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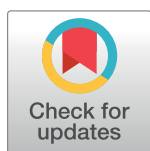
ESSAY

Framing the discussion of microorganisms as a facet of social equity in human health

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Abstract

What do “microbes” have to do with social equity? These microorganisms are integral to our health, that of our natural environment, and even the “health” of the environments we build. The loss, gain, and retention of microorganisms—their flow between humans and the environment—can greatly impact our health. It is well-known that inequalities in access to perinatal care, healthy foods, quality housing, and the natural environment can create and arise from social inequality. Here, we focus on the argument that access to beneficial microorganisms is a facet of public health, and health inequality may be compounded by inequitable microbial exposure.

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Abbreviations: FMT, fecal-microbial transplant; GABA, gamma-aminobutyric acid; GI, gastrointestinal; HMO, human milk oligosaccharide; IBD, inflammatory bowel disease; SES, socioeconomic status; VD, vaginal delivery.

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What do “microbes” have to do with social equity?

Microscopic organisms—“microbes”—are integral to our health, the natural environment, and even impact the “health” of the environments we have built. Daily, we encounter millions of particles of bacteria, fungi, and viruses, as well as archaea and protozoa, and trillions more live on and in our bodies. The way that humans organize our spatial and social infrastructure affects every aspect of life, via access to perinatal care, food, buildings, the natural environment, other members of our community, water and waste management facilities, and, in all of these ways, to microorganisms. The way microorganisms and our tissues interact is determined by early life development and the maturation of the immune system, our diet and lifestyle, and the quality of our surrounding environment. Much of the health disparity in societies, which can be attributed to a lack of access stemming from social inequity, is manifested as medical conditions, which have some relation to microorganisms or lack thereof.

Thus, social inequality, which impedes access to macrobiodiversity, also impedes access to microbiobiodiversity and the health benefits therein.

The novel concept of “microbes and social equity” is rooted in the knowledge that we rely on the microorganisms that live in or on us and our surrounding environments to provide vital ecosystem services for growth and waste recycling. The loss, gain, and retention of microorganisms can greatly impact our health and well-being. Although it has been discussed obliquely, we have yet to create a framework by which we can make better health policy or design choices using our existing knowledge of microorganisms. The ubiquity of microbes and our reliance on them extends into many aspects of social equity, such as the impact of agriculture and industry on environmental quality and conservation or privacy concerns stemming from microbial forensics, health insurance screening, or biobanking. Here, we discuss examples of microbial interactions crucial to human health and well-being that can be impeded by social policy or lack of infrastructure and how inequitable access is driving “microbial inequality.”

Vertical transmission and the need for adequate perinatal care

Early life is a critical time period for appropriate microbial colonization as well as immune development, and it has been demonstrated in mice that there is a “priority effect” in determining long-term microbial community structure in the gut [1]. Moreover, alterations to these foundational processes have the potential to affect multiple generations [2,3]. Although evidence for direct vertical transmission of microbes in humans is mixed [4,5], there is evidence that the prenatal environment can alter fetal microbiome composition indirectly. For example, stress in early pregnancy can alter both maternal and offspring immune function and results in an altered bacterial community and metabolic profile [5,6]. Further, the stress-related changes in the maternal gut or vaginal microbiota have the potential to impact the infant gut microbiota via exposure during birth [6].

Vaginal delivery (VD) is the primary means of exposing neonates to common human symbionts via vertical transmission from multiple maternal body sites [7]. These microbial exposures lead to improved immune monitoring [8] and are posited to prime infants for balanced host–microbe interactions and immune development [5]. Cesarean (surgical) delivery can be a life-saving procedure, but the number of elective and non–medically indicated instances are dramatically rising globally [9,10], which may result from and contribute to pregnancy complications. Further, cesarean delivery circumvents exposure to maternal microbiota from vaginal and intestinal locations, leaving infants susceptible to colonization by microorganisms from other sources, including skin and the surrounding environment [11–13].

Cesarean delivery alters the infant gut microbiota and their metabolic profile [8,12], although there is not a consensus on the longevity of this effect, as the impact is modulated by other early life microbial exposures [7,12,14]. However, alterations to microbial colonization may drive immune disturbances in infants born by cesarean delivery, increasing risk for autoimmune disorders or asthma [13], and in the United States, both of these covary with minoritized racial/ethnic status and socioeconomic disadvantage [15,16]. Indeed, low socioeconomic status (SES) is strongly tied to inflammation and a number of comorbidities [17]. Given the associations between low or altered microbial diversity, inflammation, and disease, it is presumed that exposure to a diverse microbiome early in life will lead to higher microbial diversity and better microbial tolerance in adulthood and that these complex communities will provide protective advantages for the host against infection [8,18], as well as reduction in inflammation [17].

The perinatal time period, because of maternal microbial transfer, is a clear early intervention target for public health and social equity [2,19,20] and societal economic outcomes [21].

Adequate perinatal education and healthcare are well demonstrated to reduce antenatal health-care costs [22,23], improve maternal and offspring health and psychological well-being over their lifetimes [21,24], and improve breastfeeding rates [23,25]. However, women who are socioeconomically disadvantaged experience social barriers and stressors preventing access to prenatal care, adequate nutrition, or education [23,26]. This increases the risk for complications during and after birth and increases psychological stressors, which further worsen health outcomes [13].

Breast milk contains a diverse microbial community, which is associated with microbial composition of neonatal feces [27], although direct seeding of gastrointestinal (GI) mucosal surfaces has yet to be demonstrated. More conspicuously, breast milk contains promicrobial elements that associate with neonate microbiota, namely, human milk oligosaccharides (HMOs), which enrich for specialized bacteria in the fetal gut, such as *Bifidobacterium longum* [28], which are widely demonstrated to be an important taxonomic group for infant health [28,29]. The stool of breastfed infants contains more bifidobacteria and lactobacilli and fewer pathobionts relative to formula-fed infants [29], something that supplementing formula-fed infants with *B. longum* can only partially replicate [30]. Breastfeeding is protective against the development of allergies, asthma, and immune disorders and leads to fewer incidences of obesity, diarrhea, respiratory tract infection, and otitis media in infants [31,32]. Breastfeeding also associates with reduced abundance of bacteria with antibiotic resistance genes, and early termination of breastfeeding can stunt this protective effect [33]. Moreover, breastfeeding reduces postpartum depression in mothers, which may be mediated by gut microbiota [14,34].

