Automated strain separation in low-complexity metagenomes using long reads

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Abstract

High-throughput short-read metagenomics has enabled large-scale species-level analysis and functional characterization of microbial communities. Microbiomes often contain multiple strains of the same species, and different strains have been shown to have important differences in their functional roles. Despite this, strain-level resolution from metagenomic sequencing remains challenging. Recent advances on long-read based methods enabled accurate assembly of bacterial genomes from complex microbiomes and an as-yet-unrealized opportunity to resolve strains. Here we present Strainberry, a metagenome assembly method that performs strain separation in single-sample low-complexity metagenomes and that relies uniquely on long-read data. We benchmarked Strainberry on mock communities and showed it consistently produces strain-resolved assemblies with near-complete reference coverage and 99.9% base accuracy. We also applied Strainberry on real datasets for which it improved assemblies generating 27-89% additional genomic material than conventional metagenome assemblies on individual strain genomes. Our results hence demonstrate that strain separation is possible in low-complexity microbiomes using a single regular long read dataset. We show that Strainberry is also able to refine microbial diversity in a complex microbiome, with complete separation of strain genomes. We anticipate this work to be a starting point for further methodological improvements aiming to provide better strain-resolved metagenome assemblies in environments of higher complexities.

Main

The analysis of bacterial communities through metagenome sequencing is a computationally challenging step which is further hampered by strain variation among species. Current techniques for *de novo* metagenome assembly are able to reconstruct the chromosomal sequences of sufficiently abundant species within a microbial sample, but ideally should also aim at reconstructing each strain present. A critical application of metagenome assembly is the identification of fine differences in the genetic makeup of organisms that end up playing major functional roles in an environment. Sequencing studies of pathogens provide evidence that microbial phenotypes could be strain-specific[1,2]. For example, unusual *Escherichia coli* strains could be highly pathogenic[3] or carcinogenic[4], different *Helicobacter pylori* strains have been associated with different risks for gastric cancer[5], some variants of *Staphylococcus epidermidis* seem to be associated with psoriatic skin[6].

While recognizing the challenges for the precise characterization of what constitutes a “strain”, here we will associate the concept of “strain” to a bacterial haplotype, *i.e.,* a contiguous sequence of nucleotides observed jointly and in sufficient abundance by sequencing reads. We therefore define

the “strain separation problem” as the reconstruction of partial or complete DNA sequences corresponding to strains, at the base level.

The strain separation problem has been extensively studied in the case of short-read sequencing[7], either without any prior knowledge (*de novo*) or reference-based. Previous works attempted to tackle the *de novo* problem using short reads, with various levels of success. DESMAN[8] managed to reconstruct haplotypes of core genes but not entire genomes. STRONG[9] addressed some of DESMAN limitations and is able to determine the number and sequence of strains in a metagenome-assembled genome by exploiting the co-assembly graph over the predicted single-copy-gene sequences and using a novel variational Bayesian algorithm. ConStrains[10] quantifies and reconstructs *conspecific* (relative to the same species) strain variations by mapping reads on a species-based marker gene set and providing a SNP-based model for each of the identified strains. LSA[11] is a short-read *de novo* pre-assembly method that aims at separating reads from multiple samples into biologically informed partitions which enable closely-related-strain separation and assembly of individual genomes. OPERA-MS[12] is a hybrid (short and long reads) metagenome *de novo* assembler, whose ability to assemble genomes at the strain level is dependent on its upstream short-read assembly phase (unassembled sequences and collapsed variants will remain so throughout the pipeline). SAVAGE[13] is a method that performs the assembly of viral quasispecies from deep-coverage short-read sequencing data and is able to reconstruct individual haplotypes of intra-host virus strains. SAVAGE is also employed in VG-flow[14], a *de novo* approach which enables full-length haplotype reconstruction from pre-assembled contigs of complex mixed samples. All the above methods are not applicable when the input consists of long reads only, and the last two are limited to small genomes (approximately up to 200 Kbp).

Related works have analyzed strains without performing separation, but rather by mapping to existing databases of genomes. StrainPhlAn[15] performs phylogenetic analysis of a population and strain-level variation profiling, through read mapping on reference species-specific markers. StrainEst[16] is a reference-based method exploiting the single-nucleotide variant profiles of available genomes of selected species to determine the number and identity of coexisting strains and their relative abundances in mixed metagenomic samples.

All previous works on strain-level assembly/characterization are based on short-read sequencing data. With the advent of long-read metagenomics sequencing, they cannot be re-used due to fundamental differences in the nature of the data. Many of them (*e.g.,* LSA and references therein) rely on the reliable detection of error-free k-mers with high k values (> 20), which cannot be performed on long reads due to the high error rate. Some methods have been specifically designed to work with multiple related samples (*e.g.,* time series), to reconstruct core genes, or to simply provide a strain-level profile of a metagenomic dataset (with no actual assembly). It would be desirable to have a method that, using long reads, produces a strain-separated *de novo* assembly from only a single sample.

Existing long-read *de novo* assembly methods can partially, but not completely, separate strains. We will focus on three state-of-the-art assembly methods (metaFlye, Canu, and Lathe), which were either designed for metagenome assembly or have been previously shown to be suitable. metaFlye[17] is, to the best of our knowledge, the only long-read assembler explicitly supporting metagenomic data. metaFlye initially generates a set of error-prone sequences called *disjointigs* representing concatenations of multiple disjoint genomic segments. They are then represented as a repeat graph in which reads are used to untangle repeats and provide an accurate set of contigs. As metaFlye is

an option within the Flye assembler, in the following we will refer to metaFlye simply as Flye. Canu[18] is the successor of the Celera Assembler and it was designed for error-prone long reads. It is based on the overlap-layout-consensus paradigm and during its development it introduced new overlapping and assembly algorithms in order to better handle the advances and challenges offered by long-read sequencing technologies. As opposed to Flye, Canu was not specifically designed for metagenomic data although it is often considered an alternative to Flye in this context[19–21]. Lathe[22] is a recently developed workflow for Nanopore reads which attempts to provide complete closed bacterial genomes from microbiomes. It combines existing methods for basecalling, long-read assembly (either Flye or Canu), extensive polishing steps to detect and correct misassemblies, and performs genome circularization.

Throughout the manuscript, we will use the term *strain-oblivious assembly* to refer to a metagenome assembly generated by an assembler which did not attempt any strain separation. Conversely, the term *strain-aware assembly* will be employed to refer to a metagenome assembly where genomic sequences are expected to be reconstructed at the strain level. Moreover, as the assembly of strain sequences from strain-oblivious sequences is a very similar problem to the reconstruction of *haplotypes* in a polyploid genome, we will interchangeably use the terms strain and haplotype in the methodological context.

In this work we show for the first time a method that performs strain separation in low-complexity metagenomes using error-prone long-read technologies. Exploiting state-of-the-art tools for variant calling, haplotype phasing, and genome assembly, we present an automated pipeline called *Strainberry*. It achieves single-sample assembly of strains with higher quality than other state-of-the-art long-read assemblers. Strainberry combines a strain-oblivious assembler with the careful use of a long-read variant calling and haplotyping tool, followed by a novel component that performs long-read metagenome scaffolding. We extensively tested Strainberry on mock communities as well as uncharacterized real samples, and showed that reanalysis of existing long-read metagenomic samples unravels novel uncharacterized strains.

Results

A software pipeline for automated strain separation using long-read sequencing data from low-complexity metagenomes

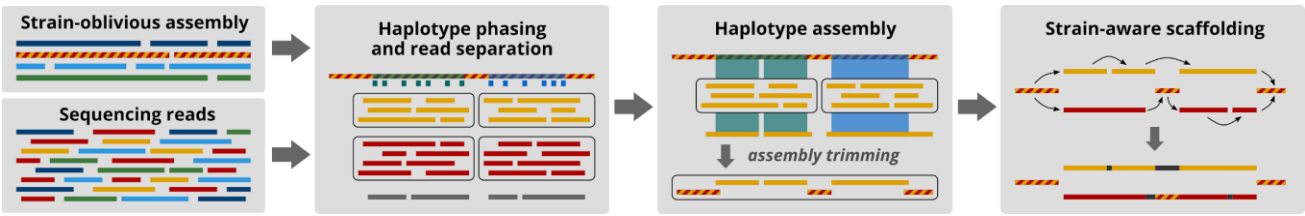

Figure 1. Strainberry pipeline. The pipeline starts from a strain-oblivious assembly and the corresponding set of reads. It then performs haplotype phasing on the strain-oblivious assembly to separate reads into groups that likely correspond to strains. Each group is assembled separately. A final scaffolding step is used to connect sequences likely corresponding to the same strain.

The Strainberry pipeline is depicted in Figure 1 and consists of three main steps: (i) haplotype phasing and read separation, (ii) haplotype assembly, and (iii) strain-aware scaffolding. It requires three inputs:

a strain-oblivious metagenome assembly, a set of long reads aligned to the assembly, and a parameter *n* which represents how many strains we will seek to reconstruct per contig. The input assembly is either one generated from the input reads, or one made from a combination of sequencing technologies. In our evaluation of Strainberry, we often used a single long-read dataset assembled using the Flye assembler which is, to the best of our knowledge, the only long-read assembler explicitly supporting metagenomic data. We additionally tested the performance of the Canu assembler. Aligned reads are used to identify single-nucleotide variants (SNVs) on assembled contigs. Sequences containing a large percentage of such SNVs likely correspond to multiple collapsed haplotypes/strains. We use those SNVs to perform haplotype phasing and therefore separate reads originating from different haplotypes. Each separated set of reads can therefore be assembled independently using a standard *de novo* assembly tool (*e.g.*, Flye). We obtain a strain-aware set of contigs by putting together the non-separated regions of the input assembly, which are either shared between multiple strains or specific to a single strain, and the haplotype-separated assemblies. The last step involves an alignment of input reads on the strain-separated contigs which is exploited to join contigs into longer scaffolds. The output of Strainberry is a multi-FASTA file containing contigs shared between multiple strains, and strain-specific contigs. Components of the pipeline are presented in more details in the Methods section.

Overview of evaluation data

Four datasets of increasing complexity were considered in order to assess to which extent our method is able to reconstruct complete strain genomes. Two low-complexity mock communities (Mock3 and Mock9) containing respectively three and nine precisely-known bacterial strains (**Supplementary Table 1**) enable an accurate assessment of the quality of results returned by our pipeline. Two metagenomic samples of real sequencing data, one with four dominant bacterial strains and another one with a higher number of species, enabled us to reconstruct novel sequences of strains. They were selected from two different studies. The first one is a low-complexity microbiome from natural whey starter cultures for which two strains of *Lactobacillus helveticus* were identified and assembled[23]. Reads were sequenced with both PacBio and Nanopore technologies which allowed us to assess the performance of our approach with different technologies and validate it with available reference genomes. The second study contains a more complex dataset that is based on Nanopore sequencing data from a human stool microbiome[22]. Previous analyses hinted at the presence of multiple uncharacterized strains: species-level binning yielded near-complete genome reconstructions characterized by a significant percentage of SNVs with respect to the assembled reads.

Evaluation metrics for strain-oblivious and strain-separated assemblies

Prior to separating strains, our method hinges on having an initial high-quality strain-oblivious assembly. We consider three criteria to be important for such an assembly, namely, 1) comprehensive species-level representation, 2) low amount of incorrectly duplicated sequences, and 3) high contiguity. Criterion 1) is a necessary (but insufficient) condition for the complete reconstruction of individual strains. Criterion 2) is not an absolute requirement for any strain separation assembler, but ours relies on similar haplotypes being “conservatively” collapsed rather than erroneously split. In general, duplicated sequences that are highly similar within an assembly either indicate that some strain-specific regions have been correctly assembled or can be produced by incorrect strain

separation. Criterion 3) enables to output more contiguous strain-aware assemblies, due to the fact that strain separation is likely to introduce additional fragmentation over the input assembly.

The evaluation of metagenome assemblies is a complex topic due to the lack of an exhaustive knowledge of the species in a sample, let alone closely-related strains. Many standard assembly evaluation metrics need in fact to be interpreted differently in the strain-aware context. We detail them in the "Strain-aware assembly evaluation" section in the Methods. Nevertheless, we will report standard evaluation metrics such as number of contigs, size of the assembly and N50 (*i.e.*, the length for which all contigs of that length or longer cover at least half of the total assembly length) on all the evaluated assemblies.

Specific to synthetic data, the NG50 variant (*i.e.*, the length for which all contigs of that length or longer cover at least half of the total genome length) is reported instead of the N50 value. We will also report the percentage of unaligned bases in both references and assemblies, which is a key metric for evaluating whether complete strain-level genomes were reconstructed. In addition, the average sequence identity, the duplication ratio (*i.e.*, the total number of aligned bases in the assembly divided by the total number of aligned bases in the reference), and the number of misassemblies, are also reported with respect to known reference genomes.

