MICROBIOME

Best practices for analysing microbiomes

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Abstract | Complex microbial communities shape the dynamics of various environments, ranging from the mammalian gastrointestinal tract to the soil. Advances in DNA sequencing technologies and data analysis have provided drastic improvements in microbiome analyses, for example, in taxonomic resolution, false discovery rate control and other properties, over earlier methods. In this Review, we discuss the best practices for performing a microbiome study, including experimental design, choice of molecular analysis technology, methods for data analysis and the integration of multiple omics data sets. We focus on recent findings that suggest that operational taxonomic unit-based analyses should be replaced with new methods that are based on exact sequence variants, methods for integrating metagenomic and metabolomic data, and issues surrounding compositional data analysis, where advances have been particularly rapid. We note that although some of these approaches are new, it is important to keep sight of the classic issues that arise during experimental design and relate to research reproducibility. We describe how keeping these issues in mind allows researchers to obtain more insight from their microbiome data sets.

Exact sequence variants
For marker gene sequencing, the exact DNA sequence for each read is used instead of operational taxonomic unit clustering.

Operational taxonomic units
(OTUs). A group of closely related individuals or sequences (often 97% sequence similarity threshold).

Machine learning
The use of algorithms to learn from and make predictions about data.

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Advances in DNA sequencing technologies have transformed our capacity to investigate the composition and dynamics of complex microbial communities that inhabit diverse environments, from mammalian gastrointestinal tracts to deep ocean sediments. These developments have led to vast increases in the number of microbiome studies being performed in many fields of science, from clinical research to biotechnology. With this transformation, researchers are often left holding massive amounts of data and are confronted with a bewildering array of computational tools and methods for analysing their data. Conducting a robust experiment is not trivial in microbiome research, and as with any study, experimental methods, environmental factors and analysis methods can affect results. Standards for data collection and analysis are still emerging in the field, yet many compelling results can be achieved with current practices.

Microbiome analysis methods and standards are rapidly advancing. In particular, recommendations concerning differential abundance testing using exact sequence variants rather than operational taxonomic units (OTUs) and performing a correlation analysis have evolved quickly in the past 2 years. We can expect a similar pace of development in several other areas, including metagenomic taxonomy and functional assignment; integration of data sets from multiple sequencing runs; and further improvement in machine learning, compositional data analysis and multi-omics analyses. However, many of the most fundamental issues that concern microbiome studies arise from statistical and experimental design issues. The most important challenge for the field is to integrate new approaches that are unique to microbiome studies, while remembering standard practices that are broadly applicable to all scientific studies.

Although it is impossible to be fully comprehensive in one article, this Review aims to provide straightforward guidelines for designing and executing a microbiome experiment and analysing the resulting data, with a particular focus on human, model organism and environmental microbiomes. We direct the reader to more specialized reviews on specific topics where these exist.

Experimental design

Designing an experiment that generates meaningful data is an important first step in your analysis. Typical scientific questions, such as those addressed in case–control and longitudinal interventions or studies, can all be studied in the context of the microbiome. Researchers can

Metadata
Information about the data. In many studies, this is structured as a matrix with samples as rows and metadata categories (age, sex, longitude, season, disease state, average monthly rainfall, and so on) as columns.

Alpha diversity
A measure of within-sample diversity.

Effect size analysis
Quantification of the magnitude of an effect of a particular metadata category (treatment group, sex and sequencing plate) on the data.

identify potential differences in microbial community structure, composition and genetics or functional variation either between separate communities or over time. Notably, the general approach to microbiome analysis is applicable regardless of sample origin (BOX 1). However, specific details of the analysis may depend on the sample origin; for example, 16S ribosomal RNA (rRNA) amplicon regions have variable success among different sample types in recapitulating results from metagenomic sequencing data[1].

Other primary considerations when assessing different sample types are experimental design and sample collection. We have observed many confounding issues during human microbiome studies, and therefore we emphasize the importance of experimental design when performing these studies, though often many of the same considerations apply to animal models and environmental samples (BOX 2).

Meticulous experimental design is crucial for obtaining accurate and meaningful results from microbiome studies. Many confounding factors, if not controlled, can obscure patterns in microbiome data (FIG. 1). Careful curation of metadata, appropriate controls, including extraction and reagent blanks, and thoughtful study designs that isolate and interrogate variables of interest are all essential.

First, the scope of the experiment must be defined and an appropriate experimental design selected for the question of interest. For example, cross-sectional studies are useful for finding differences in microbial communities between different human populations, such as healthy individuals and those with diseases, or individuals living in different geographic regions. However, owing to the large variation in the microbiome between individuals and the profound influence of lifestyle[2,3], diet[4], medication[5,6] and physiology, differences between populations may arise from factors other than the disease of interest. For example, initial reports of changes in the microbiome in individuals with diabetes were confounded by effects of the drug metformin[5]. Longitudinal studies, especially prospective longitudinal studies that collect baseline samples before disease onset, can help resolve these issues, although they are more expensive. For ease in downstream statistical analyses, longitudinal studies should plan the timing of sample collection carefully: for human studies, this may mean collecting samples at identical time points for each subject. Interestingly, community instability rather than the specific taxa present at a single time point can be a strong predictor of disease activity[7]. For example, individuals with inflammatory bowel disease exhibit greater microbiome fluctuations than control cohorts[7]. Interventional studies, including double-blind randomized control studies, are especially useful for identifying specific effects of a course of treatment on the microbiome and disease state. Designing a study with an analysis plan and specific experimental questions to interrogate can help determine the sample size. For example, to test the effects of a new broad-spectrum antibiotic on the mouse gut microbiota, more samples may be required to look at shifts in specific taxa compared with assessing how alpha diversity (a quantitative measure of community diversity) changes with antibiotic treatment, as baseline microbiota composition varies between mice. The antibiotic may be expected to decrease alpha diversity in all mice, but it could perturb their microbial community composition in different ways. For any study design, appropriate methods to assess statistical power should be employed in order to discern technical variability and real biological results[8]. However, statistical power and effect size analysis remain a challenge in microbiome research[9]. Some methods that are currently used for power and effect size analysis are based on PERMANOVA[8], Dirichlet Multinomial[10] or random forest analysis[11]. As these methods are further developed to integrate metagenomics, metatranscriptomics, metaproteomics and metabolomics data sets, study design and selection of appropriate sample size will also improve. For specific experimental design considerations, we recommend reviewing the design of other successful studies with similar sample types and desired outcomes. We expand on important considerations for microbiome experimental design below.

Defining controls and exclusion criteria. Defining clear inclusion and exclusion criteria limits confounding covariates. For instance, variability in recovery time from antibiotics among individuals[12] suggests that individuals who were treated with antibiotics in the preceding 6 months should be excluded from most microbiome studies. Similarly, recovery of the skin microbiome after hand washing takes ~2 hours[13].

