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Ecology meets human health: studies on human gut microbiota in health and disease

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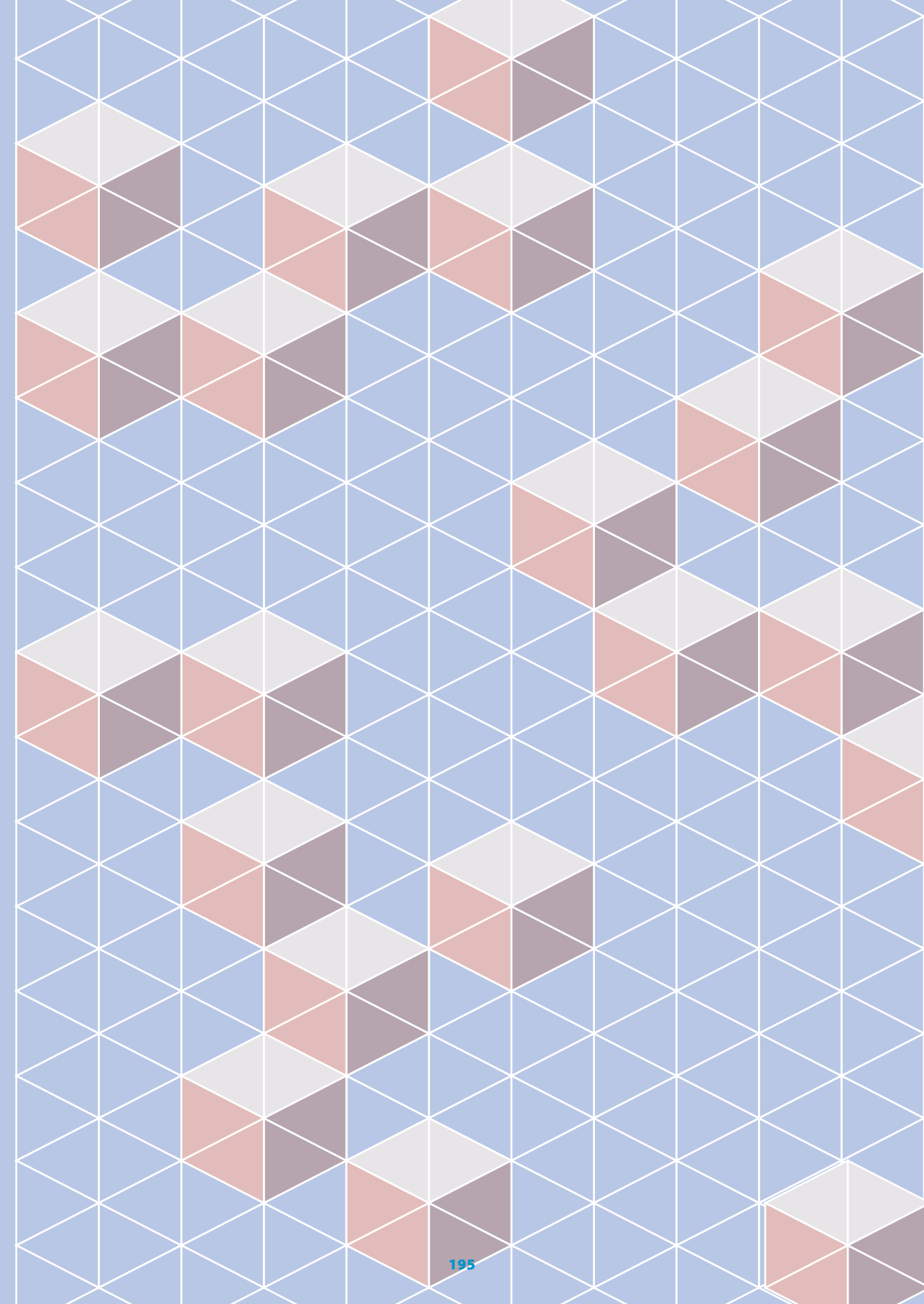
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Appendices

References

References

- 1 Lewin R. Complexity: life at the edge of chaos. 2nd ed: The university of Chicago Press; 1999.
- 2 Scheffer M. Critical transitions in nature and society: Princeton University Press; 2009.
- 3 Thurner S, Klimek P, Hanel R. Introduction to the theory of complex systems. United Kingdom: Oxford University Press; 2018.
- 4 Vermeer B, Zinsmeister S. Grip on complexity: how manageable are complex systems? Directions for future complexity research. The Hague: Netherlands Organisation for Scientific Research; 2014.
- 5 Benincà E, Huisman J, Heerkloss R, Johnk KD, Branco P, Van Nes EH, et al. Chaos in a long-term experiment with a plankton community. *Nature*. 2008;451(7180):822-825.
- 6 Benincà E, Ballantine B, Ellner SP, Huisman J. Species fluctuations sustained by a cyclic succession at the edge of chaos. *Proc Natl Acad Sci U S A*. 2015;112(20):6389-6394.
- 7 May RM. Stability and complexity in model ecosystems: Princeton University Press; 2019.
- 8 Faust K, Raes J. Microbial interactions: from networks to models. *Nat Rev Microbiol*. 2012;10(8):538-550.
- 9 Gallagher R, Appenzeller T. Beyond reductionism. *Science*. 1999;284(5411):79-79.
- 10 Parrott L, Lange H. An introduction to complexity science. In: Messier C, Puettmann KJ, Coates KD, editors. Managing forests as complex adaptive systems. London: Routledge; 2013.
- 11 Ley RE, Peterson DA, Gordon JL. Ecological and evolutionary forces shaping microbial diversity in the human intestine. *Cell*. 2006;124(4):837-848.
- 12 Gupta VK, Paul S, Dutta C. Geography, ethnicity or subsistence-specific variations in human microbiome composition and diversity. *Front Microbiol*. 2017;8:1162.
- 13 Falony G, Joossens M, Vieira-Silva S, Wang J, Darzi Y, Faust K, et al. Population-level analysis of gut microbiome variation. *Science*. 2016;352(6285):560-564.
- 14 Leviatan S, Shoer S, Rothschild D, Gorodetski M, Segal E. An expanded reference map of the human gut microbiome reveals hundreds of previously unknown species. *Nat Commun*. 2022;13(1):3863.
- 15 Nurk S, Koren S, Rhie A, Rautiainen M, Bizikadze AV, Mikheenko A, et al. The complete sequence of a human genome. *Science*. 2022;376(6588):44-53.
- 16 Deo PN, Deshmukh R. Oral microbiome: unveiling the fundamentals. *J Oral Maxillofac Pathol*. 2019;23(1):122-128.
- 17 Lee YH, Chung SW, Auh QS, Hong SJ, Lee YA, Jung J, et al. Progress in oral microbiome related to oral and systemic diseases: an update. *Diagnostics (Basel)*. 2021;11(7).
- 18 Marchesi JR, Ravel J. The vocabulary of microbiome research: a proposal. *Microbiome*. 2015;3:31.
- 19 Marchesi JR, Adams DH, Fava F, Hermes GD, Hirschfield GM, Hold G, et al. The gut microbiota and host health: a new clinical frontier. *Gut*. 2016;65(2):330-339.
- 20 Lynch SV, Pedersen O. The human intestinal microbiome in health and disease. *N Engl J Med*. 2016;375(24):2369-2379.
- 21 Human Microbiome Project Consortium. Structure, function and diversity of the healthy human microbiome. *Nature*. 2012;486(7402):207-214.
- 22 Lozupone CA, Stombaugh JI, Gordon JL, Jansson JK, Knight R. Diversity, stability and resilience of the human gut microbiota. *Nature*. 2012;489(7415):220-230.
- 23 Sommer F, Anderson JM, Bharti R, Raes J, Rosenstiel P. The resilience of the intestinal microbiota influences health and disease. *Nat Rev Microbiol*. 2017;15(10):630-638.
- 24 Yadav M, Verma MK, Chauhan NS. A review of metabolic potential of human gut microbiome in human nutrition. *Arch Microbiol*. 2018;200(2):203-217.
- 25 Gensollen T, Iyer SS, Kasper DL, Blumberg RS. How colonization by microbiota in early life shapes the immune system. *Science*. 2016;352(6285):539-544.
- 26 Thursby E, Juge N. Introduction to the human gut microbiota. *Biochem J*. 2017;474(11):1823-1836.
- 27 Zheng D, Liwinski T, Elinav E. Interaction between microbiota and immunity in health and disease. *Cell Res*. 2020;30(6):492-506.
- 28 Rastelli M, Cani PD, Knauf C. The gut microbiome influences host endocrine functions. *Endocr Rev*. 2019;40(5):1271-1284.
- 29 Zimmermann M, Zimmermann-Kogadeeva M, Wegmann R, Goodman AL. Mapping human microbiome drug metabolism by gut bacteria and their genes. *Nature*. 2019;570(7762):462-467.
- 30 Quinn RA, Melnik AV, Vrbancac A, Fu T, Patras KA, Christy MP, et al. Global chemical effects of the microbiome include new bile-acid conjugations. *Nature*. 2020;579(7797):123-129.
- 31 Ley RE, Turnbaugh PJ, Klein S, Gordon JL. Microbial ecology: human gut microbes associated with obesity. *Nature*. 2006;444(7122):1022-1023.
- 32 Manichanh C, Rigottier-Gois L, Bonnaud E, Gloux K, Pelletier E, Frangeul L, et al. Reduced diversity of faecal microbiota in Crohn's disease revealed by a metagenomic approach. *Gut*. 2006;55(2):205-211.
- 33 Willing BP, Dicksved J, Halfvarson J, Andersson AF, Lucio M, Zheng Z, et al. A pyrosequencing study in twins shows that gastrointestinal microbial profiles vary with inflammatory bowel disease phenotypes. *Gastroenterology*. 2010;139(6):1844-1854.e1841.
- 34 Chang JY, Antonopoulos DA, Kalra A, Tonelli A, Khalife WT, Schmidt TM, et al. Decreased diversity of the fecal Microbiome in recurrent *Clostridium difficile*-associated diarrhea. *J Infect Dis*. 2008;197(3):435-438.
- 35 Lloyd-Price J, Arze C, Ananthakrishnan AN, Schirmer M, Avila-Pacheco J, Poon TW, et al. Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. *Nature*. 2019;569(7758):655-662.

