

# How Quorum Sensing Interactions Affect Population Structures

02-712 Final Project

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## Abstract

example abstract

## Background

## Methods

## Basic QS Interaction Model

### Assumptions

- Very basic assumption is that QS directly controls the levels the public good production
- Signal production is constitutive and quorum response is density dependent function of signal-bound receptor
- QS system is composed of 3 genes encoding signaling molecule ( $S$ ), receptor molecule ( $R$ ), and public good product
- The public good is a secreted enzyme whose product is a usable nutrient
- Growth rate is dependent on the level of usable nutrient, Hollings type II term
- Producing the public good reduces growth rate
- Density dependent cell death, leading to a logistic form of growth equation
- In the two divergent allele model ( $R1, R2$ ) and ( $S1, S2$ ), only 1 mutation allows the transition between alleles.  $R1$  can only bind  $S1$  and  $R2$  can only bind  $S2$
- The public good is an Exo-enzyme ( $E$ ), that catalyzes the cleavage of a complex nutrient ( $P$ ) into a transportable form ( $P_d$ )
  - Level of  $P$  is constant

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- A fraction  $r$  of the growth potential is diverted from growth to enzyme production at max production level
- Quorum response function is a monotonically increasing function with maximum of 1
- $R$ - $S$  interaction occurs on a much faster time scale so they are in a quasi steady state and levels of receptor is constant  $\rightarrow$  Michaelis Menton Relationship between  $[RS]$  and  $S$
- Quorum response form is  $f(x) = x^m$

## Results

### Comparing QS interaction matrices

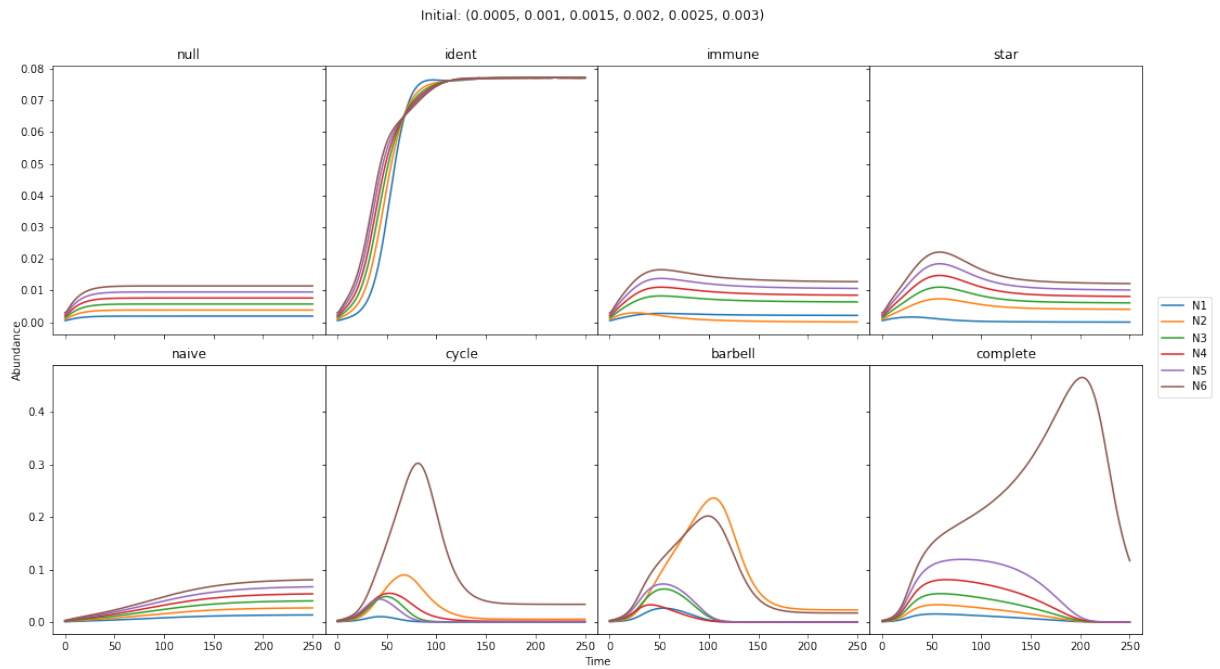


Figure 1:

Text about matrices

### Examining specific adjacency matrices

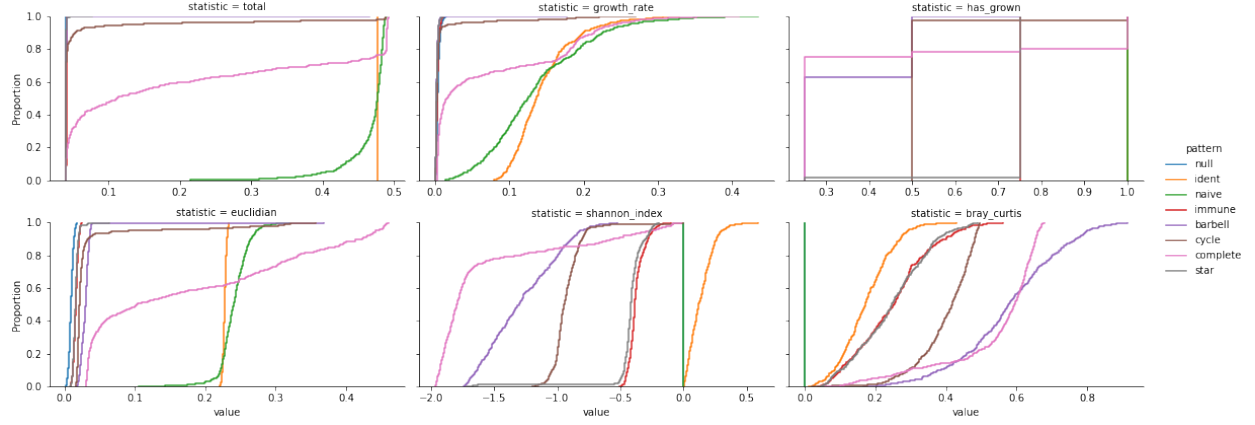


Figure 2: test

Text about patterns

## How sparsity affects model dynamics

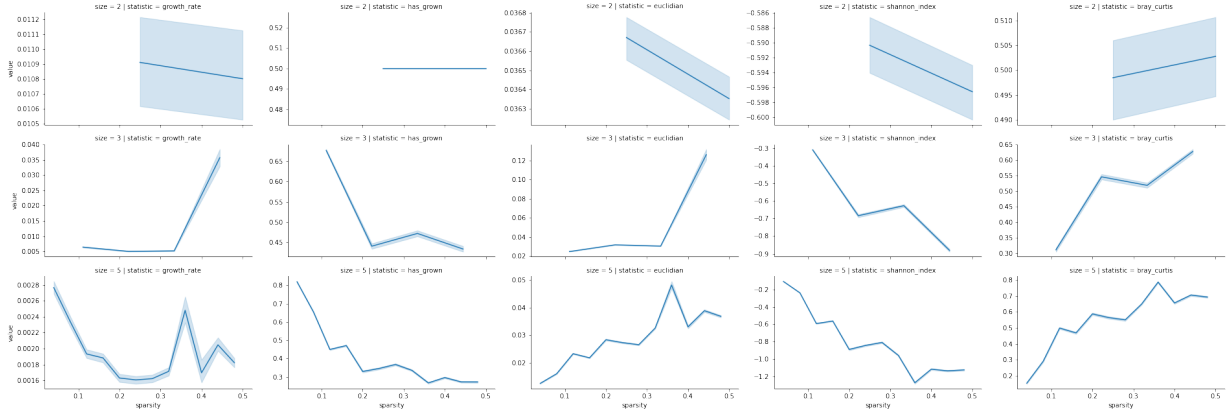


Figure 3: test

Text about sparsity

## Simulations with OTU data

The data we use is an OTU table  $O_I$ , an  $m \times n$  matrix representing the abundance of  $m$  OTUs across  $n$  samples. For each sample we use the abundance vector as our initial state and run the simulation with a given set of parameters. So after all simulations we get an OTU table  $O_T$  representing the terminal state of the model (abundance vector) for each initial state. Given the tables  $O_I, O_T$  for each sample we can calculate

- difference in  $\alpha$ -diversity (richness and Shannon Index)

- $\beta$ -diversity (Bray-Curtis distance)
- difference in skewness (Fisher's Coefficient of skewness)
- total population growth rate

and we examine how these statistics vary when using different  $K_a$  matrices and the same  $O_I$ .

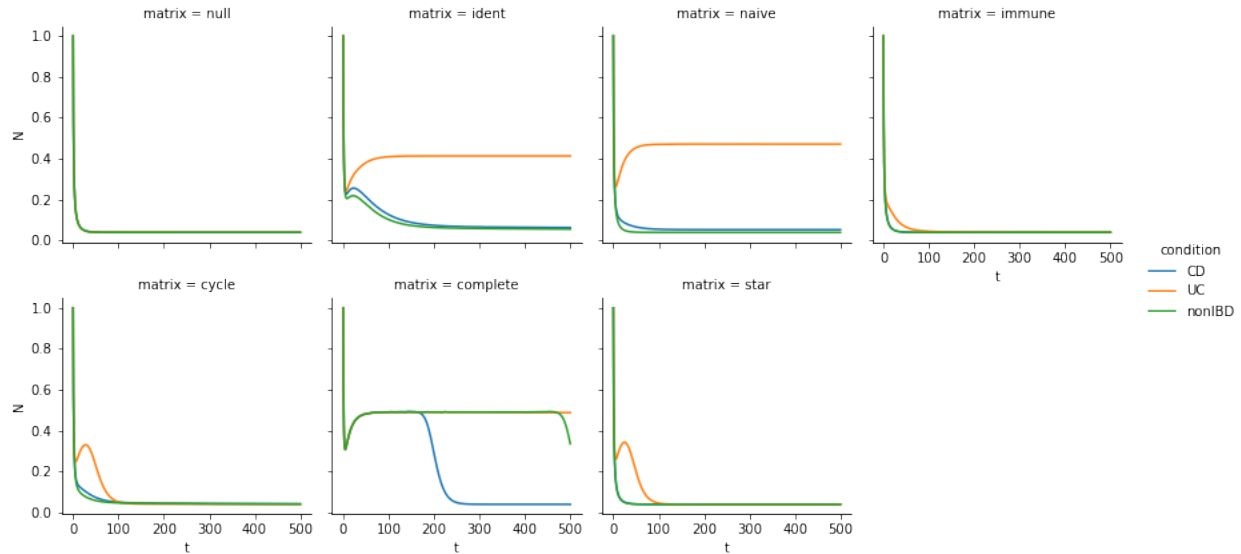


Figure 4: test

## Discussion

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