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The developing infant gut microbiota: mathematical predictions of the effects of oligosaccharides

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Citation

Versluis, D. M. (2024, April 23). *The developing infant gut microbiota: mathematical predictions of the effects of oligosaccharides*. Retrieved from <https://hdl.handle.net/1887/3748520>

Version: Publisher's Version

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Note: To cite this publication please use the final published version (if applicable).

Bibliography

- [1] K. M. Kennedy, M. J. Gerlach, T. Adam, M. M. Heimesaat, L. Rossi, M. G. Surette, D. M. Sloboda, and T. Braun, “Fetal meconium does not have a detectable microbiota before birth,” *Nature Microbiology*, vol. 6, no. 7, pp. 865–873, 2021.
- [2] K. M. Kennedy, M. C. de Goffau, M. E. Perez-Muñoz, M. C. Arrieta, F. Bäckhed, P. Bork, T. Braun, F. D. Bushman, J. Dore, W. M. de Vos, A. M. Earl, J. A. Eisen, M. A. Elovitz, S. C. Ganal-Vonarburg, M. G. Gänzle, W. S. Garrett, L. J. Hall, M. W. Hornef, C. Huttenhower, L. Konnikova, S. Lebeer, A. J. Macpherson, R. C. Massey, A. C. McHardy, O. Koren, T. D. Lawley, R. E. Ley, L. O’Mahony, P. W. O’Toole, E. G. Pamer, J. Parkhill, J. Raes, T. Rattei, A. Salonen, E. Segal, N. Segata, F. Shanahan, D. M. Sloboda, G. C. Smith, H. Sokol, T. D. Spector, M. G. Surette, G. W. Tannock, A. W. Walker, M. Yassour, and J. Walter, “Questioning the fetal microbiome illustrates pitfalls of low-biomass microbial studies,” *Nature*, vol. 613, no. 7945, pp. 639–649, 2023.
- [3] F. Bäckhed, J. Roswall, Y. Peng, Q. Feng, H. Jia, P. Kovatcheva-Datchary, Y. Li, Y. Xia, H. Xie, H. Zhong, M. T. Khan, J. Zhang, J. Li, L. Xiao, J. Al-Aama, D. Zhang, Y. S. Lee, D. Kotowska, C. Colding, V. Tremaroli, Y. Yin, S. Bergman, X. Xu, L. Madsen, K. Kristiansen, J. Dahlgren, and W. Jun, “Dynamics and stabilization of the human gut microbiome during the first year of life,” *Cell Host and Microbe*, vol. 17, no. 5, pp. 690–703, 2015.
- [4] G. Alessandri, F. Fontana, L. Mancabelli, G. A. Lugli, C. Tarracchini, C. Argentini, G. Longhi, A. Viappiani, C. Milani, F. Turrone, D. van Sinderen, and M. Ventura, “Exploring species-level infant gut bacterial biodiversity by meta-analysis and formulation of an optimized cultivation medium,” *npj Biofilms and Microbiomes*, vol. 8, no. 1, 2022.
- [5] C. Palmer, E. M. Bik, D. B. DiGiulio, D. A. Relman, and P. O. Brown, “Development of the human infant intestinal microbiota,” *PLoS Biology*, vol. 5, no. 7, pp. 1556–1573, 2007.

Bibliography

- [6] Y. Tsunoda, T. Asahara, K. Nomoto, Y. Yoshioka, and E. Fukuma, “Bacterial profile of infant feces associated with lactation infectious breasts,” *Pediatric Health, Medicine and Therapeutics*, vol. Volume 9, pp. 173–180, 2018.
- [7] T. Escherich, *Die darmbakterien des säuglings und ihre beziehungen zur physiologie der Verdauung*. Enke, 1886.
- [8] P. A. Scholtens, R. Oozeer, R. Martin, K. B. Amor, and J. Knol, “The Early Settlers: Intestinal Microbiology in Early Life,” *Annual Review of Food Science and Technology*, vol. 3, no. 1, pp. 425–447, 2012.
- [9] S. Wang, S. Zeng, M. Egan, P. Cherry, C. Strain, E. Morais, P. Boyaval, C. A. Ryan, E. M. Dempsey, R. P. Ross, and C. Stanton, “Metagenomic analysis of mother-infant gut microbiome reveals global distinct and shared microbial signatures,” *Gut Microbes*, vol. 13, no. 1, pp. 1–24, 2021.
- [10] S. Magnúsdóttir, A. Heinken, L. Kutt, D. A. Ravcheev, E. Bauer, A. Noronha, K. Greenhalgh, C. Jäger, J. Baginska, P. Wilmes, R. M. Fleming, and I. Thiele, “Generation of genome-scale metabolic reconstructions for 773 members of the human gut microbiota,” *Nature Biotechnology*, vol. 35, no. 1, pp. 81–89, 2017.
- [11] N. T. Devika and K. Raman, “Deciphering the metabolic capabilities of Bifidobacteria using genome-scale metabolic models,” *Scientific Reports*, vol. 9, no. 1, pp. 1–9, 2019.
- [12] K. Korpela and W. M. de Vos, “Infant gut microbiota restoration: state of the art,” *Gut Microbes*, vol. 14, no. 1, 2022.
- [13] J. D. Orth, I. Thiele, and B. O. Palsson, “What is flux balance analysis?,” *Nature Biotechnology*, vol. 28, no. 3, pp. 245–248, 2010.
- [14] S. Matamoros, C. Gras-Leguen, F. Le Vacon, G. Potel, and M. F. De La Cochetiere, “Development of intestinal microbiota in infants and its impact on health,” *Trends in Microbiology*, vol. 21, no. 4, pp. 167–173, 2013.
- [15] J. M. Johnson and E. D. Adams, “The Gastrointestinal Microbiome in Infant Colic,” *MCN: The American Journal of Maternal/Child Nursing*, pp. 1–12, 2022.
- [16] S. Dogra, O. Sakwinska, S. E. Soh, C. Ngom-Bru, W. M. Brück, B. Berger, H. Brüssow, N. Karnani, Y. S. Lee, F. Yap, Y. S. Chong, K. M. Godfrey, and J. D. Holbrook, “Rate of establishing the gut microbiota in infancy has consequences for future health,” *Gut Microbes*, vol. 6, no. 5, pp. 321–325, 2015.
- [17] I. O’Neill, Z. Schofield, and L. J. Hall, “Exploring the role of the microbiota member Bifidobacterium in modulating immune-linked diseases,” *Emerging Topics in Life Sciences*, vol. 1, no. 4, pp. 333–349, 2017.

-
- [18] R. M. Duar, D. Kyle, and G. Casaburi, "Colonization Resistance in the Infant Gut: The Role of *B. infantis* in Reducing pH and Preventing Pathogen Growth," *High-Throughput*, vol. 9, no. 2, p. 7, 2020.
- [19] S. Fukuda, H. Toh, K. Hase, K. Oshima, Y. Nakanishi, K. Yoshimura, T. Tobe, J. M. Clarke, D. L. Topping, T. Suzuki, T. D. Taylor, K. Itoh, J. Kikuchi, H. Morita, M. Hattori, and H. Ohno, "Bifidobacteria can protect from enteropathogenic infection through production of acetate," *Nature*, vol. 469, no. 7331, pp. 543–549, 2011.
- [20] O. Appert, A. R. Garcia, R. Frei, C. Roduit, F. Constancias, V. Neuzil-Bunesova, R. Ferstl, J. Zhang, C. Akdis, R. Lauener, C. Lacroix, and C. Schwab, "Initial butyrate producers during infant gut microbiota development are endospore formers," *Environmental Microbiology*, vol. 22, no. 9, pp. 3909–3921, 2020.
- [21] A. Cait, E. Cardenas, P. A. Dimitriu, N. Amenogbe, D. Dai, J. Cait, H. Sbihi, L. Stiemsma, P. Subbarao, P. J. Mandhane, A. B. Becker, T. J. Moraes, M. R. Sears, D. L. Lefebvre, M. B. Azad, T. Kollmann, S. E. Turvey, and W. W. Mohn, "Reduced genetic potential for butyrate fermentation in the gut microbiome of infants who develop allergic sensitization," *Journal of Allergy and Clinical Immunology*, vol. 144, no. 6, pp. 1638–1647.e3, 2019.
- [22] L. Nylund, M. Nermes, E. Isolauri, S. Salminen, W. M. De Vos, and R. Satokari, "Severity of atopic disease inversely correlates with intestinal microbiota diversity and butyrate-producing bacteria," *Allergy: European Journal of Allergy and Clinical Immunology*, vol. 70, no. 2, pp. 241–244, 2015.
- [23] H. Wopereis, K. Sim, A. Shaw, J. O. Warner, J. Knol, and J. S. Kroll, "Intestinal microbiota in infants at high risk for allergy: Effects of prebiotics and role in eczema development," *Journal of Allergy and Clinical Immunology*, vol. 141, no. 4, pp. 1334–1342.e5, 2018.
- [24] C. De Weerth, S. Fuentes, P. Puylaert, and W. M. De Vos, "Intestinal microbiota of infants with colic: Development and specific signatures," *Pediatrics*, vol. 131, no. 2, 2013.
- [25] D. R. Donohoe, N. Garge, X. Zhang, W. Sun, T. M. O'Connell, M. K. Bunger, and S. J. Bultman, "The microbiome and butyrate regulate energy metabolism and autophagy in the mammalian colon," *Cell Metabolism*, vol. 13, no. 5, pp. 517–526, 2011.
- [26] K. Meijer, P. De Vos, and M. G. Priebe, "Butyrate and other short-chain fatty acids as modulators of immunity: What relevance for health?," *Current Opinion in Clinical Nutrition and Metabolic Care*, vol. 13, no. 6, pp. 715–721, 2010.

Bibliography

- [27] V. Bunesova, C. Lacroix, and C. Schwab, “Mucin Cross-Feeding of Infant Bifidobacteria and *Eubacterium hallii*,” *Microbial Ecology*, vol. 75, no. 1, pp. 228–238, 2018.
- [28] M. S. Desai, A. M. Seekatz, N. M. Koropatkin, N. Kamada, C. A. Hickey, M. Wolter, N. A. Pudlo, S. Kitamoto, N. Terrapon, A. Muller, V. B. Young, B. Henrissat, P. Wilmes, T. S. Stappenbeck, G. Núñez, and E. C. Martens, “A Dietary Fiber-Deprived Gut Microbiota Degrades the Colonic Mucus Barrier and Enhances Pathogen Susceptibility,” *Cell*, vol. 167, no. 5, pp. 1339–1353.e21, 2016.
- [29] S. Rokhsfat, A. Lin, and E. M. Comelli, “Mucin–Microbiota Interaction During Postnatal Maturation of the Intestinal Ecosystem: Clinical Implications,” *Digestive Diseases and Sciences*, vol. 61, no. 6, pp. 1473–1486, 2016.
- [30] S. Karav, G. Casaburi, and S. A. Frese, “Reduced colonic mucin degradation in breastfed infants colonized by *Bifidobacterium longum* subsp. *infantis* EVC001,” *FEBS Open Bio*, vol. 8, no. 10, pp. 1649–1657, 2018.
- [31] N. Tsukuda, K. Yahagi, T. Hara, Y. Watanabe, H. Matsumoto, H. Mori, K. Higashi, H. Tsuji, S. Matsumoto, K. Kurokawa, and T. Matsuki, “Key bacterial taxa and metabolic pathways affecting gut short-chain fatty acid profiles in early life,” *The ISME Journal*, vol. 15, pp. 2574–2590, sep 2021.
- [32] T. Matsuki, K. Yahagi, H. Mori, H. Matsumoto, T. Hara, S. Tajima, E. Ogawa, H. Kodama, K. Yamamoto, T. Yamada, S. Matsumoto, and K. Kurokawa, “A key genetic factor for fucosyllactose utilization affects infant gut microbiota development,” *Nature Communications*, vol. 7, no. May, pp. 1–12, 2016.
- [33] S. Dogra, O. Sakwinska, S.-E. E. Soh, C. Ngom-Bru, W. M. Brück, B. Berger, H. Brüssow, Y. S. Lee, F. Yap, Y.-S. S. Chong, K. M. Godfrey, J. D. Holbrook, and GUSTO Study Group, “Dynamics of infant gut microbiota are influenced by delivery mode and gestational duration and are associated with subsequent adiposity,” *mBio*, vol. 6, no. 1, pp. 1–9, 2015.
- [34] D. Matharu, A. J. Ponsero, E. Dikareva, K. Korpela, K. L. Kolho, W. M. de Vos, and A. Salonen, “*Bacteroides* abundance drives birth mode dependent infant gut microbiota developmental trajectories,” *Frontiers in Microbiology*, vol. 13, 2022.
- [35] Q. Tang, G. Jin, G. Wang, T. Liu, X. Liu, B. Wang, and H. Cao, “Current Sampling Methods for Gut Microbiota: A Call for More Precise Devices,” *Frontiers in Cellular and Infection Microbiology*, vol. 10, no. April, 2020.
- [36] J. Rromano-Keeler, D. J. Moore, C. Wang, R. M. Brucker, C. Fannesbeck, J. C. Slaughter, H. Li, D. P. Curran, S. Meng, H. Correa, H. N. Lovvorn, Y. W. Tang, S. Bordenstein, A. L. George, and J. H. Weitkamp, “Early life