- 36 Safari Z, Gerard P. The links between the gut microbiome and non-alcoholic fatty liver disease (NAFLD). *Cell Mol Life Sci*. 2019;76(8):1541-1558.
- 37 Scher JU, Nayak RR, Ubeda C, Turnbaugh PJ, Abramson SB. Pharmacomicrobiomics in inflammatory arthritis: gut microbiome as modulator of therapeutic response. *Nat Rev Rheumatol*. 2020;16(5):282-292.
- 38 Leván SR, Stannæs KA, Lin DL, Panzer AR, Fukui E, McCauley K, et al. Elevated faecal 12,13-diHOME concentration in neonates at high risk for asthma is produced by gut bacteria and impedes immune tolerance. *Nat Microbiol*. 2019;4(11):1851-1861.
- 39 Singer JR, Blosser EG, Zindl CL, Silberberger DJ, Conlan S, Laufer VA, et al. Preventing dysbiosis of the neonatal mouse intestinal microbiome protects against late-onset sepsis. *Nat Med*. 2019;25(11):1772-1782.
- 40 van Munster KN, Bergquist A, Ponsioen CY. Inflammatory bowel disease and primary sclerosing cholangitis: One disease or two? *J Hepatol*. 2024;80(1):155-168.
- 41 Kahharova D, Pappalardo VY, Buijs MJ, de Menezes RX, Peters M, Jackson R, et al. Microbial indicators of dental health, dysbiosis, and early childhood caries. *J Dent Res*. 2023;102(7):759-766.
- 42 Othman M, Aguero R, Lin HC. Alterations in intestinal microbial flora and human disease. *Curr Opin Gastroenterol*. 2008;24(1):11-16.
- 43 Tap J, Storsrud S, Le Neve B, Cotillard A, Pons N, Dore J, et al. Diet and gut microbiome interactions of relevance for symptoms in irritable bowel syndrome. *Microbiome*. 2021;9(1):74.
- 44 Dong TS, Guan M, Mayer EA, Stains J, Liu C, Vora P, et al. Obesity is associated with a distinct brain-gut microbiome signature that connects *Prevotella* and *Bacteroides* to the brain's reward center. *Gut Microbes*. 2022;14(1):2051999.
- 45 Faith JJ, Guruge JL, Charbonneau M, Subramanian S, Seedorf H, Goodman AL, et al. The long-term stability of the human gut microbiota. *Science*. 2013;341(6141):1237439.
- 46 Caporaso JG, Lauber CL, Costello EK, Berg-Lyons D, Gonzalez A, Stombaugh J, et al. Moving pictures of the human microbiome. *Genome Biol*. 2011;12(5):R50.
- 47 Costello EK, Lauber CL, Hamady M, Fierer N, Gordon JI, Knight R. Bacterial community variation in human body habitats across space and time. *Science*. 2009;326(5960):1694-1697.
- 48 Shetty SA, Hugenholtz F, Lahti L, Smidt H, de Vos WM. Intestinal microbiome landscaping: insight in community assemblage and implications for microbial modulation strategies. *FEMS Microbiol Rev*. 2017;41(2):182-199.
- 49 Coyte KZ, Schluter J, Foster KR. The ecology of the microbiome: networks, competition, and stability. *Science*. 2015;350(6261):663-666.
- 50 Faust K, Lahti L, Gonze D, de Vos WM, Raes J. Metagenomics meets time series analysis: unraveling microbial community dynamics. *Curr Opin Microbiol*. 2015;25:56-66.
- 51 Rajilic-Stojanovic M, Heilig HG, Tims S, Zoetendal EG, de Vos WM. Long-term monitoring of the human intestinal microbiota composition. *Environ Microbiol*. 2012.
- 52 Olsson LM, Boulund F, Nilsson S, Khan MT, Gummesson A, Fagerberg L, et al. Dynamics of the normal gut microbiota: A longitudinal one-year population study in Sweden. *Cell Host Microbe*. 2022;30(5):726-739.e723.
- 53 Bonder MJ, Kurilshikov A, Tigchelaar EF, Mujagic Z, Imhann F, Vila AV, et al. The effect of host genetics on the gut microbiome. *Nat Genet*. 2016;48(11):1407-1412.
- 54 Goodrich JK, Davenport ER, Beaumont M, Jackson MA, Knight R, Ober C, et al. Genetic determinants of the gut microbiome in UK twins. *Cell Host Microbe*. 2016;19(5):731-743.
- 55 Gerber GK. The dynamic microbiome. *FEBS Lett*. 2014;588(22):4131-4139.
- 56 Sze MA, Schloss PD. Looking for a signal in the noise: revisiting obesity and the microbiome. *mBio*. 2016;7(4).
- 57 Gibbons SM, Kearney SM, Smillie CS, Alm EJ. Two dynamic regimes in the human gut microbiome. *PLOS Comput Biol*. 2017;13(2):e1005364.
- 58 Dethlefsen L, Relman DA. Incomplete recovery and individualized responses of the human distal gut microbiota to repeated antibiotic perturbation. *Proc Natl Acad Sci USA*. 2011;108 Suppl 1:4554-4561.
- 59 David LA, Materna AC, Friedman J, Campos-Baptista MI, Blackburn MC, Perrotta A, et al. Host lifestyle affects human microbiota on daily timescales. *Genome Biol*. 2014;15(7):R89.
- 60 Zoetendal EG, Raes J, van den Bogert B, Arumugam M, Booijink CC, Troost FJ, et al. The human small intestinal microbiota is driven by rapid uptake and conversion of simple carbohydrates. *ISME J*. 2012;6(7):1415-1426.
- 61 Zhang Z, Geng J, Tang X, Fan H, Xu J, Wen X, et al. Spatial heterogeneity and co-occurrence patterns of human mucosal-associated intestinal microbiota. *ISME J*. 2014;8(4):881-893.
- 62 Relman DA. The human microbiome: ecosystem resilience and health. *Nutr Rev*. 2012;70 Suppl 1(Suppl 1):S2-9.
- 63 Turnbaugh PJ, Ridaura VK, Faith JJ, Rey FE, Knight R, Gordon JI. The effect of diet on the human gut microbiome: a metagenomic analysis in humanized gnotobiotic mice. *Sci Transl Med*. 2009;1(6):6ra14.
- 64 Palmer C, Bik EM, DiGiulio DB, Relman DA, Brown PO. Development of the human infant intestinal microbiota. *PLOS Biol*. 2007;5(7):e177.
- 65 Kolenbrander PE, Andersen RN, Blehert DS, Eglund PG, Foster JS, Palmer RJ. Communication among oral bacteria. *Microbiol Mol Biol Rev*. 2002;66(3):486-505.
- 66 Koenig JE, Spor A, Scalfone N, Fricker AD, Stombaugh J, Knight R, et al. Succession of microbial consortia in the developing infant gut microbiome. *Proc Natl Acad Sci USA*. 2011;108 Suppl 1:4578-4585.
- 67 van Best N, Hornef MW, Savelkoul PH, Penders J. On the origin of species: factors shaping the establishment of infant's gut microbiota. *Birth Defects Res C Embryo Today*. 2015;105(4):240-251.
- 68 Bosch A, Levin E, van Houten MA, Hasrat R, Kalkman G, Biesbroek G, et al. Development of

- upper respiratory tract microbiota in infancy is affected by mode of delivery. *EBioMedicine*. 2016;9:336-345.
- 69 Gerber GK, Onderdonk AB, Bry L. Inferring dynamic signatures of microbes in complex host ecosystems. *PLOS Comput Biol*. 2012;8(8):e1002624.
 - 70 Dominguez-Bello MG, Costello EK, Contreras M, Magris M, Hidalgo G, Fierer N, et al. Delivery mode shapes the acquisition and structure of the initial microbiota across multiple body habitats in newborns. *Proc Natl Acad Sci USA*. 2010;107(26):11971-11975.
 - 71 Dalby MJ, Hall LJ. Recent advances in understanding the neonatal microbiome. *F1000Res*. 2020;9.
 - 72 Penders J, Thijs C, Vink C, Stelma FF, Snijders B, Kummeling I, et al. Factors influencing the composition of the intestinal microbiota in early infancy. *Pediatrics*. 2006;118(2):511-521.
 - 73 Bezirtzoglou E, Tsiotsias A, Welling GW. Microbiota profile in feces of breast- and formula-fed newborns by using fluorescence *in situ* hybridization (FISH). *Anaerobe*. 2011;17(6):478-482.
 - 74 Azad MB, Konya T, Maughan H, Guttman DS, Field CJ, Chari RS, et al. Gut microbiota of healthy Canadian infants: profiles by mode of delivery and infant diet at 4 months. *CMAJ*. 2013;185(5):385-394.
 - 75 Backhed F, Roswall J, Peng Y, Feng Q, Jia H, Kovatcheva-Datchary P, et al. Dynamics and stabilization of the human gut microbiome during the first year of life. *Cell Host Microbe*. 2015;17(5):690-703.
 - 76 Fallani M, Young D, Scott J, Norin E, Amarri S, Adam R, et al. Intestinal microbiota of 6-week-old infants across Europe: geographic influence beyond delivery mode, breast-feeding, and antibiotics. *J Pediatr Gastroenterol Nutr*. 2010;51(1):77-84.
 - 77 Azad MB, Konya T, Maughan H, Guttman DS, Field CJ, Sears MR, et al. Infant gut microbiota and the hygiene hypothesis of allergic disease: impact of household pets and siblings on microbiota composition and diversity. *Allergy Asthma Clin Immunol*. 2013;9(1):15.
 - 78 Lax S, Smith DP, Hampton-Marcell J, Owens SM, Handley KM, Scott NM, et al. Longitudinal analysis of microbial interaction between humans and the indoor environment. *Science*. 2014;345(6200):1048-1052.
 - 79 Penders J, Gerhold K, Stobberingh EE, Thijs C, Zimmermann K, Lau S, et al. Establishment of the intestinal microbiota and its role for atopic dermatitis in early childhood. *J Allergy Clin Immunol*. 2013;132(3):601-607.e608.
 - 80 Holling CS. Resilience and stability of ecological systems. *Annual Review of Ecology and Systematics*. 1973;4(1):1-23.
 - 81 Nemergut DR, Schmidt SK, Fukami T, O'Neill SP, Bilinski TM, Stanish LF, et al. Patterns and processes of microbial community assembly. *Microbiol Mol Biol Rev*. 2013;77(3):342-356.
 - 82 Sprockett D, Fukami T, Relman DA. Role of priority effects in the early-life assembly of the gut microbiota. *Nat Rev Gastroenterol Hepatol*. 2018;15(4):197-205.
 - 83 Fukami T. Historical contingency in community assembly: integrating niches, species pools, and priority effects. *Annual Review of Ecology, Evolution, and Systematics*. 2015;46(1):1-23.
 - 84 Verster AJ, Borenstein E. Competitive lottery-based assembly of selected clades in the human gut microbiome. *Microbiome*. 2018;6(1):186.
 - 85 Litvak Y, Baumlér AJ. The founder hypothesis: A basis for microbiota resistance, diversity in taxa carriage, and colonization resistance against pathogens. *PLOS Pathog*. 2019;15(2):e1007563.
 - 86 Dethlefsen L, Eckburg PB, Bik EM, Relman DA. Assembly of the human intestinal microbiota. *Trends Ecol Evol*. 2006;21(9):517-523.
 - 87 Darcy JL, Washburne AD, Robeson MS, Prest T, Schmidt SK, Lozupone CA. A phylogenetic model for the recruitment of species into microbial communities and application to studies of the human microbiome. *ISME J*. 2020;14(6):1359-1368.
 - 88 Mallon CA, Elsas JDV, Salles JF. Microbial invasions: the process, patterns, and mechanisms. *Trends Microbiol*. 2015;23(11):719-729.
 - 89 Booth DJ, Murray BR. Coexistence. *Encyclopedia of Ecology*, 2008. p. 664-668.
 - 90 Trosvik P, Stenseth NC, Rudi K. Convergent temporal dynamics of the human infant gut microbiota. *ISME J*. 2010;4(2):151-158.
 - 91 Rinninella E, Raoul P, Cintoni M, Franceschi F, Miggiano GAD, Gasbarrini A, et al. What is the healthy gut microbiota composition? A changing ecosystem across age, environment, diet, and diseases. *Microorganisms*. 2019;7(1).
 - 92 Hou K, Wu ZX, Chen XY, Wang JQ, Zhang D, Xiao C, et al. Microbiota in health and diseases. *Signal Transduct Target Ther*. 2022;7(1):135.
 - 93 Debray R, Herbert RA, Jaffe AL, Crits-Christoph A, Power ME, Koskella B. Priority effects in microbiome assembly. *Nat Rev Microbiol*. 2022;20(2):109-121.
 - 94 Guittar J, Shade A, Litchman E. Trait-based community assembly and succession of the infant gut microbiome. *Nat Commun*. 2019;10(1):512.
 - 95 Walter J, Maldonado-Gomez MX, Martinez I. To engraft or not to engraft: an ecological framework for gut microbiome modulation with live microbes. *Curr Opin Biotechnol*. 2018;49:129-139.
 - 96 Fefferman NH, Price CA, Stringham OC. Considering humans as habitat reveals evidence of successional disease ecology among human pathogens. *PLOS Biol*. 2022;20(9):e3001770.
 - 97 Scheffer M, Carpenter SR, Lenton TM, Bascompte J, Brock W, Dakos V, et al. Anticipating critical transitions. *Science*. 2012;338(6105):344-348.
 - 98 Mutshinda CM, O'Hara RB, Woivod IP. What drives community dynamics? *Proc Biol Sci*. 2009;276(1669):2923-2929.
 - 99 Faust K, Bauchinger F, Laroche B, de Buyl S, Lahti L, Washburne AD, et al. Signatures of ecological processes in microbial community time series. *Microbiome*. 2018;6(1):120.
 - 100 Stein RR, Bucci V, Toussaint NC, Buffie CG, Ratsch G, Pamer EG, et al. Ecological modeling from

