Bioinformatics: the hot interdisciplinary field

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cagccagatggggggaggggtgagcgctctcccgctcaaa
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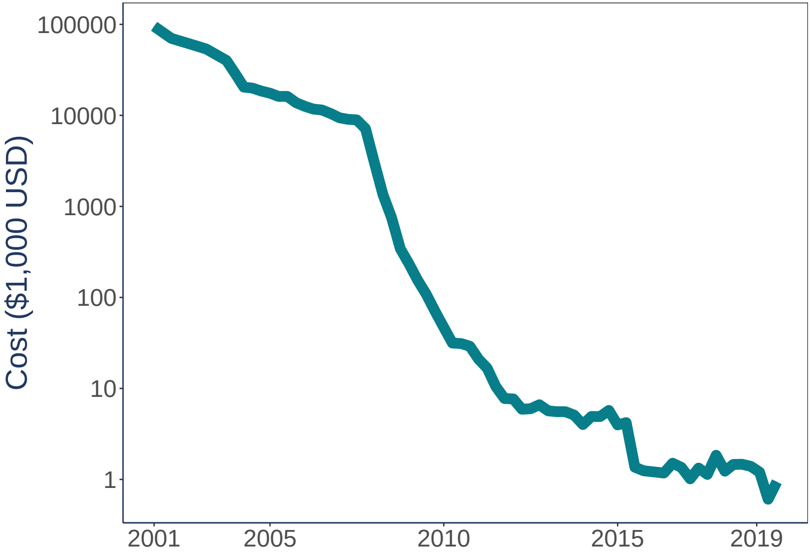
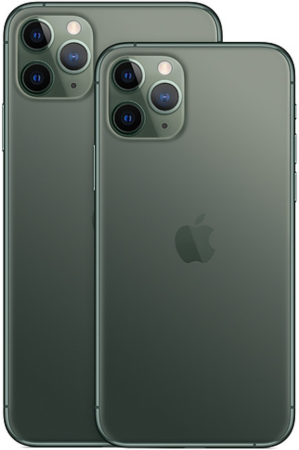
```

Sequencing Cost per Human Genome

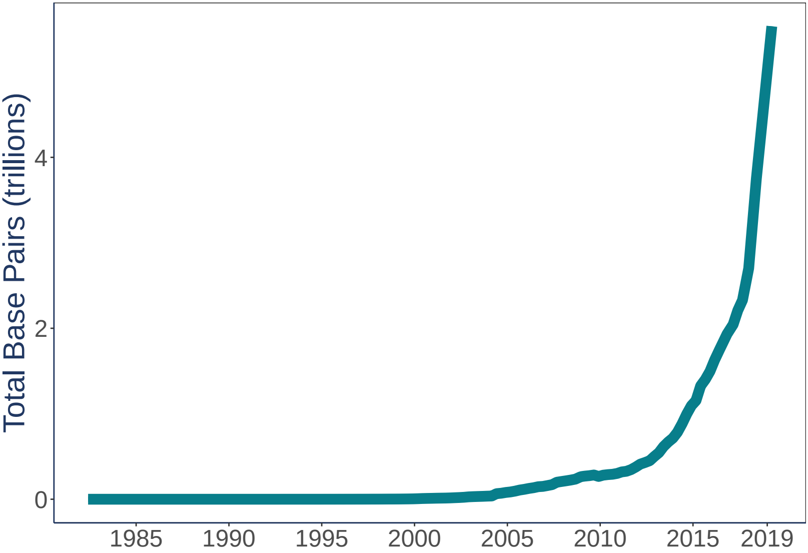


adapted from: Kris Wetterstrand, National Human Genome Research Institute

Cost to Sequence a Human Genome in 2019



EMBL Sequence Data



Data from: EMBL

How many GB is that?

All that sequence data would equal about

11,066,077,343,692 GB

How many GB is that?

$\approx$ **512GB**

22 BILLION LAPTOPS

Bioinformatics to the rescue!

What is Bioinformatics?

Bioinformatics is taking **biological data, processes and theories** and **applying** “informatics” techniques (derived from disciplines like **math, computer science, and statistics**) to understand, organize, and predict biological processes.

