

Genome Assembly

4/19/17

Let's try assembling a set of words

- Get into groups of 2-3
- Each group will get an envelope
- Those envelopes contain short sequences of words
 - Analog to Illumina Read
- Using NO outside knowledge – assemble these fragments into a well-known passage

Want help?

- Your group can now have
 - A mate-pair set
 - A low coverage, long read set

What is the phrase?

In each group, take 2 minutes to answer these questions

- What challenges did you face?
- How did you solve these challenges?

Ground Truth

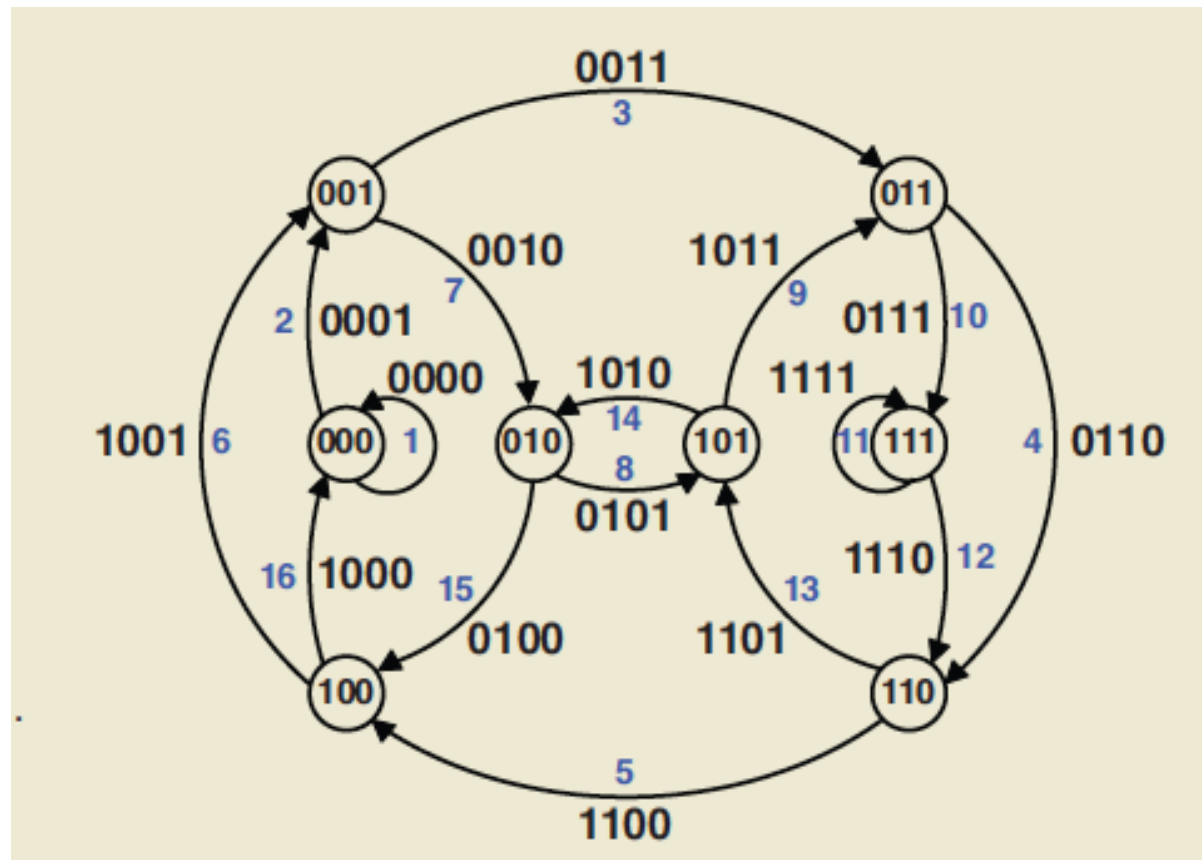
It was the best of times, it was the worst of times, it was the age of wisdom, it was the age of foolishness, it was the epoch of belief, it was the epoch of incredulity, it was the season of Light, it was the season of Darkness, it was the spring of hope, it was the winter of despair,...

- Charles Dickens, *A Tale of Two Cities*

How are these challenges similar to
genome assembly?