Specific to real datasets, for which a comprehensive set of reference genomes was not available, we used CheckM[24] to quality-control assemblies. CheckM is a reference-free tool that identifies and counts single-copy genes (SCGs) in order to estimate completeness, contamination, and strain heterogeneity of binned contigs. Completeness approximately refers to the percentage of unique SCGs found within a bin, while contamination reflects the multiplicity of the identified SCGs (as only one copy is expected in each assembled/binned species). Strain heterogeneity is a measure related to the contamination and expresses the proportion (as an index from 0 to 100) of multi-copy marker genes that likely come from closely related species. An important aspect to keep in mind regarding CheckM is that it only works well when genomes/bins are relatively complete. A wrong estimate of completeness and contamination is in fact possible for incomplete bins. We tried to avoid this problem by restricting the analysis of our results on highly contiguous contigs that likely represent complete genomes.

Separation of two *E. coli* strains in a three-strain mock community

Mock3 consists of reads sequenced from *Bacillus cereus*, and *Escherichia coli* strains K12 and W. The Flye and Canu assemblers were run on Mock3 and reads were mapped back to each assembly, and we ran Strainberry on both assemblies in order to separate the two *E. coli* strains. **Figure 2** shows reference coverage, average nucleotide identity and the duplication ratio of strain-oblivious and the resulting strain-aware assemblies. Strains K12 and W align to each other with an average identity of 98.65% and, for this reason, their entire genomes are collapsed by Flye into two consensus sequences (2 Mbp and 2.8 Mbp long, assembly graph shown in **Supplementary Figure 1**). Canu has performed partial strain separation, however it missed the 27% of both *E. coli* references and yielded an unsatisfactory identity percentage (99.65% and 99.84% for strains K-12 and W respectively). The high duplication ratio of the Canu assembly (1.22 and 1.37 for the two *E. coli* strains) excludes it from being characterized as strain-oblivious. Strainberry is able to accurately separate both the Canu and Flye assemblies into two sets of contigs (total length 9.8 Mbp) with an almost complete coverage of both reference genomes and a nearly perfect average nucleotide identity (with Flye, 99.98% and

99.97% strains K12 and W respectively). The high duplication ratio inherited from the upstream Canu assembly was slightly reduced.

Overall, the strain-aware assemblies are of high quality, as evidenced by NG50, sequence identity, duplication analysis, and misassembly analysis (**Supplementary Note 1** and **Supplementary File 1**). As an example, the strain-separated Flye assembly yielded very high NG50 values, duplication ratios close to 1, and a reasonable amount of misassemblies with respect to all references. The Flye assembly had 2 detected inversions and 5 detected relocations, while Strainberry produced 2 detected inversions and 8 detected relocations. We checked that the locations of these putative misassemblies are at the same chromosomal locations in both strains, except in *E. coli* W where one relocation was corrected by our pipeline, but a new one was introduced (**Supplementary Note 1**). Thus, identified misassemblies do not correspond to major rearrangements and, even though the amount of detected misassemblies is numerically higher, this is a natural consequence of having assembled a significantly larger number of bases.

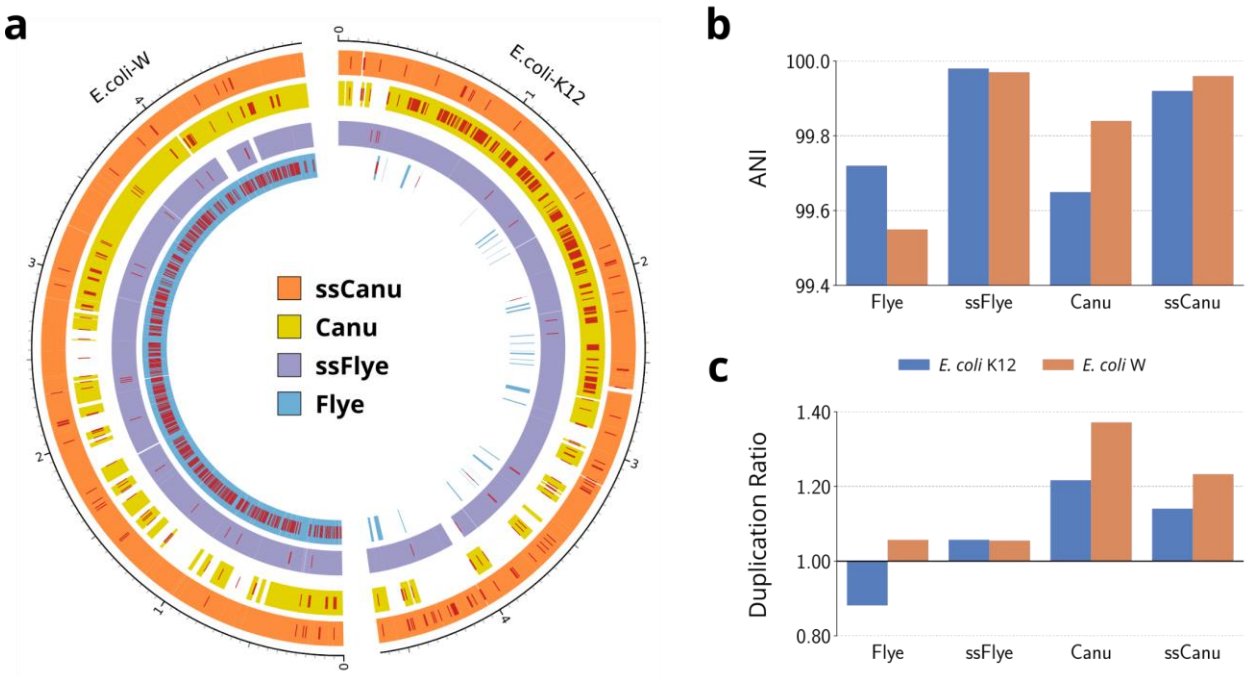

Figure 2. Mock3 dataset assembly statistics. (a) Circos[25] graph displaying the coverage and SNV-rich regions (single-nucleotide errors) of the strain-oblivious assemblies (Flye and Canu) and the strain-separated ones (ssFlye and ssCanu, respectively) compared to the reference sequences of the two *E. coli* strains. (b) Average nucleotide identity (ANI) and (c) duplication ratio of assemblies.

Separation of five close strains in a nine-strain mock community

The more challenging Mock9 dataset is composed of 9 genomes (**Supplementary Table 1**) with two strains of *E. coli* and two strains of *S. aureus*; the other genomes are of different species. As done in Mock3, a Flye assembly, a Canu assembly, and their respective read alignments were generated and provided as input to Strainberry. In this case, we aim at achieving a two-strain separation of *S. aureus* genomes, and a three-strain separation of *S. sonnei* and the two *E. coli* strains, which are three similar genomes despite *S. sonnei* being a different species. In fact, the two *E. coli* strains, *S. sonnei* but also *K. pneumoniae* all share high sequence identity. Flye was able to separate most of the *K. pneumoniae* genome, while it collapsed the other genomes into consensus contigs (**Figure 3**), as expected from

a good strain-oblivious assembler. Canu, on the other hand, completely reconstructed the *K. pneumoniae* genome but also attempted to separate individual *S. aureus*, *E. coli*, and *S. sonnei* strains. Nevertheless, while providing a significant coverage of the reference sequences, the Canu assembly is characterized by an imperfect sequence identity and a high duplication ratio (**Figure 3**).

We first look at the two *S. aureus* strains, which were most likely to be affected by our two-strain separation. They have a lower sequence identity (97.61%) compared to the two *E. coli* strains (98.65%), Flye is still unable to resolve them (**Supplementary Figure 2**). Instead, Strainberry correctly separated the Flye consensus sequences into an almost complete coverage of the reference genomes (**Figure 3a**), an average nucleotide identity of 99.97% for both *S. aureus* strains ATCC and FDAA scaffolds (**Figure 3b**), and a duplication ratio close to 1.0 (**Figure 3c**). Moreover, the final scaffolding step significantly improved contiguity achieving NG50 values of ~2.2 Mbp and ~2.7 Mbp for the two separated strains (**Supplementary File 1**). The *K. pneumoniae* genome assembly is also improved by Strainberry due to a successful separation of the 14% of genome that was not precisely reconstructed by Flye. The duplication ratio close to 1.0 additionally highlights the good quality of the strain-separated assembly. Canu attempted to separate closely-related strains, however with unsatisfactory results. Even though at least 70% of each reference genome was represented in the output assembly, the average nucleotide identity is 99.85% and 99.74% for *S. aureus* strains ATCC and FDAA, respectively. The Strainberry two-strain separation of Canu assembly greatly improves these metrics, yielding near-complete assemblies of *S. aureus* strains (**Figure 3a**) and 99.9% sequence identity (**Figure 3b**). Unfortunately, the high Canu duplication ratio propagates through the Strainberry assembly, even though duplication ratio is slightly reduced after separation and scaffolding (**Figure 3c**).

We now turn to the two *E. coli* strains and *S. sonnei,* which are expected to be affected by a three-strain separation. In this case, Flye is only able to partially separate some strain-specific regions of the three genomes, however with much lower sequence identity compared to the other near-complete assemblies (*B. cereus*, *K. pneumoniae*, *L. monocytogenes*, and *N. meningitidis*). Strainberry significantly improved the reference coverage and the average nucleotide identity with respect to the reference sequences, with a duplication ratio close to 1.0 (**Figure 3d**, **e**, and **f**), yielding a partial separation of *S. aureus* strains, albeit at a lower sequence identity than if performed with a two-strain separation (**Supplementary File 1**). Canu was unable to assemble the three reference sequences completely and, at the same time, yielded a very high duplication ratio (as previously observed in *S. aureus* assemblies and in the Mock3 dataset). The Strainberry three-strain separation of the Canu assembly overall improved all metrics or yielded comparable results (**Supplementary File 1**). We also tested a Strainberry two-strain separation of the Canu assembly which further improved reference coverage (**Figure 3d**) while yielding comparable average nucleotide identity and duplication ratio (**Figure 3e** and **f**). Unfortunately, in both cases Strainberry was only able to achieve an average nucleotide identity up to ~99.8%.

Overall, Flye yielded a better strain-oblivious assembly compared to Canu on Mock9. Strainberry was hence able to benefit from this and provided higher quality assemblies compared to the separation of the Canu assembly, as evidenced by NG50, sequence identity, duplication ratio, and misassembly analysis (**Supplementary Note 2** and **Supplementary File 1**).

