

Signs of a hospital outbreak

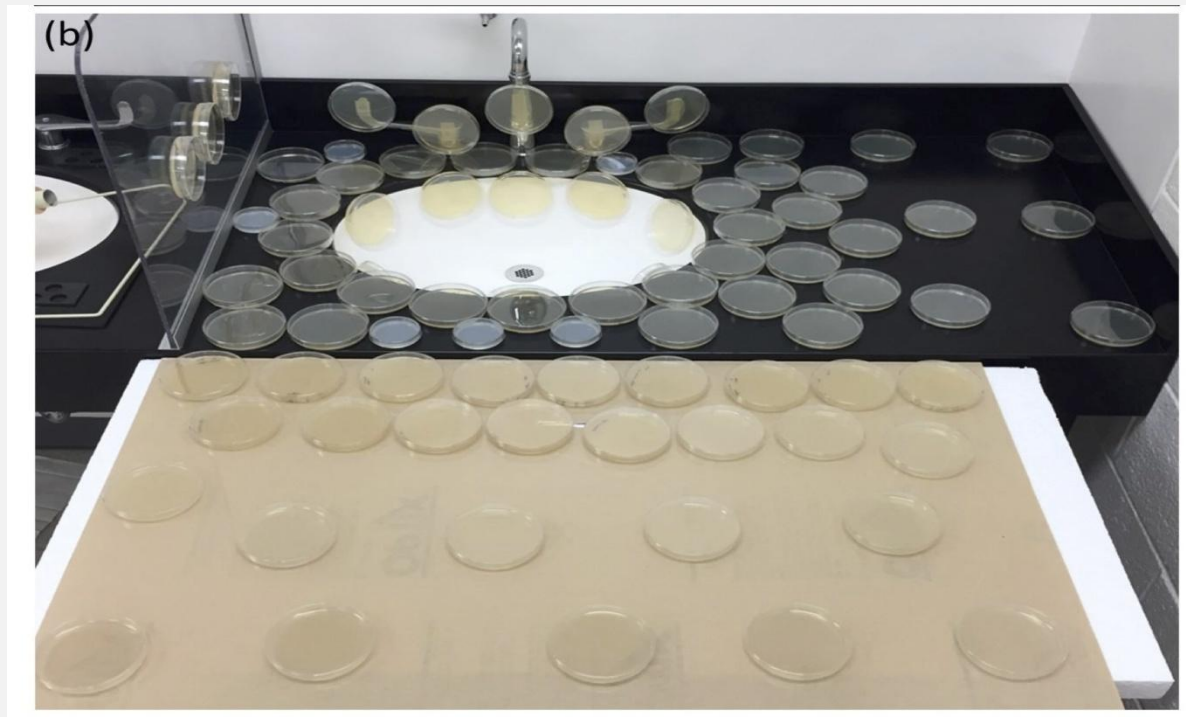
- An increase in the occurrence of a complication or disease above the background rate (e.g. blood poisoning, pneumonia)
 - A rare infection occurs (e.g. VIM, IMP producing bacteria)
 - Many episodes of common infections (MRSA surgical site infections)

Detect

- **Urine samples, rectal swabs, blood specimens**
 - This often happens routinely
- **Outbreaks have been linked to medical devices and environmental sources**
 - Catheters
 - Endoscopes
 - Sinks

The Strange Case of the Pipe-Climbing Bacteria

- Bacteria form biofilm (cells sticking together)
- Biofilms adhere to a surface
- Biofilm can climb the pipework at the extraordinary rate of one inch per day



Stop the outbreak!