- establishment of site-specific microbial communities in the gut,” *Gut Microbes*, vol. 5, no. 2, pp. 192–201, 2014.
- [37] M. Rajilić-Stojanović, H. Smidt, and W. M. De Vos, “Diversity of the human gastrointestinal tract microbiota revisited,” *Environmental Microbiology*, vol. 9, no. 9, pp. 2125–2136, 2007.
- [38] D. N. Frank and N. R. Pace, “Gastrointestinal microbiology enters the metagenomics era,” *Current Opinion in Gastroenterology*, vol. 24, no. 1, pp. 4–10, 2008.
- [39] S. R. Gill, M. Pop, R. T. DeBoy, P. B. Eckburg, P. J. Turnbaugh, B. S. Samuel, J. I. Gordon, D. A. Relman, C. M. Fraser-Liggett, and K. E. Nelson, “Metagenomic Analysis of the Human Distal Gut Microbiome,” *Science*, vol. 312, pp. 1355–1359, jun 2006.
- [40] L. Beller, W. Debutte, G. Falony, S. Vieira-Silva, R. Y. Tito, M. Valles-Colomer, L. Rymenans, D. Jansen, L. Van Espen, M. I. Papadaki, C. Shi, C. K. Yinda, M. Zeller, K. Faust, M. Van Ranst, J. Raes, and J. Matthijssens, “Successional Stages in Infant Gut Microbiota Maturation,” *mBio*, vol. 12, no. 6, 2021.
- [41] M. C. Arrieta, L. T. Stiemsma, N. Amenyogbe, E. Brown, and B. Finlay, “The intestinal microbiome in early life: Health and disease,” *Frontiers in Immunology*, vol. 5, no. AUG, pp. 1–18, 2014.
- [42] H. M. Timmerman, N. B. Rutten, J. Boekhorst, D. M. Saulnier, G. A. Kortman, N. Contractor, M. Kullen, E. Floris, H. J. Harmsen, A. M. Vlieger, M. Kleerebezem, and G. T. Rijkers, “Intestinal colonisation patterns in breast-fed and formula-fed infants during the first 12 weeks of life reveal sequential microbiota signatures,” *Scientific Reports*, vol. 7, no. 1, pp. 1–10, 2017.
- [43] V. Sagheddu, V. Patrone, F. Miragoli, E. Puglisi, and L. Morelli, “Infant early gut colonization by Lachnospiraceae: High frequency of *Ruminococcus gnavus*,” *Frontiers in Pediatrics*, vol. 4, pp. 7–12, 2016.
- [44] V. N. Rocha Martin, C. Schwab, L. Krych, E. Voney, A. Geirnaert, C. Braegger, and C. Lacroix, “Colonization of *Cutibacterium avidum* during infant gut microbiota establishment,” *FEMS Microbiology Ecology*, vol. 95, no. 1, pp. 1–14, 2018.
- [45] Y. Liu, Z. Zheng, L. Yu, S. Wu, L. Sun, S. Wu, Q. Xu, S. Cai, N. Qin, and W. Bao, “Examination of the temporal and spatial dynamics of the gut microbiome in newborn piglets reveals distinct microbial communities in six intestinal segments,” *Scientific Reports*, vol. 9, no. 1, pp. 1–8, 2019.

Bibliography

- [46] X. Cao, A. Dong, G. Kang, X. Wang, L. Duan, H. Hou, T. Zhao, S. Wu, X. Liu, H. Huang, and R. Wu, “Modeling spatial interaction networks of the gut microbiota,” *Gut Microbes*, vol. 14, no. 1, 2022.
- [47] M. V. Gryaznova, Y. D. Dvoretzskaya, M. Y. Syromyatnikov, S. V. Shabunin, P. A. Parshin, E. V. Mikhaylov, N. A. Strelnikov, and V. N. Popov, “Changes in the Microbiome Profile in Different Parts of the Intestine in Piglets with Diarrhea,” *Animals*, vol. 12, no. 3, 2022.
- [48] K. R. James, T. Gomes, R. Elmentaite, N. Kumar, E. L. Gulliver, H. W. King, M. D. Stares, B. R. Bareham, J. R. Ferdinand, V. N. Petrova, K. Polański, S. C. Forster, L. B. Jarvis, O. Suchanek, S. Howlett, L. K. James, J. L. Jones, K. B. Meyer, M. R. Clatworthy, K. Saeb-Parsy, T. D. Lawley, and S. A. Teichmann, “Distinct microbial and immune niches of the human colon,” *Nature Immunology*, vol. 21, no. 3, pp. 343–353, 2020.
- [49] C. Tropini, K. A. Earle, K. C. Huang, and J. L. Sonnenburg, “The Gut Microbiome: Connecting Spatial Organization to Function,” *Cell Host and Microbe*, vol. 21, no. 4, pp. 433–442, 2017.
- [50] Y. Liu, S. Qin, Y. Song, Y. Feng, N. Lv, Y. Xue, F. Liu, S. Wang, B. Zhu, J. Ma, and H. Yang, “The Perturbation of Infant Gut Microbiota Caused by Cesarean Delivery Is Partially Restored by Exclusive Breastfeeding,” *Frontiers in Microbiology*, vol. 10, no. March, pp. 1–11, 2019.
- [51] S. J. Song, M. G. Dominguez-Bello, and R. Knight, “How delivery mode and feeding can shape the bacterial community in the infant gut,” *Cmaj*, vol. 185, no. 5, pp. 373–374, 2013.
- [52] E. Van Daele, K. Kamphorst, A. M. Vlieger, G. Hermes, C. Milani, M. Ventura, C. Belzer, H. Smidt, R. M. van Elburg, and J. Knol, “Effect of antibiotics in the first week of life on faecal microbiota development,” *Archives of Disease in Childhood: Fetal and Neonatal Edition*, pp. 603–610, 2022.
- [53] B. Berger, N. Porta, F. Foata, D. Grathwohl, M. Delley, D. Moine, A. Charpagne, L. Siegwald, P. Descombes, P. Alliet, G. Puccio, P. Steenhout, A. Mercenier, and N. Sprenger, “Linking human milk oligosaccharides, infant fecal community types, and later risk to require antibiotics,” *mBio*, vol. 11, no. 2, pp. 1–18, 2020.
- [54] D. H. Taft, Z. T. Lewis, N. Nguyen, S. Ho, C. Masarweh, V. Dunne-Castagna, D. J. Tancredi, M. N. Huda, C. B. Stephensen, K. Hinde, E. von Mutius, P. V. Kirjavainen, J. C. Dalphin, R. Lauener, J. Riedler, J. T. Smilowitz, J. B. German, A. L. Morrow, and D. A. Mills, “Bifidobacterium Species Colonization in Infancy: A Global Cross-Sectional Comparison by Population History of Breastfeeding,” *Nutrients*, vol. 14, no. 7, 2022.

-
- [55] N. A. Bokulich, J. Chung, T. Battaglia, N. Henderson, M. Jay, H. Li, A. D. Lieber, F. Wu, G. I. Perez-Perez, Y. Chen, W. Schweizer, X. Zheng, M. Contreras, M. G. Dominguez-Bello, and M. J. Blaser, “Antibiotics, birth mode, and diet shape microbiome maturation during early life,” *Science Translational Medicine*, vol. 8, no. 343, pp. 1–14, 2016.
- [56] P. Ferretti, E. Pasolli, A. Tett, F. Asnicar, V. Gorfer, S. Fedi, F. Armanini, D. T. Truong, S. Manara, M. Zolfo, F. Beghini, R. Bertorelli, V. De Sanctis, I. Bariletti, R. Canto, R. Clementi, M. Cologna, T. Crifò, G. Cusumano, S. Gottardi, C. Innamorati, C. Masè, D. Postai, D. Savoi, S. Duranti, G. A. Lugli, L. Mancabelli, F. Turrone, C. Ferrario, C. Milani, M. Mangifesta, R. Anzalone, A. Viappiani, M. Yassour, H. Vlamakis, R. Xavier, C. M. Collado, O. Koren, S. Tateo, M. Soffiati, A. Pedrotti, M. Ventura, C. Huttenhower, P. Bork, and N. Segata, “Mother-to-Infant Microbial Transmission from Different Body Sites Shapes the Developing Infant Gut Microbiome,” *Cell Host and Microbe*, vol. 24, no. 1, pp. 133–145.e5, 2018.
- [57] F. Fouhy, C. M. Guinane, S. Hussey, R. Wall, C. A. Ryan, E. M. Dempsey, B. Murphy, R. P. Ross, G. F. Fitzgerald, C. Stanton, and P. D. Cotter, “High-throughput sequencing reveals the incomplete, short-term recovery of infant gut microbiota following parenteral antibiotic treatment with ampicillin and gentamicin,” *Antimicrobial Agents and Chemotherapy*, vol. 56, no. 11, pp. 5811–5820, 2012.
- [58] S. Tanaka, T. Kobayashi, P. Songjinda, A. Tateyama, M. Tsubouchi, C. Kiyohara, T. Shirakawa, K. Sonomoto, and J. Nakayama, “Influence of antibiotic exposure in the early postnatal period on the development of intestinal microbiota,” *FEMS Immunology and Medical Microbiology*, vol. 56, no. 1, pp. 80–87, 2009.
- [59] C. Greenwood, A. L. Morrow, A. J. Lagomarcino, M. Altaye, D. H. Taft, Z. Yu, D. S. Newburg, D. V. Ward, and K. R. Schibler, “Early empiric antibiotic use in preterm infants is associated with lower bacterial diversity and higher relative abundance of enterobacter,” *Journal of Pediatrics*, vol. 165, no. 1, pp. 23–29, 2014.
- [60] S. Arboleya, B. Sánchez, C. Milani, S. Duranti, G. Solís, N. Fernández, C. G. De Los Reyes-Gavilán, M. Ventura, A. Margolles, and M. Gueimonde, “Intestinal microbiota development in preterm neonates and effect of perinatal antibiotics,” *Journal of Pediatrics*, vol. 166, no. 3, pp. 538–544, 2015.
- [61] O. Brunser, M. Gotteland, S. Cruchet, G. Figueroa, D. Garrido, and P. Steenhout, “Effect of a milk formula with prebiotics on the intestinal microbiota of infants after an antibiotic treatment,” *Pediatric Research*, vol. 59, no. 3, pp. 451–456, 2006.

Bibliography

- [62] D. A. Medina, F. Pinto, A. Ovalle, P. Thomson, and D. Garrido, “Prebiotics mediate microbial interactions in a consortium of the infant gut microbiome,” *International Journal of Molecular Sciences*, vol. 18, no. 10, pp. 1–16, 2017.
- [63] V. Bunesova, C. Lacroix, and C. Schwab, “Fucosyllactose and L-fucose utilization of infant *Bifidobacterium longum* and *Bifidobacterium kashiwanohense*,” *BMC Microbiology*, vol. 16, no. 1, pp. 1–12, 2016.
- [64] M. Böger, S. S. Van Leeuwen, A. Lammerts Van Bueren, and L. Dijkhuizen, “Structural Identity of Galactooligosaccharide Molecules Selectively Utilized by Single Cultures of Probiotic Bacterial Strains,” *Journal of Agricultural and Food Chemistry*, vol. 67, no. 50, pp. 13969–13977, 2019.
- [65] M. A. Underwood, J. B. German, C. B. Lebrilla, and D. A. Mills, “*Bifidobacterium longum* subspecies *infantis*: Champion colonizer of the infant gut,” *Pediatric Research*, vol. 77, no. 1, pp. 229–235, 2015.
- [66] O. Ballard and A. L. Morrow, “Human Milk Composition. Nutrients and Bioactive Factors,” *Pediatric Clinics of North America*, vol. 60, no. 1, pp. 49–74, 2013.
- [67] P. Chaturvedi, C. D. Warren, M. Altaye, A. L. Morrow, G. Ruiz-Palacios, L. K. Pickering, and D. S. Newburg, “Fucosylated human milk oligosaccharides vary between individuals and over the course of lactation,” *Glycobiology*, vol. 11, no. 5, pp. 365–372, 2001.
- [68] S. D. Durham, Z. Wei, D. G. Lemay, M. C. Lange, and D. Barile, “Creation of a milk oligosaccharide database, MilkOligoDB, reveals common structural motifs and extensive diversity across mammals,” *Scientific Reports*, vol. 13, no. 1, pp. 1–26, 2023.
- [69] H. C. Bergman and C. Housley, “Chemical analyses of American opossum (*Didelphys virginiana*) milk,” *Comparative Biochemistry And Physiology*, vol. 25, pp. 213–218, apr 1968.
- [70] S. Kijner, O. Kolodny, and M. Yassour, “Human milk oligosaccharides and the infant gut microbiome from an eco-evolutionary perspective,” *Current Opinion in Microbiology*, vol. 68, p. 102156, 2022.
- [71] G. Boehm, B. Stahl, J. Jelinek, J. Knol, V. Miniello, and G. E. Moro, “Prebiotic carbohydrates in human milk and formulas,” *Acta Paediatrica, International Journal of Paediatrics, Supplement*, vol. 94, no. 449, pp. 18–21, 2005.
- [72] R. J. Gibbons and B. Kapsimalis, “Estimates of the overall rate of growth of the intestinal microflora of hamsters, guinea pigs, and mice,” *Journal of Bacteriology*, vol. 93, no. 1, pp. 510–512, 1967.

