

How Quorum Sensing Interactions Affect Population Structure

02-712 Final Project

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Background

Quorum-Sensing Systems

- Signal-Receptor molecule pairs that modulate gene expression

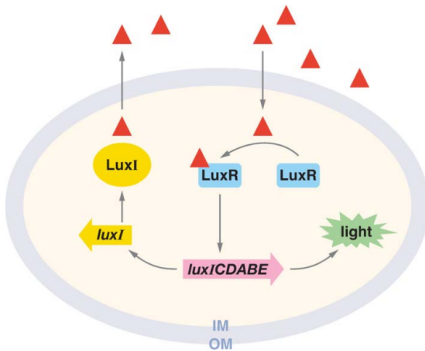


Figure 1: @qs_diagram

Quorum-Sensing Systems

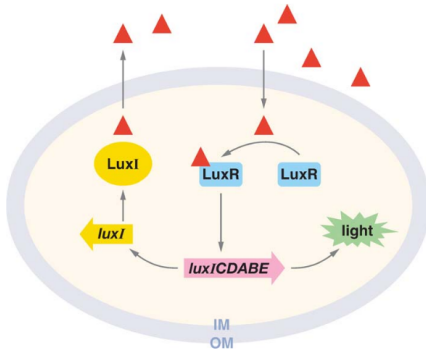


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- ▶ Once threshold density is reached, enough signal is received to upregulate target genes

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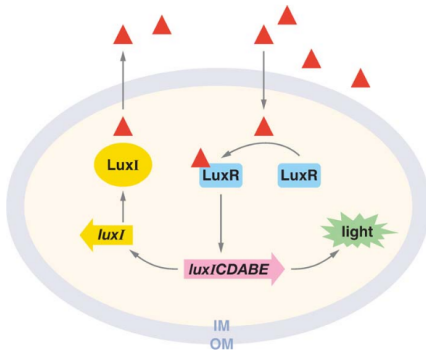
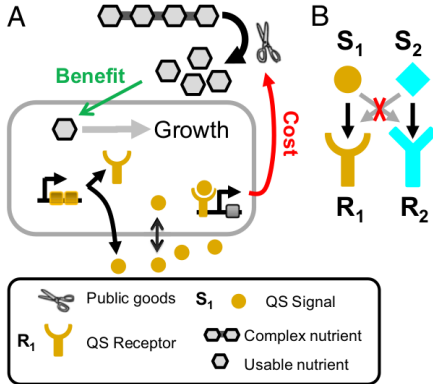


Figure 1: @qs_diagram

- ▶ Signal-Receptor molecule pairs that modulate gene expression
- ▶ Once threshold density is reached, enough signal is received to upregulate target genes
- ▶ Can lead to biofilms, antibiotic production etc.

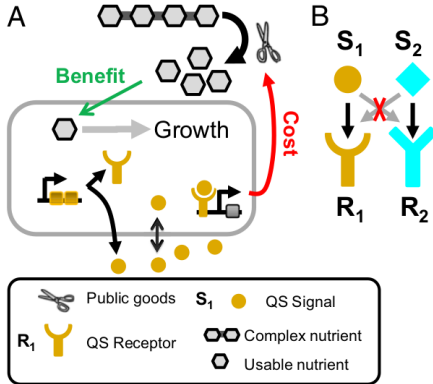
Public Goods and Cheating



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Figure 2: @eldar_2011

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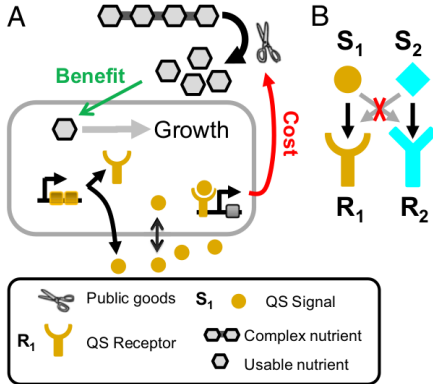