- **Disinfect the sinks**
 - Fill bathroom sink with warm water and a cup of bleach or hydrogen peroxide
 - Leave it for 10 minutes and drain

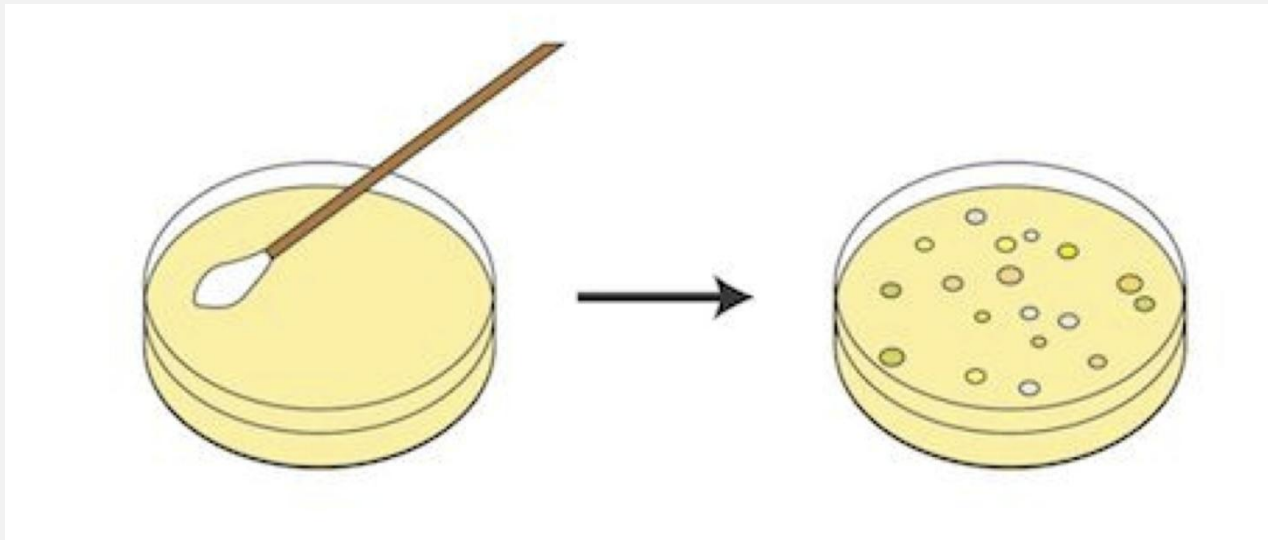
- **Clean the scopes**
 - Cleaning, disinfecting, and drying to ensure patient safety
 - Culture scope before use

- **Wash your hands often!!**
 - Healthcare workers, patients and visitors should wash hands
 - Use alcohol (vs. antibacterial soap)

How do we determine the source of the outbreak?

