# How Quorum Sensing Interactions Affect Microbial Population Structure 02712 Final Project

Sid, Neel, Sarah, Deepika, Evan

Carnegie Mellon University

November 21, 2021

## Public Goods and Cheating

# Signal-Receptor Activation Matrix $K_{ac}$

▶ Represents all receptors-signal pairs  $(R_iS_i)$  present in at least 1 OTU

# Signal-Receptor Activation Matrix $K_{ac}$

- $\triangleright$  Represents all receptors-signal pairs  $(R_iS_i)$  present in at least 1 OTU
- $K_{ac}$  is of dimension  $|R| \times |S| = |N| \times |N|$

# Signal-Receptor Activation Matrix $K_{ac}$

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

#### **Facultative Cheaters**

Background 000000

Matrix for 2 strains  $R_1S_1$  and  $R_2S_2$ 

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

#### Facultative Cheaters

Background

Matrix for 2 strains  $R_1S_1$  and  $R_2S_2$ 

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

#### **Obligate Cheater**

Matrix for 2 strains  $R_1S_1$  and  $R_0S_0$ 

#### Facultative Cheaters

Background 000000

Matrix for 2 strains  $R_1S_1$  and  $R_2S_2$ 

#### **Obligate Cheater**

Matrix for 2 strains  $R_1S_1$  and  $R_0S_0$ 

#### **Custom Matrix**

Matrix for 2 strains  $R_1R_2S_1$  and  $R_2S_2$ 

## Model

## Results

## **Example Section**

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

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

- ▶ the citation file is at ./Documents/citations.bib
  - bibtex foramtted file
  - zotero/mendel/citation websites can produce this format automatically for papers

- ▶ the citation file is at ./Documents/citations.bib
  - bibtex foramtted file
  - zotero/mendel/citation websites can produce this format automatically for papers
- here is the syntax @eldar\_2011

- ▶ the citation file is at ./Documents/citations.bib
  - bibtex foramtted file
  - zotero/mendel/citation websites can produce this format automatically for papers
- here is the syntax @eldar\_2011
  - eldar\_2011 is the cite key in the citation file

- ▶ the citation file is at ./Documents/citations.bib
  - bibtex foramtted file
  - zotero/mendel/citation websites can produce this format automatically for papers
- here is the syntax @eldar\_2011
  - eldar\_2011 is the cite key in the citation file
- ▶ here is a citation of the main paper Eldar (2011)

- ▶ the citation file is at ./Documents/citations.bib
  - bibtex foramtted file
  - zotero/mendel/citation websites can produce this format automatically for papers
- here is the syntax @eldar\_2011
  - eldar\_2011 is the cite key in the citation file
- ▶ here is a citation of the main paper Eldar (2011)
- ▶ here is a citation of the main paper (Eldar 2011)

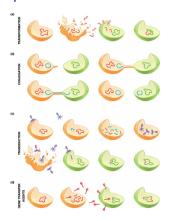


Figure 1: HGT Mechanisms

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

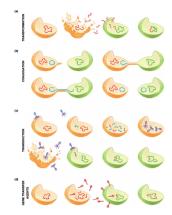


Figure 1: HGT Mechanisms

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

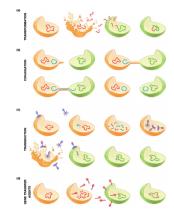


Figure 1: HGT Mechanisms

- 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

Genotype	Environment		
	En	$E_b$	E <sub>a</sub>
RCH	$1-2s_m$	$(1+s_p)(1-2s_m)$	$(1+s_p)(1-2s_m)$
RCh	$1-s_m$	$(1+s_p)(1-s_m)$	$(1+s_p)(1-s_m)$
RcH	$1-s_m$	$1-s_m$	$(1+s_p)(1-s_m)$
Rch	1	1	$1+s_p$
rCH	$1-2s_m$	$(1+s_p)(1-2s_m)$	$1-2s_m$
rCh	$1-s_m$	$(1+s_p)(1-s_m)$	$1-s_m$
rcH	$1-s_m$	$1-s_m$	$1-s_m$
rch	1	1	1

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

▶ g represents each genotype

- ▶ g represents each genotype
- 1. Gene Transfer:  $x_g^t = x_g + \sum_{x_R} x_{\neg g} x_R h(x_{\neg g}, x_R)$

- ▶ g represents each genotype
- 1. **Gene Transfer:**  $x_g^t = x_g + \sum_{x_R} x_{\neg g} x_R h(x_{\neg g}, x_R)$  $\Rightarrow$  if g = RCH then  $\neg g = rCH$ , same for CH, CH, CH, CH, CH

- g represents each genotype
- 1. Gene Transfer:  $x_g^t = x_g + \sum_{x_R} x_{\neg g} x_R h(x_{\neg g}, x_R)$ 
  - $\diamond$  if g = RCH then  $\neg g = rCH$ , same for CH, cH, Ch, ch
  - $\diamond$  defined for R genotypes ( $x_R$ ), for r genotypes subtract the sum