- time-series inference: insight into dynamics and stability of intestinal microbiota. *PLOS Comput Biol*. 2013;9(12):e1003388.
- 101 Sloan WT, Nnaji CF, Lunn M, Curtis TP, Colloms SD, Couto JM, et al. Drift dynamics in microbial communities and the effective community size. *Environ Microbiol*. 2021;23(5):2473–2483.
 - 102 Lahti L, Salojärvi J, Salonen A, Scheffer M, de Vos WM. Tipping elements in the human intestinal ecosystem. *Nat Commun*. 2014;5:4344.
 - 103 Gonze D, Lahti L, Raes J, Faust K. Multi-stability and the origin of microbial community types. *ISME J*. 2017;11(10):2159–2166.
 - 104 Folke C, Carpenter S, Walker B, Scheffer M, Elmqvist T, Gunderson L, et al. Regime shifts, resilience, and biodiversity in ecosystem management. *Annual Review of Ecology, Evolution, and Systematics*. 2004;35(1):557–581.
 - 105 Scheffer M, Carpenter S, Foley JA, Folke C, Walker B. Catastrophic shifts in ecosystems. *Nature*. 2001;413(6856):591–596.
 - 106 Scheffer M, Carpenter S, Young B. Cascading effects of over-fishing marine systems. *Trends Ecol Evol*. 2005;20(11):579–581.
 - 107 Potts LD, Douglas A, Perez Calderon LJ, Anderson JA, Witte U, Prosser JJ, et al. Chronic environmental perturbation influences microbial community assembly patterns. *Environ Sci Technol*. 2022;56(4):2300–2311.
 - 108 Daniels L, Budding AE, de Korte N, Eck A, Bogaards JA, Stockmann HB, et al. Fecal microbiome analysis as a diagnostic test for diverticulitis. *Eur J Clin Microbiol Infect Dis*. 2014;33(11):1927–1936.
 - 109 Ye H, Sugihara G. Information leverage in interconnected ecosystems: overcoming the curse of dimensionality. *Science*. 2016;353(6302):922–925.
 - 110 Das P, Marcisauskas S, Ji B, Nielsen J. Metagenomic analysis of bile salt biotransformation in the human gut microbiome. *BMC Genomics*. 2019;20(1):517.
 - 111 Fisher CK, Mehta P. Identifying keystone species in the human gut microbiome from metagenomic timeseries using sparse linear regression. *PLOS One*. 2014;9(7):e102451.
 - 112 Röttgers L, Faust K. From hairballs to hypotheses—biological insights from microbial networks. *FEMS Microbiol Rev*. 2018;42(6):761–780.
 - 113 Röttgers L, Faust K. Can we predict keystones? *Nat Rev Microbiol*. 2019;17(3):193.
 - 114 Berry D, Widder S. Deciphering microbial interactions and detecting keystone species with co-occurrence networks. *Front Microbiol*. 2014;5:219.
 - 115 Power ME, Tilman D, Estes JA, Menge BA, Bond WJ, Mills LS, et al. Challenges in the quest for keystones. *BioScience*. 1996;46(8):609–620.
 - 116 Pester M, Bittner N, Deevong P, Wagner M, Loy A. A 'rare biosphere' microorganism contributes to sulfate reduction in a peatland. *ISME J*. 2010;4(12):1591–1602.
 - 117 Ze X, Duncan SH, Louis P, Flint HJ. *Ruminococcus bromii* is a keystone species for the degradation of resistant starch in the human colon. *ISME J*. 2012;6(8):1535–1543.
 - 118 Faust K. Open challenges for microbial network construction and analysis. *ISME J*. 2021;15(11):3111–3118.
 - 119 Freilich S, Zarecki R, Eilam O, Segal ES, Henry CS, Kupiec M, et al. Competitive and cooperative metabolic interactions in bacterial communities. *Nat Commun*. 2011;2(2):589.
 - 120 Hanemaaijer M, Roling WF, Olivier BG, Khandelwal RA, Teusink B, Bruggeman FJ. Systems modeling approaches for microbial community studies: from metagenomics to inference of the community structure. *Front Microbiol*. 2015;6:213.
 - 121 Wilmes P, Martin-Gallausiaux C, Ostaszewski M, Aho VTE, Novikova PV, Laczny CC, et al. The gut microbiome molecular complex in human health and disease. *Cell Host Microbe*. 2022;30(9):1201–1206.
 - 122 San Roman M, Wagner A. An enormous potential for niche construction through bacterial cross-feeding in a homogeneous environment. *PLOS Comput Biol*. 2018;14(7):e1006340.
 - 123 Hibbing ME, Fuqua C, Parsek MR, Peterson SB. Bacterial competition: surviving and thriving in the microbial jungle. *Nat Rev Microbiol*. 2010;8(1):15–25.
 - 124 Pianka ER. On r- and K-selection. *The American Naturalist*. 1970;104(940):592–597.
 - 125 MacArthur RH, Wilson EO. *The theory of island biogeography*: Princeton University Press; 2001.
 - 126 Hoek M, Merks RMH. Emergence of microbial diversity due to cross-feeding interactions in a spatial model of gut microbial metabolism. *BMC Syst Biol*. 2017;11(1):56.
 - 127 Rabiou BA, Gibson GR. Carbohydrates: a limit on bacterial diversity within the colon. *Biol Rev Camb Philos Soc*. 2002;77(3):443–453.
 - 128 Cummings JH, Macfarlane GT. The control and consequences of bacterial fermentation in the human colon. *J Appl Bacteriol*. 1991;70(6):443–459.
 - 129 Arike L, Hansson GC. The densely O-glycosylated MUC2 mucin protects the intestine and provides food for the commensal bacteria. *J Mol Biol*. 2016;428(16):3221–3229.
 - 130 La Rosa SL, Ostrowski MP, Vera-Ponce de Leon A, McKee LS, Larsbrink J, Eijnsink VG, et al. Glycan processing in gut microbiomes. *Curr Opin Microbiol*. 2022;67:102143.
 - 131 Sicard JF, Le Bihan G, Vogelee P, Jacques M, Harel J. Interactions of intestinal bacteria with components of the intestinal mucus. *Front Cell Infect Microbiol*. 2017;7:387.
 - 132 Chng KR, Ghosh TS, Tan YH, Nandi T, Lee IR, Ng AHQ, et al. Metagenome-wide association analysis identifies microbial determinants of post-antibiotic ecological recovery in the gut. *Nat Ecol Evol*. 2020;4(9):1256–1267.
 - 133 Flint HJ, Scott KP, Duncan SH, Louis P, Forano E. Microbial degradation of complex carbohydrates in the gut. *Gut Microbes*. 2012;3(4):289–306.
 - 134 Tailford LE, Crost EH, Kavanaugh D, Juge N. Mucin glycan foraging in the human gut microbiome. *Front Genet*. 2015;6:81.
 - 135 Koh A, De Vadder F, Kovatcheva-Datchary P, Backhed F. From dietary fiber to host physiology: short-chain fatty acids as key bacterial

- metabolites. *Cell*. 2016;165(6):1332-1345.
- 136 Machado D, Maistrenko OM, Andrejev S, Kim Y, Bork P, Patil KR, et al. Polarization of microbial communities between competitive and cooperative metabolism. *Nat Ecol Evol*. 2021;5(2):195-203.
- 137 Liu W, Jacquioud S, Breynd A, Russel J, Burmolle M, Sorensen SJ. Deciphering links between bacterial interactions and spatial organization in multispecies biofilms. *ISME J*. 2019;13(12):3054-3066.
- 138 Leschine SB. Cellulose degradation in anaerobic environments. *Annu Rev Microbiol*. 1995;49:399-426.
- 139 Tait K, Sutherland IW. Antagonistic interactions amongst bacteriocin-producing enteric bacteria in dual species biofilms. *J Appl Microbiol*. 2002;93(2):345-352.
- 140 Tan CH, Koh KS, Xie C, Zhang J, Tan XH, Lee GP, et al. Community quorum sensing signalling and quenching: microbial granular biofilm assembly. *NPJ Biofilms Microbiomes*. 2015;1:15006.
- 141 Vasse M, Fiegna F, Kriesel B, Velicer GJ. Killer prey: Ecology reverses bacterial predation. *PLOS Biol*. 2024;22(1):e3002454.
- 142 Bull CT, Shetty KG, Subbarao KV. Interactions between myxobacteria, plant pathogenic fungi, and biocontrol agents. *Plant Dis*. 2002;86(8):889-896.
- 143 Raaijmakers JM, Vlami M, de Souza JT. Antibiotic production by bacterial biocontrol agents. *Antonie Van Leeuwenhoek*. 2002;81(1-4):537-547.
- 144 Haas D, Defago G. Biological control of soil-borne pathogens by fluorescent pseudomonads. *Nat Rev Microbiol*. 2005;3(4):307-319.
- 145 Askeland RA, Morrison SM. Cyanide production by *Pseudomonas fluorescens* and *Pseudomonas aeruginosa*. *Appl Environ Microbiol*. 1983;45(6):1802-1807.
- 146 Gause GF. The struggle for existence: a classic of mathematical biology and ecology: Williams & Wilkins; 1934. 163 p.
- 147 Martinson JNV, Walk ST. *Escherichia coli* residency in the gut of healthy human adults. *EcoSal Plus*. 2020;9(1).
- 148 Lidicker WZ. A clarification of interactions in ecological systems. *BioScience*. 1979;29(8):475-477.
- 149 Rodríguez-Martínez JM, Pascual A. Antimicrobial resistance in bacterial biofilms. *Reviews in Medical Microbiology*. 2006;17(3):65-75.
- 150 Russel J, Roder HL, Madsen JS, Burmolle M, Sorensen SJ. Antagonism correlates with metabolic similarity in diverse bacteria. *Proc Natl Acad Sci USA*. 2017;114(40):10684-10688.
- 151 Maynard CL, Elson CO, Hatton RD, Weaver CT. Reciprocal interactions of the intestinal microbiota and immune system. *Nature*. 2012;489(7415):231-241.
- 152 Araujo G, Montoya JM, Thomas T, Webster NS, Lurgi M. A mechanistic framework for complex microbe-host symbioses. *Trends Microbiol*. 2024.
- 153 Quaglio AEV, Grillo TG, De Oliveira ECS, Di Stasi LC, Sasaki LY. Gut microbiota, inflammatory bowel disease and colorectal cancer. *World J Gastroenterol*. 2022;28(30):4053-4060.
- 154 Wu K, Luo Q, Liu Y, Li A, Xia D, Sun X. Causal relationship between gut microbiota and gastrointestinal diseases: a mendelian randomization study. *J Transl Med*. 2024;22(1):92.
- 155 Walters WA, Xu Z, Knight R. Meta-analyses of human gut microbes associated with obesity and IBD. *FEBS Lett*. 2014;588(22):4223-4233.
- 156 Zhang X, Zhang D, Jia H, Feng Q, Wang D, Liang D, et al. The oral and gut microbiomes are perturbed in rheumatoid arthritis and partly normalized after treatment. *Nat Med*. 2015;21(8):895-905.
- 157 Murri M, Leiva I, Gomez-Zumaquero JM, Tinahones FJ, Cardona F, Soriguer F, et al. Gut microbiota in children with type 1 diabetes differs from that in healthy children: a case-control study. *BMC Med*. 2013;11:46.
- 158 Wacklin P, Kaukinen K, Tuovinen E, Collin P, Lindfors K, Partanen J, et al. The duodenal microbiota composition of adult celiac disease patients is associated with the clinical manifestation of the disease. *Inflamm Bowel Dis*. 2013;19(5):934-941.
- 159 Kostic AD, Xavier RJ, Gevers D. The microbiome in inflammatory bowel disease: current status and the future ahead. *Gastroenterology*. 2014;146(6):1489-1499.
- 160 Wei S, Bahl MI, Baunwall SMD, Hvas CL, Licht TR. Determining gut microbial dysbiosis: a review of applied indexes for assessment of intestinal microbiota imbalances. *Appl Environ Microbiol*. 2021;87(11).
- 161 Turnbaugh PJ, Ley RE, Mahowald MA, Magrini V, Mardis ER, Gordon JL. An obesity-associated gut microbiome with increased capacity for energy harvest. *Nature*. 2006;444(7122):1027-1031.
- 162 Qin J, Li R, Raes J, Arumugam M, Burgdorf KS, Manichanh C, et al. A human gut microbial gene catalogue established by metagenomic sequencing. *Nature*. 2010;464(7285):59-65.
- 163 Levine JM, D'Antonio CM. Elton revisited: a review of evidence linking diversity and invasibility. *Oikos*. 1999;87(1).
- 164 Turnbaugh PJ, Hamady M, Yatsunenko T, Cantarel BL, Duncan A, Ley RE, et al. A core gut microbiome in obese and lean twins. *Nature*. 2009;457(7228):480-484.
- 165 Rajilic-Stojanovic M, de Vos WM. The first 1000 cultured species of the human gastrointestinal microbiota. *FEMS Microbiol Rev*. 2014;38(5):996-1047.
- 166 Louis P, Young P, Holtrop G, Flint HJ. Diversity of human colonic butyrate-producing bacteria revealed by analysis of the butyryl-CoA: acetate CoA-transferase gene. *Environ Microbiol*. 2010;12(2):304-314.
- 167 Crobach MJT, Ducarmon QR, Terveer EM, Harmanus C, Sanders I, Verduin KM, et al. The bacterial gut microbiota of adult patients infected, colonized or noncolonized by *Clostridioides difficile*. *Microorganisms*. 2020;8(5).
- 168 van Rossen TM, van Beurden YH, Bogaards JA, Budding AE, Mulder CJJ, Vandenbroucke-Grauls C. Fecal microbiota composition is a better predictor of recurrent *Clostridioides difficile* infection than clinical factors in a prospective, multicentre cohort study. *BMC Infect Dis*. 2024;24(1):687.

