

How Quorum Sensing Interactions Affect Microbial Population Structure

02712 Final Project

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Background

Quorum-Sensing Systems

Public Goods and Cheating

Maintaining Freeloaders as a Diversity Reservoir

Signal-Receptor Activation Matrix K_{ac}

- Represents all receptors-signal pairs ($R_i S_i$) present in at least 1 OTU

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- ▶ Represents all receptors-signal pairs ($R_i S_j$) present in at least 1 OTU
- ▶ K_{ac} is of dimension $|R| \times |S|$
- ▶ Different sets of receptor-signal combinations can produce the same K_{ac}

Facultative Cheaters

Matrix for 2 strains R_1S_1 and R_2S_2

$$\begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix}$$

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Obligate Cheater

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Matrix for 2 strains R_1S_1 and R_0S_0

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Custom Matrix

Matrix for 2 strains $R_1R_2S_1$ and R_2S_2

$$\begin{bmatrix} 1 & 0 \\ 1 & 1 \end{bmatrix}$$

Model

Results

Example Section

Citation Example

- ▶ the citation file is at `./Documents/citations.bib`

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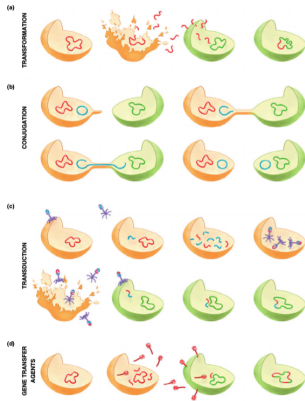
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Example 2 column slide



- **Transformation:**
Incorporation of free-floating DNA into the genome

Figure 1: HGT Mechanisms

Example 2 column slide

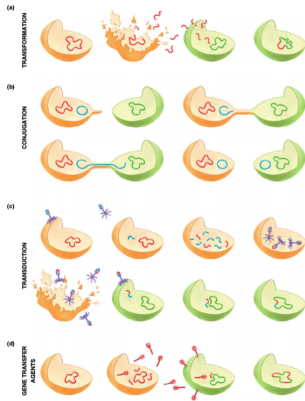


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- ▶ **Transformation:** Incorporation of free-floating DNA into the genome
- ▶ **Conjugation:** Transfer of DNA through cell-cell connections

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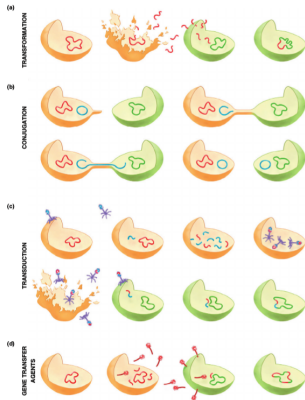


Figure 1: HGT Mechanisms

- ▶ **Transformation:** Incorporation of free-floating DNA into the genome
- ▶ **Conjugation:** Transfer of DNA through cell-cell connections
- ▶ **Transduction:** Transfer of DNA via phage

table with math

<i>Genotype</i>	<i>Environment</i>		
	E_n	E_b	E_a
<i>RCH</i>	$1 - 2s_m$	$(1 + s_p)(1 - 2s_m)$	$(1 + s_p)(1 - 2s_m)$
<i>RCh</i>	$1 - s_m$	$(1 + s_p)(1 - s_m)$	$(1 + s_p)(1 - s_m)$
<i>RcH</i>	$1 - s_m$	$1 - s_m$	$(1 + s_p)(1 - s_m)$
<i>Rch</i>	1	1	$1 + s_p$
<i>rCH</i>	$1 - 2s_m$	$(1 + s_p)(1 - 2s_m)$	$1 - 2s_m$
<i>rCh</i>	$1 - s_m$	$(1 + s_p)(1 - s_m)$	$1 - s_m$
<i>rcH</i>	$1 - s_m$	$1 - s_m$	$1 - s_m$
<i>rch</i>	1	1	1

Table 1: Relative fitness values for each genotype in each environment

Lots of math

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① **Gene Transfer:** $x_g^t = x_g + \sum_{x_R} x_{\neg g} x_R h(x_{\neg g}, x_R)$

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 - ◇ $\mu(g)$ is $\mu_{r \rightarrow R}$ for r genotypes and $\mu_{R \rightarrow r}$ for R genotypes

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 - ◇ average fitness $\bar{w} = \sum_g x_g^s f(g)$

Example code block

```
def foo(bar):  
    for i in range(69, 420):  
        if i == 69 or i == 420:  
            print('nice')  
        else:  
            print(bar)  
    return None
```

Bibliography I

Aggarwal, Surya D., Hasan Yesilkaya, Suzanne Dawid, and N. Luisa Hiller. 2020. "The Pneumococcal Social Network." *PLOS Pathogens* 16 (10). <https://doi.org/10.1371/journal.ppat.1008931>.

Calle, M. Luz. 2019. "Statistical Analysis of Metagenomics Data." *Genomics & Informatics* 17 (1). <https://doi.org/10.5808/gi.2019.17.1.e6>.

Dimitriu, Tatiana, Frances Medaney, Elli Amanatidou, Jessica Forsyth, Richard J. Ellis, and Ben Raymond. 2019. "Negative Frequency Dependent Selection on Plasmid Carriage and Low Fitness Costs Maintain Extended Spectrum Beta-Lactamases in *Escherichia Coli*." *Scientific Reports* 9 (1). <https://doi.org/10.1038/s41598-019-53575-7>.

Bibliography II

Eldar, A. 2011. "Social Conflict Drives the Evolutionary Divergence of Quorum Sensing." *Proceedings of the National Academy of Sciences* 108 (33): 13635–40.

<https://doi.org/10.1073/pnas.1102923108>.

Pérez-Escudero, Alfonso, and Jeff Gore. 2016. "Selection Favors Incompatible Signaling in Bacteria." *Proceedings of the National Academy of Sciences* 113 (8): 1968–70.

<https://doi.org/10.1073/pnas.1600174113>.

Bibliography III

Pollak, Shaul, Shira Omer-Bendori, Eran Even-Tov, Valeria Lipsman, Tasneem Bareia, Ishay Ben-Zion, and Avigdor Eldar. 2016. “Facultative Cheating Supports the Coexistence of Diverse Quorum-Sensing Alleles.” *Proceedings of the National Academy of Sciences* 113 (8): 2152–7.
<https://doi.org/10.1073/pnas.1520615113>.