Session 2.3 – Ensamblado

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Assembly

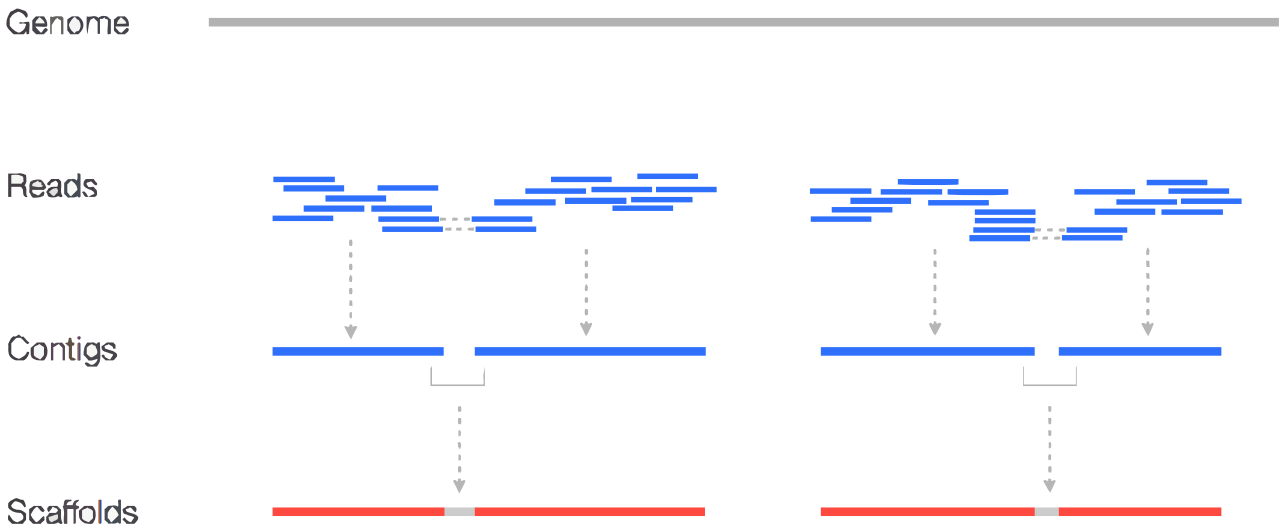
Reconstruct a representation of the original DNA from shorter DNA sequences or small fragments known as reads

- ***De novo:*** **with no previous knowledge of the genome to be assembled. It overlap the end of the end of each read in order to créate a longer sequence.**

- ***Assembly with reference:*** **A similar but not identical genome guides the assembly process. Map reads over supplied genome.**

Assembly: contig y scaffold

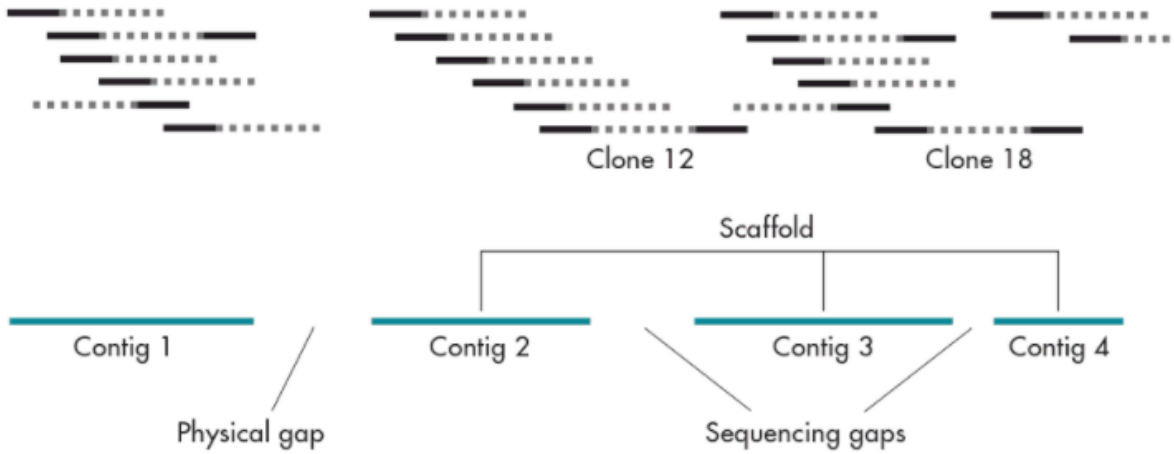
- **Contig: continuous sequence made up of overlaping shorter sequences**
- **Scaffold: two or more contigs located and rearranged according to spatial information(pair-end, mate pair, reference)**



https://www.biostars.org/p/253222/

Assembly: gaps

- **Sequencing gaps: Position and orientation known by spatial information**
- **Physical gaps: No information about adjacent contigs**

