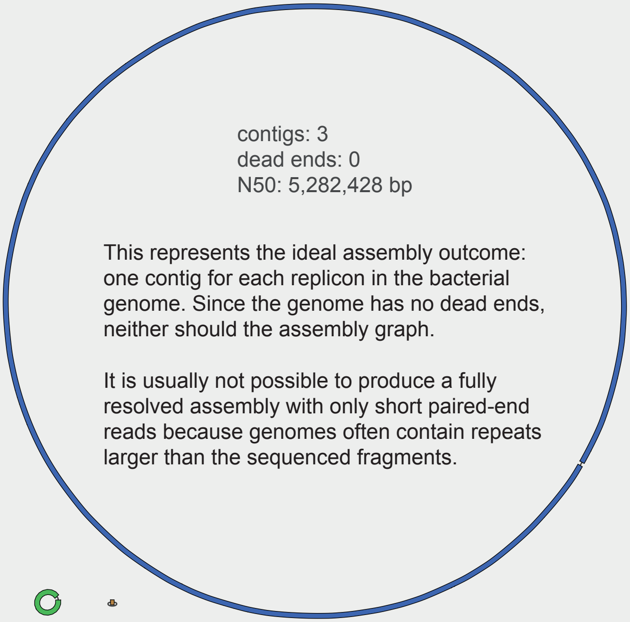
Complete genome

contigs: 3
dead ends: 0
N50: 5,282,428 bp

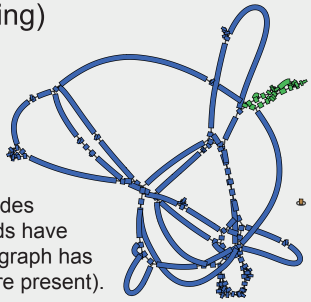


This represents the ideal assembly outcome: one contig for each replicon in the bacterial genome. Since the genome has no dead ends, neither should the assembly graph.

It is usually not possible to produce a fully resolved assembly with only short paired-end reads because genomes often contain repeats larger than the sequenced fragments.

Unicycler (before bridging)

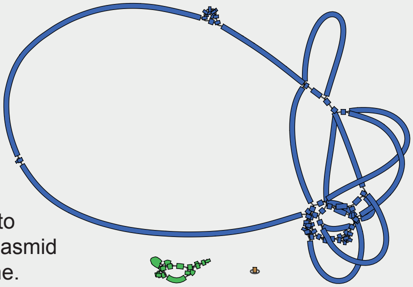
contigs: 165
dead ends: 0
N50: 208,318 bp



Unicycler's unbridged graph is made from a high k-mer SPAdes assembly graph. Since the reads have good depth and coverage, this graph has no dead ends (all sequences are present).

Unicycler graph (after bridging)

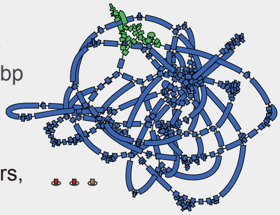
contigs: 92
dead ends: 0
N50: 478,597 bp



After bridging with the SPAdes contig paths, the graph is sufficiently resolved to separate the large plasmid from the chromosome.

SPAdes assembly graph

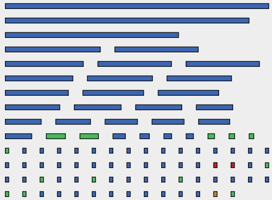
contigs: 382
dead ends: 0
N50: 93,344 bp



Due to smaller k-mers, the SPAdes assembly graph is less resolved than Unicycler's unbridged graph. It also contains erroneous contigs with sequence not in the genome.

SPAdes contigs

contigs: 95
dead ends: 190
N50: 203,689 bp

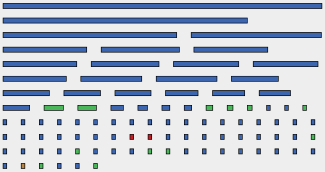


SPAdes contigs contain repeat resolution from read-pair orientation, but are no longer available in graph form. The chromosomal and plasmid contigs are interspersed.

SPAdes scaffolds

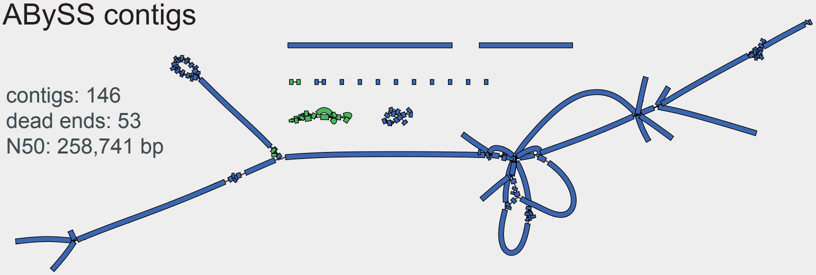
contigs: 94
dead ends: 188
N50: 215,736 bp

SPAdes scaffolds are more resolved than its contigs, but some contain Ns.



ABySS contigs

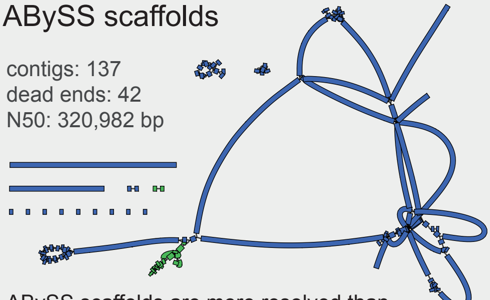
contigs: 146
dead ends: 53
N50: 258,741 bp



Unlike SPAdes, ABySS contigs are available in graph form, though with many dead ends, fragmenting the graph into pieces.

ABySS scaffolds

contigs: 137
dead ends: 42
N50: 320,982 bp



ABySS scaffolds are more resolved than its contigs, but some contain Ns.