Broad Types of Bioinformatics

1. Data Analysis
2. Software Development
3. Modeling
4. Combination

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Generating, interpreting, and explaining any biological data

Building the Human Genome

1989: The Banbury meeting at Cold Spring Harbor Laboratory in New York before the launch of the Human Genome Project.

The Human Genome is Sequenced!

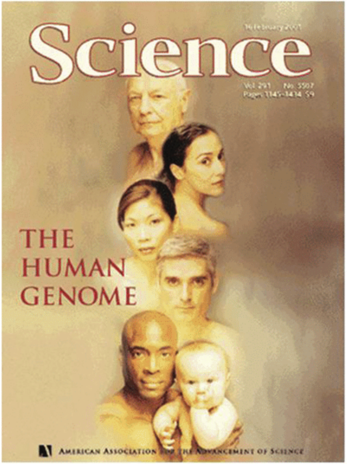
International Human Genome Sequencing Consortium Announces
“Working Draft” of Human Genome, June 2000

1. Data Analysis

The Human Genome is Sequenced...Again!

1. Data Analysis

The Human Genome is Sequenced...Again!



February 2001

1. Data Analysis

The Human Genome is Sequenced...yet AGAIN!

The Human Genome is Sequenced...yet AGAIN!

The complete Human Genome is announced by NHGRI

National Human Genome Research Institute, April 2003

But is the human genome really “Complete”?

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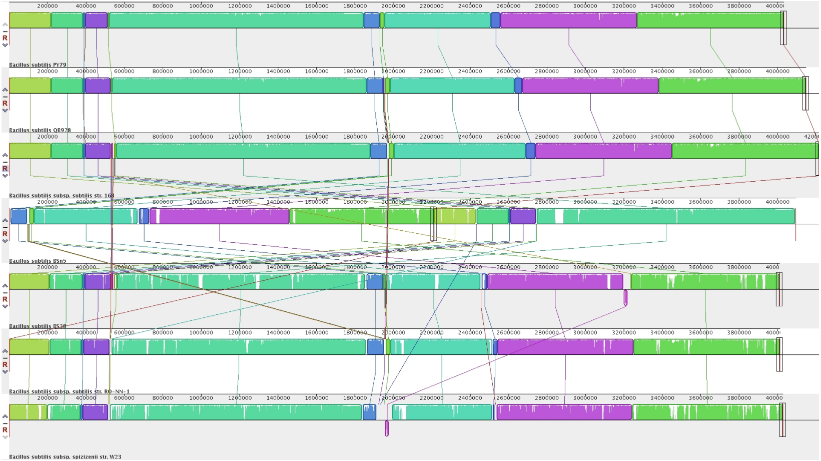
Creating bioinformatics tools for other people to use

2. Software Development

`progressiveMauve`: Whole genome alignment program

2. Software Development

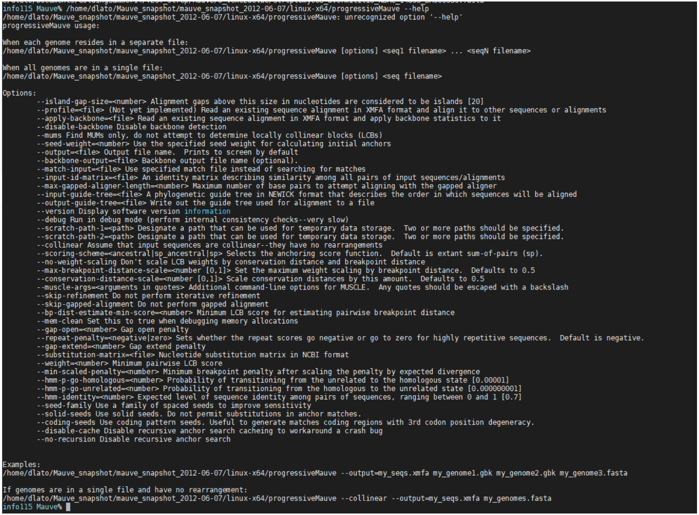
progressiveMauve: Whole genome alignment program



Darling et al. 2010

2. Software Development

progressiveMauve: Whole genome alignment program



```
info115 Mauve% /home/dlato/Mauve_snapshot/mauve_snapshot_2012-06-07/linux-x64/progressiveMauve --help
/home/dlato/Mauve_snapshot/mauve_snapshot_2012-06-07/linux-x64/progressiveMauve: unrecognized option '--help'
progressiveMauve usage:

When each genome resides in a separate file:
/home/dlato/Mauve_snapshot/mauve_snapshot_2012-06-07/linux-x64/progressiveMauve [options] <seq1 filename> ... <seqN filename>

When all genomes are in a single file:
/home/dlato/Mauve_snapshot/mauve_snapshot_2012-06-07/linux-x64/progressiveMauve [options] <seq filename>

Options:
        --island-gap-size=<number> Alignment gaps above this size in nucleotides are considered to be islands [20]
        --profile=<file> (Not yet implemented) Read an existing sequence alignment in XMFA format and align it to other sequences or alignments
        --apply-backbone=<file> Read an existing sequence alignment in XMFA format and apply backbone statistics to it
        --disable-backbone Disable backbone detection
        --mums Find MUMs only, do not attempt to determine locally collinear blocks (LCBs)
        --seed-weight=<number> Use the specified seed weight for calculating initial anchors
        --output=<file> Output file name.  Prints to screen by default
        --backbone-output=<file> Backbone output file name (optional).
