Genome assembly

Bioinformatics Applications (PLPTH813)

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Outline

- Genome assembly: concept
- Assembly algorithms: OLC/De Bruijn graph
- Error correction (Kmer counts)
- Assembly strategy to cope with the repeat problem

(mate-pair reads, long reads, others)

- Assembly evaluation (N50, comparison to a reference genome)
- A case study

Whole genome shotgun (WGS) sequencing

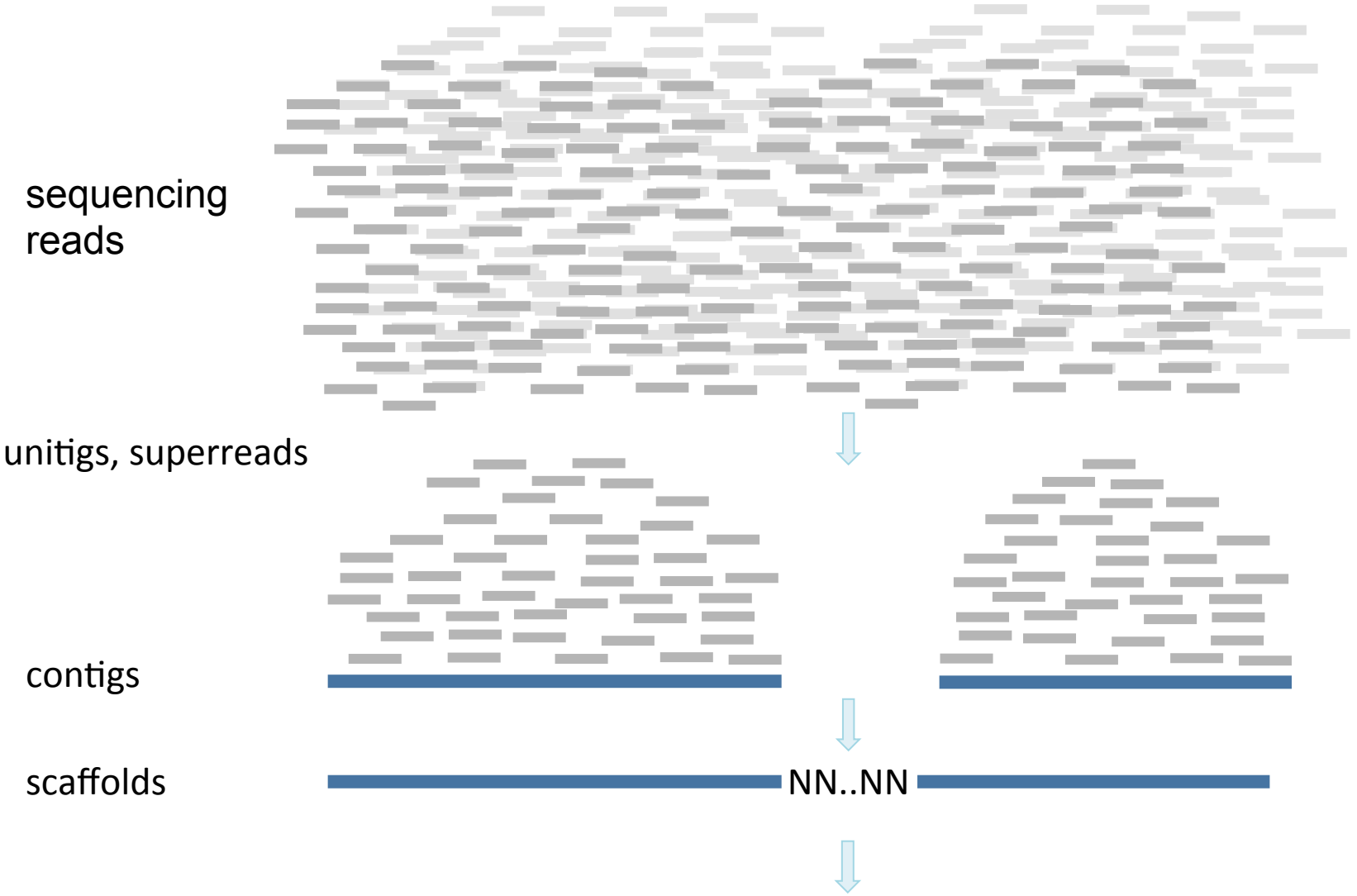
chromosome

sequencing reads

Complexity of genome assembly

Algorithm Can Solve 10, 000 Piece Jigsaw in 24 Hours

Genome assembly



Assembly algorithms

- **Overlap layout consensus (OLC)**

1. all-to-all pair-wise read alignments
2. Construct graph based on overlaps
3. Trace paths for the assembly

- **De Bruijn graph**

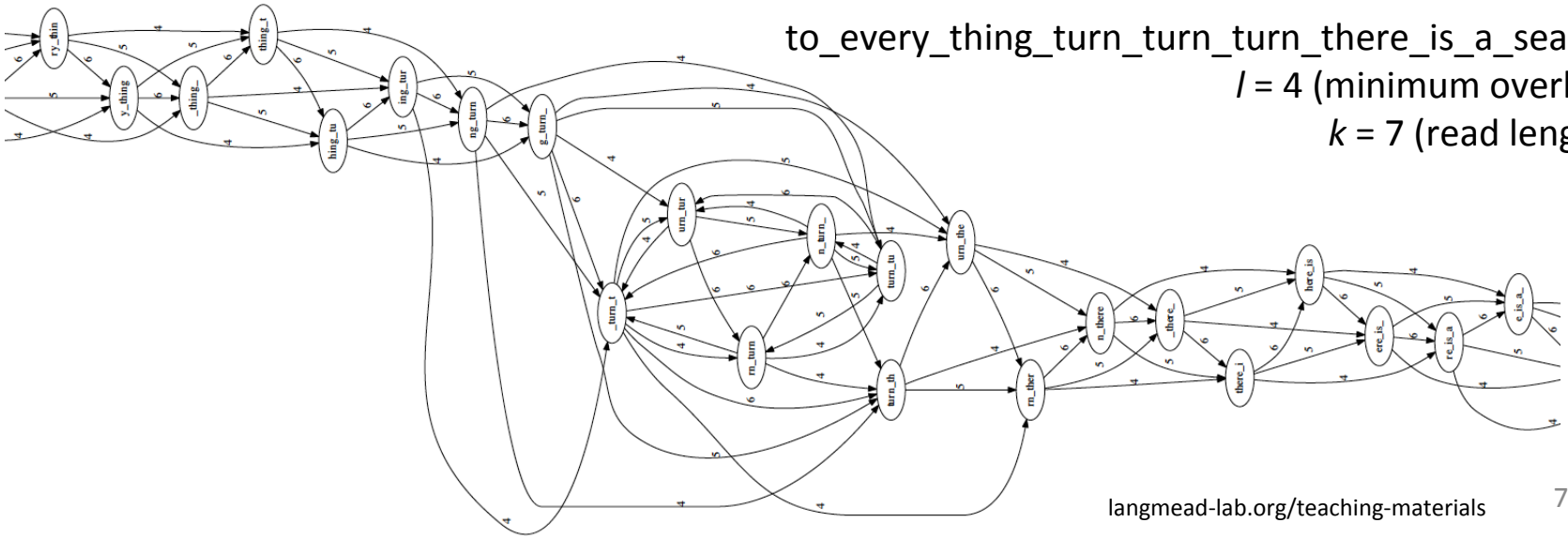
1. Determine k-mer from reads
2. Construct k-mer graph
3. Trace paths for the assembly

Overlap layout consensus (I)

Overlap → Layout → Consensus

- Overlap graph

1. identifies all pairs of reads that overlap **sufficiently well**
2. organizes the overlapping information into a graph containing a **node** for every read and an **edge** between any pair of reads that overlap each other.

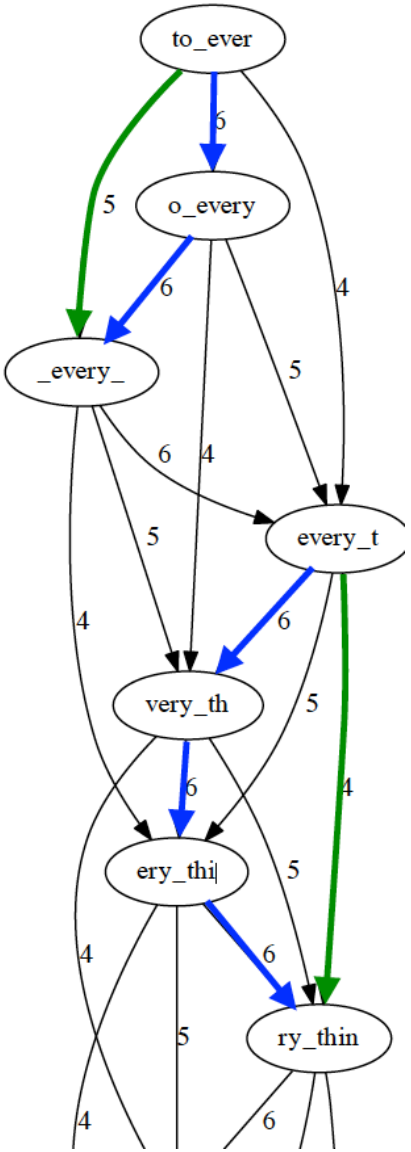


to_every_thing_turn_turn_turn_there_is_a_season
l = 4 (minimum overlap)
k = 7 (read length)

Overlap layout consensus (II)