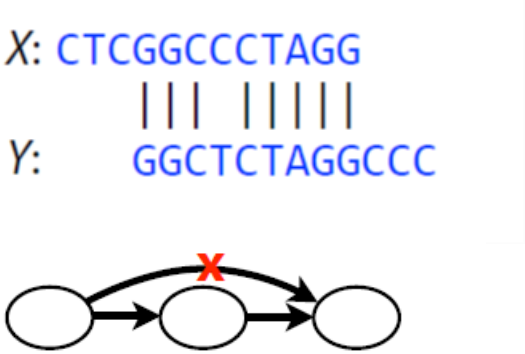


Gene Cloning, Lodge *et al*.

Assembly: Algorithms

- **Overlap, Layout, Consensus (OLC - overlap graph):**
  - O - first overlaps among all the reads are found
  - L - then it carries out a layout of all the reads and overlaps information on a graph
    - Removes redundant and low quality overlaps
  - C - and finally the consensus sequence is inferred

Ex. Newbler, Mira, Celera Assembler, CAP3, PCAP, Phrap, Phusion.



https://pt.slideshare.net/anton_alexandrov/combining-de-bruijn-graph-overlap-graph-and-microassembly/12?smtNoRedir=1

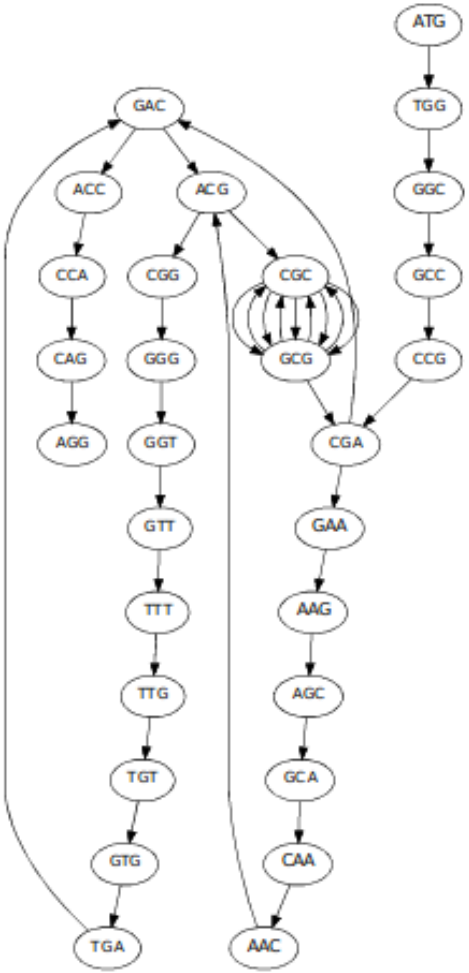
Assembly: Algorithms

- **De Brujin Graph (DBG: k-mer graph)**

Chopping reads into much shorter k-mers (fixed length fragments) and then using all the k-mers to form a DBG and infer the contigs.

- Nodes in the graph are k-mers
- Edges represent consecutive k-mers (which overlap by k-n symbols)

Ex. SPAdes, ABySS, Velvet, AllPaths, Soap….