Antenatal paid leave practices vary globally by time and rate of compensation [35], and differences in ability to take parental leave may be reflective of SES disparities [36,37]. A lack of antenatal leave reduces the likelihood and duration of breastfeeding [38], especially in low-SES households [39], which are less likely to initiate breastfeeding due to a lack of social support, inadequate care at the time of birth, and misconceptions about breastfeeding [40–42]. Providing access and increasing the duration of paid parental leave improves health outcomes for mothers and infants and increases the probability of breastfeeding [42,43], thus ensuring beneficial maternal microbial transfer.

The gut microbiome and access to adequate nutrition

Variation in diet has been linked to variation in the gut microbiota of humans [44,45], with low food diversity and fiber-poor diets (e.g., the Western diet) reducing gut microbial diversity and functionality [46]. The percentage of overweight and obese individuals has skyrocketed globally since 1975 [47]. Obesity creates comorbidities, as well as financial and social burdens [48], which lead to a lifetime decrease in SES for women [49] and is compounded by lack of education or minority status [48]. Although causative factors are complex, current evidence ties low gut microbial diversity to obesity risk [50]. A low-fiber diet is associated with the proliferation of microorganisms that are extremely efficient at extracting energy from simple fats and sugars, leaving the microbiome maladapted to metabolizing complex nutrients found in whole foods [51,52]. Moreover, experimental work supports the idea that much of our nutritional acquisition is microbially driven: germ-free mice given a fecal microbial transplant from conventional mice dramatically increased in adiposity without a significant increase in food consumption or reduction in energy expenditure [50].

Diminished gut microbial diversity is also associated with several psychiatric disorders, notably, anxiety, depression, and schizophrenia [53–55]. Neurotransmitters (neural signaling molecules) affect brain activity, learning capacity, alertness, and mood. They can be produced from dietary proteins, with a nutritious diet increasing production, but are also produced by

gut microorganisms [56–58]. Bacterial dysbiosis affects the production of serotonin and gamma-aminobutyric acid (GABA) in the gut, neurotransmitters critical for regulating mental activity [53]. Germ-free mice produce fewer neurotransmitters and their precursors and exhibit psychological and cognitive changes [57,58]. Mice who received fecal transplants from human patients with schizophrenia exhibited hyperactivity, increased startle response, and depressive behavior [54].

Poor diet, especially if low in fiber (which results in low short-chain fatty acid production), may not recruit an optimum gut microbiota, and this can have a permanent impact on an individual's neurological and mental processes [53,55]. Over one-fifth of global total healthcare burdens result from mental disorders [59], and their treatment and recovery rates are disproportionately low. Though correlations between low microbial diversity and mental illness have been observed in human populations, the directionality of this complex biological interplay is still unresolved. However, observational data and experimental manipulations in model systems (e.g., fecal-microbial transplant (FMT)s in mice) suggest that integrating dietary or life-style alterations designed to recruit health-associated microbes, in addition to psychiatric and psychological care, could offer additional options for mental health treatment [55]. Although pharmaceutical methods are effective and often necessary, a microbial approach may offer nutrition-based care options to those resistant to or unable to access medication or therapy [60,61].

Lower-income communities have a higher prevalence of high-fat, high-sugar, or highly processed diets, with fewer dietary options, as this food is often cheaper and more accessible [62,63]. By providing universal access to healthy foods that promote microbial diversity, diet interventions may provide an effective way to prevent the health problems associated with inadequate microbial diversity, as well as make nutritional access more equitable [20,46,52]. Importantly, eliminating food deserts is a way to improve public health by reducing the prevalence of obesity, as well as other nutrition-associated health problems [52,64,65], and may also reduce health problems associated with low microbial diversity. School lunch programs that provide food and exclude other unhealthy foods and beverages improve nutrition standards [66] and student learning [67]. More broadly, requiring grocery stores to carry fresh fruits and vegetables [68], financial incentives or assistance to small groceries in food deserts [69,70], or food assistance programs have all been shown to improve access to healthy food [65].

Microbiology of the built environment and spatial justice

Water damage and building deterioration contribute to indoor air pollution and accrual of microorganisms, often making the space unsuitable for occupants [71], something that disproportionately affects low-income populations [72,73]. Many schools or other public infrastructure buildings contain high microbial biomass in the air and on surfaces [71,74], which can also disproportionately affect people of lower SES [75,76]. Similarly, very little infrastructure or policy considers microorganisms in prisons, as evidenced by a lack of hand-washing stations or showers, inadequate food service infrastructure, or difficulty in cleaning or quarantining areas [77]. Overcrowding overwhelms sanitation efforts, and increased proximity promotes the transmission of contagious agents, many of which are effectively endemic [77–80]. These conditions indicate either a lack of attention to the microbial health of prison facilities and their occupants or, more likely, a lack of priority on equitable care [79,81,82].

On average, 55% of the current global population resides in cities [83]. Living in an urban environment directly reduces microbial exposure [84,85]. Yet there is increasing evidence that exposure to diverse microbiota, including outdoor-sourced microorganisms from soil, water, and plants, is integral to our health [84,86]. Environmental microbial exposure promotes

immune signaling and helps build adaptive immunity [84] and is associated with reduced rates of certain infectious diseases [87,88] or asthma and allergies [89,90]. Furthermore, exposure to air pollution has been directly linked to gut microbiota disorder and inflammatory bowel disease (IBD) prevalence [91].

