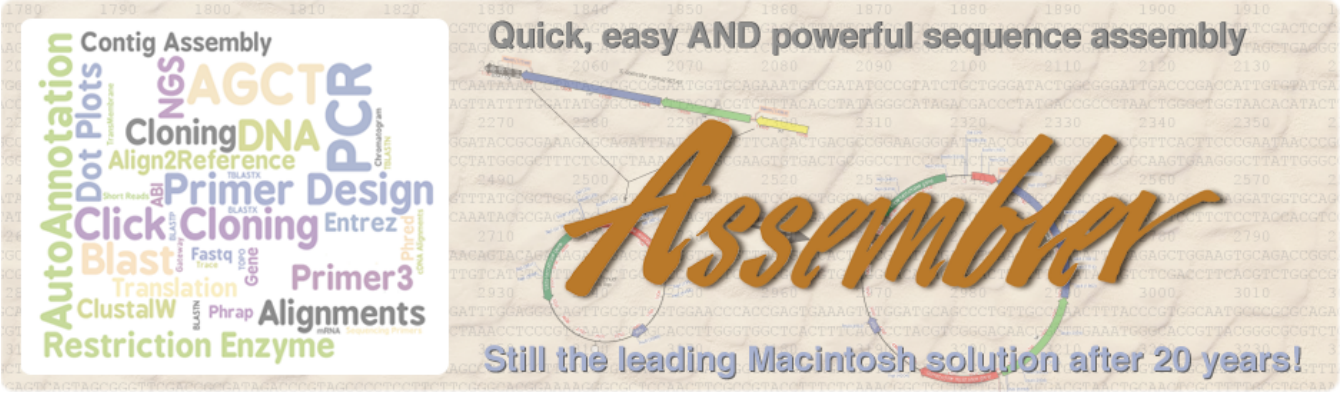


Assembler is a MacVector module designed for easy assembly of sequence reads on your desktop. From a small sequencing project to large resequencing projects, from a few hundred Sanger files to millions of Illumina , MiSeq or PacBio reads. With Assembler all you need are a few mouse clicks to get high performance and high quality sequence assemblies without needing to get technical with your data.

Base Calling. Carry out highly accurate base calling with quality values for each individual base call. An interactive trace editor allows you to view the base calls and their quality values.

***De novo* Sequence Assembly.** Perform highly accurate and fast *de novo* sequence assembly using Phrap for Sanger data and Velvet for data from short read sequencers.

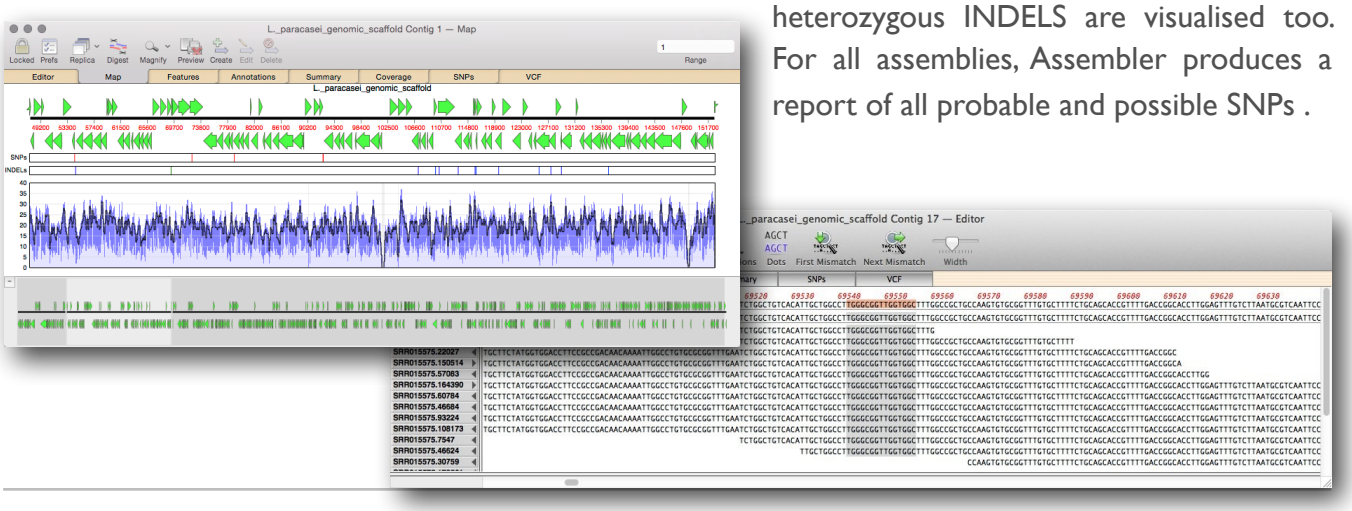
New in MacVector 16: SPAdes: offers support for mixed assemblies (e.g. Illumina, PacBio and Oxford Nanopore in one assembly), uses less RAM than Velvet and produces longer contigs.