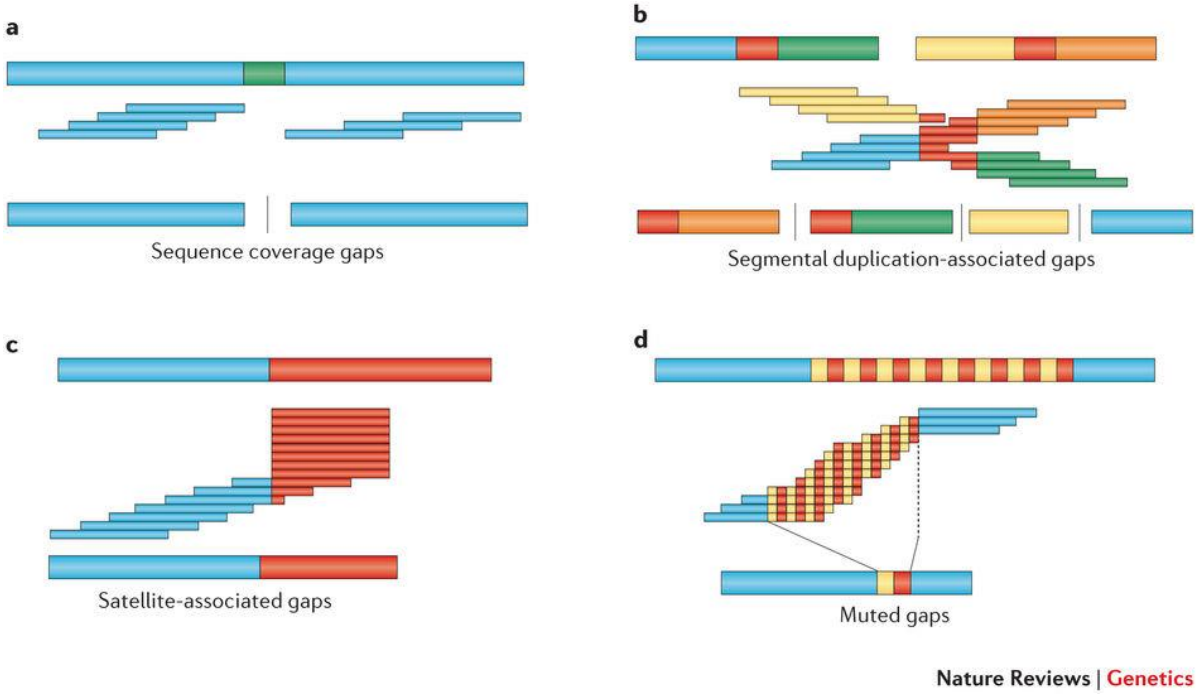
https://medium.com/@han_chen

Algorithms: DBG

- **Why choosing DBG:**
  - Sequencing bias
  - Sequence errors
  - Sequence length
- **DBG Flaws:**
  - Millions of pieces
    - Much, much shorter than the genome
    - Lots of them look similar
  - Missing pieces
    - Some parts can't be sequenced easily
    - Dirty Pieces - Multiplex
    - Lots of errors in reads
  - Repeats
    - If they are longer than the read length
    - Causes nodes to be shared, locality confusion

https://galaxyproject.github.io/training-material/topics/assembly/tutorials/debruijn-graph-assembly/slides.html#23

Assembly: Errors



- **A. Gaps – non sequenced region**
- **B. Long repeats**
  - Cuimera
- **Collapsed repetitive regions**
  - **C. Terminal**
  - **D. Intersticial**