- [73] A. W. Thorman, G. Adkins, S. C. Conrey, A. R. Burrell, Y. Yu, B. White, R. Burke, D. Haslam, D. C. Payne, M. A. Staat, A. L. Morrow, and D. S. Newburg, "Gut Microbiome Composition and Metabolic Capacity Differ by FUT2 Secretor Status in Exclusively Breastfed Infants," *Nutrients*, vol. 15, no. 2, pp. 1–13, 2023.
- [74] V. T. Pham, C. Lacroix, C. P. Braegger, and C. Chassard, "Lactate-utilizing community is associated with gut microbiota dysbiosis in colicky infants," *Scientific Reports*, vol. 7, no. 1, pp. 1–13, 2017.
- [75] R. Francavilla, M. Calasso, L. Calace, S. Siragusa, M. Ndagijimana, P. Vernocchi, L. Brunetti, G. Mancino, G. Tedeschi, E. Guerzoni, F. Indrio, L. Laghi, V. L. Miniello, M. Gobetti, and M. De Angelis, "Effect of lactose on gut microbiota and metabolome of infants with cow's milk allergy," *Pediatric Allergy and Immunology*, vol. 23, no. 5, pp. 420–427, 2012.
- [76] J. Cummings and G. Macfarlane, "The control and consequences of bacterial fermentation in the human colon," *Journal of Applied Bacteriology*, vol. 70, pp. 443–459, jun 1991.
- [77] A. Cederlund, Y. Kai-Larsen, G. Printz, H. Yoshio, G. Alvelius, H. Lagercrantz, R. Strömberg, H. Jörnvall, G. H. Gudmundsson, and B. Agerberth, "Lactose in Human Breast Milk an Inducer of Innate Immunity with Implications for a Role in Intestinal Homeostasis," *PLoS ONE*, vol. 8, no. 1, 2013.
- [78] L. T. Weaver, M. F. Laker, and R. Nelson, "Neonatal intestinal lactase activity," *Archives of Disease in Childhood*, vol. 61, no. 9, pp. 896–899, 1986.
- [79] W. C. Maclean, B. B. Fink, D. A. Schoeller, W. Wong, and P. D. Klein, "Lactose assimilation by full-term infants: Relation of [13C] and H₂ breath tests with fecal [13C] excretion," *Pediatric Research*, vol. 17, no. 8, pp. 629–633, 1983.
- [80] R. G. Heine, F. Alrefaee, P. Bachina, J. C. De Leon, L. Geng, S. Gong, J. A. Madrazo, J. Ngamphaiboon, C. Ong, and J. M. Rogacion, "Lactose intolerance and gastrointestinal cow's milk allergy in infants and children - Common misconceptions revisited," *World Allergy Organization Journal*, vol. 10, no. 1, pp. 1–8, 2017.
- [81] R. B. Jones, P. K. Berger, J. F. Plows, T. L. Alderete, J. Millstein, J. Fogel, S. N. Iablokov, D. A. Rodionov, A. L. Osterman, L. Bode, and M. I. Goran, "Lactose-reduced infant formula with added corn syrup solids is associated with a distinct gut microbiota in Hispanic infants," *Gut Microbes*, vol. 12, no. 1, 2020.
- [82] C. Schwab, H. J. Ruscheweyh, V. Bunesova, V. T. Pham, N. Beerenwinkel, and C. Lacroix, "Trophic interactions of infant bifidobacteria and eubacterium hallii during L-fucose and fucosyllactose degradation," *Frontiers in Microbiology*, vol. 8, pp. 1–14, 2017.

Bibliography

- [83] M. Centanni, S. A. Ferguson, I. M. Sims, A. Biswas, and G. W. Tannock, “Bifidobacterium bifidum ATCC 15696 and bifidobacterium breve 24b metabolic interaction based on 2-O-Fucosyl-lactose studied in steady-state cultures in a freter-style chemostat,” *Applied and Environmental Microbiology*, vol. 85, no. 7, pp. 1–17, 2019.
- [84] M. O’Connell Motherway, M. Kinsella, G. F. Fitzgerald, and D. Van Sinderen, “Transcriptional and functional characterization of genetic elements involved in galacto-oligosaccharide utilization by Bifidobacterium breve UCC2003,” *Microbial Biotechnology*, vol. 6, no. 1, pp. 67–79, 2013.
- [85] A. H. Viborg, T. Katayama, M. Abou Hachem, M. C. Andersen, M. Nishimoto, M. H. Clausen, T. Urashima, B. Svensson, and M. Kitaoka, “Distinct substrate specificities of three glycoside hydrolase family 42 β -galactosidases from Bifidobacterium longum subsp. infantis ATCC 15697,” *Glycobiology*, vol. 24, no. 2, pp. 208–216, 2014.
- [86] S. W. Hinz, M. I. Pastink, L. A. Van Den Broek, J. P. Vincken, and A. G. Vorage, “Bifidobacterium longum endogalactanase liberates galactotriose from type I galactans,” *Applied and Environmental Microbiology*, vol. 71, no. 9, pp. 5501–5510, 2005.
- [87] L. E. Tailford, E. H. Crost, D. Kavanaugh, and N. Juge, “Mucin glycan foraging in the human gut microbiome,” *Frontiers in Genetics*, vol. 6, mar 2015.
- [88] J. Gore, H. Youk, and A. Van Oudenaarden, “Snowdrift game dynamics and facultative cheating in yeast,” *Nature*, vol. 459, no. 7244, pp. 253–256, 2009.
- [89] N. W. Smith, P. R. Shorten, E. Altermann, N. C. Roy, and W. C. McNabb, “The Classification and Evolution of Bacterial Cross-Feeding,” *Frontiers in Ecology and Evolution*, vol. 7, no. May, pp. 1–15, 2019.
- [90] L. De Vuyst, F. Moens, M. Selak, A. Rivière, and F. Leroy, “Summer Meeting 2013: Growth and physiology of bifidobacteria,” *Journal of Applied Microbiology*, vol. 116, no. 3, pp. 477–491, 2014.
- [91] V. T. Pham, C. Lacroix, C. P. Braegger, and C. Chassard, “Early colonization of functional groups of microbes in the infant gut,” *Environmental microbiology*, vol. 18, no. 7, pp. 2246–2258, 2016.
- [92] S. H. Duncan, P. Louis, and H. J. Flint, “Lactate-Utilizing Bacteria, Isolated from Human Feces, That Produce Butyrate as a Major Fermentation Product,” *Applied and Environmental Microbiology*, vol. 70, no. 10, pp. 5810–5817, 2004.
- [93] J. M. Garber, H. Nothaft, B. Pluvinau, M. Stahl, X. Bian, S. Porfirio, A. Enriquez, J. Butcher, H. Huang, J. Glushka, E. Line, J. A. Gerlt, P. Azadi, A. Stintzi, A. B. Boraston, and C. M. Szymanski, “The gastrointestinal

- pathogen *Campylobacter jejuni* metabolizes sugars with potential help from commensal *Bacteroides vulgatus*,” *Communications Biology*, vol. 3, no. 1, pp. 1–11, 2020.
- [94] K. M. Ng, J. A. Ferreyra, S. K. Higginbottom, J. B. Lynch, P. C. Kashyap, S. Gopinath, N. Naidu, B. Choudhury, B. C. Weimer, D. M. Monack, and J. L. Sonnenburg, “Microbiota-liberated host sugars facilitate post-antibiotic expansion of enteric pathogens,” *Nature*, vol. 502, no. 7469, pp. 96–99, 2013.
- [95] M. Rogosa, “the Genus *Veillonella*. I. General Cultural, Ecological, and Biochemical Considerations,” *Journal of Bacteriology*, vol. 87, pp. 162–170, 1964.
- [96] B. Zabel, C. C. Yde, P. Roos, J. Marcussen, H. M. Jensen, K. Salli, J. Hirvonen, A. C. Ouwehand, and W. Morovic, “Novel Genes and Metabolite Trends in *Bifidobacterium longum* subsp. *infantis* Bi-26 Metabolism of Human Milk Oligosaccharide 2'-fucosyllactose,” *Scientific Reports*, vol. 9, no. 1, pp. 1–11, 2019.
- [97] D. Gonze, K. Z. Coyte, L. Lahti, and K. Faust, “Microbial communities as dynamical systems,” *Current Opinion in Microbiology*, vol. 44, pp. 41–49, 2018.
- [98] K. Faust and J. Raes, “Microbial interactions: From networks to models,” *Nature Reviews Microbiology*, vol. 10, no. 8, pp. 538–550, 2012.
- [99] P. Sen and M. Orešič, “Metabolic Modeling of Human Gut Microbiota on a Genome Scale: An Overview,” *Metabolites*, vol. 9, no. 2, p. 22, 2019.
- [100] R. A. Majewski and M. M. Domach, “Simple constrained-optimization view of acetate overflow in *E. coli*,” *Biotechnology and Bioengineering*, vol. 35, no. 7, pp. 732–738, 1990.
- [101] S. Magnúsdóttir and I. Thiele, “Modeling metabolism of the human gut microbiome,” *Current Opinion in Biotechnology*, vol. 51, pp. 90–96, 2018.
- [102] N. Martyushenko and E. Almaas, “ModelExplorer - software for visual inspection and inconsistency correction of genome-scale metabolic reconstructions,” *BMC Bioinformatics*, vol. 20, no. 1, pp. 1–8, 2019.
- [103] D. M. Versluis, R. Schoemaker, E. Looijesteijn, D. Muysken, P. V. Jeurink, M. Paques, J. M. W. Geurts, and R. M. H. Merks, “A Multiscale Spatiotemporal Model Including a Switch from Aerobic to Anaerobic Metabolism Reproduces Succession in the Early Infant Gut Microbiota,” *mSystems*, vol. 7, oct 2022.
- [104] T. E. Harris and F. S. Ross, “Fundamentals of a method for evaluating rail net capacities,” tech. rep., RAND Corporation, 1955.

Bibliography

- [105] G. T. Cocks, J. Aguilar, and E. C. Lin, “Evolution of L-1,2 propanediol catabolism in *Escherichia coli* by recruitment of enzymes for L-fucose and L-lactate metabolism,” *Journal of Bacteriology*, vol. 118, no. 1, pp. 83–88, 1974.
- [106] L. Bode, “Human milk oligosaccharides: Every baby needs a sugar mama,” *Glycobiology*, vol. 22, no. 9, pp. 1147–1162, 2012.
- [107] S. Gudmundsson and I. Thiele, “Computationally efficient flux variability analysis,” *BMC Bioinformatics*, vol. 11, no. 2, pp. 2–4, 2010.
- [108] J. Zanghellini, D. E. Ruckerbauer, M. Hanscho, and C. Jungreuthmayer, “Elementary flux modes in a nutshell: Properties, calculation and applications,” *Biotechnology Journal*, vol. 8, no. 9, pp. 1009–1016, 2013.
- [109] A. Vazquez and Z. N. Oltvai, “Macromolecular crowding explains overflow metabolism in cells,” *Scientific Reports*, vol. 6, pp. 1–7, 2016.
- [110] A. Hoppe, S. Hoffmann, and H. G. Holzhütter, “Including metabolite concentrations into flux balance analysis: Thermodynamic realizability as a constraint on flux distributions in metabolic networks,” *BMC Systems Biology*, vol. 1, pp. 1–12, 2007.
- [111] K. Zhuang, G. N. Vemuri, and R. Mahadevan, “Economics of membrane occupancy and respiro-fermentation,” *Molecular Systems Biology*, vol. 7, no. 500, pp. 1–9, 2011.
- [112] D. H. de Groot, J. Lischke, R. Muolo, R. Planqué, F. J. Bruggeman, and B. Teusink, “The common message of constraint-based optimization approaches: overflow metabolism is caused by two growth-limiting constraints,” *Cellular and Molecular Life Sciences*, vol. 77, no. 3, pp. 441–453, 2020.
- [113] A. Varma and B. Ø. Palsson, “Metabolic Flux Balancing: Basic Concepts, Scientific and Practical Use,” *Biotechnology*, vol. 12, no. October, pp. 994–998, 1994.
- [114] J. L. Reed and B. Palsson, “Thirteen years of building constraint-based in silico models of *Escherichia coli*,” *Journal of Bacteriology*, vol. 185, no. 9, pp. 2692–2699, 2003.
- [115] S. Stolyar, S. Van Dien, K. L. Hillesland, N. Pinel, T. J. Lie, J. A. Leigh, and D. A. Stahl, “Metabolic modeling of a mutualistic microbial community,” *Molecular Systems Biology*, vol. 3, no. 92, pp. 1–14, 2007.
- [116] R. Mahadevan, J. S. Edwards, and F. J. Doyle, “Dynamic flux balance analysis of diauxic growth,” *Biophysical Journal*, vol. 83, no. 3, pp. 1331–1340, 2002.