Reference Sequence Assembly. Perform gapped reference assembly using Bowtie2. Millions of reads can be aligned against genome reference sequences using a few mouse clicks.

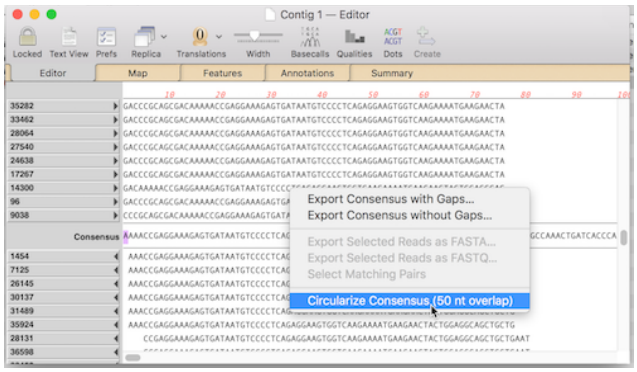
Next Generation Sequencing. Short read data may be imported in Fastq format and assembled into reference or *de novo* assemblies. Existing BAM/SAM alignments can be visualized.

Coverage Data. Read depth is plotted along contigs and reference sequence. Read depth is reported for every annotated gene and CDS region in an assembly. Useful for RNA-Seq assemblies.

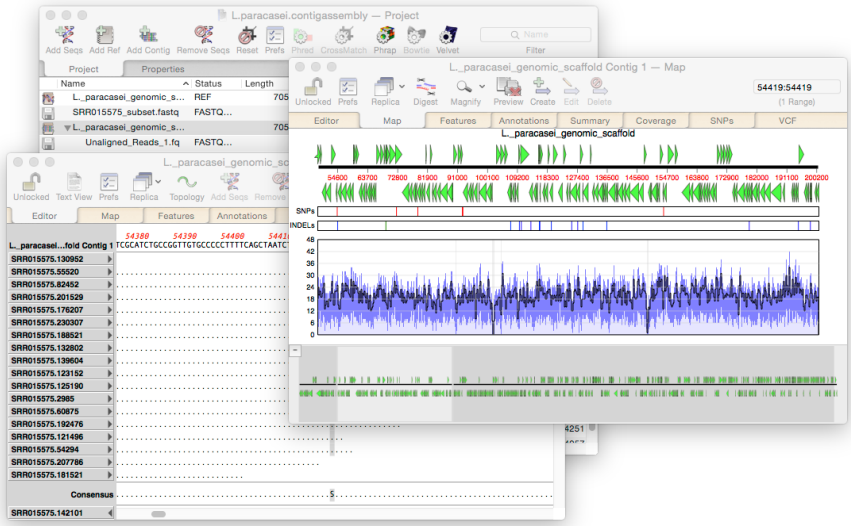
Variant Calling. SNPs and INDELS are visualised on the Map and reported in a standard VCF file. Homozygous and heterozygous INDELS are visualised too. For all assemblies, Assembler produces a report of all probable and possible SNPs .



Bacterial genome tools: Many tools for finishing bacterial genomes including circularizing genomes.

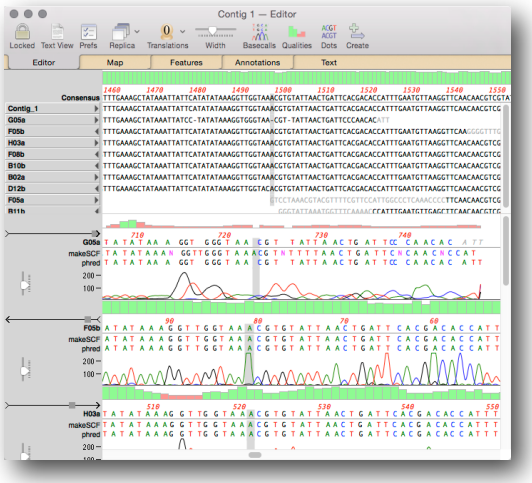


Contig Editing and Analysis. Edit individual bases in a DNA sequence to generate a new consensus. View the consensus, along with associated chromatograms, sequence reads, coverage map, and quality scores in the easy-to-use, graphical editor. When sequence variations are observed, you can quickly identify alternative protein sequences with a 3/6 frame translation of your contigs.



Advantages

Supports Numerous File Formats. Import ABI, SCF, and ALF chromatograms, MacVector, FASTQ or FASTA. Assemblies are stored in the BAM format and existing BAM/SAM alignments can be imported. Variants are



exported in VCF files.

Easy to use interface. Navigating around your assemblies has never been easier. Display an entire contig in the graphical Map and select a read to zoom straight to that region. Click on a base in a contig and see the associated trace data or the read coverage depth map of that region.

Integrated within MacVector Analyze contigs directly in MacVector. Design sequencing primers directly on your sequence, for resequencing for hybrid assembly.

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