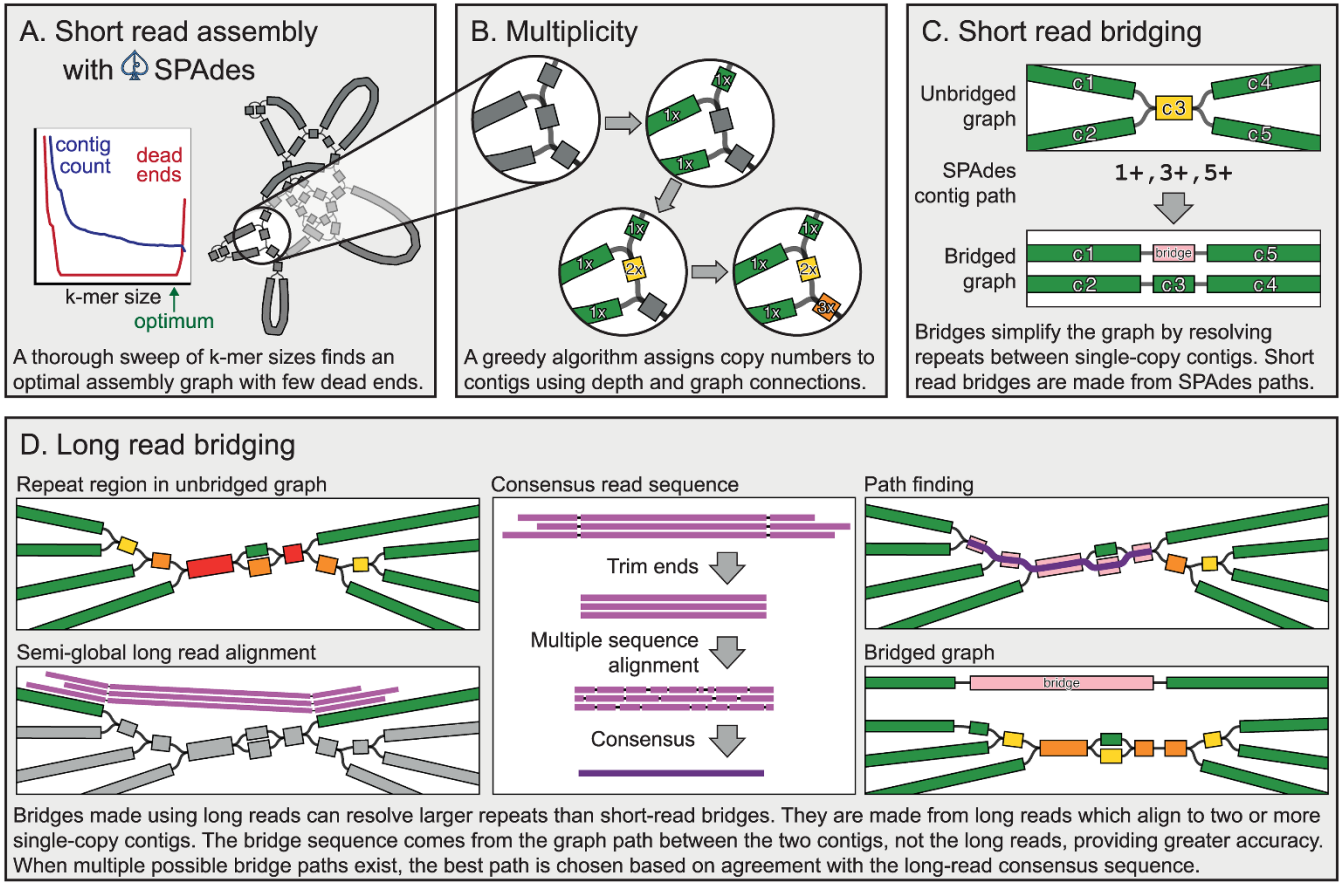
Genetic variation and the de novo assembly of human genomes
Chaisson *et al*.

Unicycler

- Lower k
  - More connections
  - Less chance of resolving small repeats
  - Higher k-mer coverage
- Higher k
  - Less connections
  - More chance of resolving small repeats
  - Lower k-mer coverage
  - Fragmented graph with dead ends
- Optimum value for k will balance these effects.