-
- [117] C. Baroukh, R. Muñoz-Tamayo, J. P. Steyer, and O. Bernard, “DRUM: A new framework for metabolic modeling under non-balanced growth. Application to the carbon metabolism of unicellular microalgae,” *PLoS ONE*, vol. 9, no. 8, 2014.
- [118] K. Zhuang, M. Izallalen, P. Mouser, H. Richter, C. Risso, R. Mahadevan, and D. R. Lovley, “Genome-scale dynamic modeling of the competition between *Rhodospirillum rubrum* and *Geobacter* in anoxic subsurface environments,” *ISME Journal*, vol. 5, no. 2, pp. 305–316, 2011.
- [119] B. Allen, J. Gore, and M. A. Nowak, “Spatial dilemmas of diffusible public goods,” *eLife*, vol. 2013, no. 2, pp. 1–11, 2013.
- [120] J. L. Welch, Y. Hasegawa, N. P. McNulty, J. I. Gordon, and G. G. Borisy, “Spatial organization of a model 15-member human gut microbiota established in gnotobiotic mice,” *Proceedings of the National Academy of Sciences of the United States of America*, vol. 114, no. 43, pp. E9105–E9114, 2017.
- [121] W. R. Harcombe, W. J. Riehl, I. Dukovski, B. R. Granger, A. Betts, A. H. Lang, G. Bonilla, A. Kar, N. Leiby, P. Mehta, C. J. Marx, and D. Segrè, “Metabolic resource allocation in individual microbes determines ecosystem interactions and spatial dynamics,” *Cell Reports*, vol. 7, no. 4, pp. 1104–1115, 2014.
- [122] M. J. A. van Hoek and R. M. H. Merks, “Emergence of microbial diversity due to cross-feeding interactions in a spatial model of gut microbial metabolism,” *BMC Systems Biology*, vol. 11, no. 1, pp. 1–18, 2017.
- [123] E. Bauer, J. Zimmermann, F. Baldini, I. Thiele, and C. Kaleta, “BacArena: Individual-based metabolic modeling of heterogeneous microbes in complex communities,” *PLoS Computational Biology*, vol. 13, no. 5, pp. 1–22, 2017.
- [124] Chan, Friedman, Wu, and Maranas, “Predicting the Longitudinally and Radially Varying Microbial Metabolic Modeling,” *Processes*, vol. 7, p. 394, 2019.
- [125] P. L. Stark and A. Lee, “The microbial ecology of the large bowel of breast-fed and formula-fed infants during the first year of life,” *Journal of Medical Microbiology*, vol. 15, no. 2, pp. 189–203, 1982.
- [126] B. M. Dotinga, J. P. Mintzer, J. E. Moore, J. B. Hulscher, A. F. Bos, and E. M. Kooi, “Maturation of Intestinal Oxygenation: A Review of Mechanisms and Clinical Implications for Preterm Neonates,” *Frontiers in Pediatrics*, vol. 8:354, 2020.
- [127] E. S. Friedman, K. Bittinger, T. V. Esipova, L. Hou, L. Chau, J. Jiang, C. Mesaros, P. J. Lund, X. Liang, G. A. FitzGerald, M. Goulian, D. Lee, B. A. Garcia, I. A. Blair, S. A. Vinogradov, and G. D. Wu, “Microbes vs. chemistry in the origin of the anaerobic gut lumen,” *Proceedings of the National Academy*

Bibliography

- of Sciences of the United States of America*, vol. 115, no. 16, pp. 4170–4175, 2018.
- [128] C. Lay, C. W. Chu, R. W. Purbojati, E. Acerbi, D. I. Drautz-Moses, P. F. de Sessions, S. Jie, E. Ho, Y. J. Kok, X. Bi, S. Chen, S. Y. Mak, M. C. Chua, A. E. Goh, W. C. Chiang, R. Rao, S. Chaithongwongwatthana, N. Khemapech, V. Chongsrisawat, R. Martin, Y. Koh, S. R. Lohar, I. C. H. Tan, W. A. Anng, C. Jie, N. Bartke, K. Ben-Amor, I. B. Renes, F. Wong, G. Roeselers, Y. S. Ho, M. L. Hibberd, S. C. Schuster, and J. Knol, “A synbiotic intervention modulates meta-omics signatures of gut redox potential and acidity in elective caesarean born infants,” *BMC Microbiology*, vol. 21, no. 1, pp. 1–17, 2021.
- [129] N. van Best, M. W. Hornef, P. H. Savelkoul, and J. Penders, “On the origin of species: Factors shaping the establishment of infant’s gut microbiota,” *Birth Defects Research Part C - Embryo Today: Reviews*, vol. 105, no. 4, pp. 240–251, 2015.
- [130] S. Magnúsdóttir and I. Thiele, “Modeling metabolism of the human gut microbiome,” *Current Opinion in Biotechnology*, vol. 51, pp. 90–96, 2018.
- [131] S. H. J. Chan, M. N. Simons, and C. D. Maranas, “SteadyCom: Predicting microbial abundances while ensuring community stability,” *PLoS Computational Biology*, vol. 13, no. 5, pp. 1–25, 2017.
- [132] I. Dukovski, D. Bajić, J. M. Chacón, M. Quintin, J. C. C. Vila, S. Sulheim, A. R. Pacheco, D. B. Bernstein, W. J. Riehl, K. S. Korolev, A. Sanchez, W. R. Harcombe, and D. Segrè, “A metabolic modeling platform for the computation of microbial ecosystems in time and space (COMETS),” *Nature Protocols*, vol. 16, pp. 5030–5082, nov 2021.
- [133] Q. K. Beg, A. Vazquez, J. Ernst, M. A. De Menezes, Z. Bar-Joseph, A. L. Barabási, and Z. N. Oltvai, “Intracellular crowding defines the mode and sequence of substrate uptake by *Escherichia coli* and constrains its metabolic activity,” *Proceedings of the National Academy of Sciences of the United States of America*, vol. 104, no. 31, pp. 12663–12668, 2007.
- [134] A. Monteagudo-Mera, J. C. Arthur, C. Jobin, T. Keku, J. M. Bruno-Barcena, and M. A. Azcarate-Peril, “High purity galacto-oligosaccharides enhance specific *Bifidobacterium* species and their metabolic activity in the mouse gut microbiome,” *Beneficial Microbes*, vol. 7, no. 2, pp. 247–264, 2016.
- [135] J. Valentin and C. Streffer, “Basic anatomical and physiological data for use in radiological protection: Reference values - ICRP Publication 89,” *Annals of the ICRP*, vol. 32, no. 3-4, pp. 1–277, 2002.
- [136] W. S. Davis, R. Parker Allen, B. E. Favara, and T. L. Slovis, “Neonatal small left colon syndrome,” *American journal of Roentgenology*, vol. 120, no. 2, pp. 322–329, 1974.

-
- [137] A. Swidsinski, V. Loening-Baucke, H. Verstraelen, S. Osowska, and Y. Doerffel, "Biostructure of Fecal Microbiota in Healthy Subjects and Patients With Chronic Idiopathic Diarrhea," *Gastroenterology*, vol. 135, no. 2, pp. 568–579, 2008.
- [138] P. Y. Hong, J. A. Croix, E. Greenberg, H. R. Gaskins, and R. I. Mackie, "Pyrosequencing-based analysis of the mucosal microbiota in healthy individuals reveals ubiquitous bacterial groups and micro-heterogeneity," *PLoS ONE*, vol. 6, no. 9, 2011.
- [139] D. Delsing, C. Lindner, H. van Dijck, E. Looijesteijn, E. S. Lima, M. Heerikhuizen, V. Agamennone, V. Triantis, and I. Bovee-Oudenhoven, "Gut microbiota modulating effects of GOS and 2'-FL studied by in vitro infant and toddler faecal fermentations," *ESPGHAN Conf. Abstr. N-P-006*, 2019.
- [140] R. Schuetz, L. Kuepfer, and U. Sauer, "Systematic evaluation of objective functions for predicting intracellular fluxes in *Escherichia coli*," *Molecular Systems Biology*, vol. 3, no. 119, 2007.
- [141] F. F. Rubaltelli and G. Largajolli, "Effect of Light Exposure on Gut Transit Time in Jaundiced Newborns," *Acta Pædiatrica*, vol. 62, no. 2, pp. 146–148, 1973.
- [142] J. S. Hyams, M. A. Geertsma, N. L. Etienne, and W. R. Treem, "Colonic hydrogen production in infants with colic," *The Journal of Pediatrics*, vol. 115, no. 4, pp. 592–594, 1989.
- [143] S. M. Lee, G. P. Donaldson, Z. Mikulski, S. Boyajian, K. Ley, and S. K. Mazmanian, "Bacterial colonization factors control specificity and stability of the gut microbiota," *Nature*, vol. 501, no. 7467, pp. 426–429, 2013.
- [144] M. J. van Hoek and R. M. H. Merks, "Redox balance is key to explaining full vs. partial switching to low-yield metabolism," *BMC Systems Biology*, vol. 6, 2012.
- [145] W. de Vries and A. H. Stouthamer, "Fermentation of glucose, lactose, galactose, mannitol, and xylose by bifidobacteria.," *Journal of Bacteriology*, vol. 96, no. 2, pp. 472–478, 1968.
- [146] S. F. Kotarski and A. A. Salyers, "Effect of long generation times on growth of *Bacteroides thetaiotaomicron* in carbohydrate-limited continuous culture," *Journal of Bacteriology*, vol. 146, no. 3, pp. 853–860, 1981.
- [147] F. P. J. Martin, S. Moco, I. Montoliu, S. Collino, L. Da Silva, S. Rezzi, R. Prieto, M. Kussmann, J. Inostroza, and P. Steenhout, "Impact of breast-feeding and high-and low-protein formula on the metabolism and growth of infants from overweight and obese mothers," *Pediatric Research*, vol. 75, no. 4, pp. 535–543, 2014.

Bibliography

- [148] C. Schwab, H. J. Ruscheweyh, V. Bunesova, V. T. Pham, N. Beerenwinkel, and C. Lacroix, “Trophic interactions of infant bifidobacteria and eubacterium hallii during L-fucose and fucosyllactose degradation,” *Frontiers in Microbiology*, vol. 8, no. JAN, pp. 1–14, 2017.
- [149] M. J. Wolin, S. Yerry, T. L. Miller, Y. Zhang, and S. Bank, “Changes in Production of Ethanol, Acids and H₂ from Glucose by the Fecal Flora of a 16- to 158-d-Old Breast-Fed Infant,” *The Journal of Nutrition*, vol. 128, no. 1, pp. 85–90, 1998.
- [150] S. L. Bridgman, M. B. Azad, C. J. Field, A. M. Haqq, A. B. Becker, P. J. Mandhane, P. Subbarao, S. E. Turvey, M. R. Sears, J. A. Scott, D. S. Wishart, and A. L. Kozyrskyj, “Fecal Short-Chain Fatty Acid Variations by Breastfeeding Status in Infants at 4 Months: Differences in Relative versus Absolute Concentrations,” *Frontiers in Nutrition*, vol. 4, no. April, 2017.
- [151] W. de Vries and A. H. Stouthamer, “Pathway of glucose fermentation in relation to the taxonomy of bifidobacteria.,” *Journal of bacteriology*, vol. 93, no. 2, pp. 574–576, 1967.
- [152] L. Albenberg, T. V. Esipova, C. P. Judge, K. Bittinger, J. Chen, A. Laughlin, S. Grunberg, R. N. Baldassano, J. D. Lewis, H. Li, S. R. Thom, F. D. Bushman, S. A. Vinogradov, and G. D. Wu, “Correlation between intraluminal oxygen gradient and radial partitioning of intestinal microbiota,” *Gastroenterology*, vol. 147, no. 5, pp. 1055–1063.e8, 2014.
- [153] L. Zheng, C. J. Kelly, and S. P. Colgan, “Physiologic hypoxia and oxygen homeostasis in the healthy intestine. A review in the theme: Cellular responses to hypoxia,” *American Journal of Physiology - Cell Physiology*, vol. 309, no. 6, pp. C350–C360, 2015.
- [154] K. Sim, A. G. Shaw, P. Randell, M. J. Cox, Z. E. McClure, M. S. Li, M. Haddad, P. R. Langford, W. O. Cookson, M. F. Moffatt, and J. S. Kroll, “Dysbiosis anticipating necrotizing enterocolitis in very premature infants,” *Clinical Infectious Diseases*, vol. 60, no. 3, pp. 389–397, 2015.
- [155] M. Mori, T. Hwa, O. C. Martin, A. De Martino, and E. Marinari, “Constrained Allocation Flux Balance Analysis,” *PLoS Computational Biology*, vol. 12, no. 6, pp. 1–24, 2016.
- [156] R. Balakrishnan, R. T. Silva, T. Hwa, and J. Cremer, “Suboptimal resource allocation in changing environments constrains response and growth in bacteria,” *Molecular Systems Biology*, vol. 17, no. 12, pp. 1–13, 2021.
- [157] E. M. Stansbridge, V. Walker, M. A. Hall, S. L. Smith, M. R. Millar, C. Bacon, and S. Chen, “Effects of feeding premature infants with Lactobacillus GG on gut fermentation,” *Archives of Disease in Childhood*, vol. 69, no. 5 SPEC NO, pp. 488–492, 1993.

