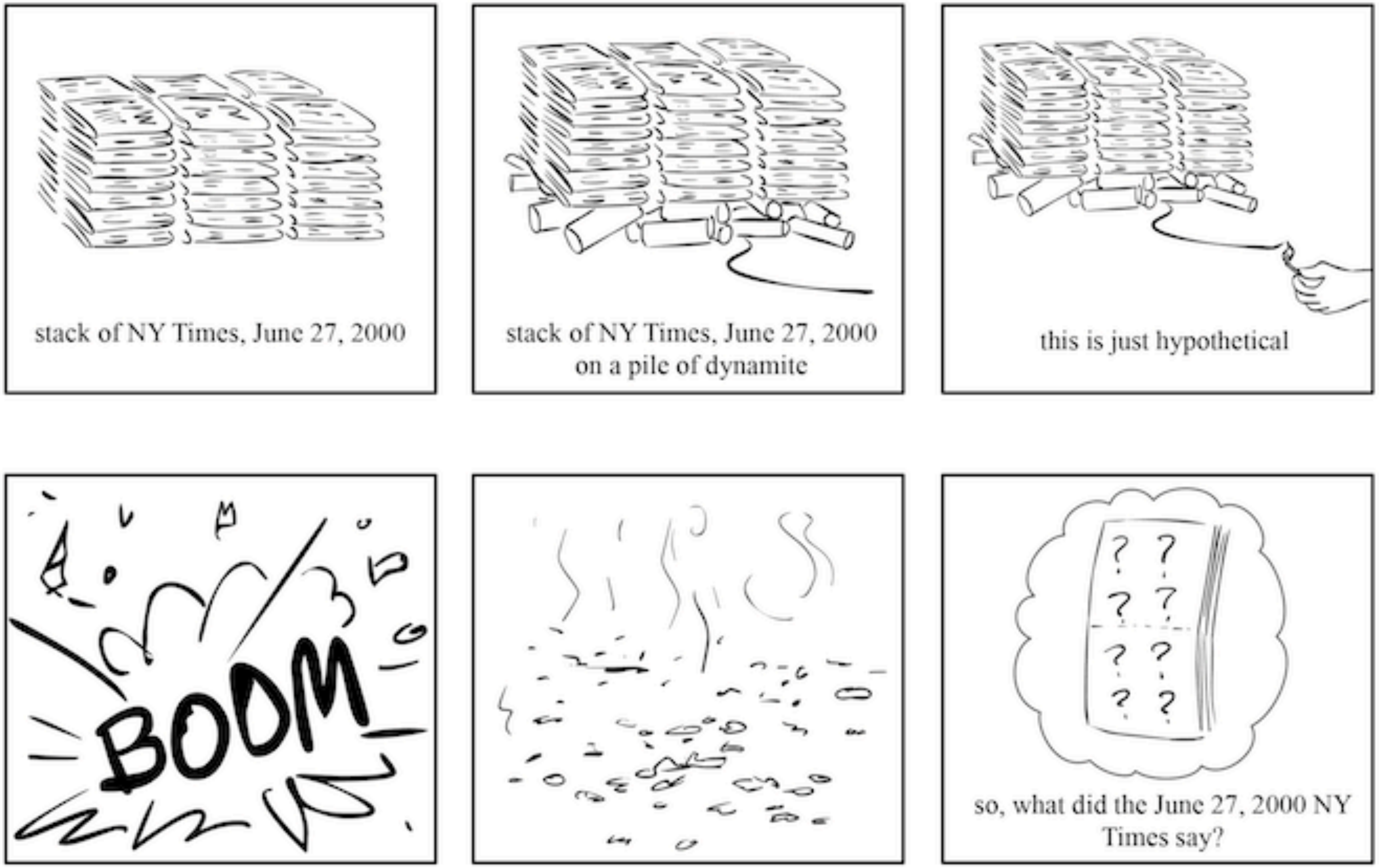
UBC Bioinformatics Class

Topic 5: de novo assembly

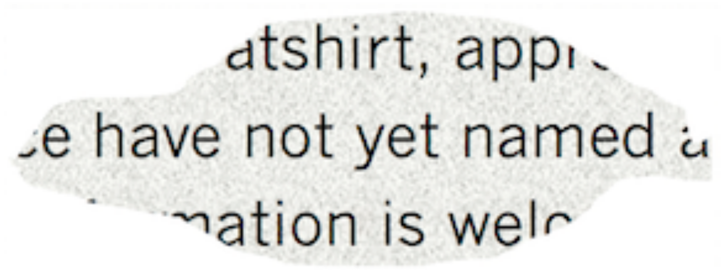
Outcomes

- Identify the difference between de novo assembly and reference guided alignment
- Evaluate two different approaches to de novo genome assembly
- Describe how repetitive elements can hamper proper assembly and compare approaches that can overcome this problem
- Describe approaches for transcriptome/ GBS de novo assembly

Introduction


stack of NY Times, June 27, 2000
stack of NY Times, June 27, 2000 on a pile of dynamite
this is just hypothetical
BOOM
so, what did the June 27, 2000 NY Times say?

Introduction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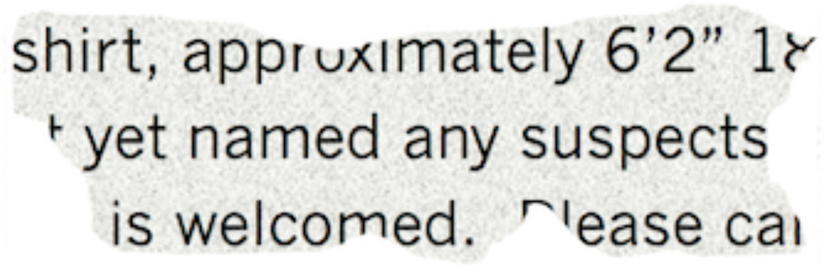
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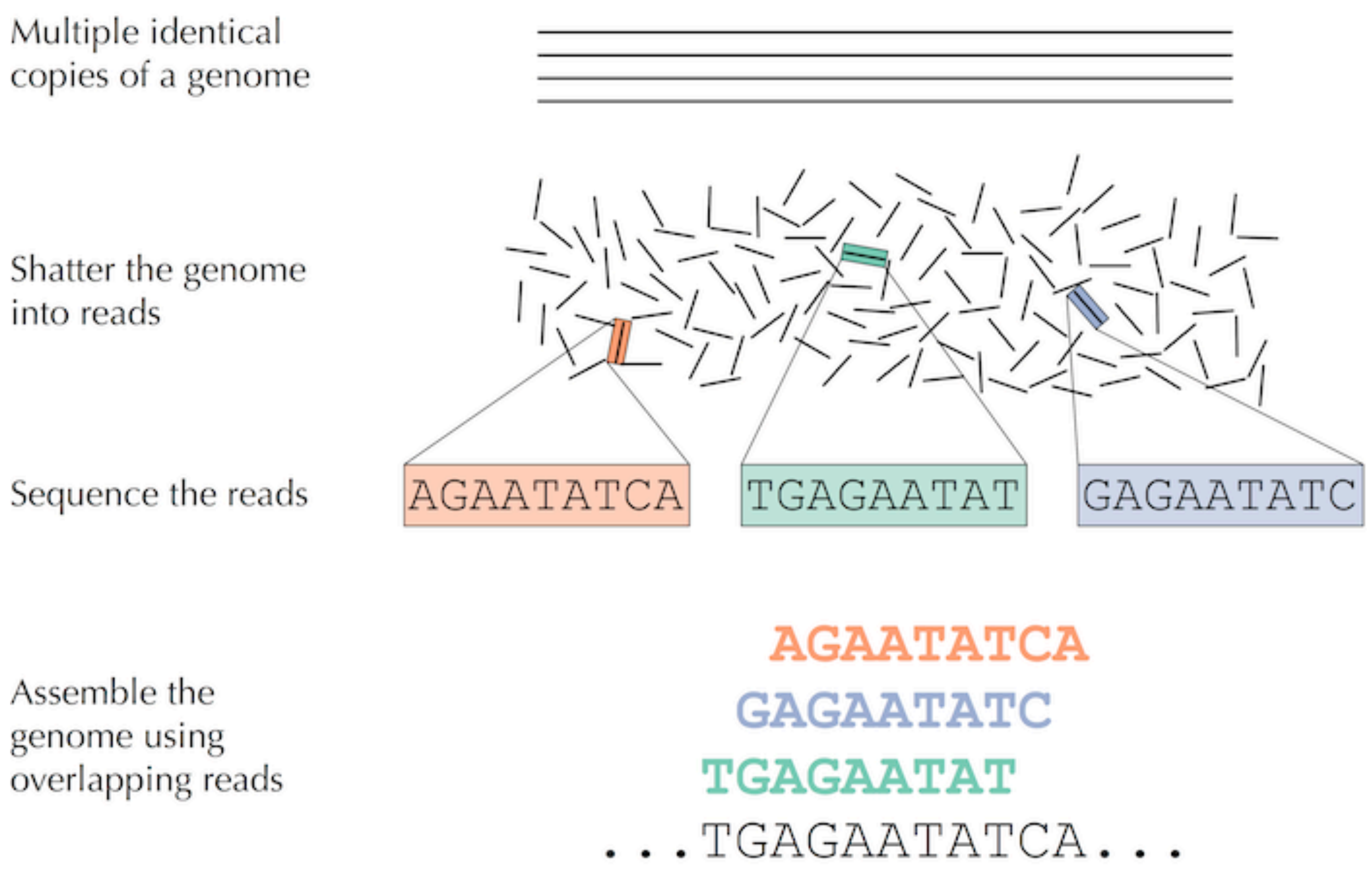
Introduction



Multiple identical copies of a genome
Shatter the genome into reads
Sequence the reads
AGAATATCA
TGAGAATAT
GAGAATATC
Assemble the genome using overlapping reads
AGAATATCA
GAGAATATC
TGAGAATAT
...TGAGAATATCA...

Alignment vs assembly

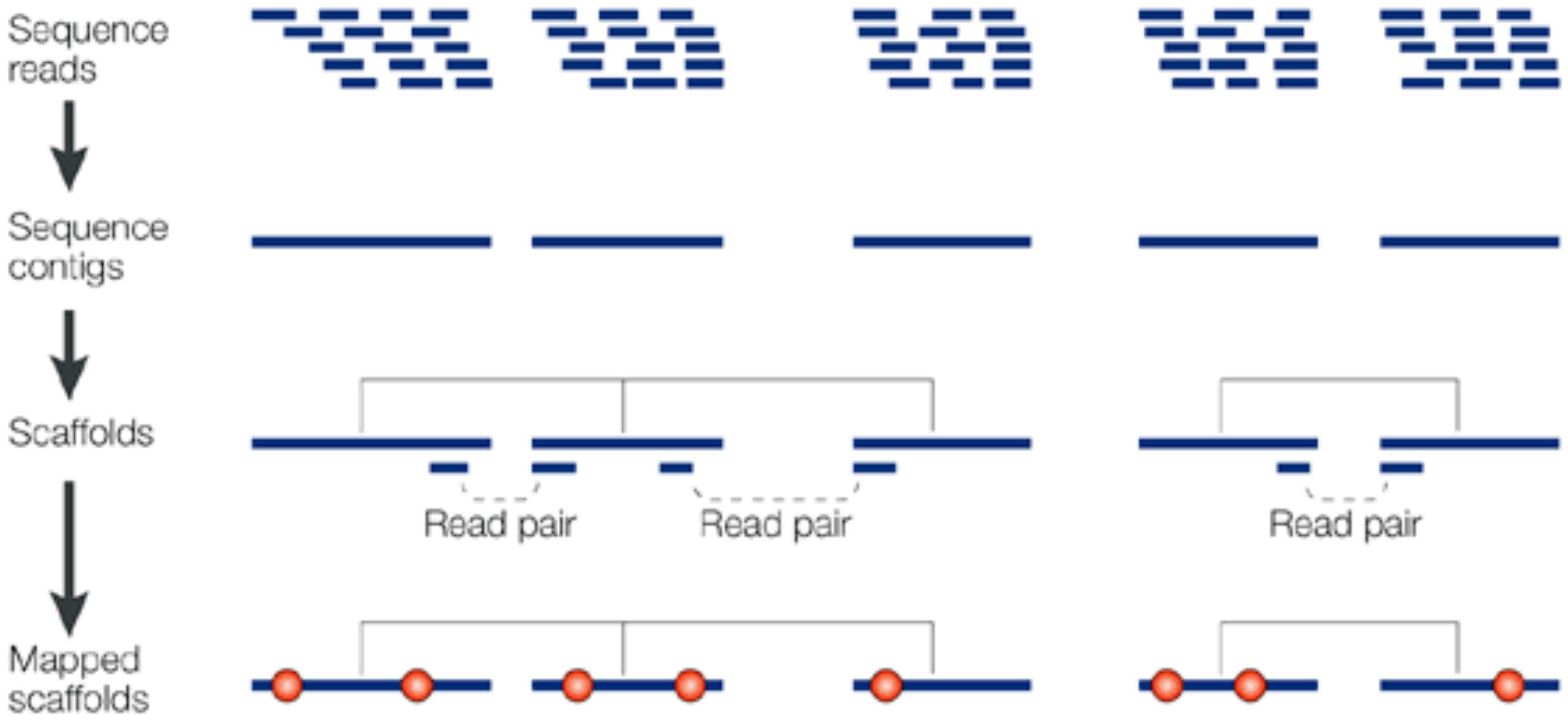
Aligning to a reference:

