

# Common principles and best practices for engineering microbiomes

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**Abstract** | Despite broad scientific interest in harnessing the power of Earth's microbiomes, knowledge gaps hinder their efficient use for addressing urgent societal and environmental challenges. We argue that structuring research and technology developments around a design–build–test–learn (DBTL) cycle will advance microbiome engineering and spur new discoveries of the basic scientific principles governing microbiome function. In this Review, we present key elements of an iterative DBTL cycle for microbiome engineering, focusing on generalizable approaches, including top-down and bottom-up design processes, synthetic and self-assembled construction methods, and emerging tools to analyse microbiome function. These approaches can be used to harness microbiomes for broad applications related to medicine, agriculture, energy and the environment. We also discuss key challenges and opportunities of each approach and synthesize them into best practice guidelines for engineering microbiomes. We anticipate that adoption of a DBTL framework will rapidly advance microbiome-based biotechnologies aimed at improving human and animal health, agriculture and enabling the bioeconomy.

## Microbiome science

Discovery and testing of fundamental principles governing microbiome assembly and function.

## Microbiome engineering

Leveraging fundamental scientific principles and quantitative design to create microbiomes that perform desired functions.

## Syntrophy

An obligately mutualistic process that is mediated by metabolite cross-feeding between two or more organisms that cannot be catalysed by one organism alone.

Microbial communities have seemingly limitless capabilities, driving Earth's biogeochemical cycles and occupying every environmental niche<sup>1,2</sup>. Engineers and scientists have tapped into this power for a long time; for example, by manipulating soil microbiomes to increase crop productivity<sup>3</sup>, by stimulating naturally occurring or introduced microbiomes to remediate contaminated groundwater<sup>4</sup> or by building reactor microbiomes to recover valuable resources from wastewater<sup>5</sup>. Although these accomplishments highlight the valuable functions of microbiomes, the vast majority of the microbial world's transformative capabilities have yet to be unlocked and harnessed. Recent insights driven by DNA sequencing have shed light on the high genetic diversity of not-yet-cultured microorganisms and their crucial roles in diverse ecosystems<sup>6,7</sup>, providing a window on potentially novel biotechnology applications.

In recognition of this unlocked potential, funding agencies and the international science community have called for a global effort to advance microbiome research<sup>8,9</sup>. These initiatives have recognized the need for microbiome science to move beyond descriptive studies and embrace a systems approach that generates the mechanistic, predictive and actionable understanding that makes possible rational microbiome engineering<sup>8</sup>.

However, achieving this transition is hindered by the lack of tractable experimental systems that permit the detailed functional investigation of microbiomes, the large pool of microbiome gene and metabolite functions that remain unknown<sup>10</sup>, the many uncharacterized interactions (for example, syntrophy) between microorganisms<sup>11</sup>, inadequate tools to accurately measure and simulate microbiome functions across time and space, and the limited availability of approaches to precisely manipulate microbiome structure and function.

Integrating basic scientific discovery with engineering can overcome these challenges and develop innovative solutions that support sustainable natural resources management and human and animal health. In particular, engineering approaches can be used to create experimental systems that permit the testing of conceptual knowledge and extraction of new knowledge that advances microbiome research. To accelerate both scientific discovery and translation into innovative solutions, we propose that microbiome engineering adopt an iterative design–build–test–learn (DBTL) cycle to structure research and the technology development process. This cycle involves developing an initial microbiome design or preliminary model system to achieve a defined engineering goal, building the microbiome,

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**Metaphenotypes**

Sets of emergent functions of a microbiome resulting from the interactions between individual microbial genomes (metagenome) and their interaction with the environment.

**Ecological engineering**

The process of designing and operating bioreactors and other engineered systems to foster the development of specific microbial communities that can perform desired functions.

**Functional guilds**

Groups of organisms that use similar resources (for example, electron donors, electron acceptors or carbon source) and occupy a similar ecological niche.

testing its function against a set of specified metrics to determine whether the design–build solution(s) produced the design objective (that is, establish causation), learning what worked and what did not work (and why) and incorporating new knowledge into the decision-making process of subsequent DBTL cycles (FIG. 1). This approach has been used successfully in manufacturing<sup>12</sup>, metabolic engineering<sup>13</sup> and entrepreneurship ('build, measure, learn')<sup>14</sup>, and could rapidly advance our ability to develop much needed tools and design concepts for harnessing microbiomes, delivering innovative solutions and advancing scientific knowledge.

In this Review, we present key elements of an iterative DBTL approach that can be implemented to advance the rational engineering of microbiomes for functions that benefit society. We review diverse approaches to harness microbiomes in medical, agricultural, energy and environmental applications, and identify current challenges and opportunities associated with implementing each DBTL phase. Finally, we discuss how the DBTL cycle can be applied to build model systems to establish basic principles of microbial ecosystems and provide an outlook on the frontiers of microbiome engineering.

**Designing microbiomes**

Because of the high complexity and limited understanding of molecular-scale microbiome processes, microbiome design has conventionally followed a top-down approach. This approach tries to predict how ecosystem-level controls can create a microbiome with desired functions. However, recent advances in multi-omics have provided opportunities to design microbiomes from the bottom up by predicting how the control of metabolic networks and their interactions can create a microbiome

with desired functions. Combined, these approaches offer complementary strategies to design microbiomes for specific engineering goals, ranging from sustainable wastewater treatment to curing microbiome-associated human diseases.

**Top-down design.** Rather than deciding which organisms and detailed metabolic pathways to use a priori, the top-down approach uses carefully selected environmental variables (such as certain substrate loading rates, mean cell retention times and redox conditions) that force an existing microbiome (naturally occurring or inoculated) through ecological selection to perform the desired biological processes (or 'metaphenotypes')<sup>15</sup> (FIG. 2). Here, 'top' refers to the ecosystem in which the desired biological process occurs and 'top-down design' denotes the methods used to predict how manipulation of the ecosystem's physical, chemical and biological processes (that is, ecosystem processes) obtains the desired function. Predicting how to manipulate an ecosystem is informed by principles of ecological engineering<sup>16</sup> (also known as microbial resource management<sup>17</sup> or microbial community engineering<sup>18</sup>). This requires engineers to conceptualize the system as an ecosystem model that captures system inputs and outputs, physicochemical conditions (pH, temperature, redox potential and so on), known abiotic and biotic processes, and environmental variables, and how their manipulation may promote or inhibit the biological process(es) being optimized<sup>19,20</sup>. Subsequently, mathematical modelling is used to perform mass balance analysis of chemicals and relevant microorganisms in the system and simulate chemical and biochemical transformation rates. These process-based models capture microbiome functions by representing key physiological or functional guilds of microorganisms (such as methanogens, fermenters, nitrifiers or phototrophs) with specific stoichiometric parameters (growth and product yields) and kinetic parameters (maximum specific growth rate, substrate uptake rate and substrate affinity)<sup>21–23</sup>. The models can also integrate equations describing the three-dimensional physical transport processes (diffusion, advection and dispersion) acting on chemicals and microorganisms, which are especially important in spatially structured systems such as biofilms<sup>24,25</sup>.

**Bottom-up design.** Although the conventional top-down design approach for microbiome engineering offers a framework for macro-scale processes and has been widely successful for wastewater treatment<sup>21</sup> and bioremediation<sup>4</sup>, it often neglects the complex in situ metabolic networks driving microbial and linked chemical transformations<sup>26</sup> and ignores processes that depend on intricate interactions between community members; for example, syntrophic interactions through direct interspecies electron transfer<sup>27</sup>. As a consequence, molecular-scale microbiome processes are often ignored during design, limiting system optimization through molecular-scale mechanistic insight. Recent advances in multi-omics and automation technology (for example, in metagenomics and microfluidics) have enabled researchers to develop bottom-up approaches and

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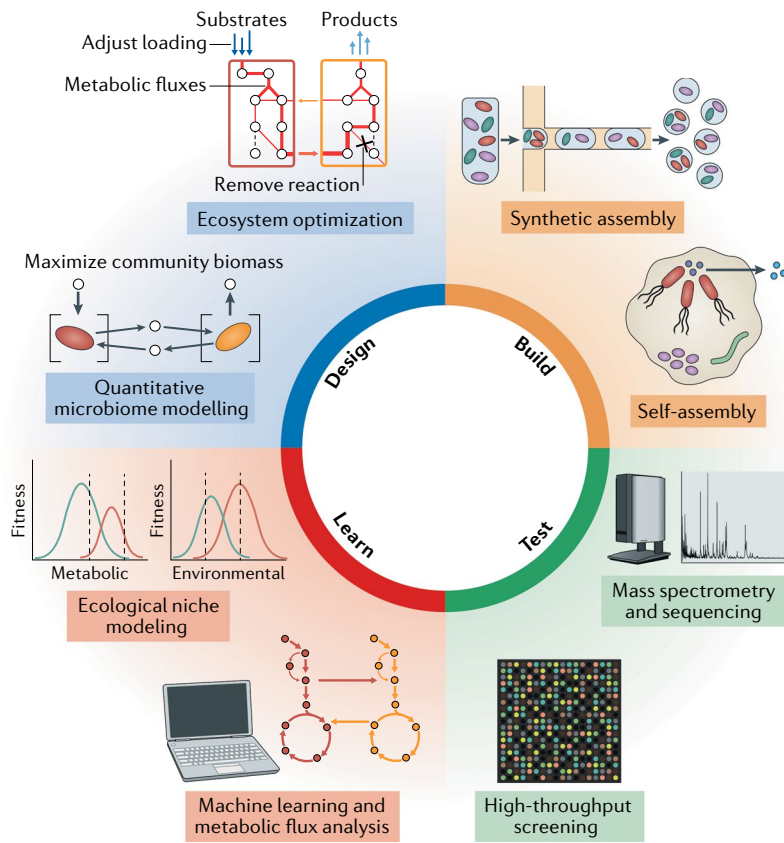
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**Fig. 1 | The design–build–test–learn cycle for microbiome engineering.** The key aspects and approaches of each phase of the design–build–test–learn cycle are presented. The cycle starts with a defined engineering objective that determines the design and produces an engineered microbiome that performs the desired function(s).