- [158] G. Falony, K. Lazidou, A. Verschaeren, S. Weckx, D. Maes, and L. De Vuyst, "In vitro kinetic analysis of fermentation of prebiotic inulin-type fructans by *Bifidobacterium* species reveals four different phenotypes," *Applied and Environmental Microbiology*, vol. 75, no. 2, pp. 454–461, 2009.
- [159] J. Cremer, M. Arnoldini, and T. Hwa, "Effect of water flow and chemical environment on microbiota growth and composition in the human colon," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 114, no. 25, pp. 6438–6443, 2017.
- [160] J. Cremer, I. Segota, C. Y. Yang, M. Arnoldini, J. T. Sauls, Z. Zhang, E. Gutierrez, A. Groisman, and T. Hwa, "Effect of flow and peristaltic mixing on bacterial growth in a gut-like channel," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 113, no. 41, pp. 11414–11419, 2016.
- [161] S. K. Sarna, *Colonic Motility From Bench Side to Bedside*. San Rafael(CA): Morgan&Claypool Life Sciences, 2010.
- [162] S. Nurko, "Motility of the Colon and Anorectum," *NeoReviews*, vol. 7, no. 1, pp. e34–e48, 2006.
- [163] M. Juntunen, P. V. Kirjavainen, A. C. Ouwehand, S. J. Salminen, and E. Isolauri, "Adherence of probiotic bacteria to human intestinal mucus in healthy infants and during rotavirus infection," *Clinical and Diagnostic Laboratory Immunology*, vol. 8, no. 2, pp. 293–296, 2001.
- [164] F. Turroni, C. Peano, D. A. Pass, E. Feroni, M. Severgnini, M. J. Claesson, C. Kerr, J. Hourihane, D. Murray, F. Fuligni, M. Gueimonde, A. Margolles, G. de Bellis, P. W. O'Toole, D. van Sinderen, J. R. Marchesi, and M. Ventura, "Diversity of bifidobacteria within the infant gut microbiota," *PLoS ONE*, vol. 7, no. 5, pp. 20–24, 2012.
- [165] S. Magnúsdóttir, A. Heinken, R. M. T. Fleming, and I. Thiele, "Reply to "Challenges in modeling the human gut microbiome"," *Nature Biotechnology*, vol. 36, no. 8, pp. 686–691, 2018.
- [166] R. Schuetz, L. Kuepfer, and U. Sauer, "Systematic evaluation of objective functions for predicting intracellular fluxes in *Escherichia coli*," *Molecular Systems Biology*, vol. 3, no. 119, 2007.
- [167] B. Sánchez, C. G. De Los Reyes-Gavilán, and A. Margolles, "The F1F0-ATPase of *Bifidobacterium animalis* is involved in bile tolerance," *Environmental Microbiology*, vol. 8, no. 10, pp. 1825–1833, 2006.
- [168] F. Krzewinski, C. Brassart, F. Gavini, and S. Bouquelet, "Characterization of the lactose transport system in the strain *Bifidobacterium bifidum* DSM 20082," *Current Microbiology*, vol. 32, no. 6, pp. 301–307, 1996.

Bibliography

- [169] D. A. Sela, A. Adeuya, J. H. Kim, T. R. Whitehead, J. Chapman, D. S. Rokhsar, P. M. Richardson, A. Lapidus, J. B. German, N. P. Price, F. Chen, C. B. Lebrilla, and D. A. Mills, “The genome sequence of *Bifidobacterium longum* subsp. *infantis* reveals adaptations for milk utilization within the infant microbiome,” *Proceedings of the National Academy of Sciences*, vol. 105, no. 48, pp. 18964–18969, 2008.
- [170] C. Lessard, A. Cochu, J. D. Lemay, D. Roy, K. Vaillancourt, M. Frenette, S. Moineau, and C. Vadeboncoeur, “Phosphorylation of *Streptococcus salivarius* Lactose Permease (LacS) by HPr(His!P) and HPr(Ser-P)(His!P) and Effects on Growth,” *Journal of Bacteriology*, vol. 185, no. 23, pp. 6764–6772, 2003.
- [171] L. V. Holdeman, “Emendation of *Bacteroidaceae* and *Butyrivibrio* and Descriptions of *Desulfomonas* gen. nov. and Ten New Species in the Genera *Desulfomonas*, *Butyrivibrio*, *Eubacterium*, *Clostridium*, and *Ruminococcus*,” *International Journal of Systematic Bacteriology*, vol. 26, no. 2, pp. 238–252, 1976.
- [172] A. Flamholz, E. Noor, A. Bar-Even, and R. Milo, “EQuilibrator - The biochemical thermodynamics calculator,” *Nucleic Acids Research*, vol. 40, no. D1, pp. 770–775, 2012.
- [173] E. Noor, H. S. Haraldsdóttir, R. Milo, and R. M. Fleming, “Consistent Estimation of Gibbs Energy Using Component Contributions,” *PLoS Computational Biology*, vol. 9, no. 7, 2013.
- [174] P. S. Stewart, “Diffusion in biofilms,” *Journal of Bacteriology*, vol. 185, no. 5, pp. 1485–1491, 2003.
- [175] L. M. Grummer-Strawn, K. S. Scanlon, and S. B. Fein, “Infant feeding and feeding transitions during the first year of life,” *Pediatrics*, vol. 122, no. SUPPL. 2, 2008.
- [176] K. Kawasaki, “Diffusion constants near the critical point for time-dependent ising models. I,” *Physical Review*, vol. 145, no. 1, pp. 224–230, 1966.
- [177] N. Koumakis, C. Devailly, and W. C. Poon, “Motile bacteria in a critical fluid mixture,” *Physical Review E*, vol. 97, jun 2018.
- [178] P. O. Anderson and V. Valdés, “Variation of milk intake over time: Clinical and pharmacokinetic implications,” *Breastfeeding Medicine*, vol. 10, no. 3, pp. 142–144, 2015.
- [179] B. Gibson, D. J. Wilson, E. Feil, and A. Eyre-Walker, “The distribution of bacterial doubling times in the wild,” *Proceedings of the Royal Society B: Biological Sciences*, vol. 285, no. 1880, 2018.

- [180] F. Turrone, C. Milani, S. Duranti, G. A. Lugli, S. Bernasconi, A. Margolles, F. Di Pierro, D. Van Sinderen, and M. Ventura, “The infant gut microbiome as a microbial organ influencing host well-being,” *Italian Journal of Pediatrics*, vol. 46, no. 1, pp. 1–13, 2020.
- [181] S. Plöger, F. Stumpff, G. B. Penner, J. D. Schulzke, G. Gäbel, H. Martens, Z. Shen, D. Günzel, and J. R. Aschenbach, “Microbial butyrate and its role for barrier function in the gastrointestinal tract,” *Annals of the New York Academy of Sciences*, vol. 1258, no. 1, pp. 52–59, 2012.
- [182] X. Wu, Y. Wu, L. He, L. Wu, X. Wang, and Z. Liu, “Effects of the intestinal microbial metabolite butyrate on the development of colorectal cancer,” *Journal of Cancer*, vol. 9, no. 14, pp. 2510–2517, 2018.
- [183] T. Feehley, C. H. Plunkett, R. Bao, S. M. Choi Hong, E. Cullen, P. Belda-Ferre, E. Campbell, R. Aitoro, R. Nocerino, L. Paparo, J. Andrade, D. A. Antonopoulos, R. Berni Canani, and C. R. Nagler, “Healthy infants harbor intestinal bacteria that protect against food allergy,” *Nature Medicine*, vol. 25, no. 3, pp. 448–453, 2019.
- [184] H. M. Hamer, D. Jonkers, K. Venema, S. Vanhoutvin, F. J. Troost, and R. J. Brummer, “Review article: The role of butyrate on colonic function,” *Alimentary Pharmacology and Therapeutics*, vol. 27, no. 2, pp. 104–119, 2008.
- [185] G. Moro, S. Arslanoglu, B. Stahl, J. Jelinek, U. Wahn, and G. Boehm, “A mixture of prebiotic oligosaccharides reduces the incidence of atopic dermatitis during the first six months of age,” *Archives of Disease in Childhood*, vol. 91, no. 10, pp. 814–819, 2006.
- [186] N. Sprenger, H. Odenwald, A. K. Kukkonen, M. Kuitunen, E. Savilahti, and C. Kunz, “FUT2-dependent breast milk oligosaccharides and allergy at 2 and 5 years of age in infants with high hereditary allergy risk,” *European Journal of Nutrition*, vol. 56, no. 3, pp. 1293–1301, 2017.
- [187] K. C. Goehring, B. J. Marriage, J. S. Oliver, J. A. Wilder, E. G. Barrett, and R. H. Buck, “Similar to those who are breastfed, infants fed a formula containing 2'-fucosyllactose have lower inflammatory cytokines in a randomized controlled trial,” *Journal of Nutrition*, vol. 146, no. 12, pp. 2559–2566, 2016.
- [188] P. Van den Abbeele, C. Duysburgh, E. Vazquez, J. Chow, R. Buck, and M. Marzorati, “2'-Fucosyllactose alters the composition and activity of gut microbiota from formula-fed infants receiving complementary feeding in a validated intestinal model,” *Journal of Functional Foods*, vol. 61, no. July, p. 103484, 2019.
- [189] S. A. Shetty, S. Zuffa, T. P. N. Bui, S. Aalvink, H. Smidt, and W. M. De Vos, “Reclassification of *eubacterium hallii* as *Anaerobutyricum hallii* gen. nov., comb. nov., and description of *Anaerobutyricum soehngenii* sp. nov., a butyrate

Bibliography

- and propionate-producing bacterium from infant faeces,” *International Journal of Systematic and Evolutionary Microbiology*, vol. 68, no. 12, pp. 3741–3746, 2018.
- [190] M. J. Gnoth, C. Kunz, E. Kinne-Saffran, and S. Rudloff, “Human milk oligosaccharides are minimally digested in vitro,” *Journal of Nutrition*, vol. 130, no. 12, pp. 3014–3020, 2000.
- [191] Y. Song, C. Liu, and S. M. Finegold, “Bacteroides,” in *Bergey’s Manual of Systematics of Archaea and Bacteria*, pp. 1–24, Wiley, sep 2015.
- [192] J. M. Macy, L. G. Ljungdahl, and G. Gottschalk, “Pathway of succinate and propionate formation in *Bacteroides fragilis*,” *Journal of Bacteriology*, vol. 134, no. 1, pp. 84–91, 1978.
- [193] C. F. Scholz and M. Kilian, “The natural history of cutaneous propionibacteria, and reclassification of selected species within the genus propionibacterium to the proposed novel genera acidipropionibacterium gen. nov., cutibacterium gen. nov. and pseudopropionibacterium gen. nov.,” *International Journal of Systematic and Evolutionary Microbiology*, vol. 66, no. 11, pp. 4422–4432, 2016.
- [194] V. T. Pham, C. Chassard, E. Rifa, C. Braegger, A. Geirnaert, V. N. Rocha Martin, and C. Lacroix, “Lactate Metabolism Is Strongly Modulated by Fecal Inoculum, pH, and Retention Time in PolyFermS Continuous Colonic Fermentation Models Mimicking Young Infant Proximal Colon,” *mSystems*, vol. 4, no. 4, 2019.
- [195] M. Goodfellow, P. Kämpfer, H.-J. Busse, M. E. Trujillo, K.-i. Suzuki, W. Ludwig, and W. B. Whitman, *Bergey’s Manual of Systematic Bacteriology: Volume Five The Actinobacteria, Part A*. Springer, 2012.
- [196] P. S. La Rosa, B. B. Warner, Y. Zhou, G. M. Weinstock, E. Sodergren, C. M. Hall-Moore, H. J. Stevens, W. E. Bennett, N. Shaikh, L. A. Linneman, J. A. Hoffmann, A. Hamvas, E. Deych, B. A. Shands, W. D. Shannon, and P. I. Tarr, “Patterned progression of bacterial populations in the premature infant gut,” *Proceedings of the National Academy of Sciences of the United States of America*, vol. 111, no. 34, pp. 12522–12527, 2014.
- [197] A. Mitchell, G. H. Romano, B. Groisman, A. Yona, E. Dekel, M. Kupiec, O. Dahan, and Y. Pilpel, “Adaptive prediction of environmental changes by microorganisms,” *Nature*, vol. 460, no. 7252, pp. 220–224, 2009.
- [198] L. Heirendt, S. Arreckx, T. Pfau, S. N. Mendoza, A. Richelle, A. Heinken, H. S. Haraldsdóttir, J. Wachowiak, S. M. Keating, V. Vlasov, S. Magnúsdóttir, C. Y. Ng, G. Preciat, A. Žagare, S. H. J. Chan, M. K. Aurich, C. M. Clancy, J. Modamio, J. T. Sauls, A. Noronha, A. Bordbar, B. Cousins, D. C. El Assal, L. V. Valcarcel, I. Apaolaza, S. Ghaderi, M. Ahookhosh, M. Ben

