

How Quorum Sensing Interactions Affect Population Structures

02-712 Final Project

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Abstract

example abstract

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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
- 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

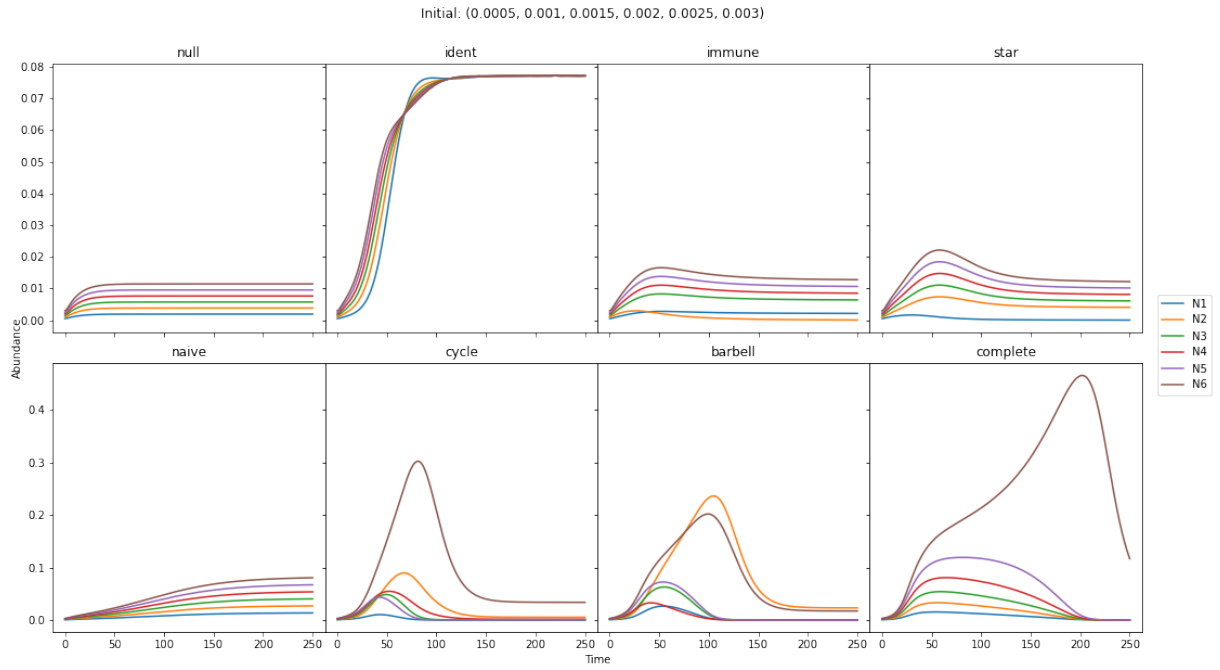


Figure 1:

Text about matrices

Examining specific adjacency matrices

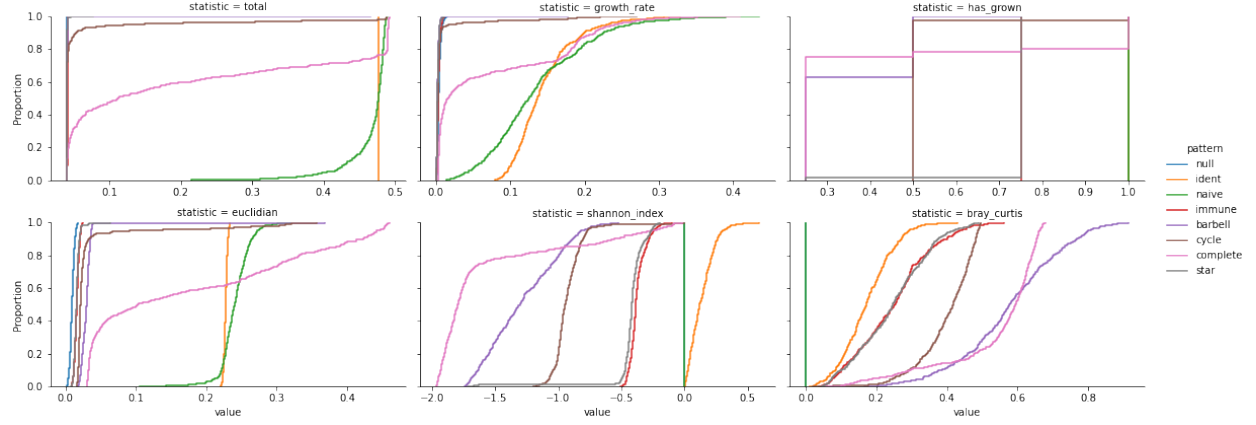


Figure 2: test

Text about patterns

How sparsity affects model dynamics

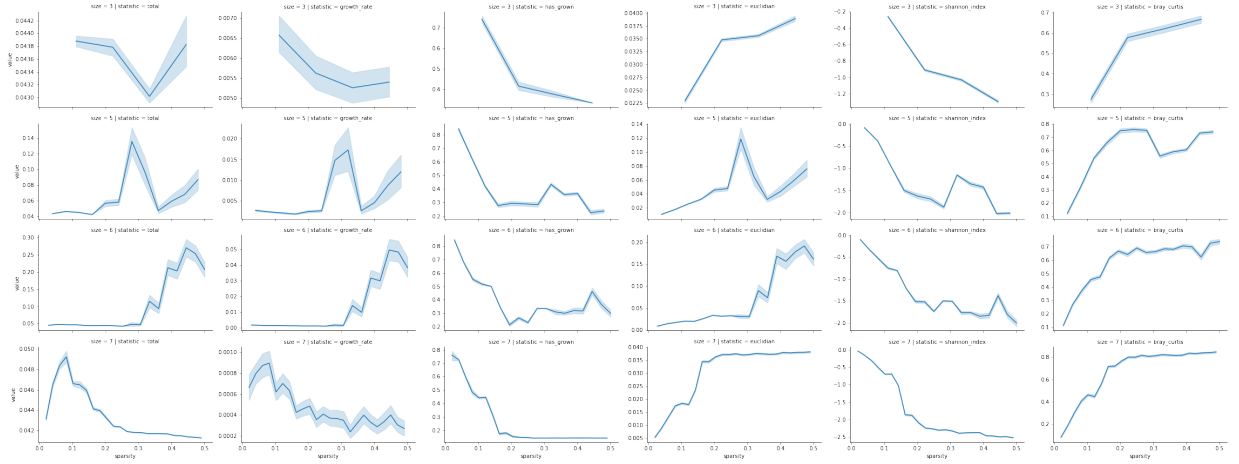


Figure 3: test

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 α -diversity (richness and Shannon Index)
- β -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 .

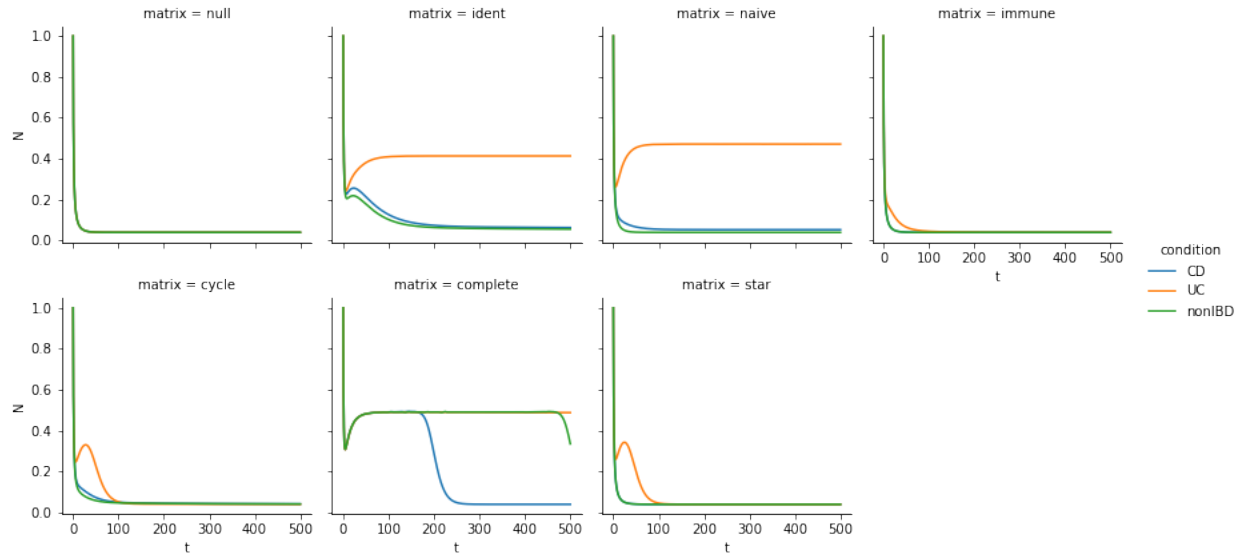


Figure 4: test

Discussion

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