

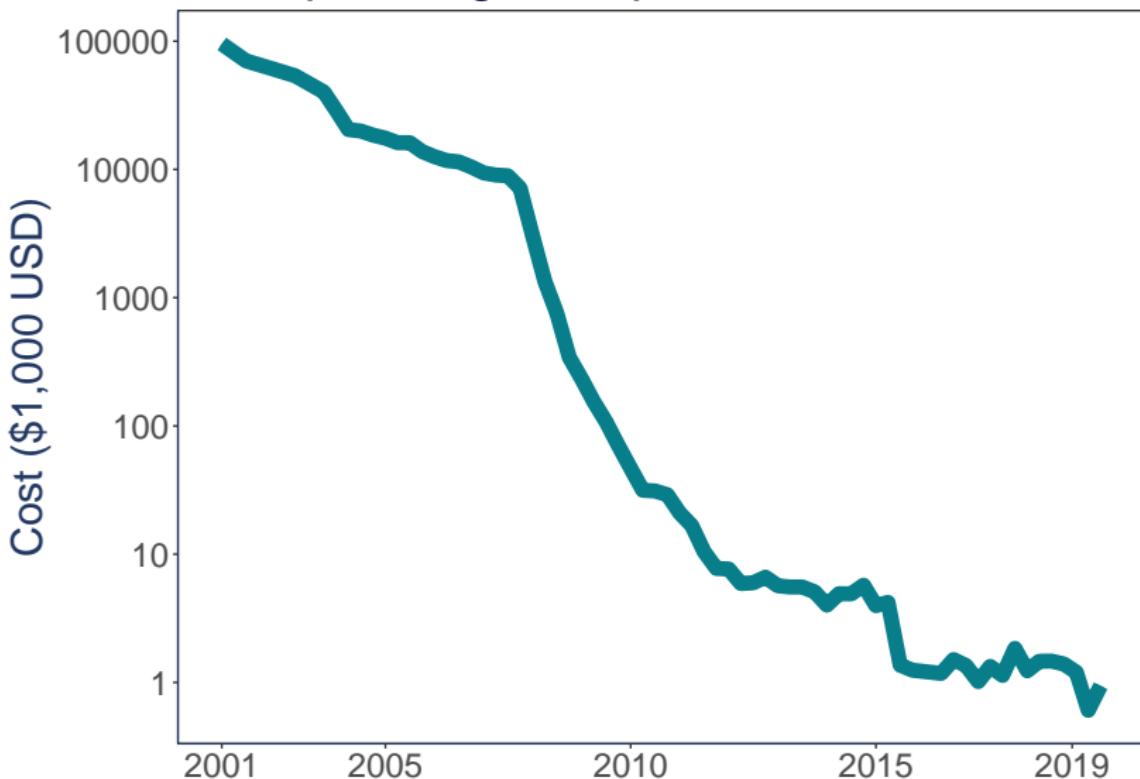
# Bioinformatics: the hot interdisciplinary field

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

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# Sequencing Cost per Human Genome