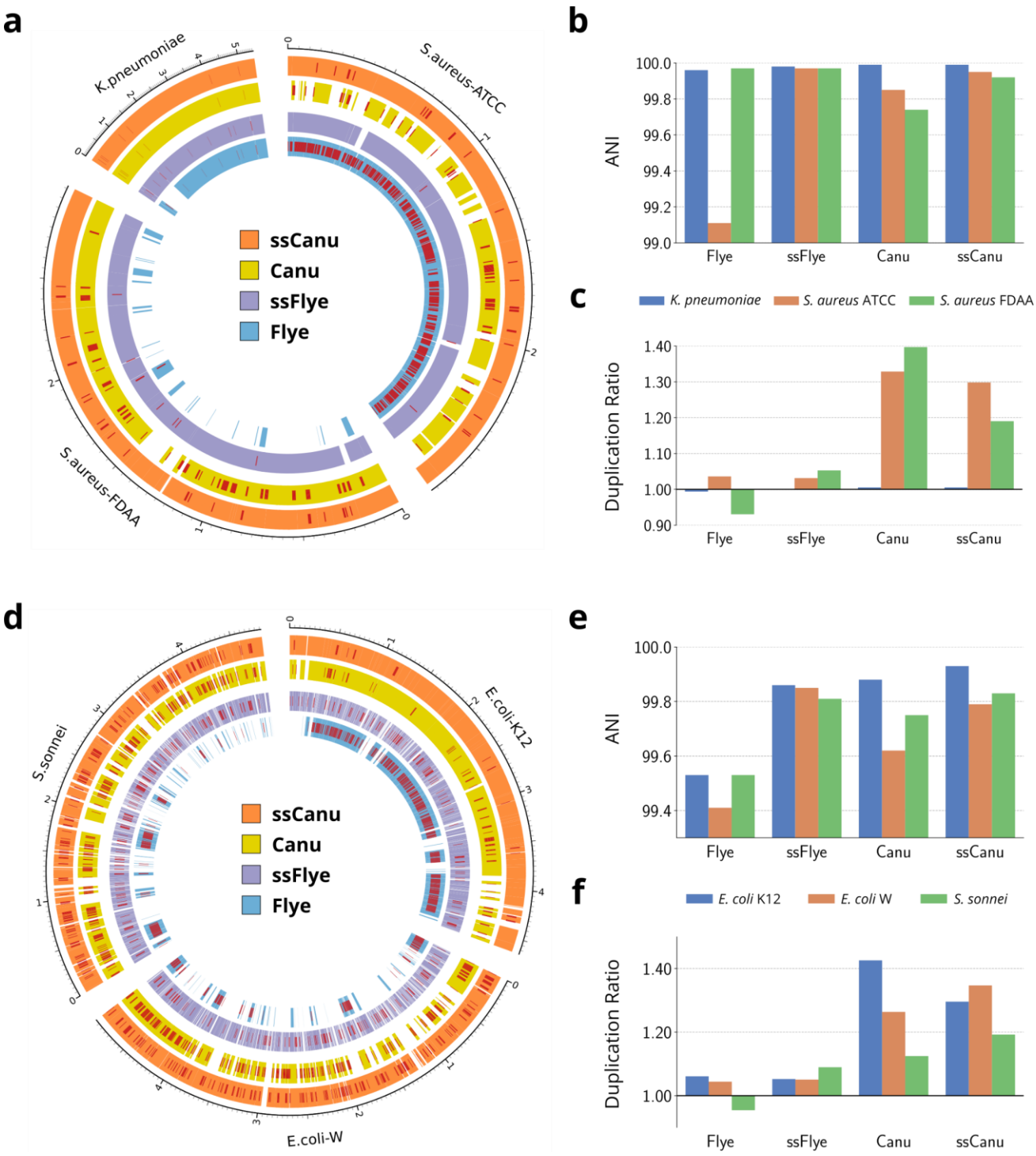

Figure 3. Mock9 dataset assembly statistics. (a) Circos[25] graph depicting reference coverage and SNV-rich regions of the strain-oblivious assemblies (Flye and Canu) and their strain-separated counterparts (ssFlye and ssCanu, respectively) compared to the reference sequences of *K. pneumoniae* and the two *S. aureus* strains. On the right-hand side, (b) the average nucleotide identity and (c) the duplication ratio of each assembly are reported. Both ssFlye and ssCanu assemblies were obtained as a result of a two-strain separation of the Flye and Canu assemblies, respectively. (d) Circos graph depicting reference coverage and SNV-rich regions of the strain-oblivious assemblies (Flye and Canu) and the strain-separated ones (ssFlye and ssCanu) with respect to the reference sequences of *S. sonnei* and the two *E. coli* strains. On the right-hand side, (e) the average nucleotide identity and (f) the duplication ratio of each assembly are reported. ssFlye was obtained as a three-strain separation of the Flye assembly, while ssCanu was obtained as a two-strain separation of the Canu assembly.

Automated strain separation on a single sample validated by manually processed and heavily curated multi-technology data

We applied Strainberry to the low-complexity microbiome NWC2 from a natural whey starter culture[23]. NWC2 contains four dominant bacterial species and, among them, two strains of the same species (*L. helveticus* strains NWC_2_3 and NWC_2_4). Therefore, it provides a good test case for our approach. Moreover, four high-quality reference sequences have been produced using a combination of Illumina, Nanopore and PacBio long-read sequencing data, and the following manual curation: Nanopore-based assembly followed by an extensive number of steps involving three PacBio-based, three Illumina-based, and two Nanopore-based runs of polishing. We independently separated strains using Strainberry applied to either the Nanopore or the PacBio dataset, without ever using short reads, in order to show that we are able to separate strains without the need of multi-technology data nor polishing, and also to assess potential differences between the two long-read technologies. A comprehensive overview of all assembly evaluation metrics computed with respect to the manually curated references are shown in **Supplementary File 2**. Significant differences between strain-oblivious and strain-aware assemblies mainly concern *L. helveticus* strain NWC_2_3 and *L. delbrueckii* (**Figure 4**), which are discussed next.

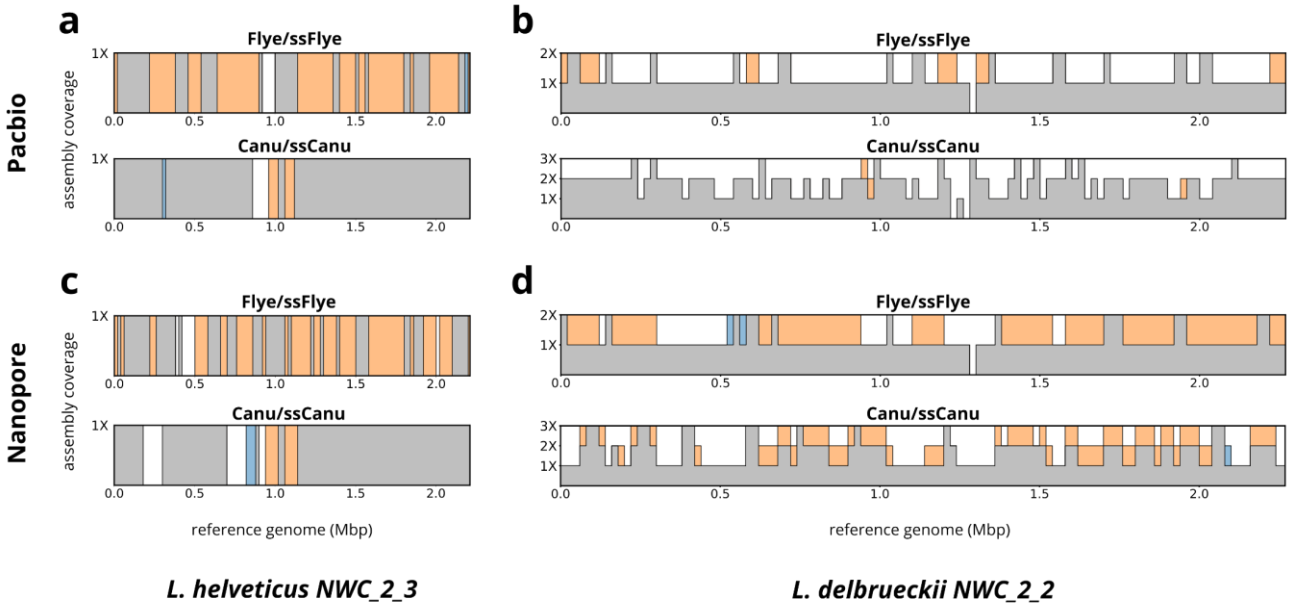

Figure 4. Assembly-level coverage of *L. helveticus* NWC_2_3 and *L. delbrueckii* NWC_2_2. Comparison between the reference coverage of the Flye and Canu assemblies and the strain-separated assemblies generated by Strainberry (ssFlye and ssCanu, respectively) for the following references and datasets: (a) *L. helveticus* NWC_2_3 reference and PacBio dataset; (b) *L. delbrueckii* NWC_2_2 reference and PacBio dataset; (c) *L. helveticus* NWC_2_3 reference and ONT dataset; (d) *L. helveticus* NWC_2_3 reference and ONT dataset. Orange regions highlight a higher coverage of the strain-separated assembly (ssFlye or ssCanu), blue regions highlight a higher coverage of the strain-oblivious assembly (Flye or Canu), and gray regions represent the minimum coverage of the depicted assemblies.

Strain separation using the PacBio technology

A strain-oblivious assembly of the NWC2 PacBio data was generated with Flye. Strainberry was run with two-strain separation. We also considered an assembly produced with Canu for comparison purposes, even though Canu produced more duplications in the Mock3 and Mock9 experiments.

Figure 4a shows that the original Flye assembly, without any additional polishing, is a strain-oblivious assembly as it fails to reconstruct a large portion (49.49%) of the reference of *L. helveticus* strain NWC_2_3 (**Figure 4a**) and a small portion (10.02%) of *L. helveticus* strain NWC_2_4 (**Supplementary File 2**). Instead, the scaffolds produced by Strainberry cover almost fully the reference strains (only 6.27% and 3.39% of the strains missing, respectively). Conversely, the original Canu assembly was able to cover almost completely both *L. helveticus* strains but Strainberry was still able to slightly improve the percentage of unaligned bases of *L. helveticus* strain NWC_2_3 from 8.22% to 4.98%. A significant number of regions of *L. delbrueckii* were also covered twice in all assemblies (**Figure 4b**), suggesting the presence of another conspecific strain in the dataset. Overall, Strainberry significantly improved Flye reconstruction of the four dominant strains with 27% additional genomic material for *L. delbrueckii* and *L. helveticus* strains, comparable sequence identity, and a reduced number of major misassembly events compared to the Flye/Canu assemblies (see **Supplementary Note 3** and **Supplementary File 2**).

Additional quality assessment of the assembled strains was carried out using CheckM (**Supplementary File 2**). The Strainberry+Flye assembly displays higher completeness values compared to the strain-oblivious Flye assembly for the two conspecific strains (*L. helveticus* strains) while yielding comparable values for other single species (*S. thermophilus* and *L. delbrueckii)*. The higher reported contamination in *L. delbrueckii* and *L. helveticus* NWC_2_4 is likely due to the number of duplicated sequences in the upstream Flye assembly, or to the presence of other closely-related strains in the metagenomic sample (only the reference sequences of the four dominant strains were available and used for the evaluation). With Canu, no major differences between the strain-oblivious and the strain-separated ones were observed.

Strain separation using the Oxford Nanopore technology

Similarly to the previous section, a strain-oblivious assembly of the NWC2 Nanopore dataset was generated with Flye using a similar protocol[23]. Also in this case a Canu assembly was produced and provided to Strainberry for comparison purposes.

Results follow the same trend as with the PacBio data (see **Supplementary Note 4** and **Supplementary File 2**). Strain-separated assemblies are able to represent reference sequences almost completely and yield just a slight improvement compared to the PacBio data for *L. helveticus* strain NWC_2_3 (**Figure 4c**). There are however some key differences for the assemblies generated with Nanopore data: an increase in contiguity, lower sequence identity to reference strains (99.34-99.76%) than with PacBio data (99.69%-99.97%), and a significant increase of strain-separated bases aligning against *L. delbrueckii* reference (**Figure 4d**). Polishing of strain-separated contigs using Nanopore-specific tools such as Medaka[26] or MarginPolish[27] yielded limited or no improvements (**Supplementary Table 2**). Overall, thanks to the longer Nanopore reads, Strainberry provided 19-49% additional genomic material on *L. delbrueckii* and *L. helveticus* strains compared to the Flye/Canu assemblies (see **Supplementary Note 4** and **Supplementary File 2**).

As expected, the CheckM analysis also follows the same trend as with PacBio data. The main difference in the Nanopore dataset is that the putative separation of a conspecific strain of *L. delbrueckii* is even more pronounced, possibly thanks to the longer reads. Moreover, a completeness greater than 90% could not be achieved for any of the strains, regardless of the assembly method. The reason for this behavior is likely due to limitations of the Nanopore technology, yielding more contiguous assemblies at the expense of higher error rates which affect sequence identity and thus

completeness (erroneous indels introduced during the assembly of separated reads likely affect marker gene annotation).

Separation of strains in a human stool microbiome dataset reveals hidden microbial diversity in a curated metagenome assembly

We applied our pipeline to a realistic strain separation instance, with no prior knowledge about strain variability. A healthy human stool microbiome (patient P1 analyzed in the work of Moss *et al.*[22]) was sequenced with Nanopore technology. A strain-oblivious reference metagenome assembly was previously generated using the Lathe workflow[22], which included extensive polishing, on which we performed a two-strain separation using Strainberry. We also created a Flye assembly for comparison purposes. In the following we will refer to the Nanopore raw data as HSM and to the strain-oblivious reference assembly as Lathe. Compared to NWC2 and the mock datasets, HSM is characterized by a higher species diversity[22]. A MetaBAT2[28] binning of the Lathe reference yields 30 bins of size greater than 2 Mbp, providing a rough estimate of the number of assembled species.

Strainberry contigs display an increased total length (+19%) and duplication ratio (+0.369) with respect to the Lathe reference assembly (**Supplementary File 3**), indicating that additional sequences (strains, as we will see next) were separated. The strain-oblivious Flye assembly also shows a slight increase in duplication ratio (+0.094) showing that it either separated some conspecific strains and/or assembled additional low-abundance material. The latter hypothesis is supported by the presence of unaligned contigs (of total size 34.6 Mbp). Compared to the Flye assembly, the Strainberry assembly also has unaligned contigs, albeit an order of magnitude less than the Flye assembly (total size 2.3 Mbp). While nearly all strain-separated contigs/scaffolds align (at least partially) to the reference metagenome, a reduced genome fraction (~90% for Flye vs. ~86% for Strainberry, see **Supplementary File 3**) is likely caused by the lower coverage of separated read sets, or, for the Flye assembly, by its different assembly strategy. The number of misassemblies, mismatches and indels shown in **Supplementary File 3** do not accurately reflect the quality of the assembly as they are obtained by mapping an assembly to the possibly imperfect and strain-oblivious Lathe reference assembly. Precisely evaluating misassemblies would require a perfect metagenome reference which is not available here (see "Evaluation metrics for strain-oblivious and strain-separated assemblies").