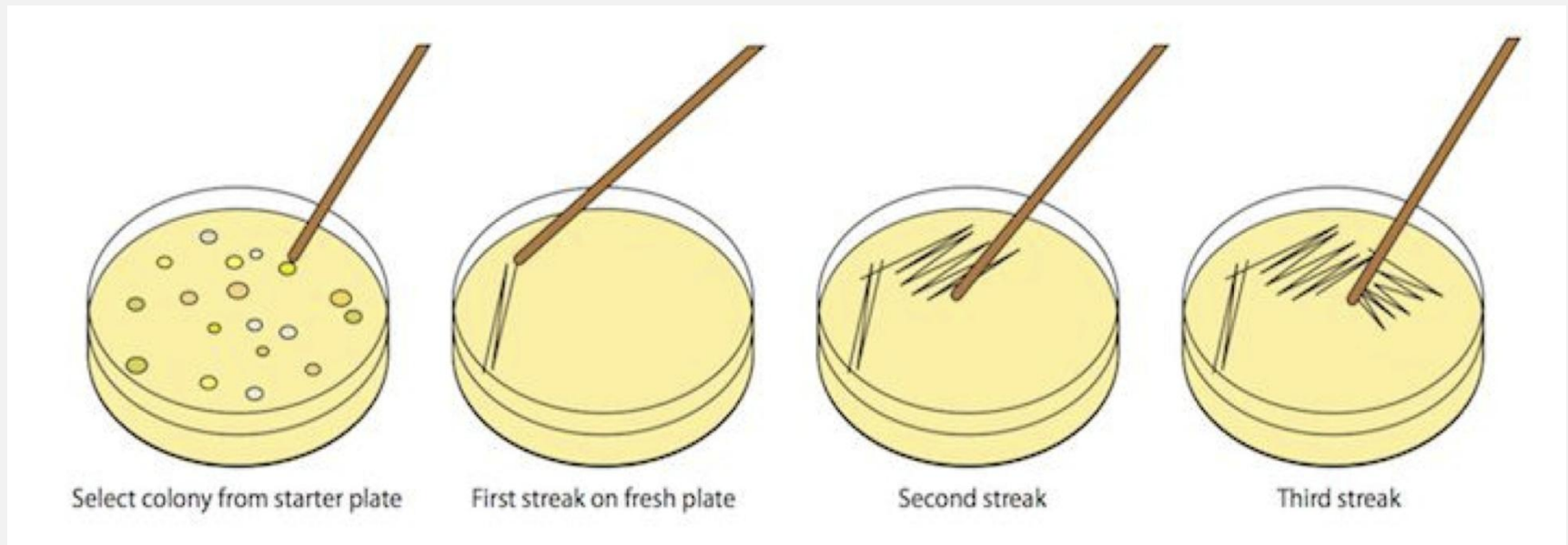
- **WGS (Whole Genome Sequencing)**
- **This can help us determine person-to-person / environmental source-to-person transmission**
- **But first we need to isolate the bacteria and get some DNA!**

Isolating bacteria: Swab sample onto starter plate



- Some microbes will grow, others will not

Pick a colony and streak it out



Colony is dominated by one organism or species

Pure colonies grow



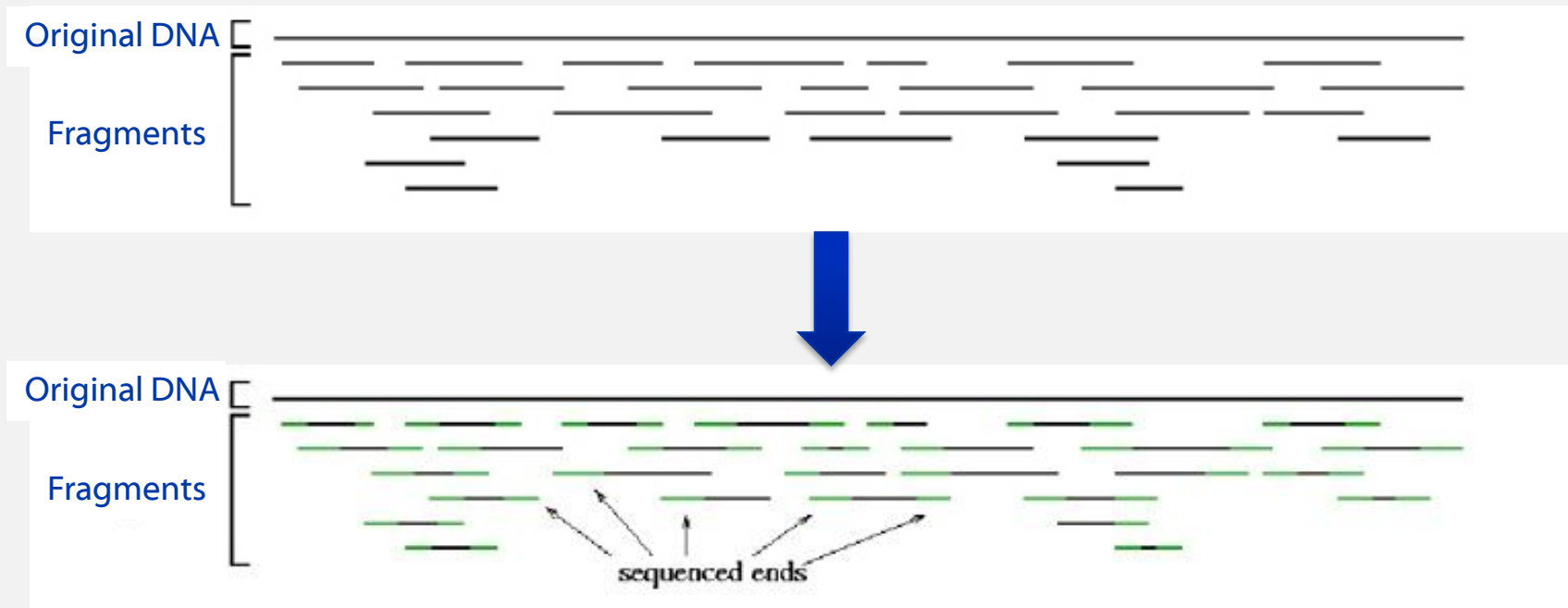
- Each streak is a dilution
- Final streaks assumed to be pure