- 169 van den Heuvel TR, Jonkers DM, Jeuring SF, Romberg-Camps MJ, Oostenbrug LE, Zeegers MP, et al. Cohort profile: the Inflammatory Bowel Disease South Limburg Cohort (IBDSL). *Int J Epidemiol*. 2017;46(2):e7.
- 170 Zhang YZ, Li YY. Inflammatory bowel disease: pathogenesis. *World J Gastroenterol*. 2014;20(1):91-99.
- 171 Gevers D, Kugathasan S, Denson LA, Vazquez-Baeza Y, Van Treuren W, Ren B, et al. The treatment-naïve microbiome in new-onset Crohn's disease. *Cell Host Microbe*. 2014;15(3):382-392.
- 172 Morgan XC, Tickle TL, Sokol H, Gevers D, Devaney KL, Ward DV, et al. Dysfunction of the intestinal microbiome in inflammatory bowel disease and treatment. *Genome Biol*. 2012;13(9):R79.
- 173 Pascal V, Pozuelo M, Borruel N, Casellas F, Campos D, Santiago A, et al. A microbial signature for Crohn's disease. *Gut*. 2016;66(5):813-822.
- 174 Walker AW, Sanderson JD, Churcher C, Parkes GC, Hudspith BN, Rayment N, et al. High-throughput clone library analysis of the mucosa-associated microbiota reveals dysbiosis and differences between inflamed and non-inflamed regions of the intestine in inflammatory bowel disease. *BMC Microbiol*. 2011;11:7.
- 175 Kolho KL, Korpela K, Jaakkola T, Pichai MV, Zoetendal EG, Salonen A, et al. Fecal microbiota in pediatric inflammatory bowel disease and its relation to inflammation. *Am J Gastroenterol*. 2015;110(6):921-930.
- 176 Papa E, Docktor M, Smillie C, Weber S, Preheim SP, Gevers D, et al. Non-invasive mapping of the gastrointestinal microbiota identifies children with inflammatory bowel disease. *PLOS One*. 2012;7(6):e39242.
- 177 Andoh A, Kobayashi T, Kuzuoka H, Tsujikawa T, Suzuki Y, Hirai F, et al. Characterization of gut microbiota profiles by disease activity in patients with Crohn's disease using data mining analysis of terminal restriction fragment length polymorphisms. *Biomed Rep*. 2014;2(3):370-373.
- 178 Sokol H, Seksik P, Furet JP, Firmesse O, Nion-Larmurier I, Beaugerie L, et al. Low counts of *Faecalibacterium prausnitzii* in colitis microbiota. *Inflamm Bowel Dis*. 2009;15(8):1183-1189.
- 179 Wang W, Chen L, Zhou R, Wang X, Song L, Huang S, et al. Increased proportions of *Bifidobacterium* and the *Lactobacillus* group and loss of butyrate-producing bacteria in inflammatory bowel disease. *J Clin Microbiol*. 2013;52(2):398-406.
- 180 Seksik P, Rigottier-Gois L, Gramet G, Sutren M, Pochart P, Marteau P, et al. Alterations of the dominant faecal bacterial groups in patients with Crohn's disease of the colon. *Gut*. 2003;52(2):237-242.
- 181 Galazzo G, Tedjo DI, Wintjens DSJ, Savelkoul PHM, Masclee AAM, Bodelier AGL, et al. Faecal microbiota dynamics and their relation to disease course in Crohn's disease. *J Crohns Colitis*. 2019;13(10):1273-1282.
- 182 Kim M, Benayoun BA. The microbiome: an emerging key player in aging and longevity. *Transl Med Aging*. 2020;4:103-116.
- 183 Gibson GR, Roberfroid MB. Dietary modulation of the human colonic microbiota: introducing the concept of prebiotics. *J Nutr*. 1995;125(6):1401-1412.
- 184 Chen Y, Zhou J, Wang L. Role and mechanism of gut microbiota in human disease. *Front Cell Infect Microbiol*. 2021;11:625913.
- 185 Gibson GR, Hutkins R, Sanders ME, Prescott SL, Reimer RA, Salminen SJ, et al. Expert consensus document: the International Scientific Association for Probiotics and Prebiotics (ISAPP) consensus statement on the definition and scope of prebiotics. *Nat Rev Gastroenterol Hepatol*. 2017;14(8):491-502.
- 186 Jacobsen CN, Rosenfeldt Nielsen V, Hayford AE, Møller PL, Michaelsen KF, Paerregaard A, et al. Screening of probiotic activities of forty-seven strains of *Lactobacillus* spp. by *in vitro* techniques and evaluation of the colonization ability of five selected strains in humans. *Appl Environ Microbiol*. 1999;65(11):4949-4956.
- 187 Kristensen NB, Bryrup T, Allin KH, Nielsen T, Hansen TH, Pedersen O. Alterations in fecal microbiota composition by probiotic supplementation in healthy adults: a systematic review of randomized controlled trials. *Genome Med*. 2016;8(1):52.
- 188 Li SS, Zhu A, Benes V, Costea PI, Herczeg R, Hildebrand F, et al. Durable coexistence of donor and recipient strains after fecal microbiota transplantation. *Science*. 2016;352(6285):586-589.
- 189 Ianiro G, Puncocchar M, Karcher N, Porcari S, Armanini F, Asnicar F, et al. Variability of strain engraftment and predictability of microbiome composition after fecal microbiota transplantation across different diseases. *Nat Med*. 2022;28(9):1913-1923.
- 190 van Nood E, Vrieze A, Nieuwdorp M, Fuentes S, Zoetendal EG, de Vos WM, et al. Duodenal infusion of donor feces for recurrent *Clostridium difficile*. *N Engl J Med*. 2013;368(5):407-415.
- 191 Colman RJ, Rubin DT. Fecal microbiota transplantation as therapy for inflammatory bowel disease: a systematic review and meta-analysis. *J Crohns Colitis*. 2014;8(12):1569-1581.
- 192 Glassner KL, Abraham BP, Quigley EMM. The microbiome and inflammatory bowel disease. *J Allergy Clin Immunol*. 2020;145(1):16-27.
- 193 El Hage Chehade N, Ghoneim S, Shah S, Chahine A, Mourad FH, Francis FF, et al. Efficacy of fecal microbiota transplantation in the treatment of active ulcerative colitis: a systematic review and meta-analysis of double-blind randomized controlled trials. *Inflamm Bowel Dis*. 2023;29(5):808-817.
- 194 Sood A, Singh A, Mahajan R, Midha V, Kaur K, Singh D, et al. Clinical predictors of response to faecal microbiota transplantation in patients with active ulcerative colitis. *J Crohns Colitis*. 2020.
- 195 Rees NP, Shaheen W, Quince C, Tselepis C, Horniblow RD, Sharma N, et al. Systematic review of donor and recipient predictive biomarkers of response to faecal microbiota transplantation in patients with ulcerative colitis. *EBioMedicine*. 2022;81:104088.
- 196 Schierova D, Brezina J, Mrazek J, Fliegerova KO, Kvasnova S, Bajar L, et al. Gut microbiome

- changes in patients with active left-sided ulcerative colitis after fecal microbiome transplantation and topical 5-aminosalicylic acid therapy. *Cells*. 2020;9(10).
- 197 Costello SP, Hughes PA, Waters O, Bryant RV, Vincent AD, Blatchford P, et al. Effect of fecal microbiota transplantation on 8-week remission in patients with ulcerative colitis: a randomized clinical trial. *JAMA*. 2019;321(2):156-164.
 - 198 Moayyedi P, Surette MG, Kim PT, Libertucci J, Wolfe M, Onischi C, et al. Fecal microbiota transplantation induces remission in patients with active ulcerative colitis in a randomized controlled trial. *Gastroenterology*. 2015;149(1):102-109.e106.
 - 199 Schmidt TSB, Li SS, Maistrenko OM, Akanni W, Coelho LP, Dolai S, et al. Drivers and determinants of strain dynamics following fecal microbiota transplantation. *Nat Med*. 2022;28(9):1902-1912.
 - 200 He R, Li P, Wang J, Cui B, Zhang F, Zhao F. The interplay of gut microbiota between donors and recipients determines the efficacy of fecal microbiota transplantation. *Gut Microbes*. 2022;14(1):2100197.
 - 201 Weiss S, Xu ZZ, Peddada S, Amir A, Bittinger K, Gonzalez A, et al. Normalization and microbial differential abundance strategies depend upon data characteristics. *Microbiome*. 2017;5(1):27.
 - 202 Budding AE, Grasman ME, Eck A, Bogaards JA, Vandenbroucke-Grauls CM, van Bodegraven AA, et al. Rectal swabs for analysis of the intestinal microbiota. *PLOS One*. 2014;9(7):e101344.
 - 203 Robinson CK, Brotman RM, Ravel J. Intricacies of assessing the human microbiome in epidemiologic studies. *Ann Epidemiol*. 2016;26(5):311-321.
 - 204 Bukin YS, Galachyants YP, Morozov IV, Bukin SV, Zakharenko AS, Zemskaya TI. The effect of 16S rRNA region choice on bacterial community metabarcoding results. *Sci Data*. 2019;6:190007.
 - 205 Callahan BJ, Sankaran K, Fukuyama JA, McMurdie PJ, Holmes SP. Bioconductor workflow for microbiome data analysis: from raw reads to community analyses. *F1000Res*. 2016;5:1492.
 - 206 Mysara M, Vandamme P, Props R, Kerckhof FM, Leys N, Boon N, et al. Reconciliation between operational taxonomic units and species boundaries. *FEMS Microbiol Ecol*. 2017;93(4).
 - 207 Ruscheweyh HJ, Milanese A, Paoli L, Sintsova A, Mende DR, Zeller G, et al. mOTUs: profiling taxonomic composition, transcriptional activity and strain populations of microbial communities. *Curr Protoc*. 2021;1(8):e218.
 - 208 Callahan BJ, McMurdie PJ, Holmes SP. Exact sequence variants should replace operational taxonomic units in marker-gene data analysis. *ISME J*. 2017;11(12):2639-2643.
 - 209 Cole JR, Wang Q, Fish JA, Chai B, McGarrell DM, Sun Y, et al. Ribosomal Database Project: data and tools for high throughput rRNA analysis. *Nucleic Acids Res*. 2014;42(Database issue):D633-642.
 - 210 Vermeire S, Joossens M, Verbeke K, Wang J, Machiels K, Sabino J, et al. Donor species richness determines faecal microbiota transplantation success in inflammatory bowel disease. *J Crohns Colitis*. 2016;10(4):387-394.
 - 211 McLaren MR, Willis AD, Callahan BJ. Consistent and correctable bias in metagenomic sequencing experiments. *Elife*. 2019;8.
 - 212 McLaren MR, Nearing JT, Willis AD, Lloyd KG, Callahan BJ. Implications of taxonomic bias for microbial differential-abundance analysis. *bioRxiv*. 2022.
 - 213 Wright RJ, Comeau AM, Langille MGI. From defaults to databases: parameter and database choice dramatically impact the performance of metagenomic taxonomic classification tools. *Microb Genom*. 2023;9(3).
 - 214 Zaura E, Pappalardo VY, Buijs MJ, Volgenant CMC, Brandt BW. Optimizing the quality of clinical studies on oral microbiome: A practical guide for planning, performing, and reporting. *Periodontol* 2000. 2021;85(1):210-236.
 - 215 Weiss SJ, Xu Z, Amir A, Peddada S, Bittinger K, Gonzalez A, et al. Effects of library size variance, sparsity, and compositionality on the analysis of microbiome data. *PeerJ Preprints*. 2015.
 - 216 Carr A, Diener C, Baliga NS, Gibbons SM. Use and abuse of correlation analyses in microbial ecology. *ISME J*. 2019;13(11):2647-2655.
 - 217 Kodikara S, Ellul S, Le Cao KA. Statistical challenges in longitudinal microbiome data analysis. *Brief Bioinform*. 2022;23(4):bbac273.
 - 218 Paulson JN, Stine OC, Bravo HC, Pop M. Differential abundance analysis for microbial marker-gene surveys. *Nat Methods*. 2013;10(12):1200-1202.
 - 219 Gloor GB, Macklaim JM, Pawlowsky-Glahn V, Egozcue JJ. Microbiome datasets are compositional: and this is not optional. *Front Microbiol*. 2017;8:2224.
 - 220 Leite MFA, Kuramae EE. You must choose, but choose wisely: model-based approaches for microbial community analysis. *Soil Biology and Biochemistry*. 2020;151.
 - 221 Gloor GB, Wu JR, Pawlowsky-Glahn V, Egozcue JJ. It's all relative: analyzing microbiome data as compositions. *Ann Epidemiol*. 2016;26(5):322-329.
 - 222 McMurdie PJ, Holmes S. Waste not, want not: why rarefying microbiome data is inadmissible. *PLOS Comput Biol*. 2014;10(4):e1003531.
 - 223 Jiang D, Armour CR, Hu C, Mei M, Tian C, Sharpton TJ, et al. Microbiome multi-omics network analysis: statistical considerations, limitations, and opportunities. *Front Genet*. 2019;10:995.
 - 224 Xia Y, Sun J. Hypothesis testing and statistical analysis of microbiome. *Genes Dis*. 2017;4(3):138-148.
 - 225 Metwally AA, Yang J, Ascoli C, Dai Y, Finn PW, Perkins DL. MetaLonDA: a flexible R package for identifying time intervals of differentially abundant features in metagenomic longitudinal studies. *Microbiome*. 2018;6(1):32.
 - 226 Costello EK, Stagaman K, Dethlefsen L, Bohannan BJ, Relman DA. The application of ecological theory toward an understanding of the human microbiome. *Science*. 2012;336(6086):1255-1262.
 - 227 Layeghifard M, Hwang DM, Guttman DS. Disentangling Interactions in the Microbiome: A Network Perspective. *Trends Microbiol*. 2017;25(3):217-228.

