

DATABASE SEARCHING AND MULTIPLE ALIGNMENT: INVESTIGATING ANTIBIOTIC RESISTANCE

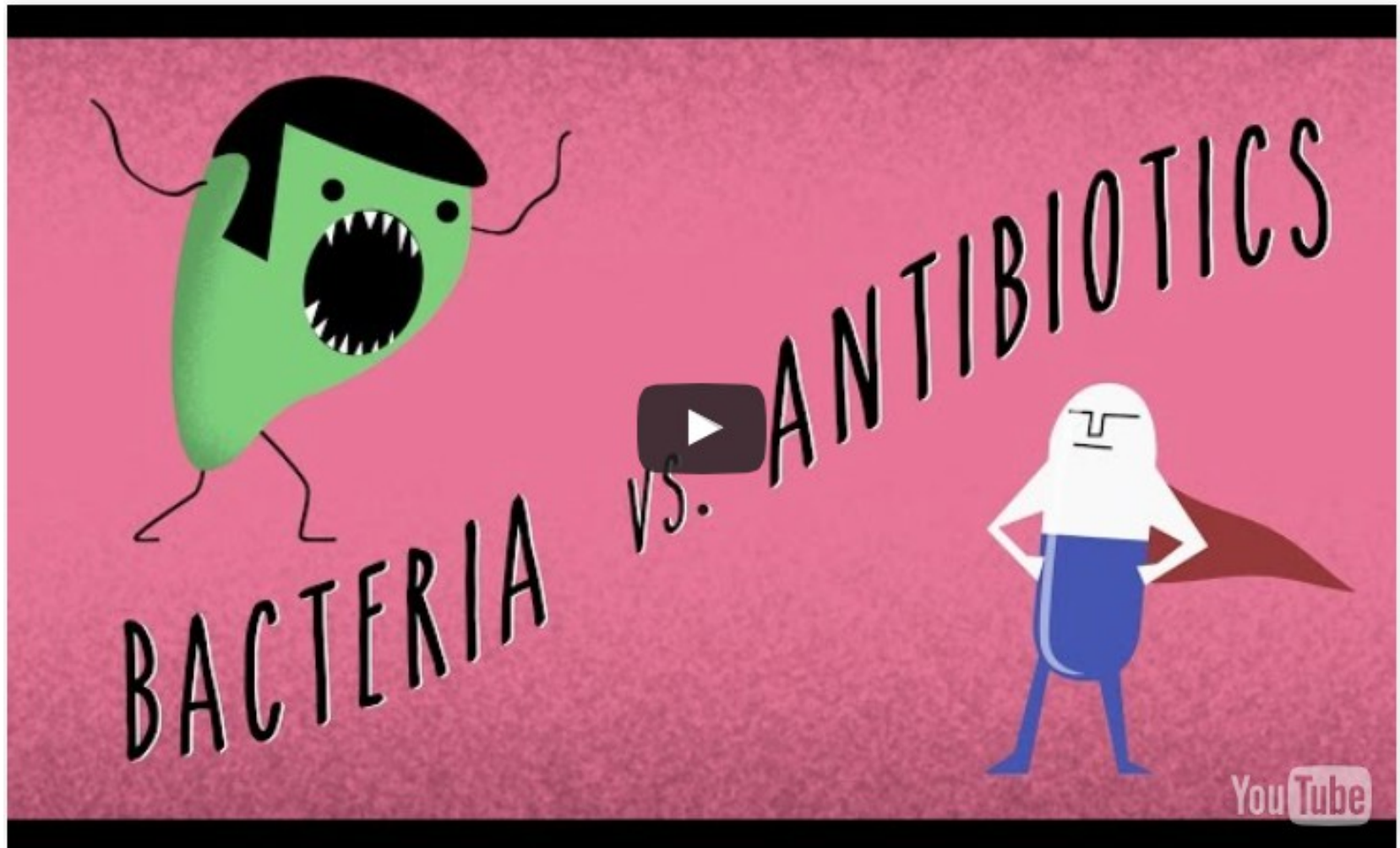
BIO 300/CMPSC 300

Dr. Kristen Webb

Spring 2016

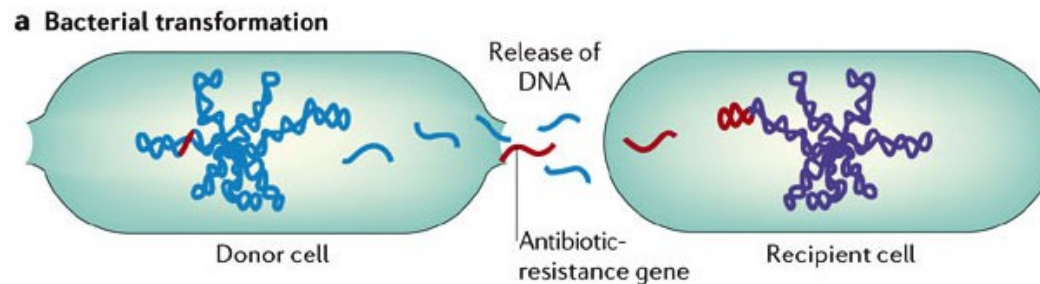
Antibiotic Resistance

<http://ed.ted.com/lessons/how-antibiotics-become-resistant-over-time-kevin-wu>



Horizontal Gene Transfer

Horizontal gene transfer (HGT) refers to the **transfer** of **genes** between organisms in a manner other than traditional reproduction.

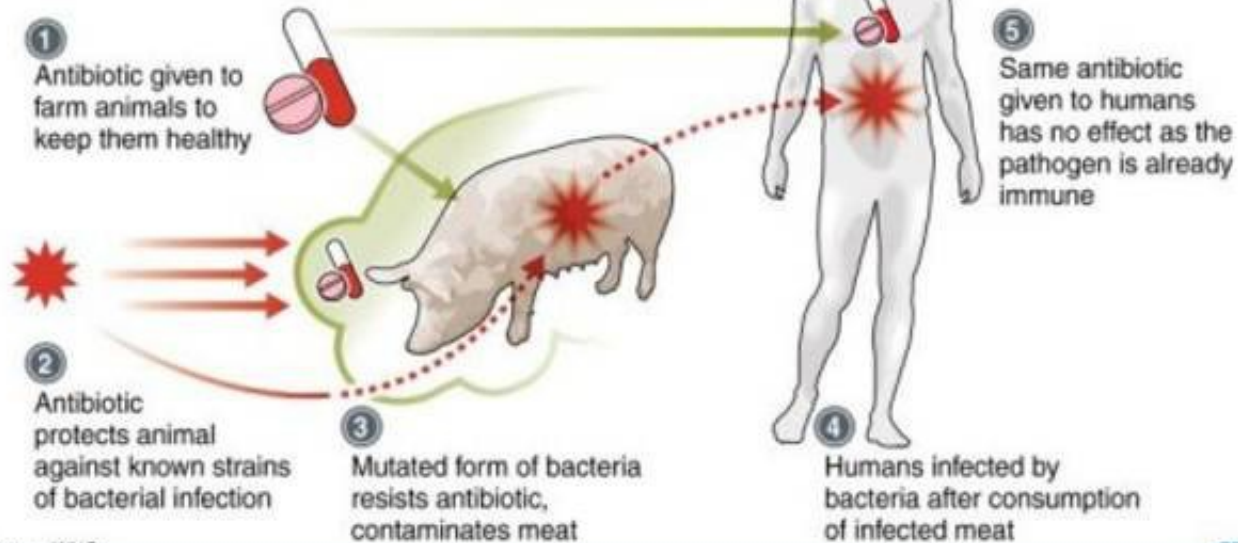


Farm-to-Fork Spread of Antibiotic Resistance

Antibiotic drug abuse

Overuse of antibiotics in agriculture is widening the spread of superbugs that are immune to common drugs

Path of resistance



Source: WHO

AFP

Farm-to-Fork Spread of Antibiotic Resistance

Salyers et al 2004

Table 1.

