Is Sharing Caring?

Elucidating the Effects of the Presence of CRISPR-Cas Systems on Rates of Horizontal Gene Transfer Using Network Analysis



Siddharth Reed MolBiol 4C12 Thesis

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April 2, 2019

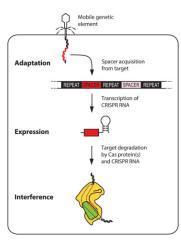
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CRISPR-Cas systems

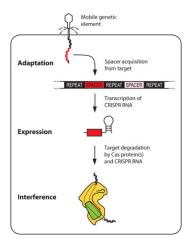
What Are They?

 Adaptive Bacterial Immune System



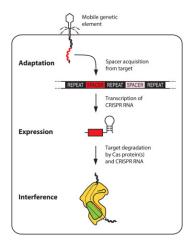
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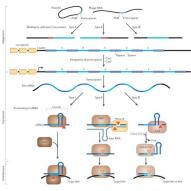


What Are They?

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

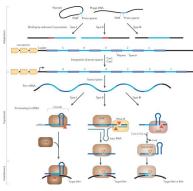


 45% of bacteria have CRISPR loci (n = 6782) (Grissa, I. and Drevet, C. and Couvin, D., 2017)



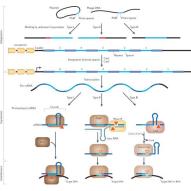
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- 3 Main Types, multiple sub types (Bondy-Denomy and Davidson, 2014)



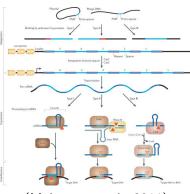
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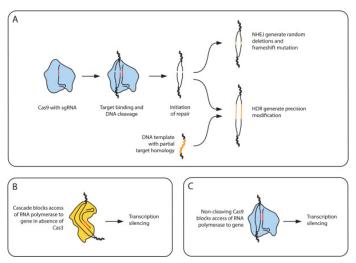
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- CRISPR arrays represent unique life history of an organism
- 11% 28% are false or orphaned CRISPR loci (Zhang and Ye, 2017)



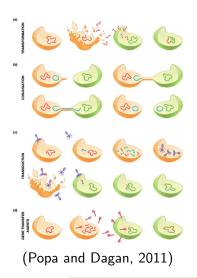
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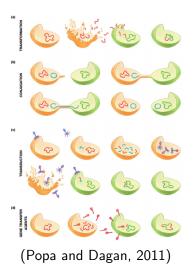
Biotech Application

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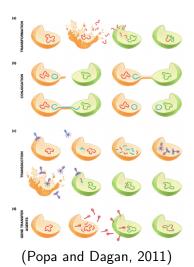


Horizontal Gene Transfer

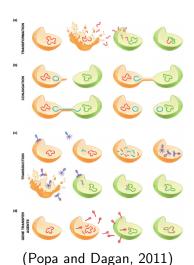




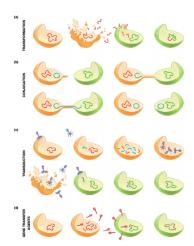
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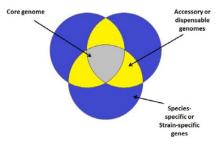


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- Conjugation: Transfer of DNA through cell-cell connections (Popa and Dagan, 2011)
- Transduction: Transfer of DNA through phage (Popa and Dagan, 2011)
- CRISPR-Cas directly affects HGT (Popa and Dagan, 2011)

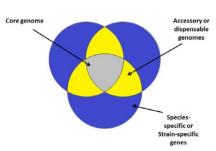
Pan-Genomes

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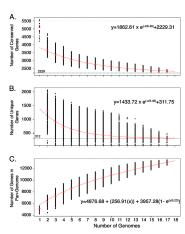


(Guimaraes et al., 2015)

Pan-Genomes



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(Rasko et al., 2008)

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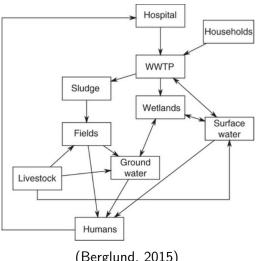
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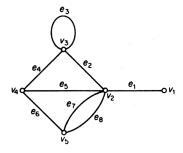
Applications

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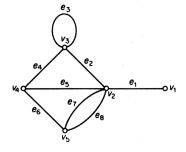


(Berglund, 2015)

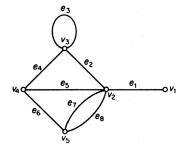
Phylogenomic Networks



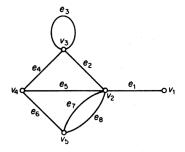
 Useful mathematical abstraction of real world system