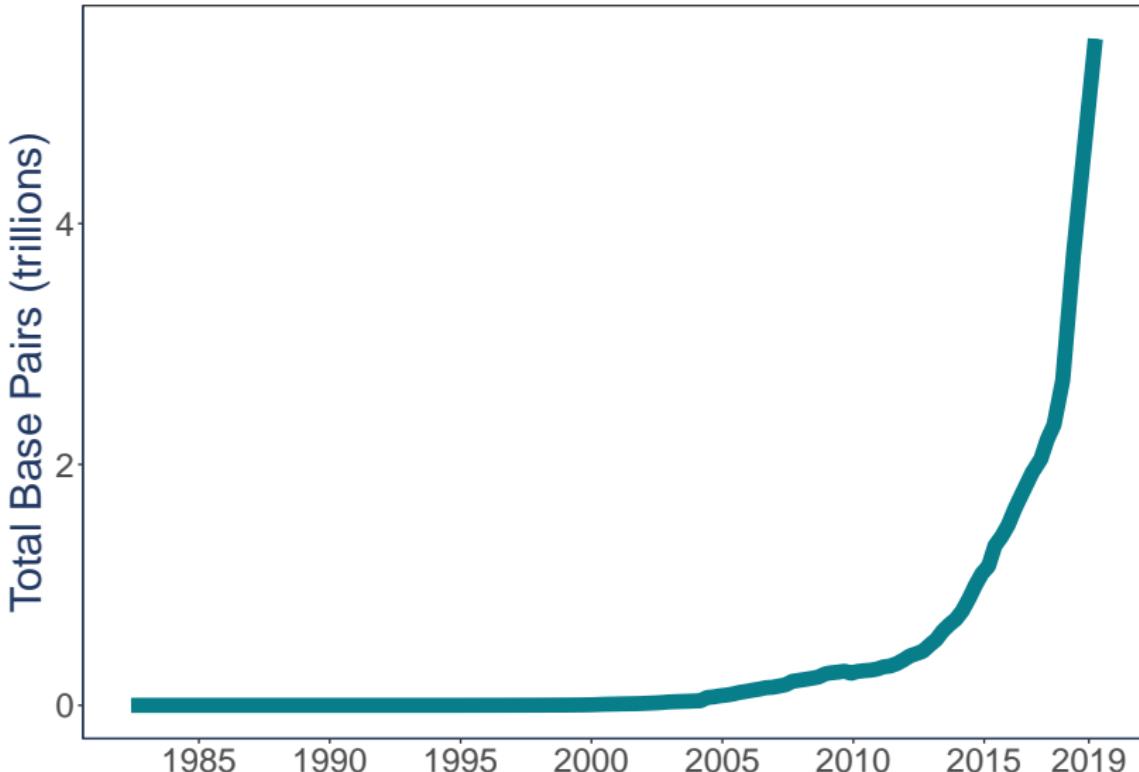


adapted from: Kris Wetterstrand, National Human Genome Research Institute

# 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

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## 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!

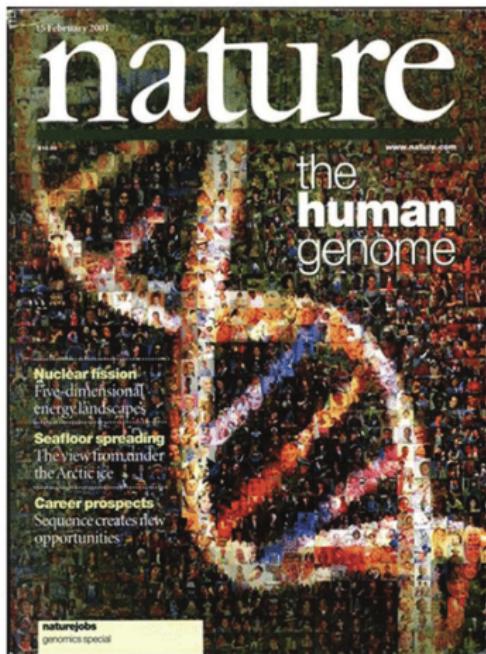
International Human Genome Sequencing Consortium Announces  
“Working Draft” of Human Genome, June 2000