Prevalence of *tetQ*, *ermF*, *ermG* and *ermB* genes in colonic *Bacteroides* spp.

Isolates	<i>ermB</i> (%)	<i>ermG</i> (%)	<i>ermF</i> (%)	<i>tetQ</i> (%)
Community (pre-1970) ^a	0	0	0	32
Clinical (pre-1970) ^b	0	0	9	22
Community (1996–1997) ^a	3	8	15	81
Clinical (1980–1995) ^b	3	18	30	86

a *Bacteroides* isolates from the colon of people who were healthy and did not have a history of recent antibiotic use.

b Isolates from people with *Bacteroides* infections.

Table options ▼

BLAST: A Heuristic Approach to Database Searching

- Basic Local Alignment Search Tool
 - NCBI – DNA and protein sequence
 - Compares one sequence to database of > 100 million
 - Finds best hits (optimal alignments) in a matter of seconds
 - (would take >3 years using Needleman-Wunsch algorithm)



BLAST: A Heuristic Approach to Database Searching

query sequence: foreviltoflourishitonlyrequiresgoodmentodonothing

k-tuples ("words"):

35	...
36	men
37	ent
38	nto
39	...

threshold = 15

database sequence A:

allthat isnecessaryfor thetriumphofevil isthatgood
mendonothing

no match

database sequence B:

allthat isnecessaryforevil tosuccedisforgoodment
ito---nl---yrequires---goodment
donothing
donothing

score: 13

database sequence C:

allthatsnecessaryfor theforcesofevil towinintheworld
isfo---renough-goodmentodonothing
it-onlyrequiresgoodmentodonothing