How do we assemble genomes?

- de Bruijn graphs



Build a graph of the sequences

- What k-mer should we work with?
- What are the nodes?
- What are the edges?

What are all the 3-mers?

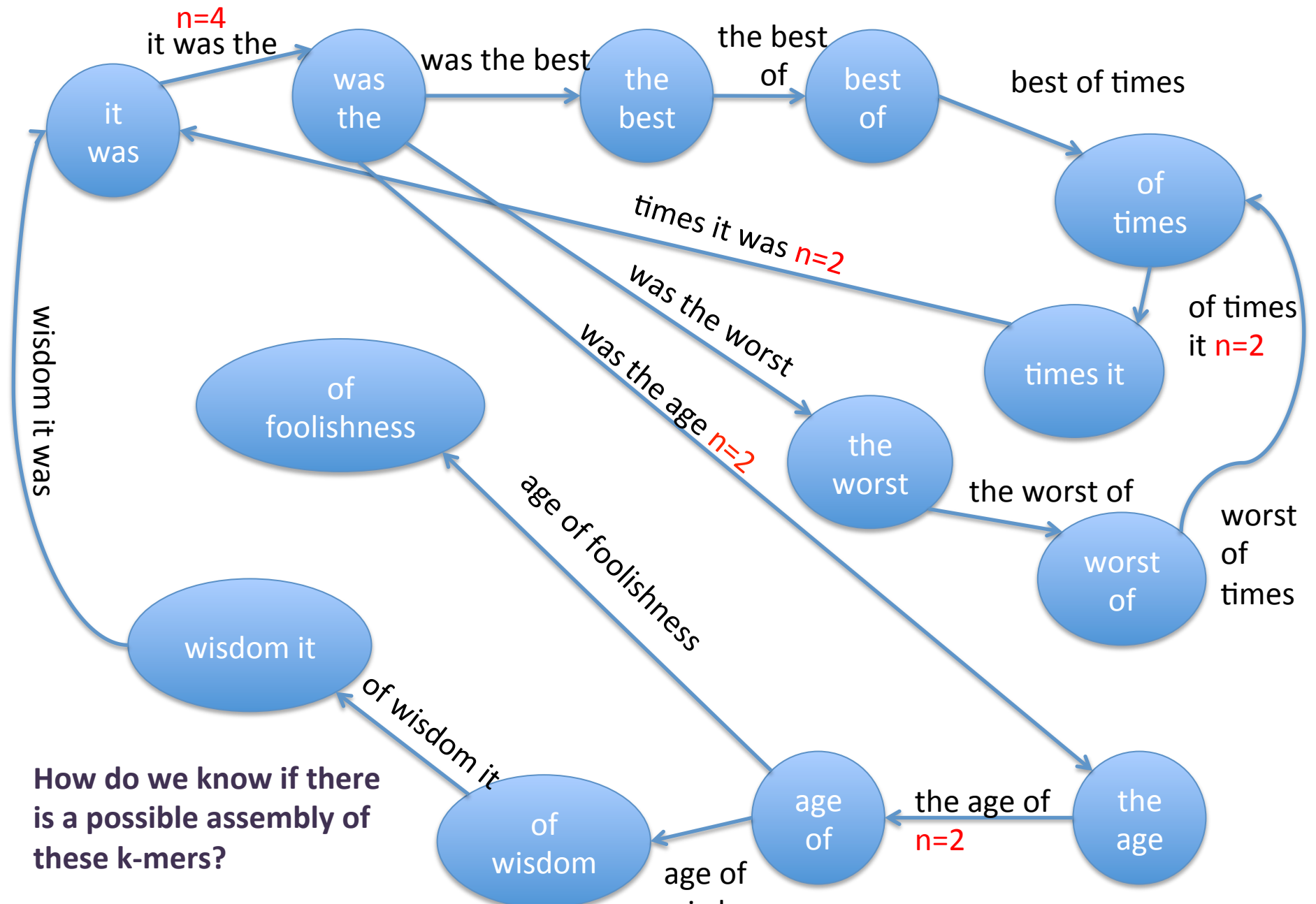
it was the	age of foolishness	of Light it
was the best	of foolishness it	Light it was
the best of	foolishness it was	season of Darkness
best of times	was the epoch	of Darkness it
of times it	the epoch of	Darkness it was
times it was	epoch of belief	was the spring
was the worst	of belief it	the spring of
the worst of	belief it was	spring of hope
worst of times	epoch of incredulity	of hope it
was the age	of incredulity it	hope it was
the age of	incredulity it was	was the winter
age of wisdom	was the season	the winter of
of wisdom it	the season of	winter of despair
wisdom it was	season of Light	

What are all the 2-mers?