**Keystone species**

An organism that has a disproportionately large effect on maintaining the microbiome’s function and microbial interactions (both between microorganisms and with the environment).

**Flux balance analysis**

A constraint-based mathematical modelling technique for simulating metabolic fluxes through a metabolic network reconstructed from genomic information.

**Ensemble modelling**

Use of multiple models to address uncertainty by simulating a set of possibilities and selecting those consistent with measured data.

**Machine learning**

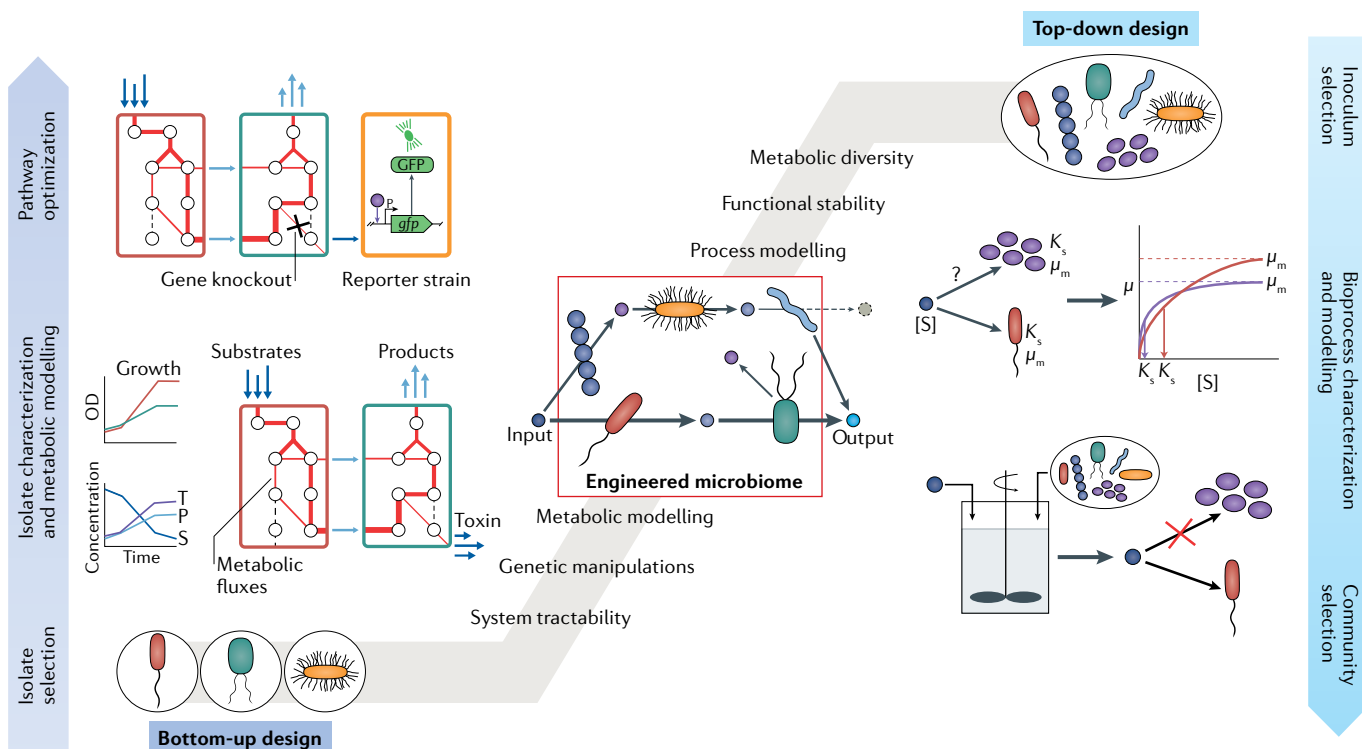
A technique used to build predictive models through patterns and inferences obtained from sample data rather than explicit or mechanistic relationships.

focus on engineering the microbiome’s metabolic network and microbial interactions. Here, ‘bottom’ refers to the metabolic networks of individual organisms in the microbiome (expressed from their genomes) and ‘bottom-up design’ denotes the methods used to predict how metabolic flux through these interacting networks generates the desired output. The general design process is to obtain the genomes of individual members of the microbiome<sup>28</sup> (especially keystone species<sup>29</sup>, when known<sup>30</sup>), reconstruct their metabolic networks<sup>31,32</sup> and use modelling<sup>33</sup> and/or network analysis tools<sup>34</sup> to guide design (FIG. 2). Existing constraint-based methods such as flux balance analysis provide a suitable framework for exploring which combinations of chemical transformations are possible using quantitative models, in which individual populations’ reactions and metabolites can be compartmentalized and metabolic fluxes within and between populations can be simulated using optimality principles<sup>35</sup>. These models can also simulate steady-state flux distributions over time and space<sup>36,37</sup> and can be integrated into process-based and/or individual-based models<sup>38</sup> to predict metaphenotypes, self-organizing spatial patterns and other emergent behaviours. Such bottom-up tools provide the engineer with a computational framework to systematically evaluate the metabolic networks driving biological processes and ecological interactions, and a platform for rationally designing microbiomes with specific properties, such

as distributed pathways<sup>39,40</sup>, modular species interactions<sup>41</sup>, community resistance and resilience<sup>42</sup> and spatiotemporal organization<sup>43</sup> that optimize ecosystem function and stability. However, most of these bottom-up design examples are based on simple communities with model organisms (such as *Escherichia coli* and *Saccharomyces cerevisiae*) that have engineered dependencies. Therefore, extending these designs to systems with non-model organisms of tens to hundreds of different species will require deeper insights into their metabolism and the principles governing their interactions and higher-order behaviour.

There are major challenges to implementing bottom-up design, including inaccurate and/or incomplete metabolic network reconstructions, unknown functions of many genes, proteins and metabolites, poorly understood evolutionary pressures driving individual and community-level phenotypes and limited understanding of gene, metabolic and ecosystem regulatory schemes (for example, quorum sensing signal–response systems)<sup>44</sup>. These limitations lead to high model uncertainty because key constraints on pathway stoichiometry and enzyme kinetics are either inappropriate or missing, and objective functions fail to capture the true evolutionary drivers of cell behaviour<sup>45</sup>, ultimately leading to poor predictions of in situ metaphenotypes. As a starting point for bottom-up design, core metabolic models that capture central carbon and energy metabolism can be reconstructed from genome annotations and known physiological information. The predictive power of these models may be limited initially, as they ignore regulatory information, pathway kinetics, secondary metabolism and evolution. However, when this knowledge is acquired and becomes incorporated into metabolic models through multiple cycles of testing and learning, accurate predictions of system function (for example, metabolic fluxes and metabolite exchange) may emerge. As a complementary approach, data-driven modelling techniques such as ensemble modelling and machine learning may offer more rapid methods to predict microbiome metabolic processes or obtain constraints and parameters required for microbiome modelling, without the need for detailed mechanistic understanding of metabolic regulation<sup>46,47</sup>. Such modelling frameworks have been used to predict pathway fluxes from proteomic and metabolomic data<sup>48</sup>, to improve metabolite cross-feeding predictions through ensemble modelling-based flux balance analysis<sup>49</sup> and to obtain key catalytic turnover numbers needed for metabolic models<sup>50</sup>. Although these approaches are flexible and generalizable enough to be applied to microbial communities, they require substantial amounts of experimental data on the metabolism of individual strains and interacting communities. This information could be leveraged from prior test phases (for example, from high-throughput phenotypic screens and multi-omics) to allow data-driven design.