Due to the lack of an accurate strain-level characterization of HSM, to assess the ability of our pipeline to identify and separate strains we considered contiguous and complete bins that were likely to represent a consensus of conspecific strains or closely related species. We focused on two nearly complete bins with low contamination (as reported by CheckM), which were likely to contain multiple strains (**Supplementary File 3**). They were classified as *Veillonella atypica* and *Eubacterium eligens* at the species level. Note that, as of July 2020, *Eubacterium* is a provisional genus name in the NCBI taxonomy. Bin sizes (2.4 and 3.2 Mbp) were also compatible with the median genome length of the assigned species (2.1 and 3.0 Mbp). In addition, Strainberry produced separations for the *V. atypica* and *E. eligens* contigs as they had a high enough percentage of SNVs (see **Supplementary Figure 3** and Methods).

Depth of coverage and sequence length for *V. atypica* and *E. eligens* contigs were evaluated before and after our pipeline as a first evidence of a plausible strain separation. The separated contigs for *V. atypica* are characterized by a halved depth of coverage compared to the Lathe contigs, suggesting

two equally abundant strains (**Figure 5a**). The *E. eligens* contigs also exhibit a similar behavior after the separation (**Figure 5b**).

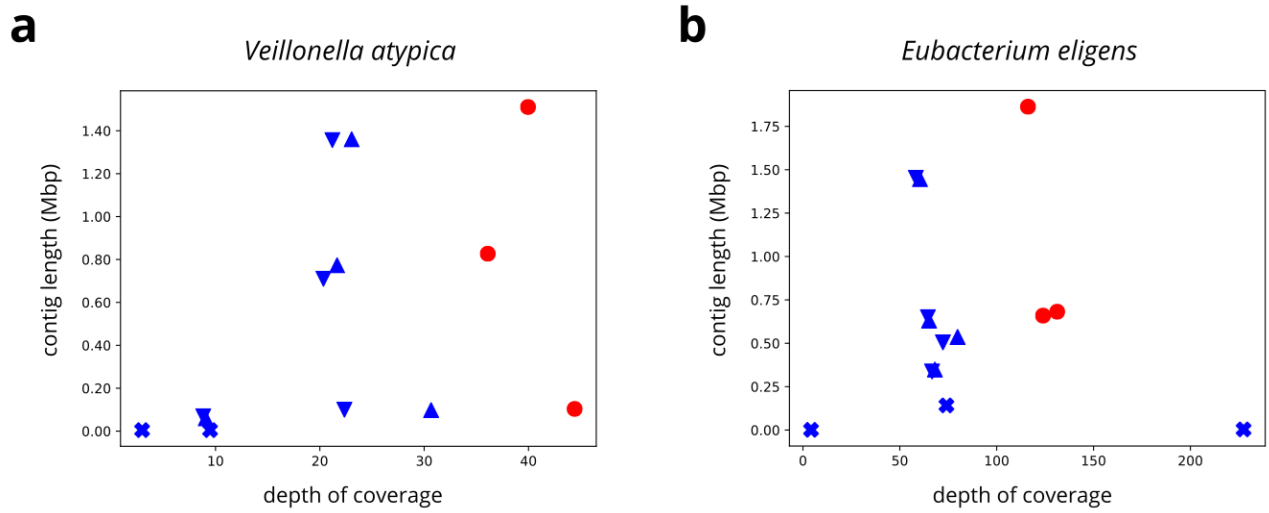

Figure 5. Depth of coverage of (a) *V. atypica* and (b) *E. eligens* Lathe bins before and after the strain separation of the Lathe reference assembly. Red circles correspond to Lathe contigs. Triangles are assemblies from separated reads and are grouped so that the up-facing (resp down-facing) ones correspond to the high-coverage (resp low-coverage) haplotype of a separation. Blue X's are non-separated regions from Lathe contigs.

V. atypica and *E. eligens* contigs were further evaluated with CheckM in order to estimate the completeness and the contamination levels of the assembled sequences (**Supplementary Table 3**). As opposed to the Lathe reference, both the strain-separated and Flye assemblies yielded a lower completeness. As expected, strain-separated contigs also displayed higher contamination and strain heterogeneity. Sequences have indeed been "duplicated" through strain separation and, for this reason, marker genes are found in multiple copies. The lower completeness of strain-aware contigs is likely due to the lower depth of coverage of the assembly (*e.g.*, from 40X to 20X for *V. atypica*) and lack of polishing. Indels appear to be one of the primary causes of frameshifts in open reading frames and hence missing marker genes. A similar behavior was previously observed in the Nanopore-based NWC2 dataset. In order to provide a fair comparison with the Lathe assembly, we polished the Strainberry and the Flye assemblies as carried out in the Lathe workflow (*i.e.*, 4 rounds of Racon[29] followed by one round of Medaka[26]). With additional polishing Strainberry yielded comparable completeness and much higher contamination and strain heterogeneity compared to the Lathe assembly. This is indeed an additional evidence that conspecific strains might have been separated. The polished Flye assembly, on the other hand, was only characterized by a limited improvement in *V. atypica* completeness (**Supplementary Table 3**). It is worth noticing that the Strainberry separation of the *V. atypica* bin yielded 86% additional genomic material, allowing to characterize separated contigs by two distinct strain-level classifications (~2 Mbp each). Specifically, Strainberry contigs have a best match and moderately cover the *V. atypica* strain ACS-134-V-Col7a and the *V. atypica* strain ACS-049-V-Sch6 available references (**Supplementary Figure 4**). Therefore, it appears that HSM contains two conspecific strains of *V. atypica*, one closer to strain ACS-134-V-Col7a, the other one to strain ACS-049-V-Sch6. This result is also observed in the raw reads: 6,222 are classified as *V. atypica* at the species level, 2,833 (~22.4 Mbp) as strain ACS-134-V-Col7a, and 2,504 (~19.4 Mbp) as strain ACS-049-V-Sch6. Strainberry also produced 89% additional genomic material on the *E. eligens* bin, yet it was not possible to classify separated contigs with at a finer level as for *V. atypica*.

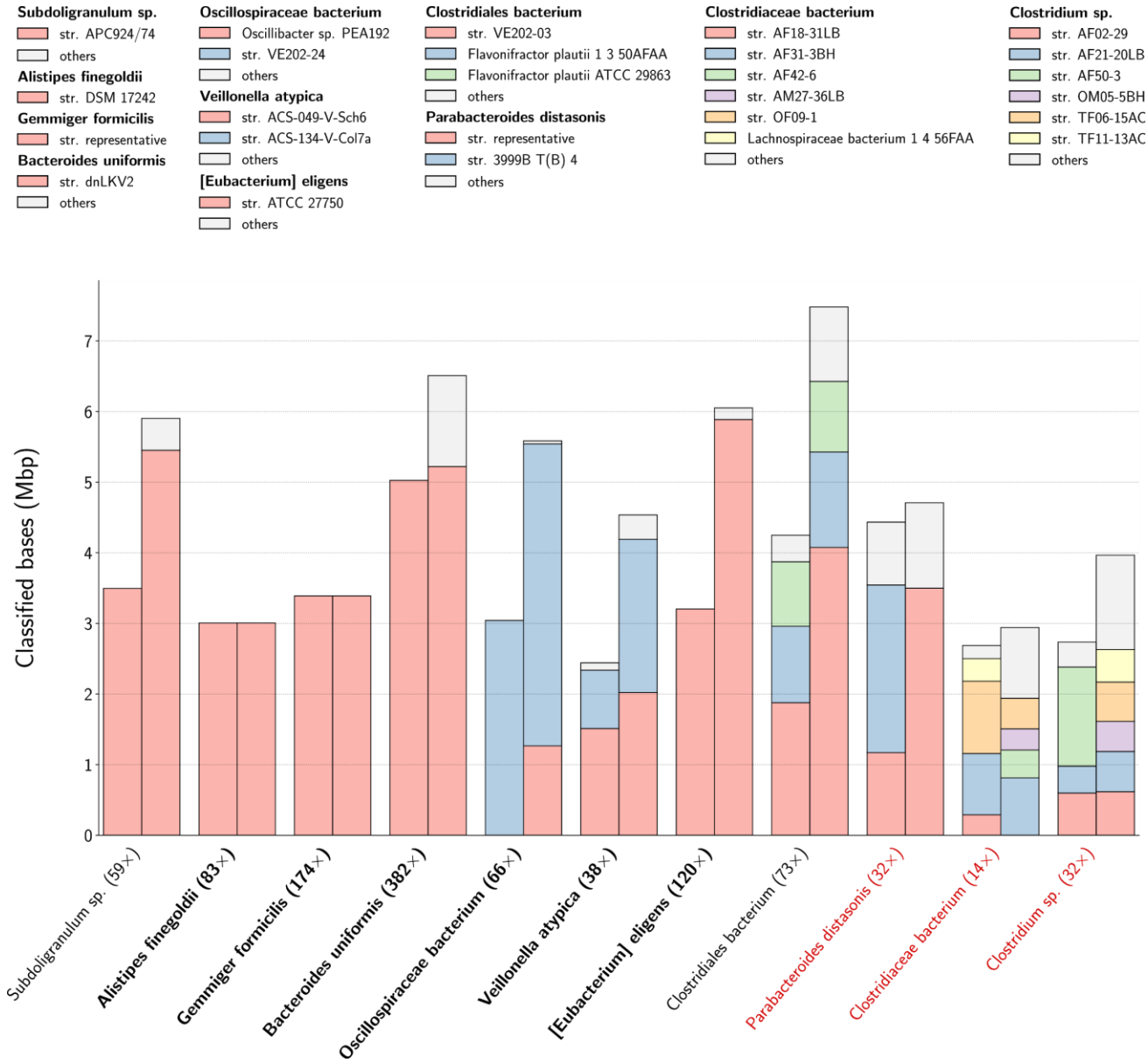

Figure 6. Assembly size and sequence classification before and after strain separation. Bins (x-axis) are named at the species level according to the most dominant Kraken2 classification. The value between parentheses represents the average depth of coverage of the bin before the strain separation. Bins highlighted with a bold font have a moderate post-separation completeness (>70%), while those highlighted in red have either poor completeness (<50%) or low read coverage (<30X). Colored bars represent the number of bases classified as a specific species/strain in a bin before and after the strain separation. Classified sequences whose size accounts for less than 10% of the bin size have been grouped as “others”.

We further performed a comprehensive comparison of good-quality Lathe bins (*i.e.*, high completeness and low contamination) with the related strain-separated contigs (**Supplementary File 3**). More precisely, we defined bin quality as $completeness - 5 \times contamination$ (as in ref.[30]) and focused on those bins having a value greater than 70. Strainberry assembly was considered in its polished form. The Kraken2 classification of bin sequences highlighted a finer strain variability after the strain-separation performed by Strainberry (**Figure 6**). Several bins also doubled (or increased significantly) in size after the Strainberry separation. Moreover, CheckM reported a completeness

greater than 70 and an increase in contamination proportional to the increase in size for 6 of the strain-separated bins (**Supplementary File 3**).

Runtimes and memory usage

All reported analyses have been run on a four-socket computing node with 14-core Intel Xeon Gold 6132 CPUs and 3 TB of memory. For all datasets we reported the time and memory usage of Flye, Minimap2, and Strainberry which were run using 12 threads. The first two tools are shown as they were used to generate the input data for Strainberry, except for the HSM dataset in which Strainberry's input consisted in the reference metagenome already available. In all cases Strainberry required less than 10 GB of memory and less time than Flye according to the dataset complexity and the input coverage (**Supplementary Table 4**). For instance, in the most complex dataset (the HSM dataset) Flye took 6.5 hours and 132 GB of RAM, while Strainberry took 4 hours and 9.5 GB of RAM. On the other hand, the Canu assembler always took 2 to 30 times more than Flye to finish (data not shown).

Discussion

In this work we presented Strainberry, an automated pipeline for performing strain-aware metagenome assembly of long reads. Strainberry makes use of well-established tools for haplotype phasing and genome assembly and introduces novel strain-aware components. Unlike other metagenome assembly methods, it does not rely on either short-read sequencing data or extensive polishing of the assembled sequences. Strainberry is able to accurately separate strains using long reads sequenced from a single metagenomic sample. An average depth of coverage of 60-80X suffices to assemble individual strains of low-complexity metagenomes with almost complete coverage and sequence identity exceeding 99.9%. Strainberry was also able to highlight finer strain variation in a human stool microbial sample which was previously characterized only to the species level. Although Strainberry showed its flexibility by generating strain-aware assemblies regardless of the employed long-read technology, we argue that the use of PacBio sequencing data yields better strain-aware assemblies in terms of sequence identity, while Nanopore sequencing data would favor assembly contiguity.