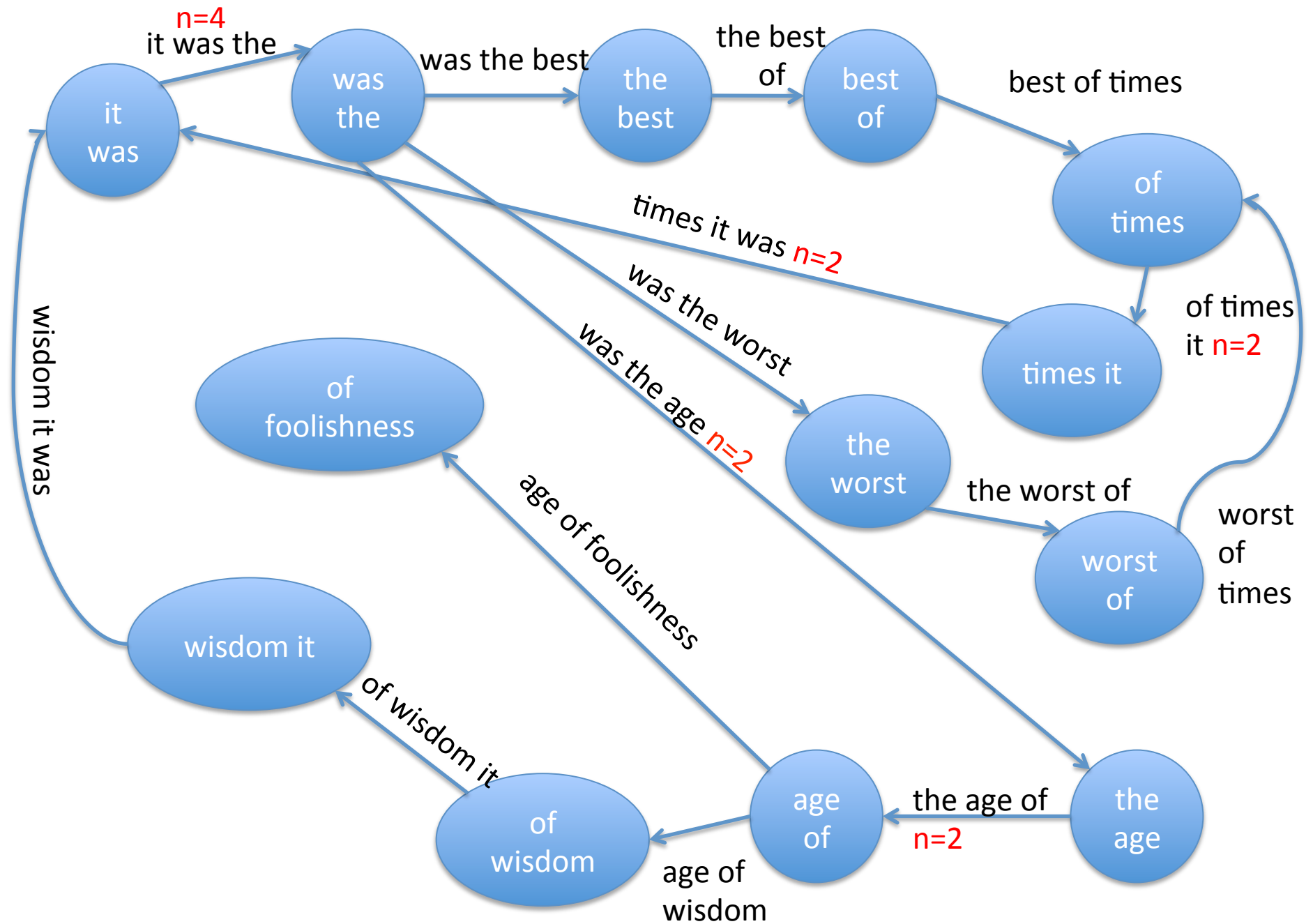
It was
was the
the best
best of
of times
times it
the worst
worst of
the age
age of
of wisdom