In case–control experimental designs, controls must be appropriately selected and matched. Age and sex are common control criteria, despite the relatively weak effect of sex on most human microbiomes across body sites[14,15], while other variables such as medication and diet are often more important confounders to control for. The relative effect sizes of these microbiome variables are still emerging[9]. Collection of comprehensive clinical data is crucial for identifying confounders that cannot be controlled. This topic has been extensively reviewed in REF.[16]. Environmental studies must also

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Box 1 | **Good working practices**

It is crucial for microbiome analyses to be reproducible. Similar microbiome studies can often have conflicting results, and without proper documentation of sample collection, data processing and analysis methods, it is difficult to re-examine the data and reconcile these differences. As the field evolves, it will be necessary to re-visit early experiments and potentially re-analyse the data with updated tools. Reproducibility is paramount for this process to be possible and efficient. When collecting samples, details of the collection process should be recorded in the experimental metadata to ensure that as much variability as possible is accounted for. Additionally, the Genome Standards Consortium minimum information standards (MIxS) for marker genes (MIMARKS) and metagenomes (MIMS)[152] should be followed. These unified standards enable comparisons across data sets. During bioinformatics processing, researchers should track all the commands that they run and all software versions that they use and deposit their raw data and metadata in public repositories. We recommend using tools such as Jupyter Notebooks or R Markdown to facilitate this and then storing the notebooks in a revision control management system such as GitHub. Some software packages, such as QIIME 2 (REF.[59]) and Galaxy, automatically track this information for researchers through an integrated data provenance tracking system. Qiita and EBI are powerful meta-analysis and data archiving tools, respectively, and when combined, allow a researcher to analyse their microbiome data in the context of tens of thousands of other samples, which enables the data to be re-used by future researchers.

account for similar confounders, as plot-to-plot variation is a widely recognized confounding phenomenon in the ecological literature that should be addressed with nested statistical tests[17].

Animal models. The predominant animal models for studying the microbiome are rodents, such as mice. Other models with varying microbial complexity, such as bobtail squid, insects or zebrafish, are often useful for studying specific interactions between hosts and microorganisms (for example, how the microbiome and the host genetics influence each other)[18]. Nevertheless, rodents are often preferred because they are well characterized and have many physiological similarities to humans. Rodent microbiome studies require particularly careful design. As rodents are coprophagic, cage mate faecal microbiomes become more homogeneous over time, so experiments must be replicated across multiple cages to control for cage effects[19]. Parental effects also necessitate randomizing littermates between cages and allowing for normalization. Single housing stresses mice[20] and is thus often technically or ethically infeasible. Even genetically identical rodents may differ in their microbiomes owing to environmental factors, including diet, litter, vendor, shipment and facility[21,22]. Additionally, early life microbial exposures greatly impact the established microbiota and can influence immune system development[23]. Similar considerations apply to other co-housed model organisms, such as zebrafish[24].

Technical variation. Technical variability among experimental methods ranging from DNA extraction to sequencing is high[25,26]. The same reagent kits must be used for all samples in a study[27], and multiple baseline samples should be collected to assess intrinsic variability among time points in longitudinal studies. The use of blanks during sampling, DNA extraction, PCR and sequencing is essential for detecting contamination. Reads that are derived from microorganisms introduced as contaminants or that grow during shipping can sometimes be reduced during analysis[28], though samples should be at −80 °C when possible[29]. For field studies or other situations where freezing is not possible, ambient storage methods, such as storage in 95% ethanol or commercial products such as RNAlater or the OMNIgene Gut kit, can be used[30]. Mock communities (reference samples with a known composition) are useful for standardizing analyses[31], as is including the same standard specimens in each DNA sequencing run[32]. In general, reconciling microbiome data that were generated using different methods remains an unsolved challenge.

Depending on the scope of their experiment (which includes the overall experimental design, sample types and source, sequencing method, and other factors that are discussed below), researchers can aim to gain a broad, community-level overview of their samples, a detailed genomic-level understanding or even a characterization of the functional variation in microbial communities.

Sequencing targets and methods

Different methods for surveying microbial communities, including marker gene, metagenome and metatranscriptome sequencing, can produce varying results. All widely used methods have strengths and weaknesses, so the question, hypothesis, sample type and analysis goals should inform the choice of method (TABLE 1). Here, we discuss the trade-offs between cost, robustness, resolution and difficulty for marker gene, metagenome and metatranscriptome sequencing. We outline the best workflow for each method in FIG. 2. To attain a high-level, but low-resolution overview, the preferred method is marker gene sequencing. Metagenomic sequencing provides more detail by analysing the total DNA in a sample, allowing strain-level resolution and detection of genes that can provide information on molecular functions. We also discuss metatranscriptomic sequencing of total RNA, which is used to characterize gene expression in the microbial community.

Marker gene analysis. Marker gene sequencing uses primers that target a specific region of a gene of interest in order to determine microbial phylogenies of a sample. This region typically contains a highly variable region that can be used for detailed identification that is flanked by highly conserved regions that can serve as binding sites for PCR primers. Marker gene amplification and sequencing (such as 16S rRNA for bacteria and archaea and internal transcribed spacer (ITS) for fungi) are well-tested, fast and cost-effective methods for obtaining a low-resolution view of a microbial community. This approach works well for samples contaminated by host DNA, such as tissue and low-biomass samples. However, because DNA sequences vary in these primer-amplified regions, primers do not have equal affinity for all possible DNA sequences and consequently induce bias during PCR amplification. Other sources of inherent bias in marker gene sequencing include variable region selection, amplicon size[33] and the number of PCR cycles[34]. Low-biomass samples are particularly susceptible to bias

Marker genes
Conserved genes (commonly 16S ribosomal RNA (rRNA), internal transcribed spacer (ITS) and 18S rRNA) that typically contain a highly variable region that can be used for detailed identification that is flanked by highly conserved regions that can serve as binding sites for PCR primers.

Nested statistical tests
Statistical tests that address variables related to the main effect. For example, soil plot would be a nested factor for testing the effects of a fertilizer on the soil microbiota.

Coprophagic
Involving the consumption of faeces. Many animal species eat faeces to more efficiently break down plant matter by digesting the material twice.

Reads
Inferred sequences of base pairs in a single DNA fragment.

Metatranscriptome
The total content of gene transcripts from a community of organisms.