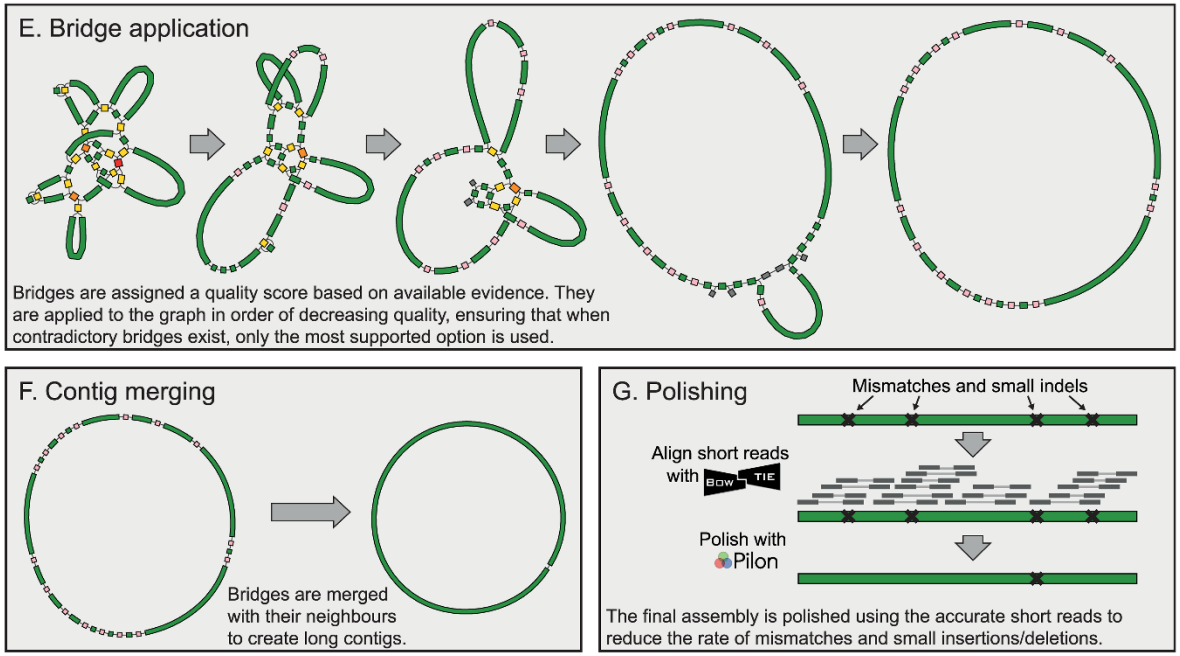
https://galaxyproject.github.io/training-material/topics/assembly/tutorials/debruijn-graph-assembly/slides.html#23

Unicycler



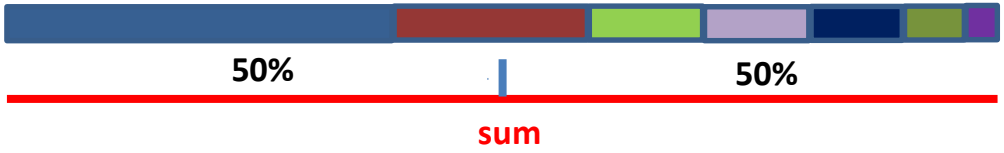
https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1005595

Unicycler

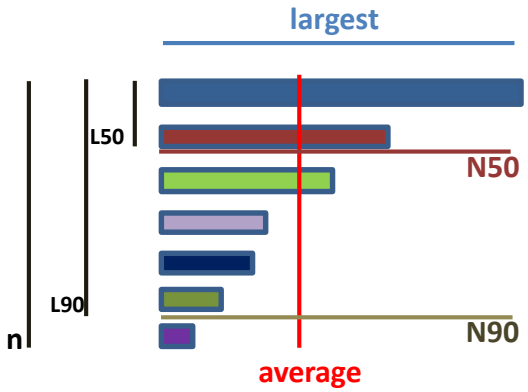


https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1005595

Assembly: Metrics



- sum = total bases number
- n = contigs number
- average = average contig length
- largest = largest contig
- N50 = length of the shortest contig where 50% of sum is held
- L50 = number of contigs which have 50% of the genome
- N90 = length of the shortest contig where 90% of sum is held.
- L90 = number of contigs which have 90% of the genome



Assembly: Scaffolding

- **From draft:**

  Order contigs (Nucmer, if there is reference it can be used to align and guide)

  Fill the GAPs (GapFiller, fill sequencing gap (not physical gap)

  Solve repeated sequence ambiguities (Expander)

  Resequence with different library:

  - Longer fragments and/or distance

- **Tools for assembly improvement**

  SSPACE (Scaffolding) REAPR (evaluate scaffolding, breaking incorrect scaffolds)

- **Assembly visualyzing**

  Artemis, ACT (comparación de dos o más secuencias)

Assembly: Evaluation

- Software that evaluate differets algorithms & parameters
  iMetAMOS, *Koren et al., BMCBioinformatics 2014, 15:126*
  GAGE-B, *Magoc et al.*, Bioinformatics 2013,29(14):1718-25