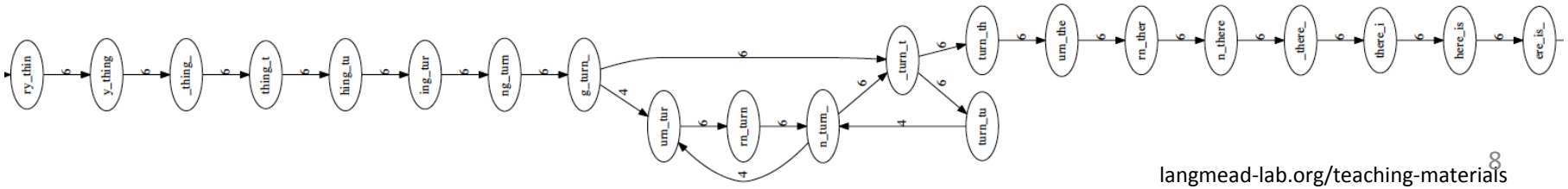
Overlap → Layout → Consensus

transitive edges: edges that skip one or more nodes

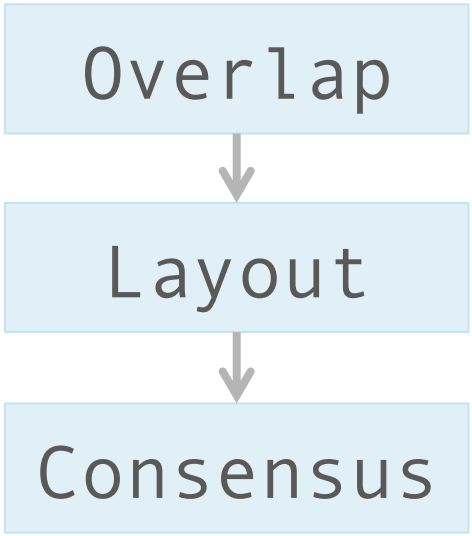


- Layout (**string graph**)

1. Simplifies the global overlap graph by removing redundant information (transitive edges)

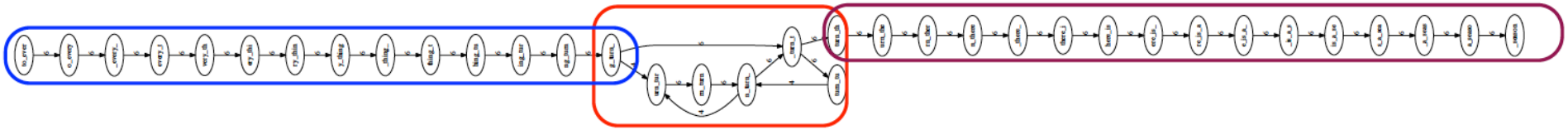


Overlap layout consensus (III)



- Layout

1. Simplifies the global overlap graph by removing redundant information
2. Emits contigs corresponding to the non-branching paths



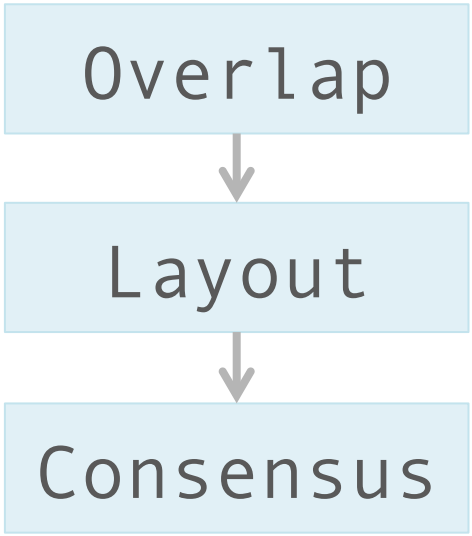
contig 1
to_every_thing_turn_

unresolved repeat (gap)

contig 2
turn_there_is_a_season

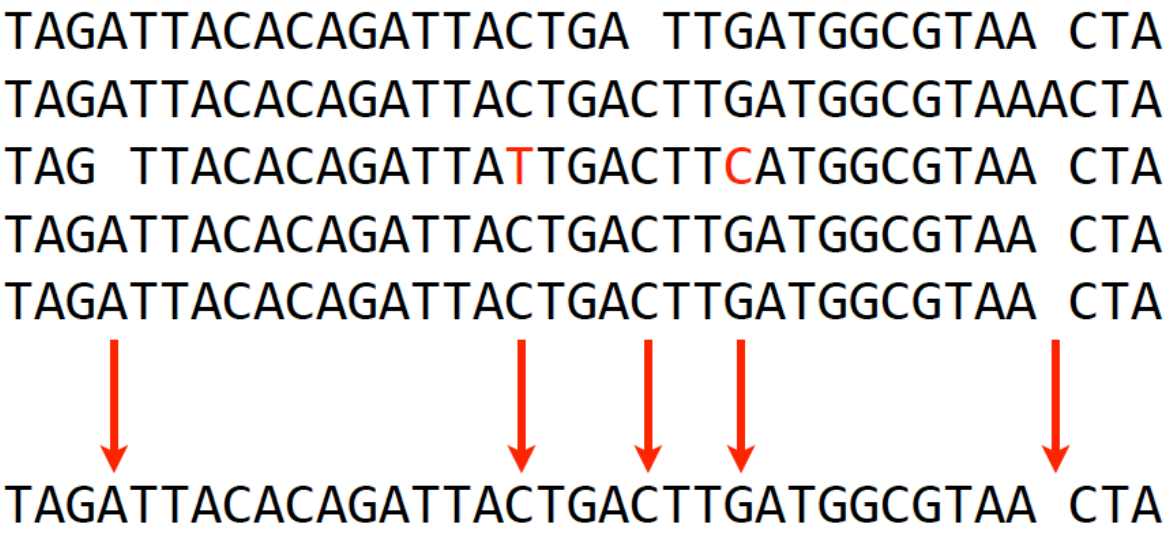
to_every_thing_turn_turn_turn_there_is_a_season

Overlap layout consensus (IV)



- Consensus

Extract consensus sequences (major votes) based on the alignment of reads that make up a contig



OLC drawbacks

- Identifying all-to-all overlaps is a slow procedure, especially when read number is millions or billions.

- Overlap graph is big when read number is huge. One node per read, and in practice the number of edges grows superlinearly with the number of reads.

- The computational complexity limits its application.

De Bruijn graph – k-mer

De Bruijn graph assemblers model the relationship between **exact substrings** of length *k* (k-mer) extracted from input reads.

(k=3)

reads A T G G C G T

k-mer (k=3)

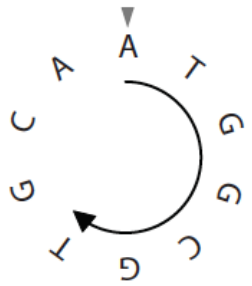
1.ATG
2.TGG
3.GGC
4.GCG
5.CGT

Compeau et al., 2011. Nature Biotechnology 29: 987-991.

De Bruijn graph - assembly

De Bruijn graph assemblers model the relationship between **exact substrings** of length *k* (k-mer) extracted from input reads.

genome sequence



reads

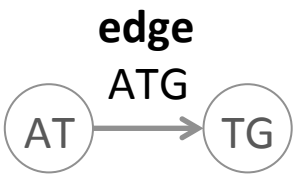
b

1. ATGGCGT
2. GGCGTCG
3. CTTGCAA
4. TGCAATG
5. CAATGGC
6. ATGGCGT

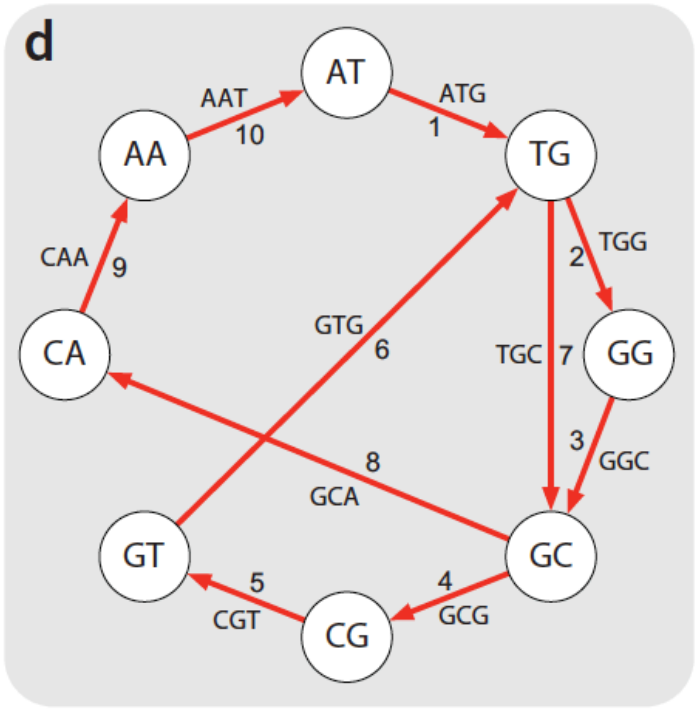
k-mer (k=3)

c

1. ATG
2. TGG
3. GGC
4. GCG
5. CGT
6. GTG
7. TGC
8. GCA
9. CAA
10. AAT



De Bruijn graph



ATGGCGTGCAATG

Compeau et al., 2011. Nature Biotechnology 29: 987-991.

