Results from Prior NSF Support

A Objectives

Our Specific Aims are to

1. Develop and parameterize models of *T. gondii* behavior for epithelial, muscle, neuron, and [immune response cell] *in vivo*

2. Combine cell population model into a cell community model to describe organ level processes and (b) link gut, muscle, brain, and vascular organs together. Use to guide and fit to *in vitro* data.

3. Between Host Model

A direct outcome of our research will be the ability to ...

B Background

C Preliminary Results

D Research Design & Methods

Specific Aim 1:

Text

Specific Aim 2: Organ and Within-Host Modeling

Limitations to our Work

Timeline of Proposed Research

Relationship of Proposed Work to Long-Term Goals

E Broader Impacts

Box 1: Calculating the Likelihood of a Parameter Set $\mathbf{\Lambda}$

If we are interested in first estimating the set of parameters $\mathbf{\Lambda}$ used to calculate η we can treat the protein production rate of a gene ϕ as a nuisance parameter and integrate over it. Combining Eqn. (**??** with the assumption that $\phi \sim \text{Exp}(\zeta)$, the probability of observing a sequence fixed in a population as a function of $\mathbf{\Lambda}$ is,

$$a + b = c \tag{1}$$

Formally, Eqn. (1) represents the likelihood of $\mathbf{\Lambda}$ given a codon sequence. Thus, the total likelihood of $\mathbf{\Lambda}$ given the n observed gene sequences within a genome is simply,

$$\text{Lik}(\mathbf{\Lambda}|Z) = \prod_{i=1}^{n} P(Z|\mathbf{\Lambda}). \tag{2}$$

Whether likelihood function of Eqn. (2) is analyzed directly or, as we propose, weighted by a prior distribution, it provides method for estimating $\mathbf{\Lambda}$ using genomic data alone. These $\mathbf{\Lambda}$ values, in turn, can be used to predict ϕ (see Figure 1).

Figure 1: Illustration of SEMPPR's ability to accurately predict ϕ using parameters $\mathbf{\Lambda}$ generated from a simple MCMC algorithm and Eqn. (2).