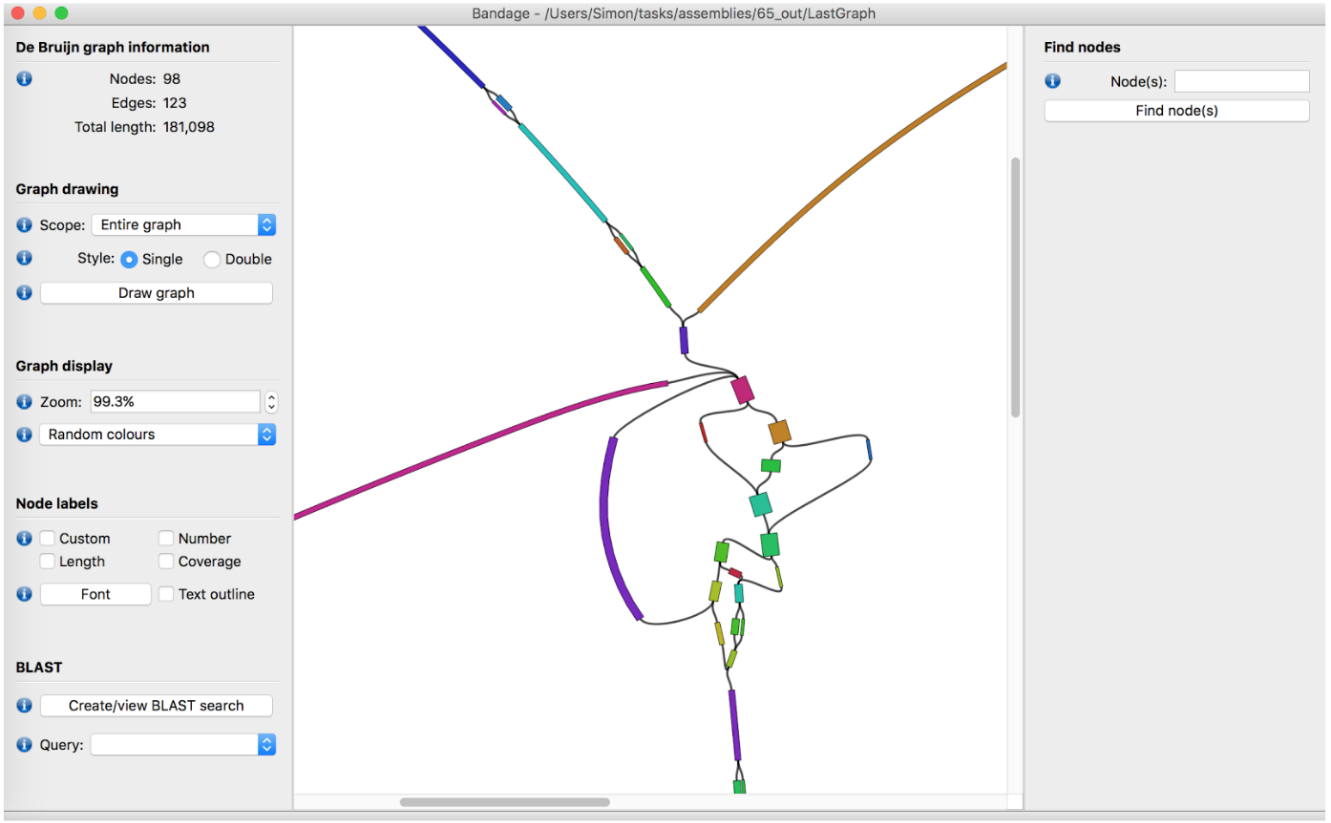
- Graph evaluation: Bandage, Wick R.R., Schultz M.B., Zobel J. & Holt K.E. (2015)

- Assembly evaluation: Quast, *Gurevich et al., Bioinformatics 2013, 29:8*

- **Metrics for a good assembly:**
  Large N50
  Sum closest to expected
  Low n
  Low L50

Assembly: Evaluation - Quast

- Graph evaluation: Bandage, Wick R.R., Schultz M.B., Zobel J. & Holt K.E. (2015)



