How Quorum Sensing Interactions Affect Microbial Population Structures

02712 Final Project

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Carnegie Mellon University

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Example Section Title 1

Citation Example

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Example 2 column slide

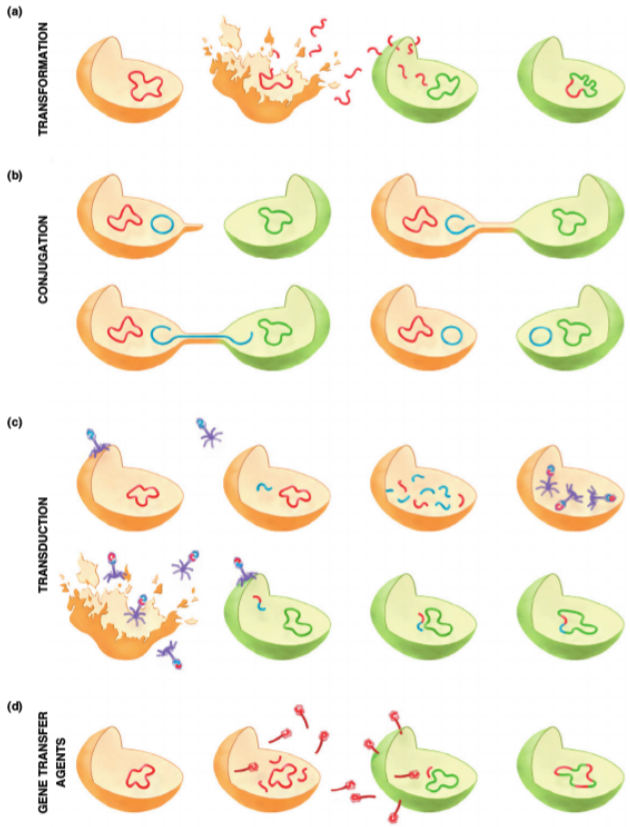

Figure 1: HGT Mechanisms

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

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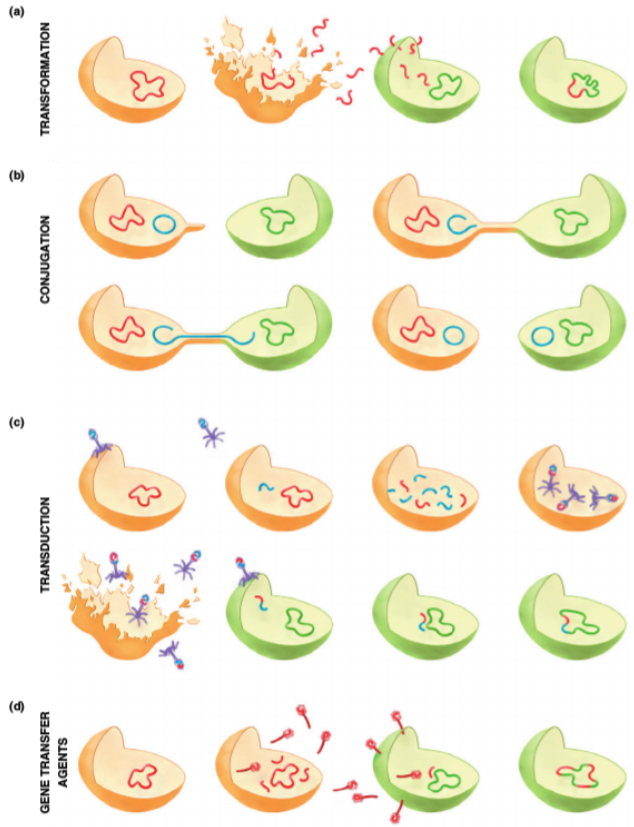

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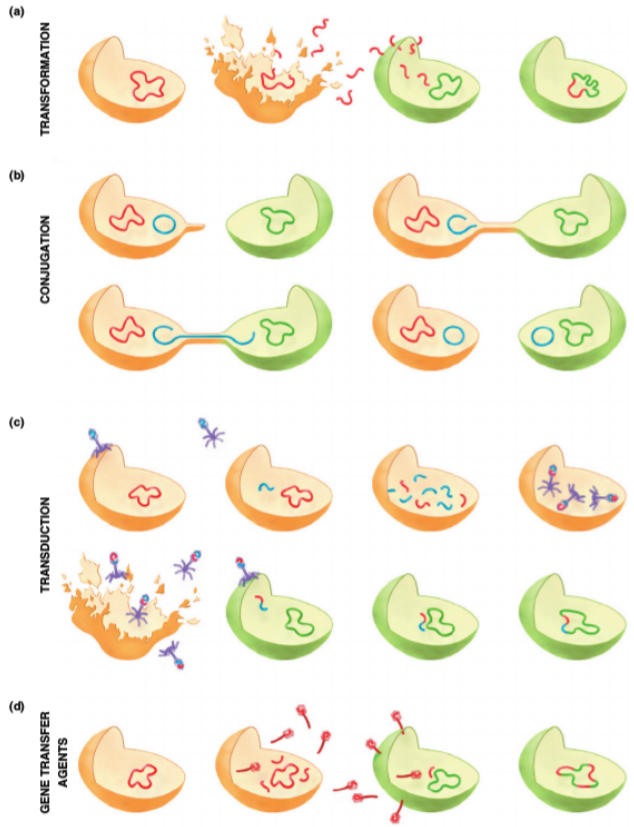

Figure 1: HGT Mechanisms

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

Math and sub lists

- Haploid population

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  - no sexual reproduction, consider gene transfer step
  - Gene transfer is analogous to oblique learning from Fogarty L. 2018
  - mutation is $r \rightarrow R$ or $R \rightarrow r$

Example Section Title 2

Example Table

Allele		Description
Major	Minor	
R	r	has/does not have resistance gene
H	h	HGT machinery is expressed/not expressed
C	c	CRISPR-Cas is expressed/not expressed

Table 1: Allele definitions

More complicated table with math

Genotype	*Environment*		
	E_n	E_b	E_a
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 2: Relative fitness values for each genotype in each environment

Lots of math

- g represents each genotype

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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
```

slide with subsections

Slide subsection 1

- resistance allele dominates even outside of antibiotic pressure

Slide subsection 2

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- environmental turnover rate significantly affects genotype frequencies

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- model phage population dynamics directly

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Slide subsection 2

- explore parameter space and look for empirical justifications
- model phage population dynamics directly
- incorporate terms that reflect biological trade-off of HGT/CRISPR

Bibliography I

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