Box 2 | **Considerations for different microbiomes**

Although microbiome data analysis methods are widely applicable to many sample types and environments, experimental design and method selection require careful consideration for different sample types. First, one must consider the composition of the sample and feasibility of use for different methods. For samples that are heavily contaminated with non-microbial DNA, such as tissue, shotgun metagenomic sequencing may not be feasible without non-microbial DNA depletion. Depending on the experimental question, samples heavily contaminated with relic DNA from dead microorganisms, such as soil samples, may require physical removal of relic DNA by propidium monoazide[46] or other methods before DNA extraction. The amount of sample to collect is also determined by sample type. Whereas a high-biomass faecal sample may only require a swab, samples with low microbial density may necessitate larger volumes and potentially concentration for sufficient DNA extraction. For example, ocean microbiome samples are usually large volumes of water run though a filter to trap and concentrate the target organisms before DNA extraction[84]. Though in all cases, appropriate controls should be included, and low-biomass environments, such as blood, spinal fluid or laboratory clean rooms, particularly necessitate controls that have gone through the entire sampling process to fully characterize contaminants. DNA contaminants can be found in numerous reagents, including swabs, DNA extraction kits and PCR reagents[27]. Furthermore, the method of sample preservation is dictated by both analysis method and sample type. For example, metatranscriptomics requires an RNase inhibitor, and metabolomics requires sample preservation that does not interfere with metabolite extraction or data collection.

In addition to sampling considerations, study design and metadata collection also require careful tailoring to sample type and environment. For example, animal studies require an evaluation of co-housing cage effects and should stratify experimental groups into multiple cages. Fresh samples should be collected, and the mouse of origin should be recorded in the metadata. Environmental samples require collection of metadata related to environmental conditions, such as pH, salinity, elevation, and depth for soil samples. The manner of collection is highly dependent on sample type and cannot be detailed for all possible samples in this Review. We recommend consulting well-validated protocols related to the sample type of interest. In any case, methods of collection, preservation and storage in a study should remain consistent across all samples to avoid introducing confounding variation. Sample composition can be affected by outgrowth of certain microorganisms during storage at room temperature[28].

introduced by overamplification — as the PCR cycle number increases, contaminating microorganisms are increasingly over-represented[35]. Optimizing primer selection can help mitigate bias, but this requires a priori knowledge of microbial community composition to assess taxonomic resolution and coverage of the target community[36]. However, even well-optimized primers are often limited to genus level taxonomic resolution. Marker gene sequencing generally correlates well with genomic content[37–41] and is applicable to the broadest range of sample types and study designs.

Whole metagenome analysis. Metagenomics is the method of sequencing all microbial genomes within a sample. Metagenomic sequencing yields more detailed genomic information and taxonomic resolution than marker gene sequencing alone, but it is relatively expensive to prepare, sequence and analyse the samples. This method captures all DNA present in the sample, including viral and eukaryotic DNA. Given adequate sequencing depth (the number of sequencing reads per sample), taxonomic resolution to species or strain level[42] and the assembly of whole microbial genomes from short DNA sequence reads are possible[43]. However, de novo annotation of functional genes is not possible in such settings. Metagenomic sequencing profiles the functional capacity of an entire community at the gene level[44], moving well beyond the limits of marker gene analysis. However, biases that are introduced by library construction, assembly and reference databases for annotation are less understood than biases that exist in well-characterized marker gene approaches. As the metagenomics field matures, these annotation steps will continue to be improved and validated. For a comprehensive review on metagenomics, we direct the reader to REF.[45].

Humic substances
Produced by biodegrading organic matter; humic substances are the main component of humus (soil).

Metagenomes
The collection of genetic material from a community of organisms, for example, the genetic material from all microorganisms in the human gut microbiome.

Metatranscriptome analysis. Metatranscriptomics uses RNA sequencing to profile transcription in microbiomes, providing information on gene expression and the active functional output of the microbiome. Metatranscriptomics differs from both marker gene and metagenomic sequencing that sequence DNA in a sample regardless of cell viability or activity. Although there are methods for depleting relic DNA from dead cells[46], sequencing microbial RNA provides better insight into the functional activity of a microbial community, though it is biased towards organisms with higher rates of transcription. It is worth noting that propidium monoazide (PMA) depletion of relic DNA is an alternative method to identify live microorganisms[47]. Host RNA contamination, particularly from the highly abundant rRNAs, is also an important consideration, and methods to exclude rRNAs from samples should be considered[48]. RNA must be carefully preserved to avoid degradation in all cases, though certain sample types may warrant specialized protocols for RNA purification. For example, soil samples require removal of enzyme-inhibiting humic substances[49,50]. Despite these technical difficulties, metatranscriptomic data can offer unique insight; transcriptomes vary more within individuals than metagenomes[51], and metatranscriptomics can reveal microbial community responses to perturbations such as xenobiotic exposure[52]. For a comprehensive review on metatranscriptomics analysis of the microbiome, we direct the reader to REF.[53].

Analyses

Ideally, each microbiome study would analyse samples with all three of the methods discussed above. In most cases, however, there is not enough sample material or enough project funding for performing all three

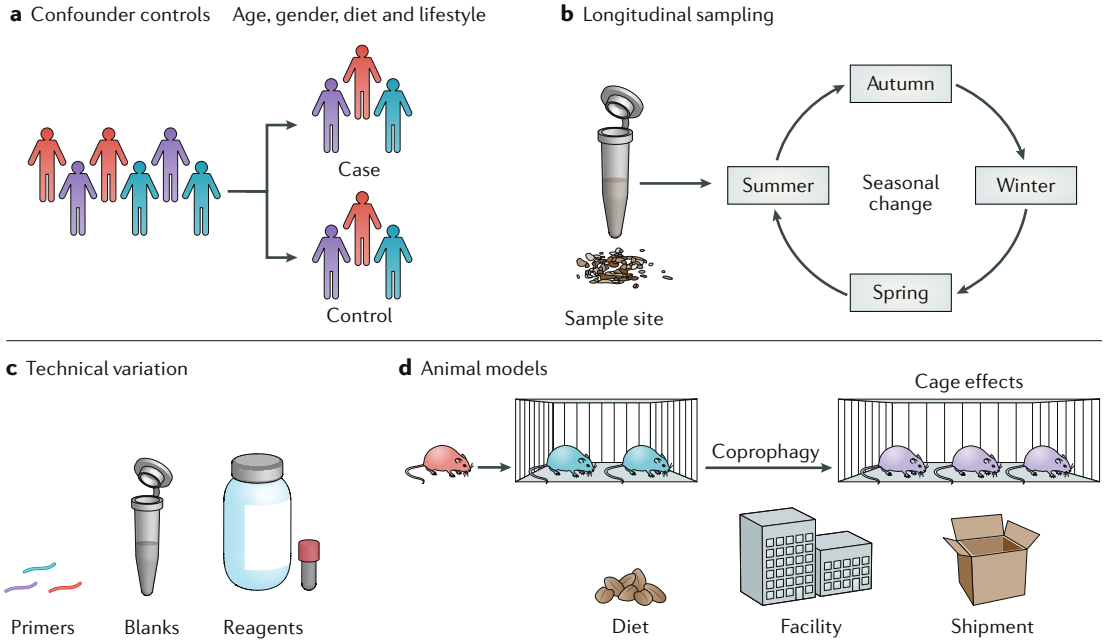

Fig. 1 | **Experimental design considerations for microbiome experiments.** Conducting a robust microbiome experiment warrants careful attention to numerous factors. **a** | Stratification by potential confounders (for example, age, gender, diet, lifestyle factors and medications) can help resolve differences in microbiota between groups of interest that might otherwise be masked by a confounder effect[5]. **b** | Longitudinal studies are especially powerful as they both control for confounding factors and allow for the assessment of community stability[7]. **c** | For all studies, standardizing technical factors and sample processing are essential to control for variation introduced by kit reagents, primers, sample storage and other factors. The collection and curation of metadata about all aspects of each sample, from clinical variables to sample processing, are crucial for data interpretation; without metadata, it is difficult to draw meaningful conclusions from sequencing data. **d** | Similar considerations apply to animal studies, though the additional impact of coprophagy must be addressed in experimental design.