Sequencing errors complicate assemblies

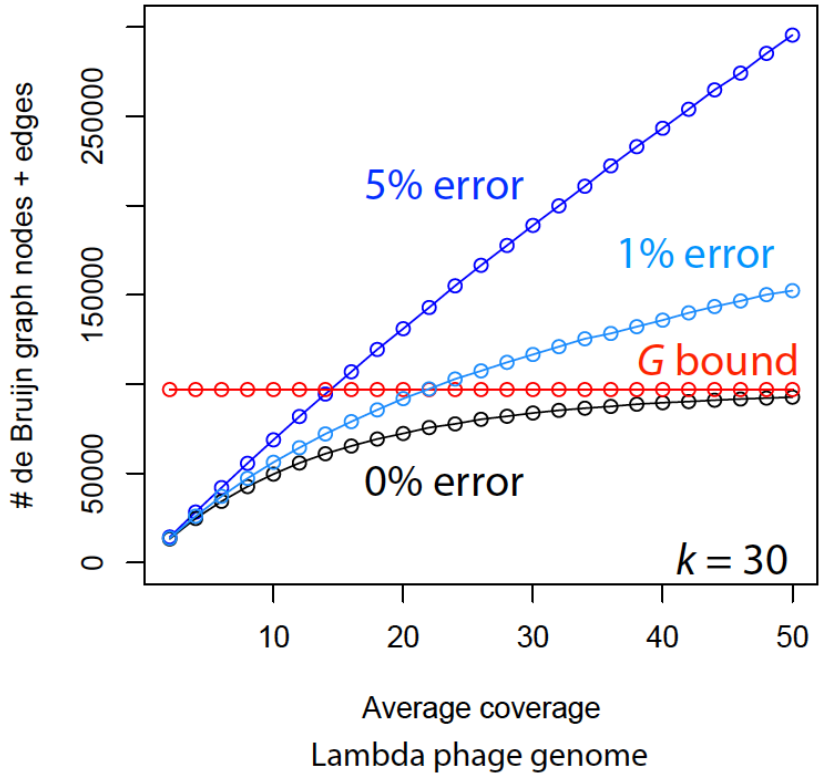
The complexity of De Bruijn graph grows when reads contain errors.

Reads

TGCGTGA
TGCGTGA
TGCGTGA
TGGGTGA

k-mer count profile (k=5)

TGCGT
GCGTG
CGTGA
TGGGT
GGGTG
GGTGA



G: genome

langmead-lab.org/teaching-materials

Sequence error correction before graph construction is a critical step for De Bruijn graph assembly.

Error identification

Reads (depth = 10)

```
TGCGTGATACG
TGCGTGATACG
TGGGTGATACG
TGCGTGATACG
TGCGTGATACG
TGCGTGATACG
TGCGTGATACG
TGCGTGATACG
TGCGTGATACG
TGCGTGATACG
```

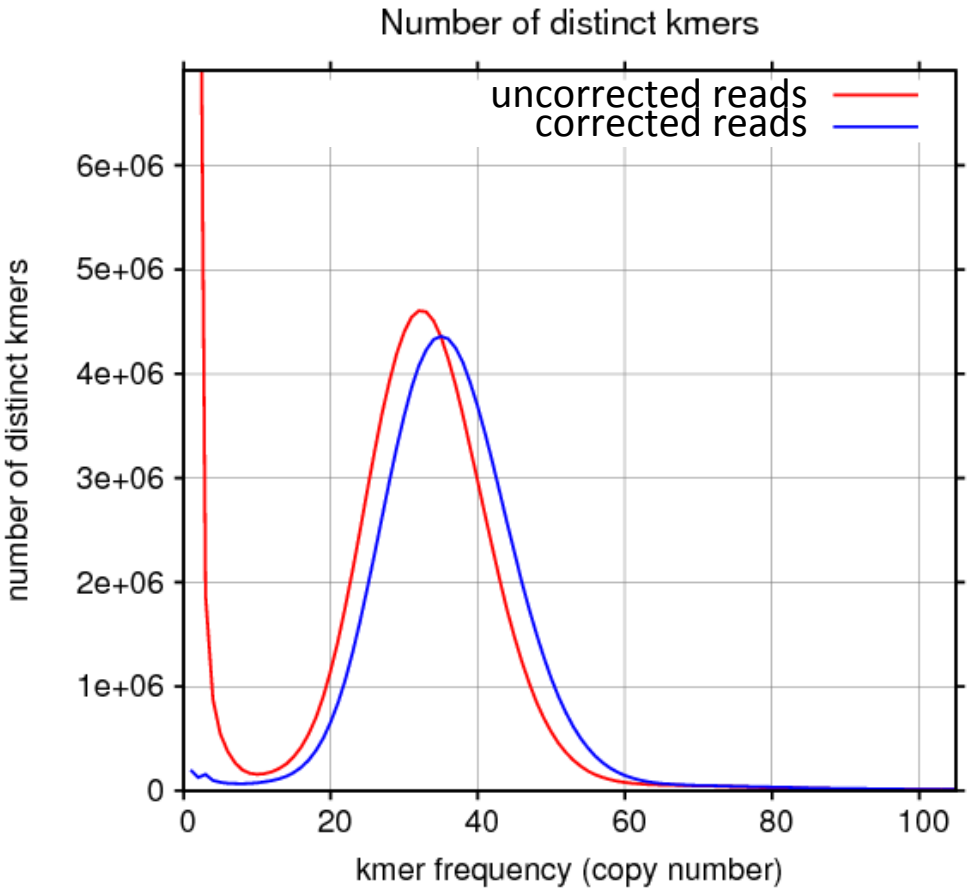
k-mer count profile (k=5)

TGGGT	1
GGGTG	1
GGTGA	1
TGCGT	9
GCGTG	9
CGTGA	9
GTGAT	10
TGATA	10
GATAC	10
ATACG	10

k-mer count profile indicates where errors are.

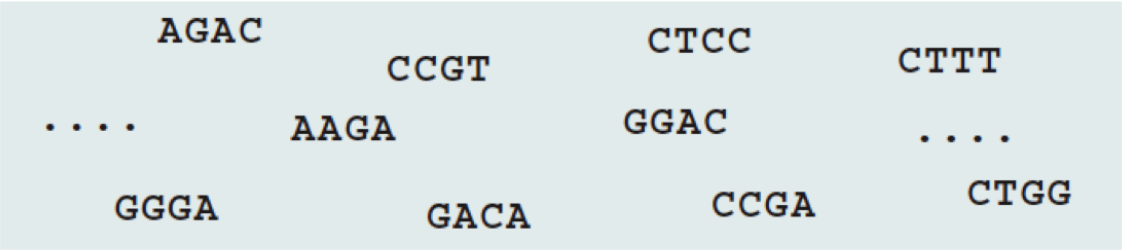
Error correction

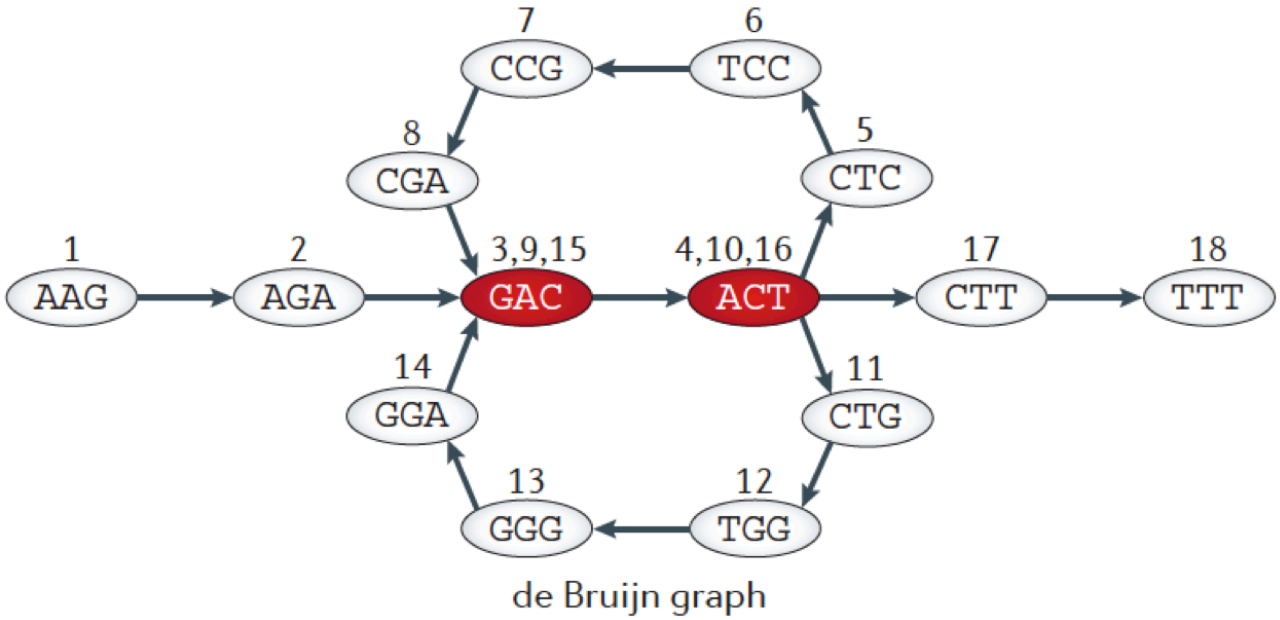
Essentially, the error correction algorithm removes k-mers with a few copies and correct reads carrying these errors.



from Allpaths-LG

Repeats





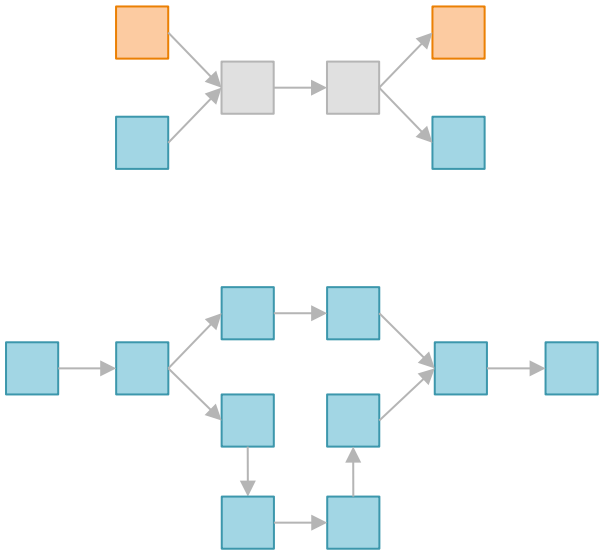
de Bruijn graph

AAGACTCCGACTGGGACTTT

Berger, B., et al., 2013 Nature Reviews Genetics 14: 333-346.