# 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”?**

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## 2. Software Development

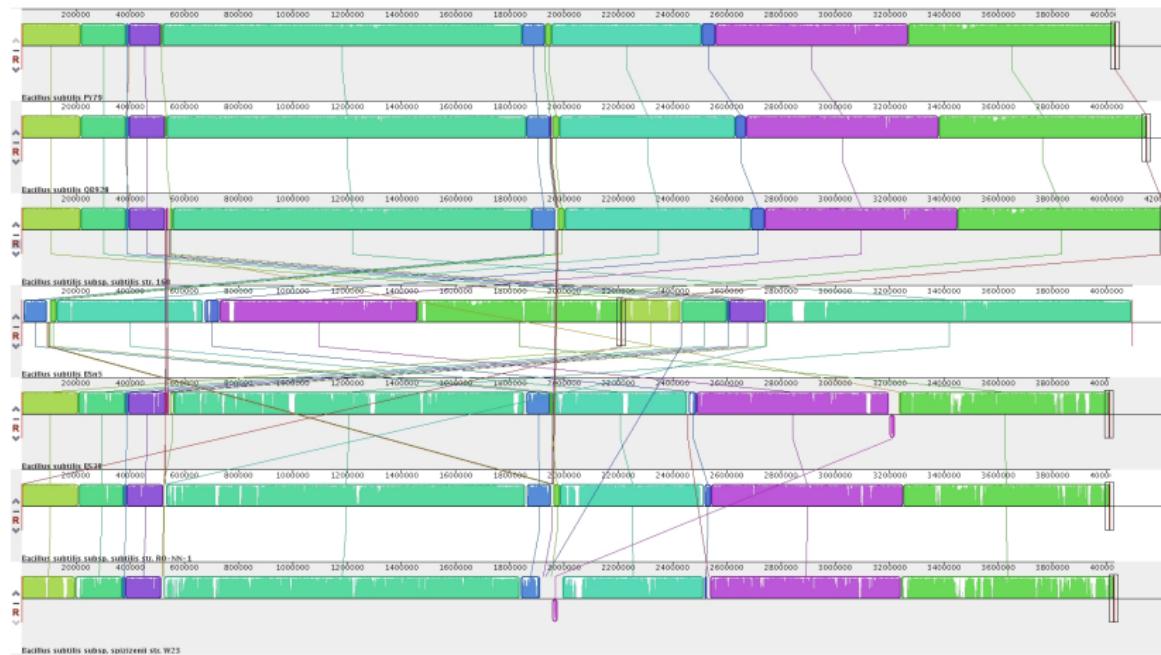
**Creating bioinformatics  
tools for other people to  
use**

## 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

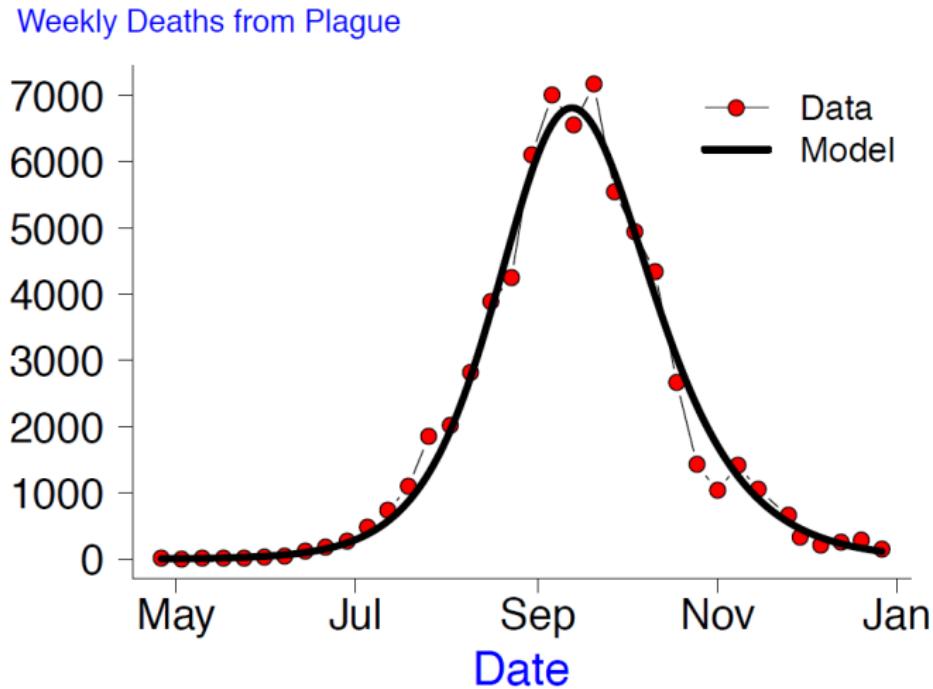
1. Data Analysis
2. Software Development
3. Modeling

