

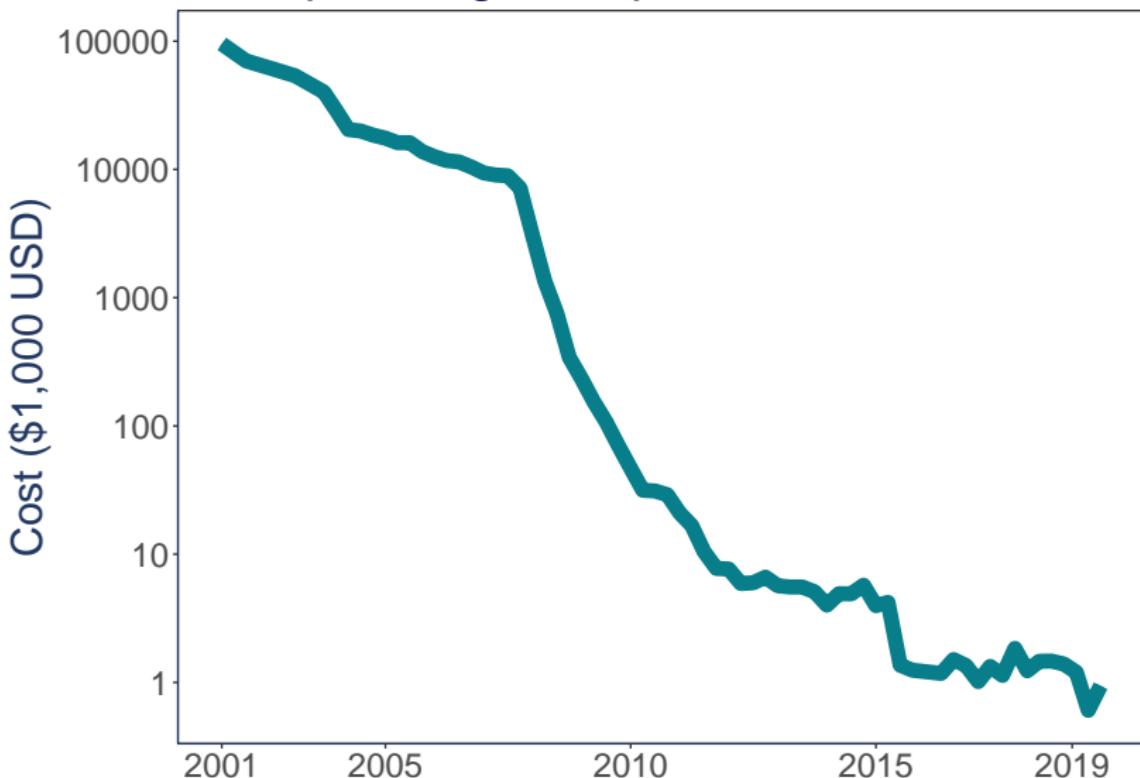
Bioinformatics: the hot interdisciplinary field

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GitHub: <https://github.com/dlato>

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Sequencing Cost per Human Genome

