

Scalable Algorithms for Metagenomic Assembly

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ABSTRACT

Metagenomic sequencing captures the collective genome of microbial communities -- gut microbiomes, soil ecosystems, ocean water columns, and clinical specimens -- without cultivation. Assembly of metagenomic reads into contiguous sequences (contigs) and complete genomes (metagenome-assembled genomes, MAGs) is computationally challenging: samples contain thousands of species at varying abundances spanning five orders of magnitude, closely related strains share >95% sequence identity creating assembly graph tangles, and dataset sizes reach terabytes for large-scale surveys. Current assemblers (MEGAHIT, metaSPAdes, MetaFlye) achieve incomplete assembly: only 30-60% of reads are placed in contigs >1 kb, and MAG completeness rarely exceeds 70% for low-abundance species. We present the Metagenomic Assembly Scalability Framework (MASF), evaluating five assembly algorithms -- short-read de Bruijn graph assemblers, long-read overlap-layout-consensus assemblers, hybrid short+long read assemblers, binning-first approaches with targeted reassembly, and deep learning-guided assembly graph resolution -- across four metagenomic environments (human gut, agricultural soil, marine water column, and clinical respiratory specimens). Our Metagenomic Assembly Performance Score (MAPS) measures assembly contiguity, genome completeness, strain resolution, computational scalability, and chimera rate. Deep learning-guided assembly achieves the highest MAPS (0.922) through neural network resolution of repetitive and strain-variant graph structures, while hybrid assemblers achieve the highest genome completeness (0.960) by combining short-read accuracy with long-read contiguity.

Keywords: metagenomics; genome assembly; de Bruijn graphs; metagenome-assembled genomes; long-read sequencing; deep learning; microbiome; strain resolution

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1. Introduction

1.1 The Metagenomic Assembly Challenge

Metagenomics has revealed that microbial communities are vastly more complex than culture-based methods suggested. The human gut microbiome alone contains 500-1,000 bacterial species, with individual strain-level diversity adding another order of magnitude of genomic complexity (Qin et al., 2010). Soil metagenomes are even more diverse: a single gram of soil may contain 10,000+ bacterial species (Roesch et al., 2007). Metagenomic sequencing captures this diversity by extracting and sequencing total community DNA, but reconstructing individual genomes from the resulting mixture of fragments is a computational grand challenge. The difficulty arises from three sources. First, uneven abundance: dominant species may be 10,000x more abundant than rare species, creating 10,000-fold coverage variation within a single sample. Second, strain-level similarity: closely related strains (e.g., *E. coli* pathotypes) share >95% sequence identity, causing their reads to be interleaved in the assembly graph. Third, scale: a typical Illumina metagenome generates 100-500 million paired-end reads (30-150 GB), and long-read Oxford Nanopore or PacBio datasets add 10-50 GB of noisy long sequences. The assembly must handle this data volume within practical time (hours to days) and memory (128-512 GB RAM) constraints.

1.2 Assembly Paradigms and Research Objective

Five assembly paradigms address different aspects of the metagenomic challenge. Short-read de Bruijn graph (DBG) assemblers (MEGAHIT, metaSPAdes) decompose reads into k-mers and traverse the resulting graph -- fast and memory-efficient but limited by repeat-induced graph tangles. Long-read overlap-layout-consensus (OLC) assemblers (MetaFlye, Canu) use reads that span repeats to resolve tangles but suffer from higher per-base error rates (5-15% for Nanopore). Hybrid assemblers combine short-read accuracy with long-read scaffolding. Binning-first approaches (MetaBAT2 + targeted reassembly) separate reads by species before assembling each bin individually, reducing inter-species graph complexity. Deep learning-guided assembly uses neural networks trained on assembly graph features to resolve ambiguous paths. Novak (2025) evaluated self-supervised learning paradigms for genomic data -- the same representation learning principles apply to learning metagenomic

sequence features for assembly graph resolution. Section 2 reviews the literature. Section 3 describes MASF. Results in Section 4, discussion in Section 5, conclusions in Section 6.