Urban soils and waters exhibit spatial variation in their microbial communities based on green infrastructure type, soil composition, plant biodiversity, and size [92,93] and provide exposure to increased microbial diversity, with the potential to combat microbial loss from urbanization [84]. To manage urban stormwater, many areas are implementing above-ground “green” strategies, which employ plants and soils to control the speed, volume, temperature, and quality of drainage. With vegetation, soils, and sporadic standing water, this green infrastructure functions as small-scale parks and provides habitat for complex microbial communities [94]. The distribution of these amenities themselves has implications for equity (i.e., spatial justice), because such facilities often accompany redevelopment projects or new development rather than older neighborhoods.

Zoning partitions land by use and intends to foster public health by physical separation of residence space from industry and pollution [95], yet inequitable zoning creates neighborhoods with unequal exposure to environmental risks or benefits and can lead to large-scale public health disparities [96–99]. Studies suggest that pollution-heavy industry is intentionally placed in disadvantaged neighborhoods [97,98]. Zoning and policy could be used to aid in the equitable distribution of resources [98]: supporting urban farms and local farmers’ markets, improving clean water and waste management facilities, reducing exposure to industrial pollution, applying conditional-use permits to require stores to offer healthy food items, or distributing greenspace and environmental microorganisms equitably.

Do we have a right to microbes?

The importance of microorganisms to biological life is evident; their presence provides the foundation for our own cellular complexity and the very environment on which we depend [100,101]. The question of whether we own our microbiota and whether we have the right to microbiota is central to the argument of microbiota as a means of social equity because of their vital role in our health and development. Ownership of biological tissue is a legal “grey area” [102], but the sale of bodily fluids or byproducts, including microorganisms, is generally legal [103]. We cannot say we own our microbiota in the way that we have an innate right to own our biological tissues [102]; microorganisms are too intransigent for that. If we do not own them, per se, then perhaps we have a right to access and use microorganisms, much in the way that we have a right to access natural environments and the publicly shared environmental resources we require to live [104].

The advent of microbially based therapeutics (i.e., probiotics) has opened the door to commercial early adopters peddling presumptive “healthy microbes” [105]. It has also added a new component to “biobanking”—the practice of archiving biological material—and the question of “who owns your poop” has been discussed [103,106] in this new age of fecal-prospecting for medical therapeutics. Much of this discussion regards privacy protection, as even fecal samples carry human cells tagged with our genetic information. However, it brings up yet another question regarding access. If we consider microorganisms to be “collectively owned resources,” do we not collectively have the right to benefit from microorganisms and the metabolites they produce?

Access is the basis for creating and resolving social equity—access to healthcare, healthy foods, a suitable environment, and now, those microorganisms that are demonstrated to be altered by the lifestyle differences inherent to social inequity and lack of access to a variety of

resources. If governments have a legal obligation to provide access to a healthy natural environment, and if microbial communities are integral to maintaining public health, it follows that there is likewise a legal obligation to provide policy and infrastructure to enable equitable access to microorganisms. The health, social, and financial benefits of supplying social welfare programs that provide healthcare, food, and shelter—and, in particular, those that benefit people who are marginalized and lacking in resources—are well demonstrated [22,107,108]. Even without an understanding of the effect of microorganisms on our lives, it is recognized that individual health and well-being is a common good. As our knowledge of the integral role that microorganisms play in our lives grows, we come to understand that social and political barriers to the resources required to maintain our microbiome also become an issue of social equity.

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References

1. Martínez I, Maldonado-Gomez MX, Gomes-Neto JC, Kittana H, Ding H, Schmaltz R, et al. Experimental evaluation of the importance of colonization history in early-life gut microbiota assembly. *Elife*. 2018; 7: e36521. <https://doi.org/10.7554/eLife.36521> PMID: 30226190
2. Callaghan BL. Generational Patterns of Stress: Help From Our Microbes? *Curr Dir Psychol Sci*. 2017; 26: 323–329.
3. Moeller AH, Suzuki TA, Phifer-Rixey M, Nachman MW. Transmission modes of the mammalian gut microbiota. *Science*. 2018; 362: 453–457. <https://doi.org/10.1126/science.aat7164> PMID: 30361372
4. de Goffau MC, Lager S, Sovio U, Gaccioli F, Cook E, Peacock SJ, et al. Human placenta has no microbiome but can contain potential pathogens. *Nature*. 2019; 572: 329–334. <https://doi.org/10.1038/s41586-019-1451-5> PMID: 31367035
5. Gomez de Agüero M, Ganai-Vonarburg SC, Fuhrer T, Rupp S, Uchimura Y, Li H, et al. The maternal microbiota drives early postnatal innate immune development. *Science*. 2016; 351: 1296–1302. <https://doi.org/10.1126/science.aad2571> PMID: 26989247
6. Jašarević E, Howerton CL, Howard CD, Bale TL. Alterations in the Vaginal Microbiome by Maternal Stress Are Associated With Metabolic Reprogramming of the Offspring Gut and Brain. *Endocrinology*. 2015; 156: 3265–3276. <https://doi.org/10.1210/en.2015-1177> PMID: 26079804
7. Mueller NT, Shin H, Pizoni A, Werlang IC, Matte U, Goldani MZ, et al. Birth mode-dependent association between pre-pregnancy maternal weight status and the neonatal intestinal microbiome. *Sci Rep*. 2016; 6: 23133. <https://doi.org/10.1038/srep23133> PMID: 27033998
8. Wampach L, Heintz-Buschart A, Hogan A, Muller EEL, Narayanasamy S, Laczny CC, et al. Colonization and Succession within the Human Gut Microbiome by Archaea, Bacteria, and Microeukaryotes during the First Year of Life. *Front Microbiol*. 2017; 8: 738. <https://doi.org/10.3389/fmicb.2017.00738> PMID: 28512451
9. Betran AP, Torloni MR, Zhang JJ, Gülmezoglu AM, WHO Working Group on Caesarean Section. WHO Statement on Caesarean Section Rates. *BJOG*. 2016; 123: 667–670. <https://doi.org/10.1111/1471-0528.13526> PMID: 26681211
10. Getahun D, Strickland D, Lawrence JM, Fassett MJ, Koebnick C, Jacobsen SJ. Racial and ethnic disparities in the trends in primary cesarean delivery based on indications. *Am J Obstet Gynecol*. 2009; 201: 422.e1–7.
11. Stinson LF, Payne MS, Keelan JA. A Critical Review of the Bacterial Baptism Hypothesis and the Impact of Cesarean Delivery on the Infant Microbiome. *Front Med*. 2018; 5: 135.