### 3. Modelling

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

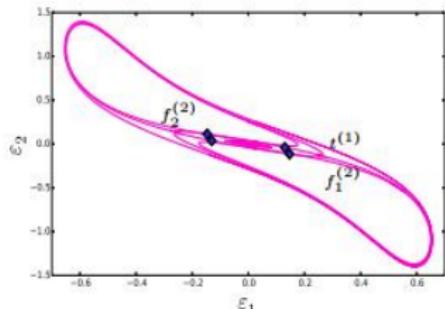
### 3. Modelling

#### SIR model and the Great Plague of London

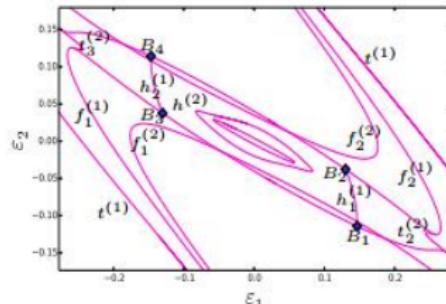


### 3. Modelling

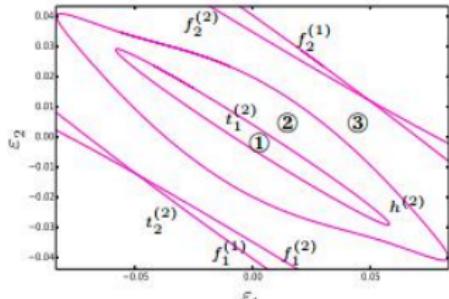
#### Bifurcation theory and predator-prey relationships



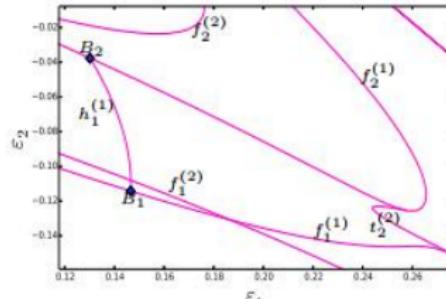
(A)



(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?)

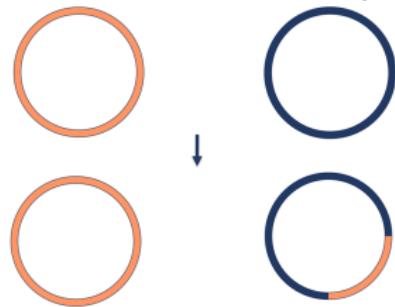
## Bacteria are bizarre!

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!

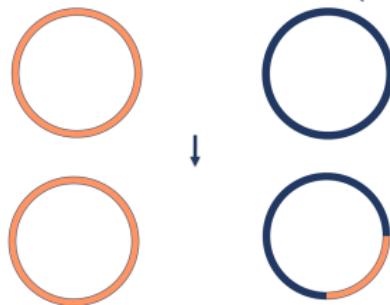
should I replace this slide with just one crazy pic of HGT?? should I remove this all together? or just shorten it?

