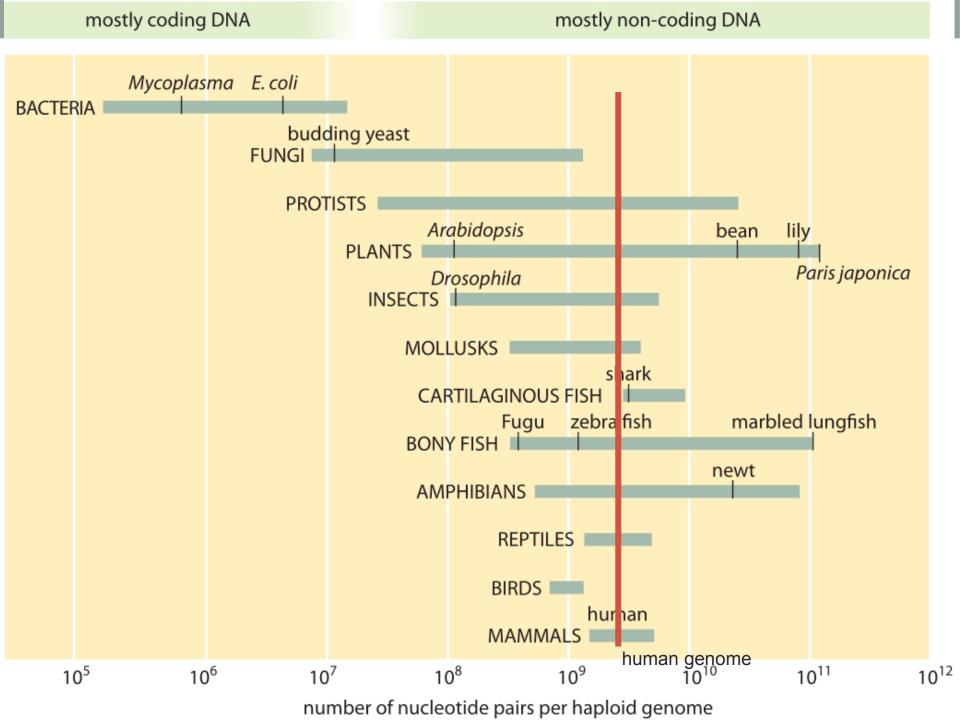
# GENOME SEQUENCING AND ASSEMBLY

BIO 300/CMPSC 300 Spring 2016

## What is a Genome?

- an organism's complete set of DNA, including all of its genes, regulatory regions, non-coding regions, etc.
- an organism's complete set of genetic instructions



	Organism	Number of genes in the genome
3	Myscoplasma genitalium	517
	Saccharomyces cerevisiae	6,275
O	Arabidopsis thaliana	~ 20,000
	Caenorhabditis elegans	19,099
8	Haemophilus influenzae	1,743
	Drosophila melanogaster	13,601
A Park	Neisseria meningitdis	2,158
	Homo sapiens	20,000- 25,000

# Genome Projects

- Goals:
  - Determine complete genome sequence of an organism
  - Annotate protein-coding genes and other important genomeencoded features

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#### Projects:

Over 15,000 genome projects in progress or completed

## Genome Projects

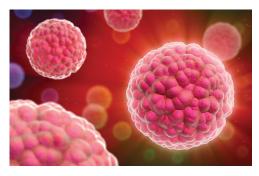
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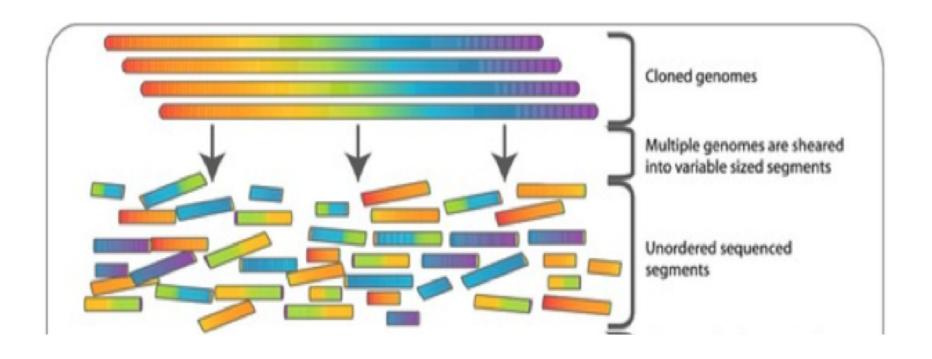
**Cancer Genomics** 



#### **Shotgun Metagenomics**



# Genome Sequencing



## Tale of Two Cities – Charles Dickens

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, we had everything before us, we had nothing before us, we were all going direct to Heaven, we were all going direct the other way - in short, the period was so far like the present period, that some of its noisiest authorities insisted on its being received, for good or for evil, in the superlative degree of comparison only.