**Integrated design.** Moving forward, we envision that a judiciously balanced blend of top-down and bottom-up approaches will be needed for successful microbiome design, especially when one is working with complex



**Fig. 2 | Top-down and bottom-up approaches to design microbiomes.** The left panel illustrates a bottom-up design workflow starting from isolates. Physiological characterization of individual organisms is performed, and metabolic modelling is used to design consortia for the desired function (produce light blue compound from dark blue compound). Genetic engineering and synthetic biology strategies are used to optimize system function (identifying gene editing targets that reroute metabolic flux away from toxin (purple) and towards the desired product; designing of toxin reporter strain). The right panel illustrates a top-down design starting with an inoculum containing uncultivated microorganisms from the environment. Community characterization of an undefined microbiome is performed, and bioprocess modelling (mass balance analysis including kinetics and microbial growth) is used to develop selection strategies to achieve the desired function (produce light blue compound from dark blue compound). Bioprocess engineering (for example, reactor design) is used to optimize system function. The middle panel shows an integrated top-down, bottom-up design. Combinations of undefined consortia and defined cultures are selected to achieve desired functions. Community characterization is performed, and microbiome modelling that integrates process-based simulation with metabolic modelling is used to develop selection strategies and analyse microbiome metabolic fluxes. The shapes of the microorganisms represent different isolates or communities selected during design. OD, optical density; S, substrate.

microbiomes, such as human microbiota or activated sludge (FIG. 2). A blended approach could involve selecting both undefined mixtures and defined consortia to achieve desired microbiome functions, merging process-based models with bottom-up metabolic models reconstructed from meta-omic information to simulate ecosystem processes, mass balances and metabolite fluxes, and using genome-derived information to develop community selection strategies. Capturing higher-order properties in design, such as functional stability and dynamics, will likely also require top-down and bottom-up approaches to converge. In particular, new mathematical modelling approaches that quantify mechanisms of functional degeneracy, niche complementarity and network buffering<sup>51</sup> using a metabolic framework may allow microbiome diversity to be optimized to sustain desired functions in situ. The need for a more comprehensive representation of microbiome metabolism will depend on the specific engineering objective and the degree of ecosystem tractability. For example, a more detailed representation of anaerobic

microbiome metabolism is likely required to convert biomass into a specific commodity chemical instead of methane because finer control over metabolism would be needed. In either case, the design phase encompasses defining the engineering problem, developing conceptual and quantitative models, identifying key biological processes to be manipulated and evaluating multiple candidate design alternatives.

**Practical design steps.** There are five key steps when one is designing microbiomes, in particular complex microbiomes: defining the engineering problem, developing a conceptual ecosystem model, creating an quantitative model, identifying the microbiome process(es) to be engineered and developing and evaluating candidate design strategies.

To drive the DBTL cycle, a clear definition of the problem with measurable design objectives must be established. These objectives could specify desired outcomes such as product titre, rates and yields, pollutant removal efficiency, crop productivity, or degree of



functional stability and robustness. Design objectives should be complemented by technoeconomic assessments and/or life cycle analysis to ensure that solutions are economically feasible and have positive environmental and societal impacts<sup>52,53</sup>.

Conceptual ecosystem models can be used to contextualize the problem. Such models capture system boundaries, inputs and outputs, major pathways of carbon and nutrient flows, key organisms and interspecies interactions responsible for those transformations and factors influencing their activity (for example, pH, temperature, redox potential and residence times)<sup>19</sup>. They provide a concept map that describes current understanding of interactions between the microbiome and physical, chemical and biological components of the ecosystem, helping to identify important gaps in system understanding and needs for data collection. At this stage, all relevant information should be collected from the literature, existing data (for example, from the Human Microbiome Project)<sup>54</sup> and online databases (for example, MiDAS (microbial database for activated sludge))<sup>55</sup> for ecosystem characterization. This includes reference genomes and physiological information for keystone organisms, previous multi-omic datasets, ecosystem physicochemical properties (such as pH, temperature and chemical concentrations) and processes (such as photochemical reactions and hydrogeological processes), site characteristics (such as nutrient loadings and dynamics, soil profiles and gut anatomy) and all other information needed to characterize the ecosystem. Missing information, such as unknown biochemical pathways and organisms that mediate them, can be targeted during the build, test and learn phases. This conceptual ecosystem model can be used by the scientific community for proposing and testing theories and serves as a road map for developing quantitative simulation tools.

Construction of quantitative modelling tools that allow the calculation and simulation of metabolic fluxes, microorganism abundances, mass balances and ecosystem physicochemical parameters is critical for the systematic design of microbiomes. Several approaches could be used to create such models, including mechanistic metabolic modelling<sup>33</sup>, process-based modelling<sup>21</sup>, data-driven modelling (for example, machine learning)<sup>48</sup> and individual-based modelling<sup>38</sup> or their combination. Regardless of the approach, the simulation of complex microbiomes will likely require simplification based on experimentally valid assumptions. Simplification could include reducing the model to a set of core or keystone organisms that represent important functional guilds and control major carbon and energy flows, or reducing the metabolic network size of organisms to central carbon and energy metabolism. Moving forward, it will be important to ensure that models undergo rigorous experimental validation and iteration during build–test–learn cycles to increase their utility and widespread use in microbiome engineering and to identify when modelling efforts fail, revealing gaps in conceptual understanding that can further facilitate model redesign and improvement.

Quantitative microbiome modelling (such as dynamic flux balance analysis) helps to identify the core and peripheral biochemical pathways that need to be

directly manipulated, added or removed to achieve the desired engineering objective. Objectives could include increasing butyrate production and non-digestible carbohydrate degradation by fermenting bacteria in the human gut, preventing toxin biosynthesis by cyanobacteria in freshwater ecosystems or stimulating the degradation of toxic chloroorganics by bioaugmentation with organohalide-respiring bacteria.

Microbiome modelling can predict how environmental (such as substrate loading, pH and solids retention time) or genetic manipulation (such as gene knockouts, pathway additions and forced dependencies) could optimize microbiome functions towards the engineering objective. If necessary, synthetic microorganisms could be designed to improve microbiome function. Such synthetic microorganisms will need to be evaluated for their ability to cooperate and compete with existing microbiome members under relevant environmental conditions.

### Building microbiomes

The build phase consists of physically assembling the designed microbiome by either top-down manipulation of a natural community (that is, a self-assembled microbiome) or bottom-up assembly using axenic or enrichment cultures of naturally occurring or engineered microorganisms (that is, a synthetic microbiome). The build phase aims to bring the design specifications and predictions into reality.

**Building by self-assembly.** Self-assembled microbiomes may include those built as open mixed cultures using reactor engineering (for example, wastewater treatment bioreactor) or biostimulation (for example, additions to soils, sediments or groundwater aquifers), in which construction creates an environment that promotes the growth and desirable activity of resident microorganisms. Examples include manipulating reactor hydrodynamics to immobilize slow-growing microorganisms into compact granules that allow their retention and proliferation<sup>56,57</sup>, use of non-human-digestible carbohydrates to stimulate fermentative production of short-chain fatty acids in the gut<sup>58</sup> or adding electron donors to drive the metabolism of organohalide-respiring bacteria during bioremediation of toxic chlorinated contaminants<sup>4</sup>. This approach is powerful when differences in physiological and physicochemical properties between functional guilds can be exploited for assembly through environmental manipulation (for example, differences in growth rates<sup>59</sup>, main electron donors and acceptors<sup>4,60</sup>, substrate affinities, cell and/or biofilm densities<sup>61</sup> and redox gradients). However, it can be limited when more fine-scale control over microbial metabolism and interactions is necessary (for example, controlling complex competitive interactions<sup>62</sup>, producing valuable bioproducts at high yields and purity<sup>63</sup> or controlling organisms with versatile lifestyles<sup>64</sup>).

In addition, new strategies for evolutionary engineering have emerged as promising tools to build self-assembled microbiomes. Controlled exposure of an initial microbiome to multiple selection cycles and/or regimes results in the microbiome gaining or optimizing specific functions through adaptation or evolution. For example,

#### Technoeconomic assessment

A tool used to evaluate the technical and economic viability of an integrated process through a combination of process design, modelling and economic evaluation.

#### Life cycle analysis

A tool used to evaluate the environmental impacts associated with all stages of a product's life, such as energy and water consumption, and air pollutant and greenhouse gas emissions.

#### Self-assembled microbiome

A microbiome built through environmental manipulation that selects for desired functions.

#### Synthetic microbiome

A microbiome built by combining predefined axenic or enrichment cultures to achieve a desired function.

successively transferring the microbiomes that maximize plant traits has generated microbiomes that increase plant biomass<sup>65</sup> and flowering time<sup>66</sup>. Response to community-level selection will often be driven by enrichment or adaptation of single species<sup>67,68</sup>; however, selection for production of community biomass has also been shown to enhance desired species interactions in defined two-species and three-species co-cultures<sup>37,69</sup>. Re-examining selection experiments to understand when and how mutations and/or adaptations altered microbiome phenotypes could elucidate the mechanisms underlying microbiome fitness optimization and inform design, as has been shown for *E. coli* in laboratory evolution experiments<sup>70,71</sup>. As similar evolutionary approaches (for example, adaptive laboratory evolution) have also been successfully applied to optimize strains for metabolic engineering<sup>72</sup>, extension of experimental and computational protocols already developed for individual microorganisms to microbiomes could streamline the design phase and reduce the time required to complete evolution experiments.