- Guebila, A. Kostromins, N. Sompairac, H. M. Le, D. Ma, Y. Sun, L. Wang, J. T. Yurkovich, M. A. P. Oliveira, P. T. Vuong, L. P. El Assal, I. Kuperstein, A. Zinovyev, H. S. Hinton, W. A. Bryant, F. J. Aragón Artacho, F. J. Planes, E. Stalidzans, A. Maass, S. Vempala, M. Hucka, M. A. Saunders, C. D. Maranas, N. E. Lewis, T. Sauter, B. Ø. Palsson, I. Thiele, and R. M. T. Fleming, "Creation and analysis of biochemical constraint-based models using the COBRA Toolbox v.3.0," *Nature Protocols*, vol. 14, pp. 639–702, mar 2019.
- [199] R. M. Fleming, I. Thiele, and H. P. Nasheuer, "Quantitative assignment of reaction directionality in constraint-based models of metabolism: Application to *Escherichia coli*," *Biophysical Chemistry*, vol. 145, no. 2-3, pp. 47–56, 2009.
- [200] C. Rao, K. Z. Coyte, W. Bainter, R. S. Geha, C. R. Martin, and S. Rakoff-Nahoum, "Multi-kingdom ecological drivers of microbiota assembly in preterm infants," *Nature*, vol. 591, no. 7851, pp. 633–638, 2021.
- [201] G. A. Dykes and J. W. Hastings, "Selection and fitness in bacteriocin-producing bacteria," *Proceedings of the Royal Society B: Biological Sciences*, vol. 264, no. 1382, pp. 683–687, 1997.
- [202] S. Mills, F. Shanahan, C. Stanton, C. Hill, A. Coffey, and R. P. Ross, "Movers and shakers Influence of bacteriophages in shaping the mammalian gut microbiota," *Gut Microbes*, vol. 4, pp. 4–16, jan 2013.
- [203] P. Mastromarino, D. Capobianco, G. Campagna, N. Laforgia, P. Drimaco, A. Dileone, and M. E. Baldassarre, "Correlation between lactoferrin and beneficial microbiota in breast milk and infant's feces," *BioMetals*, vol. 27, no. 5, pp. 1077–1086, 2014.
- [204] P. Louis and H. J. Flint, "Formation of propionate and butyrate by the human colonic microbiota," *Environmental Microbiology*, vol. 19, no. 1, pp. 29–41, 2017.
- [205] J. A. Vogt and T. M. S. Wolever, "Fecal Acetate Is Inversely Related to Acetate Absorption from the Human Rectum and Distal Colon," *American Society for Nutritional Sciences*, vol. 133, no. 10, pp. 3145–3148, 2003.
- [206] S. S. Van Leeuwen, B. J. Kuipers, L. Dijkhuizen, and J. P. Kamerling, "1 H NMR analysis of the lactose/ β -galactosidase-derived galacto-oligosaccharide components of Vivinal® GOS up to DP5," *Carbohydrate Research*, vol. 400, pp. 59–73, 2014.
- [207] K. M. Van Laere, T. Abee, H. A. Schols, G. Beldman, and A. G. Voragen, "Characterization of a novel β -galactosidase from *Bifidobacterium adolescentis* DSM 20083 active towards transgalactooligosaccharides," *Applied and Environmental Microbiology*, vol. 66, no. 4, pp. 1379–1384, 2000.

Bibliography

- [208] D. P. Clark, “The fermentation pathways of *Escherichia coli*,” *FEMS Microbiology Letters*, vol. 63, no. 3, pp. 223–234, 1989.
- [209] S. Parche, M. Beleut, E. Rezzonico, D. Jacobs, F. Arigoni, F. Titgemeyer, and I. Jankovic, “Lactose-over-Glucose Preference in *Bifidobacterium longum* NCC2705: *glcP*, Encoding a Glucose Transporter, Is Subject to Lactose Repression,” *Journal of Bacteriology*, vol. 188, pp. 1260–1265, feb 2006.
- [210] M. J. Pichler, C. Yamada, B. Shuoker, C. Alvarez-Silva, A. Gotoh, M. L. Leth, E. Schoof, T. Katoh, M. Sakanaka, T. Katayama, C. Jin, N. G. Karlsson, M. Arumugam, S. Fushinobu, and M. Abou Hachem, “Butyrate producing colonic Clostridiales metabolise human milk oligosaccharides and cross feed on mucin via conserved pathways,” *Nature Communications*, vol. 11, no. 1, 2020.
- [211] K. A. Hamed, P. R. Dormitzer, C. K. Su, and D. A. Relman, “*Haemophilus parainfluenzae* endocarditis: application of a molecular approach for identification of pathogenic bacterial species,” *Clinical Infectious Diseases*, vol. 19, no. 4, pp. 677–683, 1994.
- [212] C. C. Uranga, P. Arroyo, B. M. Duggan, W. H. Gerwick, and A. Edlund, “Commensal Oral *Rothia mucilaginosa* Produces Enterobactin, a Metal-Chelating Siderophore,” *mSystems*, vol. 5, no. 2, 2020.
- [213] E. T. Hillman, A. J. Kozik, C. A. Hooker, J. L. Burnett, Y. Heo, V. A. Kiesel, C. J. Nevins, J. M. Oshiro, M. M. Robins, R. D. Thakkar, S. T. Wu, and S. R. Lindemann, “Comparative genomics of the genus *Roseburia* reveals divergent biosynthetic pathways that may influence colonic competition among species,” *Microbial Genomics*, vol. 6, no. 7, pp. 7–24, 2020.
- [214] S. I. Yokoyama and T. Suzuki, “Isolation and characterization of a novel equol-producing bacterium from human feces,” *Bioscience, Biotechnology and Biochemistry*, vol. 72, no. 10, pp. 2660–2666, 2008.
- [215] P. Vos, G. Garrity, D. Jones, N. R. Krieg, W. Ludwig, F. A. Rainey, K.-H. Schleifer, and W. B. Whitman, *Bergey’s manual of systematic bacteriology: Volume 3: The Firmicutes*, vol. 3. Springer Science & Business Media, 2011.
- [216] M. Allen, D. Poggiali, K. Whitaker, T. R. Marshall, and R. A. Kievit, “Raincloud plots: A multi-platform tool for robust data visualization [version 1; peer review: 2 approved],” *Wellcome Open Research*, vol. 4, pp. 1–52, 2019.
- [217] J. Fu, B. Wei, T. Wen, M. E. V. Johansson, X. Liu, E. Bradford, K. a. Thomson, S. McGee, L. Mansour, M. Tong, J. M. McDaniel, T. J. Sferra, J. R. Turner, H. Chen, G. C. Hansson, J. Braun, and L. Xia, “Loss of intestinal core 1-derived O-glycans causes spontaneous colitis in mice.,” *The Journal of clinical investigation*, vol. 121, pp. 1657–66, apr 2011.

- [218] R. H. Yolken, C. Ojeh, I. A. Khatri, U. Sajjan, and J. F. Forstner, “Intestinal Mucins Inhibit Rotavirus Replication in an Oligosaccharide-Dependent Manner,” *Journal of Infectious Diseases*, vol. 169, pp. 1002–1006, may 1994.
- [219] A.-C. Midtvedt, B. Carlstedt-Duke, and T. Midtvedt, “Establishment of a Mucin-Degrading Intestinal Microflora During the First Two Years of Human Life,” *Journal of Pediatric Gastroenterology and Nutrition*, vol. 18, pp. 321–326, apr 1994.
- [220] M. Sakanaka, A. Gotoh, K. Yoshida, T. Odamaki, H. Koguchi, J. Z. Xiao, M. Kitaoka, and T. Katayama, “Varied pathways of infant gut-associated Bifidobacterium to assimilate human milk oligosaccharides: Prevalence of the gene set and its correlation with bifidobacteria-rich microbiota formation,” *Nutrients*, vol. 12, no. 1, pp. 1–21, 2020.
- [221] M. K. McGuire, C. L. Meehan, M. A. McGuire, J. E. Williams, J. Foster, D. W. Sellen, E. W. Kamau-Mbuthia, E. W. Kamundia, S. Mbugua, S. E. Moore, A. M. Prentice, L. J. Kvist, G. E. Otoo, S. L. Brooker, W. J. Price, B. Shafii, C. Placek, K. A. Lackey, B. Robertson, S. Manzano, L. Ruíz, J. M. Rodríguez, R. G. Pareja, and L. Bode, “What’s normal? Oligosaccharide concentrations and profiles in milk produced by healthy women vary geographically,” *American Journal of Clinical Nutrition*, vol. 105, no. 5, pp. 1086–1100, 2017.
- [222] D. Garrido, S. Ruiz-Moyano, D. G. Lemay, D. A. Sela, J. B. German, and D. A. Mills, “Comparative transcriptomics reveals key differences in the response to milk oligosaccharides of infant gut-associated bifidobacteria,” *Scientific Reports*, vol. 5, no. May, pp. 1–18, 2015.
- [223] D. Garrido, S. Ruiz-Moyano, R. Jimenez-Espinoza, H. J. Eom, D. E. Block, and D. A. Mills, “Utilization of galactooligosaccharides by *Bifidobacterium longum* subsp. *infantis* isolates,” *Food Microbiology*, vol. 33, no. 2, pp. 262–270, 2013.
- [224] M. N. Ojima, L. Jiang, A. A. Arzamasov, K. Yoshida, T. Odamaki, J. Xiao, A. Nakajima, M. Kitaoka, J. Hirose, T. Urashima, T. Katoh, A. Gotoh, D. van Sinderen, D. A. Rodionov, A. L. Osterman, M. Sakanaka, and T. Katayama, “Priority effects shape the structure of infant-type *Bifidobacterium* communities on human milk oligosaccharides,” *ISME Journal*, vol. 16, no. 9, pp. 2265–2279, 2022.
- [225] Z. T. Lewis, S. M. Totten, J. T. Smilowitz, M. Popovic, E. Parker, D. G. Lemay, M. L. Van Tassell, M. J. Miller, Y. S. Jin, J. B. German, C. B. Lebrilla, and D. A. Mills, “Maternal fucosyltransferase 2 status affects the gut bifidobacterial communities of breastfed infants,” *Microbiome*, vol. 3, no. 1, pp. 15–17, 2015.
- [226] P. Thomson, D. A. Medina, and D. Garrido, “Human milk oligosaccharides and infant gut bifidobacteria: Molecular strategies for their utilization,” *Food Microbiology*, vol. 75, pp. 37–46, 2018.

Bibliography

- [227] J. Cremer, A. Melbinger, K. Wienand, T. Henriquez, H. Jung, and E. Frey, “Cooperation in Microbial Populations: Theory and Experimental Model Systems,” *Journal of Molecular Biology*, vol. 431, no. 23, pp. 4599–4644, 2019.
- [228] H. Celiker and J. Gore, “Competition between species can stabilize public-goods cooperation within a species,” *Molecular Systems Biology*, vol. 8, no. 621, pp. 1–9, 2012.
- [229] D. M. Versluis, R. Schoemaker, E. Looijesteijn, J. M. W. Geurts, and R. M. H. Merks, “2'-Fucosyllactose helps butyrate producers outgrow competitors in infant gut microbiota simulations,” *iScience*, vol. 27, 2024.
- [230] P. L. Møller, F. Jørgensen, O. C. Hansen, S. M. Madsen, and P. Stougaard, “Intra- and Extracellular β -Galactosidases from *Bifidobacterium bifidum* and *B. infantis*: Molecular Cloning, Heterologous Expression, and Comparative Characterization,” *Applied and Environmental Microbiology*, vol. 67, no. 5, pp. 2276–2283, 2001.
- [231] M. O’Connell Motherway, M. Kinsella, G. F. Fitzgerald, and D. Van Sinderen, “Transcriptional and functional characterization of genetic elements involved in galacto-oligosaccharide utilization by *Bifidobacterium breve* UCC2003,” *Microbial Biotechnology*, vol. 6, no. 1, pp. 67–79, 2013.
- [232] R. J. Kelly, S. Rouquier, D. Giorgi, G. G. Lennon, and J. B. Lowe, “Sequence and expression of a candidate for the human Secretor blood group $\alpha(1,2)$ fucosyltransferase gene (FUT2). Homozygosity for an enzyme-inactivating nonsense mutation commonly correlates with the non-secretor phenotype,” *Journal of Biological Chemistry*, vol. 270, no. 9, pp. 4640–4649, 1995.
- [233] W. Holms, “The Central Metabolic Pathways of *Escherichia coli*: Relationship between Flux and Control at a Branch Point, Efficiency of Conversion to Biomass, and Excretion of Acetate,” *Current Topics in Cellular Regulation*, pp. 69–105, 1986.
- [234] A. L. Francl, J. L. Hoeflinger, and M. J. Miller, “Identification of lactose phosphotransferase systems in *Lactobacillus gasser* ATCC 33323 required for lactose utilization,” *Microbiology*, vol. 158, no. 4, pp. 944–952, 2012.
- [235] A. Gotoh, T. Katoh, M. Sakanaka, Y. Ling, C. Yamada, S. Asakuma, T. Urashima, Y. Tomabechi, A. Katayama-Ikegami, S. Kurihara, K. Yamamoto, G. Harata, F. He, J. Hirose, M. Kitaoka, S. Okuda, and T. Katayama, “Sharing of human milk oligosaccharides degradants within bifidobacterial communities in faecal cultures supplemented with *Bifidobacterium bifidum*,” *Scientific Reports*, vol. 8, no. 1, pp. 1–14, 2018.
- [236] F. Turrone, C. Milani, S. Duranti, L. Mancabelli, M. Mangifesta, A. Viapiani, G. A. Lugli, C. Ferrario, L. Gioiosa, A. Ferrarini, J. Li, P. Palanza,