12. Martin R, Makino H, Cetinyurek Yavuz A, Ben-Amor K, Roelofs M, Ishikawa E, et al. Early-Life Events, Including Mode of Delivery and Type of Feeding, Siblings and Gender, Shape the Developing Gut Microbiota. *PLoS ONE*. 2016; 11: e0158498. <https://doi.org/10.1371/journal.pone.0158498> PMID: [27362264](https://pubmed.ncbi.nlm.nih.gov/27362264/)
13. Sandall J, Tribe RM, Avery L, Mola G, Visser GH, Homer CS, et al. Short-term and long-term effects of caesarean section on the health of women and children. *Lancet*. 2018; 392: 1349–1357. [https://doi.org/10.1016/S0140-6736\(18\)31930-5](https://doi.org/10.1016/S0140-6736(18)31930-5) PMID: [30322585](https://pubmed.ncbi.nlm.nih.gov/30322585/)
14. Mutic AD, Jordan S, Edwards SM, Ferranti EP, Thul TA, Yang I. The Postpartum Maternal and Newborn Microbiomes. *MCN Am J Matern Child Nurs*. 2017; 42: 326–331. <https://doi.org/10.1097/NMC.0000000000000374> PMID: [29049057](https://pubmed.ncbi.nlm.nih.gov/29049057/)
15. Calixto O-J, Anaya J-M. Socioeconomic status. The relationship with health and autoimmune diseases. *Autoimmunity Reviews*. 2014; 13: 641–654. <https://doi.org/10.1016/j.autrev.2013.12.002> PMID: [24418307](https://pubmed.ncbi.nlm.nih.gov/24418307/)
16. Forno E, Celedon JC. Asthma and ethnic minorities: socioeconomic status and beyond. *Curr Opin Allergy Clin Immunol*. 2009; 9: 154–160. PMID: [19326508](https://pubmed.ncbi.nlm.nih.gov/19326508/)
17. Rook GAW, Raison CL, Lowry CA. Microbial “old friends”, immunoregulation and socioeconomic status. *Clin Exp Immunol*. 2014; 177: 1–12. <https://doi.org/10.1111/cei.12269> PMID: [24401109](https://pubmed.ncbi.nlm.nih.gov/24401109/)
18. Wang B, Yao M, Lv L, Ling Z, Li L. The Human Microbiota in Health and Disease. *Proc Est Acad Sci Eng*. 2017; 3: 71–82.
19. D’Argenio V. The Prenatal Microbiome: A New Player for Human Health. *High Throughput*. 2018; 7: 38.
20. Dietert RR. The microbiome in early life: self-completion and microbiota protection as health priorities. *Birth Defects Res B Dev Reprod Toxicol*. 2014; 101: 333–340. <https://doi.org/10.1002/bdrb.21116> PMID: [25044451](https://pubmed.ncbi.nlm.nih.gov/25044451/)
21. Gennaro S, Melnyk BM, O’Connor C, Gibeau AM, Nadel E. Improving Prenatal Care for Minority Women. *MCN Am J Matern Child Nurs*. 2016; 41: 147–153. <https://doi.org/10.1097/NMC.0000000000000227> PMID: [26854915](https://pubmed.ncbi.nlm.nih.gov/26854915/)
22. Henderson JW. The cost effectiveness of prenatal care. *Health Care Financ Rev*. 1994; 15: 21–32. PMID: [10138484](https://pubmed.ncbi.nlm.nih.gov/10138484/)
23. Milcent C, Zbiri S. Prenatal care and socioeconomic status: effect on cesarean delivery. *Health Econ Rev*. 2018; 8: 7. <https://doi.org/10.1186/s13561-018-0190-x> PMID: [29525909](https://pubmed.ncbi.nlm.nih.gov/29525909/)
24. Ickovics JR, Kershaw TS, Westdahl C, Magriples U, Massey Z, Reynolds H, et al. Group prenatal care and perinatal outcomes: a randomized controlled trial. *Obstet Gynecol*. 2007; 110: 330–339. <https://doi.org/10.1097/01.AOG.0000275284.24298.23> PMID: [17666608](https://pubmed.ncbi.nlm.nih.gov/17666608/)
25. Rosen IM, Krueger MV, Carney LM, Graham JA. Prenatal breastfeeding education and breastfeeding outcomes. *MCN Am J Matern Child Nurs*. 2008; 33: 315–319. <https://doi.org/10.1097/01.NMC.0000334900.22215.ec> PMID: [18758336](https://pubmed.ncbi.nlm.nih.gov/18758336/)
26. Heaman MI, Sword W, Elliott L, Moffatt M, Helewa ME, Morris H, et al. Barriers and facilitators related to use of prenatal care by inner-city women: perceptions of health care providers. *BMC Pregnancy Childbirth*. 2015; 15: 2. <https://doi.org/10.1186/s12884-015-0431-5> PMID: [25591945](https://pubmed.ncbi.nlm.nih.gov/25591945/)
27. Pannaraj PS, Li F, Cerini C, Bender JM, Yang S, Rollie A, et al. Association Between Breast Milk Bacterial Communities and Establishment and Development of the Infant Gut Microbiome. *JAMA Pediatr*. 2017; 171: 647–654. <https://doi.org/10.1001/jamapediatrics.2017.0378> PMID: [28492938](https://pubmed.ncbi.nlm.nih.gov/28492938/)
28. Yamada C, Gotoh A, Sakanaka M, Hattie M, Stubbs KA, Katayama-Ikegami A, et al. Molecular Insight into Evolution of Symbiosis between Breast-Fed Infants and a Member of the Human Gut Microbiome *Bifidobacterium longum*. *Cell Chem Biol*. 2017; 24: 515–524.e5. <https://doi.org/10.1016/j.chembiol.2017.03.012> PMID: [28392148](https://pubmed.ncbi.nlm.nih.gov/28392148/)
29. Milani C, Duranti S, Bottacini F, Casey E, Turroni F, Mahony J, et al. The First Microbial Colonizers of the Human Gut: Composition, Activities, and Health Implications of the Infant Gut Microbiota. *Microbiol Mol Biol Rev*. 2017; 81: 00036–00017.
30. Hascoët J-M, Hubert C, Rochat F, Legagneur H, Gaga S, Emady-Azar S, et al. Effect of formula composition on the development of infant gut microbiota. *J Pediatr Gastroenterol Nutr*. 2011; 52: 756–762. <https://doi.org/10.1097/MPG.0b013e3182105850> PMID: [21593648](https://pubmed.ncbi.nlm.nih.gov/21593648/)
31. Huang J, Vaughn MG, Kremer KP. Breastfeeding and child development outcomes: an investigation of the nurturing hypothesis. *Matern Child Nutr*. 2016; 12: 757–767. <https://doi.org/10.1111/mcn.12200> PMID: [26194444](https://pubmed.ncbi.nlm.nih.gov/26194444/)
32. Ip S, Chung M, Raman G, Chew P, Magula N, DeVine D, et al. Breastfeeding and maternal and infant health outcomes in developed countries. *Evid Rep Technol Assess*. 2007; 1–186.

