Visualizing Molecular Trends in Bacterial Genomes

Daniella Lato and Jana Taha

Stats 744: Final Project December 3, 2019

The Organisms

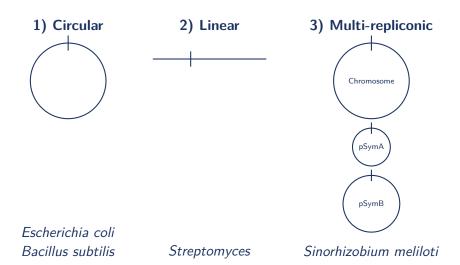
Bacteria:

- Escherichia coli
- Bacillus subtilis
- Streptomyces
- Sinorhizobium meliloti



Photo: Streptomyces by Stephanie Jones, McMaster University

Biological Background

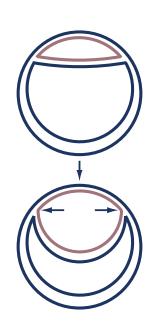


Bacterial Genome Properties

Bidirectional Replication

- Gene dosage
- Sequence composition
- Codon bias
- Replication errors
- Strand differences

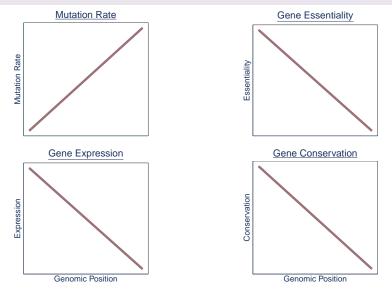
- new DNA
- old DNA



Bacterial Genomes

Different **replicons** and **positions** of bacterial genomes can have **varying molecular trends**

Spatial Molecular Trends



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

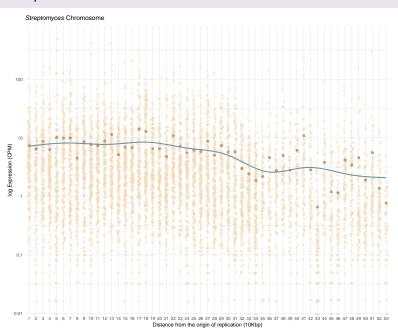
The Data

Gene Expression

- E. coli, B. subtilis, Streptomyces, and S. meliloti
- Gene expression + distance from the origin of replication
- Expectation: Near the origin of replication = Higher Expression

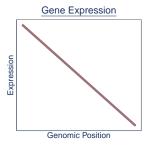
We will focus on Streptomyces

Gene Expression



Spatial Molecular Trends

Expectation:



Observation:

Gene expression decreases with increasing distance from the origin of replication in a non-linear manner

- \bullet dN = non-synonymous substitution rate
 - change in amino acid sequence
 - can alter function of the protein

- **dN** = non-synonymous substitution rate
 - change in amino acid sequence
 - can alter function of the protein
- **dS** = synonymous substitution rate
 - no change in amino acid sequence
 - will not alter function of protein

- **dN** = non-synonymous substitution rate
 - change in amino acid sequence
 - can alter function of the protein
- **dS** = synonymous substitution rate
 - no change in amino acid sequence
 - will not alter function of protein
- $\omega = (dN/dS)$

- dN = non-synonymous substitution rate
 - change in amino acid sequence
 - can alter function of the protein
- **dS** = synonymous substitution rate
 - no change in amino acid sequence
 - will not alter function of protein
- $\omega = (dN/dS)$
 - $\omega > \mathbf{1} o \mathsf{positive}$ selection
 - beneficial to the organism and will likely be maintained over time

- dN = non-synonymous substitution rate
 - change in amino acid sequence
 - can alter function of the protein
- **dS** = synonymous substitution rate
 - no change in amino acid sequence
 - will not alter function of protein
- $\omega = (dN/dS)$
 - $\omega > \mathbf{1} o \mathsf{positive}$ selection
 - beneficial to the organism and will likely be maintained over time
 - $\omega = 1 \rightarrow$ neutral selection
 - neither beneficial nor deleterious to the organism

- dN = non-synonymous substitution rate
 - change in amino acid sequence
 - can alter function of the protein
- **dS** = synonymous substitution rate
 - no change in amino acid sequence
 - will not alter function of protein
- $\omega = (dN/dS)$
 - $\omega > \mathbf{1} o \mathsf{positive}$ selection
 - beneficial to the organism and will likely be maintained over time
 - $\omega = 1 \rightarrow$ neutral selection
 - neither beneficial nor deleterious to the organism
 - $\omega < \mathbf{1} o$ negative selection
 - deleterious to the organism and will likely not be maintained over time

The Data

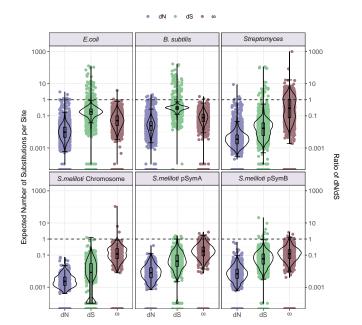
Selection

- E. coli, B. subtilis, Streptomyces, and S. meliloti
- \bullet dN, dS, and ω + distance from the origin of replication
- $\omega > 1$ (positive selection), $\omega = 1$ (neutral), $\omega < 1$ (negative selection)

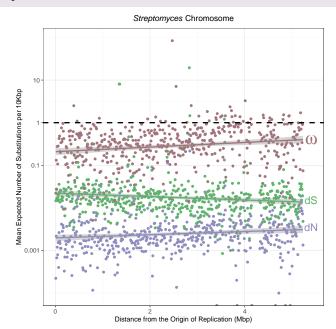
Expectations:

- 1. dS > dN
- 2. Most genes are under neutral or negative selection
- 3. Genes that are under positive selection should most likely be accessory genes
- Core genes are near the origin of replication
- Accessory genes are usually near the terminus

Selection Summary



Streptomyces Selection



Summary

- \checkmark Gene expression decreases (non-linearly) with increasing distance from the origin of replication
 - Wave-like pattern at the end of the graph?
- $\sqrt{dS} > dN$
- ✓ Most genes are under neutral or negative selection ($\omega \leq 1$)
- \checkmark In Streptomyces, genes under positive selection ($\omega>1$) were near the terminus and most likely part of the accessory genome