- M. Delledonne, D. Van Sinderen, and M. Ventura, “Deciphering bifidobacterial-mediated metabolic interactions and their impact on gut microbiota by a multi-omics approach,” *ISME Journal*, vol. 10, no. 7, pp. 1656–1668, 2016.
- [237] J. P. H. Wong, M. Fischer-Stettler, S. C. Zeeman, T. J. Battin, and A. Persat, “Fluid flow structures gut microbiota biofilm communities by distributing public goods,” *Proceedings of the National Academy of Sciences*, vol. 120, p. 2017, jun 2023.
- [238] R. F. Inglis, J. M. Biernaskie, A. Gardner, and R. Kümmerli, “Presence of a loner strain maintains cooperation and diversity in well-mixed bacterial communities,” *Proceedings of the Royal Society B: Biological Sciences*, vol. 283, no. 1822, 2016.
- [239] R. J. Lindsay, B. J. Pawlowska, and I. Gudelj, “Privatization of public goods can cause population decline,” *Nature Ecology and Evolution*, vol. 3, no. 8, pp. 1206–1216, 2019.
- [240] A. M. Feist and B. O. Palsson, “The biomass objective function,” *Current Opinion in Microbiology*, vol. 13, no. 3, pp. 344–349, 2010.
- [241] C. Belzer, L. W. Chia, S. Aalvink, B. Chamlagain, V. Piironen, J. Knol, and W. M. de Vos, “Microbial metabolic networks at the mucus layer lead to diet-independent butyrate and vitamin B12 production by intestinal symbionts,” *mBio*, vol. 8, no. 5, 2017.
- [242] J. M. Hascoët, C. Hubert, F. Rochat, H. Legagneur, S. Gaga, S. Emady-Azar, and P. G. Steenhout, “Effect of formula composition on the development of infant gut microbiota,” *Journal of Pediatric Gastroenterology and Nutrition*, vol. 52, no. 6, pp. 756–762, 2011.
- [243] A. P. Corfield, “The interaction of the gut microbiota with the mucus barrier in health and disease in human,” *Microorganisms*, vol. 6, no. 3, pp. 18–26, 2018.
- [244] S. Thurl, M. Munzert, J. Henker, G. Boehm, B. Mller-Werner, J. Jelinek, and B. Stahl, “Variation of human milk oligosaccharides in relation to milk groups and lactational periods,” *British Journal of Nutrition*, vol. 104, no. 9, pp. 1261–1271, 2010.
- [245] T. Shiba, Y. Aiba, H. Ishikawa, A. Ushiyama, A. Takagi, T. Mine, and Y. Koga, “The suppressive effect of bifidobacteria on *Bacteroides vulgatus*, a putative pathogenic microbe in inflammatory bowel disease,” *Microbiology and Immunology*, vol. 47, no. 6, pp. 371–378, 2003.
- [246] Y. Belkaid and T. W. Hand, “Role of the microbiota in immunity and inflammation,” *Cell*, vol. 157, no. 1, pp. 121–141, 2014.

Bibliography

- [247] E. Klement, R. V. Cohen, J. Boxman, A. Joseph, and S. Reif, “Breastfeeding and risk of inflammatory bowel disease: a systematic review with meta-analysis,” *The American Journal of Clinical Nutrition*, vol. 80, pp. 1342–1352, nov 2004.
- [248] Y. Kang, H. Park, B. H. Choe, and B. Kang, “The Role and Function of Mucins and Its Relationship to Inflammatory Bowel Disease,” *Frontiers in Medicine*, vol. 9, no. May, pp. 1–7, 2022.
- [249] I. Azagra-Boronat, M. Massot-Cladera, J. Mayneris-Perxachs, K. Knipping, B. Van’t Land, S. Tims, B. Stahl, J. Garsen, À. Franch, M. Castell, M. J. Rodríguez-Lagunas, and F. J. Pérez-Cano, “Immunomodulatory and Prebiotic Effects of 2'-Fucosyllactose in Suckling Rats,” *Frontiers in immunology*, vol. 10, no. July, p. 1773, 2019.
- [250] C. Agostoni, E. Riva, and M. Giovannini, “Dietary fiber in weaning foods of young children,” *Pediatrics*, vol. 96, no. 5 II SUPPL., pp. 1002–1005, 1995.
- [251] M. Sakanaka, M. E. Hansen, A. Gotoh, T. Katoh, K. Yoshida, T. Odamaki, H. Yachi, Y. Sugiyama, S. Kurihara, J. Hirose, T. Urashima, J. zhong Xiao, M. Kitaoka, S. Fukiya, A. Yokota, L. L. Leggio, M. A. Hachem, and T. Katayama, “Evolutionary adaptation in fucosyllactose uptake systems supports bifidobacteria-infant symbiosis,” *Science Advances*, vol. 5, no. 8, pp. 1–16, 2019.
- [252] H. Ashida, A. Miyake, M. Kiyohara, J. Wada, E. Yoshida, H. Kumagai, T. Katayama, and K. Yamamoto, “Two distinct α -L-fucosidases from *Bifidobacterium bifidum* are essential for the utilization of fucosylated milk oligosaccharides and glycoconjugates,” *Glycobiology*, vol. 19, no. 9, pp. 1010–1017, 2009.
- [253] D. Szatmári, P. Sárkány, B. Kocsis, T. Nagy, A. Miseta, S. Barkó, B. Longauer, R. C. Robinson, and M. Nyitrai, “Intracellular ion concentrations and cation-dependent remodelling of bacterial MreB assemblies,” *Scientific Reports*, vol. 10, no. 1, pp. 1–13, 2020.
- [254] J. L. Slonczewski, M. Fujisawa, M. Dopson, and T. A. Krulwich, “Cytoplasmic pH Measurement and Homeostasis in Bacteria and Archaea,” *Advances in Microbial Physiology*, vol. 55, 2009.
- [255] H. Siegmundfeldt, K. Björn Rechinger, and M. Jakobsen, “Use of fluorescence ratio imaging for intracellular pH determination of individual bacterial cells in mixed cultures,” *Microbiology*, vol. 145, no. 7, pp. 1703–1709, 1999.
- [256] W. H. Press, *Numerical recipes 3rd edition: The art of scientific computing*. Cambridge university press, 2007.

- [257] N. D. Rivera-Chaparro, M. Cohen-Wolkowicz, and R. G. Greenberg, “Dosing antibiotics in neonates: Review of the pharmacokinetic data,” *Future Microbiology*, vol. 12, no. 11, pp. 1001–1016, 2017.
- [258] A. H. Kim, M. P. Hogarty, V. C. Harris, and M. T. Baldrige, “The Complex Interactions Between Rotavirus and the Gut Microbiota,” *Frontiers in Cellular and Infection Microbiology*, vol. 10, jan 2021.
- [259] M. Pop, A. W. Walker, J. Paulson, B. Lindsay, M. Antonio, M. A. Hossain, J. Oundo, B. Tamboura, V. Mai, I. Astrovskaya, H. C. Bravo, R. Rance, M. Stares, M. M. Levine, S. Panchalingam, K. Kotloff, U. N. Ikumapayi, C. Ebruke, M. Adeyemi, D. Ahmed, F. Ahmed, M. T. Alam, R. Amin, S. Siddiqui, J. B. Ochieng, E. Ouma, J. Juma, E. Mailu, R. Omore, J. G. Morris, R. F. Breiman, D. Saha, J. Parkhill, J. P. Nataro, and O. C. Stine, “Diarrhea in young children from low-income countries leads to large-scale alterations in wintestinal microbiota composition,” *Genome Biology*, vol. 15, no. 6, pp. 1–12, 2014.
- [260] E. Goksör, B. Alm, R. Pettersson, P. Möllborg, L. Erdes, N. Åberg, and G. Wennergren, “Early fish introduction and neonatal antibiotics affect the risk of asthma into school age,” *Pediatric Allergy and Immunology*, vol. 24, no. 4, pp. 339–344, 2013.
- [261] B. C. Oosterloo, R. M. van Elburg, N. B. Rutten, C. M. Bunkers, C. E. Crijs, C. B. Meijssen, J. H. Oudshoorn, G. T. Rijkers, C. K. van der Ent, and A. M. Vlieger, “Wheezing and infantile colic are associated with neonatal antibiotic treatment,” *Pediatric Allergy and Immunology*, vol. 29, no. 2, pp. 151–158, 2018.
- [262] S. Salvatore, M. E. Baldassarre, A. Di Mauro, N. Laforgia, S. Tafuri, F. P. Bianchi, E. Dattoli, L. Morando, L. Pensabene, F. Meneghin, D. Dilillo, V. Mancini, V. Talarico, F. Tandoi, G. Zuccotti, and M. Agosti, “Neonatal Antibiotics and Prematurity Are Associated with an Increased Risk of Functional Gastrointestinal Disorders in the First Year of Life,” *Journal of Pediatrics*, vol. 212, pp. 44–51, 2019.
- [263] M. F. Endika, D. J. Barnett, C. E. Klostermann, H. A. Schols, I. C. Arts, J. Penders, A. Nauta, H. Smidt, and K. Venema, “Microbiota-dependent influence of prebiotics on the resilience of infant gut microbiota to amoxicillin/clavulanate perturbation in an in vitro colon model,” *Frontiers in Microbiology*, vol. 14, no. May, 2023.
- [264] M. Reyman, M. A. van Houten, R. L. Watson, M. L. J. Chu, K. Arp, W. J. de Waal, I. Schiering, F. B. Plötz, R. J. Willems, W. van Schaik, E. A. Sanders, and D. Bogaert, “Effects of early-life antibiotics on the developing infant gut microbiome and resistome: a randomized trial,” *Nature Communications*, vol. 13, no. 1, 2022.

Bibliography

- [265] D. L. Dai, C. Petersen, C. Hoskinson, K. L. Del Bel, A. B. Becker, T. J. Moraes, P. J. Mandhane, B. B. Finlay, E. Simons, A. L. Kozyrskyj, D. M. Patrick, P. Subbarao, L. Bode, M. B. Azad, and S. E. Turvey, “Breastfeeding enrichment of *B. longum* subsp. *infantis* mitigates the effect of antibiotics on the microbiota and childhood asthma risk,” *Med*, vol. 4, no. 2, pp. 92–112.e5, 2023.
- [266] M. K. Gibson, T. S. Crofts, and G. Dantas, “Antibiotics and the developing infant gut microbiota and resistome,” *Current Opinion in Microbiology*, vol. 27, pp. 51–56, 2015.
- [267] M. F. Laursen, M. I. Bahl, and T. R. Licht, “Settlers of our inner surface-factors shaping the gut microbiota from birth to toddlerhood,” *FEMS Microbiology Reviews*, vol. 45, no. 4, pp. 1–14, 2021.
- [268] A. T. Reese, E. H. Cho, B. Klitzman, S. P. Nichols, N. A. Wisniewski, M. M. Villa, H. K. Durand, S. Jiang, F. S. Midani, S. N. Nimmagadda, T. M. O’connell, J. P. Wright, M. A. Deshusses, and L. A. David, “Antibiotic-induced changes in the microbiota disrupt redox dynamics in the gut,” *eLife*, vol. 7, pp. 1–22, 2018.
- [269] S. E. Winter, M. G. Winter, M. N. Xavier, P. Thiennimitr, V. Poon, A. M. Keestra, R. C. Laughlin, G. Gomez, J. Wu, S. D. Lawhon, I. E. Popova, S. J. Parikh, L. G. Adams, R. M. Tsohis, V. J. Stewart, and A. J. Bäumlner, “Host-derived nitrate boosts growth of *E. coli* in the inflamed gut,” *Science*, vol. 339, no. 6120, pp. 708–711, 2013.
- [270] M. Yassour, T. Vatanen, H. Siljander, A. M. Hämäläinen, T. Härkönen, S. J. Ryhänen, E. A. Franzosa, H. Vlamakis, C. Huttenhower, D. Gevers, E. S. Lander, M. Knip, and R. J. Xavier, “Natural history of the infant gut microbiome and impact of antibiotic treatment on bacterial strain diversity and stability,” *Science Translational Medicine*, vol. 8, no. 343, 2016.
- [271] A. J. Eherer and J. S. Fordtran, “Fecal osmotic gap and pH in experimental diarrhea of various causes,” *Gastroenterology*, vol. 103, no. 2, pp. 545–551, 1992.
- [272] K. Shimizu, I. Seiki, Y. Goto, and T. Murata, “Measurement of the intestinal pH in mice under various conditions reveals alkalization induced by antibiotics,” *Antibiotics*, vol. 10, no. 2, pp. 1–10, 2021.
- [273] K. Faust, F. Bauchinger, B. Laroche, S. de Buyl, L. Lahti, A. D. Washburne, D. Gonze, and S. Widder, “Signatures of ecological processes in microbial community time series,” *Microbiome*, vol. 6, no. 1, pp. 1–13, 2018.
- [274] I. Ormaasen, K. Rudi, D. B. Diep, and L. Snipen, “Metagenome-mining indicates an association between bacteriocin presence and strain diversity in the infant gut,” *BMC Genomics*, vol. 24, no. 1, pp. 1–12, 2023.