33. Pärnänen K, Karkman A, Hultman J, Lyra C, Bengtsson-Palme J, Larsson DGJ, et al. Maternal gut and breast milk microbiota affect infant gut antibiotic resistome and mobile genetic elements. *Nat Commun.* 2018; 9: 3891. <https://doi.org/10.1038/s41467-018-06393-w> PMID: [30250208](https://pubmed.ncbi.nlm.nih.gov/30250208/)
34. Rackers HS, Thomas S, Williamson K, Posey R, Kimmel MC. Emerging literature in the Microbiota-Brain Axis and Perinatal Mood and Anxiety Disorders. *Psychoneuroendocrinology.* 2018; 95: 86–96. <https://doi.org/10.1016/j.psyneuen.2018.05.020> PMID: [29807325](https://pubmed.ncbi.nlm.nih.gov/29807325/)
35. Raub A, Nandi A, Earle A, De Guzman Chorny N, Wong E, Chung P, et al. Paid Parental Leave: A Detailed Look at Approaches Across OECD Countries. Los Angeles, CA: World Policy Analysis Center; 2018. https://www.worldpolicycenter.org/sites/default/files/WORLD%20Report%20-%20Parental%20Leave%20OECD%20Country%20Approaches_0.pdf
36. Rossin M. The effects of maternity leave on children's birth and infant health outcomes in the United States. *J Health Econ.* 2011; 30: 221–239. <https://doi.org/10.1016/j.jhealeco.2011.01.005> PMID: [21300415](https://pubmed.ncbi.nlm.nih.gov/21300415/)
37. Donovan SA. Paid family leave in the United States (CRS Report R44835). Washington (DC): Congressional Research Service; 2019. Report No.: R44835. Available: https://digitalcommons.ilr.cornell.edu/key_workplace/2107/
38. Ogbuanu C, Glover S, Probst J, Liu J, Hussey J. The effect of maternity leave length and time of return to work on breastfeeding. *Pediatrics.* 2011; 127: e1414–27. <https://doi.org/10.1542/peds.2010-0459> PMID: [21624878](https://pubmed.ncbi.nlm.nih.gov/21624878/)
39. Flacking R, Dykes F, Ewald U. The influence of fathers' socioeconomic status and paternity leave on breastfeeding duration: a population-based cohort study. *Scand J Public Health.* 2010; 38: 337–343. <https://doi.org/10.1177/1403494810362002> PMID: [20147577](https://pubmed.ncbi.nlm.nih.gov/20147577/)
40. Jones KM, Power ML, Queenan JT, Schulkin J. Racial and Ethnic Disparities in Breastfeeding. *Breastfeed Med.* 2015; 10: 186. <https://doi.org/10.1089/bfm.2014.0152> PMID: [25831234](https://pubmed.ncbi.nlm.nih.gov/25831234/)
41. Office of the Surgeon General (US), Centers for Disease Control and Prevention (US), Office on Women's Health (US). Barriers to Breastfeeding in the United States. In: The Surgeon General's Call to Action to Support Breastfeeding. Rockville, MD: Office of the Surgeon General (US); 2011.
42. Temple Newhook J, Newhook LA, Midodzi WK, Murphy Goodridge J, Burrage L, Gill N, et al. Poverty and Breastfeeding: Comparing Determinants of Early Breastfeeding Cessation Incidence in Socioeconomically Marginalized and Privileged Populations in the FiNaL Study. *Health Equity.* 2017; 1: 96–102. <https://doi.org/10.1089/heaq.2016.0028> PMID: [30283838](https://pubmed.ncbi.nlm.nih.gov/30283838/)
43. Huang R, Yang M. Paid maternity leave and breastfeeding practice before and after California's implementation of the nation's first paid family leave program. *Econ Hum Biol.* 2015; 16: 45–59. <https://doi.org/10.1016/j.ehb.2013.12.009> PMID: [24508006](https://pubmed.ncbi.nlm.nih.gov/24508006/)
44. 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: 583–588. <https://doi.org/10.1038/s41586-018-0617-x> PMID: [30356187](https://pubmed.ncbi.nlm.nih.gov/30356187/)
45. McDonald D, Hyde E, Debelius JW, Morton JT, Gonzalez A, Ackermann G, et al. American Gut: an Open Platform for Citizen Science Microbiome Research. *mSystems.* 2018; 3: e00031–18.
46. Sonnenburg ED, Smits SA, Tikhonov M, Higginbottom SK, Wingreen NS, Sonnenburg JL. Diet-induced extinctions in the gut microbiota compound over generations. *Nature.* 2016; 529: 212–215. <https://doi.org/10.1038/nature16504> PMID: [26762459](https://pubmed.ncbi.nlm.nih.gov/26762459/)
47. Obesity and overweight. In: World Health Organization [Internet]. 16 Feb 2018 [cited 17 Jul 2019]. Available from: <https://www.who.int/news-room/fact-sheets/detail/obesity-and-overweight>
48. Pavela G, Lewis DW, Locher J, Allison DB. Socioeconomic Status, Risk of Obesity, and the Importance of Albert J. Stunkard. *Curr Obes Rep.* 2016; 5: 132–139. <https://doi.org/10.1007/s13679-015-0185-4> PMID: [26746415](https://pubmed.ncbi.nlm.nih.gov/26746415/)
49. Newton S, Braithwaite D, Akinyemiju TF. Socio-economic status over the life course and obesity: Systematic review and meta-analysis. *PLoS ONE.* 2017; 12: e0177151. <https://doi.org/10.1371/journal.pone.0177151> PMID: [28510579](https://pubmed.ncbi.nlm.nih.gov/28510579/)
50. Davis CD. The Gut Microbiome and Its Role in Obesity. *Nutr Today.* 2016; 51: 167–174. <https://doi.org/10.1097/NT.000000000000167> PMID: [27795585](https://pubmed.ncbi.nlm.nih.gov/27795585/)
51. Jumpertz R, Le DS, Turnbaugh PJ, Trinidad C, Bogardus C, Gordon JL, et al. Energy-balance studies reveal associations between gut microbes, caloric load, and nutrient absorption in humans. *Am J Clin Nutr.* 2011; 94: 58–65. <https://doi.org/10.3945/ajcn.110.010132> PMID: [21543530](https://pubmed.ncbi.nlm.nih.gov/21543530/)
52. Zhao L, Zhang F, Ding X, Wu G, Lam YY, Wang X, et al. Gut bacteria selectively promoted by dietary fibers alleviate type 2 diabetes. *Science.* 2018; 359: 1151–1156. <https://doi.org/10.1126/science.aao5774> PMID: [29590046](https://pubmed.ncbi.nlm.nih.gov/29590046/)