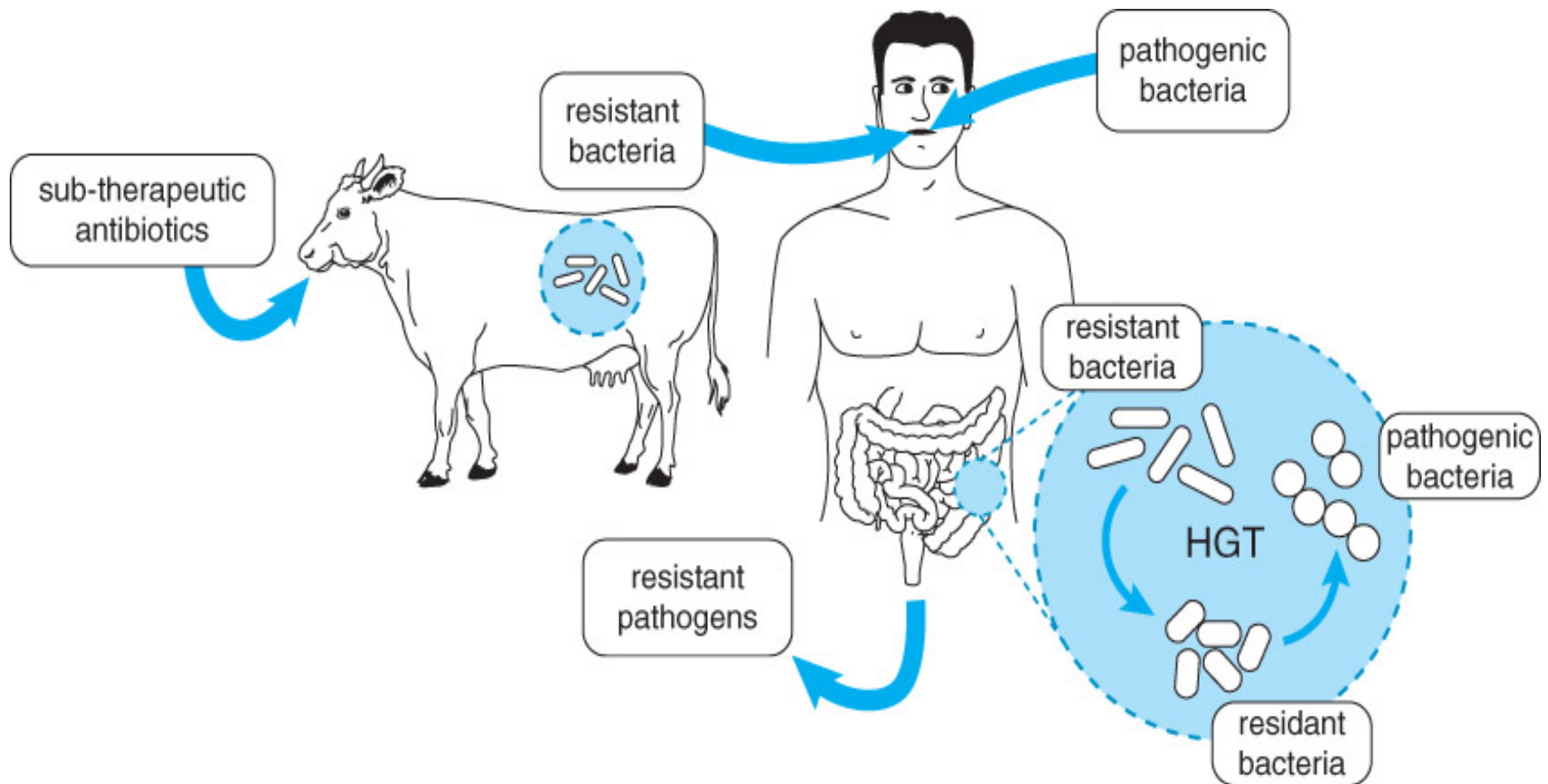
score: 17

extend initial
 match

← extend →

initial