Assembly: Evaluation - Quast

- Assembly evaluation: Quast, *Gurevich et al., Bioinformatics 2013, 29:8*

Worst Median Best ☑ Show heatmap

Genome statistics	RA_L2073_paired_assembly	RA_L2391_paired_assembly	RA_L2677_paired_assembly	RA_L2978_paired_assembly	RA_L2281_paired_assembly	RA_L2450_paired_assembly	RA_L2701_paired_assembly
Genome fraction (%)	81.079	88.828	84.92	90.172	85.733	88.172	92.463
Duplication ratio	1	1	1.001	1.001	1.001	1	1
# genomic features	1736 + 824 part	2113 + 600 part	1881 + 768 part	2157 + 611 part	1992 + 637 part	2073 + 643 part	2368 + 412 part
Largest alignment	16 612	33 033	21 336	25 068	29 638	30 305	40 471
Total aligned length	2 405 510	2 635 297	2 519 300	2 675 166	2 543 440	2 615 874	2 743 222
NGA50	3176	6162	4234	5948	5104	5358	9519
LGA50	267	151	219	153	166	166	96
Misassemblies							
# misassemblies	23	1	14	2	17	12	4
Misassembled contigs length	84 193	9611	45 868	6390	111 490	72 879	37 962
Mismatches							
# mismatches per 100 kbp	17	18.78	15	16.71	341.39	15.75	13.49
# indels per 100 kbp	1.21	1.25	1.87	1.94	7.27	1.45	0.87
# N's per 100 kbp	0	0	0	0	0	0	0
Statistics without reference							
# contigs	748	546	684	569	569	584	392
Largest contig	16 612	33 033	21 336	25 068	30 915	30 305	40 471
Total length	2 440 656	2 676 227	2 562 578	2 714 287	2 629 607	2 618 624	2 787 129
Total length (>= 1000 bp)	2 439 127	2 676 227	2 559 569	2 714 287	2 628 029	2 615 105	2 785 415
Total length (>= 10000 bp)	257 236	739 181	320 638	811 392	700 516	658 319	1 419 641
Total length (>= 50000 bp)	0	0	0	0	0	0	0