- [275] K. L. Fields and S. E. Luria, “Effects of Colicins E1 and K on Cellular Metabolism,” *Journal of Bacteriology*, vol. 97, pp. 64–77, jan 1969.
- [276] T. L. Czárán, R. F. Hoekstra, and L. Pagie, “Chemical warfare between microbes promotes biodiversity,” *Proceedings of the National Academy of Sciences*, vol. 99, pp. 786–790, jan 2002.
- [277] D. Podlesny and W. F. Fricke, “Strain inheritance and neonatal gut microbiota development: A meta-analysis,” *International Journal of Medical Microbiology*, vol. 311, no. 3, p. 151483, 2021.
- [278] S. Shimamura, F. Abe, N. Ishibashi, H. Miyakawa, T. Yaeshima, T. Araya, and M. Tomita, “Relationship Between Oxygen Sensitivity and Oxygen Metabolism of Bifidobacterium Species,” *Journal of Dairy Science*, vol. 75, no. 12, pp. 3296–3306, 1992.
- [279] A. Goelzer, V. Fromion, and G. Scorletti, “Cell design in bacteria as a convex optimization problem,” *Automatica*, vol. 47, no. 6, pp. 1210–1218, 2011.
- [280] D. Rios Garza, D. Gonze, H. Zafeiropoulos, B. Liu, and K. Faust, “Metabolic models of human gut microbiota: Advances and challenges,” *Cell Systems*, vol. 14, no. 2, pp. 109–121, 2023.
- [281] S. Labarthe, B. Polizzi, T. Phan, T. Goudon, M. Ribot, and B. Laroche, “A mathematical model to investigate the key drivers of the biogeography of the colon microbiota,” *Journal of Theoretical Biology*, vol. 462, pp. 552–581, 2019.
- [282] M. Arnoldini, J. Cremer, and T. Hwa, “Bacterial growth, flow, and mixing shape human gut microbiota density and composition,” *Gut microbes*, vol. 9, no. 6, pp. 559–566, 2018.
- [283] D. Labavić, C. Loverdo, and A. F. Bitbol, “Hydrodynamic flow and concentration gradients in the gut enhance neutral bacterial diversity,” *Proceedings of the National Academy of Sciences of the United States of America*, vol. 119, no. 1, 2022.
- [284] T. Jiang, F. L. Suarez, M. D. Levitt, S. E. Nelson, and E. E. Ziegler, “Gas production by feces of infants,” *Journal of Pediatric Gastroenterology and Nutrition*, vol. 32, no. 5, pp. 534–541, 2001.
- [285] A. L. Morrow, A. J. Lagomarcino, K. R. Schibler, D. H. Taft, Z. Yu, B. Wang, M. Altaye, M. Wagner, D. Gevers, D. V. Ward, M. A. Kennedy, C. Huttenhower, and D. S. Newburg, “Early microbial and metabolomic signatures predict later onset of necrotizing enterocolitis in preterm infants,” *Microbiome*, vol. 1, no. 1, pp. 1–16, 2013.

Bibliography

- [286] Z. T. Yu, C. Chen, and D. S. Newburg, “Utilization of major fucosylated and sialylated human milk oligosaccharides by isolated human gut microbes,” *Glycobiology*, vol. 23, no. 11, pp. 1281–1292, 2013.
- [287] A. Heinken, J. Hertel, G. Acharya, D. A. Ravcheev, M. Nyga, O. E. Okpala, M. Hogan, S. Magnúsdóttir, F. Martinelli, B. Nap, G. Preciat, J. N. Edirisinghe, C. S. Henry, R. M. Fleming, and I. Thiele, “Genome-scale metabolic reconstruction of 7,302 human microorganisms for personalized medicine,” *Nature Biotechnology*, 2023.
- [288] M. E. Beber, M. G. Gollub, D. Mozaffari, K. M. Shebek, A. I. Flamholz, R. Milo, and E. Noor, “EQuilibrator 3.0: A database solution for thermodynamic constant estimation,” *Nucleic Acids Research*, vol. 50, no. D1, pp. D603–D609, 2022.
- [289] K. Faust and J. Raes, “Rules of the game for microbiota,” *Nature*, vol. 534, no. 7606, pp. 182–183, 2016.
- [290] M. Ghoul and S. Mitri, “The Ecology and Evolution of Microbial Competition,” *Trends in Microbiology*, vol. 24, no. 10, pp. 833–845, 2016.
- [291] A. Bashan, T. E. Gibson, J. Friedman, V. J. Carey, S. T. Weiss, E. L. Hohmann, and Y. Y. Liu, “Universality of human microbial dynamics,” *Nature*, vol. 534, no. 7606, pp. 259–262, 2016.
- [292] S. Shibasaki and S. Mitri, “A spatially structured mathematical model of the gut microbiome reveals factors that increase community stability,” *iScience*, vol. 26, no. 9, p. 107499, 2023.
- [293] A. Marantos, N. Mitarai, and K. Sneppen, “From kill the winner to eliminate the winner in open phage-bacteria systems,” *PLoS Computational Biology*, vol. 18, no. 8, pp. 1–15, 2022.
- [294] D. Bajić, J. C. Vila, Z. D. Blount, and A. Sánchez, “On the deformability of an empirical fitness landscape by microbial evolution,” *Proceedings of the National Academy of Sciences of the United States of America*, vol. 115, no. 44, pp. 11286–11291, 2018.
- [295] B. Van Dijk, J. Meijer, T. D. Cuypers, and P. Hogeweg, “Trusting the hand that feeds: Microbes evolve to anticipate a serial transfer protocol as individuals or collectives,” *BMC Evolutionary Biology*, vol. 19, no. 1, pp. 1–18, 2019.
- [296] S. A. Becker, A. M. Feist, M. L. Mo, G. Hannum, B. Palsson, and M. J. Hergard, “Quantitative prediction of cellular metabolism with constraint-based models: The COBRA Toolbox,” *Nature Protocols*, vol. 2, no. 3, pp. 727–738, 2007.

-
- [297] A. R. Zomorodi and C. D. Maranas, “OptCom: A multi-level optimization framework for the metabolic modeling and analysis of microbial communities,” *PLoS Computational Biology*, vol. 8, no. 2, 2012.
- [298] J. Chen, J. A. Gomez, K. Höffner, P. Phalak, P. I. Barton, and M. A. Henson, “Spatiotemporal modeling of microbial metabolism,” *BMC Systems Biology*, vol. 10, no. 1, pp. 1–13, 2016.
- [299] P. Phalak, J. Chen, R. P. Carlson, and M. A. Henson, “Metabolic modeling of a chronic wound biofilm consortium predicts spatial partitioning of bacterial species,” *BMC Systems Biology*, vol. 10, no. 1, pp. 1–20, 2016.
- [300] B. Teusink, A. Wiersma, D. Molenaar, C. Francke, W. M. De Vos, R. J. Siezen, and E. J. Smid, “Analysis of growth of *Lactobacillus plantarum* WCFS1 on a complex medium using a genome-scale metabolic model,” *Journal of Biological Chemistry*, vol. 281, no. 52, pp. 40041–40048, 2006.
- [301] D. R. Garza, M. C. Van Verk, M. A. Huynen, and B. E. Dutilh, “Towards predicting the environmental metabolome from metagenomics with a mechanistic model,” *Nature Microbiology*, vol. 3, no. 4, pp. 456–460, 2018.
- [302] C. Diener, S. M. Gibbons, and O. Resendis-Antonio, “MICOM: Metagenome-Scale Modeling To Infer Metabolic Interactions in the Gut Microbiota,” *mSystems*, vol. 5, no. 1, 2020.
- [303] A. Noronha, J. Modamio, Y. Jarosz, E. Guerard, N. Sompairac, G. Preciat, A. D. Daniëlsdóttir, M. Krecke, D. Merten, H. S. Haraldsdóttir, A. Heinken, L. Heirendt, S. Magnúsdóttir, D. A. Ravcheev, S. Sahoo, P. Gawron, L. Friscioni, B. Garcia, M. Prendergast, A. Puente, M. Rodrigues, A. Roy, M. Rouquaya, L. Wiltgen, A. Žagare, E. John, M. Krueger, I. Kuperstein, A. Zinovyevev, R. Schneider, R. M. Fleming, and I. Thiele, “The Virtual Metabolic Human database: Integrating human and gut microbiome metabolism with nutrition and disease,” *Nucleic Acids Research*, vol. 47, no. D1, pp. D614–D624, 2019.
- [304] D. Popp and F. Centler, “ μ BialSim: Constraint-Based Dynamic Simulation of Complex Microbiomes,” *Frontiers in Bioengineering and Biotechnology*, vol. 8, no. June, 2020.
- [305] E. Karimian and E. Motamedian, “ACBM: An Integrated Agent and Constraint Based Modeling Framework for Simulation of Microbial Communities,” *Scientific Reports*, vol. 10, no. 1, pp. 1–10, 2020.
- [306] B. Yu, I. Dukovski, D. Kong, J. Bobrow, A. Ostrinskaya, D. Segrè, and T. Thorsen, “Experiments and simulations on short chain fatty acid production in a colonic bacterial community,” *bioRxiv*, 2018.

Bibliography

- [307] A. R. Pacheco, M. Moel, and D. Segrè, “Costless metabolic secretions as drivers of interspecies interactions in microbial ecosystems,” *Nature communications*, vol. 10, no. 1, p. 103, 2019.
- [308] J. J. Faith, J. L. Guruge, M. Charbonneau, S. Subramanian, H. Seedorf, A. L. Goodman, J. C. Clemente, R. Knight, A. C. Heath, R. L. Leibel, M. Rosenbaum, and J. I. Gordon, “The long-term stability of the human gut microbiota,” *Science*, vol. 341, no. 6141, 2013.
- [309] M. A. Henson and P. Phalak, “Suboptimal community growth mediated through metabolite crossfeeding promotes species diversity in the gut microbiota,” *PLoS Computational Biology*, vol. 14, no. 10, pp. 1–21, 2018.
- [310] Q. Garrigues, E. Apper, S. Chastant, and H. Mila, “Gut microbiota development in the growing dog: A dynamic process influenced by maternal, environmental and host factors,” *Frontiers in Veterinary Science*, vol. 9, 2022.
- [311] R. B. Guevarra, J. H. Lee, S. H. Lee, M. J. Seok, D. W. Kim, B. N. Kang, T. J. Johnson, R. E. Isaacson, and H. B. Kim, “Piglet gut microbial shifts early in life: Causes and effects,” *Journal of Animal Science and Biotechnology*, vol. 10, no. 1, pp. 1–10, 2019.
- [312] C. Zhang, J. Chen, Q. Wu, B. Xu, and Z. Huang, “The Gut Microbiota of Young Asian Elephants with Different Milk-Containing Diets,” *Animals*, vol. 13, no. 5, 2023.
- [313] J. Kambe, Y. Sasaki, R. Inoue, S. Tomonaga, T. Kinjo, G. Watanabe, W. Jin, and K. Nagaoka, “Analysis of infant microbiota composition and the relationship with breast milk components in the asian elephant (*Elephas maximus*) at the zoo,” *Journal of Veterinary Medical Science*, vol. 82, no. 7, pp. 983–989, 2020.
- [314] Y. Shigeno, H. Zhang, T. Banno, K. Usuda, T. Nochi, R. Inoue, G. Watanabe, W. Jin, Y. Benno, and K. Nagaoka, “Gut microbiota development in mice is affected by hydrogen peroxide produced from amino acid metabolism during lactation,” *FASEB Journal*, vol. 33, no. 3, pp. 3343–3352, 2019.
- [315] C. Kunz, S. Rudloff, W. Schad, and D. Braun, “Lactose-derived oligosaccharides in the milk of elephants: comparison with human milk,” *British Journal of Nutrition*, vol. 82, pp. 391–399, nov 1999.
- [316] M. Messer and K. R. Kerry, “Milk Carbohydrates of the Echidna and the Platypus,” *Science*, vol. 180, pp. 201–203, apr 1973.
- [317] M. A. O’Malley, “The nineteenth century roots of ‘everything is everywhere’,” *Nature Reviews Microbiology*, vol. 5, no. 8, pp. 647–651, 2007.

- [318] J. Walter, A. M. Armet, B. B. Finlay, and F. Shanahan, “Establishing or Exaggerating Causality for the Gut Microbiome: Lessons from Human Microbiota-Associated Rodents,” *Cell*, vol. 180, no. 2, pp. 221–232, 2020.
- [319] N. D. Aluthge, W. A. Tom, A. C. Bartenslager, T. E. Burkey, P. S. Miller, K. D. Heath, C. Kreikemeier-Bower, H. Kittana, R. J. Schmaltz, A. E. Ramer-Tait, and S. C. Fernando, “Differential longitudinal establishment of human fecal bacterial communities in germ-free porcine and murine models,” *Communications Biology*, vol. 3, no. 1, pp. 1–14, 2020.
- [320] G. Trujillo-de Santiago, M. J. Lobo-Zegers, S. L. Montes-Fonseca, Y. S. Zhang, and M. M. Alvarez, “Gut-microbiota-on-a-chip: an enabling field for physiological research,” *Microphysiological Systems*, vol. 1, no. 27, pp. 1–1, 2018.
- [321] N. Ashammakhi, R. Nasiri, N. R. de Barros, P. Tebon, J. Thakor, M. Goudie, A. Shamloo, M. G. Martin, and A. Khademhosseni, “Gut-on-a-chip: Current progress and future opportunities,” *Biomaterials*, vol. 255, no. June, 2020.