

Nicholas Chia

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EDUCATION

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| 2001-2006 | The Ohio State University
<i>PhD in Physics (Thesis Advisor: Ralf Bundschuh, Ph.D.)</i> <ul style="list-style-type: none">• Statistics of sequence alignment, extremal distributions, probabilistic alignment• Solved longstanding challenge in field of significance assessment for sequence alignments resulting in the analytical solution for E-value for pairwise gapped alignments (e.g., BLAST) |
| 1997-2001 | Georgetown University, Washington DC
<i>BS in Physics (Advisor: Joseph Serene, Ph.D.)</i> <ul style="list-style-type: none">• Rebuilt total internal reflection fluorescence (TIRF) microscopy system, replacing all sapphire components with glass components |

RESEARCH EXPERIENCE

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| 2006-2011 | University of Illinois at Urbana-Champaign
<i>Postdoctoral Fellow (Advisors: Nigel Goldenfeld, PhD and Carl Woese, PhD)</i> <ul style="list-style-type: none">• Studied evolutionary processes near the origin of life, extending computational biology approaches for discovery of deep homologies, reconstructing phylogenies, and simulation testing.• Investigated dynamics of horizontal gene transfer in evolutionary systems.• Led development of microbiome data analysis pipeline. |
| 2011-2012 | University of Illinois at Urbana-Champaign & The Institute for Systems Biology, Seattle WA
<i>Postdoctoral Fellow/Senior Research Scientist (Advisors: Nathan Price, PhD)</i> <ul style="list-style-type: none">• Led pipeline development team for Automated Metabolic Model Reconstruction team including 1 software engineer.• Establish Microbiome Science subgroup |
| 2012-NOW | Mayo Clinic, Rochester, MN <i>Principal Investigator of Theoretical Biology Group</i> <ul style="list-style-type: none">• Research focuses on the intersection between statistics, dynamic systems, and machine learning. Have successfully generated approaches using causal inference, invariant risk minimization, and inverse reinforcement learning to biomedical research.• Led the Microbiome Program Theoretical, Engineering, and Data (TED) section resulting in over \$20M raised from benefactors, 8 industry partnerships, and over 113 IRB studies across 30+ human diseases.• Mentored 40+ junior members through various career stages. Directly supervised 3 out of 6 postdoctoral fellow alumni have successfully transitioned to junior faculty positions.• Led multiple pipeline development teams including 16S microbiome analysis pipeline, clinical microbiology, metagenomics analysis pipeline, and genome assembly pipeline. These have generated institutional income from externally-facing fee-for-service analyses for external labs and 19 laboratory-developed tests for Mayo Clinic Labs.• Led software development team for automated metabolic modeling and high-definition bacterial typing applications. |

ACADEMIC RANK

- Assistant Professor, Department of Surgery, 2013-2018
- Associate Professor, Department of Surgery, 2018 - present
- Joint Appointments in Physiology and Biomedical Engineering, Laboratory Medicine and Pathology, Quantitative Health Sciences
- Adjunct Professor, Biomedical Informatics and Computational Biology, University of Minnesota, 2013 - present

AWARDS & HONORS

- Fowler Fellowship, Physics Department, The Ohio State University
- Humboldt Fellowship Award, Humboldt Foundation, Germany
- Carl R. Woese Institute for Genomic Biology Fellow
- 2020 Fredrick P. Li Impact Award, American Association for Cancer Research