wisdom it
of foolishness
foolishness it
the epoch
epoch of
of belief
belief it
of incredulity
incredulity it
the season
season of

of Light
Light it
of Darkness
Darkness it
the spring
spring of
of hope
hope it
the winter
winter of
of despair



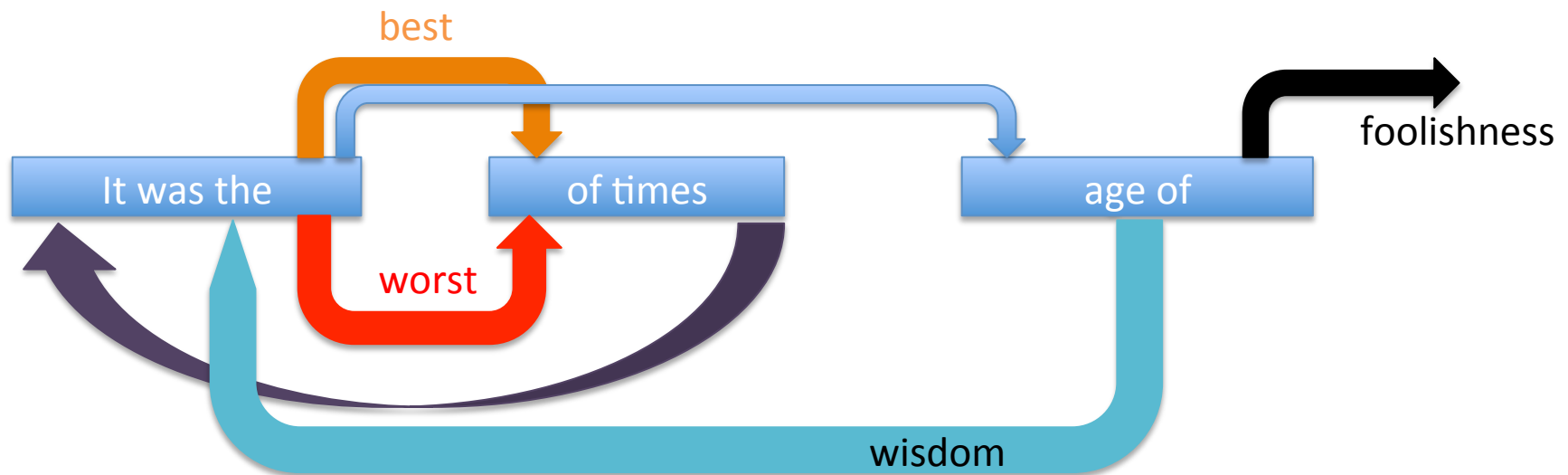
All nodes except beginning and end have equal indegrees and outdegrees



It was the best of times it was the worst of times it was the age of wisdom it was the age of foolishness

It was the worst of times it was the best of times it was the age of wisdom it was the age of foolishness

It was the age of wisdom it was the best of times it was the worst of time it was the age of foolishness



Other permutations that begin with it was and end with of foolishness

How determine what order these phrases go in?

Mate-Pairs

16 word long fragments, we have the beginning and end of each, with the end backwards.

It was the ... age the was of wisdom it ... was it belief
the epoch of ... Darkness of season it was the ... age the was
of foolishness it ... it incredulity of
was the season ... of spring the

How do you align these?

It was the best of times it was the worst of times it was the age of wisdom it was the age of foolishness it was the epoch of belief it was the epoch of incredulity it was the season of Light it was the season of Darkness it was the spring of hope it was the winter of despair

it was the _____ was the age
_____ it was the _____ was the
age
of foolishness it _____ of incredulity it
_____ of wisdom _____
_____ belief it was
_____ the epoch of _____
_____ season of Darkness
_____ was the
season _____ the spring of

How did these help?