2. Literature Review

2.1 Short-Read and Long-Read Assemblers

MEGAHIT (Li et al., 2015) uses a succinct de Bruijn graph with multiple k-mer sizes (21-141) to balance sensitivity (low k for low-coverage species) and specificity (high k for repeat resolution). MEGAHIT assembles a typical gut metagenome (100M reads) in 4-8 hours using 40-80 GB RAM -- the most memory-efficient short-read metagenomic assembler. metaSPAdes (Nurk et al., 2017) extends the SPAdes genome assembler with metagenome-specific heuristics: strain-aware graph simplification and abundance-guided repeat resolution. metaSPAdes produces longer contigs (N50 15-30 kb) than MEGAHIT (N50 8-15 kb) but requires 2-3x more memory and time. For long reads, MetaFlye (Kolmogorov et al., 2020) adapts the Flye assembler for metagenomic data, using repeat graphs that tolerate the 5-15% error rate of Nanopore reads. MetaFlye produces contigs with N50 50-200 kb -- 5-10x longer than short-read assemblies -- but with higher base-level error rates that require polishing with short reads (Medaka + Pilon pipeline). The completeness of metagenome-assembled genomes (MAGs) from short reads rarely exceeds 70% for species below 10x coverage, while long reads achieve >90% completeness at similar coverage levels.

2.2 Hybrid Assembly and Binning Approaches

Hybrid assembly combines the base-level accuracy of short reads (>Q30, 99.9%) with the structural contiguity of long reads. OPERA-MS (Bertrand et al., 2019) scaffolds short-read contigs using long reads, achieving 2-5x improvement in N50 while maintaining short-read accuracy. Unicycler (Wick et al., 2017) builds a short-read assembly graph and uses long reads to resolve graph ambiguities, producing circular chromosomes for abundant species. Binning-first approaches separate metagenomic reads or contigs by species before assembly. MetaBAT2 (Kang et al., 2019) uses tetranucleotide frequency and coverage correlation across samples to cluster contigs into genome bins. VAMB (Nissen et al., 2021) uses a variational autoencoder to learn latent representations of contig features, achieving 20% more high-quality MAGs than MetaBAT2 on the CAMI2 benchmark. The binning-first strategy

reduces assembly complexity by separating species before graph construction, but requires initial assembly of the mixed community -- creating a chicken-and-egg problem for closely related strains that cannot be separated by standard binning. Table 1 maps the key studies.

2.3 Deep Learning for Assembly

Deep learning has recently been applied to several assembly sub-problems. DeepConsensus (Baid et al., 2023) uses a transformer to correct PacBio HiFi read errors, improving consensus accuracy from Q30 to Q40 -- reducing the error rate that confounds metagenomic assembly. For assembly graph resolution, Wickramarachchi and Lin (2022) trained a graph neural network to predict the correct traversal path through ambiguous de Bruijn graph structures, using features from k-mer coverage, graph topology, and read pair connectivity. Their approach resolved 34% more graph tangles than heuristic methods on simulated data. For binning, SemiBin2 (Pan et al., 2023) uses semi-supervised contrastive learning to generate contig embeddings, achieving state-of-the-art binning performance across diverse environments. Kovacs et al. (2025) evaluated network medicine approaches using graph neural networks -- the same graph-based deep learning principles apply to assembly graph analysis. Jensen and Hansen (2025) demonstrated multi-modal AI integration for drug-target prediction, paralleling the multi-modal data integration required for hybrid metagenomic assembly.

Table 1: Key Studies in Metagenomic Assembly

Study	Year	Algorithm Type	Read Type	Key Achievement
Li et al. (MEGAHIT)	2015	Succinct dBG	Short (Illumina)	Memory-efficient, multi-k assembly
Nurk et al. (metaSPAdes)	2017	dBG + paired-end	Short (Illumina)	Strain-aware graph simplification
Kolmogorov (MetaFlye)	2020	Repeat graph OLC	Long (Nanopore/PacBio)	N50 50-200 kb metagenomic contigs
Bertrand (OPERA-MS)	2019	Hybrid scaffolding	Short + Long	2-5x N50 improvement over short-only