- Reference guided alignments: align the reads to a reference genome and looks for differences

Building a reference:

- De novo assembly: no previous genome assembly is used
- Comparative genome assembly: assemble a newly sequenced genome by mapping it on to a reference
- Hybrid approach: reference-guided and de novo for unused reads or de novo and then reference guided alignments

Introduction



Adams 2008

Introduction

Original sequence

GATAGAAGGGTCCGCTCGCTCAGCTACCGGTTTTTATAGATCTA

GATAGAAGGGTCCGCT
AGAAGGGTCCGCTC
GGGTCCGCTCGCTCA
CCGCTCGCTCAGC
CTCGCTCAGCTACC
TCAGCTACCGGTTT
CTACCGGTTTTT
AGCTACCGGTTTTTAT
TTTTTATAGATCTA

fragmented sequences
from sequencer
(reads)

Introduction

assembled

fragmented sequences
from sequencer
(reads)

```
                              TTTTTATAGATCTA
                     AGCTACCGGTTTTTAT
                    CAGCTACCGGTTTTT
                   TCAGCTACCGGTTT
              CTCGCTCAGCTACC
           CCGCTCGCTCAGC
       GGGTCCGCTCGCTCA
   AGAAGGGTCCGCTC
GATAGAAGGGTCCGCT

GATAGAAGGGTCCGCTCGCTCAGCTACCGGTTTTTATAGATCTA
```

We want to reconstruct this from the reads

Introduction

Simplified scenario

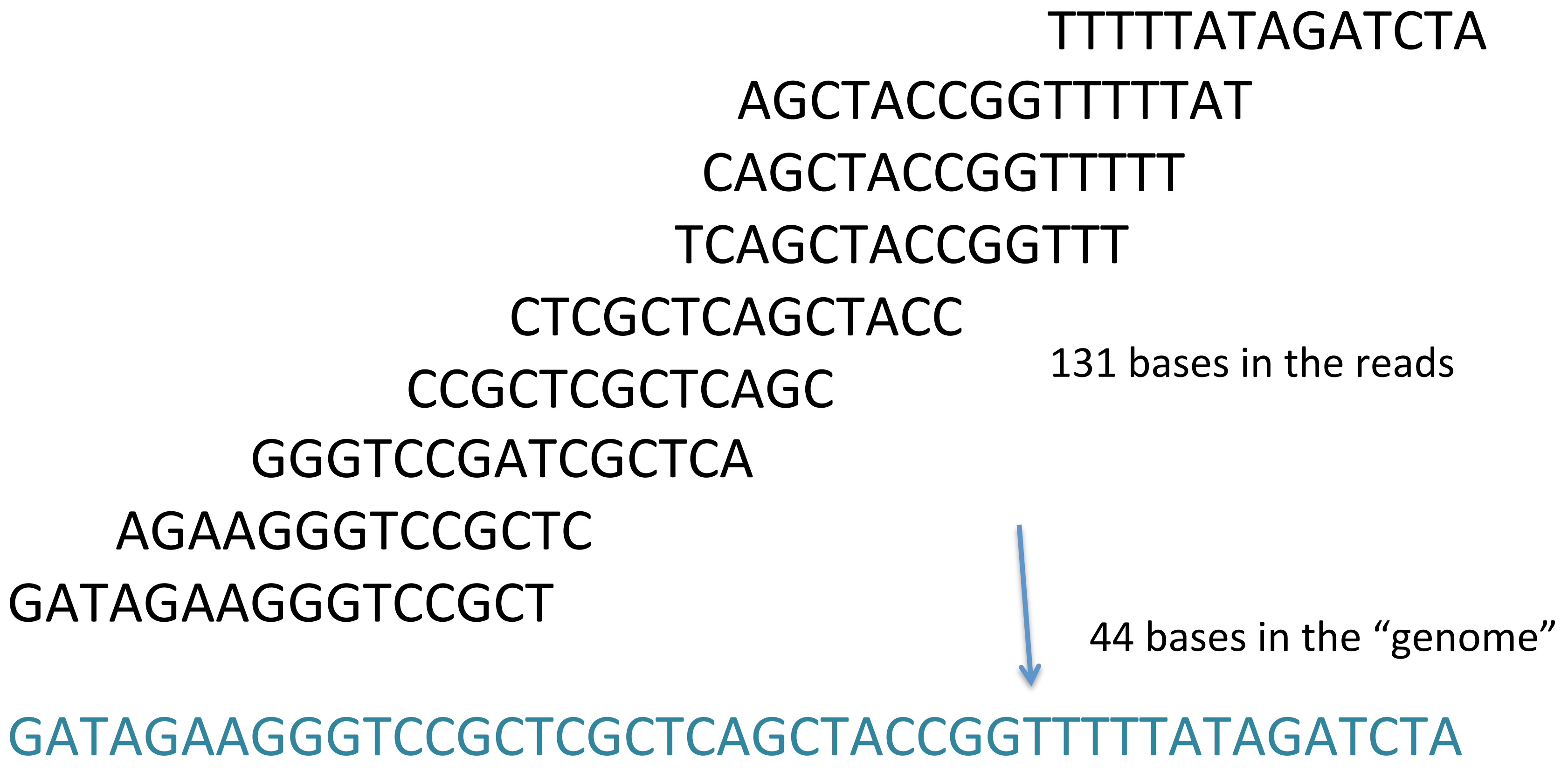
- Single strand
- Error free
- Complete coverage

```
                              TTTTTATAGATCTA
                     AGCTACCGGTTTTTAT
                    CAGCTACCGGTTTTT
                   TCAGCTACCGGTTT
              CTCGCTCAGCTACC
           CCGCTCGCTCAGC
       GGGTCCGCTCGCTCA
   AGAAGGGTCCGCTC
GATAGAAGGGTCCGCT

GATAGAAGGGTCCGCTCGCTCAGCTACCGGTTTTTATAGATCTA
```

Introduction

Coverage: reads “covering” a position in the genome (average or at a single base or region)



What is our average coverage?

What is the coverage at the arrow?

Introduction

```
                              TTTTTATAGATCTA
                     AGCTACCGGTTTTTAT
                    CAGCTACCGGTTTTT
                   TCAGGTACCGGTTT
              CTCGCTCAGCTACC
           CCGCTCGCTCAGC
       GGGTCCGATTGCTCA
   AGAAGGGTCCGCTC
GATAGAAGGGTCCGCT

GATAGAAGGGTCCGCTCGCTCAGCTACCGGTTTTTATAGATCTA
```

Why might there be differences among reads covering the same position?

Introduction

CCGCTCGCTCAGC

TCAGCTACCGGTTT

CTCGCTCAGCTACC

CAGCTACCGGTTTTT

AGAAGGGTCCGCTC

GATAGAAGGGTCCGCT

AGCTACCGGTTTTTAT

TTTTTATAGATCTA

GGGTCCGCTCGCTCA

How would you go about “assembling” these reads when you have no reference?

Code break

Write a one liner to find all the overlaps exactly 4 bp in length between CTCTAGGCC and a list of other sequences in the file ~/Topic5/data/overlaps.fa

Overlap-layout-consensus

Overlap: make an overlap graph

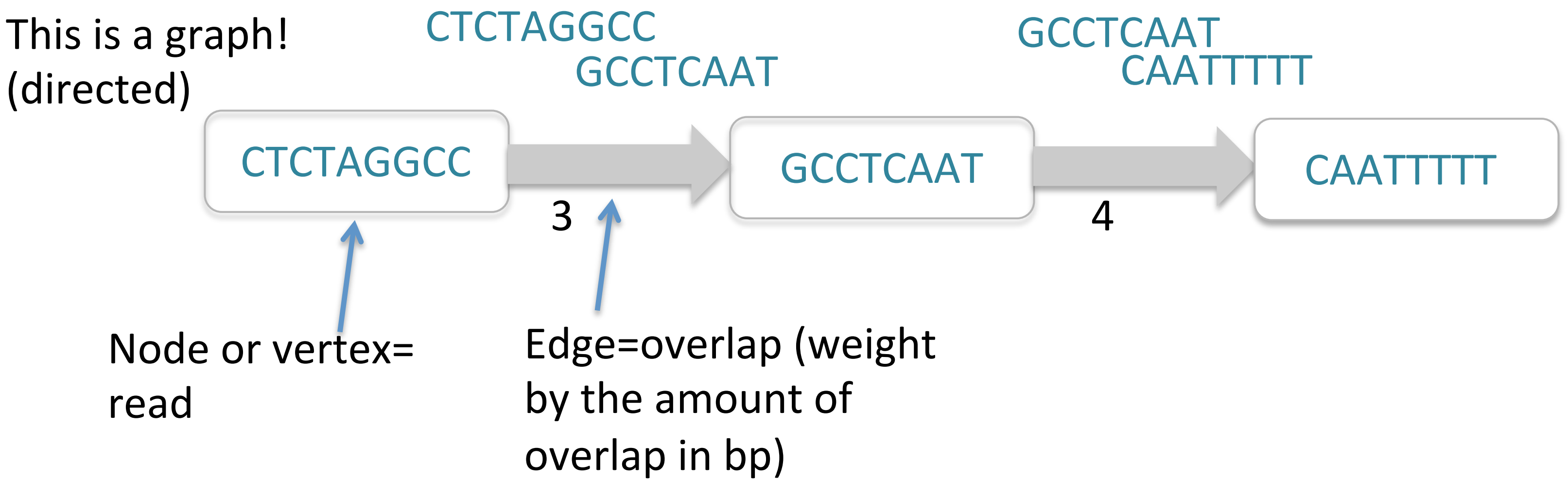
Layout: find the path through the graph

Consensus: find the most likely contig sequence

OLC programs:
ARACHNE, PHRAP, CAP, TIGR, CELERA

Overlap-layout-consensus

Reads: CTCTAGGCC GCCTCAAT CAATTTTT

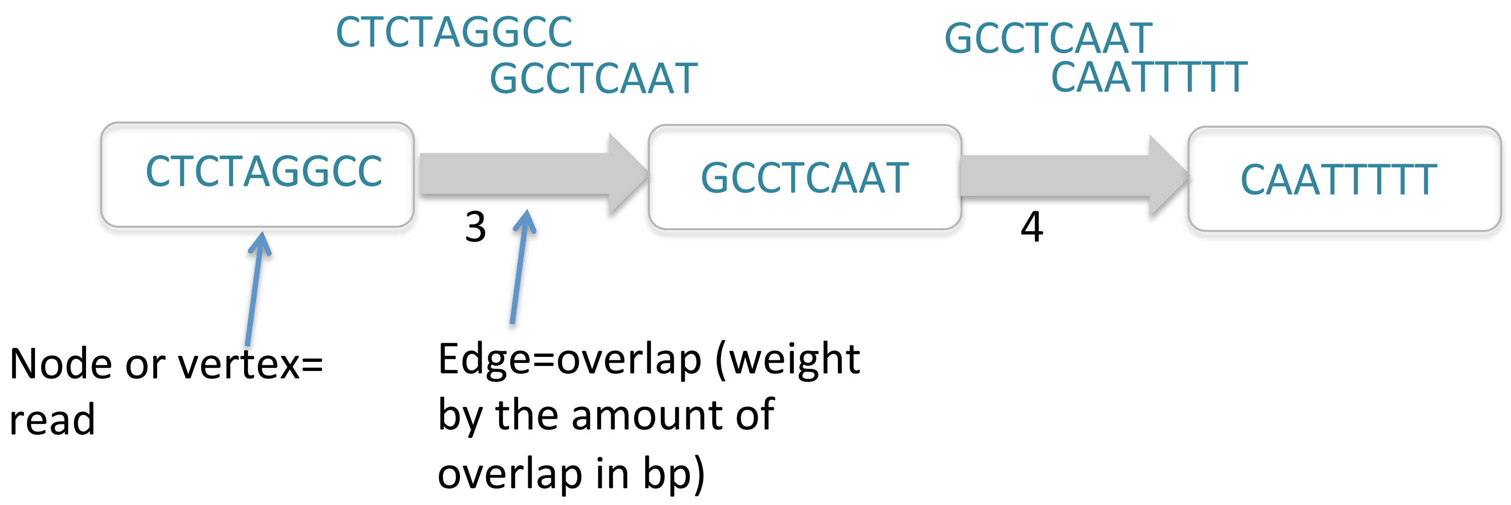


Can pick a minimum overlap length (e.g. 3 bp)

Finding overlaps can be computationally challenging when you have millions of reads!