**Building synthetic microbiomes.** Direct construction of microbiomes using axenic or enrichment cultures is also promising because of reduced complexity and the use of microorganisms that are genetically tractable and/or well characterized. This bottom-up approach makes the growing suite of synthetic biology tools accessible for microbiome construction and optimization. An early approach for building microbiomes directly from cultured microorganisms was bioaugmentation. Here, defined laboratory consortia are added back to the environment to enhance the degradation rates of specific contaminants. A successful example was the addition of consortia containing organohalide-respiring bacteria of the class Dehalococcoidia to contaminated groundwater aquifers and sediments to speed up the degradation of toxic chlorinated pollutants. Crucial for the success of this approach was detailed knowledge of the physiology, nutritional requirements and potential ecological interactions of the keystone dechlorinators with other microorganisms and the geochemical environment<sup>4</sup>. However, in contrast to the success for chlorinated contaminants, bioaugmentation approaches have largely failed for oil spills. Unlike organohalide-respiring Dehalococcoidia members, which fill a unique ecological niche and cannot grow without the chlorinated contaminants, organisms capable of degrading oil hydrocarbons (especially aerobic bacteria) are ubiquitous, metabolically versatile and do not depend on a specific substrate or redox couple for growth<sup>64</sup>. This metabolic versatility limits their utility for bioaugmentation given their unpredictable in situ activity. Other reasons why bioaugmentation can fail are that unrecognized mutualistic interactions and microorganisms performing critical functions are missing (for example, production of polysaccharide surfactants to increase hydrocarbon bioavailability)<sup>73</sup> or that consortia selected under laboratory conditions are no longer competitive enough under harsh and/or variable field conditions<sup>74–76</sup>. These examples highlight the need to better understand the interaction networks of synthetic consortia, especially the roles of supporting

interactions (secondary functions), and the competitive landscape in situ, which are often difficult to predict in complex ecosystems.

Despite the appeal of building microbiomes from the bottom up and the growing collection of cultured microorganisms from specific habitats<sup>77,78</sup>, most microorganisms relevant for human health, agriculture and environmental applications remain uncultured, poorly characterized, genetically intractable and difficult to maintain, making the construction of synthetic microbiomes challenging. To capture this uncharacterized metabolic diversity, innovative isolation and controlled microbiome assembly techniques are needed, such as single-cell sorting<sup>79</sup> coupled with high-throughput culturing (culturomics)<sup>80,81</sup> and phenotyping<sup>82,83</sup> across multiple conditions in parallel. Microfluidics<sup>84,85</sup> (that is, creation and manipulation of microlitre droplets) can facilitate this approach. Microfluidic chips can allow automated assembly and analysis of microbial communities from axenic or enrichment cultures through droplet combination<sup>86</sup>, elimination of specific species<sup>87</sup>, sequencing, and multi-omics phenotyping of individual cells<sup>88,89</sup>. Combined with new gene editing techniques, such as CRISPR-based genomic tools<sup>90</sup> that increase the efficiency of homologous recombination-based gene editing<sup>91,92</sup>, microfluidics could also automate synthetic biology techniques for the engineering of cells and microbiomes with novel capabilities<sup>93</sup>.

Another challenge with synthetic microbiomes is maintaining their functional stability in the laboratory or in open systems (for example, human gut, soil and wastewater treatment plants), which are susceptible to invasion by naturally occurring microorganisms and dynamic heterogeneous environments. As mentioned earlier, the major reason for the success of bioaugmentation with organohalide-respiring Dehalococcoidia members is their highly specialized lifestyle that enables them to occupy an open ecological niche using chlorinated electron acceptors. However, the functional stability of organisms with versatile lifestyles in open systems is much less predictable. Few studies have examined the functional stability of synthetic consortia in open systems, and the knowledge required to rationally engineer stable ecological interactions is limited. However, engineered bacteria have been successfully deployed as diagnostic sensors in the mammalian gut for up to 200 days maintaining robust function<sup>94,95</sup>. This feat, together with the bioaugmentation example of Dehalococcoidia<sup>4</sup>, demonstrates that synthetic consortia can form stable microbiomes with previously established community members, provided key players can compete with resident microorganisms.

Observations from self-assembled microbiomes suggest that building communities with spatiotemporal organization will be important for achieving stable and multifunctional synthetic microbiomes. Highly diverse microbial communities, such as human microbiota or those used for wastewater treatment, self-assemble as biofilms, flocs or granules comprising multiple single-species microcolonies attached together via species-specific extracellular polymeric substances (including polysaccharides, proteins and DNA) and other poorly

defined macromolecules (such as humics)<sup>96,97</sup>. These self-organizing microbial assemblages create diverse microenvironments and ecological niches that support the combination of seemingly incompatible functions (for example, both aerobic and anaerobic processes)<sup>98,99</sup> and functionally diverse population structures that can compensate for disturbances, such as changes in nutrients, changes in physicochemical conditions or predation<sup>100,101</sup>. Although building such fine-scale and sophisticated architectures into synthetic microbiomes is nascent, microfluidic-based systems have been used to assemble simple communities with improved functional stability by controlling spatial structure and chemical communication<sup>102</sup>. Additionally, three-dimensional bioprinting platforms could allow the construction of spatially organized systems, in which populations can be physically separated while remaining chemically interactive<sup>103,104</sup>. How to scale these spatially defined structures from experimental laboratory systems to real-world applications remains to be resolved, although knowledge gained from test and learn phases with model systems (such as synthetic polysaccharide particles)<sup>105,106</sup> should provide more insights. Until then, existing approaches based on top-down assembly and/or engineered biofilm carrier media<sup>107</sup> could be used to build self-organized synthetic microbiomes with greater stability and functionality.

Designing synthetic genetic circuits in engineered hosts that can robustly perform sense–compute–respond programmes in complex environments also remains a major challenge<sup>108</sup>. Therefore, it will be important to examine the molecular mechanisms that determine microbiome stability and adaptation to environmental perturbation in natural and engineered ecosystems to extract design principles that can be used for rationally engineering robust functions. Given the potential utility of genetically engineered microorganisms and microbiomes in diverse open environments, safeguards such as biocontainment systems (such as two-layered gene circuits and essential synthetic auxotrophies)<sup>109</sup> will also require further development and will be needed as integral components of constructed synthetic microbiomes that use genetically modified organisms in the future.

**Integrating approaches.** The ultimate goal for rational microbiome design is to develop tools that enable engineers to directly add, remove or modify specific functions and phenotypes in situ over a range of desirable operational conditions. One emerging technique with promise to achieve such flexibility is in situ metagenomic engineering<sup>110,111</sup>, which involves delivery of engineered mobile genetic elements to resident microorganisms. For example, donor strains engineered with integrative and conjugative elements have transferred DNA carrying a reporter and antibiotic resistance genes or multigene pathways (for example, nitrogen fixation gene (*nif*) cluster)<sup>112</sup> to bacteria in highly heterogeneous and diverse environments, such as soil<sup>112</sup> and the mammalian gut<sup>111</sup>. Further development of such tools in combination with existing CRISPR–Cas gene editing techniques would allow the

precise manipulation of the microbiome’s metabolic network in situ, effectively combining self-assembled and synthetic microbiomes (BOX 1; FIG. 3).

### Testing microbiome function

The test phase involves measuring microbiome-associated phenotypes and properties to determine the efficacy of the design–build solution. The measurements should determine whether the design outcomes were achieved (for example, measuring the titre, rate and yield of a bioproduct, pollutant removal efficiency or crop productivity) and whether the design–build solution was responsible for the observed outcome (establishing cause and effect). This typically requires readouts of ecosystem physicochemical properties (such as pH, temperature and chemical concentrations), as well as the stoichiometry and kinetics of key ecosystem processes and microbiome functions (such as biomass growth, chemical transformations, nutrient assimilation and metabolic fluxes). For example, acetate degradation rates and pathways to methane in an anaerobic digester microbiome could be tested using <sup>13</sup>C-labelled acetate and online biogas analysis that measures the flux through acetoclastic methanogenesis versus syntrophic acetate oxidation coupled to hydrogenotrophic methanogenesis<sup>113</sup>. While the level of microbiome granularity measured during testing will depend on the specific design objectives and ecosystem complexity, the ability to quantify molecular microbial processes (for example, metabolic pathway rates and routes, enzyme activities and individual organism growth rates) goes beyond bulk activity measurements and allows testing of the specific mechanisms responsible for the observed microbiome functions. The challenge will be to develop tools that have high-throughput and are quantitative, affordable and easy to use, such that routine analyses of the microbiome over time and space and under dynamic conditions can be accomplished.

Towards this goal, we envision a test phase comprising high-throughput phenotypic screening of microbiome design–build solutions, followed by deeper investigation of promising solutions using multi-omic and metabolic flux analyses to obtain greater insights into underlying mechanisms (FIG. 4). High-throughput phenotypic testing of constructed microbiomes could be achieved using droplet microfluidics, as recently demonstrated for screening ~100,000 synthetic communities<sup>114</sup>. Fully automated microbioreactor platforms that combine liquid handling and advanced sensing with microtitre plates or scaled-down bioreactor cultivation could also be used<sup>82,83</sup>. Combined with emerging methods to measure metabolic network activity and metabolic processes in heterogeneous environments (BOX 2), rich information will be obtained to facilitate learning.

**Microbiome metabolic network activity.** To test predictions of microbiome function at a systems level, measurement of the microbiome’s in situ metabolic network structure and activity is critical. Multi-omic approaches (metagenomics, metatranscriptomics, metaproteomics and metabolomics) combined with bioinformatic tools have allowed the genome-centric analysis of

#### Integrative and conjugative elements

Mobile genetic elements able to integrate into DNA sites via site-specific recombination that carry genes encoding the machinery necessary for conjugation.