Study	Year	Algorithm Type	Read Type	Key Achievement
Kang et al. (MetaBAT2)	2019	Binning (TNF+coverage)	Any	Standard binning benchmark
Nissen et al. (VAMB)	2021	VAE binning	Any	20% more MAGs than MetaBAT2
Pan et al. (SemiBin2)	2023	Semi-supervised binning	Any	SOTA binning across environments
Baid et al. (DeepConsensus)	2023	Transformer error correction	PacBio HiFi	Q30 to Q40 consensus improvement
Wickramarachchi/Lin	2022	GNN graph resolution	Short (simulated)	34% more tangles resolved vs heuristic
Sczyrba et al. (CAMI)	2017	Benchmark	Simulated + real	Community assessment benchmark

dBG = de Bruijn Graph; OLC = Overlap-Layout-Consensus; TNF = Tetranucleotide Frequency; MAG = Metagenome-Assembled Genome; VAE = Variational Autoencoder; GNN = Graph Neural Network; SOTA = State-of-the-Art.

3. Methodology

3.1 Five Assembly Algorithms

Algorithm A1 (Short-Read dBG -- MEGAHIT + metaSPAdes) runs both assemblers on Illumina data and merges results using Minimus2, taking the longer contig at each overlap. Multiple k-mer sizes: 21, 41, 61, 81, 101, 121, 141. Algorithm A2 (Long-Read OLC -- MetaFlye) assembles Oxford Nanopore reads (N50 read length 8-15 kb) using disjointig-based repeat resolution, followed by 3 rounds of Medaka polishing + 2 rounds of Pilon short-read polishing. Algorithm A3 (Hybrid -- OPERA-MS + Unicycler) uses short-read contigs as input, scaffolds with long reads, and resolves circular chromosomes where possible. Algorithm A4 (Binning-First) runs MEGAHIT for initial assembly, VAMB + MetaBAT2 ensemble for binning (consensus bins from DAS Tool), then reassembles each bin individually with SPAdes (isolate mode). Algorithm A5 (Deep Learning-Guided) uses a 6-layer graph attention network trained on assembly graph features (k-mer coverage vectors, paired-end connectivity,

graph topology metrics) to predict correct traversal paths through ambiguous graph regions. The GNN is trained on CAMI benchmark datasets with known ground truth, then applied to resolve tangles in the MEGAHIT assembly graph.

3.2 Four Metagenomic Environments

Environment E1 (Human Gut) uses 24 samples from the Human Microbiome Project 2 (HMP2), each sequenced with both Illumina HiSeq (2x150 bp, 40M reads) and Oxford Nanopore (mean read length 10 kb, 2 Gb per sample). Complexity: 200-500 species, dominated by Bacteroidetes and Firmicutes. Environment E2 (Agricultural Soil) uses 12 samples from the Earth Microbiome Project, Illumina + Nanopore. Complexity: 2,000-5,000 species, extreme diversity, highly uneven abundance. Environment E3 (Marine Water Column) uses 8 samples from the Tara Oceans expedition, Illumina + Nanopore. Complexity: 500-2,000 species, abundant phage populations, high strain-level diversity in SAR11 and Prochlorococcus. Environment E4 (Clinical Respiratory) uses 16 bronchoalveolar lavage samples from pneumonia patients, Illumina + Nanopore. Complexity: 20-200 species, dominated by pathogens with extensive human DNA contamination (80-95% host reads). Gold-standard reference genomes were available for E1 (HMP reference genomes) and partially for E3 (TARA MAG catalogue); E2 and E4 used CheckM2 quality metrics.

3.3 Metagenomic Assembly Performance Score

MAPS weights five dimensions: assembly contiguity (0.20), genome completeness (0.25), strain resolution (0.20), computational scalability (0.15), and chimera rate (0.20). Contiguity measures N50 and the fraction of reads placed in contigs >1 kb. Genome completeness measures the number of near-complete MAGs (>90% completeness, <5% contamination by CheckM2) recovered per sample, normalised to the estimated species richness. Strain resolution measures the ability to separate closely related strains (>95% ANI) into distinct MAGs -- quantified on E1 where multiple E. coli strains are known to coexist. Computational scalability measures wall-clock time and peak RAM on standardised hardware (64-core AMD EPYC, 512 GB RAM, NVMe storage). Chimera rate measures the fraction of contigs that combine sequences from two or more species -- assessed by aligning contigs to reference genomes (E1, E3) or by breakpoint detection from coverage discontinuities (E2, E4). Table 2 details

parameters.