What about the long reads?

How did you use these?

Which was more useful, mate-pairs or long reads?

Genome Assemblers

- Most use a De Bruijn graph assembly

Challenges

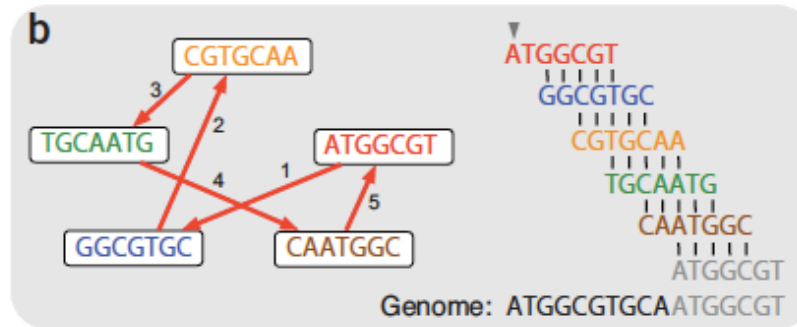
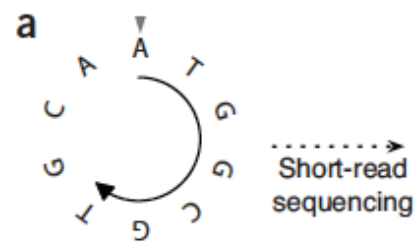
- Need a lot of data
 - 5-6 fold coverage in short reads
 - Mate-pairs or long reads
- Need a lot of memory
 - Building large graphs then traversing them to build up contigs
- Many designed for short reads so don't fully take advantage of longer reads

Creating DeBruijn graphs for genomes

- We don't use full length reads to assemble the graph.
 - Why?
 - Did you have all possible 4-mers from phrase in your library?

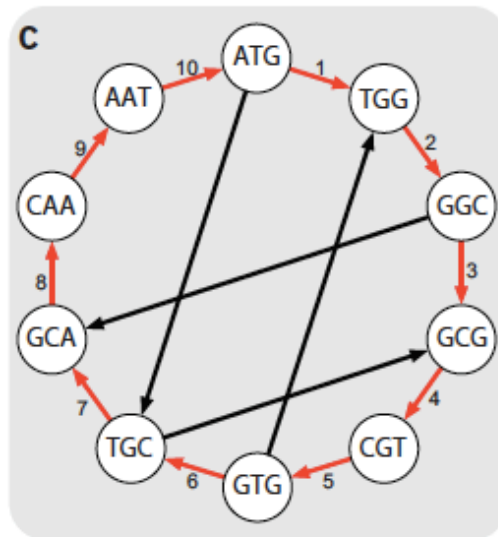
Creating DeBruijn graphs for genomes

- We don't use full length reads to assemble the graph.
 - Need all possible k-mers to be represented in graph, so breaks reads into small chunks to represent all possible k-mers
 - Usually 21-100 bp k-mers used

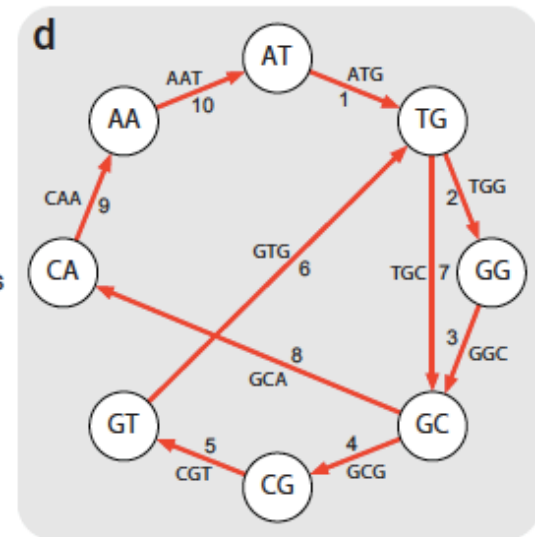
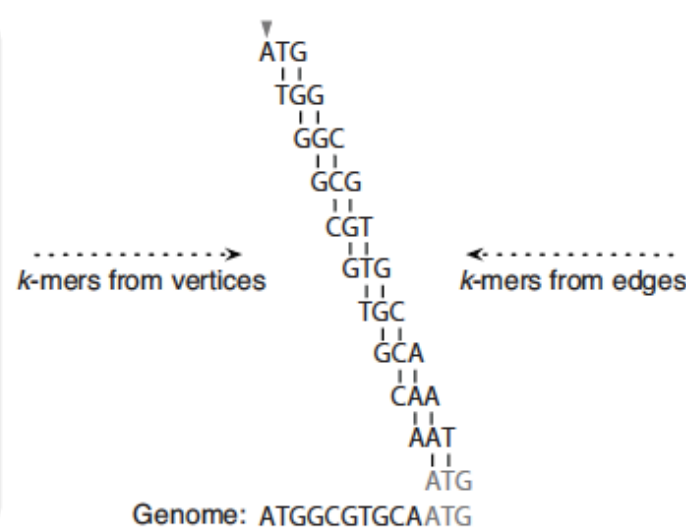