## Horizontal Gene Transfer (HGT)

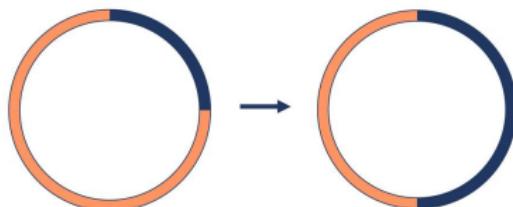


# Bacteria are bizarre!

## Horizontal Gene Transfer (HGT)

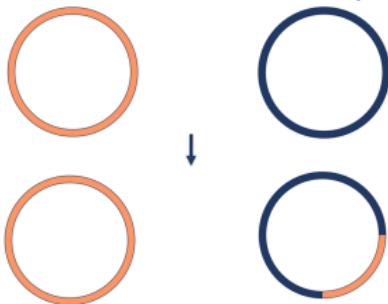


## Duplication

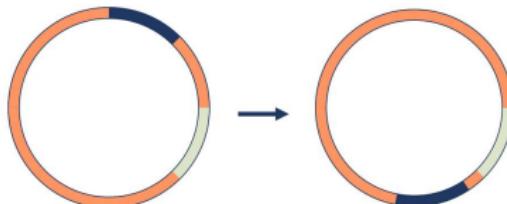


# Bacteria are bizarre!

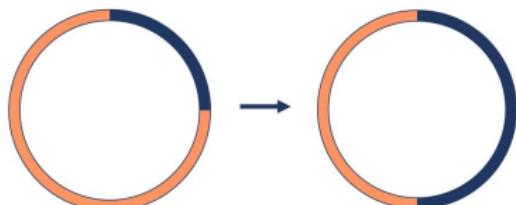
Horizontal Gene Transfer (HGT)



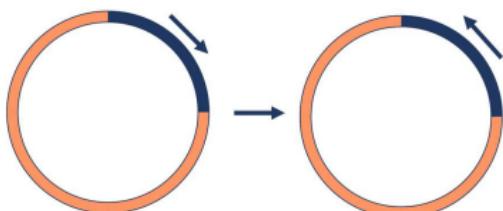
Rearrangement and Translocation



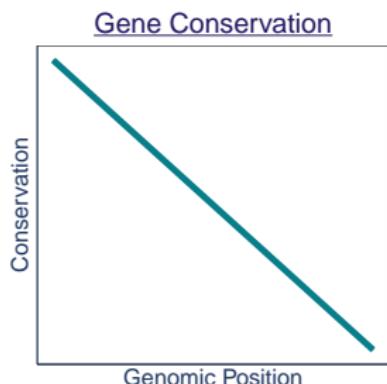
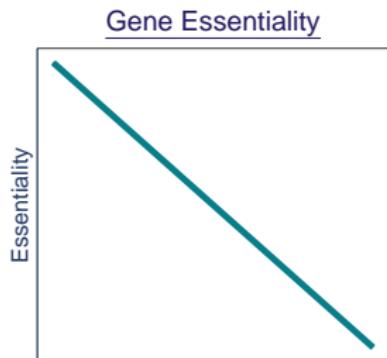
Duplication



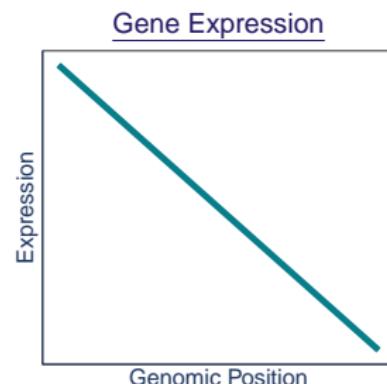
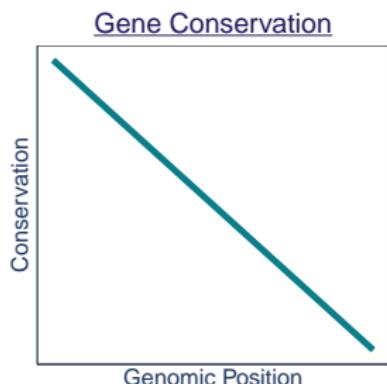
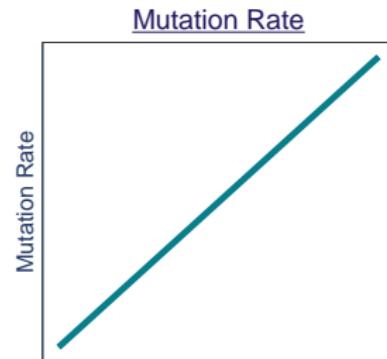
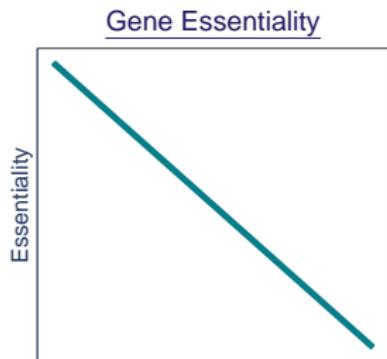
Inversion