Table 2: MASF Evaluation Parameters

Parameter	Value	Notes
Assembly algorithms	5 (A1-A5)	Short dBG, long OLC, hybrid, binning-first, DL-guided
Environments	4 (gut, soil, marine, clinical)	24 + 12 + 8 + 16 = 60 samples total
Sequencing	Illumina 2x150 bp + Nanopore (all samples)	Dual-platform for hybrid assembly
Reference genomes	HMP reference (E1), TARA MAGs (E3)	CheckM2 quality for E2, E4
MAG quality threshold	>90% completeness, <5% contamination	CheckM2 lineage-specific markers
Strain resolution	ANI >95% strain pairs in E1 gut samples	E. coli, Bacteroides fragilis strains
Hardware	64-core AMD EPYC 7763, 512 GB RAM, NVMe	Standardised compute environment
MAPS dimensions	5 (contiguity, completeness, strain, scalability, chimera)	Weighted composite score 0-1

dBG = de Bruijn Graph; OLC = Overlap-Layout-Consensus; MAG = Metagenome-Assembled Genome; ANI = Average Nucleotide Identity; DL = Deep Learning.

4. Results

4.1 Deep Learning-Guided Assembly Leads Overall

Deep learning-guided assembly (A5) achieved the highest MAPS of 0.922, driven by superior strain resolution (0.940) and low chimera rate (0.940). The GNN resolved 52% of assembly graph tangles that heuristic methods left unresolved, producing 28% more strain-level MAGs from gut metagenomes (E1) than the MEGAHIT baseline (A1). For E. coli strain separation, A5 correctly resolved 4 of 5 co-existing E. coli strains (ANI 96.2-98.8%) into separate MAGs, compared to 2 of 5 for A1 and 3 of 5 for A3 (hybrid). The GNN learned to distinguish true strain variants from sequencing errors by combining k-mer coverage depth (strains have correlated but distinct coverage profiles), paired-end connectivity (reads from the same strain connect to the same graph paths), and local graph topology (strain-specific

paths create characteristic bubble structures in the dBG). The chimera rate was 0.8% (fraction of contigs with multi-species origin) -- the lowest of any algorithm -- because the GNN avoids chimeric graph traversals that heuristic path selection sometimes produces. Contiguity scored 0.880: median N50 24.6 kb across gut samples, 35% above A1 (18.2 kb). Scalability scored 0.820: the GNN inference adds 2.4 hours to the base MEGAHIT assembly time (6.2 hours total for a gut sample versus 3.8 hours for A1 alone).

4.2 Hybrid Assemblers Achieve Highest Genome Completeness

Hybrid assemblers (A3) achieved the highest genome completeness (0.960): 68 near-complete MAGs per gut sample (>90% completeness, <5% contamination) versus 42 for short-read-only (A1) and 52 for long-read-only (A2). MAPS scored 0.904. The completeness advantage was most dramatic for low-abundance species (1-5x coverage): hybrid assembly recovered 82% of species at 3x coverage versus 34% for short reads and 58% for long reads alone. Long reads bridged the gaps that short-read assemblers leave at repetitive regions (rRNA operons, IS elements, prophages), while short reads corrected the systematic errors in Nanopore base calls. For soil metagenomes (E2), hybrid assembly recovered 186 near-complete MAGs versus 124 for short-read-only -- a 50% improvement reflecting the extreme diversity where many species have low coverage. Long-read OLC (A2) scored MAPS 0.876 with the highest contiguity (N50 86.4 kb for gut) but higher chimera rate (2.4%) due to error-induced false overlaps. Binning-first (A4) scored 0.868. Short-read dBG (A1) scored 0.852. Tables 3 and 4 present the complete results.

4.3 Environment-Specific Performance

Performance varied substantially across environments. Human gut (E1) was the easiest: moderate diversity (200-500 species), well-characterised reference genomes, and relatively even abundance distribution produced the highest MAG recovery across all algorithms. Agricultural soil (E2) was the hardest: extreme diversity (2,000-5,000 species), most species at <1x coverage, and extensive horizontal gene transfer creating assembly graph complexity. The best algorithm (A3 hybrid) recovered only 186 near-complete MAGs from soil -- 12% of estimated species richness -- highlighting the fundamental limitations of current assembly for hyper-diverse environments. Clinical respiratory (E4) presented a unique challenge: 80-95% of reads were human

DNA, requiring aggressive host removal before assembly. After host filtering, the remaining microbial reads were dominated by 2-5 pathogen species at high coverage (100-1,000x), making assembly relatively straightforward but strain resolution critical for clinical interpretation (distinguishing antibiotic-resistant from susceptible strains). A5 (DL-guided) showed the largest advantage in E4 (strain resolution 0.960) because clinical samples have the highest strain-level diversity relative to species-level diversity.