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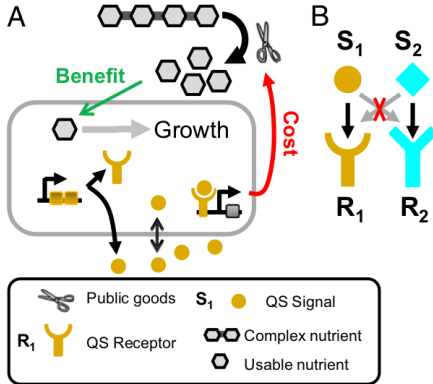


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- ▶ When quorum is reached, bacteria produce a “public good”
- ▶ Everyone benefits from this even if they don’t contribute
- ▶ Must produce the receptor, signal molecule and good to contribute
- ▶ Cheaters DO prosper (if you are a bacterium)

Who Cares?

- ▶ check the discussion from @eldar_2011 for references

Maintaining Freeloaders as a Diversity Reservoir

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Kin Recognition for Strains

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Maintaining Freeloaders as a Diversity Reservoir

Kin Recognition for Strains

Designing Cheaters to Disrupt Pathogen Growth

Methods

Basic ODE Model

Social conflict drives the evolutionary divergence of quorum sensing

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Model Equations

$$\frac{dn_i}{dt} = n_i \left(\frac{P_d}{P_d + 1} (1 - rf(R_i^{\text{active}})) - n_{\text{tot}} - \gamma_n \right)$$

$$\frac{dS_i}{dt} = \beta_S (n_i - S_i)$$

$$\frac{dE}{dt} = -\beta_E E + \sum_i f(R_i^{\text{active}}) n_i$$

$$\frac{dP_d}{dt} = J_{P_d} + V_{\text{max}} E - \beta_{P_d} \left(\frac{P_d}{P_d + 1} \right) n_{\text{tot}}$$

Signal-Receptor Activation Matrix K_{ac}

- ▶ The interaction term is defined as $R^{active} = \frac{K_{ac}\vec{S}}{K_{RS} + K_{ac}\vec{S}}$

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- ▶ K_{ac} is of dimension $|R| \times |S| = |n| \times |n|$

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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Custom Matrix

Matrix for 2 strains $R_1R_2S_1$ and R_2S_2

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Our Work

- ▶ Implemented in python using `scipy.integrate.solve_ivp`

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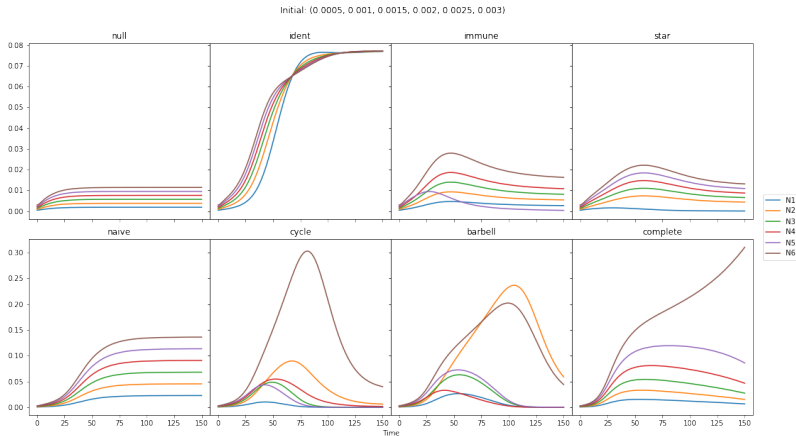
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- ▶ Simulate using gut microbiome data as initial state
- ▶ All code/results easily available to use on Github

Results

Comparing Different K_{ac} Matrices



How K_{ac} Sparsity Affects Population Structure

Simulating With Human Gut Microbiome Data

Discussion

Moral of the Study

Moral of the Study

Cheating works...

Moral of the Study

Cheating works...
(for bacteria)

Moral of the Study

Cheating works...

(for bacteria)

but cooperating is better!

Bibliography I