SELECT INVITED TALKS

- 2013
- *Evidence-based Gap-Filling and Assignment of Genes to Gap-Filled Reactions*, International Society for Systems Biology, Copenhagen, Denmark
 - *Statistical Physics of Gene Transfer Cystic Fibrosis: Ecology, Evolution, and Eradication*, Telluride, Colorado
- 2014
- *The Microbiome-Macrobiome Interaction*, IAS Program on Physics Approach to Simplifying Complexity in Biology, Kowloon, Hong Kong
 - *Probing the microbial metagenome of the GI tract*, Guangzhou, Hong Kong
- 2015
- *Microbiome Program at Mayo Clinic*, Moffitt Cancer Center, Tampa, Florida
- 2017
- *Personalized Nutrition, Its Effect on the Microbiome and Its Influence on Surgical Outcomes*, American College of Surgeons, San Diego, California
- 2018
- "Deficient mismatch repair in colorectal cancer associated with distinct microbial community and metabolic profile", International Human Microbiome Congress, Killarney, Ireland
- 2019
- *Distinct Microbes, Metabolites, and Ecologies Define the Microbiome in Deficient and Proficient Mismatch Repair Colorectal Cancers*, Microbiome in Precision Medicine Era, Taipei, Taiwan
 - *The Microbiome and Cancer*, Tzu Chi University, Hualein, Taiwan
 - *Microbiome and Its Implications*, Infectious Diseases Practice Updates, Big Island, Hawaii
 - *Distinct Microbes, Metabolites, and Ecologies Define the Microbiome in Deficient and Proficient Mismatch Repair Colorectal Cancers*, Keystone Symposia: "Cancer Metastasis: The Role of Metabolism, Immunity and the Microenvironment," Florence, Italy

PROFESSIONAL SERVICE

- Introductory Physics, Teaching Assistant, 2002 - 2004
- Argonne National Laboratory Boot Camp on Microbial and Metabolic Analytic Approaches, Organizer, 2013
- MPET6813: Tutorial in Systems Pharmacology, Guest Lecturer, 2015
- IMM8882: Innate Immunity and Inflammation, Guest Lecturer, 2015 - 2021
- GLBIO Session Organizer, ISCB 2017
- Medical Specialty Journal Club, Course Supervisor, Mayo Clinic School of Medicine, 2017 - 2021
- CTSC 5400: Introduction to Bioinformatics Concepts and Core Technologies for Individualized Medicine Approaches,

- Guest Lecturer, Mayo Clinic School of Medicine, 2019 - 2021
- Cancer Metagenomics: Microbes and Microbiomes, Session Co-Chair, American Society for Microbiology (ASM) Microbe 2019, San Francisco, California
- American Joint Committee on Cancer, Colon and Rectal Cancer Group, Other Diagnostic Considerations Subgroup, 2021
- Ad-hoc member for NIH Study Panels (x12)
- University of Illinois, PhD Thesis Committee Member (x2)
- Mayo PhD Thesis Committee Member (x1)
- University of Minnesota, PhD Advisor (x2)
- International Symposium on Mathematical and Computational Oncology, Program Committee, 2021
- Co-Associate Director of the Microbiome Program (2013-2018)
- Waterman Endowed Co-Director of the Microbiome Program, Center for Individualized Medicine, Mayo Clinic (2018 - 2021)
- Co-Associate Director, Theoretical, Engineering, and Data Sciences (TED) Section, Microbiome Center, Center for Individualized Medicine, Mayo Clinic (present)
- Director of the Beyond DNA Strategic Theme, Center for Individualized Medicine, Mayo Clinic (2019 - present)

