Predictive modeling and parameter inference of gut microbial community from time-series data

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Introduction

$$\text{Human} = 10^{13} \text{ cells} + 10^{14} \text{ microbes}$$

Figure 1 : Gastrointestinal tract ilustration

Introduction

- ▶ Relationship between gut microbes and their host;
- ▶ Health and Disease;
- ▶ Mathematical models can predict the microbiota dynamics;
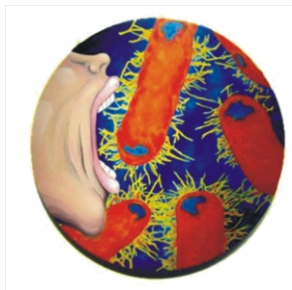
The gLV model

The generalized Lotka-Volterra model:

$$\dot{x}_i = x_i \left(r_i - \sum_j c_{ij} \; x_j \right)$$

where x_i is the abundance of species i;
r_i is the intrinsic growth rate;
and c_{ij} is the interaction from species j to i.

Immigration

$$\dot{x}_i = m_i + x_i\left(r_i - \sum_j c_{ij}\ x_j\right)$$

Where m_i is the immigration rate.

Materials and Methods

Python – simulation of the ODEs
Data collection – from a previous experiment (Marino et al., Jan 2014)

- DNA of 5 mice;
- 27 kinds of bacteria in each mouse;
- Abundance of 17 OTUs;
- Modeling the OTUs.

Materials and Methods

The gLV with m_i can be rewrite as:

$$\dot{x}_i = m_i + r_i \ x_i + \sum_j c_{ij} \ x_i \ x_j$$

Given the time-series data $x_i(t)$, all $x_i(t) \ x_j(t)$ are known.

- Linear regression to infer the parameters
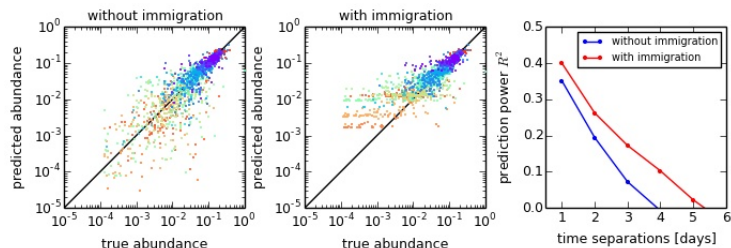- Compare both models

Results and Discussion

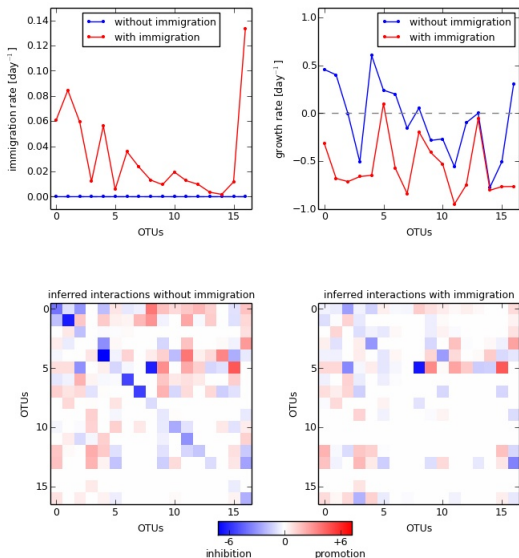Figure 2 : Linear regression and prediction results.

Results and Discussion

Figure 3 : m_i and r_i inference; interactions between OTUs.

Conclusion

- Prediction power;
- Importance of the m_i.

   Future works:

- Analyzing stability of the model with empirical parameters;
- Predict future evolutions of gut microbiome systems.

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THANK YOU!