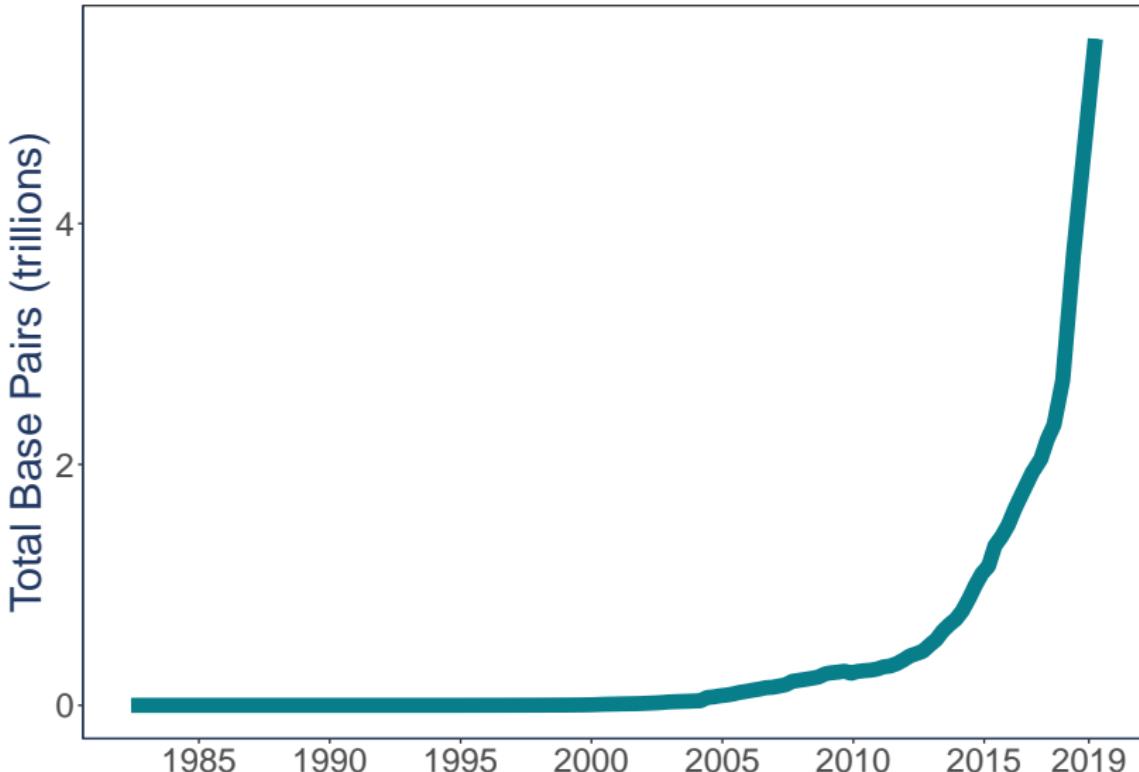


adapted from: Kris Wetterstrand, National Human Genome Research Institute

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**

The background consists of numerous laptops, all showing a blue screen with a white wavy pattern. The laptops are oriented in various directions, creating a dense, overlapping texture.

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

Broad Types of Bioinformatics

1. Data Analysis
2. Software Development
3. Modeling

1. Data Analysis

**Generating, interpreting,
and explaining any
biological data**

1. Data Analysis

Building the Human Genome



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

1. Data Analysis

The Human Genome is Sequenced!

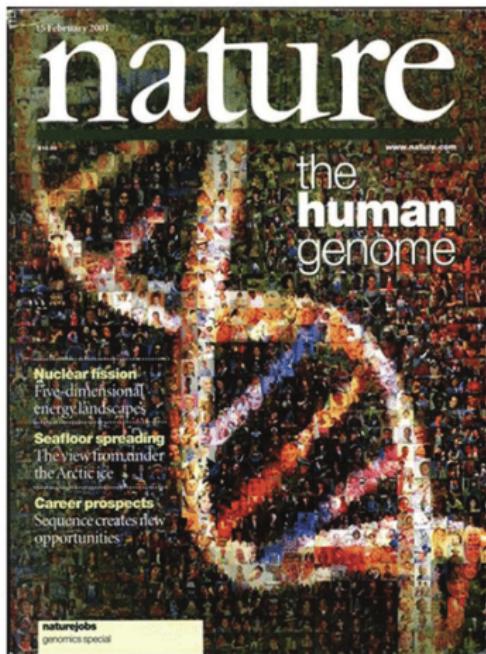
International Human Genome Sequencing Consortium Announces
“Working Draft” of Human Genome, June 2000

1. Data Analysis

The Human Genome is Sequenced...Again!

1. Data Analysis

The Human Genome is Sequenced...Again!



1. Data Analysis

The Human Genome is Sequenced...yet AGAIN!

1. Data Analysis

The Human Genome is Sequenced...yet AGAIN!