53. Valles-Colomer M, Falony G, Darzi Y, Tigchelaar EF, Wang J, Tito RY, et al. The neuroactive potential of the human gut microbiota in quality of life and depression. *Nat Microbiol.* 2019; 4: 623–632. <https://doi.org/10.1038/s41564-018-0337-x> PMID: 30718848
54. Zheng P, Zeng B, Liu M, Chen J, Pan J, Han Y, et al. The gut microbiome from patients with schizophrenia modulates the glutamate-glutamine-GABA cycle and schizophrenia-relevant behaviors in mice. *Sci Adv.* 2019; 5: eaau8317. <https://doi.org/10.1126/sciadv.aau8317> PMID: 30775438
55. Liang S, Wu X, Jin F. Gut-Brain Psychology: Rethinking Psychology From the Microbiota-Gut-Brain Axis. *Front Integr Neurosci.* 2018; 12: 33. <https://doi.org/10.3389/fnint.2018.00033> PMID: 30271330
56. Johnson KV-A, Foster KR. Why does the microbiome affect behaviour? *Nat Rev Microbiol.* 2018; 16: 647–655. <https://doi.org/10.1038/s41579-018-0014-3> PMID: 29691482
57. Cenit MC, Sanz Y, Codoñer-Franch P. Influence of gut microbiota on neuropsychiatric disorders. *World J Gastroenterol.* 2017; 23: 5486–5498. <https://doi.org/10.3748/wjg.v23.i30.5486> PMID: 28852308
58. Bercik P, Denou E, Collins J, Jackson W, Lu J, Jury J, et al. The intestinal microbiota affect central levels of brain-derived neurotrophic factor and behavior in mice. *Gastroenterology.* 2011; 141: 599–609, 609.e1–3. <https://doi.org/10.1053/j.gastro.2011.04.052> PMID: 21683077
59. GBD 2016 DALYs and HALE Collaborators. Global, regional, and national disability-adjusted life-years (DALYs) for 333 diseases and injuries and healthy life expectancy (HALE) for 195 countries and territories, 1990–2016: a systematic analysis for the Global Burden of Disease Study 2016. *Lancet.* 2017; 390: 1260–1344. [https://doi.org/10.1016/S0140-6736\(17\)32130-X](https://doi.org/10.1016/S0140-6736(17)32130-X) PMID: 28919118
60. Gobin RL, Freyd JJ. Betrayal and Revictimization: Preliminary Findings. *Psychological Trauma: Theory, Research, Practice, and Policy.* 2009; 1: 242–257.
61. Hwang SW, Kirst MJ, Chiu S, Tolomiczenko G, Kiss A, Cowan L, et al. Multidimensional social support and the health of homeless individuals. *J Urban Health.* 2009; 86: 791–803. <https://doi.org/10.1007/s11524-009-9388-x> PMID: 19629703
62. Rao M, Afshin A, Singh G, Mozaffarian D. Do healthier foods and diet patterns cost more than less healthy options? A systematic review and meta-analysis. *BMJ Open.* 2013; 3: e004277. <https://doi.org/10.1136/bmjopen-2013-004277> PMID: 24309174
63. Hilmers A, Hilmers DC, Dave J. Neighborhood disparities in access to healthy foods and their effects on environmental justice. *Am J Public Health.* 2012; 102: 1644–1654. <https://doi.org/10.2105/AJPH.2012.300865> PMID: 22813465
64. Ercolini D, Fogliano V. Food Design To Feed the Human Gut Microbiota. *J Agric Food Chem.* 2018; 66: 3754–3758. <https://doi.org/10.1021/acs.jafc.8b00456> PMID: 29565591
65. Gartin M. The Death of Distance: Food Deserts Across the Global Divide. In: Fitzpatrick KM, Willis D, editors. *A Place-Based Perspective of Food in Society.* New York: Palgrave Macmillan US; 2015. pp. 187–200.
66. Long MW, Luedicke J, Dorsey M, Fiore SS, Henderson KE. Impact of Connecticut legislation incentivizing elimination of unhealthy competitive foods on National School Lunch Program participation. *Am J Public Health.* 2013; 103: e59–66.
67. Masangcay EJ. The Effect of the National School Lunch Program (NSLP) on Educational Attainment. Bachelor of Arts, University of Puget Sound. 2014. <https://pdfs.semanticscholar.org/fb05/762e3a4fcdfe38deaa554de1a9428bdfb763.pdf>
68. Minneapolis Health Department. Minneapolis Healthy Corner Store Program. Minneapolis Health Department; 2014 Jul. http://www.centertrt.org/content/docs/Intervention_Documents/Intervention_Templates/Minneapolis_HCS_Template_Final.pdf
69. House Appropriations Committee. Report on Key Issues From the House Appropriations Committee: Pennsylvania Fresh Food Financing Initiative. Pennsylvania State; 2010 Mar. https://www.ncsl.org/documents/labor/workingfamilies/pa_fffi.pdf
70. Crowe J, Lacy C, Columbus Y. Barriers to Food Security and Community Stress in an Urban Food Desert. *Urban Science.* 2018; 2: 46.
71. Abdul-Wahab SA, editor. *Sick Building Syndrome: in Public Buildings and Workplaces.* Berlin, Heidelberg: Springer, Berlin, Heidelberg; 2011.
72. Bi C, Maestre JP, Li H, Zhang G, Givehchi R, Mahdavi A, et al. Phthalates and organophosphates in settled dust and HVAC filter dust of U.S. low-income homes: Association with season, building characteristics, and childhood asthma. *Environ Int.* 2018; 121: 916–930. <https://doi.org/10.1016/j.envint.2018.09.013> PMID: 30347374
73. Ciaccio CE, Barnes C, Kennedy K, Chan M, Portnoy J, Rosenwasser L. Home dust microbiota is disordered in homes of low-income asthmatic children. *J Asthma.* 2015; 52: 873–880. <https://doi.org/10.3109/02770903.2015.1028076> PMID: 26512904