match

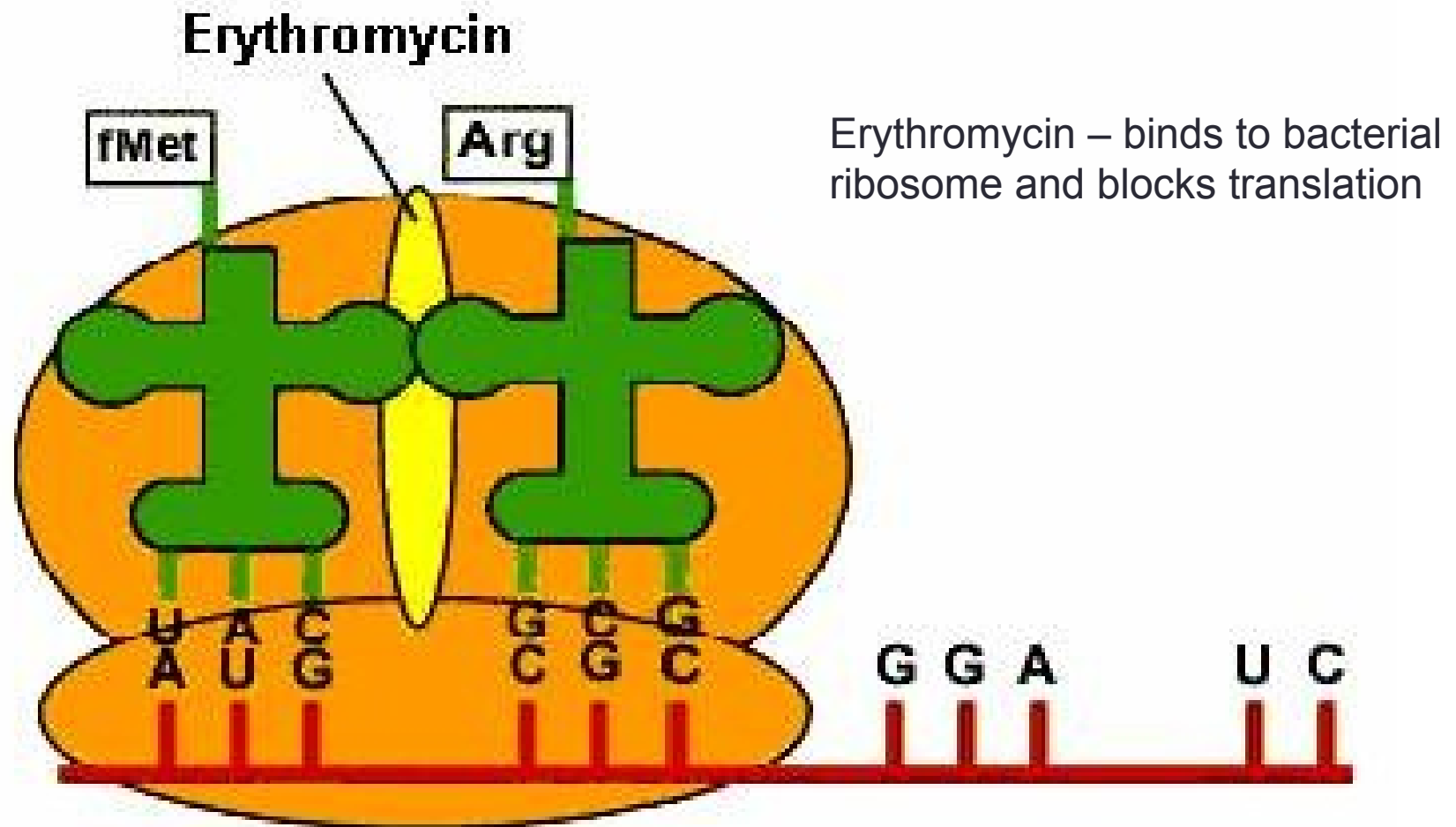
Horizontal Gene Transfer of Antibiotic Resistance