The complete Human Genome is announced by NHGRI

1. Data Analysis

**But is the human genome
really “Complete”?**

Broad Types of Bioinformatics

1. Data Analysis
2. Software Development
3. Modeling

2. Software Development

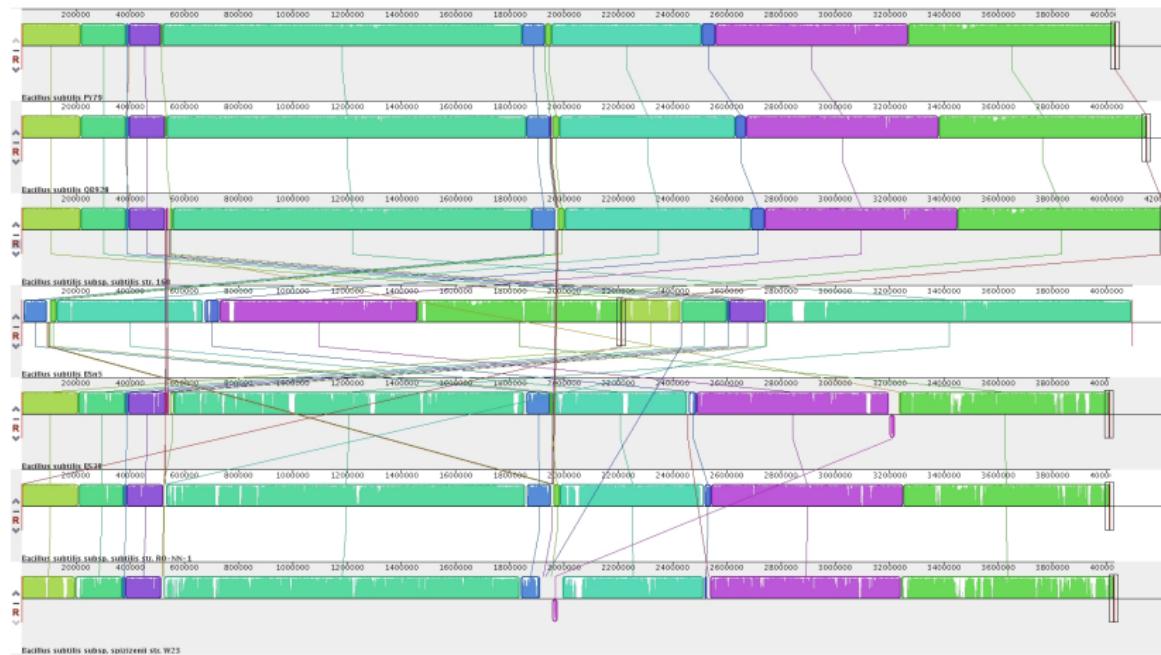
**Creating bioinformatics
tools for other people to
use**

2. Software Development

`progressiveMauve`: Whole genome alignment program

2. Software Development

progressiveMauve: Whole genome alignment program



2. Software Development

progressiveMauve: Whole genome alignment program

```
info15 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]
--profilefile=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
--numS 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-pairs-align=<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.
--extant=1=<path> Designate a path that can be used for temporary data storage. Two or more paths should be specified.
--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> Additional command-line options for MUSCLE. Any quotes should be escaped with a backslash
--skip-refinement Do not perform iterative refinement
--skip-rearrangement Do not perform rearrangement
--hp-dist-estimate=min|score|number Minimum LCD 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-exclude=<number> Gap extend penalty
--substitution-matrix=<file> Nucleotide substitution matrix in NCBI format
--weight-penalty=<number> Minimize pair wise LCD score
--hmm-scaled-penalty=<number> Minimize pair wise LCD score 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 caching 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
info15 Mauve%
```

Broad Types of Bioinformatics

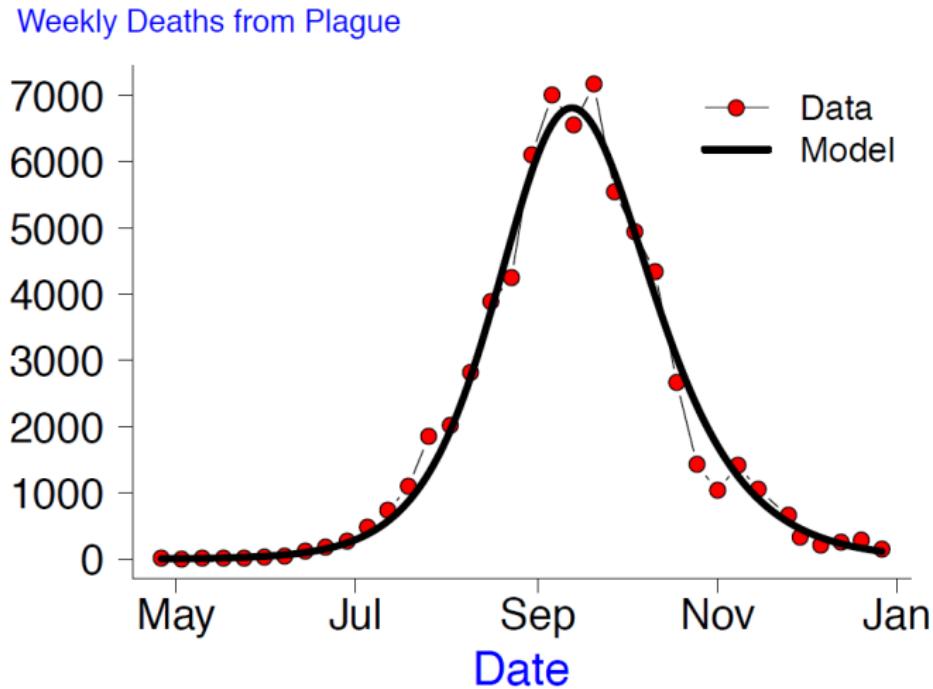
1. Data Analysis
2. Software Development
3. Modeling