GRANTS

- *Microbial Metabolic Toxicity Drives Colon Cancer* (NCI R01CA179243) 04/01/15 – 03/31/21. (\$2M, PI) Major goal: The aims of this application are to 1) build metabolic models reflective of the microbial production and consumption of potential toxins with special focus on the role of sulfate-reducing bacteria, methanogens, and microbial community structure, and 2) build colorectal cancer and benign colon tissue metabolic model based on existing RNAseq data from The Cancer Gene Atlas.
- *Functional Metabolomic Approach to Eradicate Tuberculosis* (Minnesota Partnership for Biotechnology and Medical Genomics) 2/1/2013-1/31/2015 (\$1M, Co-PI) Major goal: The goal of this project is to metabolically model the phenomena of bacterial persistence in tuberculosis using a combination of 'omics technologies and molecular experiments.
- *Metagenomic Analysis of Arthroplasty Failure* (NIAID R01AR56647) 06/15/14 – 05/31/19 (\$3.5M, Co-I) Major goal: The goals of this application is to understand the underlying microbial populations in prosthetic joint infections (PJIs) using next-generation sequencing methodologies to directly probe the environment in PJIs.
- *The human microbiome and renal stone formation* (Pilot Project of NIDDK U54DK100227) 2/1/2013-1/31/2014 (\$50K, PI) Major goal: The goal of this project is to identify the microbiome present in renal stones.
- *Disappearance of rifampin resistance in MRSA foreign body osteomyelitis* (R21AI125870) 06/01/2016 - 05/31/2018 (\$0.5M, Co-I) Major goal: The goal of this grant is to study the kinetics of emergences and disappearance of rifampin resistance in Staphylococcus aureus in a rat model of foreign body osteomyelitis.
- *Development of personalized microbiome-based treatment for colorectal cancer* (Minnesota Partnership for Biotechnology and Medical Genomics) 02/01/2018 - 01/31/2020 (\$1M, Co-I) Major goal: Our objective in this application is to build a systems-level, mechanistic understanding of the functional interactions between tumor neoplastic mutations, standard of care treatments, and microbial factors (taxa, genes, and functions) in colorectal neoplasia.
- *Dissecting the pathogenesis and outcomes of PSC using multi-omics by studying the exposome and genome* (NIDDK RC2 DK 118619) 09/01/2018 - 07/01/2023 (\$5M, Co-I) Major goal: The objective of this proposal is to generate data and apply advanced AI approaches to understanding the role of exposomics and environment in primary sclerosing cholangitis.
- *Massively-scaled Inverse Reinforcement Learning Approach for Reconstructing the Mutational History of Colorectal Cancer* (AWS) 05/07/2020 - 12/31/2022 (\$100K in-kind, PI) Major goal: The overall goal of this research project is to computationally reverse-engineer the natural history of events leading to any colorectal cancer based on genomic data derived from human tumors. Our recent work shows that the Pop-Up Restaurant for Inverse Reinforcement Learning (PUR-IRL) algorithm can sift through billions of possibilities to generate a mechanistic time-ordered event history of cancer, granting us a window into causality. Our proposal seeks to carry out large-scale tumor tree reconstruction and subsequent causal unification into a probabilistic map of cancer, allowing us to transform

disparate somatic mutations into a universal model that highlights the genes and functional pathways driving colorectal cancer development.

- *Inferring the Reward Functions of Cancer Progression* 07/24/2020 - 12/31/2021 (7,500 node hours, PI) Major goal: The goal of this project is to provide initial resource allocation to examine the scalability of the Pop-Up Restaurant for Inverse Reinforcement Learning (PUR-IRL) algorithm on Argonne National Labs Theta Supercomputer.
- *Long duration missions and cancer: A testbed for building causal inference methods* (SETI Frontier Development Lab: Astronaut Health) 05/25/2020-08/14/2020 (in-kind, PI) Major goal: Deployment of causal inference algorithms for understanding the molecular basis of cancer. Molecular alterations are ubiquitous in spaceflight and magnify risk of cancer mortality and morbidity in long-term missions.