Overlap-**layout**-consensus

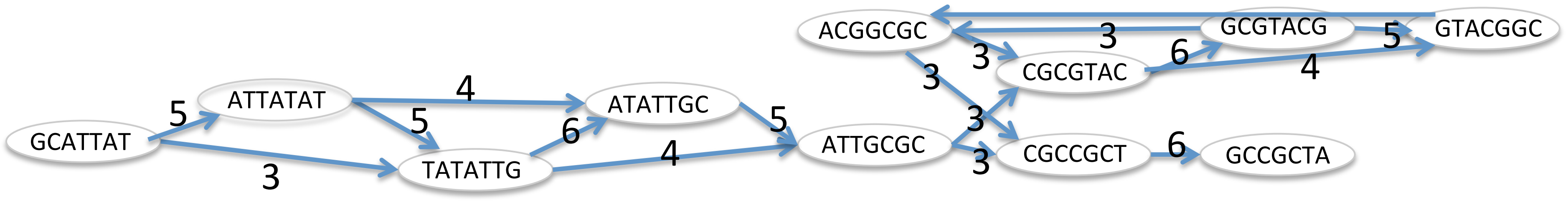
Reads: CTCTAGGCC GCCTCAAT CAATTTTT



Here we have only one path through the graph

Overlap-**layout**-consensus

These graphs get complicated!



Minimum overlap = 3

Read length = 7

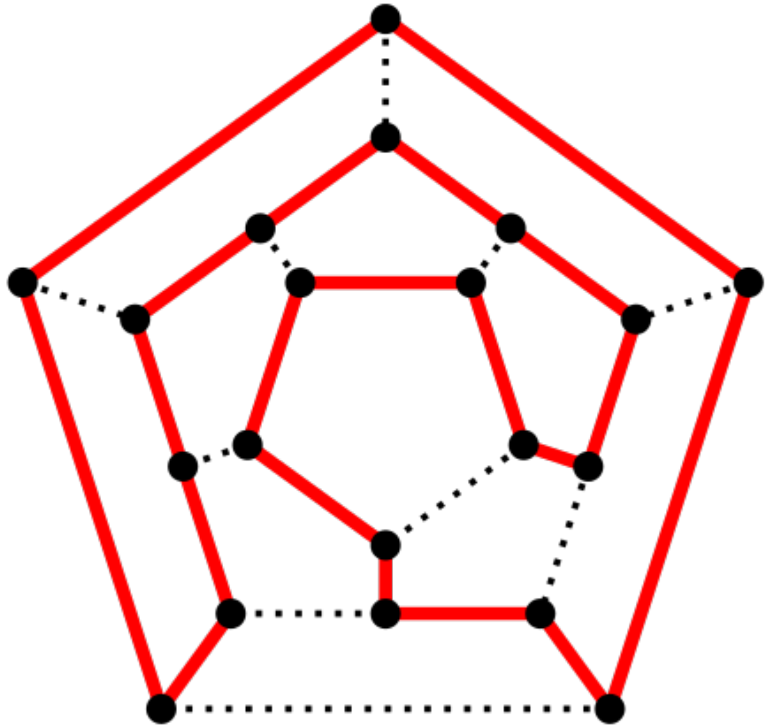
GCATTATATATTGCGCGTACGGCGCCGCTACA

Original sequence

How can we find the best path?

Overlap-**layout**-consensus

Hamiltonian path: hit each node (read) once
–no quick way to figure it out (NP-complete)
–not practical and not implemented



Overlap-**layout**-consensus

Shortest superstring: find the shortest final sequence (greatest overlap between reads)
-hit each node (read) once
-NP-hard

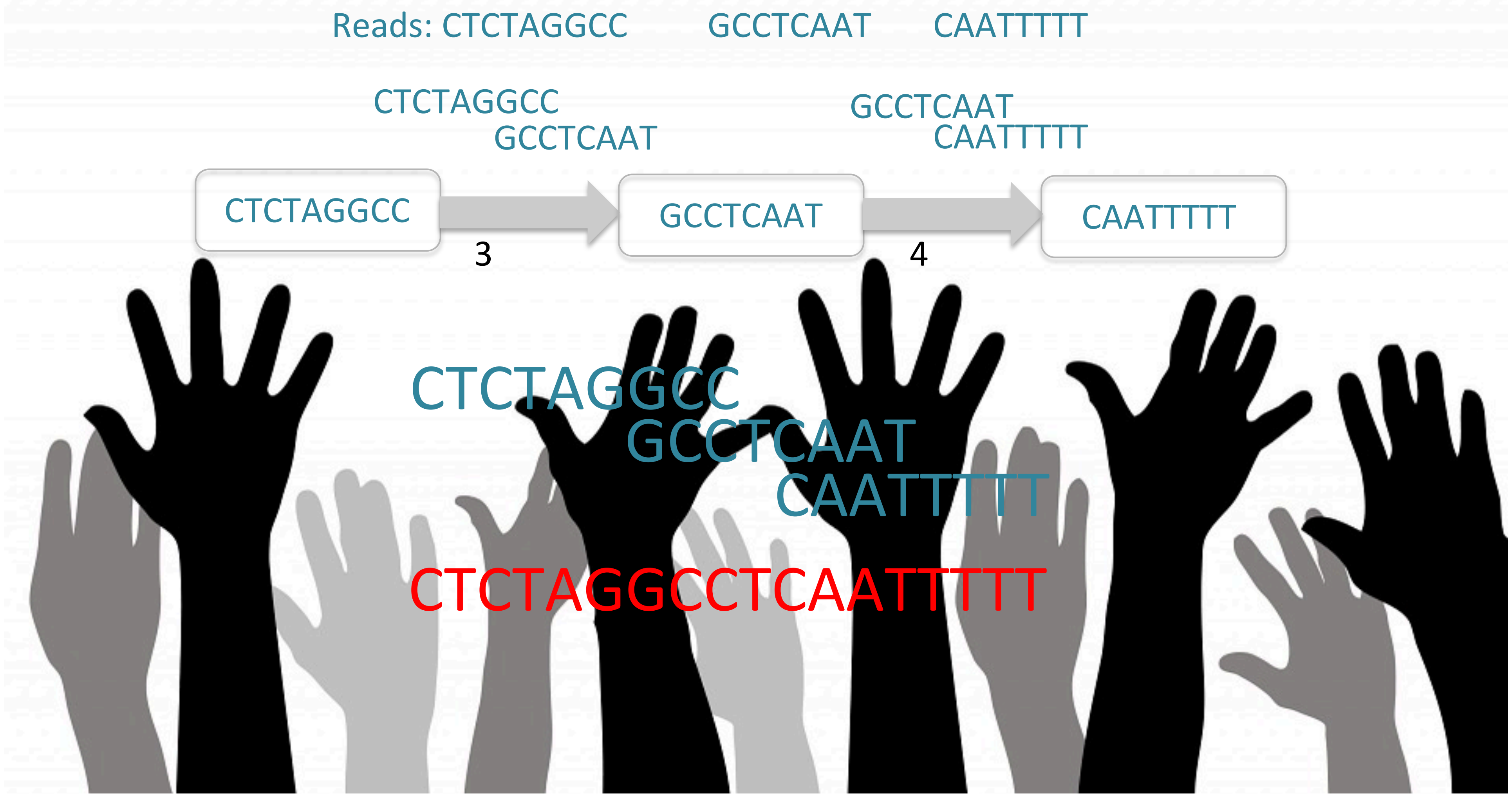
Overlap-**layout**-consensus

Greedy algorithm (example)

1) Pairwise alignments between all fragments
2) Pick the two with the largest overlap
3) Merge chosen fragments
4) Repeat

Overlap-layout-**consensus**

Join sequences together into one sequence



Limitations of OLC

- require overlaps to be scored between all possible pairs of reads. This is a problem when you have millions of reads

- finding the best path through the graph with a huge number of nodes (reads) is computationally challenging

Is there a faster way to assemble many short reads?

De Bruijn graphs

What are all the 5-mers (5 bp fragments) in these reads?

	read 1	read 2
2 reads of 9 bp	ATGGGGAAC	GGGAACCCC
	ATGGG	GGGAA
	TGGGG	GGAAC
	GGGGA	GAACC
	GGGAA	AACCC
	GGAAC	ACCCC

If a read is L bp long, how many kmers of size k can you make?

Code break

Find all the unique 9mers in a fasta sequence and sort them alphabetically ~/Topic5/data/kmer.fa

1. Find all the kmers in this fasta sequence.

   Hints: test out the following commands

   ```
   cut -c2- kmer.fa
   cut -c1-4 kmer.fa

   for num in {1..10}
   do
   echo $num >> file.txt
   done
   ```

2. Sort them and keep the unique ones

   Hint: try `sort`

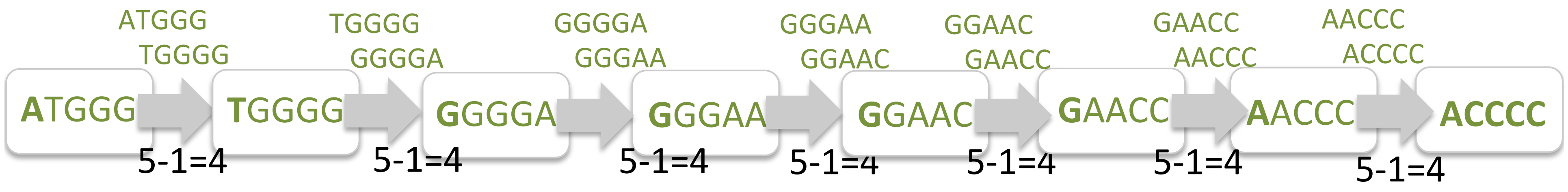
De Bruijn graphs

- Join up all the k-mers (length = k bp) into a graph with an overlap of k-1 (here k=5)

read 1
ATGGGGAAC

read 2
GGGAACCCC

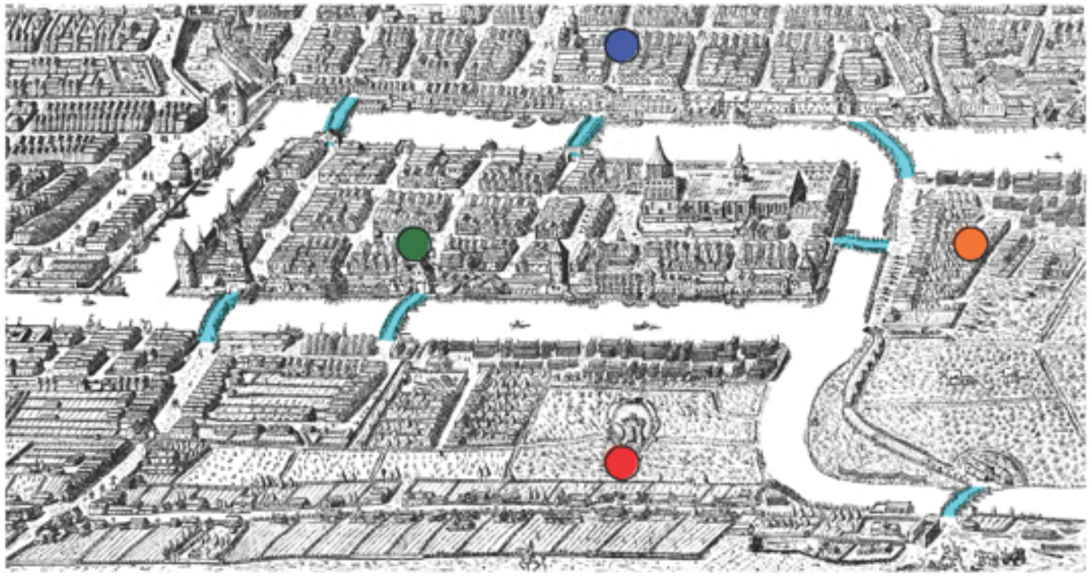
```
ATGGG
 TGGGG
  GGGGA
   GGGAA
    GGAAC
     GAACC
      AACCC
       ACCCC
```