analyses, and in some cases, the samples might not be amenable to one of the sequencing methods. It is therefore paramount that the researcher chooses the method of sequencing that is most effective for answering their specific questions. If there are no budget constraints, we recommend performing metagenomics rather than marker gene sequencing. However, it is common practice to perform marker gene sequencing to gain a low-resolution understanding of the microbial community composition. Next, depending on the focus of the study, the researcher can move on to metagenomic and metatranscriptomic sequencing, though this may require a second study for appropriate sample collection and processing.

Marker gene analyses. As noted above, marker gene approaches are sensitive to technical factors such as primer choice[54], so well-validated protocols such as those used with the diverse sample set in the Earth Microbiome Project should be used[55]. The first step in analysing marker gene amplicon data is to remove sequencing errors: despite very low sequencing error rates (for example, in Illumina sequencing, the rate is ~0.1% per nucleotide[56]), most of the apparent sequence diversity arises from sequencing errors[57,58]. Until recently, this problem was addressed by clustering similar sequences into OTUs[59,60]. Clustering sequences into OTUs, termed OTU picking, consolidates similar sequences (usually with a 97% similarity threshold) into single features, merging sequence variants, including those introduced by sequence error, into a single OTU that can be used in subsequent analysis. However, this method misses subtle and real biological sequence variation, such as SNPs that would be consolidated into single OTUs[61]. Oligotyping[62] improves upon traditional OTU picking by including position-specific information from 16S rRNA sequencing to identify subtle nucleotide variation and by discriminating between closely related but distinct taxa. Algorithms such as Deblur[63] and DADA2 (REF.[64]) use error profiles to resolve sequence data into exact sequence features (the marker gene sequence) called sub-OTUs (sOTUs). The resulting output from these methods is a table of DNA sequences and counts of these different sequences per sample rather than OTU groups. We recommend that these methods replace OTU-based approaches for all applications, except when it is necessary to combine sequence data that were generated using different technologies (that is, Illumina sequencing and 454 pyrosequencing) or with different primer sets, when mapping to a common reference database of full-length sequences is often still needed[65].

One key analysis step is to assign taxonomic names to microbial sequences in the data. Taxonomy is typically assigned by machine learning approaches such as the RDP classifier[66], a naive Bayesian classifier, which uses naive Bayes models that are trained on oligonucleotide frequencies at the genus level to achieve ~80% accuracy in genus-level assignments. Popular microbiome

Naive Bayesian classifier
A simple probabilistic classifier used in machine learning that is based on applying Bayes' theorem assuming strong independence between the features.

Table 1 | **Pros and cons of genomic analyses for evaluating microbial communities**

Method	Pros	Cons
Marker gene analysis	• Quick, simple and inexpensive sample preparation and analysis[55,59] • Correlates well with genomic content[37–41] • Amenable to low-biomass and highly host-contaminated samples • Large existing public data sets for comparison[16,55,160]	• No live, dead or active discrimination • Subject to amplification biases[34] • Choice of primers and variable region magnifies biases[33,54,159] • Requires a priori knowledge of microbial community[36] • Resolution typically limited to genus level at best • Appropriate negative controls required • Functional information is limited[39,40]
Whole metagenome analysis	• Can directly infer the relative abundance of microbial functional genes; microbial taxonomic and phylogenetic identity to species and strains level is attainable for known organisms[42] • Does not assume knowledge of microbial community (that is, captures phages, viruses, plasmids, microbial eukaryotes, etc.) • No PCR-related biases • Can estimate in situ growth rates for target organisms with sequenced genomes[161] • Can allow assembly of population-averaged microbial genomes[43,162] • Can be mined for novel gene families	• Relatively expensive, laborious and complex sample preparation and analysis • Contamination from host-derived DNA and organelles may obscure microbial signatures • Viruses and plasmids are not typically well annotated by default pipelines • Deep sequencing depths are typically required relative to other methods • No live, dead or active discrimination • Population-averaged microbial genomes tend to be inaccurate owing to assembly artefacts
Metatranscriptome analysis	• Can estimate which microorganisms in a community are actively transcribing when paired with marker gene analysis • Inherently discriminates between active live organisms versus dormant or dead microorganisms and extracellular DNA • Captures dynamic intra-individual variation[51] • Directly evaluates microbial activity, including responses to intervention and event exposure[52]	• Most expensive, laborious and complex sample preparation and analysis[163] • Host mRNA contamination and rRNA must be removed[48,164,165] • Requires careful sample collection and storage • Data are biased towards organisms with high transcription rates • Requires paired DNA sequencing to decouple transcription rates from bacterial abundance changes

rRNA, ribosomal RNA.

analysis packages, such as QIIME[59] and Mothur[60], provide support for taxonomic classification. In principle, exact matching to reference databases (three of the most characterized and frequently used are Greengenes, RDP and Silva) should provide better specificity in taxonomic assignment, but the sensitivity of this approach is poor given the large number of unknown taxa. Furthermore, de novo phylogenetic trees that are constructed from short marker gene sequences are typically poorly resolved, so insertion of marker gene sequences into a characterized reference tree that is based on full-length sequences[67] is desirable given the importance of phylogenetic metrics[68]. Unclassified microorganisms should be checked for organelle sequences, and for many studies, chloroplast-derived and mitochondrial sequences should be excluded before proceeding with analysis (although for intestinal samples, these sequences can be useful for identifying consumed foods and thus should not be disregarded completely).

Predictive functional profiling[38–41] is a technique for linking marker gene data with available microbial genomes to make predictions about metagenomic content and thus the putative biological functions of a microbial community. This analysis generally requires a reference-based OTU table. Methods based on evolutionary models (for example, PICRUSt[39]) provide confidence intervals on these predictions of gene content, which will tend to be wider in regions of the tree distant from reference genome sequences and narrower where many reference genomes are available. Thus, the availability of sufficient closely related reference genomes is a main factor that influences the accuracy of these results. Another limitation for predictive functional profiling is that some families of bacteria possess a very similar 16S rRNA variable region, despite being phenotypically and genotypically divergent.