Unresolved repeats produce gaps

Long repeats, especially for those whose lengths are longer than read length, and high-copy repeats are challenging to resolve. If no other information can be used to assist in resolving repeats, gaps will be introduced.



Miller et al., 2010. Genomics 95: 315-327

Gaps due to other reasons

- Low sequence coverage (depth)
- Sequencing biases (e.g., regions recalcitrant to sequencing)

```
CGGATCTGCGTGATACGGAATAGCCTAGCA
  GATCTGCGTGATACGGAAT
   ATCTGCGTGATACGGAATA
    TCTGCGTGATACGGAATAG
     CTGCGTGATACGGAATAGC
      TGCGTGATACGGAATAGCC
        CGTGATACGGAATAGCCT
           6 (coverage; depth)
```

Recalcitrant genomic regions:

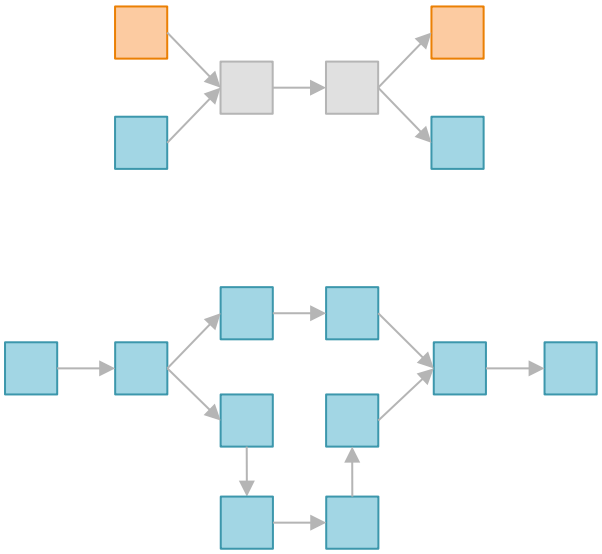
1. extremely high GC or AT
2. complicated secondary structure

Preferred genome sequencing reads:

1. Long reads
2. High-quality reads
3. High sequencing depth (>30x)
4. No sequencing biases

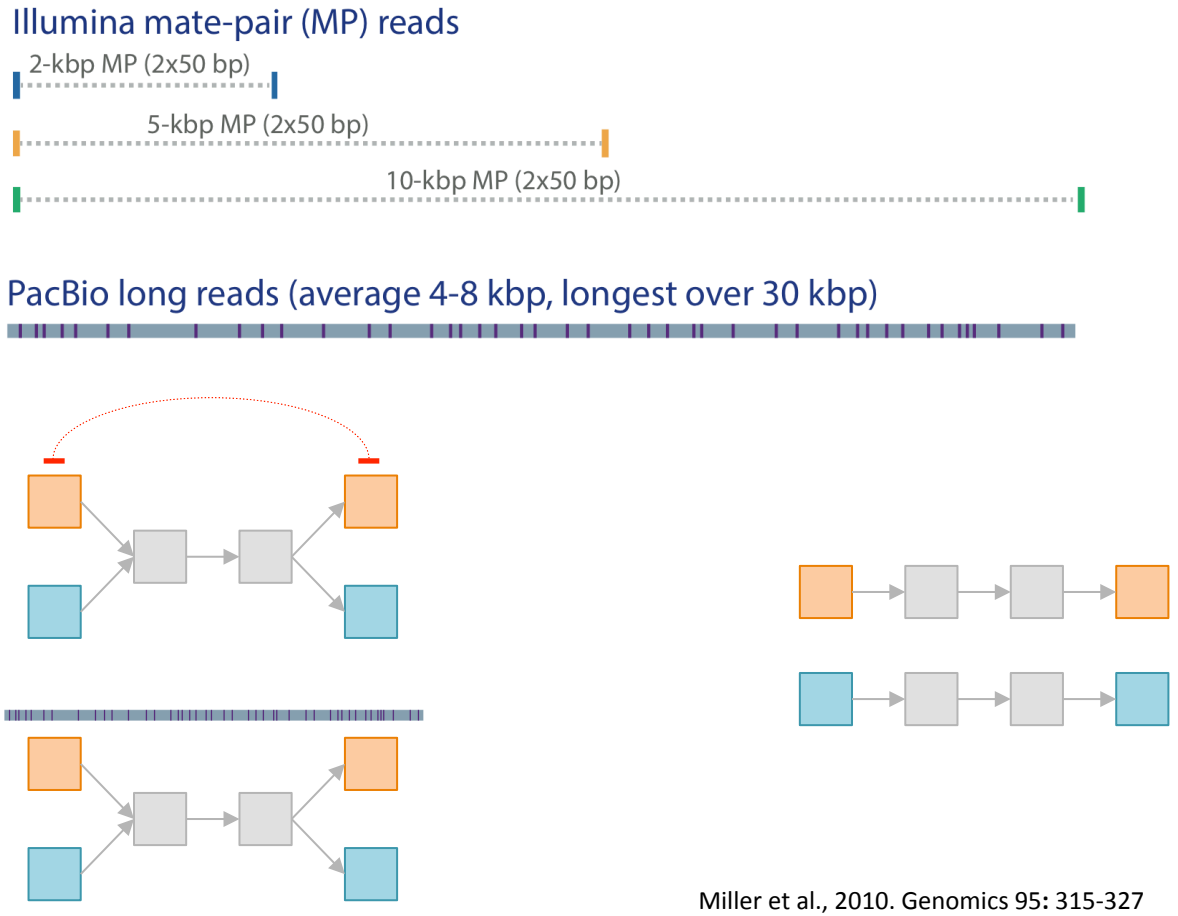
Question

What strategies can be used to resolve repeats?



Some strategies to resolve repeats

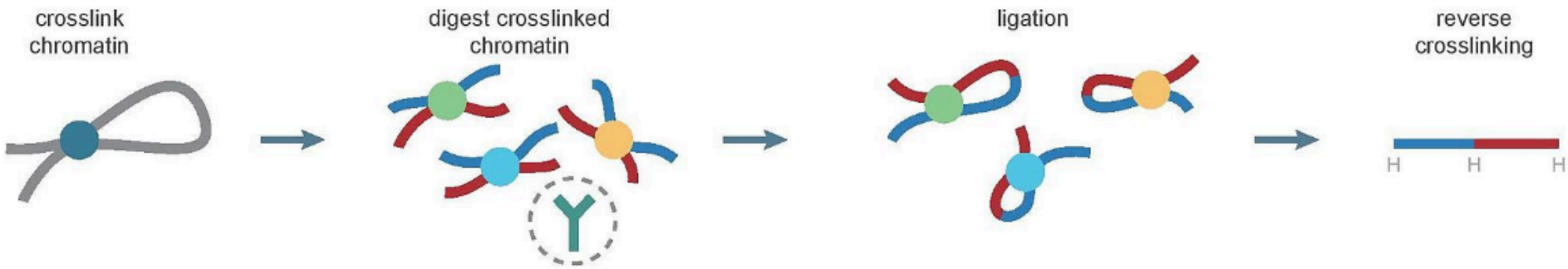
Mate-pair reads, long reads (e.g., PacBio), genetic map, Hi-C data, and physical map (BioNano) can resolve some repeats



Miller et al., 2010. Genomics 95: 315-327

Hi-C: the method to quantify physical interactions between all possible pairs of genomic regions simultaneously

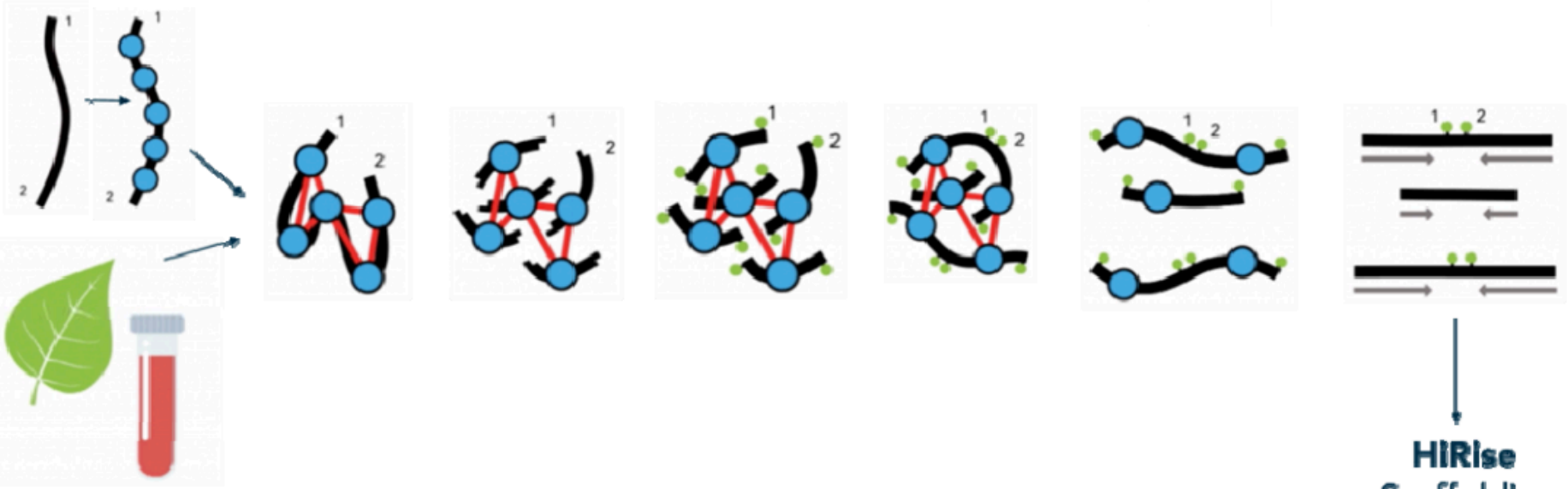
Inside a cell, genomic regions in a chromosome are physically connected to form chromosome conformation. Closer genomic regions generally have higher frequent physical contacts than regions far apart in distance.



https://en.wikipedia.org/wiki/Chromosome_conformation_capture

Chicago + Dovetail Hi-C

Chicago generated libraries start from pure DNA that is reconstituted into chromatin.