Strainberry has some intrinsic limitations which pave the way to future developments of the method. First, it relies on some prior knowledge of the number of strains present in the dataset. We have pragmatically shown that employing two- or three-strain separation is sufficient for improving the characterization of the microbial diversity of the low-complexity microbial samples in our tests. Yet we recognize that correctly estimating the number of strains is an important avenue for future work. For instance, we observed in the Mock9 dataset a two-strain separation allowed for the reconstruction of the two *S. aureus* strains, while a three-strain separation was needed for untangling *S. sonnei* and the two *E. coli* strains. A possible workaround is to perform strain separation at the level of a bin instead of an entire metagenome assembly.

A key aspect that would merit further study is the relationship between depth of coverage of the sample, read length, and ability to resolve haplotypes. Strains need to be sufficiently covered, and with long enough reads, in order to be fully and precisely resolved. The lack of easy-to-use DNA extraction methods producing high molecular weight DNA for all bacteria in a microbial community limits read length (to around a N50 of 5 Kbp). As we showed on the human stool microbial sample, low-coverage strains are likely separated into shorter contigs/scaffolds compared to the input

sequences due to poorly covered regions. This limitation also affects strain-oblivious assemblies, to a lesser extent given that species-level assembly is achieved by pooling the depth of coverage of all strains present.

Strainberry finds strain variations and separates reads by exploiting state-of-the-art haplotype phasing tools that are typically designed for genomes. For this reason, such tools typically assume read coverage is evenly split among the different haplotypes. This assumption however does not typically hold in a metagenomic context where haplotypes/strains might exhibit quite different abundance/coverage levels. While we showed this is not a limitation for the actual separation of a limited number of well-represented strains, we believe it is an important development worth pursuing. Moreover, in the presence of high strain variability, strain-oblivious sequences might need to be separated into a variable number of strains within the same contig. Finally, we did not evaluate Strainberry's ability to resolve plasmid genomes, which we leave for future work.

Methods

Datasets and preparation

Mock communities were constructed from a 10-plex PacBio Sequel dataset (see "Data availability"). Sequenced reads were demultiplexed and assigned to two mock communities: Mock3 and Mock9. The former contains a ~400X coverage of *Bacillus cereus*, *Escherichia coli* strains K12 and W. The latter instead contains a ~430X coverage of the same genomes in Mock3, with the addition of *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Neisseria meningitidis*, *Staphylococcus aureus* strains ATCC 25923 and FDAARGOS 766, and *Shigella sonnei*. The precise depth of coverage of each single genome is available in **Supplementary Table 1**. Assemblies of Mock3 and Mock9 datasets were generated with Flye v2.7 with parameters `--meta` (corresponding to metaFlye) and `--pacbio-raw`. The estimated genome size (`--genome-size` option) was set to 15 Mbp and 42 Mbp for Mock3 and Mock9, respectively. Reads were aligned to the assemblies using minimap v2.17 with parameter `-axmap-pb`, sorted with the `sort` command of samtools v1.10. Due to the extremely high depth of coverage, the Mock3 and Mock9 alignments were downsampled to obtain approximately 75X and 86X coverage respectively (command `samtools view -s 0.15`) in order to run our pipeline in reasonable time. For evaluation, the reference sequences of the genomes in the mock datasets were downloaded from NCBI (**Supplementary Table 1**). Assembly graphs for the Flye assemblies (**Supplementary Fig. 1 and 2**) were generated using Bandage[31] v0.8.1.

The PacBio and Nanopore reads of the NWC2 sample and the reference sequences were retrieved from NCBI (see "Data availability"). The PacBio dataset contains a total of 763,335 reads sequenced using PacBio's Sequel platform, however only the 385,106 reads longer than 5 Kbp were retained for generating an assembly. The Nanopore dataset contains a total of 407,027 reads sequenced with the MinION platform. In this case only the 33,364 reads longer than 10 Kbp were retained for generating an assembly. Both assemblies were constructed with Flye v2.7 using a minimum read overlap of 3 Kbp, an estimated metagenome size of 8 Mbp, and four polishing iterations (options `--meta --min-overlap 3000 --genome-size 8m --iterations 4`). Flye was run with parameters `--pacbio-raw` and `--nano-raw` for PacBio and Nanopore data, respectively. Reads were aligned to the assemblies using minimap v2.17 with parameters `-axmap-pb` and `-axmap-ont` for the PacBio and Nanopore datasets respectively, and position-sorted with the `sort` command of samtools v1.10.

The alignment of PacBio reads was further downsampled to obtain approximately a 66X coverage (command `samtools view -s 0.1743`). The alignment of Nanopore reads already yielded a 63X coverage of the assembly and therefore no downsampling was applied.

Finally, the HSM dataset was also retrieved from the NCBI database (see “Data availability” for accession numbers). More precisely, 4,003,772 Nanopore reads and the 163-Mbp metagenome assembly generated with the Lathe workflow were downloaded and used as input for Strainberry. Reads were aligned to the Lathe assembly using minimap v2.17 with parameter `-axmap-ont` and sorted with the `sort` command of samtools v1.10. Since the alignment yielded a 61X coverage of the assembly, no downsampling was applied. The Flye assembly for this dataset was generated with parameters `--meta`, `--nano-raw`, and an estimated metagenome size (`--genome-size` option) set to 160 Mbp.

Components of the strain separation pipeline

Haplotype phasing and read separation

The input of the first step of the strain separation pipeline consists in a strain-oblivious assembly and an alignment of the long reads against it. The rationale is to perform a variant call and identify single-nucleotide variants (SNVs) on assembled contigs, then make use of them to separate reads into different haplotypes (each haplotype will then correspond to a strain). Unfortunately, the literature does not yet offer many variant callers that are designed to handle efficiently long, error-prone reads, and at the same time supporting ploidy above 2. For this reason, we devised an approach that differently handles two-strain separation and n-strain separation (for $n > 2$). Two-strain separation was performed using the Longshot[32] diploid long-read SNV caller, that is also able to tag (separate) reads according to their most likely haplotype. Read separation is automatically performed by its companion phasing tool HapCUT2[33]. The n-strain separation, on the other hand, still makes use of SNVs identified by Longshot but then refined them using a polyploid variant caller, freebayes[34] which is run with ploidy level n. This manner of "guiding" polyploid calls from diploid calls was deemed necessary by the high computational resources demanded by running freebayes to detect all variants instead of refining a known list. The VCF file generated by freebayes and the read alignments are consequently provided as input to WhatsHap Polyphase[35], a recent long-read polyploid phasing tool that is also able to separate reads. The output of the first step of the strain separation pipeline is therefore a set of phased haplotypes (or phasesets) that partition the input assembly, and, for each one of the haplotypes, n sets of reads where n is the number of strains to be separated.

All variant calling and read separation tools were run with their default parameters. Only SNV calls having a QUAL value greater than 50 were retained for haplotype phasing. Moreover, the Longshot SNVs that were classified as belonging to a dense cluster (likely to be false positives) were filtered out before running freebayes. We also tried other combinations of Longshot, freebayes, and WhatsHap, as follows. We applied WhatsHap on the Longshot output for two-strain separation. We also considered the exclusive use of freebayes and WhatsHap for a "polyploid" strain separation. Overall, these alternative strategies did not provide major improvements on the mock datasets (**Supplementary File 4**) and were not further evaluated. Computational time was also considered to select an appropriate combination of tools (**Supplementary Table 5**).

Assembly of strain-aware contigs from separated reads

A *phaseset* is usually defined as a list of phased SNVs along a sequence (*e.g.,* a contig), that is SNVs assigned to a specific haplotype. In this work, we slightly redefine a phaseset to be the interval which includes the phased SNVs (and not the SNVs themselves). More formally, given a strain-oblivious contig C_i, we define a *phaseset* over C_i as a tuple $PS = (i, s, e)$, where i is the contig identifier, and s and e are the first and last positions, respectively, of the SNVs belonging to PS. Moreover, we define $dens(PS)$ as the percentage of SNVs that have been detected in the interval $[s, e]$ of C_i.

Assembly of haplotype-separated reads

The separated reads can be independently assembled by a standard (genome) assembly tool. We expect this task to be much simpler compared to the assembly of the whole metagenome, as the read separation step should in principle yield reads that correspond to a single strain. For this reason, and to handle a potentially large number of separated regions, we opted for the fast long-read assembler wtdbg2[36]. Moreover, as phasesets could be identified in quite short regions (couple of thousands bases) and the depth of coverage is reduced by the read separation, we decided to run wtdbg2 with fine-tuned parameters. We slightly increased the minimum read depth of a valid edge to 5 (option `-e 5`), we decreased the minimum length of alignment to 1,000 bp (option `-l 1000`), we decreased to 3,000 bp the threshold to drop short reads (option `-L 3000`), we disabled k-mer subsampling (option `-S 1`) and enabled the realignment mode (option `-R`). Note that these parameters were not tuned according to a particular dataset but were set rationally and identically for all evaluated datasets. Finally, phasesets PS where $dens(PS) < 0.1\%$ were discarded. This allows, first, to avoid the separation of strains having extremely high sequence identity (greater than 99.9%) and, second, to evade splitting contigs due to "false" phasesets identified due to a small number false positive SNVs.

Assembly post-processing

The assembly of separated reads posed some additional difficulties that needed to be handled in order to provide an accurate strain-aware assembly. More precisely, let $PS = (i, s, e)$ be a phaseset over the contig C_i defined on the interval $[s, e]$. The depth of coverage of a separated set of reads with respect to PS is expected to progressively decrease at positions $j < s$ and $j > e$, resulting in a low-quality assembly at the extremities of phasesets. Therefore, to reduce this effect, each haplotype-separated assembled contig is mapped to its corresponding strain-oblivious contig C_i and its extremities are trimmed in order to keep exclusively the aligned sequence corresponding to the interval $[s, e]$ of C_i. Moreover, the strain-oblivious unphased (non-separated) subsequences longer than 500 bp are retained. The set of the haplotype-assembled and unphased sequences constitutes the Strainberry strain-aware set of contigs.

Strain-aware scaffolding

We explored the possibility of implementing a simple scaffolding algorithm to produce a more contiguous assembly. Ideally, strain-aware contigs belong to three types: *strain-resolved* (contigs that align to multiple strains but map better to one than the other(s)), *strain-specific* (contigs belonging to one strain only), *core* (contigs that correspond to regions that are near-exactly shared by both strains). Therefore, aligning the original set of reads against the strain-aware assembly might allow for properly joining strain-resolved contigs, possibly including strain-specific and core contigs in between. Strain-aware scaffolding is implemented as follows. First, the input reads are aligned against the strain-aware contigs. Second, a *scaffolding graph* is built according to those reads whose alignments bridge

different contigs. Third, the graph is simplified, and unambiguous paths are processed to generate a set of strain-aware scaffolds.

Definitions

A *dovetail alignment* between a contig C and a read r is an alignment between either the suffix of C and the prefix of r or vice versa, the prefix of C and the suffix of r. We define a (*strain-aware) scaffolding graph* based on the string graph formalism[37]. A vertex is associated to each contig (henceforth the two terms will be used interchangeably), while edges are the dovetail alignments, indicating adjacency between contigs. More formally, a *scaffolding graph* is a bi-directed weighted graph $G = (V, E, w)$. V is the set of all strain-aware contigs S_i. A bi-directed edge $e_{ij} \in E$ is put between two vertices $S_i$and S_j if and only if there exists at least one read r having two dovetail alignments, one with S_i and the other with S_j, and those dovetails alignments are such that one must involve the prefix the read, and the other the suffix of the read. Moreover, e_{ij} is modeled as a bi-directed edge by adding oriented arrows at both its endpoints. The direction of the arrow on S_i's side of e_{ij} is defined as follows: if the dovetail alignment involves the suffix of S_i, it points away from S_i; otherwise, if the dovetail alignment involves the prefix of S_i, it points towards S_i. The number of reads connecting $S_i$and S_j defines the weight $w(e_{ij})$ of the edge e_{ij}.

During a graph traversal, entering a vertex corresponding to S_i with an arrow pointing towards it, tells us to consider the contig S_i as it is. Otherwise, the reverse complement of S_i must be considered (arrow pointing away from S_i). The same reasoning applies to S_j. Moreover, when entering a vertex from an arrow pointing towards it, an edge with the arrow pointing away from it must be used to exit, and vice versa.

Read alignment and filtering

Reads are mapped against the strain-aware contigs using minimap2 with option `-cxmap-pb` (`-cxmap-ont`) in order to perform a base-level alignment of PacBio (Nanopore) reads. Unique alignments (*i.e.*, primary minimap2 alignments with mapping quality greater than 40) which are also dovetail alignments are retained in order to build the scaffolding graph. An overhang (*i.e.*, the unaligned extremity) that is the minimum between 50 bp and the 10% of the match length is however allowed for identifying prefix and suffix matches.