**Box 1 | A design–build–test–learn cycle to create synthetic microbiomes with desired functions**

We present a generalized design–build–test–learn cycle for creating synthetic microbiomes with desired functions, integrating both top–down and bottom–up approaches. We briefly describe two iterations of the cycle and identify opportunities for incorporating high–throughput approaches and automation to increase speed and reproducibility.

**Top–down approach**

**Design: identify biological process(es).** An example of a process to harness or replicate is anaerobic conversion of complex lignocellulosic biomass into valuable commodity chemicals. The initial design step includes selection of different inocula that may contain microorganisms with desired functions (for example, acid phase anaerobic digester sludge, herbivore rumen microbiome or others). Conceptual ecosystem models that include environmental parameters (pH, temperature, nutrients and so on) and expected functional guilds (hydrolytic bacteria, fermenting bacteria, methanogens and so on) are used to select enrichment variables.

**Build: enrich microbiomes from multiple sources.** Source inocula are cultivated under different environmental conditions to select for the desired function using real (for example, lignocellulosic hydrolysate or rumen fluid) and synthetic media. Modulation of environmental conditions and medium composition is done to improve the desired function. For complex environments (such as soil), model laboratory ecosystems could be ideal platforms for microbiome enrichment<sup>146</sup>.

**Test: evaluate performance.** The performance of enriched microbiomes is tested on real and synthetic media using high–throughput phenotypic screens. High–throughput screens could be developed using microfluidic or automated microbioreactor experiments. Deeper multi–omic measurements (such as metagenomics, metatranscriptomics and metaproteomics) are collected from high–performing microbiomes.

**Learn: identify key functional roles of microbiome members.** Besides key functions, bottlenecks for the desired function are identified using metabolic reconstruction and multi–omic analysis. This understanding helps to refine conceptual models of microbiome function and create quantitative models.

**Bottom–up approach**

**Design: identify new potential microbial partners.** In silico metabolic modelling is used to screen high–performing microbiome enrichments for interacting microorganisms. Metagenome–assembled genomes can be used to reconstruct metabolic models of key microbiome members. Automated computational workflows (together with manual curation) will accelerate model building. Flux balance analysis is used to predict each microorganism's requirements for optimal growth and activity, and unify individual metabolic models into a microbiome model to identify new potential partners that improve the design objective (for example, higher titres, rates or yields of valuable product).

**Build: recombine key microorganisms into new synthetic consortia.** Following their isolation or enrichment, key microorganisms are assembled into new synthetic consortia on the basis of in silico predictions at various ratios (for example, 1:1, 1:10). Microfluidic devices and/or liquid–handling robots could be used for high–throughput isolation and recombination.

**Test: test function and stability of consortia.** High–throughput phenotypic screening coupled with multi–omic measurements can be used for testing. This step should also include validation of predicted metabolisms of individual isolates or enrichments.

**Learn: identify microbial interactions that control function.** Analysing the metabolism of microorganisms growing in consortia versus in isolation using metabolic flux analysis can identify important mechanisms and interactions. This understanding can be used to propose how microbiome function and stability could be optimized by environmental manipulation and/or in situ genome engineering.

individual species (or even strains)<sup>115</sup> within microbiomes and global measurement of sequences, proteins and metabolites<sup>116–118</sup>. These tools measure the microbiome's components on a spectrum from functional potential (for example, gene abundance) to expressed products (for example, protein and metabolite abundance) and through their combined activity produce microbiome metaphenotypes that drive system function. Currently, multi–omic approaches used to infer microbiome function have focused on correlating gene abundances or gene expression data across time and space with ecosystem geochemical data or process rates. This has included measurements of key functional genes and transcripts using quantitative PCR assays (for example, ammonia monooxygenase)<sup>119</sup>, microarrays (for example, GeoChip)<sup>120</sup> or untargeted high–throughput approaches (metatranscriptome and/or metaproteome). Although useful for overall system characterization and discovery, these approaches

focus on measuring the components or 'parts list' of the system, which are often limited predictors of emergent phenotypes due to metabolic network complexity, interactions and regulation<sup>121,122</sup>. Therefore, new approaches and tools are needed to measure the in situ stoichiometry and fluxes of microbiome metabolic networks to permit the direct testing of design predictions and offer mechanistic insights into metabolic regulation.

Metabolic flux analysis is the most authoritative method for measuring in vivo fluxes. This method calculates fluxes from metabolite stable isotope measurements obtained during isotopic labelling experiments using metabolic network modelling<sup>123</sup>. Although metabolic flux analysis has been used to measure fluxes in co–cultures<sup>124</sup>, flux analysis in communities is challenging because metabolite pools cannot be easily assigned to individual cells, and the number of possible reactions in a microbiome greatly exceed those of an individual organism. Nonetheless, isotopic tracers combined with



**Exometabolomics**

An analytical technique to quantify extracellular small-molecule metabolites from environmental and/or biological samples typically through gas/liquid chromatography–mass spectrometry or nuclear magnetic resonance spectroscopy.

**Off-gas analysis**

The monitoring of gas flow rate and chemical composition (for example, carbon dioxide, hydrogen, methane) produced from a biological system.

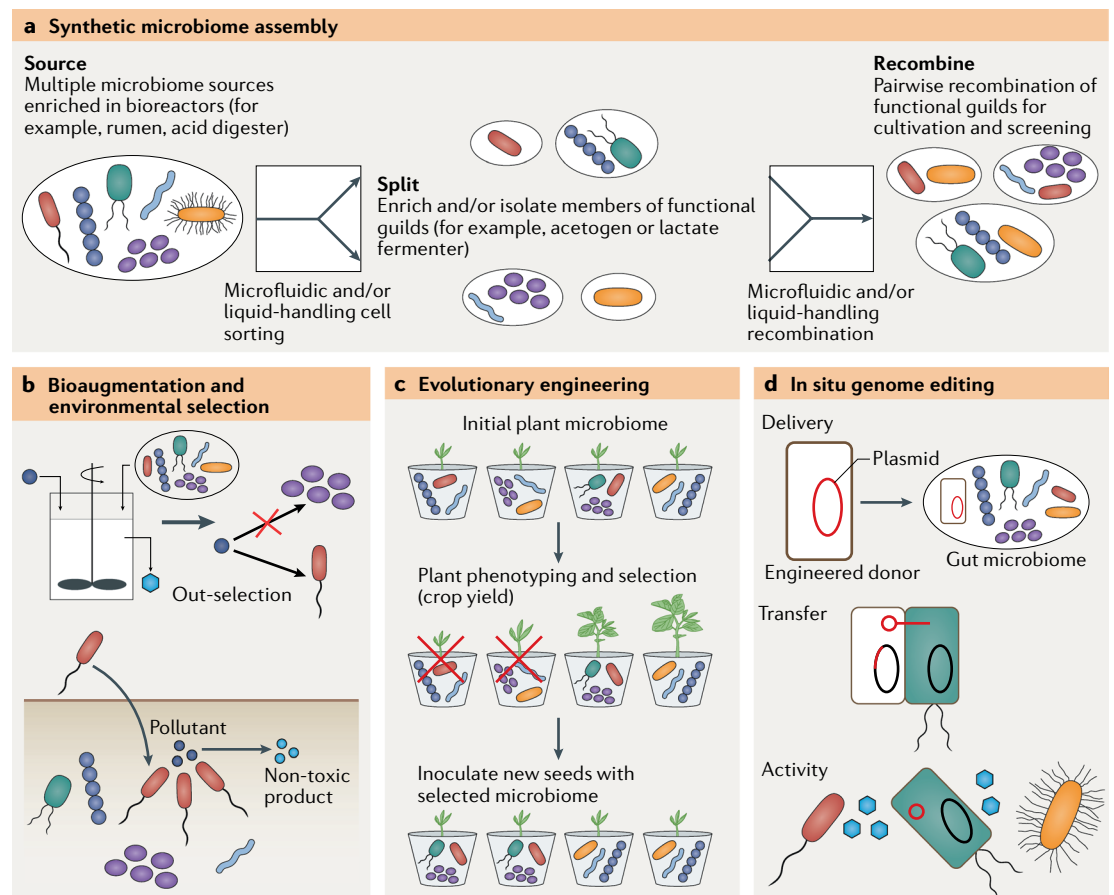
**Structure–function relationships**

The influence of the microbiome’s three-dimensional spatial organization on its function.