Dovetail Hi-C generated libraries start from tissue or cell culture and endogenous chromatin is extracted after fixation.

https://www.biorxiv.org/content/biorxiv/early/2018/08/15/392126.full.pdf

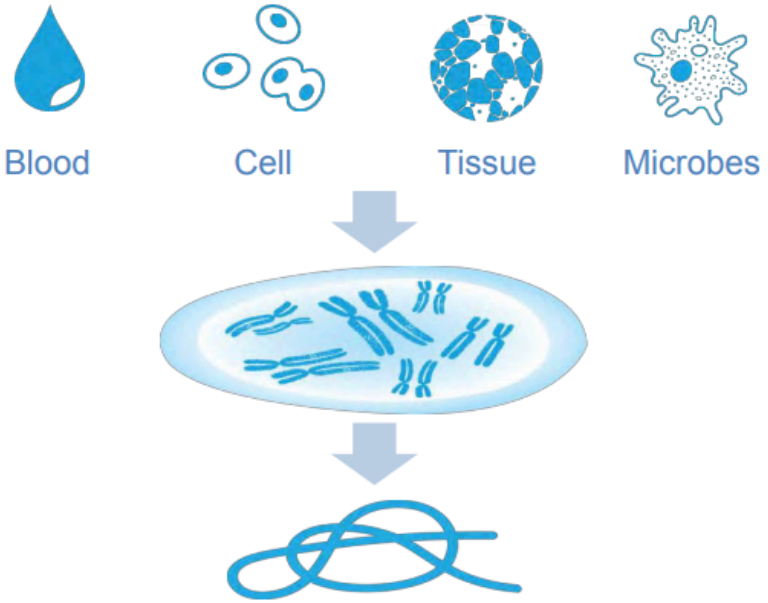
BioNano – library preparation

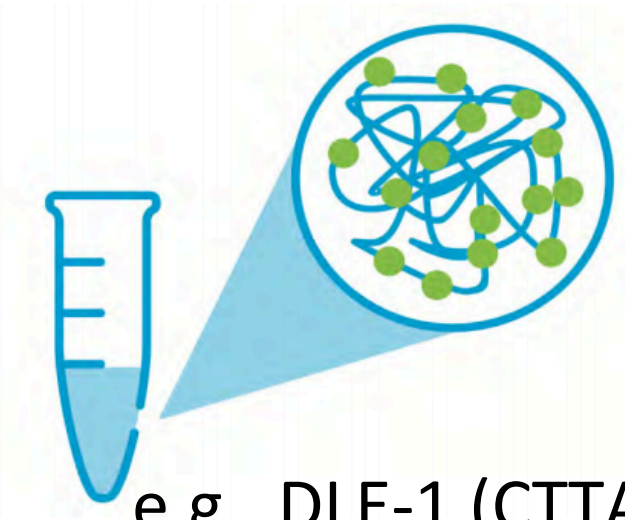
1

Extraction of long DNA molecules

2

Label DNA at specific sequence motifs





e.g., DLE-1 (CTTAAG)
Direct label enzyme

https://bionanogenomics.com/wp-content/uploads/2019/03/Bionano-Genomics_Poster_PAG-2019_A-Lee_S-Bocklandt_Hybrid-Scaffold.pdf

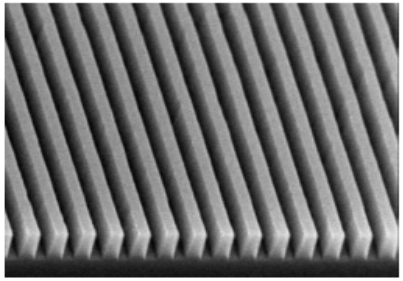
BioNano – running on Saphyr

3

Saphyr Chip linearizes DNA in NanoChannel arrays

4

Saphyr automates imaging of single molecules in NanoChannel arrays



https://bionanogenomics.com/wp-content/uploads/2019/03/Bionano-Genomics_Poster_PAG-2019_A-Lee_S-Bocklandt_Hybrid-Scaffold.pdf

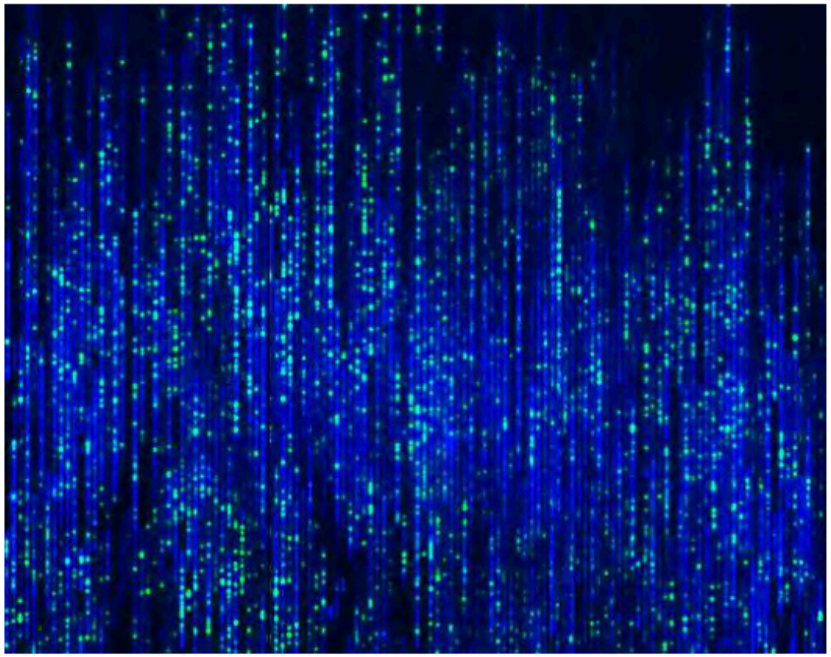
BioNano – image analysis and assembly of molecular data

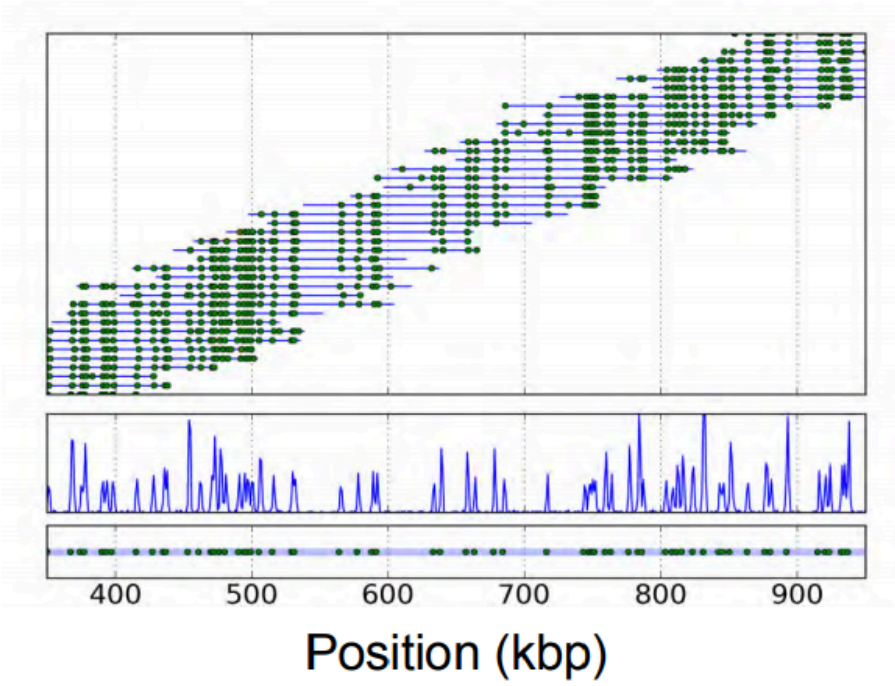
5

Molecules and labels detected in images

6

Bionano Access software assembles optical maps





https://bionanogenomics.com/wp-content/uploads/2019/03/Bionano-Genomics_Poster_PAG-2019_A-Lee_S-Bocklandt_Hybrid-Scaffold.pdf

BioNano scaffolding

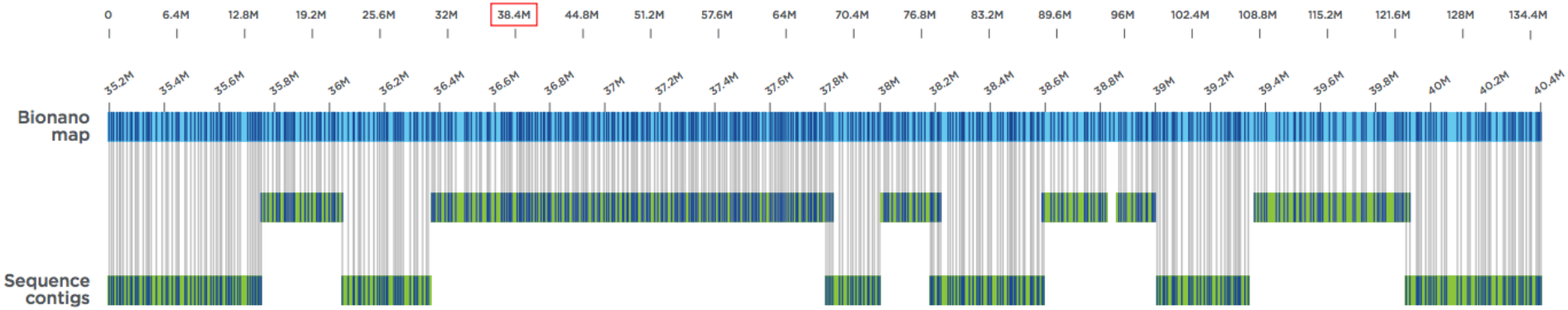


Figure 1:
Combining Bionano maps with sequence assemblies. Sequence contigs are anchored and oriented using the de novo generated Bionano maps.

https://bionanogenomics.com/wp-content/uploads/2017/02/Bionano_HumanPAG_Hybrid-Scaffolding-White-Paper.pdf

Assembly statistics – N50 and L50

- N50: A statistic used for assessing the contiguity of a genome assembly.
- L50: The number of contigs whose summed length is N50.