# My Research: Spatial molecular trends

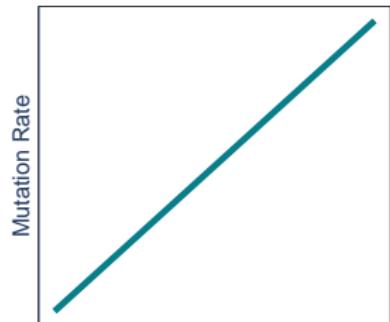


# My Research: Spatial molecular trends

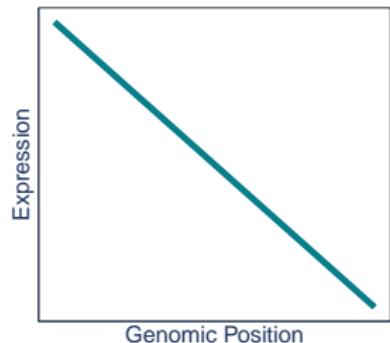


# My Research: Spatial molecular trends

Mutation Rate

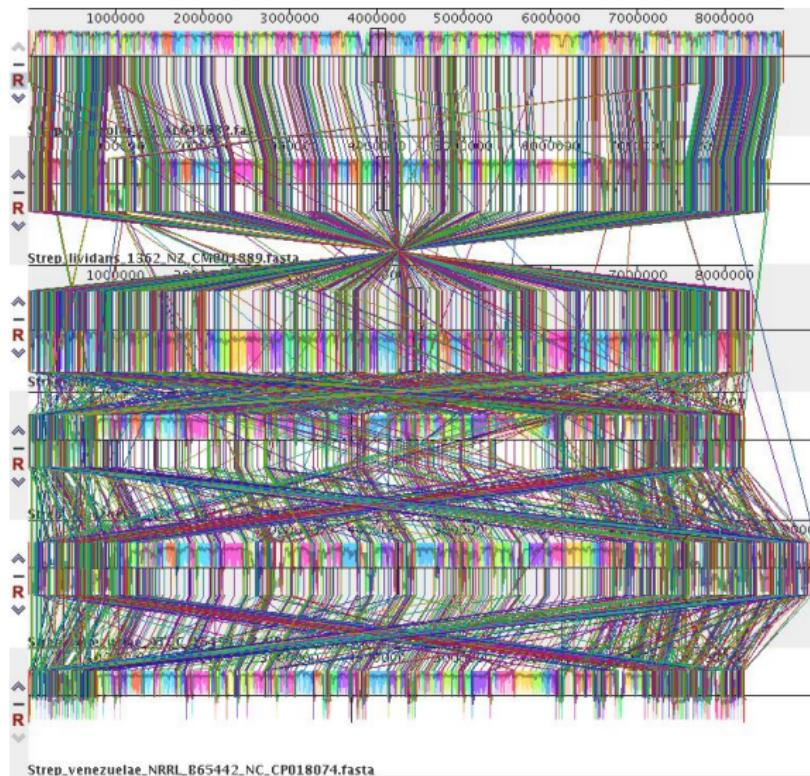


Gene Expression



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

# My Research: Shaking it Up!



# My Research: The Organisms

Bacteria:

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

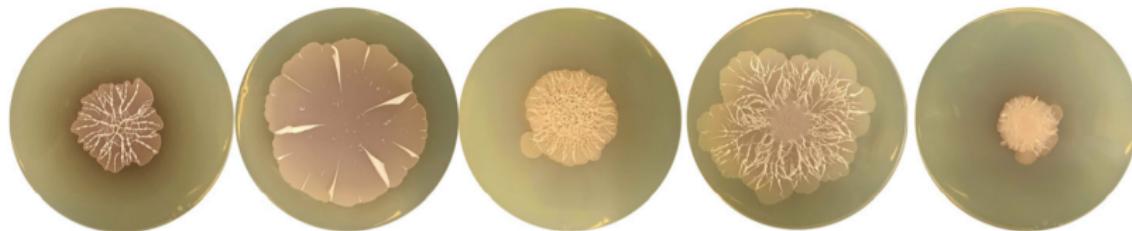
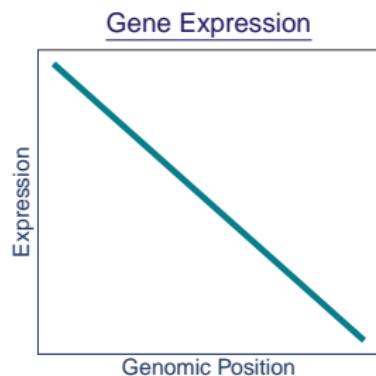
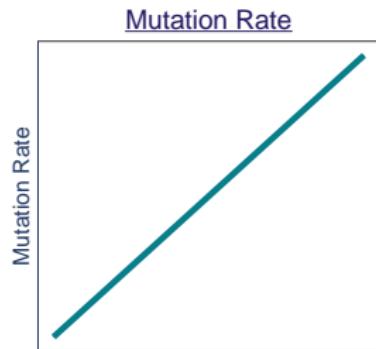


Photo: *Streptomyces* by Stephanie Jones, Marie Elliot's Lab at McMaster University

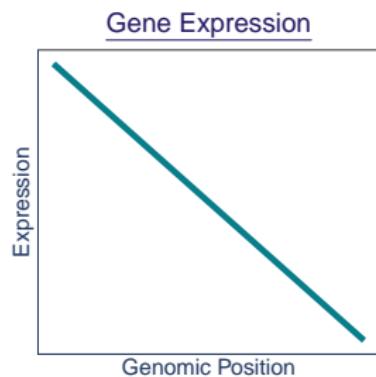
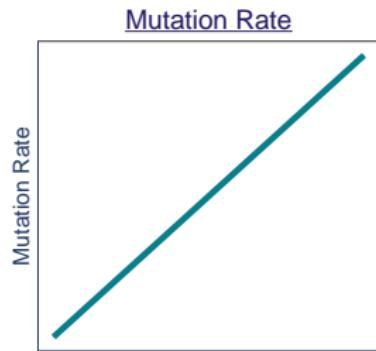
# My Research: Conclusions

## Previous Studies:

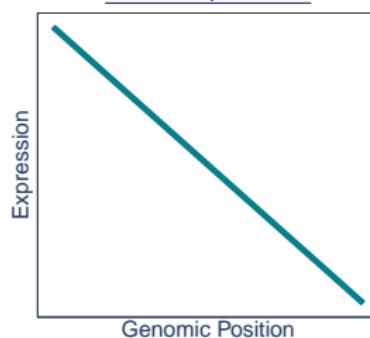
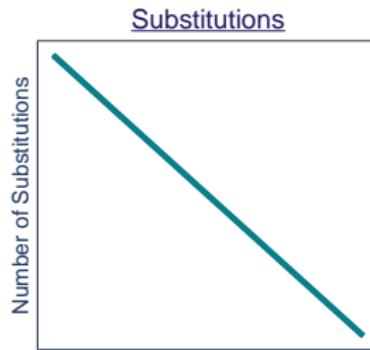


# My Research: Conclusions

## Previous Studies:



## My Research:



# Why become a Comp Bio Geek?



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?

latodf@mcmaster.ca

insert QR code linking to the github for this  
persentation