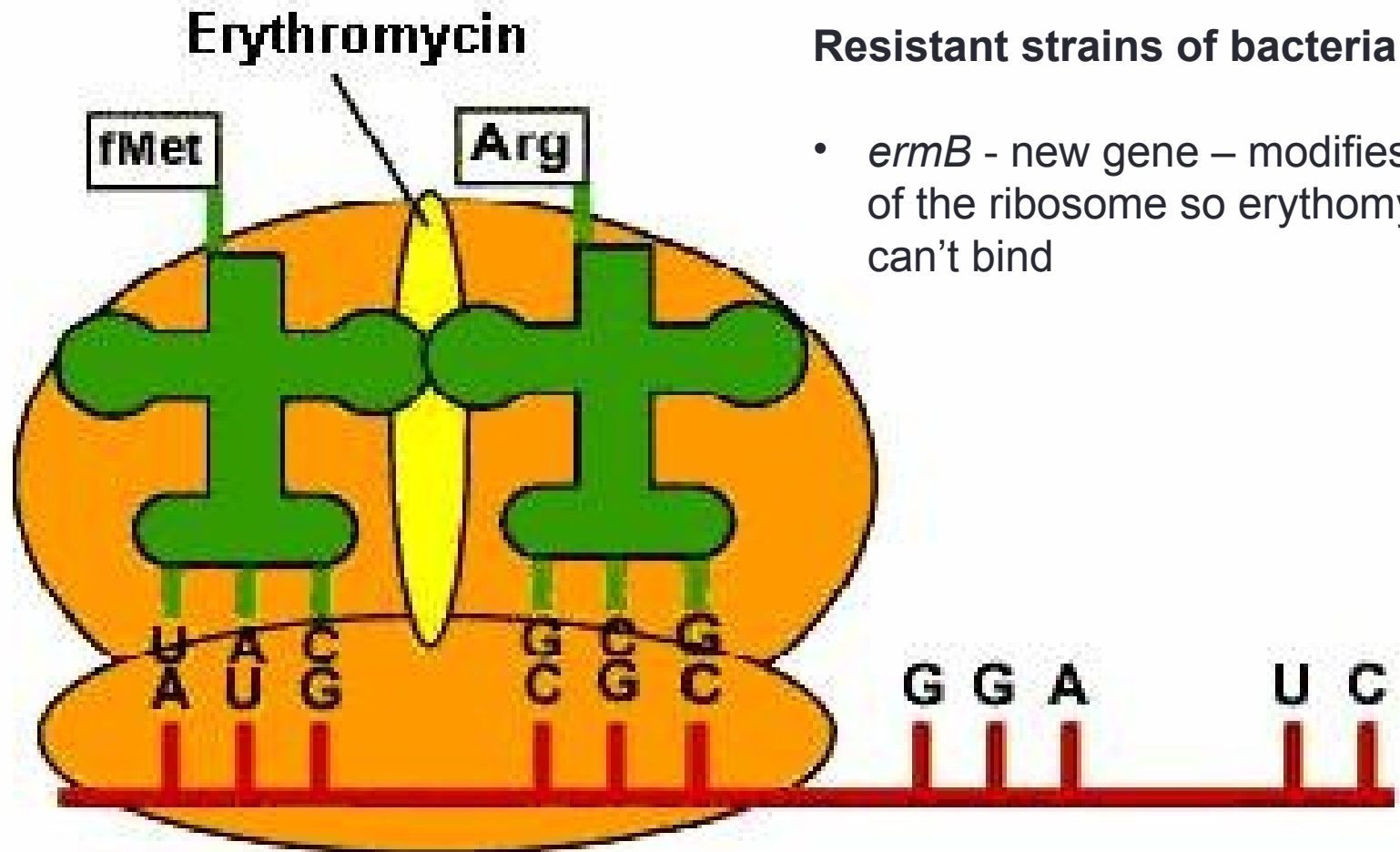
What is the likelihood that agricultural use of antibiotics is resulting in resistant human gut bacteria and/or resistant human pathogens?