Extended report

Assembly: Evaluation - Quast

- Assembly evaluation: Quast, *Gurevich et al., Bioinformatics 2013, 29:8*

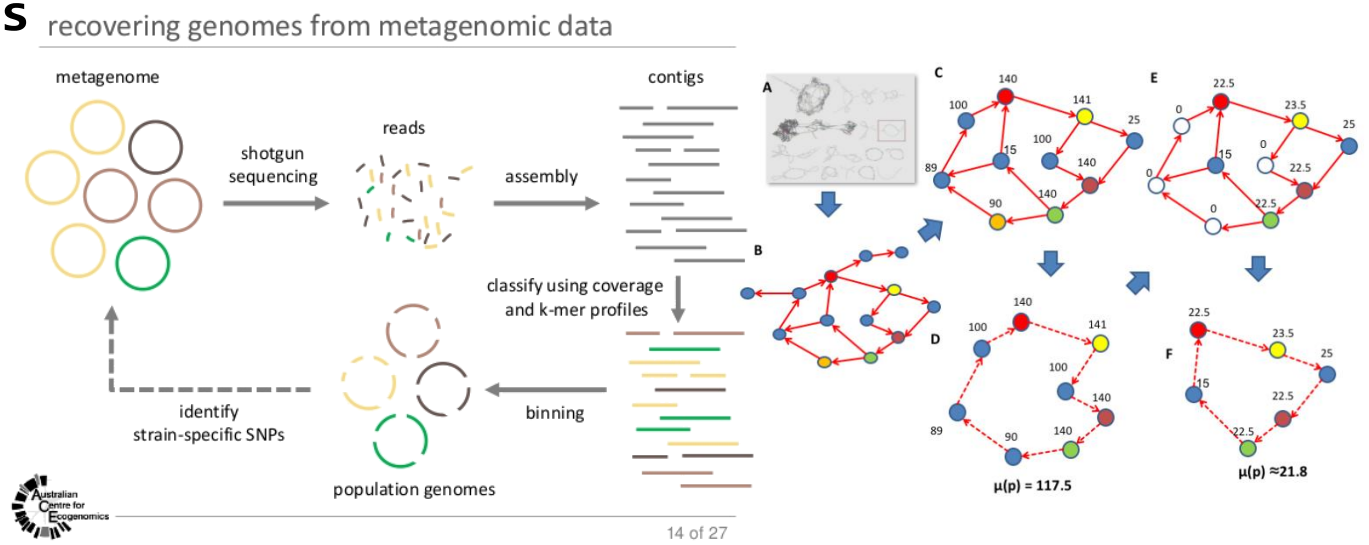
Assembly: Assemblers

Name	Type	Technologies	Author	Presented /Last updated	Licence*	Homepage
DNASTAR Lasergene Genomics Suite	(large) genomes, exomes, transcriptomes, metagenomes, ESTs	Illumina, ABI SOLiD, Roche 454, Ion Torrent, Solexa, Sanger	DNASTAR	2007 / 2016	C	link
Newbler	genomes, ESTs	454, Sanger	454/Roche	2004/2012	C	link
Canu	Small and large, haploid/diploid genomes	PacBio/Oxford Nanopore reads	Koren et al.[8]	2001 / 2018	OS	link
SPAdes	(small) genomes, single-cell	Illumina, Solexa, Sanger, 454, Ion Torrent, PacBio, Oxford Nanopore	Bankevich, A et al.	2012 / 2017	OS	link
Velvet	(small) genomes	Sanger, 454, Solexa, SOLiD	Zerbino, D. et al.	2007 / 2011	OS	link

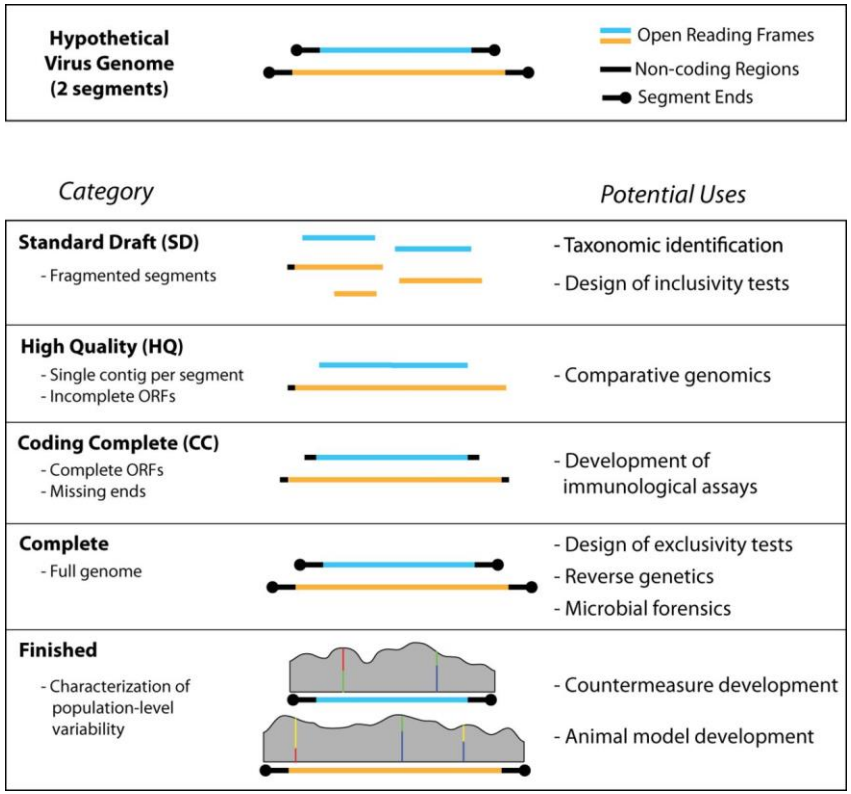
***Licences:** OS = Open Source; C = Commercial; C / NC-A = Commercial but free for non-commercial and academics

Assembly: Specials assemblers

- **Diploid genomes**
- **Metagenomics**
- **Plasmids**
- **Transcriptome**



Assembly: Categories



Standards for Sequencing Viral Genomes in the Era of HighThroughput Sequencing. Ladner *et al*.