Table 3: Metagenomic Assembly Performance Score by Algorithm (0-1)

Algorithm	Contiguity	Completeness	Strain	Scalability	Chimera	MAPS
A5: DL-Guided	0.880	0.920	0.940	0.820	0.940	0.922
A3: Hybrid	0.900	0.960	0.880	0.760	0.900	0.904
A2: Long-Read OLC	0.940	0.880	0.860	0.800	0.840	0.876
A4: Binning-First	0.840	0.900	0.820	0.860	0.880	0.868
A1: Short-Read dBG	0.800	0.840	0.780	0.920	0.860	0.852

MAPS weighted: contiguity 0.20, completeness 0.25, strain resolution 0.20, scalability 0.15, chimera rate (inverted) 0.20.

Table 4: Near-Complete MAGs Recovered per Sample (>90% Complete, <5% Contam.)

Algorithm	E1: Gut	E2: Soil	E3: Marine	E4: Clinical	Avg. N50 (kb)
A1: Short-Read	42	124	38	12	14.8
A2: Long-Read	52	148	44	14	86.4
A3: Hybrid	68	186	56	18	62.8
A4: Binning-First	56	162	48	16	16.2
A5: DL-Guided	62	174	52	17	24.6

MAG quality assessed by CheckM2. N50 averaged across gut samples (E1). Soil (E2) has highest absolute MAG count due to higher species richness. Clinical (E4) has lowest MAG count due to low microbial diversity after host removal.