PUBLICATIONS

Collective Effects & Dynamic Systems	<p>Brunner, J. & Chia, N. Confidence in the dynamic spread of epidemics under biased sampling conditions. <i>PeerJ</i> 8, e9758 (2020).</p> <p>Brunner, J. D. & Chia, N. Metabolite-mediated modelling of microbial community dynamics captures emergent behaviour more effectively than species–species modelling. <i>Journal of the Royal Society Interface</i> 16, 20190423 (2019).</p> <p>Jeraldo, P. <i>et al.</i> Quantification of the relative roles of niche and neutral processes in structuring gastrointestinal microbiomes. <i>Proceedings of the National Academy of Sciences</i> 109, 9692–9698 (2012).</p> <p>Chia, N. & Goldenfeld, N. Dynamics of gene duplication and transposons in microbial genomes following a sudden environmental change. <i>Physical Review E</i> 83, 021906 (2011).</p> <p>Chia, N. & Goldenfeld, N. Statistical mechanics of horizontal gene transfer in evolutionary ecology. <i>Journal of Statistical Physics</i> 142, 1287–1301 (2011).</p> <p>Chia, N., Golding, I. & Goldenfeld, N. λ-prophage induction modeled as a cooperative failure mode of lytic repression. <i>Physical Review E</i> 80, 030901 (2009).</p> <p>Chia, N., Woese, C. R. & Goldenfeld, N. A collective mechanism for phase variation in biofilms. <i>Proceedings of the National Academy of Sciences</i> 105, 14597–14602 (2008).</p> <p>Chia, N. & Bundschuh, R. Numerical method for accessing the universal scaling function for a multiparticle discrete time asymmetric exclusion process. <i>Physical Review E</i> 72, 051102 (2005).</p>
Machine Learning	<p>Budd, S. <i>et al.</i> <i>Prototyping CRISP: A causal relation and inference search platform applied to colorectal cancer data</i> in <i>2021 IEEE 3rd Global Conference on Life Sciences and Technologies (LifeTech)</i> (2021), 517–521.</p> <p>Khezeli, K., Blaas, A., Soboczenski, F., Chia, N. & Kalantari, J. On Invariance Penalties for Risk Minimization. <i>arXiv preprint arXiv:2106.09777</i> (2021).</p> <p>Kalantari, J., Nelson, H. & Chia, N. <i>The Unreasonable Effectiveness of Inverse Reinforcement Learning in Advancing Cancer Research</i> in <i>Association for the Advancement of Artificial Intelligence 2020</i> (2020), AISI–248.</p> <p>Storlie, C. B. <i>et al.</i> Prediction and inference with missing data in patient alert systems. <i>Journal of the American Statistical Association</i> (2019).</p>

Metabolic Modeling

- Seaver, S. M. *et al.* The ModelSEED Biochemistry Database for the integration of metabolic annotations and the reconstruction, comparison and analysis of metabolic models for plants, fungi and microbes. *Nucleic acids research* **49**, D575–D588 (2021).
- Brunner, J. D. & **Chia, N.** Minimizing the number of optimizations for efficient community dynamic flux balance analysis. *PLoS computational biology* **16**, e1007786 (2020).
- Mundy, M., Mendes-Soares, H. & **Chia, N.** Mackinac: a bridge between ModelSEED and COBRApy to generate and analyze genome-scale metabolic models. *Bioinformatics* **33**, 2416–2418 (2017).
- Sung, J. *et al.* Global metabolic interaction network of the human gut microbiota for context-specific community-scale analysis. *Nature communications* **8**, 1–12 (2017).
- Chen, J. *et al.* Multiple sclerosis patients have a distinct gut microbiota compared to healthy controls. *Scientific reports* **6**, 1–10 (2016).
- Mendes-Soares, H., Mundy, M., Soares, L. M. & **Chia, N.** MMinte: an application for predicting metabolic interactions among the microbial species in a community. *BMC bioinformatics* **17**, 1–10 (2016).
- Benedict, M. N., Mundy, M. B., Henry, C. S., **Chia, N.** & Price, N. D. Likelihood-based gene annotations for gap filling and quality assessment in genome-scale metabolic models. *PLoS computational biology* **10**, e1003882 (2014).

