

# Project: Biological Modeling & Simulations 02-712

## How Quorum Sensing Interactions Affect Microbial Population Structures

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# Example Section Title 1

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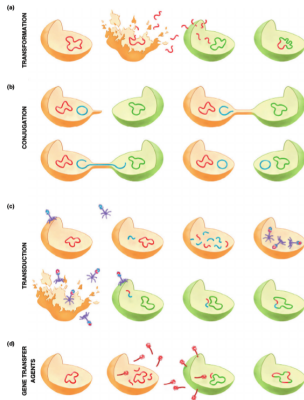
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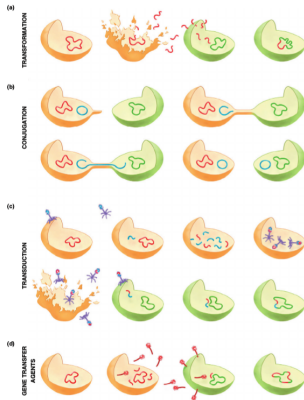
## Example 2 column slide



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

Figure 1: HGT Mechanisms

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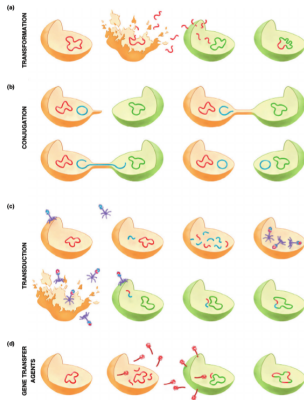


Figure 1: HGT Mechanisms

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

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  - ▶ 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	
<i>R</i>	<i>r</i>	has/does not have resistance gene
<i>H</i>	<i>h</i>	HGT machinery is expressed/not expressed
<i>C</i>	<i>c</i>	CRISPR-Cas is expressed/not expressed

Table 1: Allele definitions

## More complicated 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 2: Relative fitness values for each genotype in each environment

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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

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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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