The Effects Of CRISPR-Cas Systems On The Rate Of Horizontal Gene Transfer

A Network Theoretic Approach



Siddharth Reed Undergraduate Thesis

Golding Lab, Biology Department, McMaster University

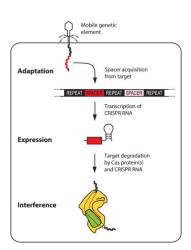
November 27, 2018

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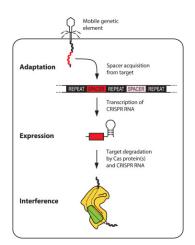
- 1. CRISPR-Cas systems
- 2. Horizontal Gene Transfer
- 3. Phylogenomic Networks
- 4. Do CRRISPR Systems Affect Horizontal Gene Transfer?
- 5. My Project

CRISPR-Cas systems

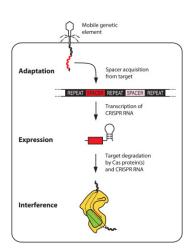
 Adaptive Bacterial Immune System



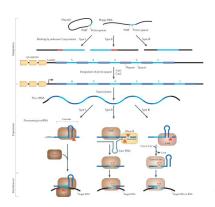
- Adaptive Bacterial Immune System
- Protects against foreign DNA



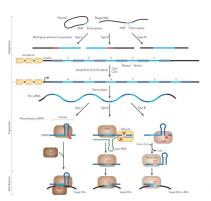
- Adaptive Bacterial Immune System
- Protects against foreign DNA
- Requires Cas proteins and CRISPR loci



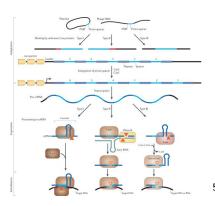
• 45% of bacteria have CRISPR loci $(n = 6782)^2$



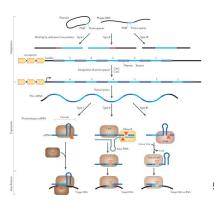
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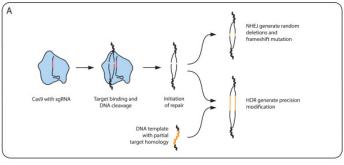


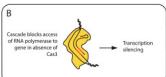
- 45% of bacteria have CRISPR loci $(n = 6782)^2$
- 3 Main Types, multiple subtypes³
- CRISPR arrays represent unique life history of an organism
- 11% 28% are false or orphaned CRISPR loci⁴

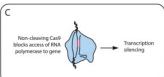


Biotech Application

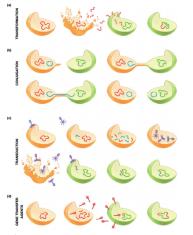
Biotech Application





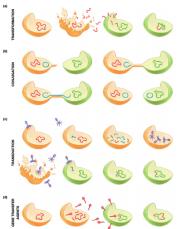


Horizontal Gene Transfer

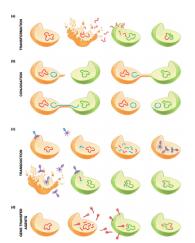


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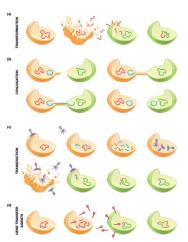


 Conjugation: Transfer of DNA through cell-cell connections⁶



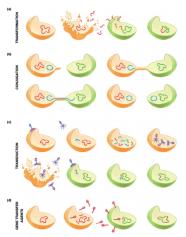
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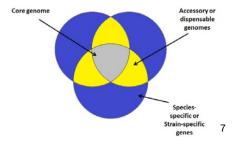
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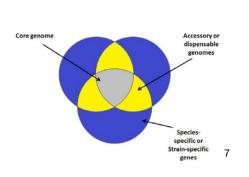
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- Transformation: Incorportaion of free-floating DNA into the genome⁶
- Transduction: Transfer of DNA through phage⁶
- CRISPR-Cas directly affects Transduction and Transformation⁶

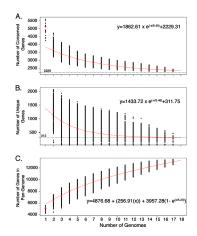
Pan-Genomes

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Amount of exogenous DNA/cell density/phage density

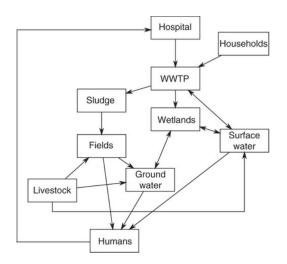
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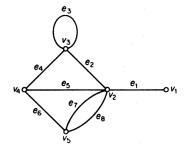
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- Metabolic costs
- Sequence compatibility

Applications

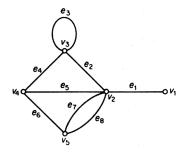
Applications



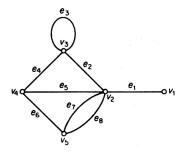
Phylogenomic Networks



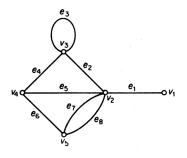
 Useful mathematical abstraction of real world system



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- Nodes can have attributes



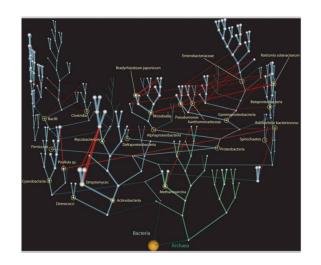
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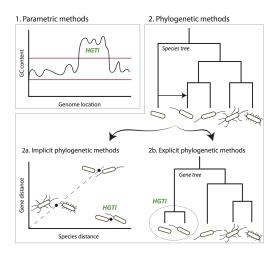
- Useful mathematical abstraction of real world system
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- Directed or Undirected Edges
- Weighted or Unweighted Edges

Prokaryotic "Net of Life"

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Construction



Do CRRISPR Systems Affect Horizontal Gene Transfer?