WGS (Whole Genome Sequencing)

- Sequencing
 - Assembly (solve the jigsaw puzzle)
 - SNP calling
 - SNP phylogenetic trees
-
- These are the methods for your project

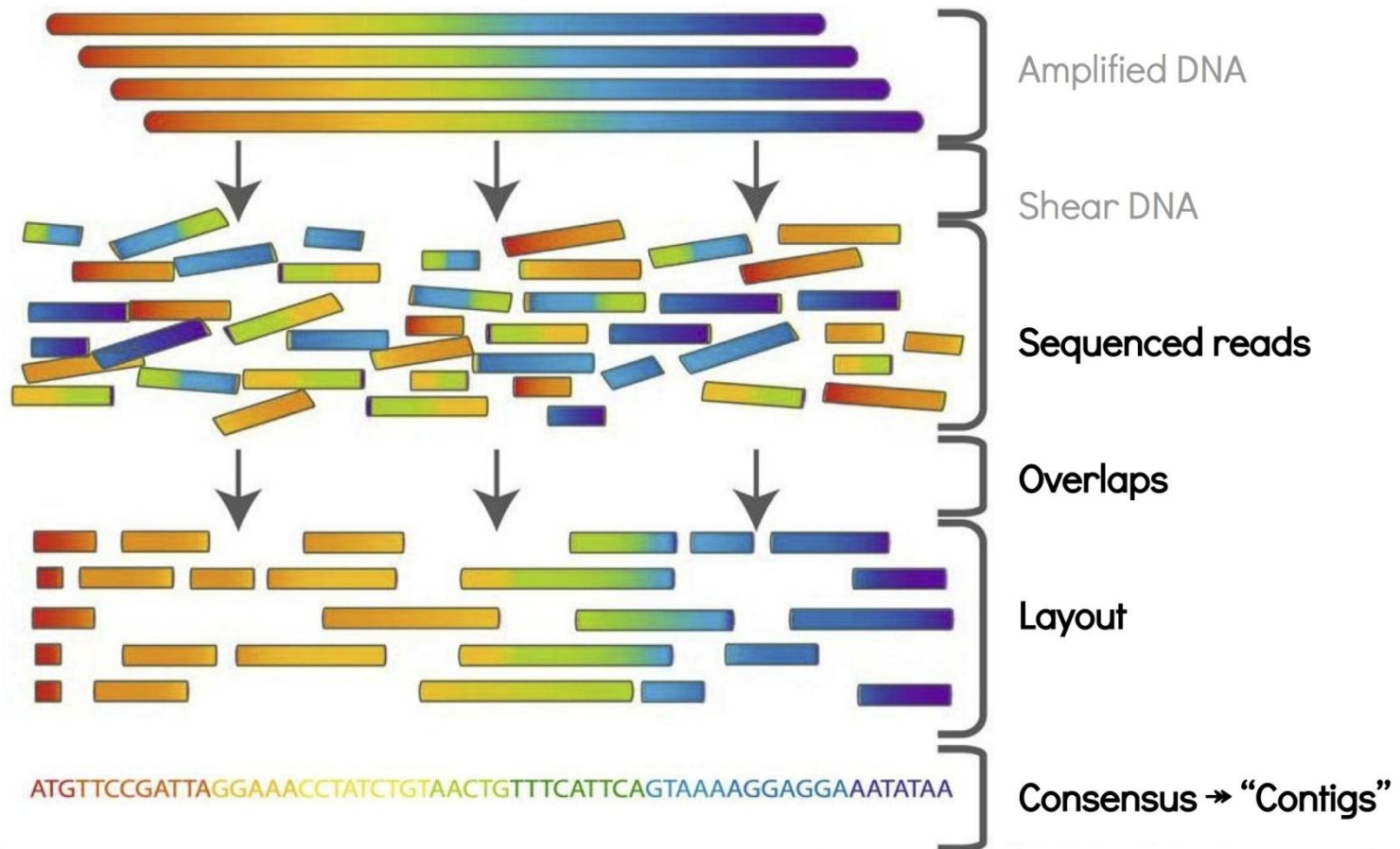
Sequencing in brief



Genome assembly: an analogy



Genome assembly: Not an analogy



Sequence files – the FASTA format

Start symbol

Sequence ID
(no spaces)

Sequence description
(spaces allowed)

>NM_006361.5 Alcohol dehydrogenase (ADH) EC 1.1.1.1

ATGTGCGTCAAGACGGCCGTGCTGAGCGAATGCAGGCGACTTGCGAGCTGGGAGCGAT
TTGGATTCCCCCGGCCTGGGTGGGGAGAGCGAGCTGGGTGCCCCCTAGATTCCCCGCC
CCCGGCCGACCCTCGGCTCCATGGAGCCCGGCAATTATGCCACCTTGGATGGAGCCAA
GGATATCTGGGAGCGGGAGGGGGGCGGAATTGA

The sequence
(usually 60 letters per line)

The diagram illustrates the FASTA format with three labels and arrows pointing to their respective parts in a sample entry. The 'Start symbol' label points to the green '>' character. The 'Sequence ID (no spaces)' label points to the red 'NM_006361.5'. The 'Sequence description (spaces allowed)' label points to the blue 'Alcohol dehydrogenase (ADH) EC 1.1.1.1'. Below these is a multi-line DNA sequence in brown. An arrow points from the text 'The sequence (usually 60 letters per line)' to the sequence lines.