Most statistical analyses that are applied to microbiome data that are generated from marker gene sequencing can also be applied to other types of omics analyses and are described below in the higher-level analyses section.

Metagenome and metatranscriptome analyses. Surveying the complete nucleic acid profile of a sample yields rich information that can be used to investigate a broad range of taxonomic, functional and evolutionary aspects of microbial communities — even contaminants can provide important details[69]. As with marker gene-based surveys, the analytical methods must be carefully chosen to consider the sample origin and the specific hypotheses under investigation. Here, we discuss the best approaches to perform these analyses.

Read-based profiling takes the unassembled DNA or mRNA sequence reads and compares them against reference databases to assign taxonomy or annotate genes. With the ever-increasing size of modern

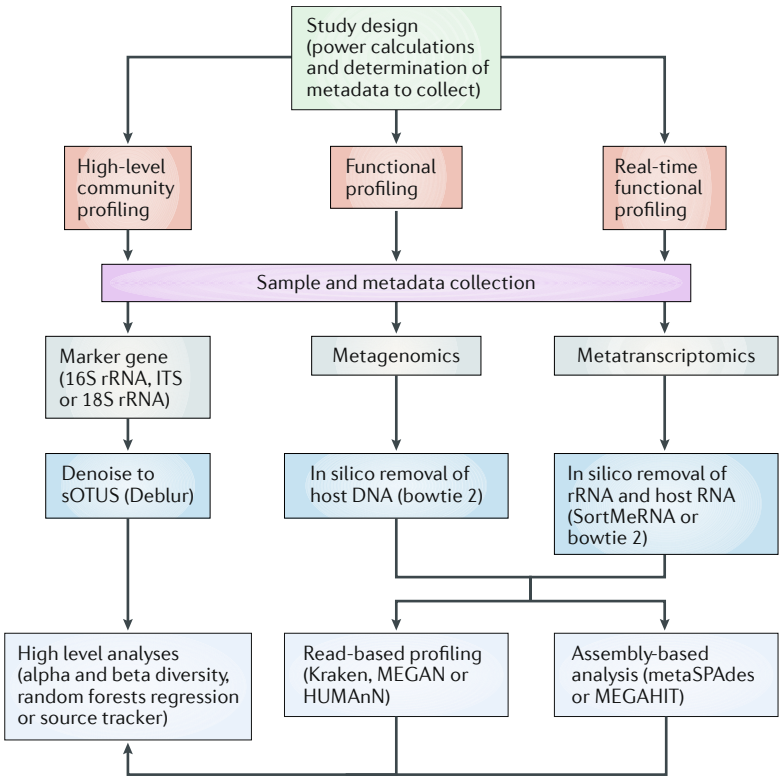

Fig. 2 | **Best workflow for 16S ribosomal RNA, metagenomic and metatranscriptomic sequencing.** After careful design and sample collection, microbiome data are generated from 16S ribosomal RNA (rRNA), metagenomic or metatranscriptomic sequencing. After performing 16S rRNA sequencing, we recommend using Deblur[63] to resolve sequence data into single-sequence variants called sub-operational taxonomic units (sOTUs). Although DADA2 and Deblur achieve similar results, Deblur is an order of magnitude faster than DADA2, is parallelizable and shows greater stability (that is, it obtains the same sOTUs across different samples)[63]. Metagenomics and metatranscriptomics first require preprocessing to remove either host DNA or rRNA and host RNA The resultant sequencing data can be analysed by either read-based profiling using state-of-the-art tools, such as Kraken[70], MEGAN[76] or HUMAnN[44], or by assembly-based analyses, with tools such as metaSPAdes[92] and MEGAHIT[93]. For each of these three methods, higher-level analyses (for example, alpha and beta diversity, taxonomic profiling and machine learning) are subsequently used to find overall patterns in microbiome variation. Random forests regression has been effective in many applications, ranging from dating time since death of a corpse[128] to providing an index for microbiome maturation[129]. SourceTracker[130], a Bayesian estimator of the sources that make up each unknown community, is useful for classifying microbial samples according to environment of origin[131]. ITS, internal transcribed spacer.

query data sets and databases, methods are continually being refined to improve the speed of read-based profiling. Many tools utilize k-mers, assigning taxonomy to short DNA fragments of length k, such as Kraken[70], or employ the Burrows–Wheeler transform, which compresses the database by merging similar sequences (for example, Bowtie2 (REF.[71])) and Centrifuge[72]). For a more comprehensive guide to tool selection, we direct the reader to REF.[73]. Marker gene methods (such as MetaPhlAn2 (REF.[74]) and TIPP[75]) use specific genomic regions for taxonomy assignment, focusing on universal, single-copy elements. Beyond taxonomy assignment, other tools, such as HUMAnN2 (REF.[44]), can also be used for annotating genes and metabolic pathways. Some tools, including MEGAN[76], incorporate both of these functionalities and can be a preferred method when both annotations are desired. Because each read is considered independently, read-based methods scale efficiently to large, complex data sets, such as soil microbiome data sets. It is important to note that as taxonomic or functional assignment depends on homology between the single read and a reference, database choice is crucial. For well-characterized environments such as the human gut, curated genome databases such as RefSeq[77] and protein family databases such as Pfam[78] or UniRef[79] increase the accuracy of results and decrease computational costs. For samples from poorly characterized environments, the use of large databases such as NCBI nr and nt and IMG/M[80] should be considered because the databases are larger, despite the increased computational complexity and decreased assignment specificity. Specialized databases must be used to annotate specific taxonomic or functional categories, such as PHASTER[81] for bacteriophages, Resfams[82] for antibiotic resistance genes and FOAM for environmental samples[83]. Additionally, numerous metagenomic data catalogues are available for many sample types, including Tara for ocean samples[84], the BGI catalogue for mouse gut samples[85] and MetaHit for human gut samples[86].