- 228 Zuo Y, Yu G, Tadesse MG, Resson HW. Biological network inference using low order partial correlation. *Methods*. 2014;69(3):266-273.
- 229 Hirano H, Takemoto K. Difficulty in inferring microbial community structure based on co-occurrence network approaches. *BMC Bioinformatics*. 2019;20(1):329.
- 230 Faust K, Raes J. CoNet app: inference of biological association networks using Cytoscape. *F1000Res*. 2016;5:1519.
- 231 Park SY, Ufodu A, Lee K, Jayaraman A. Emerging computational tools and models for studying gut microbiota composition and function. *Curr Opin Biotechnol*. 2020;66:301-311.
- 232 Gonze D, Coyte KZ, Lahti L, Faust K. Microbial communities as dynamical systems. *Curr Opin Microbiol*. 2018;44:41-49.
- 233 Knights D, Ward TL, McKinlay CE, Miller H, Gonzalez A, McDonald D, et al. Rethinking "enterotypes". *Cell Host Microbe*. 2014;16(4):433-437.
- 234 Gower JC. Some distance properties of latent root and vector methods used in multivariate analysis. *Biometrika*. 1966;53(3-4):325-338.
- 235 Coenen AR, Hu SK, Luo E, Muratore D, Weitz JS. A primer for microbiome time-series analysis. *Front Genet*. 2020;11:310.
- 236 Stewart CJ, Ajami NJ, O'Brien JL, Hutchinson DS, Smith DP, Wong MC, et al. Temporal development of the gut microbiome in early childhood from the TEDDY study. *Nature*. 2018;562(7728):583-588.
- 237 Kumar M, Ji B, Zengler K, Nielsen J. Modelling approaches for studying the microbiome. *Nat Microbiol*. 2019;4(8):1253-1267.
- 238 Mounier J, Monnet C, Vallaeys T, Arditi R, Sarthou AS, Helias A, et al. Microbial interactions within a cheese microbial community. *Appl Environ Microbiol*. 2008;74(1):172-181.
- 239 Kuntal BK, Gadgil C, Mande SS. Web-gLV: a web based platform for Lotka-Volterra based modeling and simulation of microbial populations. *Front Microbiol*. 2019;10:288.
- 240 Momeni B, Xie L, Shou W. Lotka-Volterra pairwise modeling fails to capture diverse pairwise microbial interactions. *Elife*. 2017;6:1-34.
- 241 Chan SHJ, Simons MN, Maranas CD. SteadyCom: Predicting microbial abundances while ensuring community stability. *PLOS Comput Biol*. 2017;13(5):e1005539.
- 242 Shoaie S, Ghaffari P, Kovatcheva-Datchary P, Mardinoglu A, Sen P, Pujos-Guillot E, et al. Quantifying diet-induced metabolic changes of the human gut microbiome. *Cell Metab*. 2015;22(2):320-331.
- 243 Zengler K, Palsson BO. A road map for the development of community systems (CoSy) biology. *Nat Rev Microbiol*. 2012;10(5):366-372.
- 244 Diener C, Gibbons SM. More is different: metabolic modeling of diverse microbial communities. *mSystems*. 2023;8(2):e0127022.
- 245 Karkman A, Lehtimäki J, Ruokolainen L. The ecology of human microbiota: dynamics and diversity in health and disease. *Ann N Y Acad Sci*. 2017;1399(1):78-92.
- 246 Woyke T, Teeling H, Ivanova NN, Huntemann M, Richter M, Gloeckner FO, et al. Symbiosis insights through metagenomic analysis of a microbial consortium. *Nature*. 2006;443(7114):950-955.
- 247 Chaffron S, Rehrauer H, Pernthaler J, von Mering C. A global network of coexisting microbes from environmental and whole-genome sequence data. *Genome Res*. 2010;20(7):947-959.
- 248 Riera J, Baldo L. Animal Microbial co-occurrence networks of gut microbiota reveal community conservation and diet-associated shifts in cichlid fishes. *Microbiome*. 2020;2:36.
- 249 Vemuri R, Martoni CJ, Kavanagh K, Eri R. *Lactobacillus acidophilus* DDS-1 modulates the gut microbial co-occurrence networks in aging mice. *Nutrients*. 2022;14.
- 250 Friedman J, Alm EJ. Inferring correlation networks from genomic survey data. *PLOS Comput Biol*. 2012;8(9):e1002687.
- 251 Kurtz ZD, Muller CL, Miraldi ER, Littman DR, Blaser MJ, Bonneau RA. Sparse and compositionally robust inference of microbial ecological networks. *PLOS Comput Biol*. 2015;11(5):e1004226.
- 252 Faust K, Sathirapongsasuti JF, Izard J, Segata N, Gevers D, Raes J, et al. Microbial co-occurrence relationships in the human microbiome. *PLOS Comput Biol*. 2012;8(7):e1002606.
- 253 Weiss S, Van Treuren W, Lozupone C, Faust K, Friedman J, Deng Y, et al. Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. *ISME J*. 2016;10(7):1669-1681.
- 254 Bucci V, Tzen B, Li N, Simmons M, Tanoue T, Bogart E, et al. MDSINE: Microbial Dynamical Systems INference Engine for microbiome time-series analyses. *Genome Biol*. 2016;17(1):121.
- 255 Xiao Y, Angulo MT, Friedman J, Waldor MK, Weiss ST, Liu YY. Mapping the ecological networks of microbial communities. *Nat Commun*. 2017;8(1):2042.
- 256 Jones EW, Shankin-Clarke P, Carlson JM. Navigation and control of outcomes in a generalized Lotka-Volterra model of the microbiome. In: Kotas J, editor. *Advances in nonlinear biological systems: modeling and optimal control*. 11. USA: American Institute of Mathematical Sciences; 2020. p. 97-120.
- 257 Yodzis P. *Introduction to theoretical ecology*: Longman Higher Education; 1989.
- 258 Gause GF. Experimental studies on the struggle for existence. *Journal of Experimental Biology*. 1932;9(4):389-402.
- 259 Hardin G. The competitive exclusion principle. *Science*. 1960;131(3409):1292-1297.
- 260 Cho I, Blaser MJ. The human microbiome: at the interface of health and disease. *Nat Rev Genet*. 2012;13(4):260-270.
- 261 Burnham P, Gomez-Lopez N, Heyang M, Cheng AP, Lenz JS, Dadhania DM, et al. Separating the signal from the noise in metagenomic cell-free DNA sequencing. *Microbiome*. 2020;8(1):18.
- 262 Hindmarsh AC, Petzold LR. Algorithms and software for ordinary differential equations and differential algebraic equations, Part II: Higher-order methods and software packages. *Computers in Physics* 1995;9:148-155.

- 263 Soetaert K, Petzoldt T, Setzer RW. Solving differential equations in R: package deSolve. *Journal of Statistical Software*. 2010;33(9).
- 264 Goh K-II, Oh E, Jeong H, Kahng B, Kim D. Classification of scale-free networks. *PNAS*. 2002;99(20):12583–12588.
- 265 Barabási A. *Network science*. 1st ed: Cambridge University Press; 2016.
- 266 Benjamini Y, Hochberg Y. Controlling the false discovery rate: a practical and powerful approach to multiple testing. *Journal of the Royal Statistical Society Series B: Statistical Methodology*. 1995;57(1):289–300.
- 267 Sasaki Y. *The truth of the F-measure*. University of Manchester: School of Computer Science. 2007: 1–5.
- 268 Cougoul A, Bailly X, Vourc'h G, Gasqui P. Rarity of microbial species: In search of reliable associations. *PLOS One*. 2019;14(3):e0200458.
- 269 Gupta S, Hjelmso MH, Lehtimäki J, Li X, Mortensen MS, Russel J, et al. Environmental shaping of the bacterial and fungal community in infant bed dust and correlations with the airway microbiota. *Microbiome*. 2020;8(1):115.
- 270 Ma ZS. The P/N (positive-to-negative links) ratio in complex networks—a promising *in silico* biomarker for detecting changes occurring in the human microbiome. *Microb Ecol*. 2018;75(4):1063–1073.
- 271 Seelbinder B, Chen J, Brunke S, Vazquez-Urbe R, Santhaman R, Meyer AC, et al. Antibiotics create a shift from mutualism to competition in human gut communities with a longer-lasting impact on fungi than bacteria. *Microbiome*. 2020;8(1):133.
- 272 Stone L, Roberts A. Conditions for a species to gain advantage from the presence of competitors. *Ecology*. 1991;72:947–957.
- 273 Freilich MA, Wieters E, Broitman BR, Marquet PA, Navarrete SA. Species co-occurrence networks: can they reveal trophic and non-trophic interactions in ecological communities? *Ecology*. 2018;99(3):690–699.
- 274 Mayfield MM, Stouffer DB. Higher-order interactions capture unexplained complexity in diverse communities. *Nat Ecol Evol*. 2017;1(3):62.
- 275 Tilman D. The importance of the mechanisms of interspecific competition. *The American Naturalist*. 1987;129(5):769–774.
- 276 Pace ML, Cole JJ, Carpenter SR, Kitchell JF. Trophic cascades revealed in diverse ecosystems. *Trends Ecol Evol*. 1999;14(12):483–488.
- 277 Højsgaard S, Edwards D, Lauritzen S. *Graphical models with R*: Springer Science & Business Media; 2012.
- 278 Wootton J. Predicting direct and indirect effects: an integrated approach using experiments and path analysis. *Ecology*. 1994;75(1):151–165.
- 279 Succurro A, Ebenhoj O. Review and perspective on mathematical modeling of microbial ecosystems. *Biochem Soc Trans*. 2018;46(2): 403–412.
- 280 Moran NA, Wernegreen JJ. Lifestyle evolution in symbiotic bacteria: insights from genomics. *Trends Ecol Evol*. 2000;15(8):321–326.
- 281 Costantino RF, Desharnais RA, Cushing JM, Dennis B. Chaotic dynamics in an insect population. *Science*. 1997;275(5298):389–391.
- 282 Becks L, Hilker FM, Malchow H, Jurgens K, Arndt H. Experimental demonstration of chaos in a microbial food web. *Nature*. 2005;435(7046): 1226–1229.
- 283 Scheffer M, Bascompte J, Brock WA, Brovkin V, Carpenter SR, Dakos V, et al. Early-warning signals for critical transitions. *Nature*. 2009;461(7260): 53–59.
- 284 Faust K, Raes J. Host-microbe interaction: rules of the game for microbiota. *Nature*. 2016;534(7606):182–183.
- 285 Rottjers L, Faust K. Manta: a clustering algorithm for weighted ecological networks. *mSystems*. 2020;5(1).
- 286 Claussen JC, Skieveciene J, Wang J, Rausch P, Karlsen TH, Lieb W, et al. Boolean analysis reveals systematic interactions among low-abundance species in the human gut microbiome. *PLOS Comput Biol*. 2017;13(6):e1005361.
- 287 Blanchet FG, Cazelles K, Gravel D. Co-occurrence is not evidence of ecological interactions. *Ecol Lett*. 2020;23(7):1050–1063.
- 288 Steinway SN, Biggs MB, Loughran TP, Jr., Papin JA, Albert R. Inference of network dynamics and metabolic interactions in the gut microbiome. *PLOS Comput Biol*. 2015;11(5):e1004338.
- 289 Bjornstad ON, Grenfell BT. Noisy clockwork: time series analysis of population fluctuations in animals. *Science*. 2001;293(5530):638–643.
- 290 Rouyer T, Fromentin JM, Menard F, Cazelles B, Briand K, Pianet R, et al. Complex interplays among population dynamics, environmental forcing, and exploitation in fisheries. *Proc Natl Acad Sci U S A*. 2008;105(14):5420–5425.
- 291 Levy R, Borenstein E. Metabolic modeling of species interaction in the human microbiome elucidates community-level assembly rules. *Proc Natl Acad Sci U S A*. 2013;110(31):12804–12809.
- 292 David LA, Maurice CF, Carmody RN, Gootenberg DB, Button JE, Wolfe BE, et al. Diet rapidly and reproducibly alters the human gut microbiome. *Nature*. 2014;505(7484):559–563.
- 293 Schwartz DJ, Langdon AE, Dantas G. Understanding the impact of antibiotic perturbation on the human microbiome. *Genome Med*. 2020;12(1):82.
- 294 Joseph TA, Pasarkar AP, Pe'er I. Efficient and accurate inference of mixed microbial population trajectories from longitudinal count data. *Cell Syst*. 2020;10(6):463–469 e466.
- 295 Shenhav L, Furman O, Briscoe L, Thompson M, Silverman JD, Mizrahi I, et al. Modeling the temporal dynamics of the gut microbial community in adults and infants. *PLOS Comput Biol*. 2019;15(6):e1006960.
- 296 Joseph TA, Shenhav L, Xavier JB, Halperin E, Pe'er I. Compositional Lotka-Volterra describes microbial dynamics in the simplex. *PLOS Comput Biol*. 2020;16(5):e1007917.
- 297 Rouyer T, Fromentin JM, Stenseth NC, Cazelles B. Analysing multiple time series and extending significance testing in wavelet analysis. *Marine Ecology Progress Series*. 2008;359:11–23.
- 298 Addison PS. *The illustrated wavelet transform handbook: introductory theory and applications in science, engineering, medicine, and finance*: CRC Press; 2017.