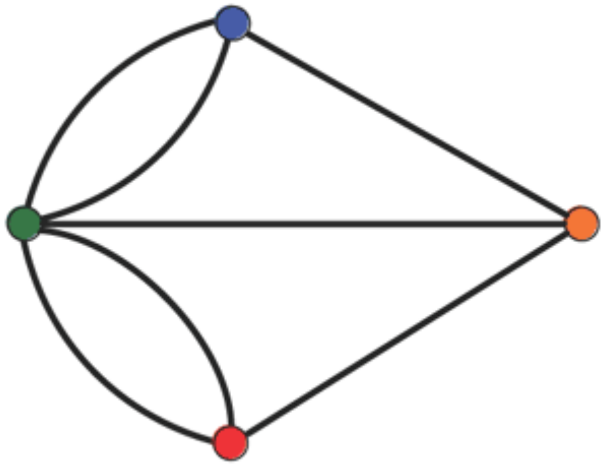
- Traverse through the graph
- The first base of each node spells out the sequence

De Bruijn graphs

a

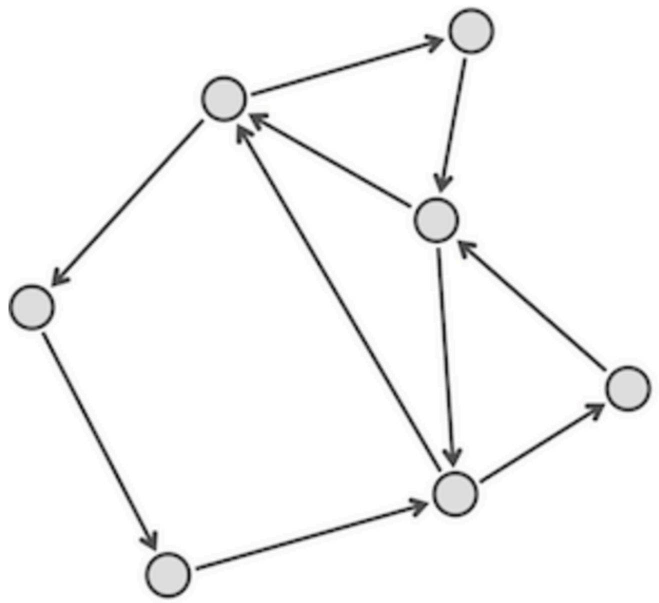


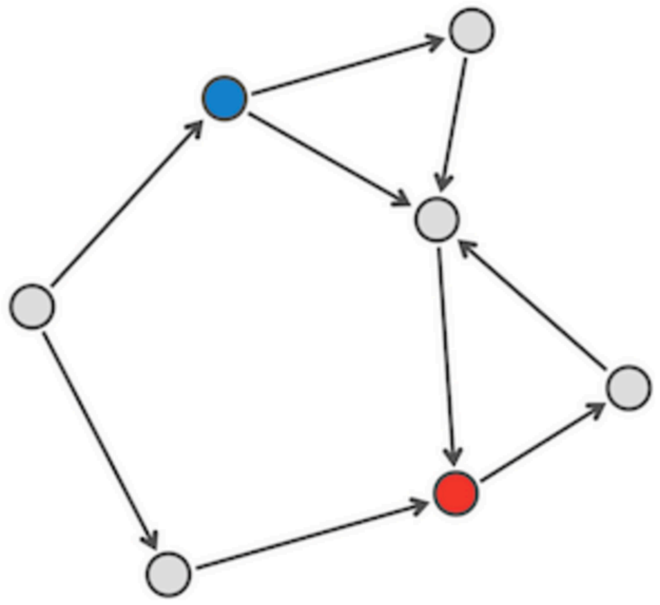
b



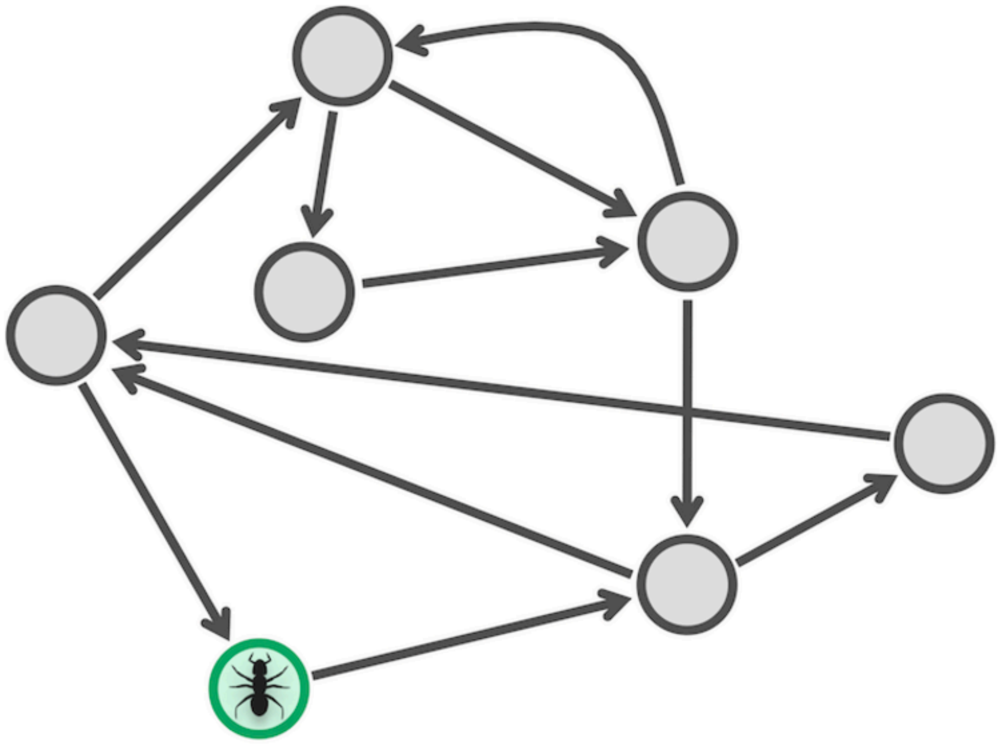
De Bruijn graphs

Eulerian graph must be both balanced and strongly connected



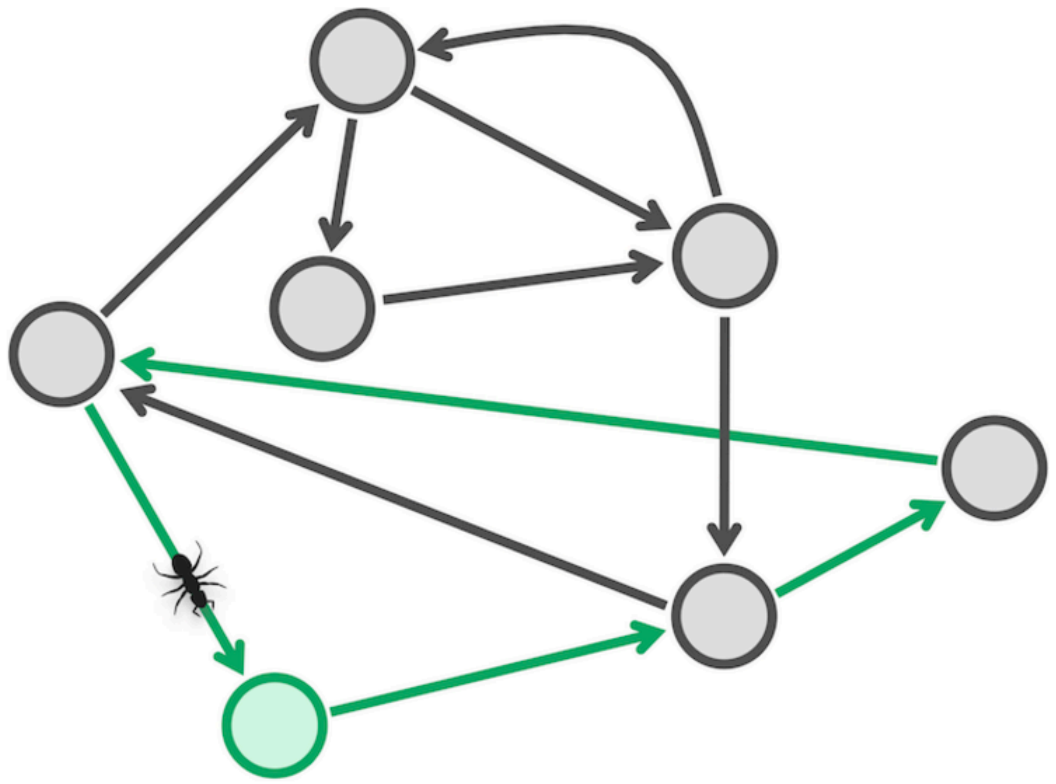


De Bruijn graphs



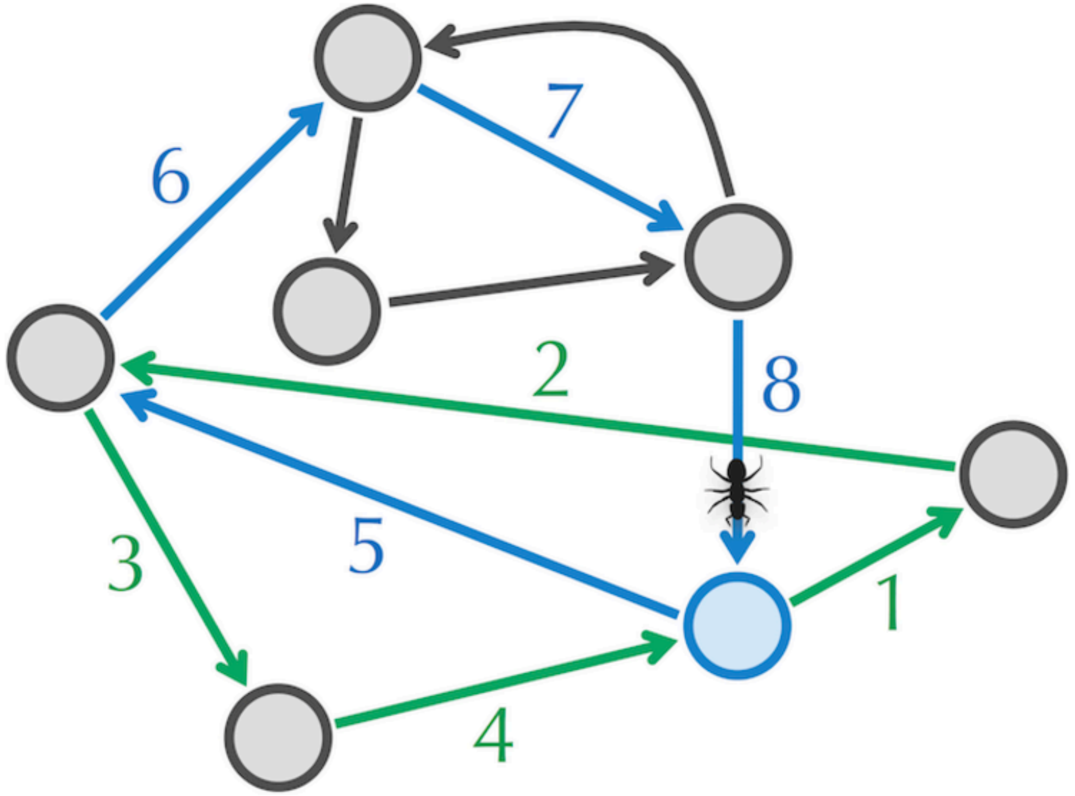
Algorithm to find a path through an Eulerian graph