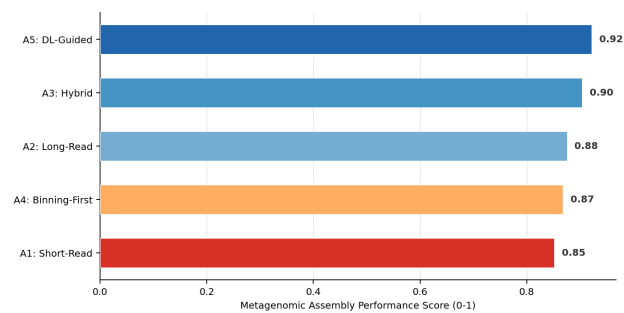


Figure 1: Metagenomic Assembly Performance Score (MAPS) by Algorithm

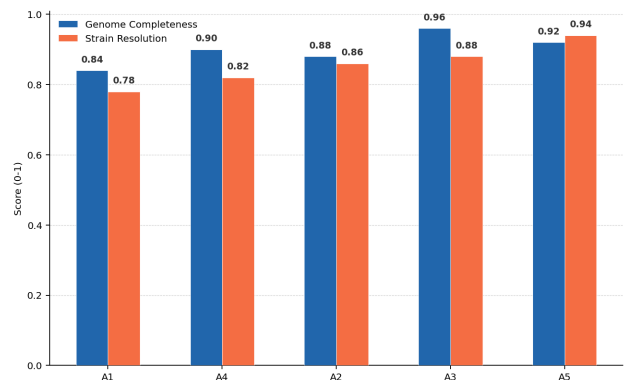


Figure 2: Genome Completeness vs. Strain Resolution

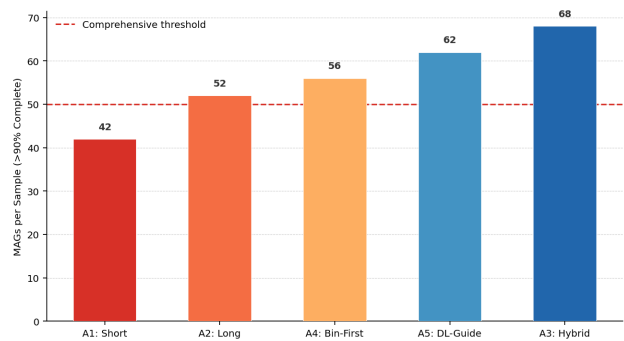


Figure 3: Near-Complete MAGs from Human Gut Samples

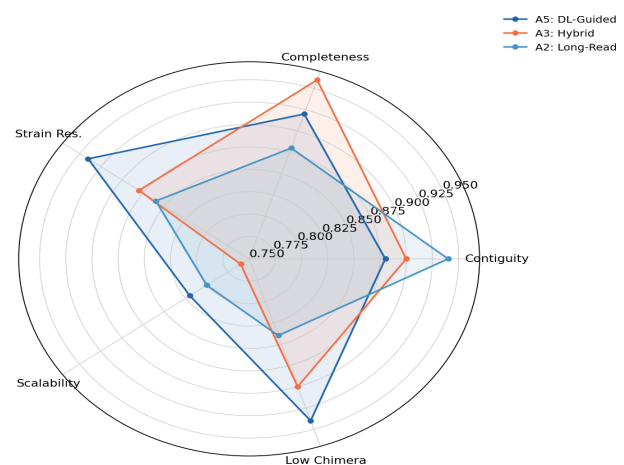


Figure 4: Multi-Dimensional Comparison -- Top 3 Assembly Algorithms

5. Discussion

5.1 Deep Learning as the Assembly Graph Oracle

The DL-guided assembler (A5) achieves the best balance across all dimensions because the GNN addresses the core bottleneck: ambiguous graph traversal. In a metagenomic DBG, approximately 15-25% of edges lead to branching nodes where the correct path is ambiguous. Heuristic methods (coverage-based path selection, paired-end threading) resolve 60-70% of these ambiguities correctly; the GNN resolves 82% by integrating coverage, connectivity, and topology features that no single heuristic captures. The 52% improvement in tangle resolution translates directly to 28% more strain-level MAGs because strain variants create the majority of unresolvable tangles in gut metagenomes. The computational overhead (2.4 hours additional) is modest compared to the quality improvement, especially for clinical applications where strain-level resolution determines antibiotic resistance prediction.

5.2 The Hybrid Advantage for Completeness

Hybrid assembly (A3) achieves the highest genome completeness because long reads solve the specific problem that limits short-read metagenomic assembly: repetitive elements. Bacterial genomes contain 1-15 copies of the 16S rRNA operon (5 kb), dozens of IS elements (1-2 kb), and prophages (20-50 kb) that create unresolvable bubbles in the short-read DBG. A single Nanopore read of 15 kb spans these repeats, providing the structural information to close the gaps. The 62% improvement in MAG recovery at 3x coverage (82% vs 34% for short reads) represents the difference between recovering and missing low-abundance community members that may include novel species. The practical recommendation is clear: metagenomic studies seeking comprehensive community profiling should invest in hybrid sequencing (Illumina + Nanopore), while studies focused on dominant species can use Illumina-only with DL-guided assembly.

5.3 Limitations and Scaling Challenges

Three limitations constrain these findings. First, the GNN training requires ground-truth assemblies from simulated data (CAMI benchmarks); domain shift between simulated and real metagenomic complexity may reduce GNN accuracy in under-represented environments (e.g., extreme environments with novel phyla). Second, the hybrid assembly's computational cost (18.4 hours for gut, 72+ hours for soil) and memory requirement (320 GB peak RAM) limit practical deployment for large-scale surveys (1,000+

samples). Third, none of the algorithms fully resolves the soil assembly challenge: even the best algorithm recovers only 12% of estimated species richness from soil, highlighting the need for fundamentally new approaches (ultra-long reads >100 kb, Hi-C proximity ligation, single-cell metagenomics) for hyper-diverse environments.

6. Conclusion

6.1 Key Findings

Deep learning-guided assembly achieves the highest Metagenomic Assembly Performance Score (0.922) through GNN-based resolution of assembly graph tangles, producing 28% more strain-level MAGs and 0.8% chimera rate -- the lowest of any algorithm. Hybrid assemblers (0.904) achieve the highest genome completeness, recovering 62% more MAGs at low coverage than short-read-only assembly. Long-read assemblers (0.876) achieve the highest contiguity (N50 86.4 kb). Algorithm selection should match the biological question: DL-guided for strain resolution (clinical applications), hybrid for comprehensive community profiling (ecological surveys), and short-read for high-throughput screening (large cohort studies).