Vertices are k -mers
Edges are pairwise alignments

Vertices are $(k-1)$ -mers
Edges are k -mers



Hamiltonian cycle
Visit each vertex once
(harder to solve)



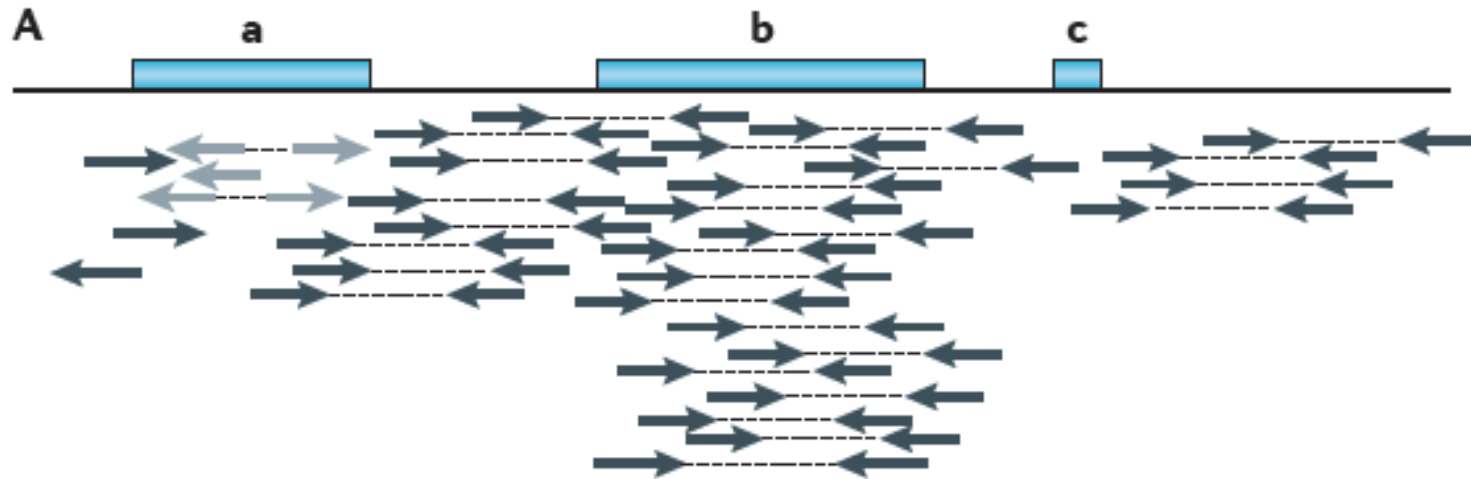
Eulerian cycle
Visit each edge once
(easier to solve)

Hamiltonian cycle is NP-
complete

How do we know we have correctly
assembled the genome?

