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# A GENETIC SIGNATURE OF HOST-PARASITE COEVOLUTION IN CONTINUOUS SPACE

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A PREPRINT

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## Abstract

Here we identify a genetic signature of host-parasite coevolution in continuous space using spatial patterns of linkage-disequilibrium.

**Keywords** blah · bleee · bloo · these are optional and can be removed

## 1 Introduction

We consider a biallelic haploid two-locus model of fitness for each species. For the host and parasite we denote the possible haplotypes respectively by  $p_{AB}^H, p_{Ab}^H, p_{aB}^H, p_{ab}^H$  and  $p_{AB}^P, p_{Ab}^P, p_{aB}^P, p_{ab}^P$ . Similarly, gene frequencies are denoted by  $p_A^X$  and  $p_B^X$  for species  $X = H, P$ . Linkage disequilibrium within species  $X$  can be written as  $D_X = p_{AB}^X - p_A^X p_B^X$  or  $D_X = p_{AB}^X p_{ab}^X - p_{Ab}^X p_{aB}^X$ . We assume that individuals encounter each at random and that when a host individual with haploid genotype  $i$  encounters a parasite individual with haploid genotype  $j$ , infection occurs with probability  $\alpha_{ij}$ . Given an infection occurs, we assume the host experiences a reduction in fitness by the amount  $s_H$ . Hence, per-capita growth rates of host haplotypes are given by

$$m_{AB}^H = -s_H(\alpha_{AB,AB}p_{AB}^P + \alpha_{AB,Ab}p_{Ab}^P + \alpha_{AB,aB}p_{aB}^P + \alpha_{AB,ab}p_{ab}^P), \quad (1a)$$

$$m_{aB}^H = -s_H(\alpha_{aB,AB}p_{AB}^P + \alpha_{aB,Ab}p_{Ab}^P + \alpha_{aB,aB}p_{aB}^P + \alpha_{aB,ab}p_{ab}^P), \quad (1b)$$

$$m_{Ab}^H = -s_H(\alpha_{Ab,AB}p_{AB}^P + \alpha_{Ab,Ab}p_{Ab}^P + \alpha_{Ab,aB}p_{aB}^P + \alpha_{Ab,ab}p_{ab}^P), \quad (1c)$$

$$m_{ab}^H = -s_H(\alpha_{ab,AB}p_{AB}^P + \alpha_{ab,Ab}p_{Ab}^P + \alpha_{ab,aB}p_{aB}^P + \alpha_{ab,ab}p_{ab}^P). \quad (1d)$$

Similarly, by assuming infection increases per-capita growth rates of parasite haplotypes by the amount  $s_P$ , we obtain

$$m_{AB}^P = -s_H(\alpha_{AB,AB}p_{AB}^H + \alpha_{Ab,AB}p_{Ab}^H + \alpha_{aB,AB}p_{aB}^H + \alpha_{ab,AB}p_{ab}^H), \quad (2a)$$

$$m_{Ab}^P = -s_H(\alpha_{AB,Ab}p_{AB}^H + \alpha_{Ab,Ab}p_{Ab}^H + \alpha_{aB,Ab}p_{aB}^H + \alpha_{ab,Ab}p_{ab}^H), \quad (2b)$$

$$m_{aB}^P = -s_H(\alpha_{AB,aB}p_{AB}^H + \alpha_{Ab,aB}p_{Ab}^H + \alpha_{aB,aB}p_{aB}^H + \alpha_{ab,aB}p_{ab}^H), \quad (2c)$$

$$m_{ab}^P = -s_H(\alpha_{AB,ab}p_{AB}^H + \alpha_{Ab,ab}p_{Ab}^H + \alpha_{aB,ab}p_{aB}^H + \alpha_{ab,ab}p_{ab}^H). \quad (2d)$$

The per-capita population growth rate of species  $X$  can then be written as  $\bar{m}_X = m_{AB}^X p_{AB}^X + m_{aB}^X p_{aB}^X + m_{Ab}^X p_{Ab}^X + m_{ab}^X p_{ab}^X$ . Assuming clonal reproduction, we can write down the evolution of haploid genotype frequency  $p_i^X$  as

$$\frac{dp_i^X}{dt} = (m_i^X - \bar{m}_X) p_i^X. \quad (3)$$

However, since our interests are in sexually reproducing diploid organisms we need to extend this model.

## 2 Approximation

Modeling IBD in 2D space will be challenging since the SPDE approach breaks down here. One option is simulate the rescaled process that approximates the superprocess solution. Another is to assume allele frequencies are sufficiently close to 0.5 to remove the multiplicative noise term. However, for just two loci this assumption may not hold (for a polygenic trait it may...).