Yes

• Cost tradeoff factors:

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 - Metabolic maintenace¹

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 - Prophage abundance¹⁵

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- Selective CRISPR inactivation¹
- CRISPR can enhance transduction-mediated HGT¹⁵

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 - Higher gene indel rates for CRISPR containing genera than non-CRISPR containing outgroups

My Project

Hypothesis

Null Hypothesis

Bacterial strains or genera with known CRISPR systems will show no significant differences in network statistics compared to those strains or genera without known CRISPR systems.

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Alternative Hypothesis

Bacterial strains or genera with known CRISPR systems will show a significant difference in at least 1 network statistic compared to those strains or genera without known CRISPR systems.

Within Network Comparisons

For genera with CRISPR conatining strains, compare the node statistics of CRIPSR-containing strain to non-CRISPR-containing strains.

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For genera with CRISPR conatining strains, compare the node statistics of CRIPSR-containing strain to non-CRISPR-containing strains.

Between Network Comparisons

For genera with no CRISPR conatining strains, compare the network statistics of mixed to non-CRISPR-containing networks.

Within Network Comparisons

For genera with CRISPR conatining strains, compare the node statistics of CRIPSR-containing strain to non-CRISPR-containing strains.

Between Network Comparisons

For genera with no CRISPR conatining strains, compare the network statistics of mixed to non-CRISPR-containing networks.

Gene Indel Rates vs. Network Statistics

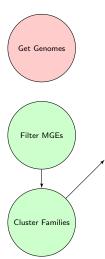
Compare gene InDel rates to node/network statistics for CRISPR-containing and non-CRISPR-containing strains/genera.

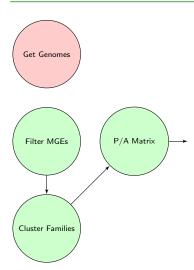


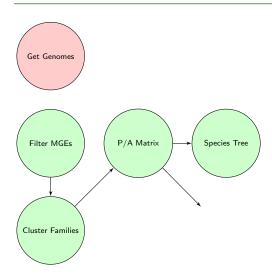
Filter MGEs

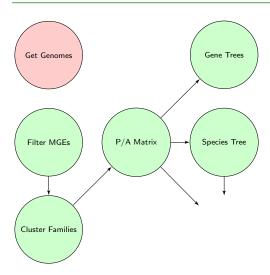


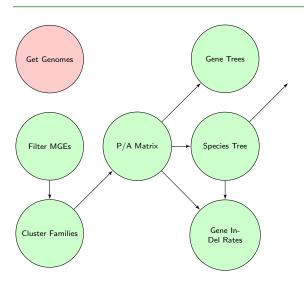


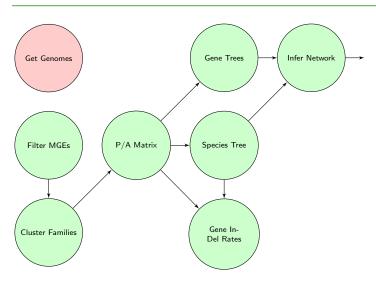


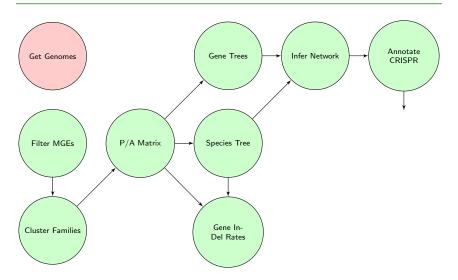


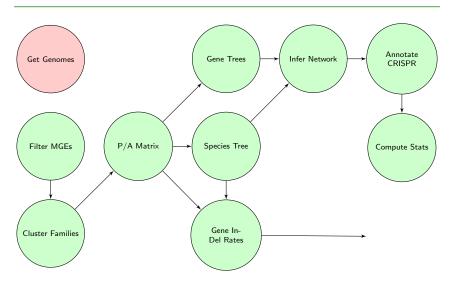


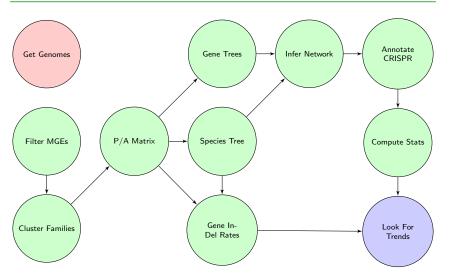




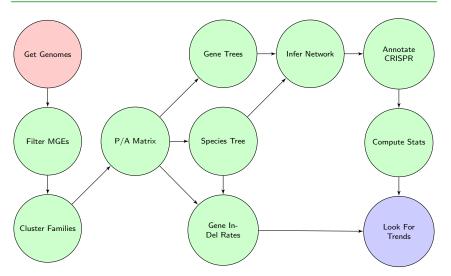








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• Total/Average edge weight: $\sum_i w_i, \frac{\sum_i w_i}{N}$

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- Node Associativity: $\frac{j(j+1)(\overline{k}-\mu_q)}{2E\sigma_q^2}$ where j is the excess degree of the node and \overline{k} is the average excess degree of the node's neighbors and μ_q and σ_q are the mean and standard variation of the excess degree distribution.

Thanks

Thank you to

- Dr. G. Brian Golding
- The Golding lab
 - Caitlin Simopoulos
 - o Daniella Lato
 - Zachery Dickson
 - Sam Long
 - Lucy Zhang
 - Brianne Laverty
 - Nicole Zhang
- · Everyone here for listening

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