Another method for analysing metagenome and metatranscriptome sequencing reads is to assemble the short reads into longer sequences (contigs). These contigs can be further sorted or binned by similarity to assemble partial to full genomes of microorganisms. This allows data exploration beyond taxa and gene annotation, enabling the prediction of multi-gene biosynthetic pathways or even metabolic reconstructions with tools such as antiSMASH[87]. However, assembly-based analyses are not universally applicable; higher biodiversity, the presence of many related strains in samples, or low coverage yields fragmented assemblies and can obscure taxa from downstream analyses. For example, soil samples are often difficult to assemble owing to the high microbial diversity and uneven distribution[88]. For samples that avoid these complications, metagenome assemblies provide valuable bespoke reference databases for read-based and assembly-based metatranscriptome analyses[89,90], thus recovering the 'microbial dark matter' that is absent in curated databases[91]. Recommended tools for assembly-based analyses include metaSPAdes[92] and MEGAHIT[93]. A comprehensive discussion of these and other tools can be found in REF.[94]. To assemble partial to full genomes of individual microorganisms, contigs are sorted (binned) into separate putative genomes with tools such as MaxBin2 (REF.[95]) and CONCOCT[96], which evaluate nucleotide composition and abundance patterns across samples to perform sorting (binning). To evaluate the quality of these binned and assembled genomes, single-copy gene profiling tools such as CheckM[97] that use common single-copy genes to estimate genome completeness and contamination can be used. Additionally, visualization tools like VizBin[98] display clustering of metagenomic sequences without alignment to a reference database, allowing researchers to visually inspect the sequence clustering of related organisms and assist with evaluating bin quality. Employing integrated workflow

K-mers
All possible sequences of length k from a read obtained through DNA sequencing.

tools to automate data processing, such as Anvi'o[99], ATLAS[100] or MetAMOS[101], is highly recommended because assembly-based methods are complex.

In order to compare samples with varying sequencing read counts, various methods of normalization can be employed. Common methods of normalization include read counts per million (counts are scaled by the total number of reads), transcripts per kilobase million (counts scaled by number of reads and length of reads) and converting the data to relative abundance. Additionally, there are various tools for performing normalization, including edgeR[102] and DESeq2 (REF.[103]).

New tools for both read-based and assembly-based approaches are under rapid development. When possible, specific analytical decisions should be made based on performance on well-studied or synthetic data sets (such as the Critical Assessment of Metagenomic Information[104]) that are most similar to the microbial community of interest.

Higher-level analyses

Processing microbiome data generates a matrix that relates feature abundance (taxa or genes) to samples. This output is deceptively simple; microbiome data are highly dimensional, often representing thousands of different taxa, and sparse, with many zeros present in the matrix, requiring careful statistical treatment to extract meaningful results.

Overall patterns in microbiome variation are typically assessed by alpha and beta diversity. Alpha diversity quantifies feature diversity within individual samples and can be compared across sample groups. For example, when comparing a sample from an individual with a disease to a healthy control, the researcher can use alpha diversity to compare the mean species diversity between the two samples. Measures of species richness (for example, the number of observed species or the Chao1 abundance estimator, which estimates true species diversity) and phylogenetic measures (Faith's phylogenetic diversity) are sensitive to the number of sequences per sample, whereas measures that combine richness and evenness (Shannon index) are much less so. However, it should be noted that these methods have been evaluated exclusively for 16S rRNA data and may not apply to other microbiome data types. Beta diversity compares feature dissimilarity between each pair of samples, generating a distance matrix of beta diversity distances between all pairs of samples. Metric selection can influence the results obtained[68,105] and should be chosen with biological data interpretation in mind. Quantitative metrics (Bray–Curtis, Canberra and weighted UniFrac) use feature abundance data in calculations, whereas qualitative metrics (binary-Jaccard and unweighted UniFrac) only consider the presence or absence of features. Phylogenetic measures such as UniFrac typically provide interpretable biological patterns[106], though these metrics require a phylogenetic tree and thus cannot be used for direct comparison with omics data that lack trees. Software for performing alpha and beta diversity calculations includes QIIME[59], Mothur[60] and the R package vegan[107]. The non-parametric permutation tests PERMANOVA and ANOSIM are used for assessing significant beta diversity clustering between groups, but PERMANOVA may perform better on data sets with varying dispersions within groups[108]. Calculation of meaningful alpha and beta diversity measures requires the researcher to control for the sampling effort (that is, the number of sequences per sample obtained), as this can differ by orders of magnitude. The current best solution for UniFrac is rarefaction[109], though for the special case of pairwise differential abundance testing, the full sample set should be used[110].

For visualizing beta diversity data, ordination techniques, such as principal coordinates analysis (PCoA) or principal component analysis (PCA), are commonly used. These methods reduce large and complex distance matrices into visually manageable two-dimensional or three-dimensional representations of sample distances. Samples can then be coloured by various metadata categories to visualize clustering in an unsupervised manner. EMPeror offers an interactive framework for manipulating PCoA plots[111].

Another common analysis approach is to look at differentially abundant microorganisms or functional elements (for example, genes and pathways) in the comparison groups of interest (that is, treatment versus control). Identifying microbial taxa that explain differences between communities is particularly challenging because microbiome data sets are high-dimensional (that is, they include thousands of taxa), sparse and compositional. Compositionality is the crux of the problem[112]; when the proportion of one microorganism increases, the proportions of others must decrease for the proportions to sum to 1. For example, suppose a patient is administered a drug that increases the growth rate in only a single microbial genus while not affecting the growth of others. Although the other microorganisms are not impacted by the drug, they would have decreased in relative abundance owing to the outgrowth of the single microbial genus. This poses challenges for many classical methods, such as parametric statistical tests (for example, Student's *t*-test and ANOVA) and measures of correlation, including Spearman's rank correlation, often leading to completely unacceptable false discovery rates above 90%[109,113,114]. Recently, compositionally aware methods have addressed this problem of compositionality and relative abundance. One approach is to force strong biological assumptions on the statistical test: for example, Lovell's proportionality metric detects only positive correlations[115]. Other tools that are widely applicable and have been optimized for microbiome data, such as SparCC[116] and SPEIC-EASI[117], assume that few species are correlated, so most correlation coefficients are zero. BAnOCC[118] is another tool for addressing the compositionality problem that makes no assumptions about the data. We recommend another approach that does not assume few species are correlated, which is to test for differences between microbial communities using the isometric log ratio transform (ilr). The ilr approach controls for false positives owing to proportionality by testing for the changes in log ratios between microbial abundances, commonly referred to as balances. Balances can be constructed using previous knowledge such as evolutionary

Beta diversity
A measure of similarity between samples.

Faith's phylogenetic diversity
An alpha diversity metric that uses a phylogenetic tree to compute sample diversity.

Shannon index
A commonly used index to characterize species diversity in a community.

False discovery rates
A method of understanding the rate of type I errors in null hypothesis testing when performing multiple comparisons.

Isometric log ratio transform
(ilr). Converts a vector of proportions into a vector of log ratios using a tree as a reference. The computed log ratios consist of the difference of mean logarithms of species proportions between adjacent clades within the tree.