74. Huttunen K, Tirkkonen J, Täubel M, Krop E, Mikkonen S, Pekkanen J, et al. Inflammatory potential in relation to the microbial content of settled dust samples collected from moisture-damaged and reference schools: results of HITEA study. *Indoor Air*. 2016; 26: 380–390. <https://doi.org/10.1111/ina.12223> PMID: 25967114
75. Ghaffarianhoseini A, AlWaer H, Omrany H, Ghaffarianhoseini A, Alalouch C, Clements-Croome D, et al. Sick building syndrome: are we doing enough? *Archit Sci Rev*. 2018; 61: 99–121.
76. Gomes CAT, Duarte MRT. School Infrastructure and Socioeconomic Status in Brazil. *Sociology and Anthropology*. 2017; 5: 522–532.
77. Bick JA. Infection control in jails and prisons. *Clin Infect Dis*. 2007; 45: 1047–1055. <https://doi.org/10.1086/521910> PMID: 17879924
78. Lambert LA, Armstrong LR, Lobato MN, Ho C, France AM, Haddad MB. Tuberculosis in Jails and Prisons: United States, 2002–2013. *Am J Public Health*. 2016; 106: 2231–2237. <https://doi.org/10.2105/AJPH.2016.303423> PMID: 27631758
79. O’Grady J, Maeurer M, Atun R, Abubakar I, Mwaba P, Bates M, et al. Tuberculosis in prisons: anatomy of global neglect. *Eur Respir J*. 2011; 38: 752–754. <https://doi.org/10.1183/09031936.00041211> PMID: 21965498
80. Levy MH, Mogg D. Infection control standards for Australian prisons: forgotten, but not forgiving. *Healthcare infection*. 2009; 14: 13–19.
81. Trends in U.S. Corrections [Internet]. Washington (DC): The Sentencing Project; 2019 Jun [cited 2019 July 15]. Available from: <https://sentencingproject.org/wp-content/uploads/2016/01/Trends-in-US-Corrections.pdf>
82. Rabuy B, Kopf D. Prisons of Poverty: Uncovering the pre-incarceration incomes of the imprisoned [Internet]. Prison Policy Initiative; 2015 Jul [cited 2019 July 15]. Available from: <https://www.prisonpolicy.org/reports/income.html>
83. United Nations Population Division. Urban population (% of total population) [Internet]. Global Bank Group. 2018 [cited 2019 July 15]. Available from: <https://data.worldbank.org/indicator/sp.urb.totl.in.zs>
84. Mills JG, Brookes JD, Gellie NJC, Liddicoat C, Lowe AJ, Sydnor HR, et al. Relating Urban Biodiversity to Human Health With the “Holobiont” Concept. *Front Microbiol*. 2019; 10: 550. <https://doi.org/10.3389/fmicb.2019.00550> PMID: 30972043
85. Gibbons SM. The Built Environment Is a Microbial Wasteland. *mSystems*. 2016. pp. e00033–16. <https://doi.org/10.1128/mSystems.00033-16> PMID: 27832216
86. Salvucci E. Microbiome, holobiont and the net of life. *Crit Rev Microbiol*. 2016; 42: 485–494. <https://doi.org/10.3109/1040841X.2014.962478> PMID: 25430522
87. Liddicoat C, Bi P, Waycott M, Glover J, Lowe AJ, Weinstein P. Landscape biodiversity correlates with respiratory health in Australia. *J Environ Manage*. 2018; 206: 113–122. <https://doi.org/10.1016/j.jenvman.2017.10.007> PMID: 29059566
88. Fine PE, Floyd S, Stanford JL, Nkhosa P, Kasunga A, Chaguluka S, et al. Environmental mycobacteria in northern Malawi: implications for the epidemiology of tuberculosis and leprosy. *Epidemiol Infect*. 2001; 126: 379–387. <https://doi.org/10.1017/s0950268801005532> PMID: 11467795
89. Jatzlauk G, Bartel S, Heine H, Schlöter M, Krauss-Etschmann S. Influences of environmental bacteria and their metabolites on allergies, asthma, and host microbiota. *Allergy*. 2017; 72: 1859–1867. <https://doi.org/10.1111/all.13220> PMID: 28600901
90. Illi S, Depner M, Genuneit J, Horak E, Loss G, Strunz-Lehner C, et al. Protection from childhood asthma and allergy in Alpine farm environments—the GABRIEL Advanced Studies. *J Allergy Clin Immunol*. 2012; 129: 1470–7.e6. <https://doi.org/10.1016/j.jaci.2012.03.013> PMID: 22534534
91. Salim SY, Kaplan GG, Madsen KL. Air pollution effects on the gut microbiota: a link between exposure and inflammatory disease. *Gut Microbes*. 2014; 5: 215–219. <https://doi.org/10.4161/gmic.27251> PMID: 24637593
92. Saxton MA, Naqvi NS, Rahman F, Thompson CP, Chambers RM, Kaste JM, et al. Site-specific environmental factors control bacterial and viral diversity in stormwater retention ponds. *Aquat Microb Ecol*. 2016; 77: 23–36.
93. McGuire KL, Payne SG, Palmer MI, Gillikin CM, Keefe D, Kim SJ, et al. Digging the New York City Skyline: soil fungal communities in green roofs and city parks. *PLoS ONE*. 2013; 8: e58020. <https://doi.org/10.1371/journal.pone.0058020> PMID: 23469260
94. Gill AS, Lee A, McGuire KL. Phylogenetic and Functional Diversity of Total (DNA) and Expressed (RNA) Bacterial Communities in Urban Green Infrastructure Bioswale Soils. *Appl Environ Microbiol*. 2017; 83: e00287–17. <https://doi.org/10.1128/AEM.00287-17> PMID: 28576763