3. Modelling

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

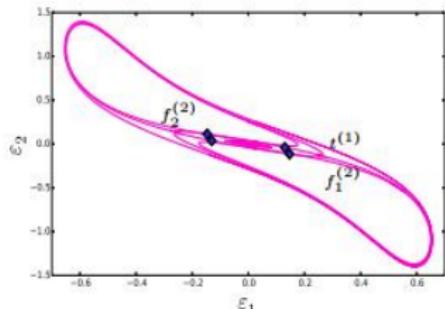
3. Modelling

SIR model and the Great Plague of London

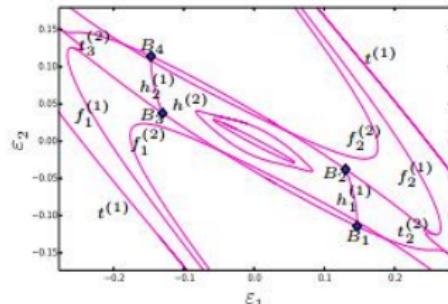


3. Modelling

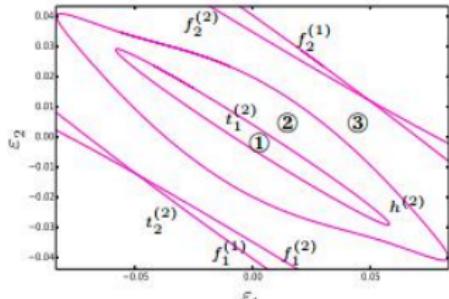
Bifurcation theory and predator-prey relationships



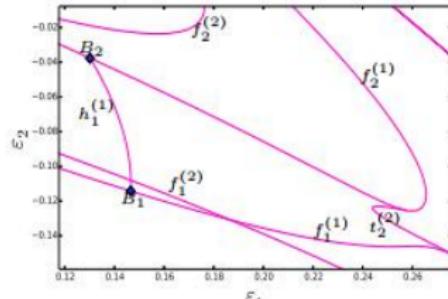
(A)



(B)



(C)



(D)

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

Broad Types of Bioinformatics

1. Data Analysis
2. Software Development
3. Modeling

Broad Types of Bioinformatics

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

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?)

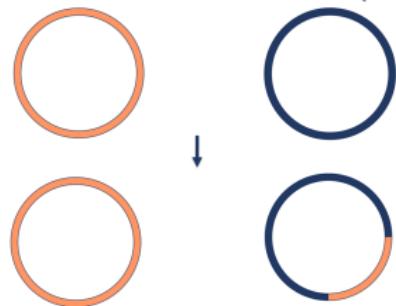
Bacteria are bizarre!

should I replace this slide with just one crazy pic of HGT?? should I remove this all together? or just shorten it?

Bacteria are bizarre!

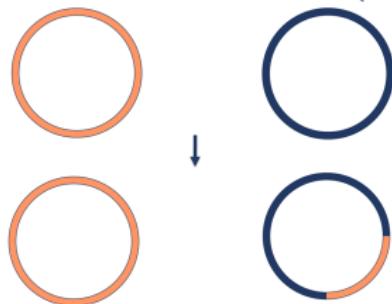
should I replace this slide with just one crazy pic of HGT?? should I remove this all together? or just shorten it?

Horizontal Gene Transfer (HGT)

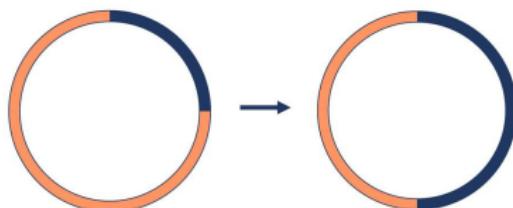


Bacteria are bizarre!