## Shredded Book Reconstruction

- Dickens accidently shreds first printing of Tale of Two Cities
  - first printing = 5 copies

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### Shredded Book Reconstruction

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  - shredding was random (can cut between different words in each copy)
  - always 5 words per fragment

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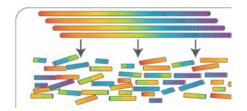
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5 copies x 138, 656 words/5 words per fragment = 138k fragments

All short fragments are mixed together



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Repeats pile up – actual placement of each individual fragment unknown

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Repeats pile up – actual placement of each individual fragment unknown

Repeats can cause ambiguity and prevent proper assembly

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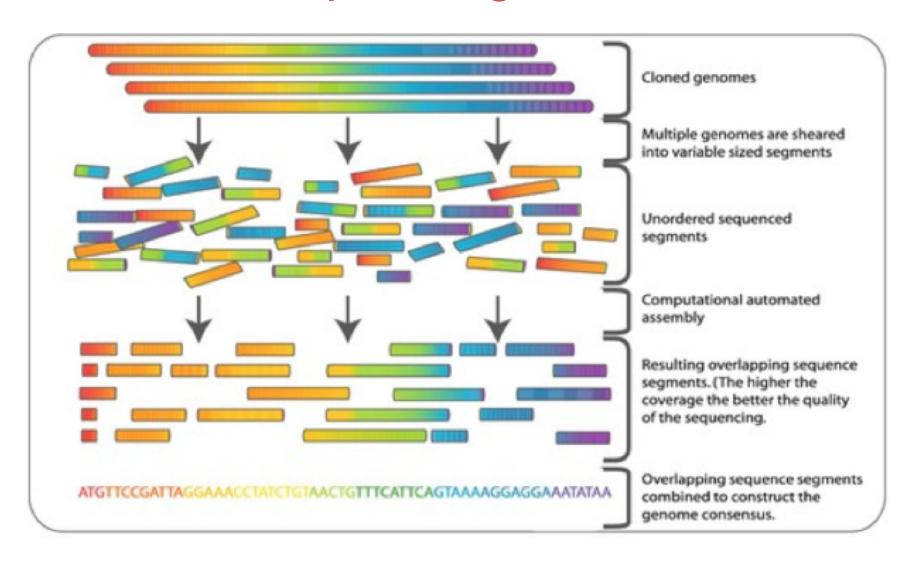
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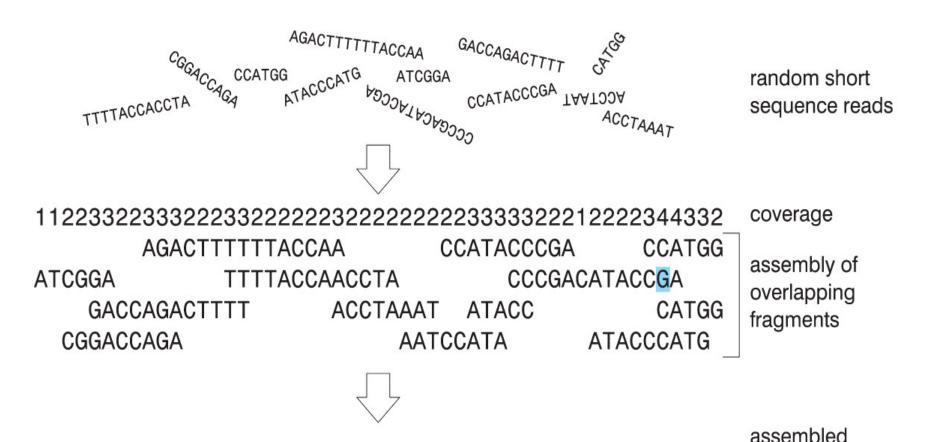
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## Genome Sequencing



## Coverage



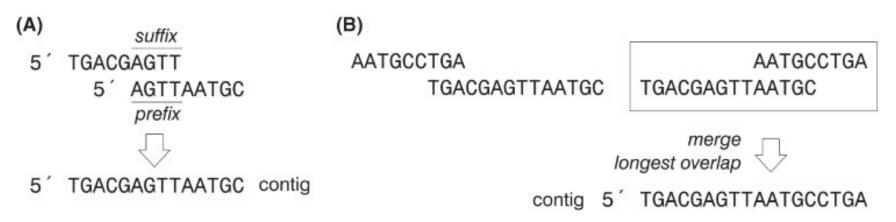
contig sequence

ATCGGACCAGACTTTTTTACCAACCTAAATCCATACCCGACATACCCATGG

## Finding the Largest Overlap

- Consider two fragment assembly:
  - If there is more than one overlap, choose the longest overlap
  - Assume the sequences are not identical
  - Assume neither sequence is a substring of the other
  - The longest **possible** overlap is length of the shorter sequence-1

# Finding the Largest Overlap



- Start with s1 and s2
- 2. n = size of the smallest sequence 1
- Compare n suffix/prefix characters from s1 with n prefix/suffix characters s2
- 4. Count matching bases in the prospective overlap region. If the number of matches = n, found the largest overlap
- 5. If the number of matches < n, n = n-1 If n=0 no overlap, go to step 3

## Finding the Largest Overlap

 Removing assumptions of identical subsequences and substrings:

• set the initial **n** to the length of the sequence rather than the length of the sequence – 1.

# Dealing with Noisy Sequencing Data

- Sequencing errors
- Ambiguities leading to incorrect base-calling
- Modify the algorithm so that the overlap exceeds some threshold value (instead of being perfect match)
  - Check if the number of matching bases is threshold
     value x n
  - With the threshold value being between 0 and 1

# Assembling a Contig

Table 8.3 Overlaps for a hypothetical set of sequence reads.

Fragments	Overlaps (Length)
1. TACCTTG	2 (3), 3 (1), 4 (1), 7 (1)
2. TTGAT	1 (1), 3 (3)
3. GATATGG	4 (2), 7 (1)
4. GGAG	3 (1), 7 (1)
5. CTCTA	1 (2), 6 (3)
6. CTAGT	1 (1), 2 (1)
7. GCTCT	1 (1), 2 (1), 5 (4), 6 (2)

## Assembling a Contig: graph representation