        --match-input=<file> Use specified match file instead of searching for matches
        --input-id-matrix=<file> An identity matrix describing similarity among all pairs of input sequences/alignments
        --max-gapped-aligner-length=<number> Maximum number of base pairs to attempt aligning with the gapped aligner
        --input-guide-tree=<file> A phylogenetic guide tree in NEWICK format that describes the order in which sequences will be aligned
        --output-guide-tree=<file> Write out the guide tree used for alignment to a file
        --version Display software version information
        --debug Run in debug mode (perform internal consistency checks--very slow)
        --scratch-path-1=<path> Designate a path that can be used for temporary data storage.  Two or more paths should be specified.
        --scratch-path-2=<path> Designate a path that can be used for temporary data storage.  Two or more paths should be specified.
        --collinear Assume that input sequences are collinear--they have no rearrangements
        --scoring-scheme=<ancestral|sp_ancestral|sp> Selects the anchoring score function.  Default is extant sum-of-pairs (sp).
        --no-weight-scaling Don't scale LCB weights by conservation distance and breakpoint distance
        --max-breakpoint-distance-scale=<number [0,1]> Set the maximum weight scaling by breakpoint distance.  Defaults to 0.5
        --conservation-distance-scale=<number [0,1]> Scale conservation distances by this amount.  Defaults to 0.5
        --muscle-args=<arguments in quotes> Additional command-line options for MUSCLE.  Any quotes should be escaped with a backslash
        --skip-refinement Do not perform iterative refinement
        --skip-gapped-alignment Do not perform gapped alignment
        --bp-dist-estimate-min-score=<number> Minimum LCB score for estimating pairwise breakpoint distance
        --mem-clean Set this to true when debugging memory allocations
        --gap-open=<number> Gap open penalty
        --repeat-penalty=<negative|zero> Sets whether the repeat scores go negative or go to zero for highly repetitive sequences.  Default is negative.
        --gap-extend=<number> Gap extend penalty
        --substitution-matrix=<file> Nucleotide substitution matrix in NCBI format
        --weight=<number> Minimum pairwise LCB score
        --min-scaled-penalty=<number> Minimum breakpoint penalty after scaling the penalty by expected divergence
        --hmm-p-go-homologous=<number> Probability of transitioning from the unrelated to the homologous state [0.00001]
        --hmm-p-go-unrelated=<number> Probability of transitioning from the homologous to the unrelated state [0.000000001]
        --hmm-identity=<number> Expected level of sequence identity among pairs of sequences, ranging between 0 and 1 [0.7]
        --seed-family Use a family of spaced seeds to improve sensitivity
        --solid-seeds Use solid seeds. Do not permit substitutions in anchor matches.
        --coding-seeds Use coding pattern seeds. Useful to generate matches coding regions with 3rd codon position degeneracy.