Graph construction and simplification

The identified dovetail alignments are used to build the scaffolding graph according to the previous definition. In this process, we consider the input strain-oblivious assembly as a “backbone” and we allow only certain links according to the position of contigs on the input assembly. We say that two contigs are *consecutive* if they map to the same backbone contig and no other contig maps in between them. Two haplotype-assembled contigs are *adjacent* if they map to the same backbone contig and no other phaseset exists in between them (*i.e.*, two adjacent contigs are not necessarily consecutive). Two contigs are *read-linked* if there exists at least one read showing evidence of these two contigs being close in a strain. An edge is then allowed only between contigs of the following types: (i) two consecutive contigs; (ii) two adjacent haplotype-assembled contigs; (iii) a non-separated backbone contig and a haplotype-assembled contig which are read-linked; (iv) two contigs both mapping on the extremity of a backbone contig.

Once the scaffolding graph has been constructed it is trimmed to remove simple transitive edges and weak edges. The former is an edge e_{ij} between two vertices $S_i$and S_j (where $i \neq j$) for which there exists a path $S_i \rightarrow S_z \rightarrow S_j$ from S_i to S_j traversing a distinct node S_z ($z \neq i$ and $z \neq j$) and whose arrows at the sides of S_i and S_j are of the same type as e_{ij}. A weak edge is an edge exiting a vertex S_i either being supported by less than 10 reads or such that its supporting reads are less than the 90% of the reads supporting all edges exiting S_i. The simplified graph is traversed, and a scaffold is produced for each maximal unambiguous path (*i.e.*, a path without bifurcations that cannot be extended) introducing gaps when needed. More precisely, gap lengths are computed as the median distance between two contigs according to the reads supporting the corresponding edge, when such a distance is positive. Conversely, contigs are simply joined one after the other if the median distance has a negative value.

Strain-aware assembly evaluation

When only a single reference genome is available for a given species and used to evaluate the assembly of multiple strains, metrics such as sequence identity, duplication rate, and number of misassemblies need to be evaluated with caution. As an example, in an isolate-genome assembly, a duplication ratio much greater than 1 would typically indicate a problem in the assembly. On the contrary, in a strain-aware metagenome context with limited knowledge of the organisms, a higher duplication ratio might be simply an indication that multiple strains have been resolved. A similar observation could be made when observing a lower sequence identity and/or the presence of misassemblies. The former is expected when only a single reference is compared against strain-resolved sequences as the consensus sequence will diverge from individual strains. On the other hand, misassemblies such as SNVs and indels could be due to strain differences. For these reasons, metrics need to be evaluated differently with respect to the datasets considered in this study. Mock datasets are precisely evaluated as all the genomes are known and accurate references are available. Evaluation metrics computed on the real datasets, on the other hand, need to be analyzed with care.

All generated strain-oblivious and strain-aware assemblies were compared to a set of reference sequences corresponding to genomes and strains known to be present in the sample, when available. Each contig/scaffold was assigned to the best-identity reference sequence using the MUMmer4[38]. More precisely, we aligned each contig/scaffold against all the references with the command `nucmer --maxmatch`. The output delta-file was then filtered with the command `delta-filter -q` and sequences that align for at least 90% of their length were assigned to the reference sequence which yielded the highest sequence identity.

The following metrics were computed: number of contigs, assembly size, N50/NG50, reference and assembly aligned percentages, average sequence identity, number of duplicated/compressed bases, and number of misassemblies. Misassemblies can be divided into four major categories, following the terminology and criteria of QUAST[39]: SNPs, relocations, translocations, and inversions. SNPs are simply single-base mismatches with respect to the reference sequence. Relocations arise instead when the consistent ordering of aligned blocks is disrupted. Translocations are relocations involving two adjacent blocks in the assembly that align to different sequences/chromosomes in the reference genome. Inversions are characterized by subsequences that align on opposite strands.

A custom script was finally used to assess whether a contig aligned for at least the 90% of its length against a reference sequence. Each set of sequences was precisely compared against its closest

reference using the MUMmer4 command `dnadiff` whose output files were processed (using again a custom script) to obtain the GAGE[40] assembly evaluation metrics. Circular and bar graphs in Figures 2 and 3 were generated from the MUMmer output with Circos[25] and custom Python scripts (see "Code availability").

Assembly-level coverage plots of NWC2 available references (**Figure 4**) were produced by aligning the contigs assigned to a reference with minimap2 (parameters `-ax asm20 --cs`) and computing the assembly-level coverage in 20-Kbp windows with mosdepth[41] (parameters `--by 20000 -m -x`). CheckM v1.1.2 was run with the Bacteria marker-gene set in order to evaluate completeness and contamination percentages of the assembled sequences.

Some specific and more appropriate evaluation procedures were considered for the HSM real dataset due to the lack of an accurate strain-level characterization and its higher complexity compared to the Mock3, Mock9, and NWC2 datasets. They are precisely detailed in the **Supplementary Note 5**.

Data availability

All described datasets are publicly available. Links and accession codes are provided in this section. PacBio sequencing data used to create the Mock3 and Mock9 datasets is available at https://github.com/PacificBiosciences/DevNet/wiki/Microbial-Multiplexing:-PacBio-Sequel-System,-Chemistry---v3.0,-Analysis---SMRT-Link-v6.0.0. NCBI RefSeq accession codes of the reference genomes used for the assembly evaluation are listed in **Supplementary Table 1**. NWC2 reads are available at the NCBI BioSample SAMN09580370 under the SRA accession codes SRX4451758 (Nanopore) and SRX4451757 (PacBio). Reference sequences used for the assembly evaluation of NWC2 are accessible under the NCBI BioSample accession codes SAMN09476686 (*S. thermophilus*), SAMN09476687 (*L. delbrueckii*), SAMN09476688 (*L. helveticus* strain NWC_2_3), and SAMN09476689 (*L. helveticus* strain NWC_2_4). HSM reads and the corresponding metagenome assembly reference are available at the NCBI BioProject PRJNA508395 under the SRA accession code SRX5235113 and the GenBank accession code GCA_011075405.1, respectively. All assemblies generated with metaFlye, Canu, and Strainberry have been made available at https://doi.org/10.5281/zenodo.4293889.

Code availability

Strainberry has been developed as a collection of Bash and Python scripts, it uses GNU parallel[42] in order to exploit multiple CPU cores, and it has been tested on a Linux platform. Strainberry is open source and available at https://github.com/rvicedomini/strainberry under the MIT License. Scripts necessary to reproduce the main results are available at https://github.com/rvicedomini/strainberry-analyses and were generated using the version 1.0 of Strainberry.

Acknowledgments

R.V. and R.C. are funded by ANR INCEPTION (PIA/ANR-16-CONV-0005) and R.C. by ANR PRAIRIE and ANR SeqDigger. C.Q. is funded through "Strain resolved metagenomics for medical microbiology" MRC MR/S037195/1 and the "CLIMB-BIG-DATA" consortium MR/T030062/1.

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Contributions

R.V. and R.C. conceived the study. R.V. developed the software, carried out all the analyses and generated the figures. R.V., C.Q., A.E.D. and R.C. wrote the manuscript. All authors read and approved the final manuscript.

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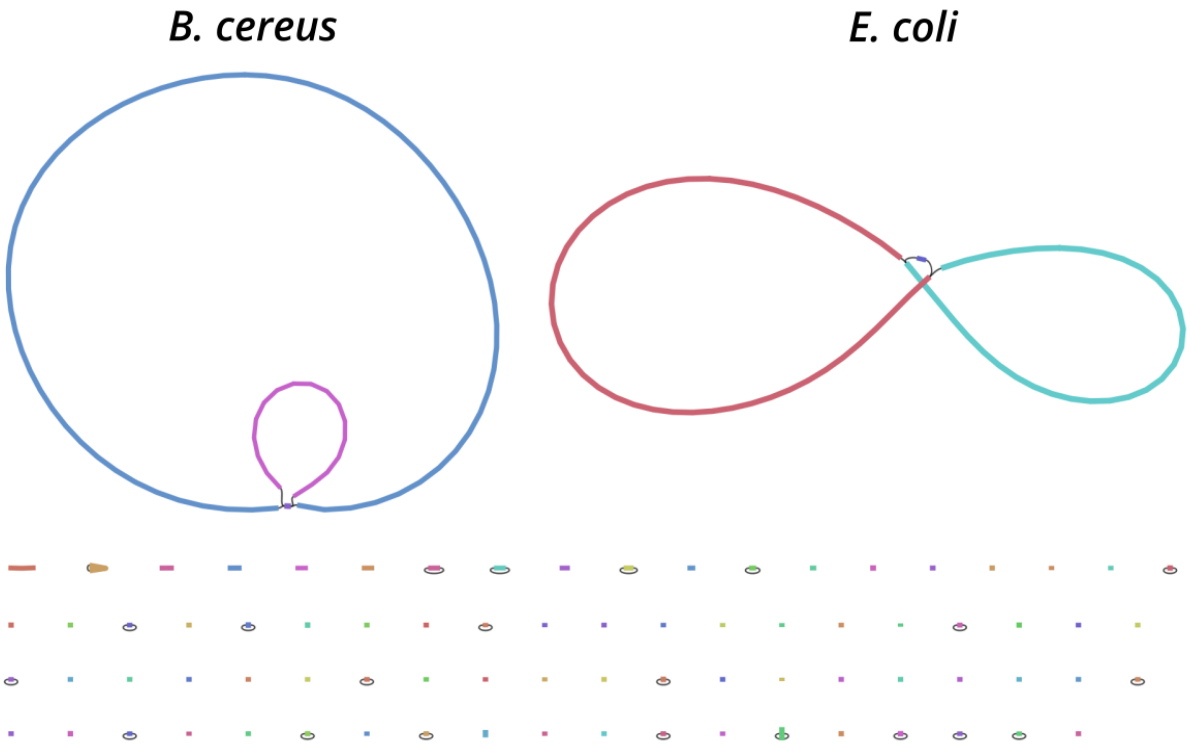
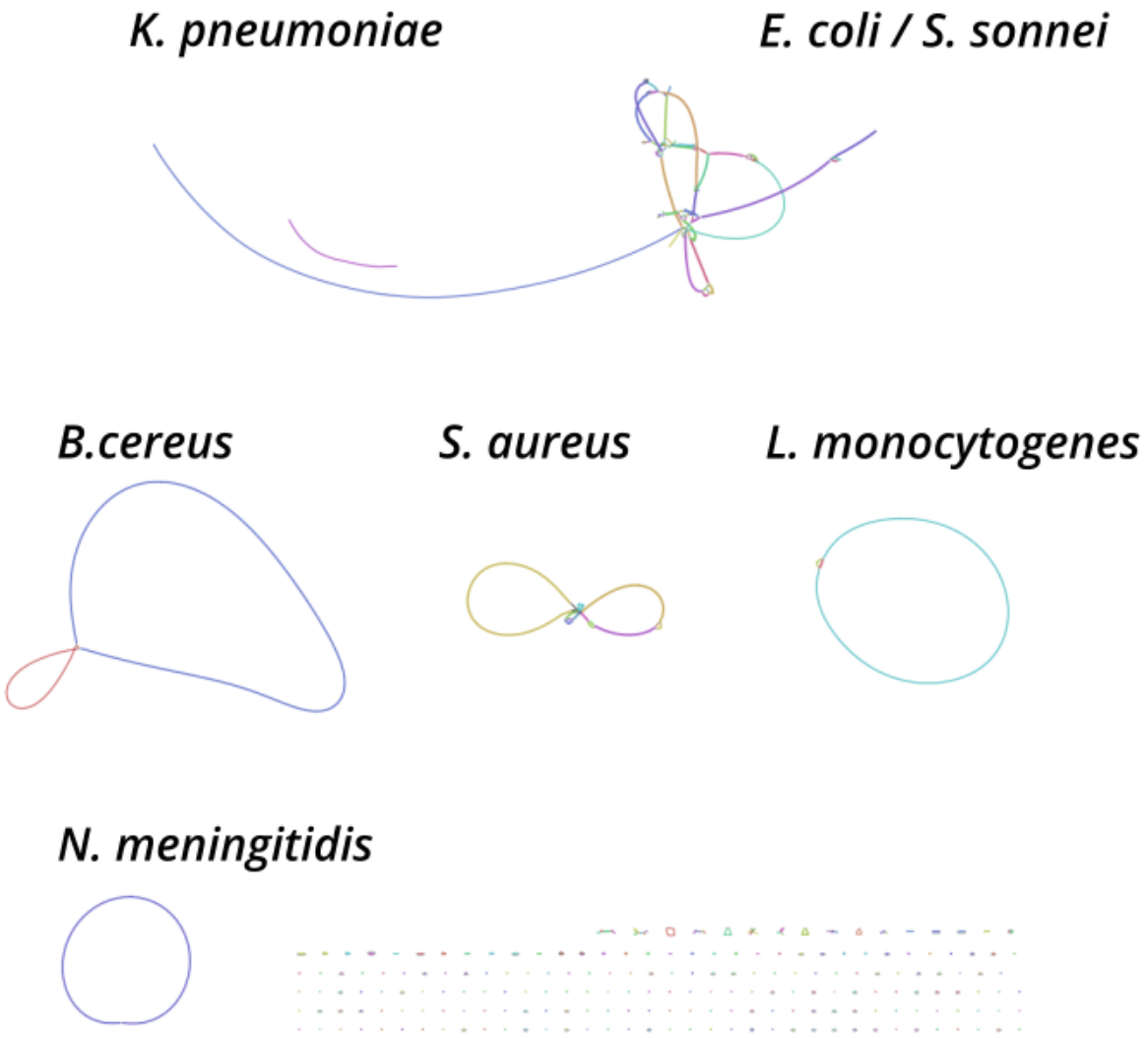
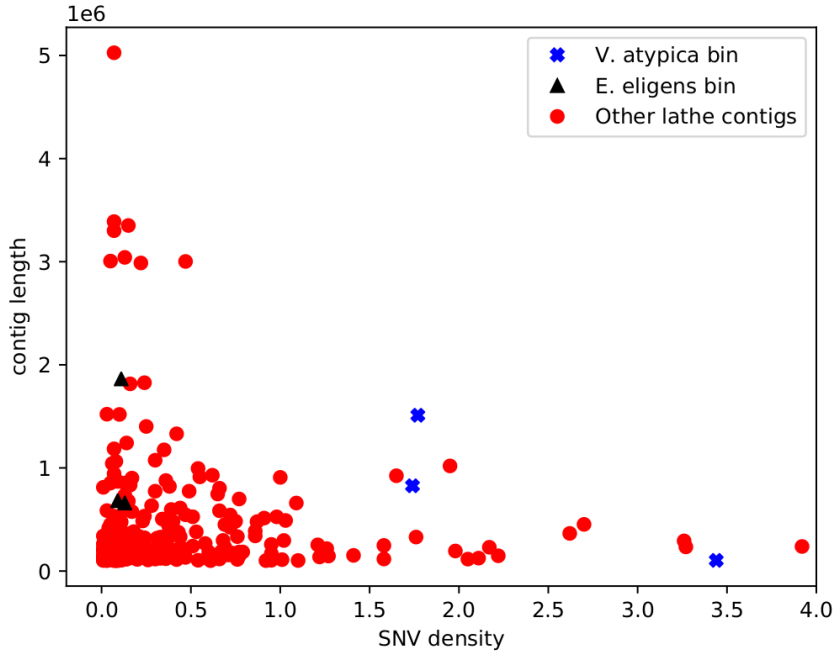
Supplementary Figures