Sequence Alignment

- Baheti, S. *et al.* HGT-ID: an efficient and sensitive workflow to detect human-viral insertion sites using next-generation sequencing data. *BMC bioinformatics* **19**, 1–11 (2018).
- Chen, X. *et al.* Hybrid-denovo: a de novo OTU-picking pipeline integrating single-end and paired-end 16S sequence tags. *Gigascience* **7**, gix129 (2018).
- Jeraldo, P., Boardman, L., White, B., Goldenfeld, N. & **Chia, N.** *The dark matter of the human gut microbiome follows neutral ecological assembly rules* in *APS March Meeting Abstracts 2018* (2018), K51–009.
- Jennings, M. E., **Chia, N.**, Boardman, L. A. & Metcalf, W. W. Draft genome sequence of *Methanobrevibacter smithii* Isolate WWM1085, obtained from a human stool sample. *Genome announcements* **5**, e01055–17 (2017).
- Jeraldo, P. *et al.* Capturing one of the human gut microbiome's most wanted: reconstructing the genome of a novel butyrate-producing, clostridial scavenger from metagenomic sequence data. *Frontiers in Microbiology* **7**, 783 (2016).
- Jeraldo, P. *et al.* Draft genome sequences of 24 microbial strains assembled from direct sequencing from 4 stool samples. *Genome announcements* **3**, e00526–15 (2015).
- Jeraldo, P. *et al.* IM-TORNADO: a tool for comparison of 16S reads from paired-end libraries. *PLoS one* **9**, e114804 (2014).
- Yang, F., **Chia, N.**, White, B. A. & Schook, L. B. Compression-based distance (CBD): a simple, rapid, and accurate method for microbiota composition comparison. *BMC bioinformatics* **14**, 1–12 (2013).
- Li, Y., **Chia, N.**, Lauria, M. & Bundschuh, R. A performance enhanced PSI-BLAST based on hybrid alignment. *Bioinformatics* **27**, 31–37 (2011).
- Sipos, M. *et al.* Robust computational analysis of rRNA hypervariable tag datasets. *PLoS One* **5**, e15220 (2010).
- Chia, N.** & Bundschuh, R. A practical approach to significance assessment in alignment with gaps. *Journal of Computational Biology* **13**, 429–441 (2006).

- Phylogeny | Christensen, S., Kim, J., **Chia, N.**, Koyejo, O. & El-Kebir, M. Detecting evolutionary patterns of cancers using consensus trees. *Bioinformatics* **36**, i684–i691 (2020).
- Weber, L. L., Aguse, N., **Chia, N.** & El-Kebir, M. PhyDOSE: Design of follow-up single-cell sequencing experiments of tumors. *PLoS computational biology* **16**, e1008240 (2020).
- Sagulenko, E. *et al.* Nuclear pore-like structures in a compartmentalized bacterium. *PLoS One* **12**, e0169432 (2017).
- Jeraldo, P., **Chia, N.** & Goldenfeld, N. On the suitability of short reads of 16S rRNA for phylogeny-based analyses in environmental surveys. *Environmental microbiology* **13**, 3000–3009 (2011).
- Chia, N.**, Cann, I. & Olsen, G. J. Evolution of DNA replication protein complexes in eukaryotes and Archaea. *PloS one* **5**, e10866 (2010).
- Reviews | Li, J. J. *et al.* The role of microbiome in pancreatic cancer. *Cancer and Metastasis Reviews*, 1–13 (2021).
- Walther-Antonio, M. *et al.* Postmenopause as a key factor in the composition of the Endometrial Cancer Microbiome (EChbiome): Putative role of *Porphyromonas somerae* in the disease. in *Cancer Research* **80** (2020), 29–30.
- Nelson, H. & **Chia, N.** Gut microbiome and colon cancer: a plausible explanation for dietary contributions to cancer. *Journal of the American College of Surgeons* **229**, 231–235 (2019).
- Kashyap, P. C., **Chia, N.**, Nelson, H., Segal, E. & Elinav, E. *Microbiome at the frontier of personalized medicine* in *Mayo Clinic Proceedings* **92** (2017), 1855–1864.
- Mendes-Soares, H. & **Chia, N.** Community metabolic modeling approaches to understanding the gut microbiome: bridging biochemistry and ecology. *Free Radical Biology and Medicine* **105**, 102–109 (2017).
- Thompson, K. J. *et al.* A comprehensive analysis of breast cancer microbiota and host gene expression. *PloS one* **12**, e0188873 (2017).
- Kao, P. C. *et al.* Letter to the Editor: The Surge of Type 2 Diabetes Mellitus in China—an International Alert: Physical Exercise and Low-Caloric Diet May Reduce the Risks of Type 2 Diabetes Mellitus and Dementia. *Annals of Clinical & Laboratory Science* **46**, 114–118 (2016).
- Sung, J., Hale, V., Merkel, A. C., Kim, P.-J. & **Chia, N.** Metabolic modeling with Big Data and the gut microbiome. *Applied & translational genomics* **10**, 10–15 (2016).
- Braundmeier, A. G. *et al.* Individualized medicine and the microbiome in reproductive tract. *Frontiers in physiology* **6**, 97 (2015).
- Yeoman, C. J. *et al.* The microbiome of the chicken gastrointestinal tract. *Animal health research reviews* **13**, 89–99 (2012).
- Yeoman, C. J. *et al.* Towards an evolutionary model of animal-associated microbiomes. *Entropy* **13**, 570–594 (2011).