        --disable-cache Disable recursive anchor search cacheing to workaround a crash bug
        --no-recursion Disable recursive anchor search


Examples:
/home/dlato/Mauve_snapshot/mauve_snapshot_2012-06-07/linux-x64/progressiveMauve --output=my_seqs.xmfa my_genome1.gbk my_genome2.gbk my_genome3.fasta

If genomes are in a single file and have no rearrangement:
/home/dlato/Mauve_snapshot/mauve_snapshot_2012-06-07/linux-x64/progressiveMauve --collinear --output=my_seqs.xmfa my_genomes.fasta
info115 Mauve%
```

Darling et al. 2010

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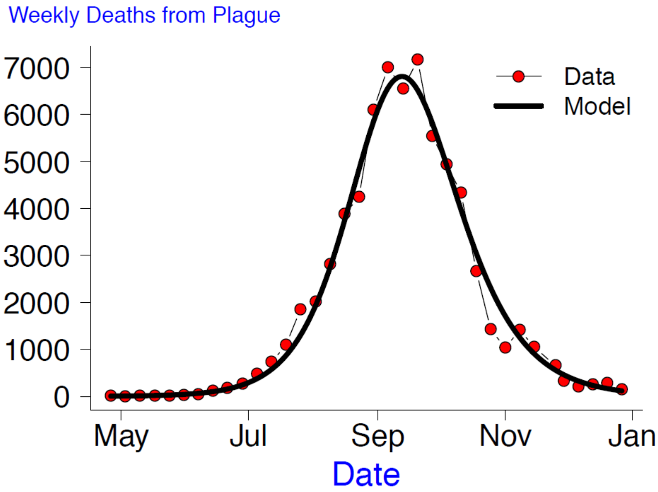
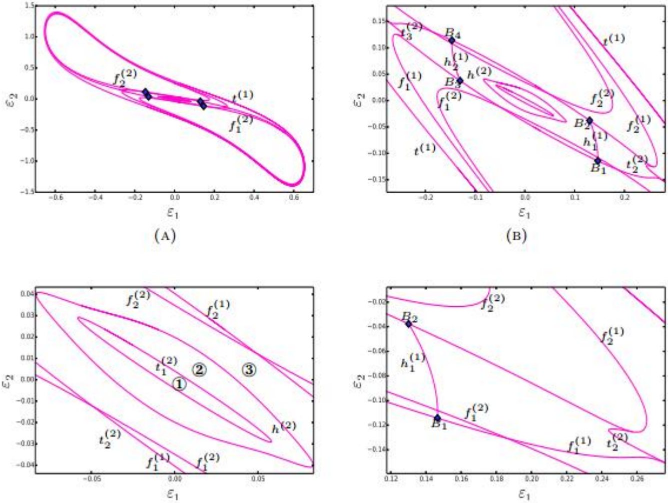
Using mathematical and statistical principals to represent and predict biological systems or data

SIR model and the Great Plague of London



3. Modelling

Bifurcation theory and predator-prey relationships



(A)

(B)

(C)

(D)

Li et al. 2018, from Gail Wolkowicz's lab at McMaster University

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4. Combination

- Modelling + Software Development
- Data Analysis + Modelling
- Data Analysis + Software Development
- Data Analysis + Modelling + Software Development

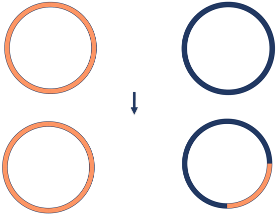
Spatial Patterns of Molecular Trends in Bacterial Genomes

(How do molecular trends change with position in the genome?)

Bacteria are bizarre!

Bacteria are bizarre!

Horizontal **G**ene **T**ransfer (**HGT**)



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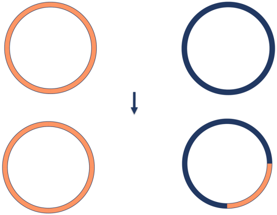
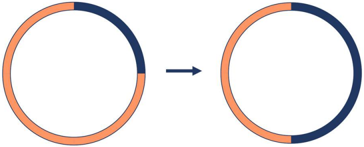
Horizontal **G**ene **T**ransfer (**HGT**)

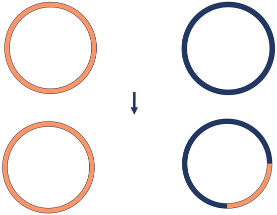


Duplication

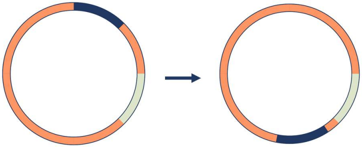


Bacteria are bizarre!