De Bruijn graphs



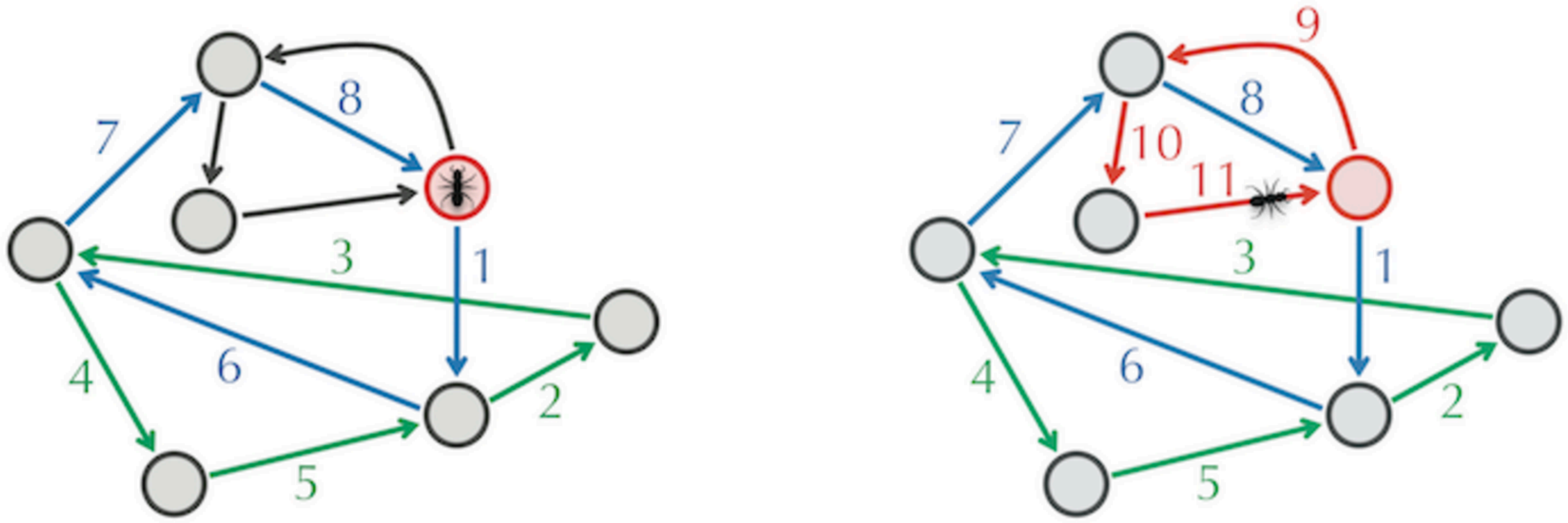
Algorithm to find a path through an Eulerian graph

De Bruijn graphs



Algorithm to find a path through an Eulerian graph

De Bruijn graphs



Algorithm to find a path through an Eulerian graph

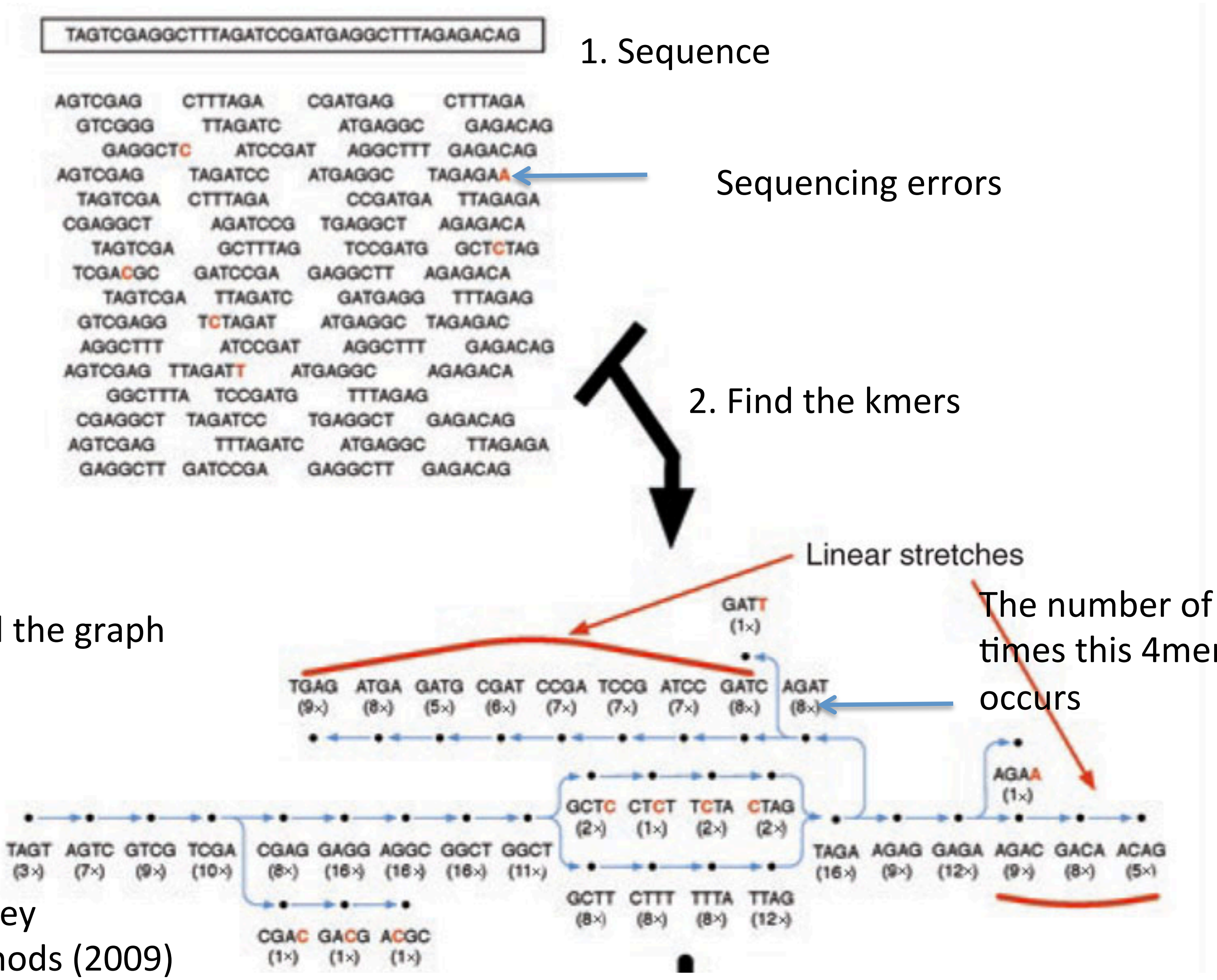
De Bruijn graphs

Limitations of the Eulerian path:

- With “perfect” genomic data there are usually many Eulerian tours

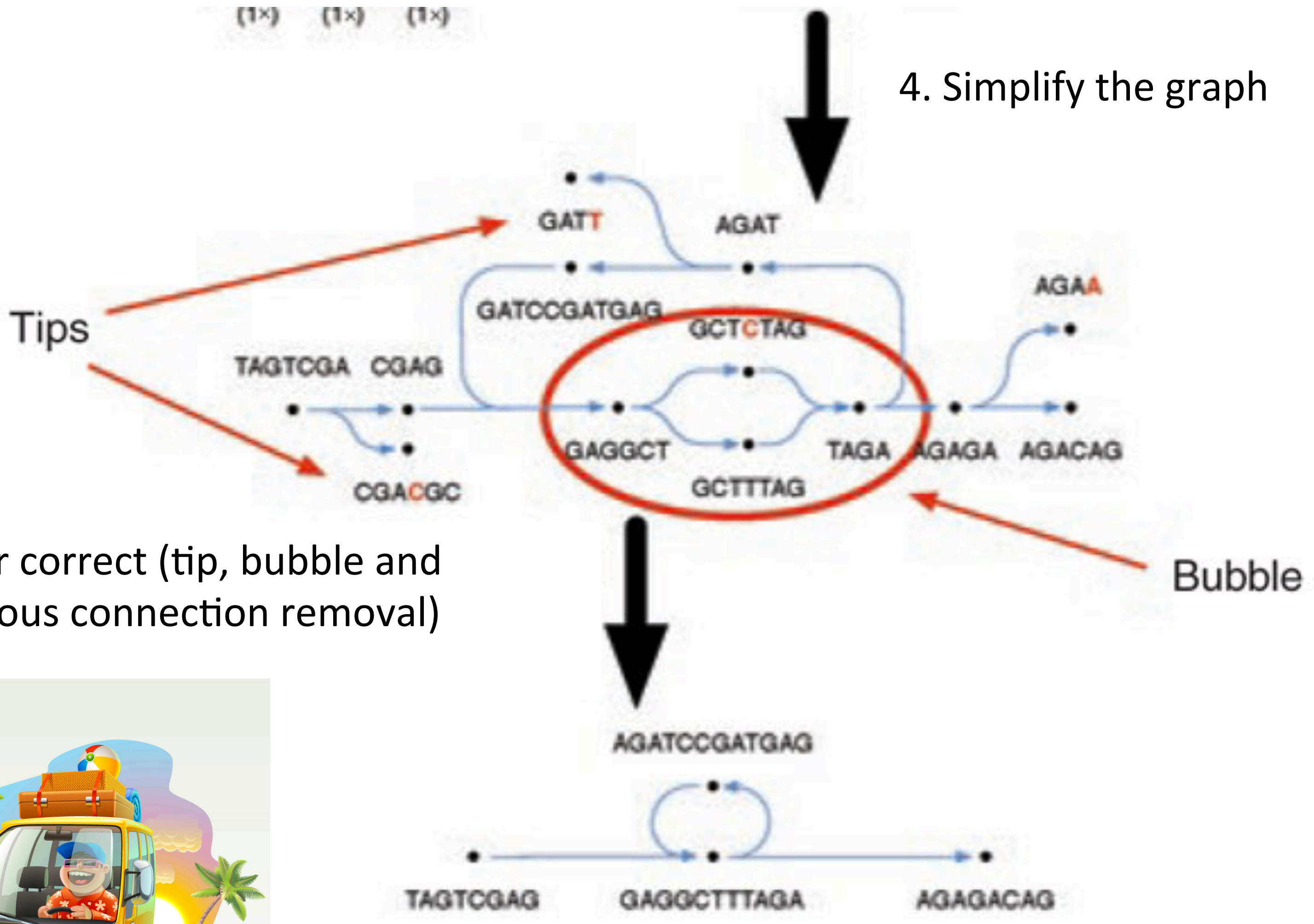
- Data is not perfect (areas of low coverage, errors, repeats, etc.)