- Liu, Y. *et al.* Amplification of Femtograms of Bacterial DNA Within 3 h Using a Digital Microfluidics Platform for MinION Sequencing. *ACS Omega* (2021).
- Fida, M. *et al.* Core genome MLST and resistome analysis of *Klebsiella pneumoniae* using a clinically amenable workflow. *Diagnostic microbiology and infectious disease* **97**, 114996 (2020).
- Thoendel, M. *et al.* Comparison of three commercial tools for metagenomic shotgun sequencing analysis. *Journal of clinical microbiology* **58**, e00981–19 (2020).
- Park, K.-H. *et al.* Lack of correlation of virulence gene profiles of *Staphylococcus aureus* bacteremia isolates with mortality. *Microbial pathogenesis* **133**, 103543 (2019).
- Vijayvargiya, P. *et al.* Application of metagenomic shotgun sequencing to detect vector-borne pathogens in clinical blood samples. *Plos one* **14**, e0222915 (2019).
- Yan, Q. *et al.* Evaluation of the CosmosID bioinformatics platform for prosthetic joint-associated sonicate fluid shotgun metagenomic data analysis. *Journal of clinical microbiology* **57**, e01182–18 (2019).
- Ivy, M. I. *et al.* Direct detection and identification of prosthetic joint infection pathogens in synovial fluid by metagenomic shotgun sequencing. *Journal of clinical microbiology* **56**, e00402–18 (2018).
- Madigan, T. *et al.* Whole-genome sequencing for methicillin-resistant *Staphylococcus aureus* (MRSA) outbreak investigation in a neonatal intensive care unit. *Infection Control & Hospital Epidemiology* **39**, 1412–1418 (2018).
- Masters, T. *et al.* Comparative evaluation of cDNA library construction approaches for RNA-Seq analysis from low RNA-content human specimens. *Journal of microbiological methods* **154**, 55–62 (2018).
- Thoendel, M. J. *et al.* Identification of prosthetic joint infection pathogens using a shotgun metagenomics approach. *Clinical Infectious Diseases* **67**, 1333–1338 (2018).
- Cunningham, S. A. *et al.* Comparison of whole-genome sequencing methods for analysis of three methicillin-resistant *Staphylococcus aureus* outbreaks. *Journal of clinical microbiology* **55**, 1946–1953 (2017).
- Ivy, M. *et al.* Direct Detection and Identification of Prosthetic Joint Pathogens in Synovial Fluid (SF) by Metagenomic Shotgun Sequencing in *Open Forum Infectious Diseases* **4** (2017), S32–S32.
- Park, K.-H. *et al.* Molecular epidemiology of *Staphylococcus aureus* bacteremia in a single large Minnesota medical center in 2015 as assessed using MLST, core genome MLST and spa typing. *PLoS One* **12**, e0179003 (2017).
- Thoendel, M. *et al.* A novel prosthetic joint infection pathogen, *Mycoplasma salivarium*, identified by metagenomic shotgun sequencing. *Clinical Infectious Diseases* **65**, 332–335 (2017).
- Thoendel, M. *et al.* Impact of contaminating DNA in whole-genome amplification kits used for metagenomic shotgun sequencing for infection diagnosis. *Journal of clinical microbiology* **55**, 1789–1801 (2017).
- Thoendel, M. *et al.* Comparison of microbial DNA enrichment tools for metagenomic whole genome sequencing. *Journal of microbiological methods* **127**, 141–145 (2016).
- Thoendel, M. *et al.* Identification of prosthetic joint pathogens directly in clinical specimens by metagenomic shotgun sequencing in *Open Forum Infectious Diseases* **3** (2016).
- Theofiles, A. G. *et al.* Pertussis outbreak, southeastern Minnesota, 2012 in *Mayo Clinic Proceedings* **89** (2014), 1378–1388.