- 299 Benincà E, van Boven M, Hagenaars T, van der Hoek W. Space-time analysis of pneumonia hospitalisations in the Netherlands. *PLOS One*. 2017;12(7):e0180797.
- 300 Ben-Ari T, Neerincx S, Agier L, Cazelles B, Xu L, Zhang Z, et al. Identification of Chinese plague foci from long-term epidemiological data. *Proc Natl Acad Sci U S A*. 2012;109(21):8196-8201.
- 301 Teissier Y, Paul R, Aubry M, Rodo X, Dommar C, Salje H, et al. Long-term persistence of monotypic dengue transmission in small size isolated populations, French Polynesia, 1978-2014. *PLOS Negl Trop Dis*. 2020;14(3):e0008110.
- 302 Martin-Platero AM, Cleary B, Kauffman K, Preheim SP, McGillicuddy DJ, Alm EJ, et al. High resolution time series reveals cohesive but short-lived communities in coastal plankton. *Nat Commun*. 2018;9(1):266.
- 303 Torrence C, Compo GP. A practical guide to wavelet analysis. *Bulletin of the American Meteorological Society*. 1998;79(1):61-78.
- 304 Cazelles B, Cazelles K, Chavez M. Wavelet analysis in ecology and epidemiology: impact of statistical tests. *J R Soc Interface*. 2014;11(91):20130585.
- 305 Cazelles B, Chavez M, Berteaux D, Menard F, Vik JO, Jenouvrier S, et al. Wavelet analysis of ecological time series. *Oecologia*. 2008;156(2):287-304.
- 306 Cazelles B, Chavez M, Magny GC, Guegan JF, Hales S. Time-dependent spectral analysis of epidemiological time-series with wavelets. *J R Soc Interface*. 2007;4(15):625-636.
- 307 Chavez M, Cazelles B. Detecting dynamic spatial correlation patterns with generalized wavelet coherence and non-stationary surrogate data. *Sci Rep*. 2019;9(1):7389.
- 308 Fowlkes EB, Mallows CL. A method for comparing two hierarchical clusterings. *Journal of the American Statistical Association*. 1983;78(383):553-569.
- 309 Galili T. dendextend: an R package for visualizing, adjusting and comparing trees of hierarchical clustering. *Bioinformatics*. 2015;31(22):3718-3720.
- 310 Oksanen J, Kindt R, Legendre P, O'Hara B, Simpson G, Solymos P, et al. vegan: community ecology package, R package version 2.6-4 2022.
- 311 Amir A, McDonald D, Navas-Molina JA, Kopylova E, Morton JT, Zech Xu Z, et al. Deblur rapidly resolves single-nucleotide community sequence patterns. *mSystems*. 2017;2(2).
- 312 Thompson LR, Sanders JG, McDonald D, Amir A, Ladau J, Locey KJ, et al. A communal catalogue reveals Earth's multiscale microbial diversity. *Nature*. 2017;551(7681):457-463.
- 313 Lahti L, Shetty S, Blake T, Salojärvi J. Tools for microbiome analysis in R. Version 1. 2017;507.
- 314 McMurdie PJ, Holmes S. phyloseq: an R package for reproducible interactive analysis and graphics of microbiome census data. *PLOS One*. 2013;8(4):e61217.
- 315 van den Boogaart KG, Tolosana-Delgado R. "compositions": a unified R package to analyze compositional data. *Computers & Geosciences*. 2008;34(4):320-338.
- 316 Millard S. EnvStats: an R package for environmental statistics. New York: Springer; 2013.
- 317 Ward JH. Hierarchical grouping to optimize an objective function. *Journal of the American Statistical Association*. 1963;58(301):236-244.
- 318 Vandermeer J. Coupled oscillations in food webs: balancing competition and mutualism in simple ecological models. *Am Nat*. 2004;163(6):857-867.
- 319 Benincà E, Johnk KD, Heerkloss R, Huisman J. Coupled predator-prey oscillations in a chaotic food web. *Ecol Lett*. 2009;12(12):1367-1378.
- 320 Massoud EC, Huisman J, Benincà E, Dietze MC, Bouten W, Vrugt JA. Probing the limits of predictability: data assimilation of chaotic dynamics in complex food webs. *Ecol Lett*. 2018;21(1):93-103.
- 321 Wang Y, Niu Q, Zhang X, Liu L, Wang Y, Chen Y, et al. Exploring the effects of operational mode and microbial interactions on bacterial community assembly in a one-stage partial-nitrification anammox reactor using integrated multi-omics. *Microbiome*. 2019;7(1):122.
- 322 Gilbert JA, Steele JA, Caporaso JG, Steinbrink L, Reeder J, Temperton B, et al. Defining seasonal marine microbial community dynamics. *ISME J*. 2012;6(2):298-308.
- 323 Giovannoni SJ, Vergin KL. Seasonality in ocean microbial communities. *Science*. 2012;335(6069):671-676.
- 324 Fuhrman JA, Hewson I, Schwalbach MS, Steele JA, Brown MV, Naeem S. Annually reoccurring bacterial communities are predictable from ocean conditions. *Proc Natl Acad Sci U S A*. 2006;103(35):13104-13109.
- 325 Newton RJ, Kent AD, Triplett EW, McMahon KD. Microbial community dynamics in a humic lake: differential persistence of common freshwater phylotypes. *Environ Microbiol*. 2006;8(6):956-970.
- 326 Matulich KL, Weihe C, Allison SD, Amend AS, Berlemont R, Goulden ML, et al. Temporal variation overshadows the response of leaf litter microbial communities to simulated global change. *ISME J*. 2015;9(11):2477-2489.
- 327 Carini P, Delgado-Baquerizo M, Hinkley ES, Holland-Moritz H, Brewer TE, Rue G, et al. Effects of spatial variability and relic DNA removal on the detection of temporal dynamics in soil microbial communities. *mBio*. 2020;11(1).
- 328 Flores GE, Caporaso JG, Henley JB, Rideout JR, Domogala D, Chase J, et al. Temporal variability is a personalized feature of the human microbiome. *Genome Biol*. 2014;15(12):531.
- 329 Vandeputte D, De Commer L, Tito RY, Kathagen G, Sabino J, Vermeire S, et al. Temporal variability in quantitative human gut microbiome profiles and implications for clinical research. *Nat Commun*. 2021;12(1):6740.
- 330 Kugathasan S, Denson LA, Walters TD, Kim MO, Marigorta UM, Schirmer M, et al. Prediction of complicated disease course for children newly diagnosed with Crohn's disease: a multicentre inception cohort study. *Lancet*. 2017;389(10080):1710-1718.
- 331 Petchey OL, Gaston KJ. Functional diversity: back to basics and looking forward. *Ecol Lett*. 2006;9(6):741-758.
- 332 Shetty SA, Kostopoulos I, Geerlings SY, Smidt H, de Vos WM, Belzer C. Dynamic metabolic interactions and trophic roles of human gut

- microbes identified using a minimal microbiome exhibiting ecological properties. *ISME J*. 2022;16(9):2144-2159.
- 333 Louis P, Duncan SH, Sheridan PO, Walker AW, Flint HJ. Microbial lactate utilisation and the stability of the gut microbiome. *Gut Microbiome*. 2022;3.
- 334 Granger CWJ. Investigating causal relations by econometric models and cross-spectral methods. *Econometrica*. 1969;37(3).
- 335 Friston KJ, Bastos AM, Oswal A, van Wijk B, Richter C, Litvak V. Granger causality revisited. *Neuroimage*. 2014;101:796-808.
- 336 Tsonis AA, Deyle ER, Ye H, Sugihara G. Convergent cross mapping: theory and an example. In: Tsonis AA, editor. *Advances in Nonlinear Geosciences*: Springer; 2018.
- 337 Ye H, Deyle ER, Gilarranz LJ, Sugihara G. Distinguishing time-delayed causal interactions using convergent cross mapping. *Sci Rep*. 2015;5:14750.
- 338 Dhamala M, Rangarajan G, Ding M. Estimating Granger causality from fourier and wavelet transforms of time series data. *Phys Rev Lett*. 2008;100(1):018701.
- 339 Olayeni OR. Causality in continuous wavelet transform without spectral matrix factorization: theory and application. *Computational Economics*. 2015;47(3):321-340.
- 340 Cazelles B, Chavez M, McMichael AJ, Hales S. Nonstationary influence of El Nino on the synchronous dengue epidemics in Thailand. *PLOS Med*. 2005;2(4):e106.
- 341 Pascual M, Cazelles B, Bouma MJ, Chaves LF, Koelle K. Shifting patterns: malaria dynamics and rainfall variability in an African highland. *Proc Biol Sci*. 2008;275(1631):123-132.
- 342 Constantin de Magny G, Guegan JF, Petit M, Cazelles B. Regional-scale climate-variability synchrony of cholera epidemics in West Africa. *BMC Infect Dis*. 2007;7:20.
- 343 Blauw AN, Benincà E, Laane RW, Greenwood N, Huisman J. Dancing with the tides: fluctuations of coastal phytoplankton orchestrated by different oscillatory modes of the tidal cycle. *PLOS One*. 2012;7(11):e49319.
- 344 Winder M, Schindler DE, Essington TE, Litt AH. Disrupted seasonal clockwork in the population dynamics of a freshwater copepod by climate warming. *Limnology and Oceanography*. 2009;54(6part2):2493-2505.
- 345 Ménard F, Marsac F, Bellier E, Cazelles B. Climatic oscillations and tuna catch rates in the Indian Ocean: a wavelet approach to time series analysis. *Fisheries Oceanography*. 2006;16(1):95-104.
- 346 Murdoch WW, Kendall BE, Nisbet RM, Briggs CJ, McCauley E, Bolser R. Single-species models for many-species food webs. *Nature*. 2002;417(6888):541-543.
- 347 Mondal D, Percival DB. Wavelet variance analysis for gappy time series. *Annals of the Institute of Statistical Mathematics*. 2008;62(5):943-966.
- 348 Foster G. Wavelets for period analysis of unevenly sampled time series. *Astron J*. 1996;112:1709-1729.
- 349 Thiebaut C, Roques S. Time-scale and time-frequency analyses of irregularly sampled astronomical time series. *EURASIP Journal on Advances in Signal Processing*. 2005;2005(15).
- 350 Azuara J, Sabatier P, Lebreton V, Jalali B, Sicre M-A, Dezileau L, et al. Mid- to late-holocene mediterranean climate variability: contribution of multi-proxy and multi-sequence comparison using wavelet spectral analysis in the northwestern Mediterranean basin. *Earth-Science Reviews*. 2020;208.
- 351 Dong F-T, Gai N, Tang Y, Wang Y-F, Yi T-F. Evidence of quasi-periodic oscillation in the optical band of the blazar 1ES 1959+650. *Research in Astronomy and Astrophysics*. 2022;22(11).
- 352 Mouchet M, Guilhaumon F, Villéger S, Mason NWH, Tomasini JA, Mouillot D. Towards a consensus for calculating dendrogram-based functional diversity indices. *Oikos*. 2008;117(5):794-800.
- 353 Seyedian SS, Nokhostin F, Malamir MD. A review of the diagnosis, prevention, and treatment methods of inflammatory bowel disease. *J Med Life*. 2019;12(2):113-122.
- 354 Khor B, Gardet A, Xavier RJ. Genetics and pathogenesis of inflammatory bowel disease. *Nature*. 2011;474(7351):307-317.
- 355 Halfvarson J, Brislawn CJ, Lamendella R, Vazquez-Baeza Y, Walters WA, Bramer LM, et al. Dynamics of the human gut microbiome in inflammatory bowel disease. *Nat Microbiol*. 2017;2:17004.
- 356 Sha S, Xu B, Wang X, Zhang Y, Wang H, Kong X, et al. The biodiversity and composition of the dominant fecal microbiota in patients with inflammatory bowel disease. *Diagn Microbiol Infect Dis*. 2013;75(3):245-251.
- 357 Andoh A, Kuzuoka H, Tsujikawa T, Nakamura S, Hirai F, Suzuki Y, et al. Multicenter analysis of fecal microbiota profiles in Japanese patients with Crohn's disease. *J Gastroenterol*. 2012;47(12):1298-1307.
- 358 Dey N, Soergel DA, Repo S, Brenner SE. Association of gut microbiota with post-operative clinical course in Crohn's disease. *BMC Gastroenterol*. 2013;13:131.
- 359 Luo A, Leach ST, Barres R, Hesson LB, Grimm MC, Simar D. The microbiota and epigenetic regulation of T helper 17/regulatory T cells: in search of a balanced immune system. *Front Immunol*. 2017;8:417.
- 360 Vester-Andersen MK, Prosberg MV, Jess T, Andersson M, Bengtsson BG, Blixt T, et al. Disease course and surgery rates in inflammatory bowel disease: a population-based, 7-year follow-up study in the era of immunomodulating therapy. *Am J Gastroenterol*. 2014;109(5):705-714.
- 361 Cade B, Noon B. A gentle introduction to quantile regression for ecologists. *Front Ecol Environ*. 2003.
- 362 Koenker R. Quantile regression. in: *Econometric Society Monographs*: Cambridge: Cambridge University Press; 2005.
- 363 Knight CA, Ackerly DD. Variation in nuclear DNA content across environmental gradients: a quantile regression analysis. *Ecology Letters*. 2002.
- 364 Mujagic Z, Ludidi S, Keszthelyi D, Hesselink M, Kruimel J, Lenaerts K, et al. Small intestinal permeability is increased in diarrhoea predominant IBS, while alterations in