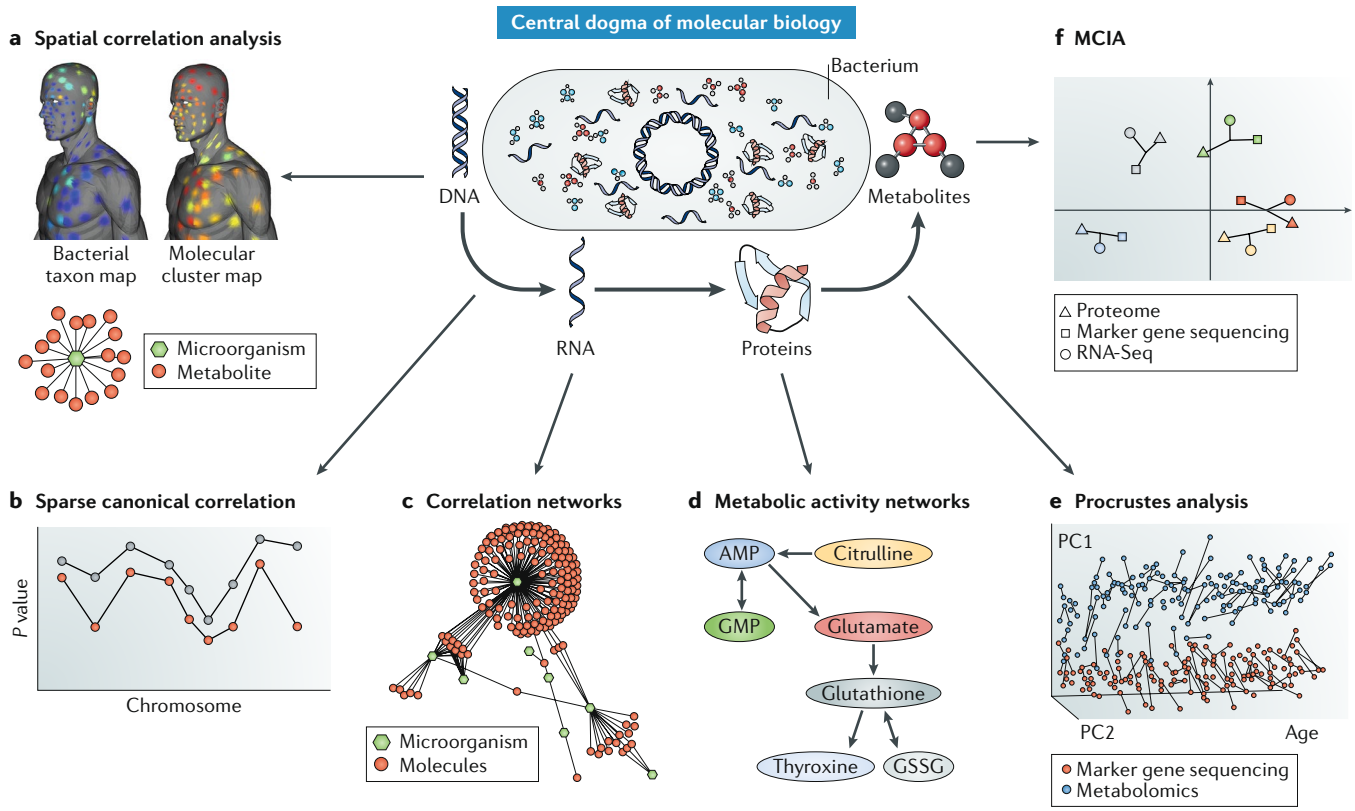

Fig. 3 | **Integrating omics data with microbiome data.** The central dogma of molecular biology of progression from genes to downstream metabolic products is reflected by the compendia of corresponding 'omes' co-occurring within the cell. Linking the knowledge from different omics studies constitutes a multi-omics analysis. Panels around the cell represent some integration examples of various omics data with marker gene sequencing: **a** | Three-dimensional visualization of mapped molecular and microbial (or any other) features aids our understanding of spatial correlation thereof. **b** | Sparse canonical correlation analysis[140] identifies linear combinations of the two sets of variables that are highly correlated with each other. **c** | Correlation network analysis shows clustering of a particular microorganism with metabolites that are potentially produced and/or processed by it. **d** | Metabolic activity networks help to predict microbial community structure and function by mathematical modelling of the molecular mechanisms of particular organisms. **e** | Procrustes analysis enables the direct comparison of different omics data sets with the same internal structure on a single principal coordinates (PC) analysis plot to reveal trends in the data. **f** | Multiple co-inertia analysis (MCIA) enables multidimensional comparisons through graphical representation so that the similarity of different omics data can be more easily understood. GSSG, oxidized glutathione; RNA-Seq, RNA sequencing.

history[106,119,120] or microbial niche differentiation in response to environmental factors such as pH (REF.[121]). After the ilr is applied, standard statistical tools, such as multivariate response, linear regression and classification, can effectively test for differences in the balances or log ratios between microorganisms rather than the raw microbial abundances, controlling for compositionally. Other recent methods use absolute quantification to address compositionality by complementing sequencing with microbial cell counts in each sample[122,123].

Machine learning is emerging as an especially useful technique for determining how microbiome data can be used to separate samples based on the current state (usually determined by metadata categories, such as healthy state versus diseased state)[124,125] or, excitingly, to predict a future state[126,127]. For instance, it is possible to model the severity and susceptibility of gingivitis based on an individual's oral microbiota[126]. Random forests regression, a machine learning technique, has been effective in many applications, ranging from dating time since death of a corpse[128] to providing a model for determining microbiome maturation in child development[129]. SourceTracker[130], a Bayesian estimator of the microbial sources that make up an unknown community, is useful for classifying microbial samples according to environment of origin[131]. Importantly, machine learning analyses need a substantial sample size and should always be coupled with cross validation, independent test sets or other experimental and biological confirmation to ensure robust findings.

Random forests regression
A machine learning technique that uses decision trees to perform classification.

Integrating other omics data

Knowing the composition of a microbial community is no longer a sufficient research goal; we want to know the function of the community. Integrating other data types — including marker gene sequencing, metagenomics, metatranscriptomics, metaproteomics, metabolomics and other techniques — for a given study is crucial for a comprehensive understanding of the composition and function of microbial communities. For example, changes in the metabolite profile of a microbial

Box 3 | **Metabolomics and the microbiome**

Microbially produced metabolites influence host physiology, can shape microbial community dynamics and are involved in both health and disease. These metabolites can have both beneficial (for example, short-chain fatty acids[153]) and detrimental (for example, the genotoxin colibactin[154]) effects on the host. However, identifying a metabolite as sourced from the microbiome is particularly challenging. Even more challenging is identifying which microorganism or collection of microorganisms produced or modified a particular metabolite. Here are several strategies to address this problem:

- Compare metabolites from natural samples to those from cultured isolates of microbiome-isolated microorganisms. One useful approach is matching tandem mass spectrometry data from cultured isolates to data from clinical or environmental samples, showing that a particular metabolite signature can be sourced from the cultured microorganism[155].
- Map metabolites detected in a microbiome sample to paired genome or metagenomic data. Some metabolites are unique to particular microbial taxa. Detection of these metabolites in a natural sample can enable determination of their likely source by mining paired genomic data for genes known to produce that metabolite. For example, 2,3-butanedione, a unique fermentation product, is a microbial metabolite produced by *Streptococcus* spp. Detection of this metabolite in clinical samples along with the biosynthetic genes facilitates mapping of reads to the biochemical pathway back to the genome of the organism of origin[146].
- Build co-occurrence networks of microorganisms and metabolites. Co-occurrence or correlation methods associate microorganisms with metabolite features. This is an active area of research, but available algorithms that have been optimized for detecting correlations between microorganisms in sparse microbiome data include SparCC[116], CCLasso[156] and others[114,157]. However, this approach warrants caution because of the high false discovery rates across the large multivariate data sets.
- Germ-free versus specific pathogen-free murine models. These comparisons identify metabolites from the microbiome as metabolites detected in colonized mice but not in uncolonized mice are likely produced by microorganisms. Gnotobiotic mice (mono-colonized or with defined communities) help identify specific microorganisms that produce metabolites of interest[158].

community reflect changes in its biosynthetic activity, mRNA and protein expression, and protein activity[132]. Multi-omics analysis integrates chemical and biological knowledge to provide a more complete picture of a biological system and is an active area of research with largely untested methods (FIG. 3).

Integrating multi-omics data types is inherently difficult. For example, gene expression and metabolism operate on different timescales[133], and microorganisms produce many metabolites, often only in response to molecular signals from other species[134]. Also, metagenomic and metabolomic data sets (where the data matrices are composed mostly of zeros) are much sparser than metaproteomic data sets, and this may pose technical problems for some methods. Although the integration of different omics data sets is a work in progress, tools that integrate these data sets are becoming increasingly available. For example, XCMS Online integrates metabolomic data with metabolic pathways, as well as transcriptomic and proteomic data[135]. Traditional correlation methods such as Pearson and Spearman could enable pairwise correlation between features across omics data sets. However, these are prone to false positives owing to the sparsity and high dimensionality of microbiome and metabolome data sets. Procrustes analysis[136] uses dimensionally reduced data to test whether patterns (distances) between samples in one data set are observed in the other, essentially correlating ordination spaces rather than individual features (tested using Mantel[137] or PROcrustes randomization TEST). Other methods integrate omics data sets by not only taking into account the relationships between samples but also associating samples to particular metadata categories of interest (such as examining healthy versus diseased groups or control versus treatment groups). These methods include co-inertia analysis, which uses dimensionality reduction to associate sample patterns in two data sets and relevant metadata[138], and partial least-squares[139], as well as related methods such as canonical correlation analysis[140] or robust sparse canonical correlation analysis, which is a variation of the method to deal with sparse omics data[141].

Advanced integrative analysis tools include molecular networking with Global Natural Product Social (GNPS)[142] to identify metabolites and pathway annotations[143] and general systems biology tools, exemplified by XCMS Online[135]. Increasingly, multi-omics studies are investigating temporal patterns in addition to spatial patterns. Spatial mapping[144], which can now be performed with the tool 'ili[144], adds a powerful dimension to multi-omics studies through visual representations that are readily amenable to human interpretation.

Integration with other omics data can be performed using various statistical methodologies[145]. However, these techniques have been shown to perform suboptimally on microbiome data sets[114]. Furthermore, simply finding correlations in various omics data by itself is only the first step. Establishing causation and correlation across data sets is the next challenge. BOX 3 gives an example of the integration of metabolome and microbiome data sets and corresponding approaches to move beyond correlation and determine causation. Correction for multiple comparisons is crucial in multi-omic analyses; data sets can contain thousands of different microorganisms and metabolites, so significant correlations are expected by random chance. Measures to correct significance testing for multiple comparisons include the false discovery rate (for example, Benjamini–Hochberg correction) or, for more conservative corrections, the family-wise error (for example, Bonferroni correction). The use of these methods to penalize multiple comparisons in conjunction with statistical models that incorporate sparsity and compositionality[114] can reduce false discovery rates in large multi-omic comparisons.

Family-wise error
The probability of making one or more type I errors (false discoveries) when performing multiple hypotheses tests.

Despite these challenges, the future potential for omics data integration is promising. In particular, there are numerous examples where metagenome, metatranscriptome and metabolome data have been successfully integrated, illuminating gene regulation in microbiomes[37] and correlating the presence of microorganisms with metabolites[146]. Such studies have provided insights beyond the capacity of single omics studies, such as studies of gut bacterial metabolism of xenobiotics[52] and how antibiotic-induced microbiome depletion creates a favourable metabolomic environment for *Clostridium difficile*[147]. Comparatively, the integration of metaproteomics data with microbiome data is a relatively new field of investigation, though there are many recent examples of successful integration ranging from identifying biomarkers of Crohn's disease[148] to examining microbial protein production in layers of permafrost[149]. Additionally, tool development for metaproteomics annotations and analysis is ongoing[150,151]. Overall, integrating omics data can provide a more holistic and mechanistic understanding of microbiomes — from DNA identification to functional production of metabolites and proteins — and ideally lead to more actionable scientific insights.

Conclusions

In this Review, we discuss how all stages of conducting a microbiome study, from designing the experiment to collecting and storing the samples to obtaining insight from graphical displays of the sequence data, can substantially impact the results and their biological interpretation. As the effects of many of these technical steps are large compared with the real biological variability to be explained, standardization is necessary in order to compare and combine separate studies, and the first efforts to do this and to provide recommendations and best practices, such as the International Human Microbiome Standards and the Microbiome Quality Control (MBQC) project, are already underway. Including bioinformatics pipelines and controls into these standardization efforts, and in particular using cloud-enabled reproducible computing resources that run open-source code on publicly available data to reproduce scientific claims of publications, is a rapidly emerging area that will bring consistency and comparability to the microbiome field. An important part of such efforts will be spike-in standards (which have already been so important to standardizing microarrays) and standardized, biologically realistic samples that can be used to quantify systems-level accuracy in microbiome assays.

This article is focused primarily on DNA-level analyses at the whole-community level, but as expression-level profiling and single-cell profiling techniques continue to advance, many similar considerations will apply to those types of data also. Avoiding the mistakes that have been repeated frequently in other expensive assays, such as inadequate sample size and validation, and employing best practices for standards, sample handling, compositional data analysis and other frequent pitfalls will accelerate progress in these areas. Using standardized and well-characterized sample sets, such as those developed in the MBQC project and in the Earth Microbiome Project, can greatly shorten the time needed to understand the value and unique insights provided by a new technique.

As the field trends towards ever-larger data sets, understanding subtle confounding factors long known to epidemiologists and taking more care with longitudinal study designs will become increasingly important. The value of interventional studies over observational studies is considerable, especially when human, animal model and in vitro data can be correlated across scales and systems. Increased standardization of techniques and dissemination of methods with low noise and bias will greatly increase the ability of the microbiome field to deliver on the promise of translatability from lab-scale studies to the clinic, field or natural environment.

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