De Bruijn graphs



Flicek & Birney
Nature Methods (2009)

De Bruijn graphs



5. Error correct (tip, bubble and erroneous connection removal)

Flicek & Birney Nature Methods (2009)

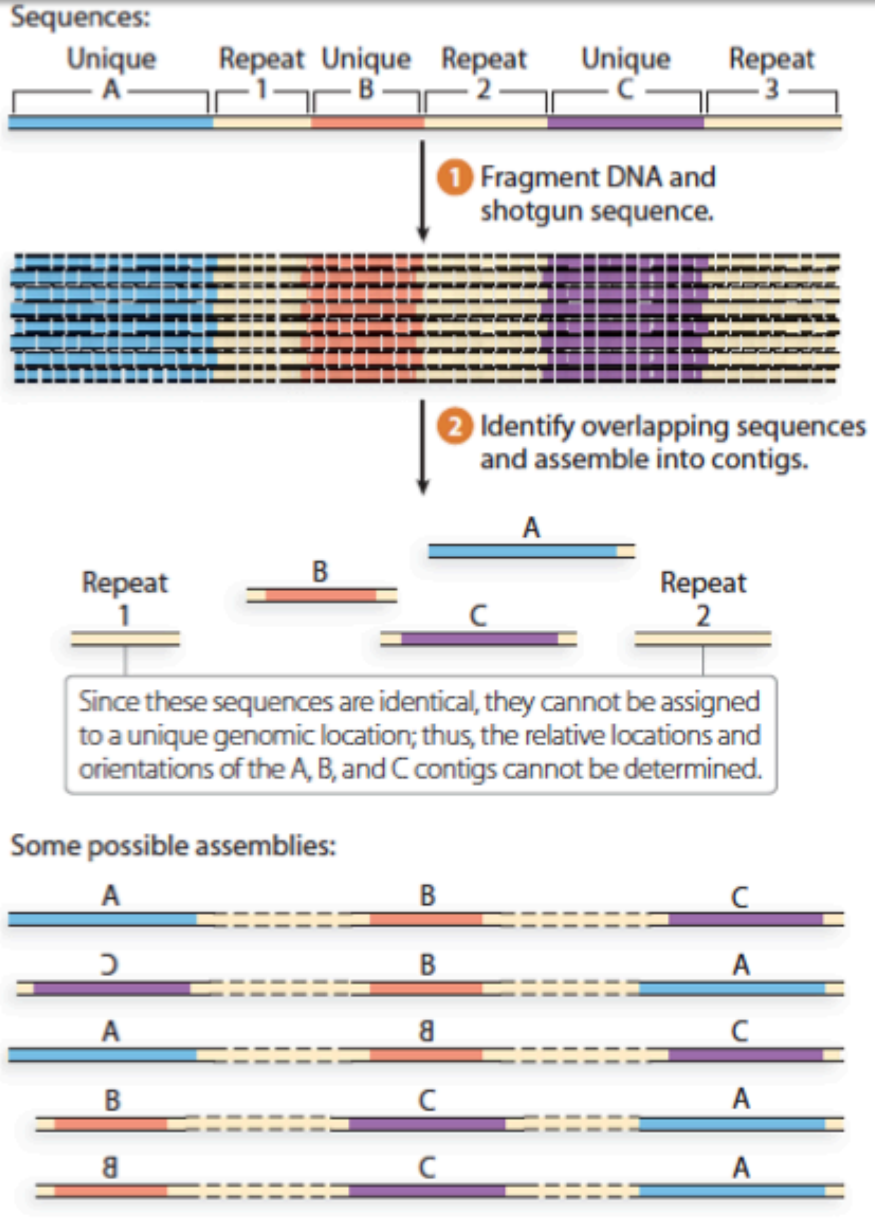
De Bruijn graphs

Advantages:
1) Set node length (no overlap algorithm)
2) Easy approaches for traversing through the graph
3) Simpler representation of repeats in the graph

Disadvantages:
1) Lose information
2) Shorter contigs

For PacBio and other long read sequences, what type of assembly strategy would you use?

Repetitive regions

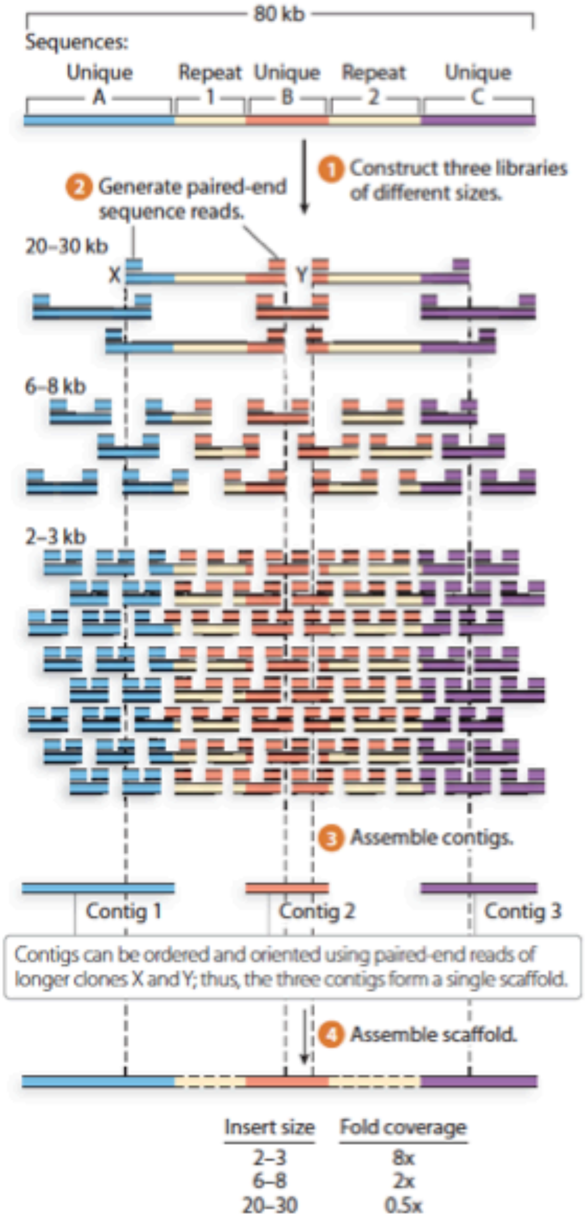


Sequences:
Unique A
Repeat 1
Unique B
Repeat 2
Unique C
Repeat 3
1 Fragment DNA and shotgun sequence.
2 Identify overlapping sequences and assemble into contigs.
A
B
C
Repeat 1
Repeat 2
Since these sequences are identical, they cannot be assigned to a unique genomic location; thus, the relative locations and orientations of the A, B, and C contigs cannot be determined.
Some possible assemblies:
A B C
Ↄ B A
A ᗺ C
B C A
ᗺ C A

Sanders and Bowman

Figure 18.2 The problem of repetitive DNA.

Repetitive regions



80 kb
Sequences:
Unique A
Repeat 1
Unique B
Repeat 2
Unique C
1 Construct three libraries of different sizes.
2 Generate paired-end sequence reads.
20–30 kb
X
Y
6–8 kb
2–3 kb
3 Assemble contigs.
Contig 1
Contig 2
Contig 3
Contigs can be ordered and oriented using paired-end reads of longer clones X and Y; thus, the three contigs form a single scaffold.
4 Assemble scaffold.

Insert size	Fold coverage
2–3	8x
6–8	2x
20–30	0.5x

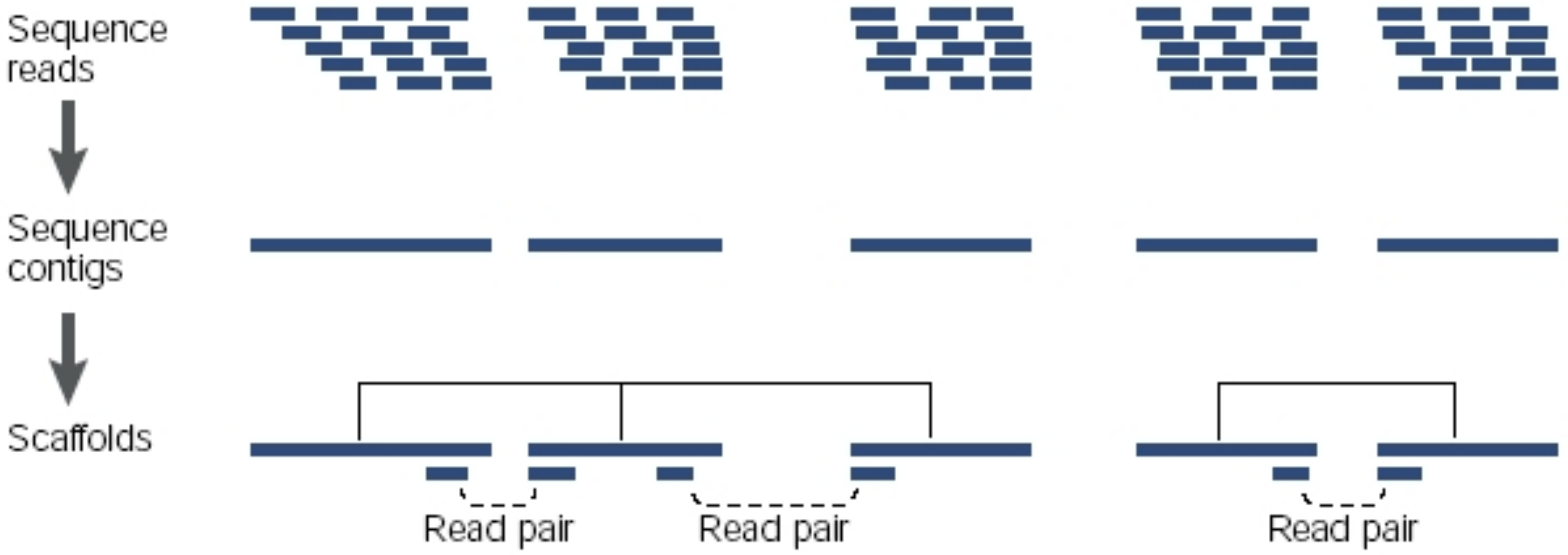
Figure 18.3 Paired-end shotgun sequencing strategy.

Sanders and Bowman

Finishing genomes

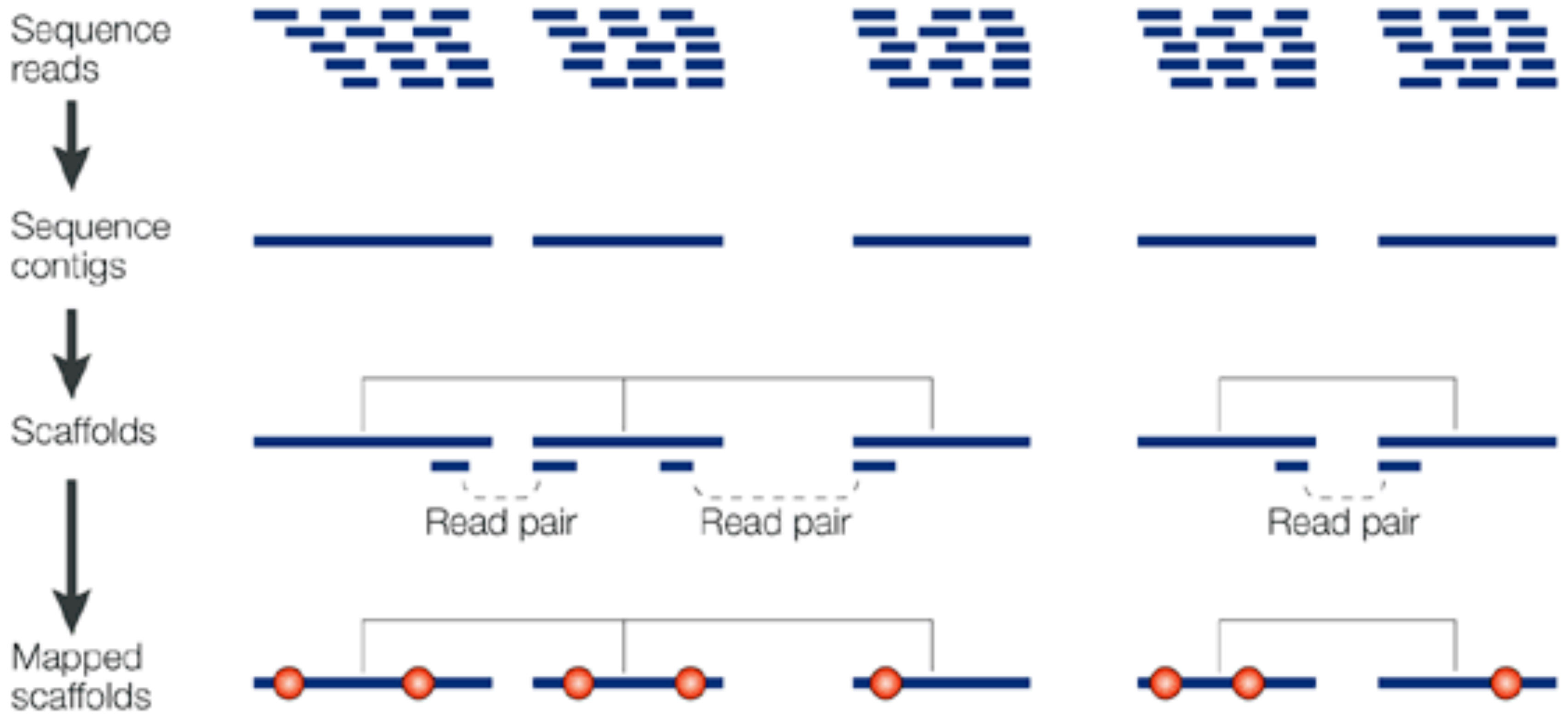
- Finishing eukaryotic genome assemblies can be challenging because much of the genome is repetitive
- This repetitive DNA breaks up the assembly and obscures the order and orientation of the assembled contigs
- Even well studied model organisms can have poorly assembled regions of their genome