Horizontal Gene Transfer (HGT)

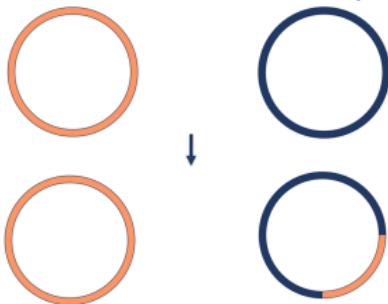


Duplication

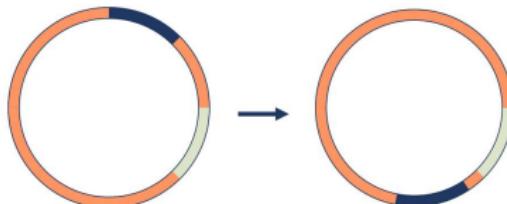


Bacteria are bizarre!

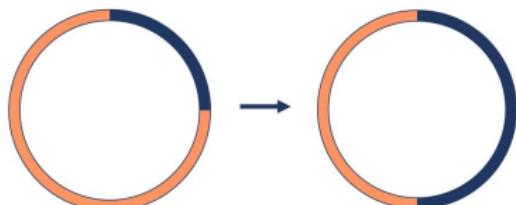
Horizontal Gene Transfer (HGT)



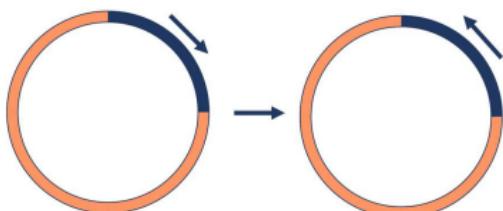
Rearrangement and Translocation



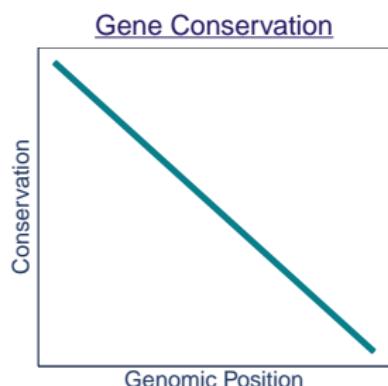
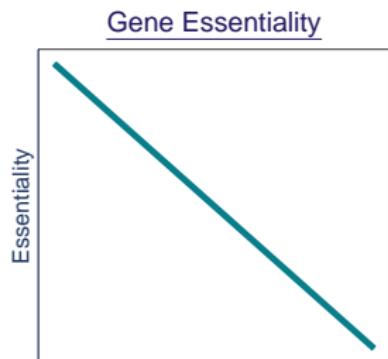
Duplication



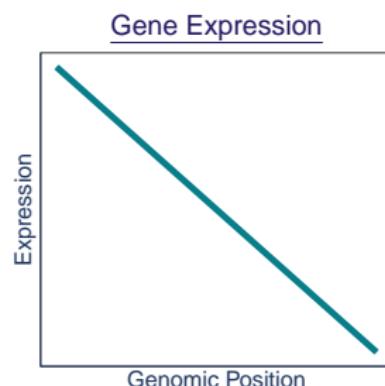
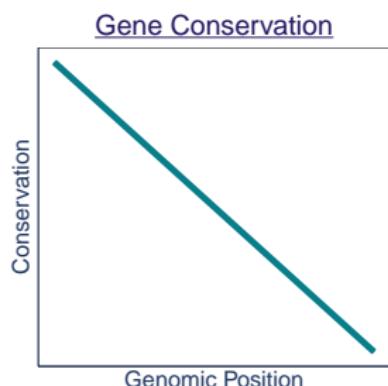
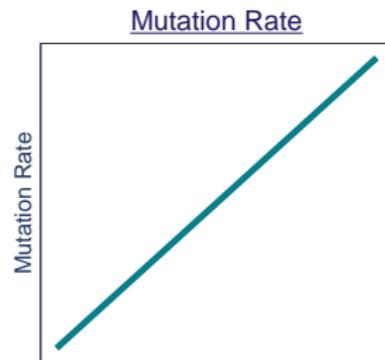
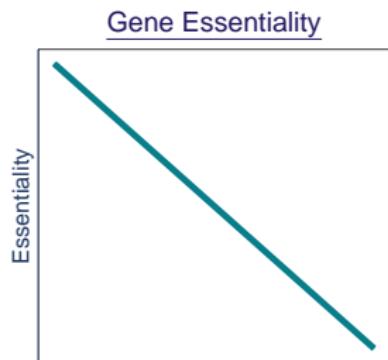
Inversion