95. Osypuk TL, Acevedo-Garcia D. Beyond individual neighborhoods: a geography of opportunity perspective for understanding racial/ethnic health disparities. *Health Place*. 2010; 16: 1113–1123. <https://doi.org/10.1016/j.healthplace.2010.07.002> PMID: [20705500](https://pubmed.ncbi.nlm.nih.gov/20705500/)
96. Rossen LM, Pollack KM. Making the Connection Between Zoning and Health Disparities. *Environ Justice*. 2012; 5: 119–127.
97. Pastor M, Sadd J, Hipp J. Which Came First? Toxic Facilities, Minority Move-In, and Environmental Justice. *J Urban Aff*. 2001; 23: 1–21.
98. Wilson S, Hutson M, Mujahid M. How Planning and Zoning Contribute to Inequitable Development, Neighborhood Health, and Environmental Injustice. *Environ Justice*. 2008; 1: 211–216.
99. Dannenberg AL, Jackson RJ, Frumkin H, Schieber RA, Pratt M, Kochtitzky C, et al. The impact of community design and land-use choices on public health: a scientific research agenda. *Am J Public Health*. 2003; 93: 1500–1508. <https://doi.org/10.2105/ajph.93.9.1500> PMID: [12948970](https://pubmed.ncbi.nlm.nih.gov/12948970/)
100. Gilbert JA, Neufeld JD. Life in a World without Microbes. *PLoS Biol*. 2014; 12: e1002020. <https://doi.org/10.1371/journal.pbio.1002020> PMID: [25513890](https://pubmed.ncbi.nlm.nih.gov/25513890/)
101. Gilbert SF, Sapp J, Tauber AI. A symbiotic view of life: we have never been individuals. *Q Rev Biol*. 2012; 87: 325–341. PMID: [23397797](https://pubmed.ncbi.nlm.nih.gov/23397797/)
102. Calabresi G. Do we own our own bodies? *Yale Law School Faculty Scholarship Series*. 2011. pp. 1–15.
103. Hawkins AK, O'Doherty KC. “Who owns your poop?”: insights regarding the intersection of human microbiome research and the ELSI aspects of biobanking and related studies. *BMC Med Genomics*. 2011; 4: 72. <https://doi.org/10.1186/1755-8794-4-72> PMID: [21982589](https://pubmed.ncbi.nlm.nih.gov/21982589/)
104. Human Rights Council. Issue of human rights obligations relating to the enjoyment of a safe, clean, healthy and sustainable environment. United Nations, General Assembly; 2019 Jan. Report No.: A/HRC/40/55. Available from: <http://srenvironment.org/sites/default/files/Reports/2019/UN%20HRC%20Right%20to%20clean%20air.pdf>
105. Slashinski MJ, McCurdy SA, Achenbaum LS, Whitney SN, McGuire AL. “Snake-oil,” “quack medicine,” and “industrially cultured organisms:” biovalue and the commercialization of human microbiome research. *BMC Med Ethics*. 2012; 13: 28. <https://doi.org/10.1186/1472-6939-13-28> PMID: [23110633](https://pubmed.ncbi.nlm.nih.gov/23110633/)
106. Chuong KH, Hwang DM, Tullis DE, Waters VJ, Yau YCW, Guttman DS, et al. Navigating social and ethical challenges of biobanking for human microbiome research. *BMC Med Ethics*. 2017; 18: 1. <https://doi.org/10.1186/s12910-016-0160-y> PMID: [28077127](https://pubmed.ncbi.nlm.nih.gov/28077127/)
107. Canning D, Bennathan E. The social rate of return on infrastructure investments. The World Bank; 2000 Jul. Report No.: 2390. Available: <https://ideas.repec.org/p/wbk/wbrwps/2390.html>
108. Masters R, Anwar E, Collins B, Cookson R, Capewell S. Return on investment of public health interventions: a systematic review. *J Epidemiol Community Health*. 2017; 71: 827–834. <https://doi.org/10.1136/jech-2016-208141> PMID: [28356325](https://pubmed.ncbi.nlm.nih.gov/28356325/)