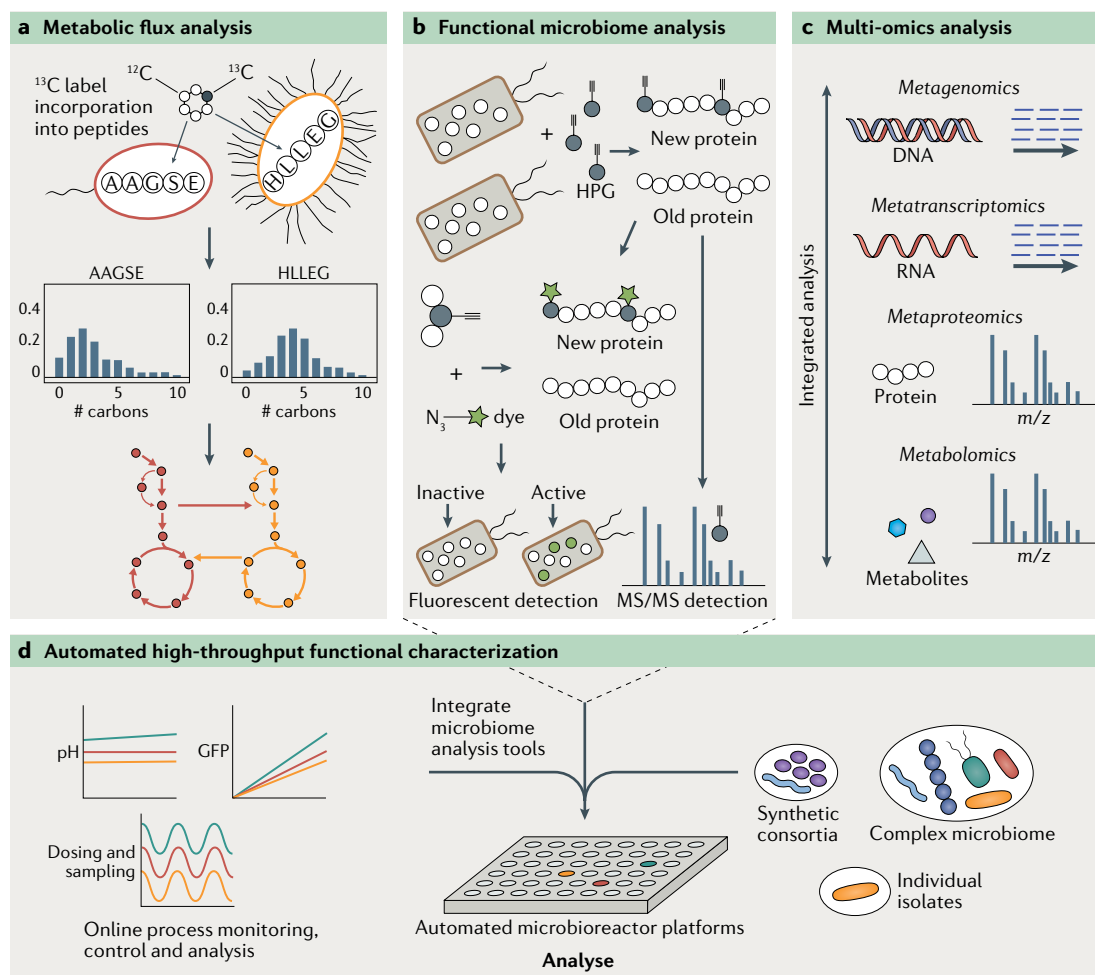
exometabolomics and/or off-gas analysis have been used to determine process fluxes driving important microbiome functions, such as syntrophic acetate oxidation and methanogenesis during anaerobic digestion<sup>116</sup>. To circumvent the challenges with metabolite measurements, a method analysing labelling patterns from short peptides instead of amino acids for metabolic flux analysis was proposed<sup>125</sup>. Peptides can be assigned to individual species in a microbiome using high-throughput metaproteomic approaches, which opens the door to determining fluxes in microbial communities (that is, to ‘metafluxomics’). Given that fluxes represent the final outcome of cellular regulation across all levels<sup>126</sup>, further development and demonstration of metafluxomics will be essential for advancing microbiome engineering efforts and our understanding of metabolic regulation in microbiomes. This will also require new software packages for associated computational analyses, similar to existing <sup>13</sup>C metabolic flux analysis software<sup>127</sup>. Such data may also allow metabolic modelers to infer, rather than assume, community-level and individual-level objective functions and to identify new constraints, allowing the

accurate prediction and measurement of reaction rates driving microbiome function.

**Measuring function in spatially heterogeneous environments.** Most natural microbiomes, such as those associated with plants (for example, rhizosphere), humans (for example, oral microbiome) and industrial processes (for example, acid mine drainage), display highly organized spatial organization across micro-scale physicochemical gradients that directly influences microbiome function. For example, the spatial proximity of microorganisms can control whether they interact through diffusible substrates or direct transfer<sup>128</sup>, whereas variations in colony size can dramatically influence apparent substrate affinity constants and substrate competition between biofilm microorganisms<sup>129</sup>. Therefore, one of the biggest challenges will be to create tools that measure and report on microbiome spatial structure and function across all relevant scales (from micrometres to kilometres). Current methods to measure structure–function relationships have focused on the micrometre to millimetre scale using approaches such as fluorescence in situ hybridization



**Fig. 3 | Building self-assembled and synthetic microbiomes. a** | A protocol for assembling synthetic microbiomes from multiple microbiome sources. Complex microbiomes can be taken apart into key functional members using automated microfluidic cell sorting techniques. Isolated or enriched members can then be recombined into synthetic consortia using liquid-handling robots for downstream screening and/or cultivation. **b** | Microbiome assembly can also be achieved through environmental selection via bioreactor manipulation or biostimulation (top) or by bioaugmentation with defined cultures (bottom). **c** | Another option is microbiome assembly through directed adaptation and/or evolution of the microbiome to acquire or optimize a desired function. **d** | In situ microbiome engineering can be used to add new functions to microbiomes residing in the environment.



**Fig. 4 | Testing microbiome function.** **a** | Isotopic tracers combined with the metaproteome could be used to measure microbiome metabolic flux by analysing isotopic labelling patterns of short peptides rather than amino acids (metabolome). **b** | Bio-orthogonal non-canonical amino acid tagging is a method for rapid profiling of anabolic processes (growth) in situ using either fluorescent detection or metaproteomics. **c** | Metagenomics, metatranscriptomics, metaproteomics and metabolomics can be integrated to reconstruct and analyse metabolic network expression in microbiomes. **d** | An automated microreactor platform allows high-throughput analysis of microbiome processes across diverse conditions (for example, with changing environmental or physiological variables). The platform can integrate tools for detailed functional analysis of individual microbiome members to complex communities. Green, red and yellow colours in process monitoring graphs correspond to microreactor well locations. HPG, homopropargylglycine; MS, mass spectrometry.

combined with stable isotope labelling<sup>130</sup>, chemical fingerprinting<sup>131</sup>, mass spectrometry imaging<sup>132</sup> and/or fluorescence-based bio-orthogonal non-canonical amino acid tagging<sup>133</sup> (BOX 2). Although these techniques have successfully identified the substrate use and activity patterns of spatially distributed microorganisms in microbiomes, they are limited by throughput and can examine and/or differentiate only a limited number of organisms. The integrated application of labelling techniques (for example, stable isotope labelling and bio-orthogonal non-canonical amino acid tagging) with metaproteomics and cell sorting (for example, fluorescence-activated cell sorting)<sup>133</sup> could be used to measure the metabolic activity of microorganisms with high-throughput and with spatial resolution. Combined with microsensor devices that profile microenvironmental chemical properties (for example, through microelectrodes<sup>134</sup> or engineered biosensors<sup>95</sup>), microbiome structure, microbiome

function and ecosystem physicochemical parameters could be monitored in real time.

**Learning microbiome design principles.** Progressing through the design, build and test phases of microbiome engineering presents a unique opportunity to learn from previous failures and successes, and to incorporate new knowledge into subsequent cycles. Indeed, the learn phase of the DBTL cycle is critical for success and for increasing microbiome engineering efficiency. To date there are no general strategies, techniques or approaches that guarantee success in translating information obtained from the test phase into new knowledge that informs the next design phase. Therefore, we stress the importance of devoting enough emphasis and resources to the learn phase early on so as to avoid, for example, the difficulties encountered in metabolic engineering due to a relative lack of investment in the learn step<sup>13</sup>.

**Generalized Lotka–Volterra equations**

A set of ordinary differential equations used to represent population dynamics based on experimentally inferred species interaction parameters.

Further development of computational methods to formalize the learn phase will be needed, including machine learning algorithms<sup>48,135,136</sup>, metabolic flux analysis and constraint-based analysis<sup>36,124,125,137</sup>, ecosystem modelling approaches<sup>138</sup> and regulatory network analysis<sup>139</sup>. Together, these analyses could isolate the principal drivers of microbiome interactions and function from large datasets to inform microbiome design. For example, generalized Lotka–Volterra equations could infer

interacting species from temporal population dynamics data that become the starting point for bottom-up design<sup>140</sup> or constraint-based analysis could be applied to identify key metabolite exchange reactions from <sup>13</sup>C metabolomic data that increase flux simulation accuracy and improve design of anaerobic consortia<sup>137</sup>.

More broadly, we envision the learn phase to focus on translating data into generalizable principles for microbiome engineering through the continuous refinement

**Box 2 | A toolbox for measuring microbiome function****Multi-omics integration**

The ability to assemble genomes from metagenomic data<sup>28</sup> has enabled the genome-resolved analysis of individual transcriptomes<sup>63</sup> and proteomes<sup>118</sup> within diverse communities and greatly increased the interpretive power of multi-omic datasets. A key challenge moving forward will be the integration of metabolic information<sup>163</sup>, both intracellular and extracellular, which cannot be readily assigned to individual members of the microbiome such as DNA, RNA and proteins can be. The large amount of unknown or poorly characterized genes, enzymes and metabolites currently limits the interpretive power of multi-omic information. It does, however, create novel targets for further biochemical studies. Advances in bioinformatic tools, such as data-driven approaches (for example, statistical or machine learning methods) and knowledge-based approaches (for example, interaction networks or genome-scale metabolic modelling)<sup>164,165</sup>, will be key to the success of systematic measurements of microbiome function through coherent multi-omics data integration.