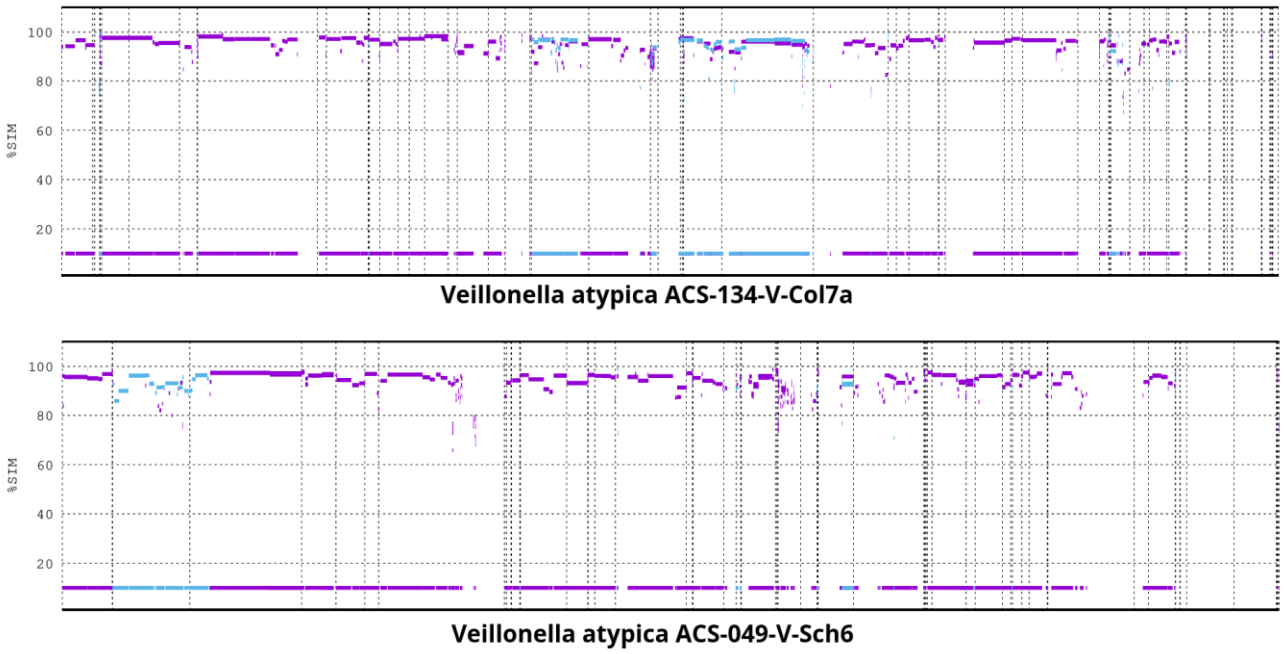
Supplementary Figure 1. Bandage plot of the Flye assembly graph of the Mock3 dataset. The picture shows assembled sequences of metaFlye for the Mock3 dataset. Lines correspond to contigs. Edges, in the form of thin black lines between the contigs, reflect adjacencies. Colors are arbitrary. While *B. cereus* genome was correctly reconstructed, *E. coli* strains K-12 and W have been mainly collapsed into two long consensus sequences. At the same time many “short” fragments appear due to genomic sequences specific to either one of the two strains.



Supplementary Figure 2. Bandage plot of Flye assembly graph of the Mock9 dataset. The picture shows assembled sequences of metaFlye for the Mock9 dataset (see caption of Supplementary Figure 1 for additional explanations). While single-strain genomes have been correctly reconstructed, the two *S. aureus* strains are mostly collapsed into long consensus sequences. Moreover, the assembly graph exhibits a more complex structure for the two *E. coli* strains due to the high similarity of the *S. sonnei* genome. As for Mock3, “short” fragments appear due to strain-specific sequences.



Supplementary Figure 3. Density of SNVs found in Lathe assembled contigs with emphasis on *Veillonella atypica* and *[Eubacterium] eligens* bins. Each data point corresponds to a contig.



Supplementary Figure 4. Mapping of the strain-separated contigs of the *V. atypica* bin classified as *V. atypica* strain ACS-134-V-Col7a and *V. atypica* strain ACS-049-V-Sch6 on the available NCBI contig-level references. X and Y axes represent the reference contigs and the sequence identity of mapped segments, respectively. The line at the 10% level represents the projection of mapped segments on the references which accounts for a ~70% coverage of both references.

Supplementary Tables

Supplementary Table 1. Mock datasets composition. Strains, genome size, reads, and coverage of the mock communities created from the PacBio Sequel data available at https://github.com/PacificBiosciences/DevNet/wiki/Microbial-Multiplexing:-PacBio-Sequel-System,-Chemistry--v3.0,-Analysis---SMRT-Link-v6.0.0. Reads sequenced with barcode BC1022 are supposed to come from *Staphylococcus aureus* strain HPV107, however through a BLAST alignment of the available isolate PacBio assembly against the RefSeq genome database we observed they likely come from *Staphylococcus aureus* strain FDAARGOS 766.

mock dataset	species	strain	RefSeq	genome size (bp)	barcode	reads	depth of coverage
Mock3	*Bacillus cereus*	ATCC 14579	NZ_CP034551.1	5,416,249	BC1010	402,216	447.13
	Escherichia coli	K-12 substr MG1655	NC_000913.3	4,641,652	BC1002	221,080	311.24
	Escherichia coli	W ATCC 9637	NC_017664.1	4,897,452	BC1019	360,041	435.21
Mock9	*Bacillus cereus*	ATCC 14579	NZ_CP034551.1	5,416,249	BC1010	402,216	447.13
	Escherichia coli	K-12 substr MG1655	NC_000913.3	4,641,652	BC1001	249,861	367.11
					BC1002	221,080	311.24
	Escherichia coli	W ATCC 9637	NC_017664.1	4,897,452	BC1019	360,041	435.21
	Klebsiella pneumoniae	ATCC BAA-2146	NZ_CP006659.2	5,435,746	BC1009	222,032	280.03
	Listeria monocytogenes	CFSAN008100	NZ_CP011398.2	3,039,878	BC1012	180,478	411.58
	Neisseria meningitidis	FAM18	NC_008767.1	2,194,961	BC1016	188,874	474.75
	Staphylococcus aureus	ATCC 25923	NZ_CP009361.1	2,778,854	BC1018	302,192	686.15
	Staphylococcus aureus	FDAARGOS 766	NZ_CP041010.1	2,877,716	BC1022	221,177	543.55
	Shigella sonnei	CFSAN030807	NZ_CP023645.1	4,813,450	BC1015	237,599	333.39

Supplementary Table 2. Assembly evaluation of the Strainberry contigs before/after polishing on the NWC2 Nanopore dataset. The following quantitative and qualitative measures are displayed for each assembly: assembly method, reference sequence, number of contigs (#seq), reference size (ref size), assembly size (asm size), NG50, unaligned reference percentage (unaligned ref %), unaligned assembly percentage (unaligned asm %), average nucleotide identity (ANI), duplicated bases (dup), compressed bases (cmp), single-nucleotide polymorphisms (SNPs), inversions (inv), relocations (reloc).

assembly	reference	#seq	ref size	asm size	NG50	unaligned ref %	unaligned asm %	ANI	dup ratio	dup	cmp	SNPs	inv	reloc
Flye	*S. thermophilus* strain NWC_2_1	7	1,971,439	1,991,691	1,929,846	0.00	0.00	99.70	1.01	23,705	0	1,033	0	1
	L. delbrueckii strain NWC_2_2	53	2,269,179	2,884,694	136,620	1.39	0.75	99.55	1.28	727,866	84,920	2,632	2	9
	***L. helveticus* strain NWC_2_3**	**93**	**2,210,811**	**1,303,109**	**7,560**	**40.85**	**0.71**	**99.51**	**0.99**	**229,718**	**358,933**	**2,084**	**3**	**4**
	***L. helveticus* strain NWC_2_4**	**78**	**2,177,422**	**2,914,528**	**190,476**	**2.99**	**1.26**	**99.76**	**1.36**	**797,523**	**44,485**	**542**	**7**	**5**
ssFlye/contigs	*S. thermophilus* strain NWC_2_1	7	1,971,439	1,991,691	1,929,846	0.00	0.00	99.70	1.01	23,705	0	1,033	0	1
	L. delbrueckii strain NWC_2_2	104	2,269,179	4,478,418	173,860	1.02	0.53	98.75	1.98	2,334,522	92,157	4,084	2	4
	***L. helveticus* strain NWC_2_3**	**128**	**2,210,811**	**2,987,292**	**95,688**	**1.54**	**1.16**	**99.34**	**1.36**	**804,215**	**51,459**	**2,010**	**1**	**5**
	***L. helveticus* strain NWC_2_4**	**108**	**2,177,422**	**3,082,925**	**96,313**	**0.83**	**0.89**	**99.47**	**1.41**	**886,812**	**41,073**	**811**	**0**	**1**
ssFlye/contigs + Medaka	*S. thermophilus* strain NWC_2_1	3	1,971,439	1,975,529	1,935,060	0.18	0.27	99.42	1.00	5,335	19,301	876	0	12
	L. delbrueckii strain NWC_2_2	57	2,269,179	4,366,916	176,031	0.96	0.76	98.93	1.93	2,014,781	73,005	4,395	5	5
	***L. helveticus* strain NWC_2_3**	**57**	**2,210,811**	**2,640,466**	**84,345**	**1.77**	**1.00**	**99.39**	**1.20**	**439,720**	**67,884**	**1,536**	**1**	**2**
	***L. helveticus* strain NWC_2_4**	**77**	**2,177,422**	**2,993,091**	**95,568**	**1.00**	**0.65**	**99.44**	**1.38**	**799,365**	**51,555**	**871**	**2**	**1**
ssFlye/contigs + MarginPolish	*S. thermophilus* strain NWC_2_1	3	1,971,439	1,978,816	1,938,248	0.18	0.00	99.42	1.01	5,654	5,163	1,173	0	2
	L. delbrueckii strain NWC_2_2	51	2,269,179	4,088,801	175,797	4.78	1.26	98.65	1.87	1,931,026	92,319	5,825	3	1
	***L. helveticus* strain NWC_2_3**	**47**	**2,210,811**	**2,260,855**	**84,286**	**7.45**	**0.96**	**99.28**	**1.09**	**290,410**	**153,920**	**1,861**	**1**	**3**
	***L. helveticus* strain NWC_2_4**	**52**	**2,177,422**	**2,352,862**	**95,496**	**7.49**	**0.62**	**99.37**	**1.16**	**356,387**	**95,986**	**914**	**2**	**3**

Supplementary Table 3. CheckM evaluation of the *V. atypica* and *E. eligens* bins of the HSM dataset. Completeness, contamination and strain heterogeneity (S.H.) percentages of the Lathe reference assembly compared to the Strainberry-separated contigs from the Lathe assembly (ssLathe) and the Flye assembly. Flye sequences were selected as the best-mapping ones against Lathe sequences.

assembly	species	size (Mbp)	completeness	contamination	s.h.
Lathe	*V. atypica*	2.44	93.9	1.5	100.0
	E. eligens	3.20	87.6	0.0	0.0
ssLathe/contigs	*V. atypica*	4.50	68.9	38.3	50.0
	E. eligens	6.03	68.5	39.4	84.8
ssLathe/contigs polished	*V. atypica*	4.54	93.0	62.1	76.9
	E. eligens	6.05	89.9	72.3	88.2
Flye	*V. atypica*	2.19	57.0	2.4	81.8
	E. eligens	2.64	69.2	0.0	0.0
Flye polished	*V. atypica*	2.35	64.1	3.1	28.6
	E. eligens	2.63	70.9	0.3	0.0

Supplementary Table 4. Runtime and memory usage of Strainberry on the different datasets. Time and memory needed to generate the input assembly (Flye), perform the read mapping (Minimap2), and separate the assembly with Strainberry. The estimated reference size of the mock and HSM datasets refers to the size of available references, while for NWC2 it refers to the size of the Flye assembly.