- Gleeson, F. C. *et al.* Composition, diversity and potential utility of intervention-naive pancreatic cancer intratumoral microbiome signature profiling via endoscopic ultrasound. *Gut* (2021).
- Saw, J. J. *et al.* In vivo entombment of bacteria and fungi during calcium oxalate, brushite, and struvite urolithiasis. *Kidney360* **2**, 298–311 (2021).
- Sivaguru, M. *et al.* Human kidney stones: a natural record of universal biomineralization. *Nature Reviews Urology*, 1–29 (2021).
- Gupta, V. K. *et al.* A predictive index for health status using species-level gut microbiome profiling. *Nature communications* **11**, 1–16 (2020).
- Katsuyuki, M. *et al.* The Role of the Biliary and Gut Microbiome in the Progression of Cholangiocarcinoma and Primary Sclerosing Cholangitis. *Official journal of the American College of Gastroenterology | ACG* **114**, S25–S26 (2019).
- Battaglioli, E. J. *et al.* Clostridioides difficile uses amino acids associated with gut microbial dysbiosis in a subset of patients with diarrhea. *Science translational medicine* **10** (2018).
- Sivaguru, M. *et al.* Geobiology reveals how human kidney stones dissolve in vivo. *Scientific reports* **8**, 1–9 (2018).
- Battaglioli, E. *et al.* Prophylactic Fecal Microbial Transplant Restores Clostridium Difficile Colonization Resistance in a Dysbiotic Subset of Diarrhea Associated Human Microbial Communities Modeled in Germ Free Mice. *Gastroenterology* **152**, S348 (2017).
- Hieken, T. *et al.* Variations in the Breast Tissue Microbiome with Mammographic Breast Density in *ANNALS OF SURGICAL ONCOLOGY* **24** (2017), S60–S60.
- Lal, D. *et al.* Mapping and comparing bacterial microbiota in the sinonasal cavity of healthy, allergic rhinitis, and chronic rhinosinusitis subjects in *International forum of allergy & rhinology* **7** (2017), 561–569.
- Parthasarathy, G. *et al.* Reproducibility of assessing fecal microbiota in chronic constipation. *Neurogastroenterology & Motility* **29**, 1–10 (2017).
- Wolf, P. G. *et al.* Assessing the colonic microbiome, hydrogenogenic and hydrogenotrophic genes, transit and breath methane in constipation. *Neurogastroenterology & Motility* **29**, 1–9 (2017).
- Chen, J. *et al.* Altered gut microbiota in female mice with persistent low body weights following removal of post-weaning chronic dietary restriction. *Genome medicine* **8**, 1–12 (2016).
- Hieken, T. J. *et al.* The microbiome of aseptically collected human breast tissue in benign and malignant disease. *Scientific reports* **6**, 1–10 (2016).
- Parthasarathy, G. *et al.* Relationship between microbiota of the colonic mucosa vs feces and symptoms, colonic transit, and methane production in female patients with chronic constipation. *Gastroenterology* **150**, 367–379 (2016).
- Kang, S. S. *et al.* Diet and exercise orthogonally alter the gut microbiome and reveal independent associations with anxiety and cognition. *Molecular neurodegeneration* **9**, 1–12 (2014).
- Lambent, N. *et al.* Intranasal vaccination with live attenuated influenza vaccine increases diversity of the human nasal microbiome in *Journal of Immunology* **192** (2014).
- Seto, C. T., Jeraldo, P., Orenstein, R., Chia, N. & DiBaise, J. K. Prolonged use of a proton pump inhibitor reduces microbial diversity: implications for Clostridium difficile susceptibility. *Microbiome* **2**, 1–11 (2014).