Finishing genomes



Adams 2008

Finishing genomes



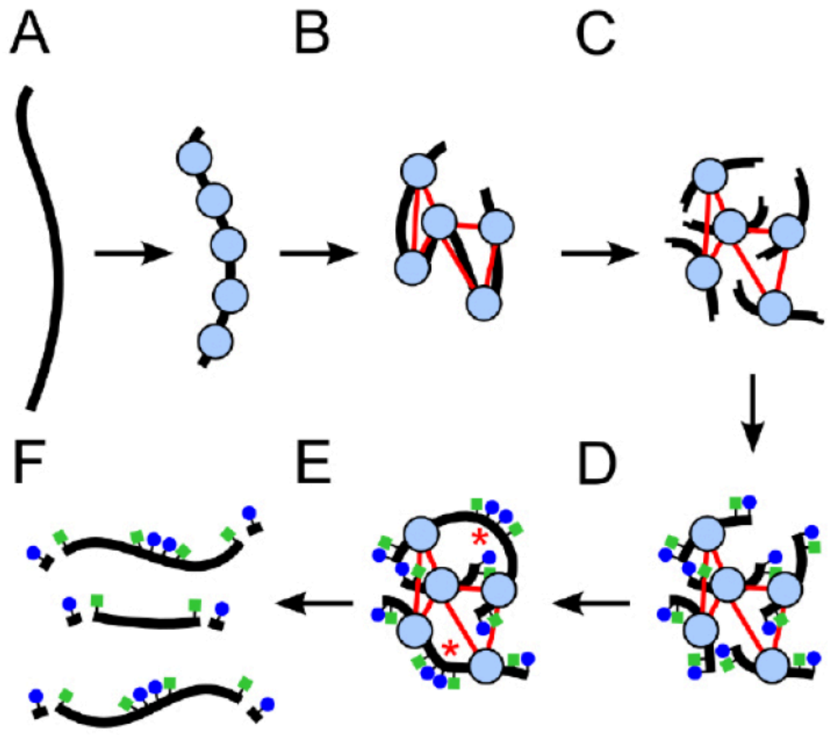
Adams 2008

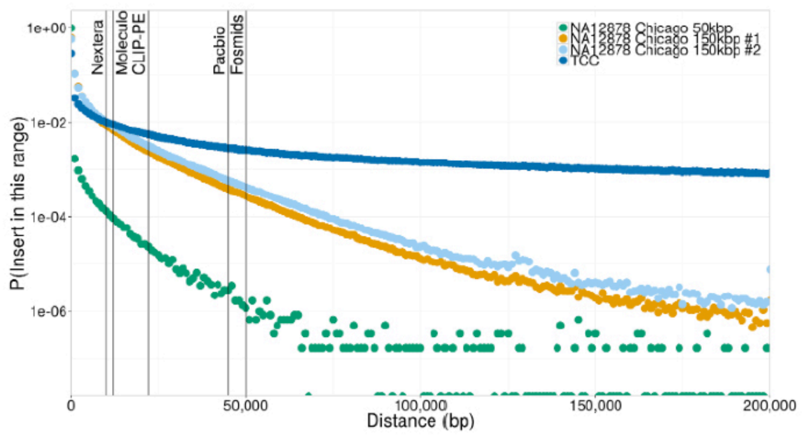
Finishing genomes

1. Long read sequencing (e.g. PacBio)
2. Optical mapping (https://vimeo.com/116090215)
3. Genetic and physical maps
4. Jumping libraries

Finishing genomes

Ragweed genome project: Chicago library





Finishing genomes

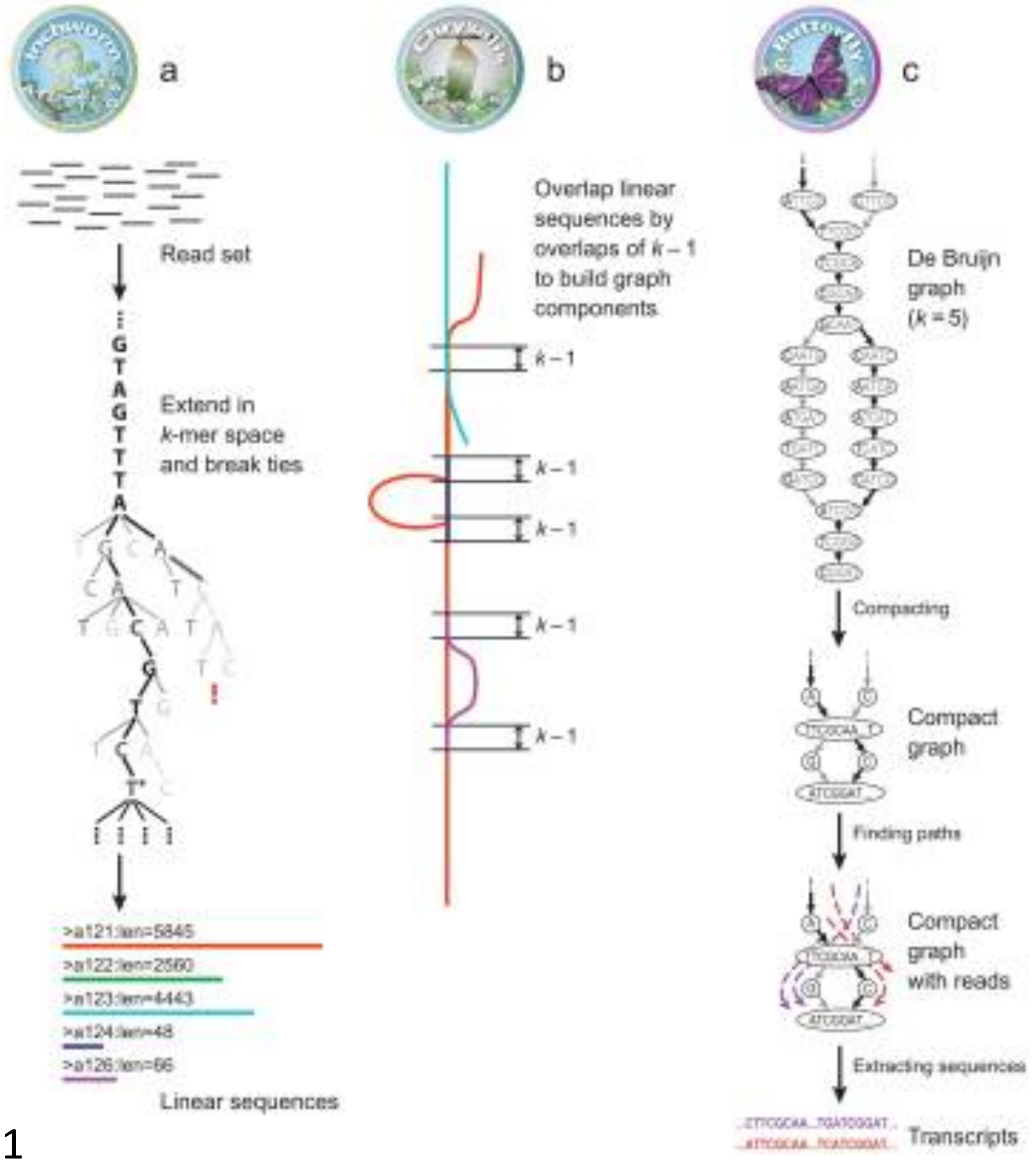
	Before HiRise	After HiRise	Fold Increase
N50 #of Scaffolds	30 Kb 12,793	522 Kb 807	17.5X -
N90 #of Scaffolds	3 Kb 65,658	88Kb 3,190	29.3X -

Other types of de novo assembly

Transcriptome

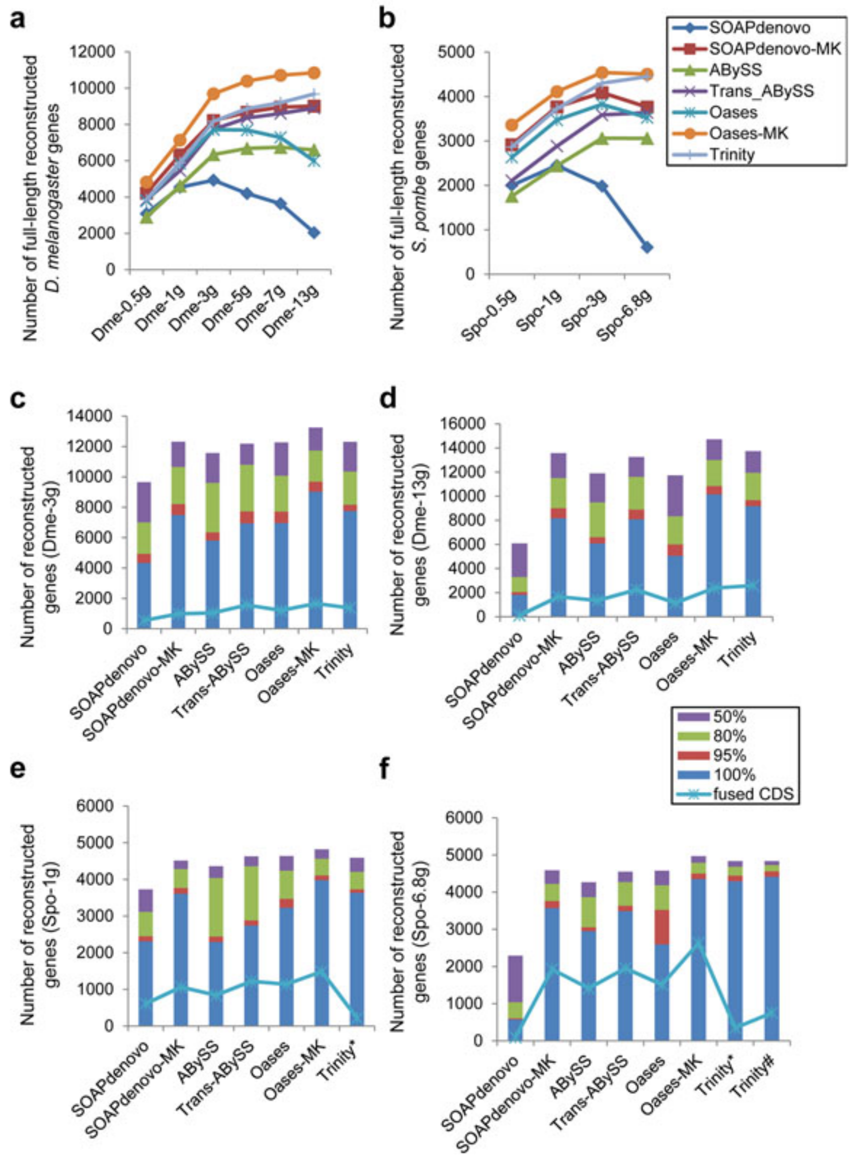
- Variable coverage among genes/isoforms
- Alternative splicing
  promotors, exons, and poly(A)