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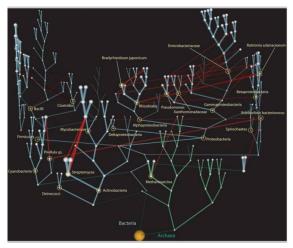
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- Weighted or Unweighted Edges

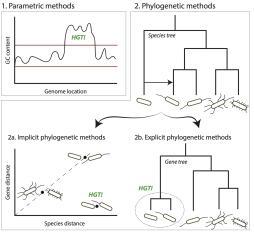
Prokaryotic "Net of Life"

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(Kunin et al., 2005)

Construction



(Ravenhall et al., 2015)

Do CRISPR Systems Affect Horizontal Gene Transfer?

Yes

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 - Prophage abundance (Watson, Staals, and Fineran, 2018)

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- Selective CRISPR inactivation (Rath et al., 2015)
- CRISPR can enhance transduction-mediated HGT (Watson, Staals, and Fineran, 2018)

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 - Can see inhibitory effects of CRIPSR on HGT over short evolutionary time scales
 - Higher gene indel rates for CRISPR containing OTUs than non-CRISPR containing outgroups

My Project

Hypothesis

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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.

Objectives

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Within Network Comparisons

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

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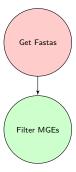
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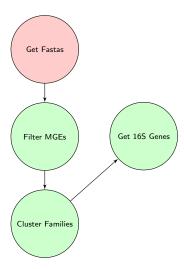
Gene Indel Rates vs. Network Statistics

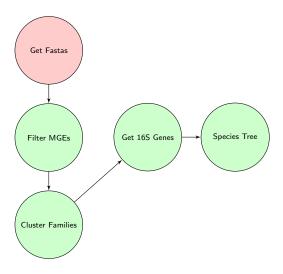
Compare gene Indel rates to node/network statistics for CRISPR containing and non-CRISPR containing OTUs

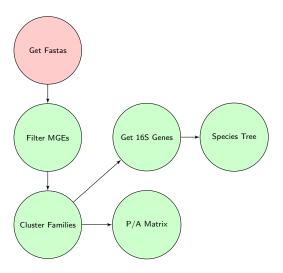


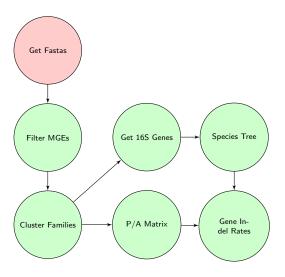


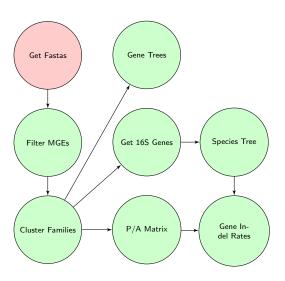


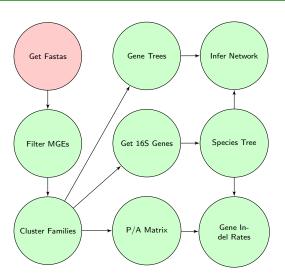


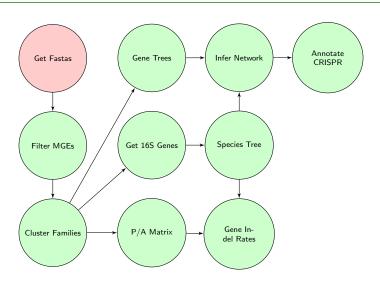


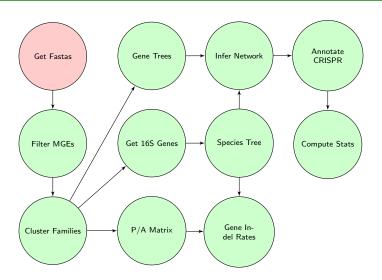


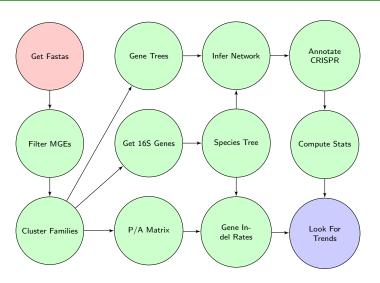












• Average Node Degree: $\frac{1}{|N_u|} \sum_{uv}^{N_u} w_{uv}$ where N_u is the set of nodes incident to u

