Sikora, N. C., Jarmusch, A. K., **Martino, Cameron**, Tripathi, A., Sayyari, E., Shaffer, J. P., Coras, R., Vargas, F., Goldasich, L. D., Schwartz, T., Bryant, M., Humphrey, G., Johnson, A. J., Spengler, K., Belda-Ferre, P., Diaz, E., McDonald, D., Zhu, Q., Nguyen, D. S., Elijah, E. O., Wang, M., Marotz, C., Sprecher, K. E., Robles, D. V., Withrow, D., Ackermann, G., Herrera, L., Bradford, B. J., Marques, L. M. M., Amaral, J. G., Silva, R. M., Veras, F. P., Cunha, T. M., Oliveira, R. D. R., Louzada-Junior, P., Mills, R. H., Galasko, D., Dulai, P. S., Wittenberg, C., Gonzalez, D. J., Terkeltaub, R., Doty, M. M., Kim, J. H., Rhee, K. E., Beauchamp-Walters, J., Wright, K. P., Dominguez-Bello, M. G., Manary, M., Oliveira, M. F., Boland, B. S., Lopes, N. P., Guma, M., Swafford, A. D., Dutton, R. J., Knight, R., and Dorrestein, P. C. (2020). Reference data based insights expand understanding of human metabolomes
 17. Sanders, J. G., Nurk, S., Salido, R. A., Minich, J., Xu, Z. Z., Zhu, Q., **Martino, Cameron**, Fedarko, M., Arthur, T. D., Chen, F., et al. (2019). Optimizing sequencing protocols for leader-board metagenomics by combining long and short reads. *Genome biology*, 20(1):1–14
 18. Fouladi, F., Bailey, M. J., Patterson, W. B., Sioda, M., Blakley, I. C., Fodor, A. A., Jones, R. B., Chen, Z., Kim, J. S., Lurmann, F., **Martino, Cameron**, Knight, R., Gilliland, F. D., and Alderete, T. L. (2020). Air pollution exposure is associated with the gut microbiome as revealed by shotgun metagenomic sequencing. *Environment International*, 138:105604
 19. Bluemel, S., Wang, L., **Martino, Cameron**, Lee, S., Wang, Y., Williams, B., Horvath, A., Stadlbauer, V., Zengler, K., and Schnabl, B. (2018). The Role of Intestinal C-type Regenerating Islet Derived-3 Lectins for Nonalcoholic Steatohepatitis. *Hepatology communications*, 2(4):393–406
 20. Bluemel, S., Wang, L., **Martino, Cameron**, Lee, S., Williams, B., Horvath, A., Stadlbauer, V., Zengler, K., and Schnabl, B. (2017). The Role of Intestinal Reg3 lectins for Non-Alcoholic Steatohepatitis. In *HEPATOLOGY*, volume 66, pages 452A–453A. WILEY 111 RIVER ST, HOBOKEN 07030-5774, NJ USA
 21. Jin Song, S., Woodhams, D. C., **Martino, Cameron**, Allaband, C., Mu, A., Javorschi-Miller-Montgomery, S., Suchodolski, J. S., and Knight, R. (2019). Engineering the microbiome for animal health and conservation. *Experimental Biology and Medicine*, 244(6):494–504
 22. Clemmons, B. A., **Martino, Cameron**, Schneider, L. G., Lefler, J., Embree, M. M., and Myer, P. R. (2019). Temporal Stability of the Ruminant Bacterial Communities in Beef Steers. *Scientific reports*, 9(1):9522
 23. Clemmons, B. A., **Martino, Cameron**, Powers, J. B., Campagna, S. R., Voy, B. H., Donohoe, D. R., Gaffney, J., Embree, M. M., and Myer, P. R. (2019). Rumen Bacteria and Serum Metabolites Predictive of Feed Efficiency Phenotypes in Beef Cattle. *Scientific Reports*, 9(1):1–8
 24. Clemmons, B., **Martino, Cameron**, Embree, M., Melchior, E., Voy, B., Campagna, S., and Myer, P. (2018). Biochemical and microbial biomarkers of feed efficiency in Black Angus steers. *Journal of Animal Science*, 96:237–237
 25. Goetz, B. M., Lefler, J., Abeyta, M. A., Horst, E. A., Mayorga, E. J., Al-Qaisi, M., Rodriguez-Jimenez, S., **Martino, Cameron**, Izzo, A., La, R., Green, H. B., Moore, C. E., Embree, M., and Baumgard, L. H. (2021). Effects of dietary microbial feed supplement on production efficacy in lactating dairy cows. *JDS Communications*

PATENTS

1. Embree, M. and **Martino, Cameron** (2018). Methods, apparatuses, and systems for analyzing microorganism strains in complex heterogeneous communities, determining functional relationships and interactions thereof, and diagnostics and biostate management based thereon
2. Embree, M., **Martino, Cameron**, Pitt, N., Embree, J., and Dodge, C. (2018). Methods for supporting grain intensive and or energy intensive diets in ruminants by administration of a synthetic bioensemble of microbes or purified strains therefor
3. Dodge, C., Embree, J., Embree, M., **Martino, Cameron**, and Pitt, N. (2019). Methods for supporting grain intensive and/or energy intensive diets in ruminants with a synthetic bioensemble of microbes
4. Embree, M., Gogul, G., **Martino, Cameron**, and Pitt, N. (2019). Methods of decreasing feed conversion ratios in fowl
5. Dodge, C., Embree, J., Pitt, N., **Martino, Cameron**, and Embree, M. (2019). Methods of supplementing diets high grain consumption and / or high energy value in ruminants by administering a synthetic bioensemble microbes or purified isolates thereof
6. Embree, M., Gogul, G., **Martino, Cameron**, and Pitt, N. (2019). Improving fowl production by administration of a synthetic bioensemble of microbes or purified strains thereof
7. Zengler, K., Varki, A., Da Silva, F., Diaz, S., **Martino, Cameron**, Chang, G., Rees, S., and Zaramela, L. S. (2021). Novel sialidases and uses thereof

OPEN SOURCE SOFTWARE CONTRIBUTIONS

- [DEICODE](#) (Lead Developer)
- [QIIME 2](#) (Contributor)
- [sourcetracker2](#) (Contributor)
- [BacDivePy](#) (Lead Developer)
- [Qurro](#) (Developer)
- [songbird](#) (Contributor)
- [gemelli](#) (Lead Developer)
- [FEAST](#) (Contributor)
- [mmvec](#) (Contributor)

SELECTED CONFERENCE PRESENTATIONS

SACMDA —2019— Simons Foundation - NYC
Animal Microbiome Congress —2018— Kansas City
ASM Microbe —2016— Boston

SKILLS

Skilled in the following wet laboratory techniques:

- Illumina Sequencing Platforms
- Metagenomics
- Microbial Isolation to Axenicity
- 16S rRNA Gene Amplicon Libraries
- Anaerobic and Aerobic Cultivation
- Protein Purification

Skilled in the following languages and computational platforms:

- Python
- C/C++
- Java
- Javascript
- Matlab
- R
- Unix
- L^AT_EX
- git

REFERENCES

- Kartsen Zengler — Asst. Professor Dept. of Pediatrics, UCSD — kzengler@ucsd.edu
- Mike Seeley — CEO Ascus Biosciences — mike@ascusbiosciences.com

FELLOWSHIPS AWARDED

- **Ascus Biosciences Fellowship**, 2018-2019
- **Frontiers of Innovation Scholars Program**, 2016-2017
- **Frontiers of Innovation Scholars Program**, 2015-2016