- The contigs in an assembly are sorted by size and added, starting with the largest. The contig N50 is the size of the contig that makes the total greater than or equal to 50% of the total contig size.

- OR: The contig N50 is the length of the smallest contig in the set that contains the fewest (largest) contigs whose combined length represents at least 50% of the assembly.

Assembly statistics – NG50

Problem of N50:

N50 values of the assemblies with significantly different total assembly space (lengths) are usually not comparable. Even if the same data set is used for the assembly.

50,000	50,000
30,000	**40,000**
10,000	30,000
	20,000
	10,000

NG50: The NG50 statistic is the same as N50 except that it is 50% of the known or estimated genome size. This allows for meaningful comparisons between different assemblies.

An example to determine N50 and NG50

- Genome size: 5 Mbp
- 20 contigs

contig N50? 360 kbp

contig NG50? 356 kbp

ctg_ID	ctg_size (kbp)	Accumulated (kbp)	% ASM	% genome
1	615	615	13%	12%
2	515	1,130	25%	23%
3	512	1,642	36%	33%
4	450	2,092	46%	42%
5	360	2,452	53%	49%
6	356	2,808	61%	56%
7	310	3,118	68%	62%
8	201	3,319	72%	66%
9	189	3,508	76%	70%
10	186	3,694	80%	74%
11	160	3,854	84%	77%
12	150	4,004	87%	80%
13	120	4,124	90%	82%
14	102	4,226	92%	85%
15	95	4,321	94%	86%
16	86	4,407	96%	88%
17	82	4,489	98%	90%
18	54	4,543	99%	91%
19	32	4,575	100%	92%
20	21	4,596	100%	92%
Total	4,596			

Software for short-read assemblies

Software	Description	URLandreference
Velvet	Original de Bruijn graph assembler	http://github.com/dzerbino/velvet
SOAPdenovo	De Bruijn graph assembler with error-correction step	http://soap.genomics.org.cn/
Meraculous	Hybrid k-mer/read-based	https://jgi.doe.gov/data-and-tools/meraculous/
ALLPATHS-LG	Uses unipath graph to collapse repeats	http://software.broadinstitute.org/allpaths-lg/blog/
SGA	Uses string graphs	https://github.com/jts/sga
ABySS	Represents de Bruijn graph with a Bloom filter	https://github.com/bcgsc/abyss
DISCOVAR de novo	Requires 250-bp PCR-free reads	https://software.broadinstitute.org/software/discovar/blog/
Supernova	Assembles 10× linked reads	https://github.com/10XGenomics/supernova

Long-read assemblies and polishing

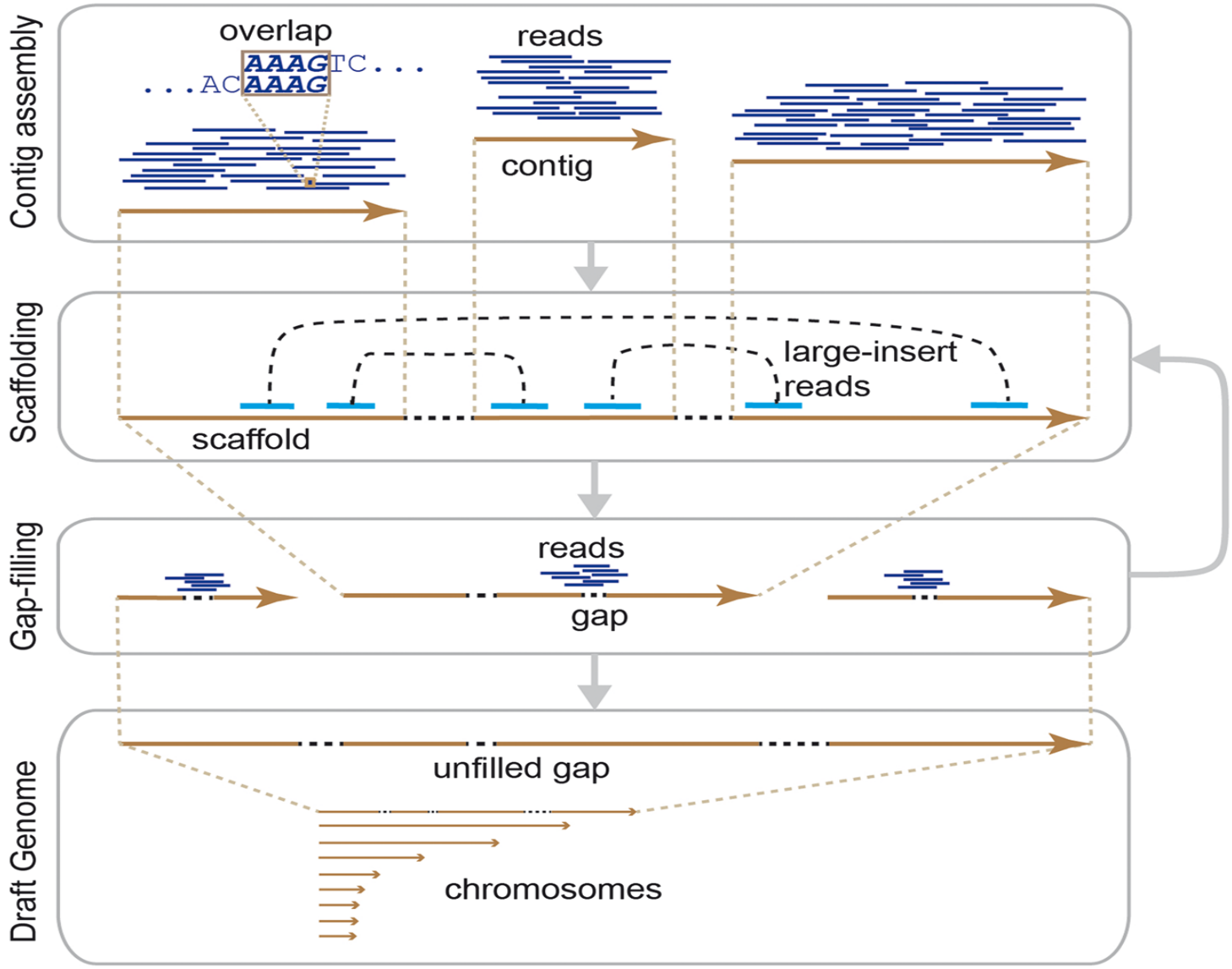
Long-read assemblies

Software	Description	URLandreference
HGAP	Error correction, OLC assembly, and polishing	https://github.com/PacificBiosciences/Bioinformatics-Training/wiki/HGAP
Canu	K-mer-based overlap computation	https://github.com/marbl/canu
FALCON	Assembles phased diploid genomes	https://github.com/PacificBiosciences/FALCON
Flye	Uses A-Bruijn graph	https://github.com/fenderglass/Flye
Miniasm	Fast, but no error correction	https://github.com/lh3/miniasm

Polishing

Software	Description	URLandreference
Pilon	Uses short-read alignments to correct errors	https://github.com/broadinstitute/pilon
Arrow	Hidden Markov model and long-read alignments	https://github.com/PacificBiosciences/GenomicConsensus
Nanopolish	Nanopore only; uses voltage data to correct errors	https://github.com/jts/nanopolish

General workflow of *de novo* assemblies



Briefings in Bioinformatics, 19:23–40, 2018

Assemblies are hypotheses

... there will always be some degree of error in the characterized genome sequence, both on the level of individual nucleotides and in the ordering of sequence blocks. Forth, every genome assembly is the result of a series of assembly heuristics and should accordingly be treated as **a working hypothesis**.

Evolutionary Conservation, 7:1026-1042, 2014

Assembly evaluation – QUAST

- QUAST: quality assessment tool for genome assemblies

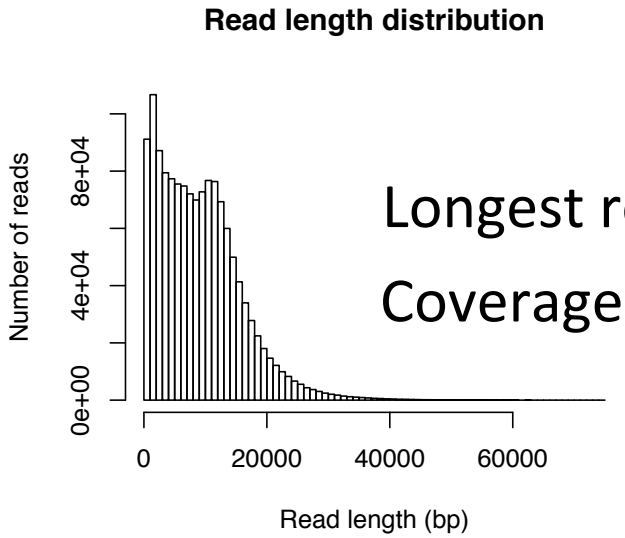
1. No. of contigs: the total number of contigs in the assembly.
2. Largest contig: the length of the largest contig in the assembly.
3. Total length: total assembly length
4. Nxx (N50), NGxx (NG50)
5. Using a reference genome, No. of misassemblies, No. INDEL per 100 kbp, and No. of mismatches per 100 kbp are reported
6. NA50: splits contigs that contain "misassemblies" and "unaligned" sequences and uses the new contigs for N50 calculation (NA50)

Gurevich et al., 2013 Bioinformatics 29: 1072-1075.