**Isotopic tracers**

Isotopic tracers have a long history in functional analysis in both pure cultures and communities, and have been combined with DNA<sup>166</sup>, RNA<sup>167</sup> and protein<sup>116</sup> measurements to link individual populations to specific *in situ* functions. Moving forward, more efforts to incorporate isotopic tracers with multi-omics (especially metaproteomics and metabolomics) are needed to illuminate the complex metabolic networks within microbiomes. The combination of these techniques should also pave the way for measurement of intracellular and extracellular reaction rates ('metaflexomics')<sup>124,125</sup>, which has been one of the most powerful tools for elucidating *in vivo* phenotypes, pathway constraints and metabolic regulation in pure cultures used for engineering purposes.

**Mass spectrometry imaging**

Mass spectrometry imaging (MSI) techniques visualize the distribution of elements and their isotopes as well as biomolecules within complex samples. MSI is well suited for the analysis of spatially structured microbiomes and for the investigation of cellular interactions. When combined with fluorescence *in situ* hybridization, MSI also allows the linking of microbiome structure with function<sup>168,169</sup>. The chemical coverage, spatial resolution and sample preparation that can be obtained with different MSI techniques depend on the ionization method used<sup>132</sup>. Although nanoscale secondary ion mass spectrometry (nanoSIMS) has superior lateral resolution compared with matrix-assisted laser desorption/ionization (MALDI) or desorption electrospray ionization (DESI; 50 nm, 3–50 mm and 100 mm, respectively), its relative chemical versatility is very low (elements and isotopes versus peptides, lipids, metabolites and other molecules). Therefore, nanoSIMS has generally been applied to study substrate use of single cells, whereas MALDI–MSI has been used to visualize chemical interactions between populations<sup>132</sup>. Although MALDI–MSI and DESI–MSI are more accessible than nanoSIMS<sup>170</sup> and could be well positioned to visualize the broad range of chemical interactions within microbiomes, they have very low throughput and their lateral resolution and sensitivity currently prohibit single-cell metabolic profiling<sup>132</sup>. A technique that combines the best of these two methods is nanostructure-initiator mass spectrometry (NIMS). NIMS is a matrix-free desorption/ionization technique that depends on initiator molecules trapped in 30-nm pores to achieve the ionization of small molecules adsorbed to the pore

surface. NIMS offers a lateral resolution of ~150 nm and is particularly well suited for the analyses of peptides and metabolites<sup>171</sup>. So far, NIMS has seen only limited application in microbiology<sup>172,173</sup>. We expect advances that resolve these issues will soon make MSI a useful and more widely applied tool for functional analysis of microbiomes<sup>174</sup>.

**Bio-orthogonal chemistry**

Metabolic labelling techniques, such as bio-orthogonal non-canonical amino acid tagging (BONCAT), offer additional approaches to measure microbiome anabolic activity *in situ*. BONCAT is based on the *in vivo* translational incorporation of a non-canonical amino acid (for example, L-azidohomoalanine, an L-methionine surrogate) followed by fluorescent labelling of tagged cellular proteins by azide–alkyne click chemistry<sup>175</sup>. The technique can be used together with ribosomal RNA-targeted fluorescence *in situ* hybridization to directly link taxonomy with *in situ* activity<sup>175</sup>. BONCAT has also been combined with fluorescence-activated cell sorting to separate active cells from complex samples and further characterize them by DNA sequencing<sup>133</sup>. In addition, tagged proteins can be selectively enriched through bead capture and subjected to proteomic analysis<sup>176</sup>. The combined application of these methods could allow the high-throughput tracking of newly synthesized proteins from uncultivated microorganisms under different physicochemical conditions. Although BONCAT can be limited due to differences in cellular amino acid uptake and metabolic perturbation, the technique offers a flexible tool for the comparatively simple, inexpensive and high-throughput analysis of *in situ* activity on a single-cell level.

**Microfluidics**

Devices that allow the high-throughput analyses of microorganisms at single-cell resolution will be important for the rapid cultivation and functional analysis of microbiomes. Microfabricated devices such as microfluidic 'lab-on-chip' technology could offer multiple applications, including isolation of individual cells and populations from complex microbiomes<sup>177</sup>, the creation of *in vitro* cell-based models that facilitate assembly of synthetic microbiomes and experimentation under heterogeneous microenvironmental conditions<sup>178</sup>, and online diagnostics for rapid monitoring and detection of desired phenotypes. These applications are still in early stages of development, and several challenges remain, including reliable detection of microorganisms in droplets, precise control of gas concentrations, cross-contamination and technology accessibility<sup>177,179</sup>.

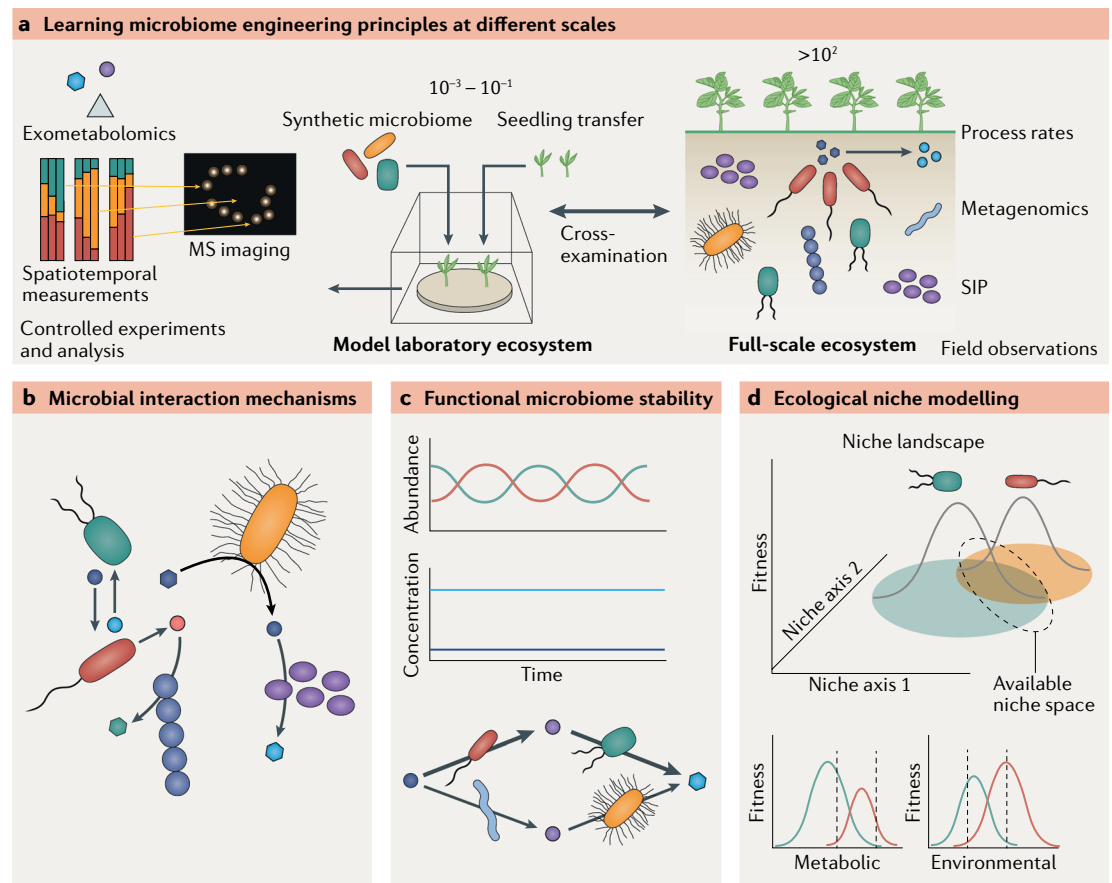
**Automation**

To increase the reproducibility, throughput, efficiency, and standardization of microbiome engineering, advances in automation will be necessary. This includes incorporating liquid-handling robots, microfluidic devices, automated cultivation systems, online physicochemical measurement sensors and software into data generation and analysis workflows. Emerging examples include the use of liquid-handling robots coupled to automated microfermentation platforms for high-throughput cultivation<sup>82</sup>, or microfluidics to automate the analysis of thousands of droplet experiments that probe microbial community interactions<sup>114,180</sup>. Such automated platforms could also integrate several functional tools (for example, single-cell analyses and multi-omics), resulting in rich reproducible datasets that could be leveraged for machine learning and other big data analytics.

of conceptual knowledge and proposed theory (for example, from traditional macroecology)<sup>51,141–144</sup> with each DBTL cycle. We propose that model laboratory ecosystems should be used to drive microbiome engineering inquiry and learning. Model laboratory ecosystems are experimental platforms that can replicate the physicochemical conditions of a complex environment (natural or engineered) in a simplified and controlled manner and contain model microbial communities (for example, the model rhizosphere microbiome THOR)<sup>145</sup> that can be used as testing grounds for learning how to design, construct and optimize engineered microbiomes. These ecosystems have reduced complexity, are accessible for experimentation and can be established in a reproducible manner, which is often not possible when one is working in natural environments.