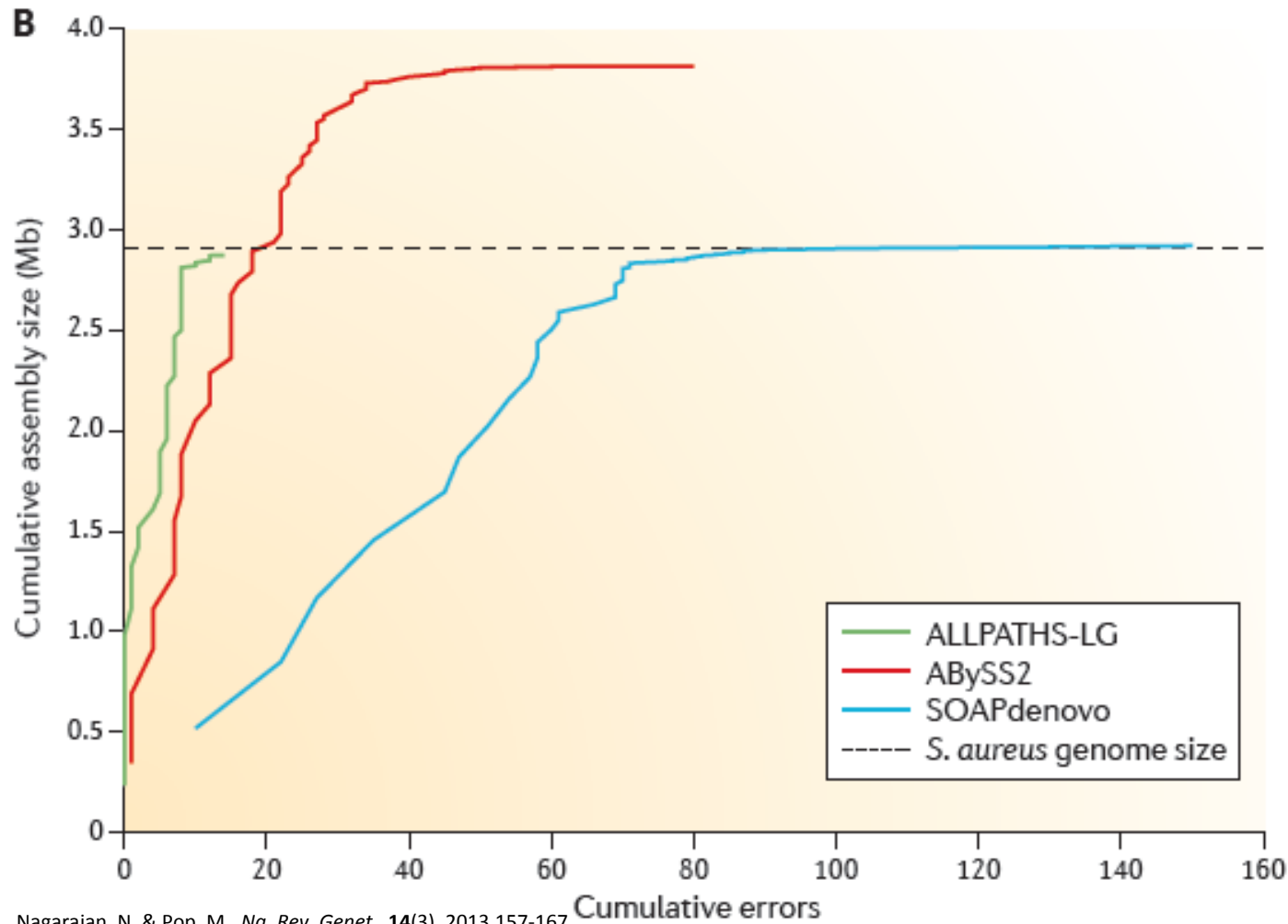
How do we know we have correctly assembled the genome?

- Hard to know – **no ground truth**
- Use measures that correlate with correctness
 - Total size
 - Contiguity (N50)
 - Mate-pair alignment orientation
 - All regions have similar coverage
 - when does this not apply?
 - Similarity to similar genomes
 - Matches to transcriptome data



Madhavan, N. & Pop, M., *Nu. Rev. Genet.*, **14**(3), 2013, 157-167.

If mate pairs misalign, what might be going on?



Nagarajan, N. & Pop, M., *Na. Rev. Genet.*, **14**(3), 2013,157-167.

Our measures of genome assembly don't always correlate with correctness