My Research: Spatial molecular trends

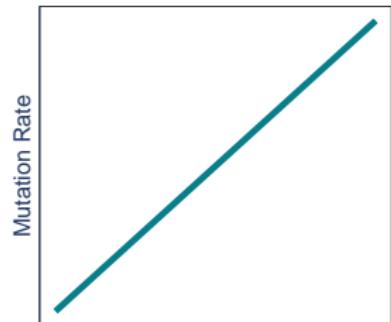


My Research: Spatial molecular trends

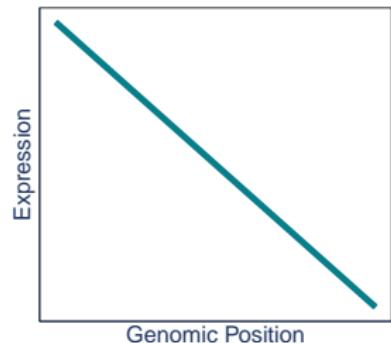


My Research: Spatial molecular trends

Mutation Rate

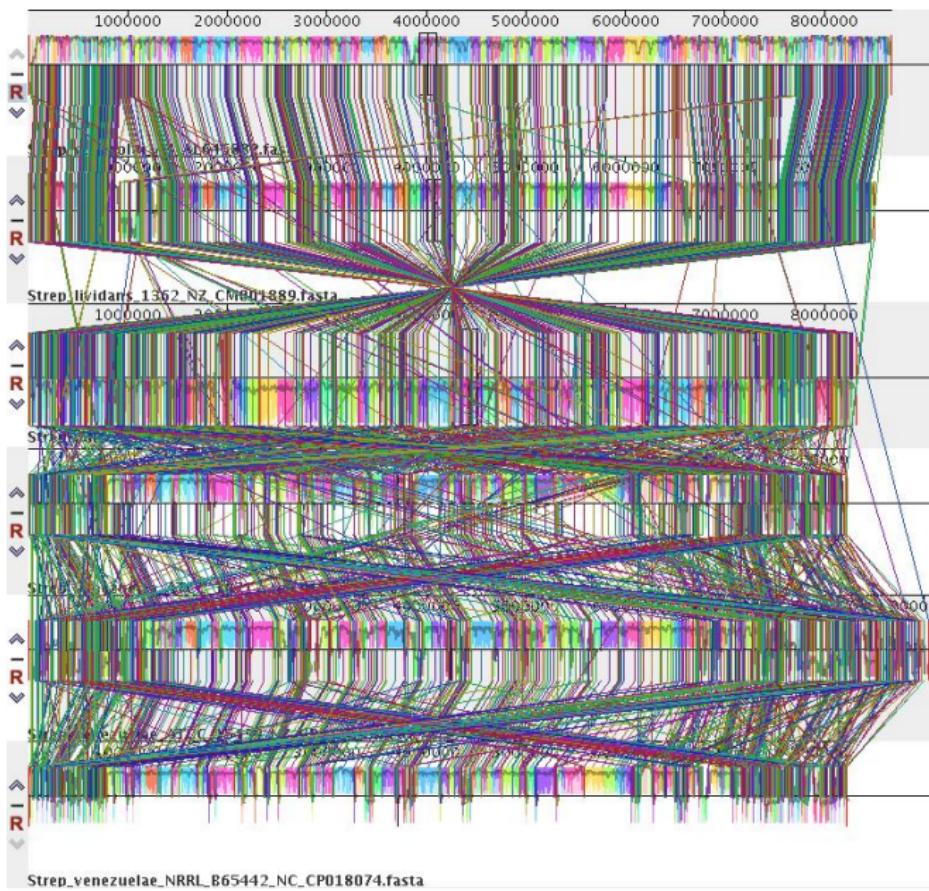


Gene Expression



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

My Research: Incorporating Bacteria Genome Shuffling!