Recently, model laboratory ecosystems have been developed to study plant–soil microbiome interactions<sup>146</sup>. These fabricated ecosystems use three-dimensional printing, sensing and analytical and imaging technologies to create an experimental device that replicates the

native soil ecosystem, in which microorganism and host phenotypes can be monitored in response to changing variables, allowing the systematic dissection of microbial interactions and metabolite exchanges influencing plant health<sup>146,147</sup>. Fabricated ecosystems offer a middle ground between model organisms and complex natural microbiomes, and can be established collaboratively between expert investigators to create standardized and reproducible devices and protocols for dissemination to the broader research community. Such model systems offer the ability to experimentally develop engineered microbiomes with desired functions in a tractable manner, and permit results to be compared with results from natural settings. This cross-examination between model and natural ecosystems will be a valuable and necessary approach for learning engineering principles and practices that are relevant to real-world systems (not laboratory artefacts), and for acquiring knowledge on scaling up laboratory-based engineering strategies to full-scale applications (FIG. 5). For example, microfluidic-based in vitro models of the human gut microbiome



**Fig. 5 | Learning fundamental principles for microbiome engineering.** Model laboratory ecosystems can be used for controlled experiments with simplified microbiomes and environmental properties, representing a system in between pure laboratory conditions (such as test tubes or flasks) and complex natural environments (such as soil or the ocean). Continuous cross-examination between laboratory-scale models and natural complex ecosystems will be needed for development of engineering principles and practices that are robust in real systems while also tractable in the laboratory. This will require close collaboration between multiple stakeholders, including researchers and end users (such as hospitals or treatment plants) that have expertise and experience with issues specific to each scale (part a). Key principles that need to be learned to make possible systematic microbiome engineering include microbial interaction mechanisms (part b), mechanisms governing functional stability and degeneracy (part c), and frameworks for quantitatively mapping and simulating ecological niches in complex ecosystems (part d). MS, mass spectrometry; SIP, stable isotope labelling.



Box 3 | Emerging principles for microbiome engineering: a case for niche modelling

Ecological niche modelling could be used to systematically design higher-order properties such as functional stability and robustness into engineered microbiomes. However, to develop such a framework, mechanistic understanding of how diversity is maintained within microbiomes and how it imparts properties such as functional stability is needed. Here, we propose that this understanding could come from applying the design–build–test–learn cycle to answer key questions:

**Does functional degeneracy lead to productivity and functional stability?**

Diversity has been correlated with productivity and functional stability in communities of macroorganisms<sup>143,181</sup>, yet the role that diversity has in improving microbiome function and functional stability remains open. For microbiome engineering, we propose that diversity be viewed, discussed and defined through the lens of functional redundancy (as described previously<sup>154</sup>), or more specifically, functional degeneracy. This is the degree to which a set of organisms perform an identical role in ecosystem functionality (for example, methane oxidation, nitrogen fixation or polymer hydrolysis) but exhibit degeneracy with respect to other physiological traits (for example, pH optima or biofilm formation), which enables them to achieve realized niche space and coexistence<sup>51</sup>. The design–build–test–learn cycle offers an excellent opportunity to understand the molecular basis of functional degeneracy and to examine how emergent community-level properties, such as resilience to perturbation or susceptibility to invasion by another species, are predictable from quantifying the fundamental and realized niche space in microbiomes. We propose that ecological niche modelling could be a particularly useful framework to achieve this goal.

**How is diversity maintained in microbial ecosystems?**

To create a framework for ecological niche modelling, it will be important to understand how diversity is maintained. Competitive exclusion suggests that two species with identical resource requirements cannot coexist in the same ecological niche<sup>144</sup>. Therefore, we need to understand the mechanisms that create niche space and allow diversity to develop and be maintained. For example, what role do the processes of spatiotemporal variability, dormancy, predation, nutrient loading, secondary metabolite production and resistance, cell motility and biofilm formation have in niche differentiation? And how can these processes be manipulated to achieve and maintain a desired level of functional degeneracy in a microbiome? Answers to these questions will offer microbiome engineering mechanisms to design and control ecological niche space for desired microbiome properties.

**How does ecological niche modelling underlie microbiome engineering?**

To allow the systematic engineering of desirable higher-order microbiome properties, we propose that microbiome engineering develops a framework for ecological niche modelling. The goal of this framework would be to quantify community and individual fundamental niche and realized niche space by integrating multi-omic data, physiological information, nutrient availability and environmental parameters, and use them to develop strategies for controlling cooperation and competition in microbiomes. To achieve this goal, new mathematical representations of the fundamental niche and the realized niche of an organism or guild will need to be defined, together with fitness functions that describe responses to environmental variables. When incorporated into microbiome modelling, this framework will allow the ecological forecasting of higher-order properties, as well as quantification of cooperative and competitive microbiome landscapes. Moreover, such frameworks will help guide important unresolved microbiome design questions, such as the trade-off between functional redundancy and minimal diversity.

that contain co-cultures of human cells with different bacterial consortia are already producing physiological (including epithelial cell monolayer formation, cell growth and viability, cytokine levels and metabolomic profiles) and environmental (including oxygen gradients and laminar flow) variables that are comparable to *in vivo* variables<sup>148</sup>.

The combination of model ecosystems with the DBTL cycle may be particularly fruitful for understanding the mechanisms governing microbial interactions and functional stability. Substantial knowledge is available on specific microorganisms that undergo co-aggregation and exchange metabolites, such as bacteria involved in nitrogen cycling<sup>2</sup>, consortia of methane-oxidizing archaea and sulfate-reducing bacteria<sup>128,149,150</sup>, and syntrophic bacteria partnered with hydrogenotrophic methanogens<sup>151,152</sup>. However, we are only beginning to understand the complex mechanisms (such as quorum sensing and secondary metabolites) involved in regulating the behaviour, interactions and kin discrimination of microorganisms in communities<sup>153</sup>. Although studies have established links between microbiome functional redundancy, diversity and stability<sup>154</sup>, a framework to predict or engineer functionally stable microbiomes has

not been attained. Through the use of model laboratory ecosystems together with existing knowledge of microbial ecology and engineering design, it may be possible to decipher the chemical language of microbiomes and discover mechanisms of other important processes (including evolution, selection, dispersal limitation and neutral processes)<sup>155</sup> that enable robust and stable microbiome function. Translating this theory into engineering design practice will require a quantitative framework that links these mechanisms to metabolic interaction networks and new approaches that allow ecological properties to emerge from metabolic models (BOX 3).

**Outlook**

True advancement in microbiome engineering will need multiple DBTL rounds to capture the necessary ecological principles to manipulate microbiomes in a precise manner with predictable outcomes (FIG. 1). For example, incorporating direct interspecies electron transfer discovered during previous DBTL cycles into metabolic models and bioreactor construction (for example, by adding conductive materials) could optimize the efficiency of biogas production from waste<sup>27</sup>, or design-engineered *E. coli* to control levels of previously

**Fundamental niche**  
The entire set of environmental conditions in which an organism can survive and reproduce (that is, an organism's niche in the absence of interspecific competition).

**Realized niche**  
The set of environmental conditions used by a species after consideration of interspecific competition (competition, predation and other factors).

discovered autoinducers could tailor gut microbiota under conditions of dysbiosis towards a healthier state<sup>156</sup>. However, developing new knowledge and tools with fast turnaround will require next-generation infrastructure for data collection, data sharing and knowledge integration. To accelerate progress, developing the predictive capabilities needed for the learn phase is a priority. Model laboratory ecosystems combined with advances in automation, such as liquid-handling robots, microfluidics and data analysis pipelines<sup>157,158</sup>, will offer a starting point for the testing of multiple designs in a rigorous and reproducible manner. Capturing new knowledge from this process and integrating information into subsequent DBTL cycles will accelerate microbiome engineering developments, creating innovative biotechnologies and practices for the management of microbiomes across medicine, agriculture, manufacturing and environmental stewardship. Examples that show particular promise for advancing microbiome engineering across these fields include illuminating the roles that phages and metabolite cross-feeding have in controlling ruminal carbon turnover<sup>159</sup>, harnessing untapped anaerobic fungal–bacterial consortia to increase biomass

conversion to valuable bioproducts<sup>160,161</sup>, creating microfluidic cell sorting techniques to automatically sort stable isotope-labelled cells from high-diversity samples for subsequent multi-omic analysis or cultivation<sup>162</sup> and developing in situ metagenomic engineering tools to introduce new functions into microbiomes in their native environment<sup>111</sup>.

To move the DBTL approach forward, interdisciplinary research teams with expertise in experimentation (for example, in culturing, molecular genetics or biochemistry), computation (for example, metabolic modelling, machine learning or bioinformatics), automation (for example, robotics or microfluidics), and practice (for example, professional engineers or medical doctors) are essential. The road ahead for microbiome engineering seems long, given our nascent understanding of microbial ecology; however, structuring research and technology developments around the DBTL cycle offers a promising approach for advancing microbiome engineering and providing innovative solutions for addressing pressing societal and environmental problems.

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