Case study: genome assembly of a wheat blast fungal strain

- 10 SMRTCell PacBio data (P6-C4)

PacBio RS II



Longest reads: 74,474 bp

Coverage*: 276x

- PCR-free Illumina TruSeq data

HiSeq 2500

>2x10^7 pairs of 2x250 paired-end reads

Coverage*: 222x

* assuming the genome size is 45 Mb

Summary of the assembly

Statistics of the assembly*

Item	Statistics
total contig number	**31**
total contig length	44,522,920
longest contig	**7,902,655**
shortest contig	12,906
N50	**5,402,116**
overall GC	0.50
min contig GC	0.28

* *Canu* for PacBio assembly
Quiver polishing
Further error correction using Illumina data

mitochondial sequence

List of contigs (N=31)

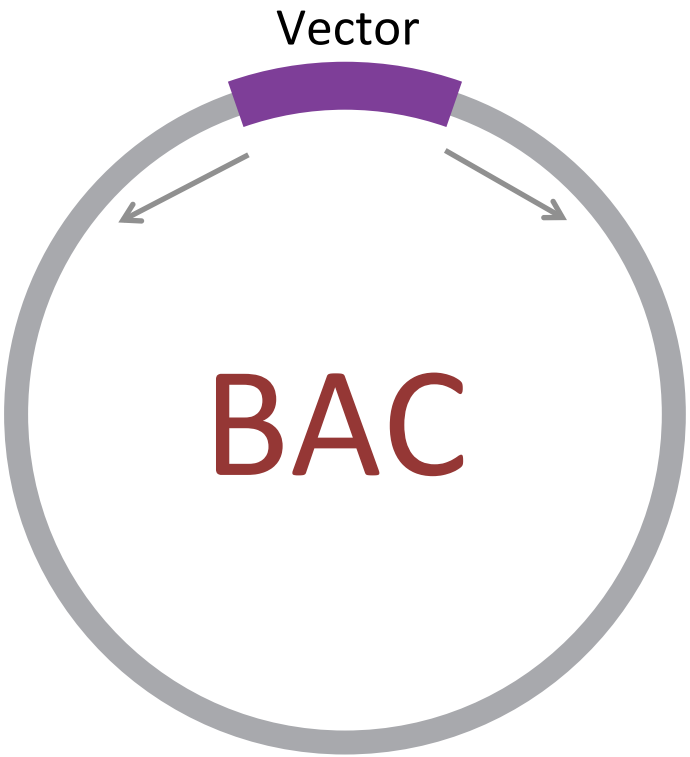
Contig	Length (bp)	GC%
tig00000000	7,902,655	51.2
tig00000024	7,531,155	49.1
tig00000030	6,090,985	50.2
tig00000003	5,402,116	51.2
tig00000011	4,657,194	49.2
tig00000004	4,442,877	51.2
tig00000005	4,042,640	49.2
tig00000001	1,778,515	46.4
tig00000014	461,599	49.4
tig00000025	398,015	44.3
tig00000039	253,502	45.1
tig00000026	240,676	43.8
tig00000018	237,459	47.4
tig00000016	184,678	48
tig00000007	138,010	49.9
tig00000022	110,918	46
tig00000020	78,737	49.6
tig00000006	69,533	51.1
tig00000033	69,131	49.2
tig00000043	57,199	28.4
tig00000015	51,862	48.5
tig00000008	47,134	47.6
tig00000031	42,261	48.6
tig00000041	36,641	52.5
tig00000023	36,455	44.2
tig00000037	35,037	48.9
tig00000032	32,608	49.7
tig00000017	28,099	51.7
tig00000038	27,162	49.5
tig00000019	25,161	51.2
tig00000027	12,906	47.3

BAC-end sequencing for assembly improvement?

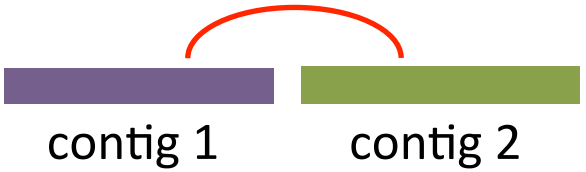
Vector

+ insert

long genomic DNA fragment (e.g., 200 kb)



scaffolding



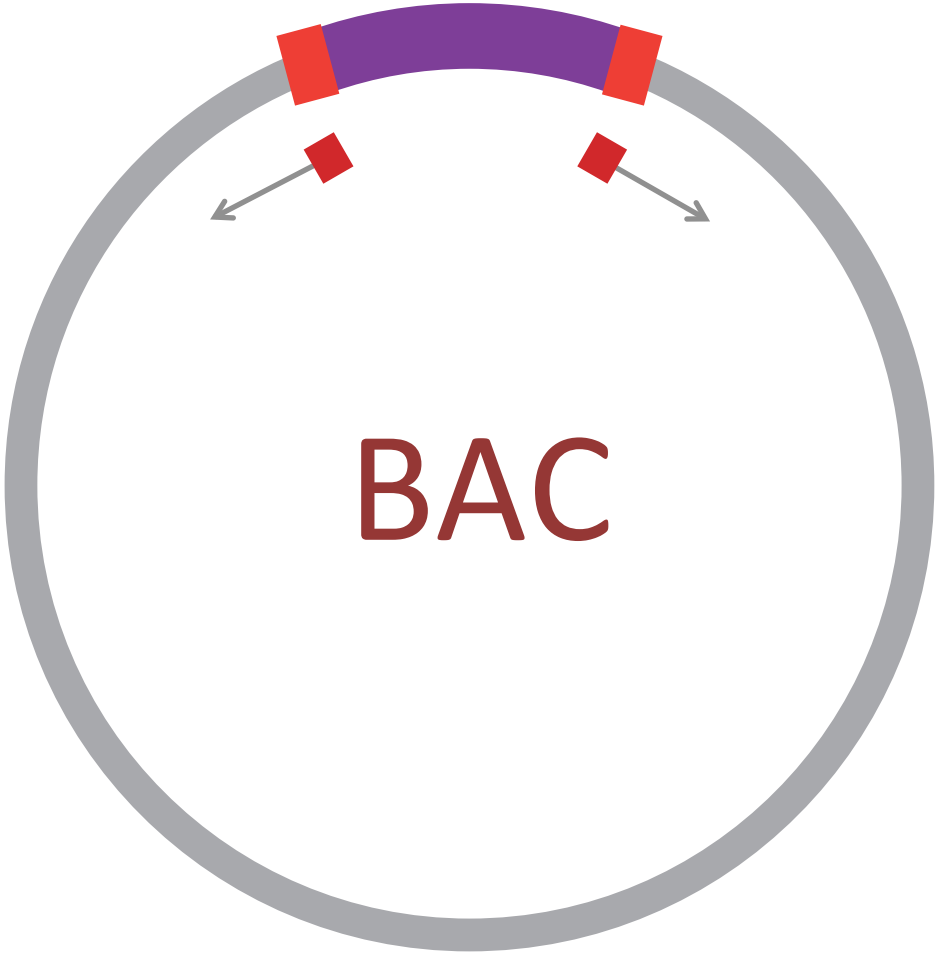
Sequence BAC ends of clones ***one by one***, which is very low-throughput and cost-inefficient.

Idea: build random barcodes in vectors to enable a high throughput (I)

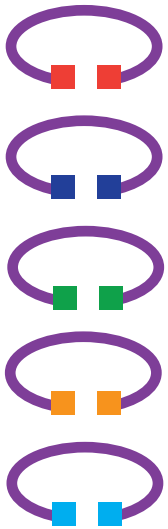
code (Red)

Vector with barcode (Red)

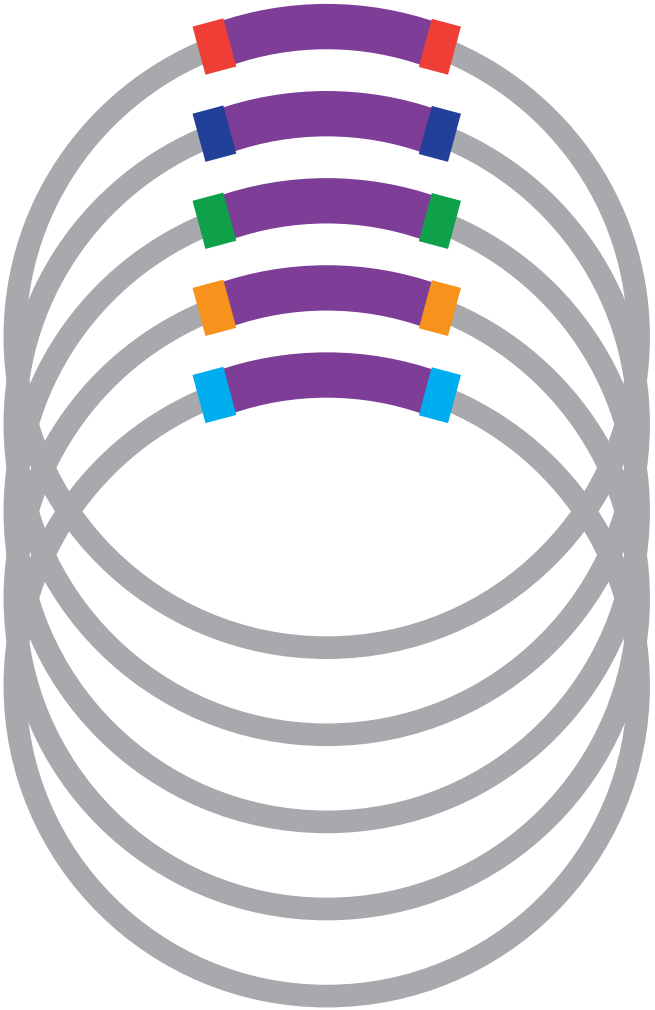
Sequences with barcode



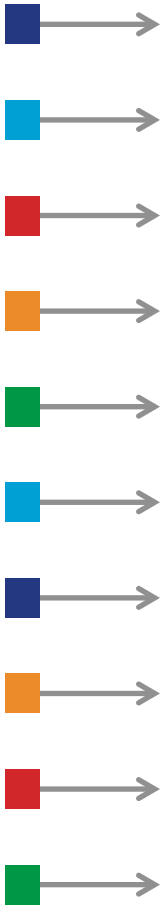
Idea: build random barcodes in vectors to enable a high throughput (II)