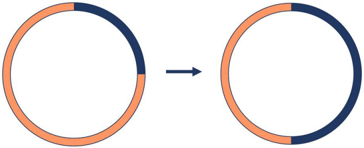
Horizontal **G**ene **T**ransfer (**HGT**)



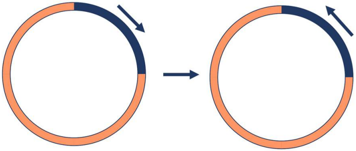
Rearrangement and Translocation



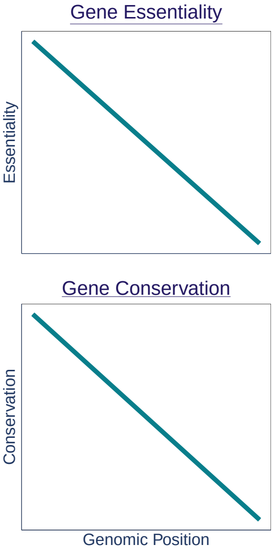
Duplication



Inversion



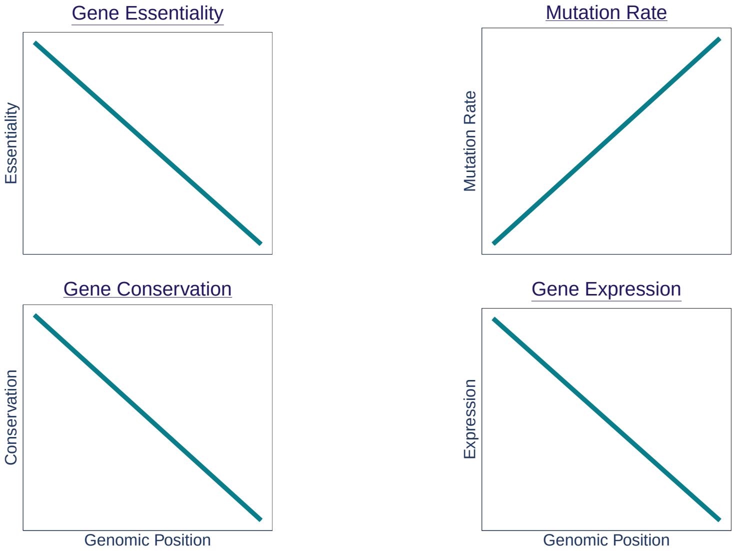
My Research: Spatial molecular trends



Gene Essentiality

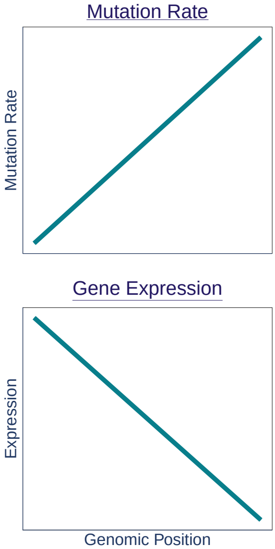
Gene Conservation

My Research: Spatial molecular trends



Couturier et al. 2006, Cooper et al. 2010, Sharp et al. 2005, Morrow et al. 2012, Cooper and Rocha 2006

My Research: Spatial molecular trends



Couturier et al. 2006, Cooper et al. 2010, Sharp et al. 2005, Morrow et al. 2012, Cooper and Rocha 2006

My Research: The Organisms

Bacteria:

- *Escherichia coli*
- *Bacillus subtilis*
- *Streptomyces*
- *Sinorhizobium meliloti*

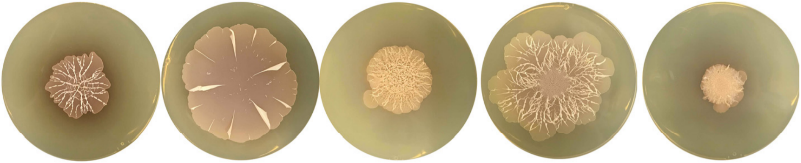
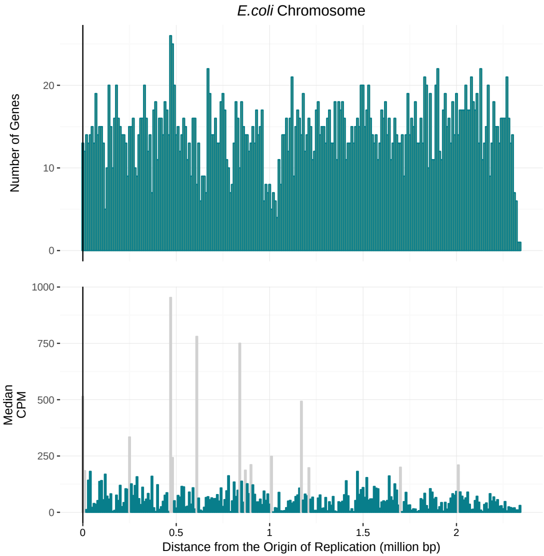


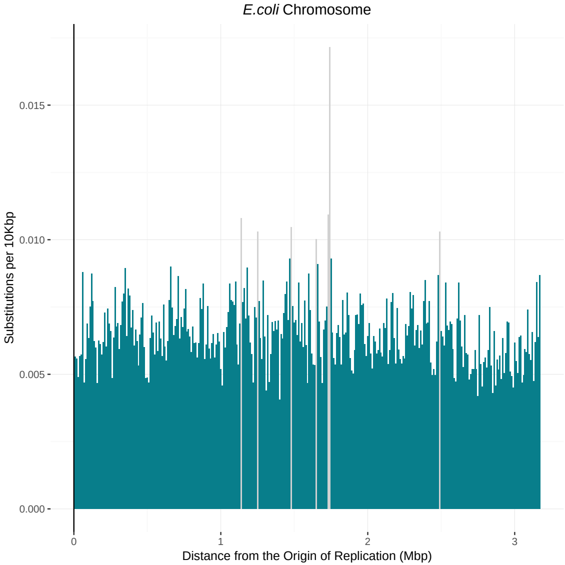