- gastroduodenal permeability in all IBS subtypes are largely attributable to confounders. *Aliment Pharmacol Ther.* 2014;40:288–297.
- 365 Lagkouravdos I, Joseph D, Kapfhammer M, Girtli S, Horn M, Haller D, et al. IMNGS: A comprehensive open resource of processed 16S rRNA microbial profiles for ecology and diversity studies. *Sci Rep.* 2016;6:33721.
 - 366 Geraci M, Bottai M. Linear quantile mixed models. *Statistics and Computing* 2014;24:461–479.
 - 367 Turnbaugh PJ, Gordon JL. The core gut microbiome, energy balance and obesity. *J Physiol.* 2009;587(Pt 17):4153–4158.
 - 368 Pinheiro J, Bates D. Mixed-effects models in S and S-PLUS. *Statistics and Computing.* 2022.
 - 369 Carpenter SR, Cole JJ, Pace ML, Batt R, Brock WA, Cline T, et al. Early warnings of regime shifts: a whole-ecosystem experiment. *Science.* 2011;332(6033):1079–1082.
 - 370 Cade BS, Noon BR, Flather CH. Quantile regression reveals hidden bias and uncertainty in habitat models. *Ecology.* 2005;86(3):786–800.
 - 371 Magro DO, Santos A, Guadagnini D, de Godoy FM, Silva SHM, Lemos WJF, et al. Remission in Crohn's disease is accompanied by alterations in the gut microbiota and mucins production. *Sci Rep.* 2019;9(1):13263.
 - 372 Pisani A, Rausch P, Bang C, Ellul S, Tabone T, Marantidis Cordina C, et al. Dysbiosis in the gut microbiota in patients with inflammatory bowel disease during remission. *Microbiol Spectr.* 2022;10(3):e0061622.
 - 373 Jackson MA, Goodrich JK, Maxam ME, Freedberg DE, Abrams JA, Poole AC, et al. Proton pump inhibitors alter the composition of the gut microbiota. *Gut.* 2016;65(5):749–756.
 - 374 Molodecky NA, Kaplan GG. Environmental risk factors for inflammatory bowel disease. *Gastroenterol Hepatol (N Y).* 2010;6(5):339–346.
 - 375 Alam MT, Amos GCA, Murphy ARJ, Murch S, Wellington EMH, Arasaradnam RP. Microbial imbalance in inflammatory bowel disease patients at different taxonomic levels. *Gut Pathog.* 2020;12(1).
 - 376 Zhang SL, Wang SN, Miao CY. Influence of microbiota on intestinal immune system in ulcerative colitis and its intervention. *Front Immunol.* 2017;8:1674.
 - 377 Kumari R, Ahuja V, Paul J. Fluctuations in butyrate-producing bacteria in ulcerative colitis patients of North India. *World J Gastroenterol.* 2013;19(22):3404–3414.
 - 378 Nishihara Y, Ogino H, Tanaka M, Ihara E, Fukaura K, Nishioka K, et al. Mucosa-associated gut microbiota reflects clinical course of ulcerative colitis. *Sci Rep.* 2021;11(1):13743.
 - 379 Iljazovic A, Roy U, Galvez EJC, Lesker TR, Zhao B, Gronow A, et al. Perturbation of the gut microbiome by *Prevotella* spp. enhances host susceptibility to mucosal inflammation. *Mucosal Immunol.* 2021;14(1):113–124.
 - 380 Maconi G, Camatta D, Cannatelli R, Ferretti F, Carvalhas Gabrielli A, Ardizzone S. Budesonide MMX in the treatment of ulcerative colitis: current perspectives on efficacy and safety. *Ther Clin Risk Manag.* 2021;17:285–292.
 - 381 Debast SB, Bauer MP, Kuijper EJ, European Society of Clinical Microbiology and Infectious Diseases. European society of clinical microbiology and infectious diseases: update of the treatment guidance document for *Clostridium difficile* infection. *Clin Microbiol Infect.* 2014;20 Suppl 2:1–26.
 - 382 Sokol H, Landman C, Seksik P, Berard L, Montil M, Nion-Larmurier I, et al. Fecal microbiota transplantation to maintain remission in Crohn's disease: a pilot randomized controlled study. *Microbiome.* 2020;8(1):12.
 - 383 Rossen NG, Fuentes S, van der Spek MJ, Tijssen JG, Hartman JH, Duflo A, et al. Findings from a randomized controlled trial of fecal transplantation for patients with ulcerative colitis. *Gastroenterology.* 2015;149(1):110–118 e114.
 - 384 van Lingen E, Nooij S, Terveer E, Crossette E, Prince A, Bhattarai S, et al. Fecal microbiota transplantation engraftment after budesonide or placebo in patients with active ulcerative colitis using pre-selected donors: a randomized pilot study. *J Crohns Colitis.* 2024;jjae043:1381–1393.
 - 385 Terveer EM, Vendrik KE, Ooijevaar RE, Lingen EV, Boeijs-Koppenol E, Nood EV, et al. Faecal microbiota transplantation for *Clostridioides difficile* infection: Four years' experience of the Netherlands Donor Feces Bank. *United European Gastroenterol J.* 2020;8(10):1236–1247.
 - 386 Langmead B, Salzberg SL. Fast gapped-read alignment with Bowtie 2. *Nat Methods.* 2012;9(4):357–359.
 - 387 Chen S, Zhou Y, Chen Y, Gu J. fastp: an ultra-fast all-in-one FASTQ preprocessor. *Bioinformatics.* 2018;34(17):i884–i890.
 - 388 Milanese A, Mende DR, Paoli L, Salazar G, Ruscheweyh HJ, Cuenca M, et al. Microbial abundance, activity and population genomic profiling with mOTUs2. *Nat Commun.* 2019;10(1):1014.
 - 389 Ruscheweyh HJ, Milanese A, Paoli L, Karcher N, Clayssen G, Keller MI, et al. Cultivation-independent genomes greatly expand taxonomic-profiling capabilities of mOTUs across various environments. *Microbiome.* 2022;10(1):212.
 - 390 Aitchison J, Barceló-Vidal C, Martín-Fernández JA, Pawłowsky-Glahn V. Logratio analysis and compositional distance. *Mathematical Geology.* 2000;32(3):271–275.
 - 391 Barnett D, Arts I, Penders J. microViz: an R package for microbiome data visualization and statistics. *Journal of Open Source Software.* 2021;6(63).
 - 392 Morgan M. Dirichlet-multinomial mixture model machine learning for microbiome data. 2022.
 - 393 Holmes I, Harris K, Quince C. Dirichlet multinomial mixtures: generative models for microbial metagenomics. *PLOS One.* 2012;7(2):e30126.
 - 394 Brooks ME, Kristensen K, van Benthem KJ, Magnusson A, Berg CW, Nielsen A, et al. glmmTMB balances speed and flexibility among packages for zero-inflated generalized linear mixed modeling. *The R Journal.* 2017;9(2):378–400.

- 395 Bates D, Mächler M, Bolker B, Walker S. Fitting linear mixed-effects models using lme4. *Journal of Statistical Software*. 2015;67(1).
- 396 Wald A. Tests of statistical hypotheses concerning several parameters when the number of observations is large. *Transactions of the American Mathematical Society*. 1943;54(3): 426-482.
- 397 Lahti L, Shetty S. microbiome R package. 2012-2019.
- 398 Pinheiro J, Bates D, R Core Team. nlme: linear and nonlinear mixed effects models. 2022.
- 399 Wilson BC, Vatanen T, Cutfield WS, O'Sullivan JM. The super-donor phenomenon in fecal microbiota transplantation. *Front Cell Infect Microbiol*. 2019;9:2.
- 400 Larsen JM. The immune response to *Prevotella* bacteria in chronic inflammatory disease. *Immunology*. 2017;151(4):363-374.
- 401 Precup G, Vodnar DC. Gut *Prevotella* as a possible biomarker of diet and its eubiotic versus dysbiotic roles: a comprehensive literature review. *Br J Nutr*. 2019;122(2):131-140.
- 402 Lahti L, Salojärvi J, Salonen A, Scheffer M, de Vos WM. Tipping elements in the human intestinal ecosystem. *Nature Communications* 2014;4344.
- 403 Pinto S, Benincà E, Galazzo G, Jonkers D, Penders J, Bogaards JA. Heterogeneous associations of gut microbiota with Crohn's disease activity. *Gut Microbes*. 2024;16(1):2292239.
- 404 Caenepeel C, Deleu S, Vazquez Castellanos JF, Arnauts K, Braekeleire S, Machiels K, et al. Rigorous donor selection for fecal microbiota transplantation in active ulcerative colitis: key lessons from a randomized controlled trial halted for futility. *Clin Gastroenterol Hepatol*. 2024.
- 405 Arumugam M, Raes J, Pelletier E, Le Paslier D, Yamada T, Mende DR, et al. Enterotypes of the human gut microbiome. *Nature*. 2011;473(7346):174-180.
- 406 Vieira-Silva S, Sabino J, Valles-Colomer M, Falony G, Kathagen G, Caenepeel C, et al. Quantitative microbiome profiling disentangles inflammation- and bile duct obstruction-associated microbiota alterations across PSC/IBD diagnoses. *Nat Microbiol*. 2019;4(11):1826-1831.
- 407 Tian Y, Zhou Y, Huang S, Li J, Zhao K, Li X, et al. Fecal microbiota transplantation for ulcerative colitis: a prospective clinical study. *BMC Gastroenterol*. 2019;19(1):116.
- 408 Crothers JW, Chu ND, Nguyen LTT, Phillips M, Collins C, Fortner K, et al. Daily, oral FMT for long-term maintenance therapy in ulcerative colitis: results of a single-center, prospective, randomized pilot study. *BMC Gastroenterol*. 2021;21(1):281.
- 409 Christensen L, Roager HM, Astrup A, Hjorth MF. Microbial enterotypes in personalized nutrition and obesity management. *Am J Clin Nutr*. 2018;108(4):645-651.
- 410 Lee SH, Yoon SH, Jung Y, Kim N, Min U, Chun J, et al. Emotional well-being and gut microbiome profiles by enterotype. *Sci Rep*. 2020;10(1):20736.
- 411 Roswall J, Olsson LM, Kovatcheva-Datchary P, Nilsson S, Tremaroli V, Simon MC, et al. Developmental trajectory of the healthy human gut microbiota during the first 5 years of life. *Cell Host Microbe*. 2021;29(5):765-776 e763.
- 412 Costea PI, Hildebrand F, Arumugam M, Backhed F, Blaser MJ, Bushman FD, et al. Enterotypes in the landscape of gut microbial community composition. *Nat Microbiol*. 2018;3(1):8-16.
- 413 Hanssen NMJ, de Vos WM, Nieuwdorp M. Fecal microbiota transplantation in human metabolic diseases: from a murky past to a bright future? *Cell Metab*. 2021;33(6):1098-1110.
- 414 Pinto S, Šajbenová D, Benincà E, Nooij S, Terveer EM, Keller JJ, et al. Dynamics of gut microbiota after fecal microbiota transplantation in ulcerative colitis: success linked to control of Prevotellaceae. *J Crohns Colitis*. 2024.
- 415 Olesen SW, Gerardin Y. Re-evaluating the evidence for faecal microbiota transplantation 'super-donors' in inflammatory bowel disease. *J Crohns Colitis*. 2021;15(3):453-461.
- 416 Danne C, Rolhion N, Sokol H. Recipient factors in faecal microbiota transplantation: one stool does not fit all. *Nat Rev Gastroenterol Hepatol*. 2021;18(7):503-513.
- 417 Peri R, Aguilar RC, Tuffers K, Erhardt A, Link A, Ehlermann P, et al. The impact of technical and clinical factors on fecal microbiota transfer outcomes for the treatment of recurrent *Clostridioides difficile* infections in Germany. *United European Gastroenterol J*. 2019;7(5): 716-722.
- 418 Xiao Y, Angulo MT, Lao S, Weiss ST, Liu YY. An ecological framework to understand the efficacy of fecal microbiota transplantation. *Nat Commun*. 2020;11(1):3329.
- 419 Schmidt TSB, Raes J, Bork P. The human gut microbiome: from association to modulation. *Cell*. 2018;172(6):1198-1215.
- 420 Grinspan AM, Kelly CR. Fecal microbiota transplantation for ulcerative colitis: not just yet. *Gastroenterology*. 2015;149(1):15-18.
- 421 Scheffer M, van Nes EH. Self-organized similarity, the evolutionary emergence of groups of similar species. *Proc Natl Acad Sci U S A*. 2006;103(16):6230-6235.
- 422 Fuentes S, Rossen NG, van der Spek MJ, Hartman JH, Huuskonen L, Korpela K, et al. Microbial shifts and signatures of long-term remission in ulcerative colitis after faecal microbiota transplantation. *ISME J*. 2017;11(8):1877-1889.
- 423 Goodrich JK, Di Rienzi SC, Poole AC, Koren O, Walters WA, Caporaso JG, et al. Conducting a microbiome study. *Cell*. 2014;158(2):250-262.
- 424 Gilbert JA, Blaser MJ, Caporaso JG, Jansson JK, Lynch SV, Knight R. Current understanding of the human microbiome. *Nat Med*. 2018;24(4): 392-400.
- 425 Nielsen HB, Almeida M, Juncker AS, Rasmussen S, Li J, Sunagawa S, et al. Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. *Nat Biotechnol*. 2014;32(8):822-828.
- 426 Bashan A, Gibson TE, Friedman J, Carey VJ, Weiss ST, Hohmann EL, et al. Universality of human microbial dynamics. *Nature*. 2016;534(7606): 259-262.