- *ermB* gene

Searching for Erythromycin Resistance Genes Using BLAST



Searching for Erythromycin Resistance Genes Using BLAST



What is the likelihood that agricultural use of antibiotics is resulting in resistant human gut bacteria and/or resistant human pathogens?

- *ermB* gene – codes for a protein that methylates rRNA so erythromycin can't bind – antibiotic resistance gene
 - Generate FASTA-formatted file of diverse *ermB* genes using BLAST
 - Diverse species

Multiple Sequence Alignment: Clustal and MUSCLE

- Align a set of sequences (2 – ~2,000)
 - May find distinctly identifiable groups - evolution
 - Can create a consensus sequence: the nucleotides (or amino acids) that appear the most frequently at each position in a set of sequences

Multiple Sequence Alignment: Clustal

- Order matters

A

GTCT
G-GT

B

GTCT
G-GT
CT--

C

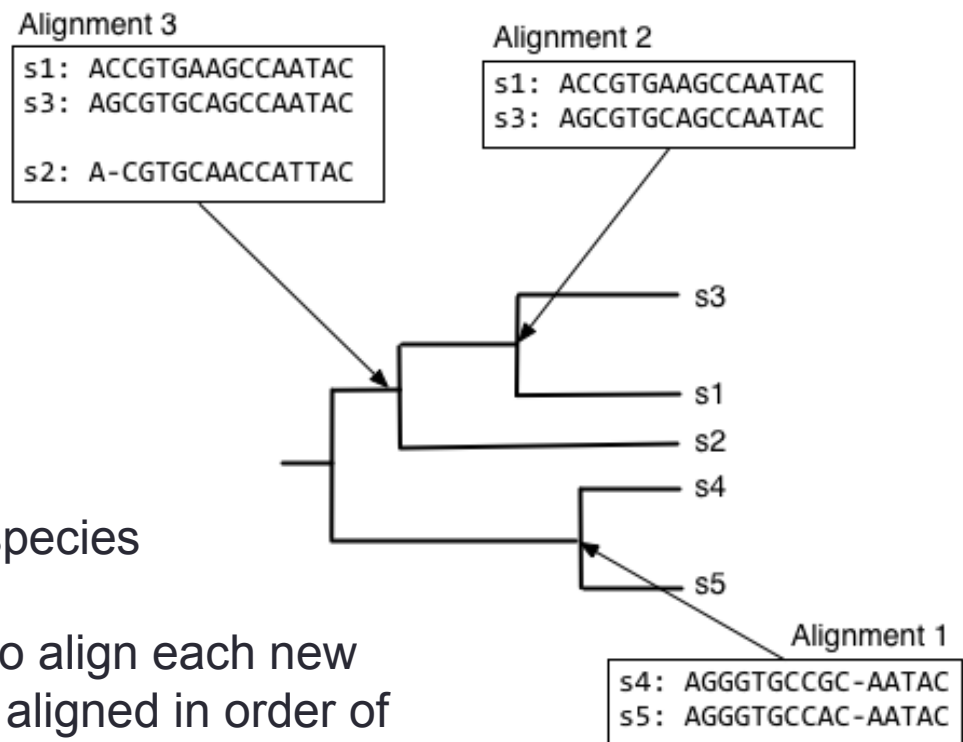
GTCT
--CT
-GGT

Solutions?

- Needleman-Wunsch $L \times M \times N$ matrix
 - Impractical for long sequences
- Heuristic
 - Progressive alignment via a guide tree

Multiple Sequence Alignment: Clustal

- Heuristic
 - Progressive alignment via a guide tree
 - Pairwise alignments, group sequences together based on similarity
 - Start with most closely related species
 - Global, pairwise alignments to align each new sequence with those already aligned in order of decreasing relatedness



Multiple Sequence Alignment: MUSCLE

MUSCLE

MUSCLE has been cited by
17,047 papers
[Google scholar](#)
Last updated 01 Mar 2016

Downloads

Documentation

Support

USEARCH

Ultra-fast sequence analysis



10 - 1,250x BLAST
1 - 1,000x CD-HIT

Popular multiple alignment software

MUSCLE is one of the most widely-used methods in biology. On average, MUSCLE is cited by seven new papers every day.

Fast, accurate and easy to use

MUSCLE is one of the best-performing multiple alignment programs according to published benchmark tests, with accuracy and speed that are consistently better than CLUSTALW. MUSCLE can align hundreds of sequences in seconds. Most users learn everything they need to know about MUSCLE in a few minutes—only a handful of command-line options are needed to perform common alignment tasks.

Papers

There are two papers. The first (NAR) introduced the algorithm, and is the primary citation if you use the program. The second (BMC Bioinformatics) gives more technical details, including descriptions of non-default options.

Edgar, R.C. (2004) MUSCLE: multiple sequence alignment with high accuracy and high throughput
Nucleic Acids Res. 32(5):1792-1797 [[Link to PubMed](#)].

Edgar, R.C. (2004) MUSCLE: a multiple sequence alignment method with reduced time and space complexity
BMC Bioinformatics, (5) 113 [[Link to PubMed](#)].

What is the likelihood that agricultural use of antibiotics is resulting in resistant human gut bacteria and/or resistant human pathogens?

- *ermB* gene – codes for a protein that methylates rRNA so erythromycin can't bind – antibiotic resistance gene
 - Generate FASTA-formatted file of diverse *ermB* genes using BLAST
 - Diverse species
 - Generate multiple alignment and tree

Summarize your findings regarding the likelihood that agricultural use of antibiotics can result in resistant human gut bacteria and/or resistant human pathogens

- Preliminary evidence to support or reject hypothesis of Horizontal Gene Transfer of *ermB*
 - Bacterial species/hosts used – why chosen/rationale?
 - Screenshot of alignment and tree
 - Evidence for or against HGT?
- Next steps to continue investigation...