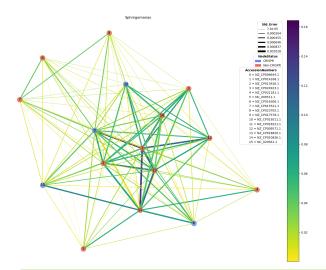
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- Node Assortativity: $A = \frac{Tr(M) ||M^2||}{1 ||M^2||}$ Where M is the mixing matrix of a given attribute and ||M|| is the sum of all elements of M. $A \in [-1,1]$. (Newman, 2002)

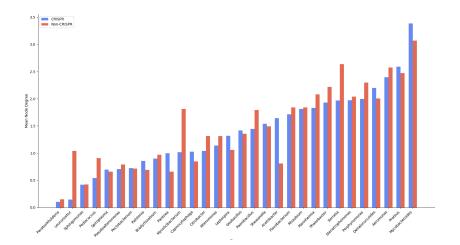
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- Network Modularity: $Q = \frac{1}{2m} \sum_{uv}^{W} [W_{uv} \frac{k_u k_v}{2m}] \delta(u, v)$ where m is the total weight of alledges, k_u is the degree of u and $\delta(u, v)$ is 1 if u and v both have or do not have CRISPR systems and 0 otherwise. $Q \in [-1, 1]$ (Newman, 2004)

Results

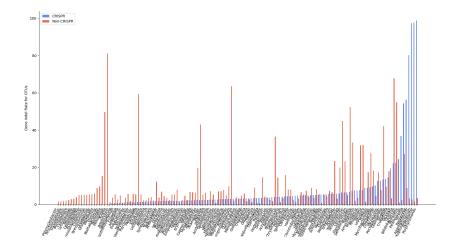
Example "Consensus" Network



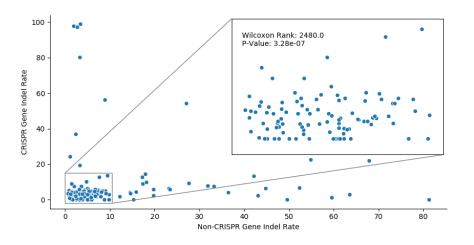
Mean Node Degree



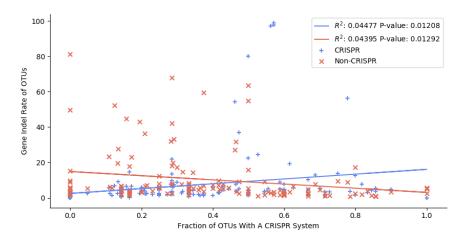
Gene Indel Rates



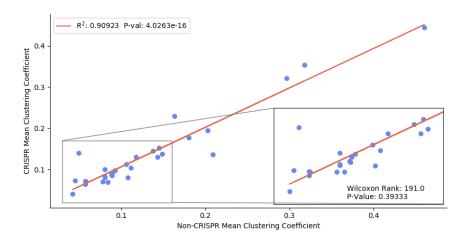
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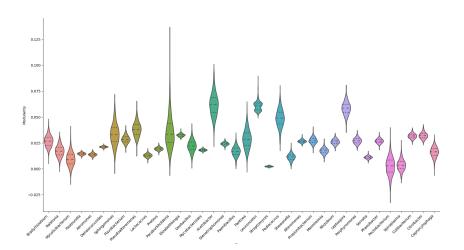
Gene Indel Rate Vs. Fraction of CRISPR OTUs



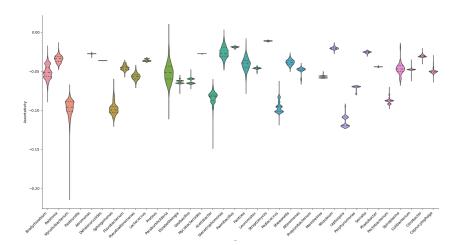
Mean Node Weighted Clustering Coefficient



Modularity Distributions



Assortativity Distributions



Conclusion

• Large variation in HGT rate between genera.

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- CRISPR-Cas systems broadly associated with lower HGT rates, with prominent exceptions

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- CRISPR-Cas systems broadly associated with lower HGT rates, with prominent exceptions
- High mixing between CRISPR and non-CRISPR OTUs
- Population level effects of CRISPR-Cas systems may decrease HGT rates
- Interplay of CRISPR-Cas systems and HGT is complex and warrants further study

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- Intergenic comparisons: Combine any set of fasta files from OTUs for analyzing transfer dynamics
- Considering bacterial ecology and environments: Consider geographically close OTUs or differences between networks due to environmental factors

Is Sharing Caring?

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Yes, for researchers

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Yes, for researchers Jury's still out for bacteria

Thanks

Thank you to

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



All code used for this project is available at https://github.com/DJSiddharthVader/thesis_SidReed

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