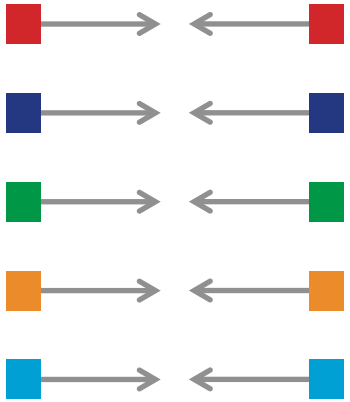
millions of barcoded vectors in a pool



tens of thousands of clones



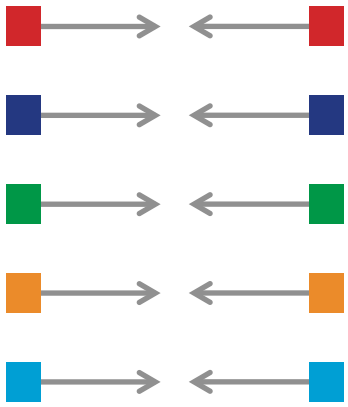
High-throughput end sequencing



Paired ends based on barcodes

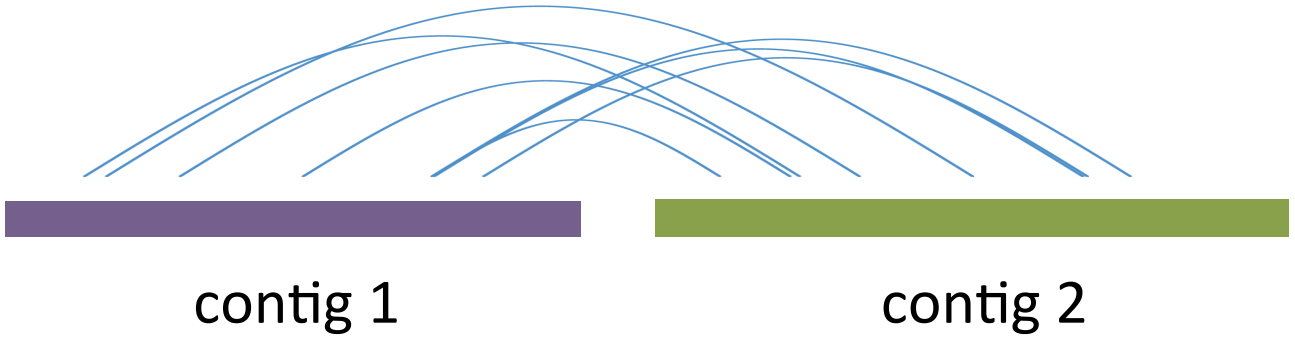
LIEP Scaffolding to improve the B71 assembly

Long Distance End Pairs (LIEP)



~95% are long-distance read pairs

LIEP scaffolding

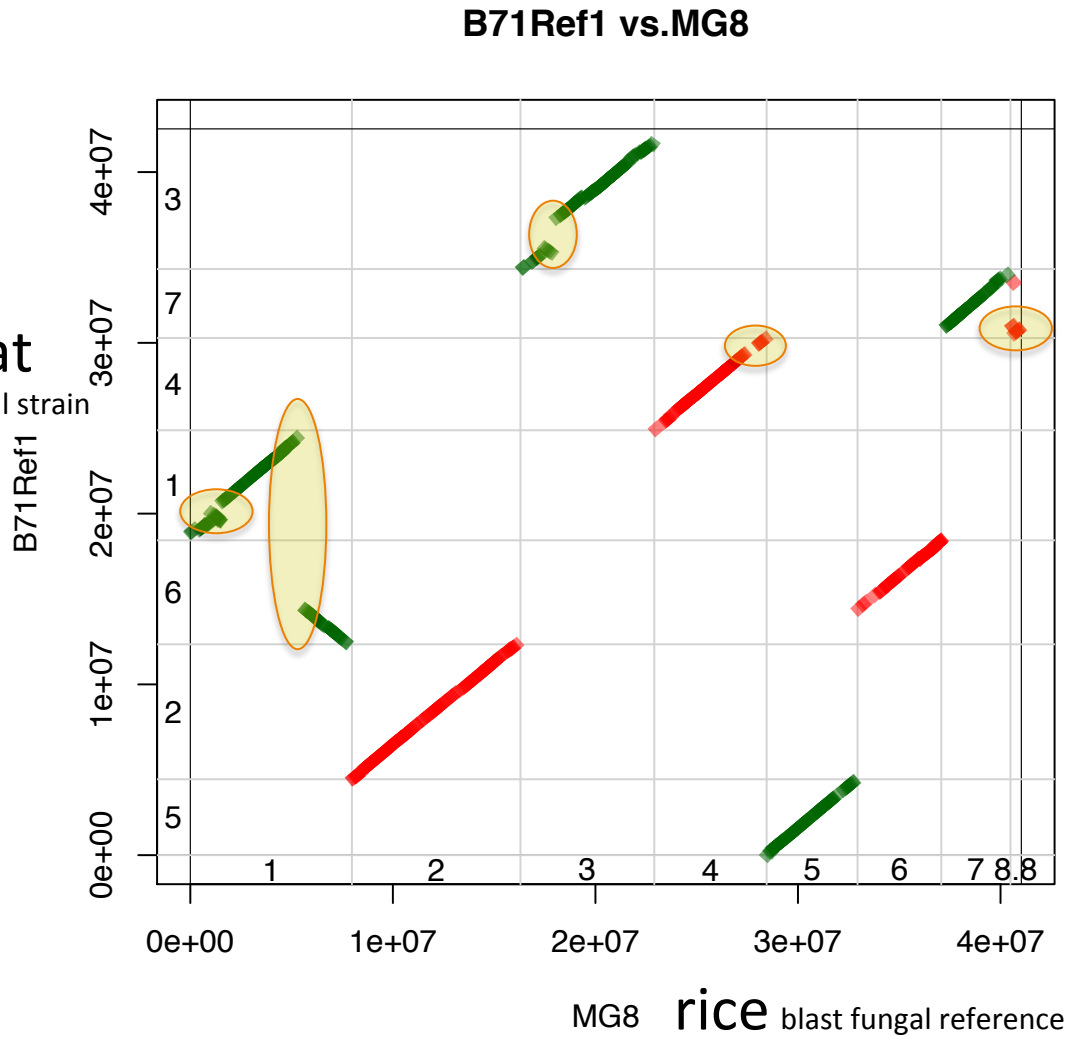


scaffolding two contigs to a sequence

MoT B71 final assembly vs. MG8 (70-15, *rice* strain)

Chr	Length (bp)
chr1	6,442,091
chr2	7,902,655
chr3	8,206,304
chr4	5,402,116
chr5	4,442,877
chr6	6,090,985
chr7	4,042,640
scaf1	941,816
scaf2	739,928
scaf3	104,670
scaf4	74,396
scaf5	69,131

Wheat
blast fungal strain

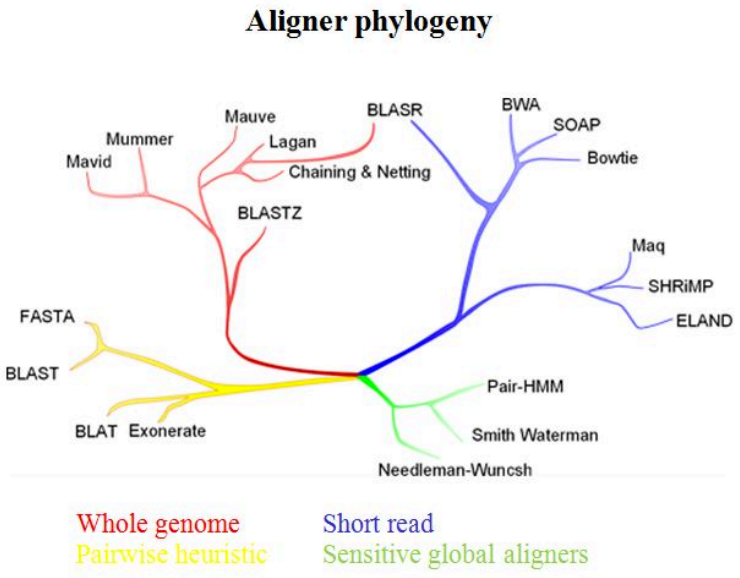


>10 kb overlap and >95% identity

An alignment tool behind QUAST - Nucmer

- **Nucmer** is a user-friendly alignment script of the MUMmer software package for DNA sequence alignment.

- For instance, a very common use for Nucmer is to determine the position and orientation of a set of sequence contigs in relation to a reference genome sequence



Citations

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- Compeau, P. E. C., P. A. Pevzner and G. Tesler, 2011 How to apply de Bruijn graphs to genome assembly. Nature Biotechnology 29**:** 987-991.
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- Miller, J. R., S. Koren and G. Sutton, 2010 Assembly algorithms for next-generation sequencing data. Genomics 95**:** 315-327.
- Gurevich, A., V. Saveliev, N. Vyahhi and G. Tesler, 2013 QUAST: quality assessment tool for genome assemblies. Bioinformatics 29**:** 1072-1075.