Other types of de novo assembly



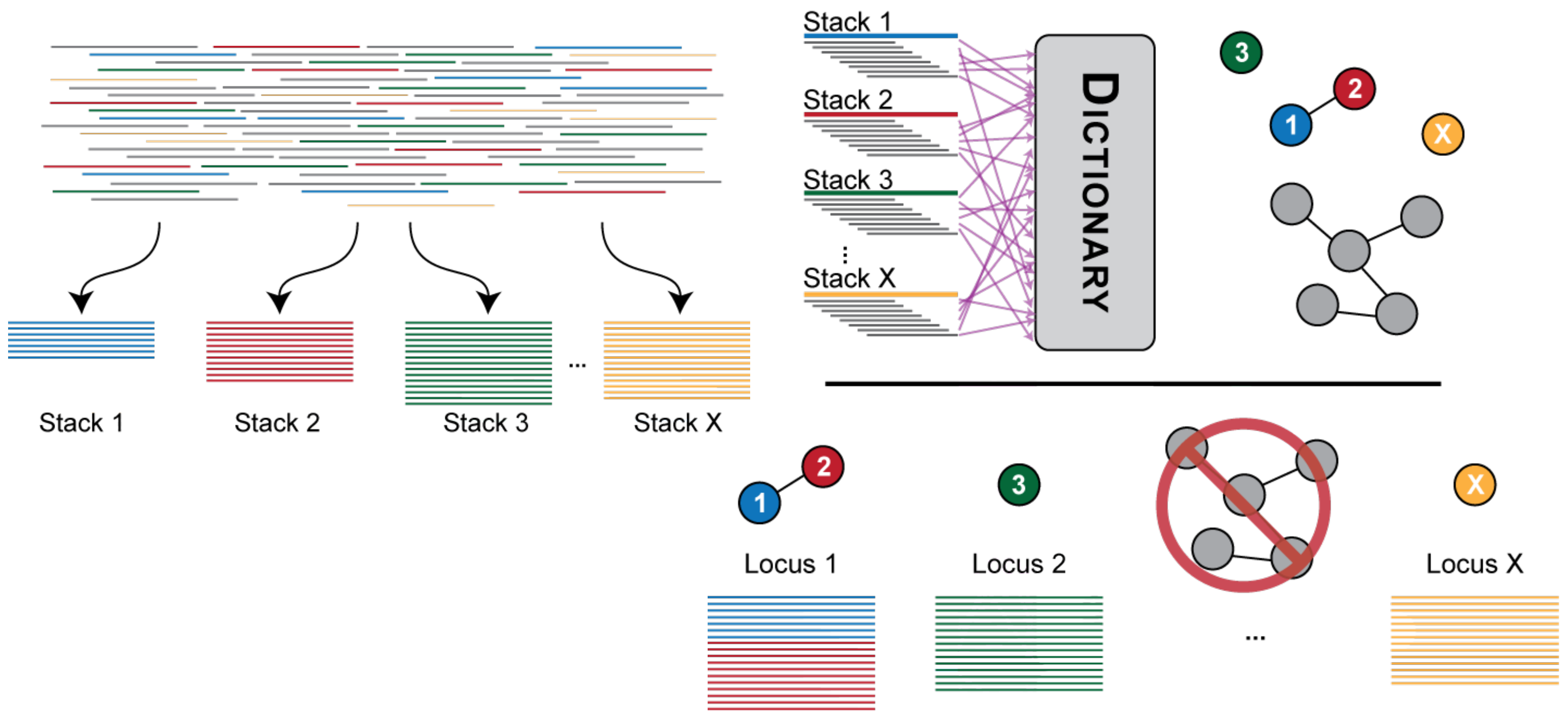
Grabherr et al 2011

Other types of de novo assembly



Other types of de novo assembly

De novo assembly of GBS reads: Stacks



http://catchenlab.life.illinois.edu/stacks/param_tut.php

Further Reading

Flicek, P., & Birney, E. (2009). Sense from sequence reads: methods for alignment and assembly. Nature methods, 6, S6-S12.

Zerbino DR, Birney E. Velvet: Algorithms for de novo short read assembly using de Bruijn graphs. Genome Research. 2008;18(5):821-829. doi:10.1101/gr.074492.107.

http://computing.bio.cam.ac.uk/local/doc/velvet.pdf

Li, Z., Chen, Y., Mu, D., Yuan, J., Shi, Y., Zhang, H., ... & Yang, B. (2012). Comparison of the two major classes of assembly algorithms: overlap–layout–consensus and de-bruijn-graph. Briefings in functional genomics, 11(1), 25-37.

Grabherr MG, Haas BJ, Yassour M, et al. Trinity: reconstructing a full-length transcriptome without a genome from RNA-Seq data. Nature biotechnology. 2011;29(7):644-652. doi:10.1038/nbt.1883.

https://github.com/trinityrnaseq/trinityrnaseq/wiki

J. Catchen, A. Amores, P. Hohenlohe, W. Cresko, and J. Postlethwait. Stacks: building and genotyping loci de novo from short-read sequences. G3: Genes, Genomes, Genetics, 1:171-182, 2011.

http://catchenlab.life.illinois.edu/stacks/

Tutorial

Today you will use the genome assembly program Velvet to assemble a bacterial genome.

Velvet overview:
1. Hash k-mers
2. Construct the graph
3. Correct for errors
4. Resolve the repeats

Refer to Github page or open ~/Topic5/README_assembly.txt and follow the instructions

Tutorial

1) Given the above information, what is the expected coverage?

2) For a k-mer of 21 what is would the k-mer coverage be for this genome assembly?

3) Can you think of other ways to assess assembly quality? What might be the trouble with only focusing on maximizing N50? Discuss this with your group.

4) Quantify the assembly metrics for your first assembly that you ran without any options. In your group of four, each person should pick different sets of parameters to run. Compare the resulting assemblies with one another and discuss which ones seemed to have improved the assembly and why that might be. Be prepared to share your findings with the class.

For next class

- Make sure R and Rstudio are installed and working on your computer
- Go over Greg's short R tutorial (Topic 2) if you are not familiar with R

1. ABySS (Assembly By Short Sequencing) (Birol et al): A denovo assembler for short read sequence data which uses a distributed representation of a de Bruijn graph, allowing parallel computation of the assembly algorithm across a network of commodity computers. Developed at Canada's Michael Smith Genome Sciences Centre.

2. ALLPATHS-LG (Gnerre et al): a de Bruijn graph-based *de novo* assembler for large (and small) genomes. ALLPATHS-LG is being developed by scientists at the Broad Institute.

3. Bambus2: The second generation Bambus scaffolder relies on a combination of a novel method for detecting genomic repeats and algorithms that analyze assembly graphs to identify biologically meaningful genomic variants. Bambus2 compares favorably to existing scaffolds generated by CABOG, Newbler and SOAPdenovo with respect to contiguity and error rate. While Bambus 2 was specifically designed for polymorphic and metagenomic scaffolding, its modular and efficient algorithm allows it to be used to scaffold mammalian genomes and used a drop-in replacement scaffolder for CABOG, Newbler, and SOAPdenovo. Bambus2 is being primarily developed by Sergey Koren and Mihai Pop, with input from Todd Treangen,

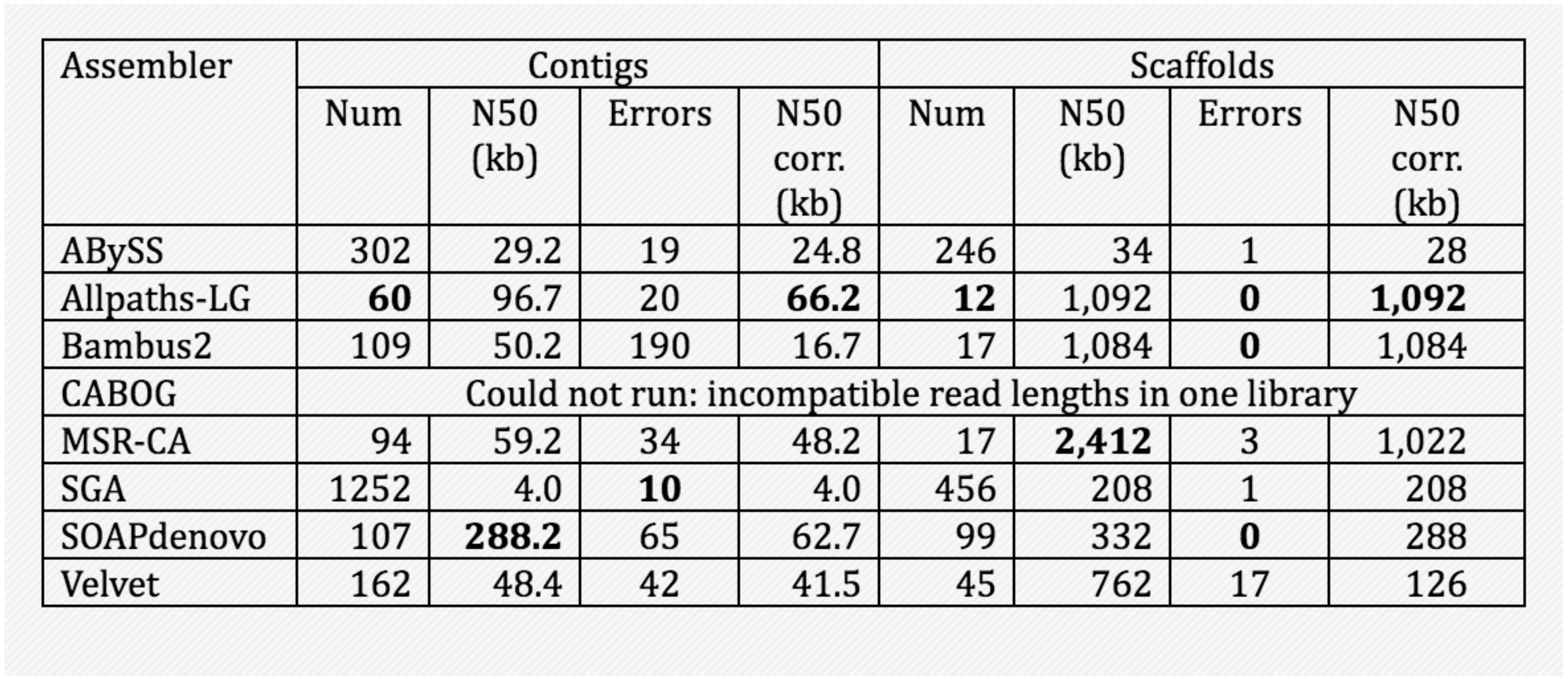
4. Celera Assembler: an Overlap-Layout-Consenus based de novo whole-genome shotgun (WGS) DNA sequence assembler. It reconstructs long sequences of genomic DNA from fragmentary data produced by whole-genome shotgun sequencing. Celera Assembler has enabled many advances in genomics, including the first whole genome shotgun sequence of a multi-cellular organism (Myers 2000) and the first diploid sequence of an individual human (Levy 2007). Celera Assembler was developed at Celera Genomics starting in 1999. It was released to SourceForge in 2004 as the wgs-assembler under the GNU General Public License. The pipeline revised for 454 data was named CABOG (Miller 2008).

5. MSR-CA (pronounced "MizerKa") is a new technique that pre-processes the short read data and then performs the final assembly using a modified version of Celera Assembler. MSR-CA stands for Maryland Super-Reads + Celera Assembler. The pre-processing steps include error correction and subsequent coverage reduction by creating "super-reads," which are produced using a de Bruijn graph. The algorithm then groups together the reads that map to the same sets of nodes and edges, and for each set replaces them by a single super-read that contains these nodes and edges. This can reduce the number of reads by a factor of 50 or more, resulting in the data set that is much easier to manage.

6. SGA (Simpson et al): stands for String Graph Assembler. Experimental de novo assembler based on string graphs. SGA is being developed by scientists at the Wellcome Trust Sanger Institute.

7. SOAPdenovo (Li et al): is the short-read assembler that was used for the panda genome, the first mammalian genome assembled entirely from Illumina reads, and for several human genomes and other genomes subsequently. It is being developed by scientists at BGI.

8. Velvet (Zerbino et al): Velvet is a *de novo* genome assembler specially designed for short read sequencing technologies, particularly Illumina reads, and was one of the first short-read assemblers to be published. It was developed by Daniel Zerbino and Ewan Birney at the European Bioinformatics Institute (EMBL-EBI), near Cambridge, England.



Assembler	Contigs				Scaffolds			
	Num	N50 (kb)	Errors	N50 corr. (kb)	Num	N50 (kb)	Errors	N50 corr. (kb)
ABySS	302	29.2	19	24.8	246	34	1	28
Allpaths-LG	**60**	96.7	20	**66.2**	**12**	1,092	**0**	**1,092**
Bambus2	109	50.2	190	16.7	17	1,084	**0**	1,084
CABOG	Could not run: incompatible read lengths in one library							
MSR-CA	94	59.2	34	48.2	17	**2,412**	3	1,022
SGA	1252	4.0	**10**	4.0	456	208	1	208
SOAPdenovo	107	**288.2**	65	62.7	99	332	**0**	288
Velvet	162	48.4	42	41.5	45	762	17	126