Look for differences

SNP	Deletion	Reference
		AGTCTGATTAGCTTAGCTTGTAGCGCTATATTAT
		AGTCTGATTAGCTTAGAT
		ATTAGCTTAGATTGTAG
		CTTAGATTGTAGC-C
		TGATTAGCTTAGATTGTAGC-CTATAT
		TAGCTTAGATTGTAGC-CTATATT
		TAGATTGTAGC-CTATATTA
		TAGATTGTAGC-CTATATTAT
Reads		

SNP fasta file

- Input for building your SNP tree

	SNP 1	SNP 2	SNP 3
1:	acggtta g ctacaattattttaaa c gggaggagggatttttattaacca g atgtg		
2:	acggtta t ctacaattattttaaa c gggaggagggatttttattaacca a atgtg		
3:	acggtta a ctacaattattttaaa t gggaggagggatttttattaacca g atgtg		
4:	acggtta a ctacaattattttaaa t gggaggagggatttttattaacca a atgtg		
5:	acggtta t ctacaattattttaaa t gggaggagggatttttattaacca a atgtg		
6:	acggtta t ctacaattattttaaa t gggaggagggatttttattaacca a atgtg		

Summary

- Outbreaks are caused by similar or near identical bacteria
- We use WGS to assess relatedness of collected isolates
- WGS can answer many questions (AR genes, SNPs, strain type and the list goes on)