Dataset	Size (Gbp)	Mean coverage	Est. ref. size (Mbp)	Tool	Wall-clock time (12 threads)	CPU time	RAM peak (GB)
Mock3	6.00	515X	14.96	*Flye*	2h 52m 46s	18h 54m 25s	20.36
	6.00	515X		*Minimap2*	6m 39s	1h 5m 49s	9.31
	0.90	75X		*Strainberry*	34m 21s	2h 0m 24s	4.17
Mock9	16.59	460X	36.18	*Flye*	7h 8m 18s	56h 19m 30s	132.80
	16.59	460X		*Minimap2*	20m 52s	3h 28m 13s	9.37
	2.48	86X		*Strainberry (n=2)*	1h 18m 34s	8h 12m 4s	7.81
	2.48	86X		*Strainberry (n=3)*	4h 17m 2s	32h 26m 37s	6.01
NWC2-PacBio	4.21	372X	9.98	*Flye*	6h 29m 38s	50h 45m 25s	25.12
	4.21	372X		*Minimap2*	9m 26s	1h 45m 18s	9.26
	0.73	66X		*Strainberry*	14m 30s	1h 37m 9s	6.45
NWC2-ONT	0.67	63X	10.10	*Flye*	1h 1m 55s	7h 56m 44s	35.96
				Minimap2	1m 58s	14m 32s	4.56
				Strainberry	18m 7s	2h 4m 23s	3.19
HSM	11.36	61X	162.81	*Flye*	6h 34m 2s	54h 51m 22s	131.97
				Minimap2	18m 12s	3h 6m 38s	9.46
				Strainberry	3h 54m 25s	33h 0m 8s	9.53

Supplementary Table 5. Runtime and memory usage of the pipeline using different combinations of SNV-detection and haplotype-phasing tools.

method (12 CPUs)	haplotype separation	haplotype assembly	scaffolding	total	RAM peak (GB)
Longshot +HapCUT2	23m 15s	9m 2s	2m 4s	34m 21s	4.17
Longshot +whatshap-poly	41m 35s	15m 0s	2m 1s	58m 36s	4.04
freebayes +whatshap-poly	26h 41m 44s	12m 37s	1m 57s	26h 56m 18s	4.09

Supplementary Notes

Supplementary Note 1 - Analysis of Mock3 assemblies

Note: in all our tests on the Mock3 dataset we used a beta version of Flye (v2.7b-b1528), which turns out to produce modestly better assemblies than Flye released version 2.7-b1585.

For the genome with only one strain present (*B. Cereus*) the NG50 of Strainberry+Flye scaffolds (5.4 Mbp) is higher than Flye (4.3 Mbp), due to additional scaffolding. For *E. coli* strain K12, Flye reports a NG50 of zero due to the low number of assembled bases, while the strain-separated assembly achieves a NG50 of ~1.3 Mbp. For *E. coli* strain W, the strain-separated scaffolds have lower NG50 (1.3 Mbp) than Flye (2.8 Mbp) since we report haplotype blocks while Flye contigs correspond to a strain consensus. There is therefore a trade-off between high NG50 and strain reconstruction accuracy.

As misassemblies are concerned, the Strainberry+Flye scaffolds yielded 2 relocations for B. cereus which were also present in the upstream Flye assembly (one due to the circularity of the genome, the other one due to an 800-bp deletion in the Flye assembly). The 3 new relocations in the Strainberry+Flye assembly of *E. coli* strain K12 are due to the circularity of the genome and the introduction of gaps during the scaffolding phase. With respect to the *E. coli* strain W reference, Strainberry+Flye is affected by the same number of misassemblies of the Flye assembly. More precisely, one relocation is due to the circularity of the genome, one is found in the same locus of the Flye assembly, one is corrected, and one is introduced by the scaffolding nearby a repeated region of the genome. Finally, inversions are identified on non-separated contigs and therefore are inherited by the Flye assembly.

Supplementary Note 2 - Analysis of Mock9 assemblies

For the genome with only one strain present (*B. cereus*, *K. pneumoniae*, *L. monocytogenes*, *N. meningitidis*) the strain-oblivious assemblies achieved a near-complete genome reconstruction with average nucleotide identity greater than 99.9% and an optimal duplication ratio. Strainberry scaffolds yielded comparable results as no major separation was performed. For *S. aureus* strain FDAA, Flye reports a NG50 of 44 Kbp due to the low number of assembled bases, while the strain-separated assembly achieves a NG50 of 2.7 Mbp. For *S. aureus* strain ATCC, the strain-separated scaffolds further increased the NG50 (2.2 Mbp) compared to Flye (1.5 Mbp). Canu yielded an NG50 of 2.4 Mbp and 56 Kbp for strains FDAA and ATCC, respectively. Even though Strainberry was able to achieve a complete coverage of the two *S. aureus* strains, the high duplication ratio of Canu assembly hindered the scaffolding of the strain-separated contigs leading to a NG50 of 82 Kbp and 63 Kbp for strains FDAA and ATCC, respectively. For *E. coli* strains K12, W and *S. sonnei*, Flye reports a NG50 of 351 Kbp, 49 Kbp and 46 Kbp, respectively. While significantly improving reference coverage and sequence identity, the three-strain separation achieves a NG50 of 16 Kbp, 13 Kbp, and 17 Kbp, respectively, highlighting the difficulty of separating more than two strains into a contiguous set of scaffolds. On the other hand, Canu reports a NG50 of 543 Kbp, 39 Kbp and 44 Kbp, for *E. coli* strains K12, W and *S. sonnei* respectively. The two-strain separation of Strainberry achieves instead a NG50 of 59 Kbp, 43 Kbp, and 40 Kbp, respectively, due to the difficulty of scaffolding a set of contigs characterized by a high duplication ratio. Misassemblies are precisely reported in **Supplementary File 1**.

Supplementary Note 3 - Analysis of NWC2 PacBio assemblies

Compared to the Flye strain-oblivious assembly, the strain-separated assembly is of higher quality as evidenced by comparable and/or improved values of NG50, sequence identity, and misassemblies. Regarding the separation of the two *L. helveticus* strains, for instance, strain-separated scaffolds of NWC_2_3 improved NG50 (Strainberry attained 107 Kbp, while Flye produced an assembly smaller than half of the reference size) and sequence identity (99.74% versus 99.69% with Flye). For *L. delbrueckii*, strain-separated sequences achieve a higher NG50 (224 Kbp) compared to Flye (190 Kbp). At the same time, the higher assembly size and duplicated bases are likely due to the potential existence of other undetected conspecific strain(s) of *L. delbrueckii*, as also evidenced by the strain-separated assembly obtained with the longer Nanopore reads. For all the four reference strains, the number of inversions and relocations of separated contigs/scaffolds is either the same as for the Flye assembly or decreased due to a correct strain reconstruction. Compared to the Canu assembly, however, the strain-separated assembly does not display major differences concerning NG50, sequence identity and misassemblies.

Supplementary Note 4 - Analysis of NWC2 Nanopore assemblies

A key difference between the Flye assemblies generated with PacBio and Nanopore data is that the latter allows to further reduce the percentage of the references that are left uncovered (40.85% of NWC_2_3 versus 49.48% with PacBio data, same trend with NWC_2_4). Conversely, strain-separated contigs and scaffolds are able to achieve near-complete reference coverage, yielding a slight improvement compared to the PacBio data (**Supplementary File 2**). The number of inversions and relocations is also reduced with respect to the Flye assembly while, at the same time, the NG50 of the separated-strain assemblies is significantly improved. Nanopore-based strain-aware assemblies have lower sequence identities to reference strains (99.34-99.76%) than with PacBio data (99.69%-99.97%). Also, the lower sequence identities in the strain-aware assemblies, compared to the strain-oblivious assembly, are likely caused by splitting reads into two haplotype groups, thus having less input coverage. We attempted to mitigate this effect by polishing the strain-separated contigs using Nanopore-specific tools such as Medaka (https://nanoporetech.github.io/medaka) and MarginPolish (https://github.com/UCSC-nanopore-cgl/MarginPolish), with limited success (**Supplementary Table 2**). The assembly evaluation also shows a 1.6-Mbp increase of strain-resolved sequences aligning against the *L. delbrueckii* reference compared to the Flye assembly. This is further evidence that, thanks to the longer Nanopore reads, a conspecific strain might have been separated by Strainberry. As for the Canu assembly, compared to the PacBio data, results show a higher uncovered percentage of *L. helveticus* strain NWC_2_3 (15.9%) and a fully represented strain NWC_2_4 (**Supplementary File 2**). The strain-separated assembly slightly improves reference coverage and increases the assembly size of scaffolds aligning to *L. delbrueckii*. It yields however comparable results according to the other evaluation metrics. As in the mock datasets, Canu reports a very high number of duplicated sequences which, again, could be due to erroneous duplications or correctly separated conspecific strains. *L. delbrueckii* reference is largely covered two and three times by the Canu and Strainberry assembly, respectively. This higher coverage is likely due to a conspecific strain (as observed for the strain-separated Flye assembly and with PacBio data). There is however the possibility that the separation performed by Canu is not optimal and could affect the performance of Strainberry, as seen for all the mock datasets.

As the CheckM analysis is concerned, compared to the Flye assembly, strain-separated sequences globally show higher completeness for *L. helveticus* strains (from 39.3% to up to 83.8% with

NWC_2_3 strain-separated contigs). On the contrary, *L. delbrueckii* sequences are characterized by a slightly lower completeness (90.5% in strain-oblivious assembly, 78.5% in strain-aware) and a much higher contamination (29.6% in strain-oblivious assembly, 55.5% in strain-aware). On the other hand, the Canu assembly and the related strain-separated Strainberry assembly yield comparable metrics.

Supplementary Note 5 - HSM dataset evaluation

Evaluation metrics of the assembled sequences were computed using QUAST v5.1.0rc1 with parameters `--fragmented --min-identity 80 --min-contig 200`.

The binning of the Lathe assembly was generated with MetaBAT v2.15. First, the average depth of coverage of each assembled contig was computed using the command `jgi_summarize_bam_contig_depths` with options `--minContigLength 1000 --minContigDepth 1 --percentIdentity 50`. The actual binning was then produced using the `metabat2` command with default parameters.

Bin and read classifications were performed using Kraken (version 2.0.9-beta) with the Maxikraken2 database (update of March 2019) retrieved at https://lomanlab.github.io/mockcommunity/mc_databases.html. In addition to sequence hashes from genomes of NCBI RefSeq that are marked as complete or representative, it includes genomes that are either incomplete or not representative for the following database types: archaea, bacteria, fungi, protozoa, viral, and human.

Plots showing contig length and mean coverage of the Lathe and strain-aware assemblies of *V. atypica* and *E. eligens* bins were generated using a custom Python script.

In order to identify the Flye contigs that corresponded to the Lathe assembly of the *V. atypica* and *E. eligens* bins, the Flye assembly was aligned against the Lathe reference and the best-mapping contigs were retained. More in detail, Flye contigs whose minimap2 primary alignments with MAPQ >= 30 cover at least 80% of their length were retained. CheckM v1.1.2 was hence run on these two sets of retrieved sequences.

In order to fairly compare Lathe bin classification before and after the strain separation carried out by Strainberry, strain-separated contigs were polished as it is done in the Lathe workflow: 4 rounds of Racon and one round of Medaka polishing (see https://github.com/bhattlab/lathe).