My Research: The Organisms

Bacteria:

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

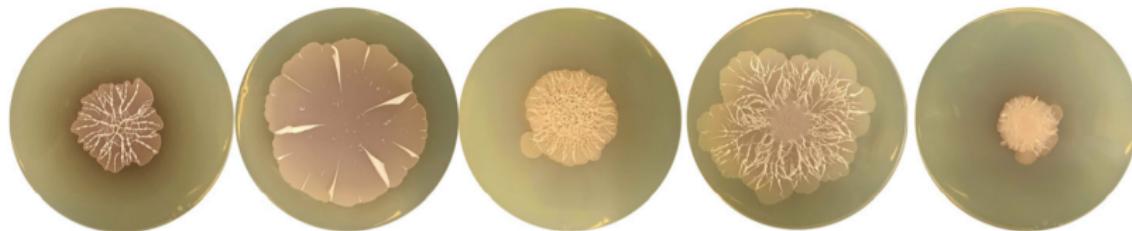
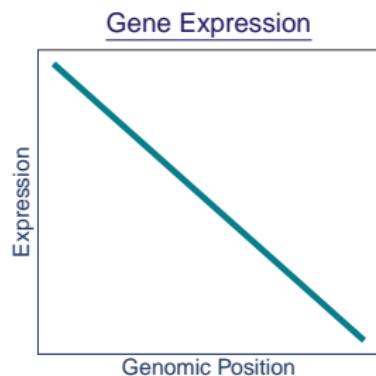
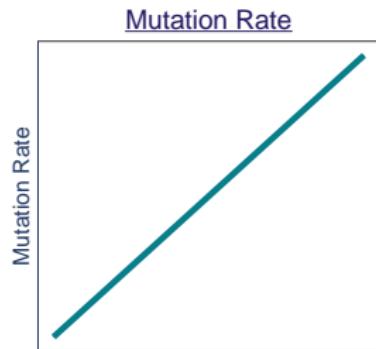


Photo: *Streptomyces* by Stephanie Jones, Marie Elliot's Lab at McMaster University

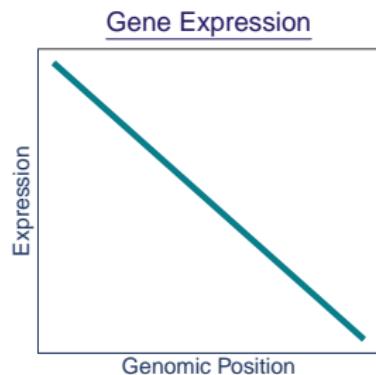
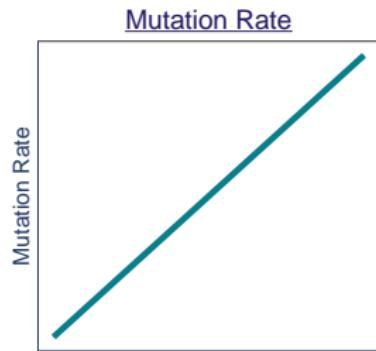
My Research: Conclusions

Previous Studies:

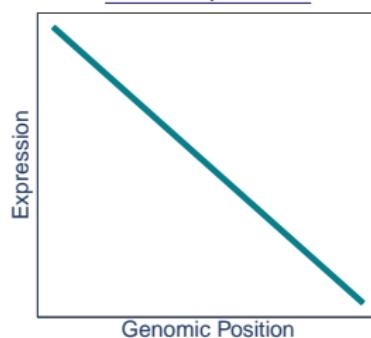
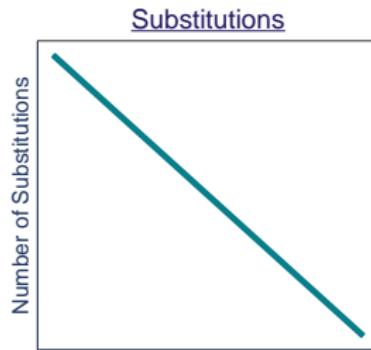


My Research: Conclusions

Previous Studies:



My Research:



Why become a Comp Bio Geek?



Not Just Biology!

Not Just Biology!

insert some pic with chemestry

here

Not Just Biology!

insert some pic with chemestry

here

insert pic about physics here

Not Just Biology!

insert some pic with chemestry

here

insert pic about physics here

insert facebook pic here

insert instagram pic here

Courses you should take or audit:

- **Online Resources!**
 - DataCamp, Corsera, CodeAcademy insert more here! (and look up spelling of these)
- **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?

latodf@mcmaster.ca

insert QR code linking to the github for this
persentation