- g represents each genotype
- 1. Gene Transfer:  $x_g^t = x_g + \sum_{x_p} x_{\neg g} x_R h(x_{\neg g}, x_R)$ 
  - $\diamond$  if g = RCH then  $\neg g = rCH$ , same for CH, cH, Ch, ch
  - $\diamond$  defined for R genotypes ( $x_R$ ), for r genotypes subtract the sum
  - $\diamond$  h() probability of transfer, increases for each H allele  $(g_h, g_H, 2g_H)$

- g represents each genotype
- 1. Gene Transfer:  $x_g^t = x_g + \sum_{x_p} x_{\neg g} x_R h(x_{\neg g}, x_R)$ 
  - $\diamond$  if g = RCH then  $\neg g = rCH$ , same for CH, cH, Ch, ch
  - $\diamond$  defined for R genotypes ( $x_R$ ), for r genotypes subtract the sum
  - $\diamond$  h() probability of transfer, increases for each H allele  $(g_h, g_H, 2g_H)$
- 2. Mutation:  $x_{\sigma}^{s} = (1 \mu(g))x_{\sigma}^{t} + \mu(g)x_{\neg \sigma}^{t}$

- g represents each genotype
- 1. Gene Transfer:  $x_g^t = x_g + \sum_{x_p} x_{\neg g} x_R h(x_{\neg g}, x_R)$ 
  - $\diamond$  if g = RCH then  $\neg g = rCH$ , same for CH, cH, Ch, ch
  - $\diamond$  defined for R genotypes ( $x_R$ ), for r genotypes subtract the sum
  - $\diamond$  h() probability of transfer, increases for each H allele  $(g_h, g_H, 2g_H)$
- 2. Mutation:  $x_{\sigma}^{s} = (1 \mu(g))x_{\sigma}^{t} + \mu(g)x_{\neg \sigma}^{t}$ 
  - $\phi$   $\mu(g)$  is  $\mu_{r\to R}$  for r genotypes and  $\mu_{R\to r}$  for R genotypes

- g represents each genotype
- 1. Gene Transfer:  $x_g^t = x_g + \sum_{x_p} x_{\neg g} x_R h(x_{\neg g}, x_R)$ 
  - $\diamond$  if g = RCH then  $\neg g = rCH$ , same for CH, cH, Ch, ch
  - $\diamond$  defined for R genotypes ( $x_R$ ), for r genotypes subtract the sum
  - $\diamond$  h() probability of transfer, increases for each H allele  $(g_h, g_H, 2g_H)$
- 2. Mutation:  $x_{\sigma}^{s} = (1 \mu(g))x_{\sigma}^{t} + \mu(g)x_{\neg \sigma}^{t}$  $\phi$   $\mu(g)$  is  $\mu_{r\to R}$  for r genotypes and  $\mu_{R\to r}$  for R genotypes
- 3. Selection:  $x'_{\sigma} = \frac{x_g^s f(g)}{\bar{x}}$

- ▶ g represents each genotype
- 1. Gene Transfer:  $x_g^t = x_g + \sum_{x_R} x_{\neg g} x_R h(x_{\neg g}, x_R)$ 
  - $\diamond$  if g = RCH then  $\neg g = rCH$ , same for CH, cH, Ch, ch
  - $\diamond$  defined for R genotypes ( $x_R$ ), for r genotypes subtract the sum
  - ⋄ h() probability of transfer, increases for each H allele  $(g_h, g_H, 2g_H)$
- 2. **Mutation:**  $x_g^s = (1 \mu(g))x_g^t + \mu(g)x_{\neg g}^t$  $\phi \ \mu(g)$  is  $\mu_{r \rightarrow R}$  for r genotypes and  $\mu_{R \rightarrow r}$  for R genotypes
- 3. Selection:  $x'_g = \frac{x_g^s f(g)}{\bar{w}}$ 
  - $\diamond$  f(g) picks the correct fitness modifier from Table 2

- g represents each genotype
- 1. Gene Transfer:  $x_g^t = x_g + \sum_{x_p} x_{\neg g} x_R h(x_{\neg g}, x_R)$ 
  - $\diamond$  if g = RCH then  $\neg g = rCH$ , same for CH, cH, Ch, ch
  - $\diamond$  defined for R genotypes ( $x_R$ ), for r genotypes subtract the sum
  - $\diamond$  h() probability of transfer, increases for each H allele  $(g_h, g_H, 2g_H)$
- 2. Mutation:  $x_{\sigma}^{s} = (1 \mu(g))x_{\sigma}^{t} + \mu(g)x_{\neg \sigma}^{t}$  $\phi$   $\mu(g)$  is  $\mu_{r\to R}$  for r genotypes and  $\mu_{R\to r}$  for R genotypes
- 3. Selection:  $x'_{\sigma} = \frac{x_g^* f(g)}{\bar{x}_{\sigma}}$ 
  - $\diamond$  f(g) picks the correct fitness modifier from Table 2
  - $\diamond$  average fitness  $\bar{w} = \sum_{\sigma} x_{\sigma}^{s} f(g)$

# 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 & Amp; 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.