Photo: *Streptomyces* by Stephanie Jones, Marie Elliot's Lab at McMaster University

My Research: Gene Expression



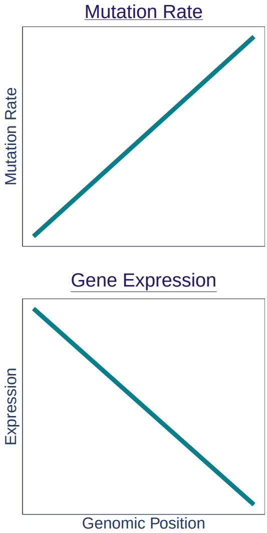
Lato and Golding 2020, Under Review

My Research: Substitutions

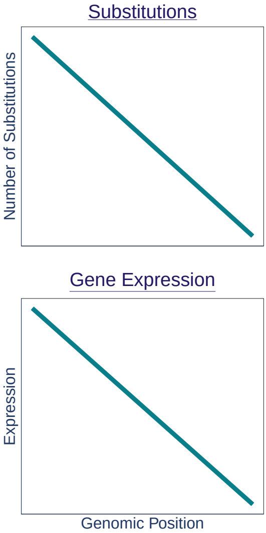


My Research: Conclusions

Previous Studies:



My Research:



Why become a Comp Bio Geek?

LY
AB
NO EATING
NO DRINKING
NO BREATHING
NO OPEN TOE SHOES
NO SHORTS
NO MINI SKIRTS
ALWAYS LAB COATS ON
Experimental Biologist
Computational Biologist
LIFE IS BEAUTIFUL
CO
Bi
LA

www.biocomicals.com

Courses you should take or audit:

- **Online Resources!**
  - DataCamp, Corsera, insert more here!
- **Bio 3S03:** Intro to Bioinformatics
- **Bio 3SS3:** Population Ecology
- **Bio 3SA3:** insert name of course here
- **Math 4MB3:** Mathematical Biology
- **Math 3MB3:** Introduction to Modelling

Questions?

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