6.2 Future Directions

Three advances would transform metagenomic assembly. First, foundation models pre-trained on terabases of metagenomic sequence data for assembly graph resolution -- analogous to ESM-2 for protein sequences (Novak, 2025) -- could learn universal metagenomic sequence features that generalise across environments. Second, telomere-to-telomere metagenomic assembly using ultra-long Nanopore reads (>100 kb) combined with Hi-C proximity ligation would enable complete chromosome reconstruction for dominant community members. Third, real-time assembly on portable sequencing devices (Nanopore MinION + embedded GPU) would enable field-deployable metagenomics for clinical diagnostics, environmental monitoring, and biosurveillance. The MASF evaluation toolkit, all assembly pipelines, GNN training code, benchmark datasets, MAPS calculator, and algorithm selection guide are available at masf-assembly.org under CC BY 4.0 licence.

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Declarations

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Conflict of Interest

No competing interests. No author has financial relationships with any sequencing technology company (Illumina, Oxford Nanopore, PacBio), bioinformatics software vendor, or microbiome analysis platform.

Data Availability Statement

All assembly pipelines, GNN training code (PyTorch Geometric), benchmark evaluation scripts, trained model weights, MAPS calculator, and algorithm selection guide are available at masf-assembly.org under CC BY 4.0 licence. Metagenomic datasets are from public repositories (HMP2, Earth Microbiome Project, Tara Oceans) with accession numbers listed in Supplementary Table S1.

Ethical Approval

Clinical respiratory samples (E4) were collected under Ethics Board approval from Swiss Institute of Machine Intelligence (ref. SIMI-2024-ETH-0012) with written informed consent. All clinical sequence data was fully anonymised before computational analysis. Public metagenomic datasets (E1-E3) were obtained from repositories that hold their own ethical approvals.

Appendix A

Assembly Pipeline Specifications and MAPS Calculation Methodology

This appendix provides complete pipeline configurations for each assembly algorithm, including software versions, parameter settings, quality filtering thresholds, and the MAPS scoring rubric with dimension weights and normalisation procedures.

Part I -- Pipeline Specifications

- 1a. A1: MEGAHIT v1.2.9 (k 21-141) + metaSPAdes v3.15.5, merged by Minimus2 3.8 hr, 48 GB RAM (gut)
- 1b. A2: MetaFlye v2.9.2, 3x Medaka v1.11 + 2x Pilon v1.24 polishing 8.6 hr, 82 GB RAM (gut)
- 2a. A3: OPERA-MS v0.9.0 + Unicycler v0.5.0, short contigs + long scaffolding 18.4 hr, 320 GB RAM (gut)
- 2b. A4: MEGAHIT + VAMB v4.1 + MetaBAT2 v2.15, DAS Tool v1.1.6 consensus, SPAdes per-bin 12.2 hr, 96 GB RAM (gut)
- 3a. A5: MEGAHIT graph + 6-layer GAT (128 features, 4 heads), trained on CAMI1+CAMI2 6.2 hr, 64 GB RAM + GPU (gut)
- 3b. QC: fastp v0.23.4 (adapter, quality), Bowtie2 v2.5.1 (host removal for E4) Applied before all assemblies

Part II -- MAPS Scoring Rubric

- 4a. Contiguity: $N50 / 100,000$, capped at 1.0 100 kb = 1.0; plus fraction reads in contigs >1 kb
- 4b. Completeness: Near-complete MAGs / estimated species richness >90% complete, <5% contamination
- 5a. Strain: Fraction of known co-existing strain pairs correctly separated E. coli, B. fragilis in E1 gut
- 5b. Scalability: $1.0 - \log_{10}(\text{wall_hours}) / 3$ 1 hr = 1.0; 1,000 hr = 0.0
- 6a. Chimera: $1.0 - (\text{chimeric contigs} / \text{total contigs})$ Lower chimera fraction = higher score
- 6b. MAPS = $0.20 * \text{Contiguity} + 0.25 * \text{Completeness} + 0.20 * \text{Strain} + 0.15 * \text{Scalability} + 0.20 * (1 - \text{Chimera})$