- 427 Ding T, Schloss PD. Dynamics and associations of microbial community types across the human body. *Nature*. 2014;509(7500):357-360.
- 428 Tipton L, Muller CL, Kurtz ZD, Huang L, Kleerup E, Morris A, et al. Fungi stabilize connectivity in the lung and skin microbial ecosystems. *Microbiome*. 2018;6(1):12.
- 429 Feng C, Jia H, Wang H, Wang J, Lin M, Hu X, et al. MicroNet-MIMRF: a microbial network inference approach based on mutual information and Markov random fields. *Bioinform Adv*. 2024;4(1):vbae167.
- 430 Venturelli OS, Carr AC, Fisher G, Hsu RH, Lau R, Bowen BP, et al. Deciphering microbial interactions in synthetic human gut microbiome communities. *Mol Syst Biol*. 2018;14(6):e8157.
- 431 de Vos MGJ, Zagorski M, McNally A, Bollenbach T. Interaction networks, ecological stability, and collective antibiotic tolerance in polymicrobial infections. *Proc Natl Acad Sci USA*. 2017;114(40):10666-10671.
- 432 Wilson WG, Lundberg P, Vázquez DP, Shurin JB, Smith MD, Langford W, et al. Biodiversity and species interactions: extending Lotka–Volterra community theory. *Ecology Letters*. 2003;6(10):944-952.
- 433 Haegeman B, Loreau M. A mathematical synthesis of niche and neutral theories in community ecology. *J Theor Biol*. 2011;269(1):150-165.
- 434 Dam P, Fonseca LL, Konstantinidis KT, Voit EO. Dynamic models of the complex microbial metapopulation of lake mendota. *NPJ Syst Biol Appl*. 2016;2:16007.
- 435 Jang SS, Oishi KT, Egbert RG, Klavins E. Specification and simulation of synthetic multicelled behaviors. *ACS Synth Biol*. 2012;1(8):365-374.
- 436 Scheffer M. *Personal Communication*. 2019.
- 437 Lyu R, Qu Y, Divaris K, Wu D. Methodological considerations in longitudinal analyses of microbiome data: a comprehensive review. *Genes (Basel)*. 2023;15(1).
- 438 Picot A, Shibasaki S, Meacock OJ, Mitri S. Microbial interactions in theory and practice: when are measurements compatible with models? *Curr Opin Microbiol*. 2023;75:102354.
- 439 Pacheco AR, Pauvert C, Kishore D, Segre D. Toward FAIR representations of microbial interactions. *mSystems*. 2022;7(5):e0065922.
- 440 Dal Co A, van Vliet S, Kiviet DJ, Schlegel S, Ackermann M. Short-range interactions govern the dynamics and functions of microbial communities. *Nature Ecology & Evolution*. 2020;4(3):366-375.
- 441 Kim HJ, Boedicker JQ, Choi JW, Ismagilov RF. Defined spatial structure stabilizes a synthetic multispecies bacterial community. *Proc Natl Acad Sci U S A*. 2008;105(47):18188-18193.
- 442 Duvallet C, Gibbons SM, Gurry T, Irizarry RA, Alm EJ. Meta-analysis of gut microbiome studies identifies disease-specific and shared responses. *Nat Commun*. 2017;8(1):1784.
- 443 Simren M, Barbara G, Flint HJ, Spiegel BM, Spiller RC, Vanner S, et al. Intestinal microbiota in functional bowel disorders: a Rome foundation report. *Gut*. 2013;62(1):159-176.
- 444 Zhang X, Pei YF, Zhang L, Guo B, Pendegraft AH, Zhuang W, et al. Negative binomial mixed models for analyzing longitudinal microbiome data. *Front Microbiol*. 2018;9:1683.
- 445 Ramaboli MC, Ocvirk S, Khan Mirzaei M, Eberhart BL, Valdivia-García M, Metwaly A, et al. Diet changes due to urbanization in South Africa are linked to microbiome and metabolome signatures of Westernization and colorectal cancer. *Nat Commun*. 2024;15(1):3379.
- 446 Gellman RH, Olm MR, Terrapon N, Enam F, Higginbottom SK, Sonnenburg JL, et al. Hadza *Prevotella* require diet-derived microbiota-accessible carbohydrates to persist in mice. *Cell Rep*. 2023;42(11).
- 447 Levin J, Passmore J-A, Williams B, editors. Role of vaginal microbiota in genital inflammation and enhancing HIV transmission. International AIDS Conference; 2016; Durban, South Africa. www.natap.org/2016/IAC/IAC_20.htm.
- 448 Lebeer S, Ahannach S, Gehrman T, Wittouck S, Eilers T, Oerlemans E, et al. A citizen-science-enabled catalogue of the vaginal microbiome and associated factors. *Nat Microbiol*. 2023;8(11):2183-2195.
- 449 Vital M, Howe AC, Tiedje JM. Revealing the bacterial butyrate synthesis pathways by analyzing (meta)genomic data. *mBio*. 2014;5(2):e00889.
- 450 O'Keefe SJ, Li JV, Lahti L, Ou J, Carbonero F, Mohammed K, et al. Fat, fibre and cancer risk in African Americans and rural Africans. *Nat Commun*. 2015;6:6342.
- 451 Marcelino VR, Welsh C, Diener C, Gulliver EL, Rutten EL, Young RB, et al. Disease-specific loss of microbial cross-feeding interactions in the human gut. *Nat Commun*. 2023;14(1):6546.
- 452 Kullberg RFJ, Wikki I, Haak BW, Kauko A, Galenkamp H, Peters-Sengers H, et al. Association between butyrate-producing gut bacteria and the risk of infectious disease hospitalisation: results from two observational, population-based microbiome studies. *Lancet Microbe*. 2024;5(9):100864.
- 453 Duizer C, de Zoete MR. The role of microbiota-derived metabolites in colorectal cancer. *Int J Mol Sci*. 2023;24(9).
- 454 Wortelboer K, Nieuwdorp M, Herrema H. Fecal microbiota transplantation beyond *Clostridioides difficile* infections. *EBioMedicine*. 2019;44: 716-729.
- 455 Ducarmon QR, Kuijper EJ, Olle B. Opportunities and challenges in development of live biotherapeutic products to fight infections. *J Infect Dis*. 2021;223(12 Suppl 2):S283-S289.
- 456 Pamer EG. Fecal microbiota transplantation: effectiveness, complexities, and lingering concerns. *Mucosal Immunol*. 2014;7(2):210-214.
- 457 Kaiser JC, Verschoor CP, Surette MG, Bowdish DM. Host cytokine responses distinguish invasive from airway isolates of the *Streptococcus milleri* anginosus group. *BMC Infect Dis*. 2014;14:498.
- 458 Besselink MG, van Santvoort HC, Buskens E, Boermeester MA, van Goor H, Timmerman HM, et al. Probiotic prophylaxis in predicted severe acute pancreatitis: a randomised,

- double-blind, placebo-controlled trial. *Lancet*. 2008;371(9613):651-659.
- 459 de Souza HSP, Fiocchi C, Iliopoulos D. The IBD interactome: an integrated view of aetiology, pathogenesis and therapy. *Nat Rev Gastroenterol Hepatol*. 2017;14(12):739-749.
- 460 Paramsothy S, Paramsothy R, Rubin DT, Kamm MA, Kaakoush NO, Mitchell HM, et al. Faecal microbiota transplantation for inflammatory bowel disease: a systematic review and meta-analysis. *J Crohns Colitis*. 2017;11(10):1180-1199.
- 461 Xu D, Chen VL, Steiner CA, Berinstein JA, Eswaran S, Waljee AK, et al. Efficacy of fecal microbiota transplantation in irritable bowel syndrome: a systematic review and meta-analysis. *Am J Gastroenterol*. 2019;114(7):1043-1050.
- 462 Taur Y, Coyte K, Schluter J, Robilotti E, Figueroa C, Gjonbalaj M, et al. Reconstitution of the gut microbiota of antibiotic-treated patients by autologous fecal microbiota transplant. *Sci Transl Med*. 2018;10(460).
- 463 Schluter J, Peled JU, Taylor BP, Markey KA, Smith M, Taur Y, et al. The gut microbiota is associated with immune cell dynamics in humans. *Nature*. 2020;588(7837):303-307.
- 464 Yelin I, Flett KB, Merakou C, Mehrotra P, Stam J, Snesrud E, et al. Genomic and epidemiological evidence of bacterial transmission from probiotic capsule to blood in ICU patients. *Nat Med*. 2019;25(11):1728-1732.
- 465 Reijnders D, Goossens GH, Hermes GD, Neis EP, van der Beek CM, Most J, et al. Effects of gut microbiota manipulation by antibiotics on host metabolism in obese humans: a randomized double-blind placebo-controlled trial. *Cell Metab*. 2016;24(1):63-74.
- 466 Liu X, Salles JF. Lose-lose consequences of bacterial community-driven invasions in soil. *Microbiome*. 2024;12(1):57.
- 467 Liu X, Salles JF. Bridging ecological assembly process and community stability upon bacterial invasions. *ISME J*. 2024;18(1).
- 468 Mallon CA, Le Roux X, van Doorn GS, Dini-Andreote F, Poly F, Salles JF. The impact of failure: unsuccessful bacterial invasions steer the soil microbial community away from the invader's niche. *ISME J*. 2018;12(3):728-741.
- 469 Stecher B, Chaffron S, Kappeli R, Hapfelmeier S, Friedrich S, Weber TC, et al. Like will to like: abundances of closely related species can predict susceptibility to intestinal colonization by pathogenic and commensal bacteria. *PLOS Pathog*. 2010;6(1):e1000711.
- 470 Rodriguez-Verdugo A, Ackermann M. Rapid evolution destabilizes species interactions in a fluctuating environment. *ISME J*. 2021;15(2):450-460.
- 471 Shepherd ES, DeLoache WC, Pruss KM, Whitaker WR, Sonnenburg JL. An exclusive metabolic niche enables strain engraftment in the gut microbiota. *Nature*. 2018;557(7705):434-438.
- 472 Kearney SM, Gibbons SM, Erdman SE, Alm EJ. Orthogonal dietary niche enables reversible engraftment of a gut bacterial commensal. *Cell Rep*. 2018;24(7):1842-1851.
- 473 Makhmalanyane TP, Bezuidt OKI, Pierneef RE, Mizrahi E, Zeze A, Fossou RK, et al. African microbiomes matter. *Nat Rev Microbiol*. 2023;21(8):479-481.
- 474 Vargas-Robles D, Morales N, Rodriguez I, Nieves T, Godoy-Vitorino F, Alcaraz LD, et al. Changes in the vaginal microbiota across a gradient of urbanization. *Sci Rep*. 2020;10(1):12487.
- 475 Asnicar F, Manara S, Zolfo M, Truong DT, Scholz M, Armanini F, et al. Studying vertical microbiome transmission from mothers to infants by strain-level metagenomic profiling. *mSystems*. 2017;2(1).
- 476 Rossetto Marcelino V. Gut health: The value of connections. *Elife*. 2023;12.
- 477 Viertel TM, Ritter K, Horz HP. Viruses versus bacteria-novel approaches to phage therapy as a tool against multidrug-resistant pathogens. *J Antimicrob Chemother*. 2014;69(9):2326-2336.
- 478 Maslov S, Sneppen K. Population cycles and species diversity in dynamic Kill-the-Winner model of microbial ecosystems. *Sci Rep*. 2017;7:39642.
- 479 Thingstad TF. Elements of a theory for the mechanisms controlling abundance, diversity, and biogeochemical role of lytic bacterial viruses in aquatic systems. *Limnology and Oceanography*. 2000;45(6):1320-1328.
- 480 Tautz D, Domazet-Loso T. The evolutionary origin of orphan genes. *Nat Rev Genet*. 2011;12(10):692-702.
- 481 Malik AA, Martiny JBH, Brodie EL, Martiny AC, Treseder KK, Allison SD. Defining trait-based microbial strategies with consequences for soil carbon cycling under climate change. *ISME J*. 2020;14(1):1-9.
- 482 Ballal SA, Gallini CA, Segata N, Huttenhower C, Garrett WS. Host and gut microbiota symbiotic factors: lessons from inflammatory bowel disease and successful symbionts. *Cell Microbiol*. 2011;13(4):508-517.
- 483 Perez-Cobas AE, Gosalbes MJ, Friedrichs A, Knecht H, Artacho A, Eismann K, et al. Gut microbiota disturbance during antibiotic therapy: a multi-omic approach. *Gut*. 2013;62(11):1591-1601.
- 484 McNulty NP, Yatsunenkov T, Hsiao A, Faith JJ, Muegge BD, Goodman AL, et al. The impact of a consortium of fermented milk strains on the gut microbiome of gnotobiotic mice and monozygotic twins. *Sci Transl Med*. 2011;3(106):106ra106.
- 485 Maurice CF, Haiser HJ, Turnbaugh PJ. Xenobiotics shape the physiology and gene expression of the active human gut microbiome. *Cell*. 2013;152(1-2):39-50.
- 486 Goers L, Freemont P, Polizzi KM. Co-culture systems and technologies: taking synthetic biology to the next level. *J R Soc Interface*. 2014;11(96).
- 487 Pearce SC, Coia HG, Karl JP, Pantoja-Feliciano IG, Zachos NC, Racicot K. Intestinal *in vitro* and *ex vivo* models to study host-microbiome interactions and acute stressors. *Front Physiol*. 2018;9:1584.
- 488 Shah P, Fritz JV, Glaab E, Desai MS, Greenhalgh K, Frachet A, et al. A microfluidics-based *in vitro* model of the gastrointestinal human-microbe interface. *Nat Commun*. 2016;7:11535.

- 489 Puschhof J, Pleguezuelos-Manzano C, Clevers H. Organoids and organs-on-chips: Insights into human gut-microbe interactions. *Cell Host Microbe*. 2021;29(6):867-878.
- 490 Min S, Kim S, Cho SW. Gastrointestinal tract modeling using organoids engineered with cellular and microbiota niches. *Exp Mol Med*. 2020;52(2):227-237.
- 491 Mirzayi C, Renson A, Genomic Standards Consortium, Massive Analysis and Quality Control Society, Zohra F, Elsafoury S, et al. Reporting guidelines for human microbiome research: the STORMS checklist. *Nat Med*. 2021;27(11):1885-1892.
- 492 Chistoserdova L. Recent progress and new challenges in metagenomics for biotechnology. *Biotechnol Lett*. 2010;32(10):1351-1359.
- 493 Liu YX, Qin Y, Chen T, Lu M, Qian X, Guo X, et al. A practical guide to amplicon and metagenomic analysis of microbiome data. *Protein Cell*. 2021;12(5):315-330.
- 494 Wilkinson MD, Dumontier M, Aalbersberg IJ, Appleton G, Axton M, Baak A, et al. The FAIR guiding principles for scientific data management and stewardship. *Sci Data*. 2016;3:160018.
- 495 Tedersoo L, Kungas R, Oras E, Koster K, Eenmaa H, Leijen A, et al. Data sharing practices and data availability upon request differ across scientific disciplines. *Sci Data*. 2021;8(1):192.
- 496 Sinha R, Abnet CC, White O, Knight R, Huttenhower C. The microbiome quality control project: baseline study design and future directions. *Genome Biol*. 2015;16:276.
- 497 Wen H, Wang HY, He X, Wu CI. On the low reproducibility of cancer studies. *Natl Sci Rev*. 2018;5(5):619-624.
- 498 Vujkovic-Cvijin I, Sklar J, Jiang L, Natarajan L, Knight R, Belkaid Y. Host variables confound gut microbiota studies of human disease. *Nature*. 2020;587(7834):448-454.
- 499 Langille MGI, Ravel J, Fricke WF. "Available upon request": not good enough for microbiome data! *Microbiome*. 2018;6(1):8.
- 500 Christian TM, Gooch A, Vision T, Hull E. Journal data policies: exploring how the understanding of editors and authors corresponds to the policies themselves. *PLOS One*. 2020;15(3):e0230281.