A GENETIC SIGNATURE OF HOST-PARASITE COEVOLUTION IN CONTINUOUS SPACE

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 \cdot blee \cdot bloo \cdot 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 i, infection occurs with probability α_{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

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

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

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

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

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

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

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

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

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

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

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

2 Headings: first level

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2.1 Headings: second level

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$$\xi_{ij}(t) = P(x_t = i, x_{t+1} = j | y, v, w; \theta) = \frac{\alpha_i(t) a_{ij}^{w_t} \beta_j(t+1) b_j^{v_{t+1}}(y_{t+1})}{\sum_{i=1}^{N} \sum_{j=1}^{N} \alpha_i(t) a_{ij}^{w_t} \beta_j(t+1) b_j^{v_{t+1}}(y_{t+1})}$$

2.1.1 Headings: third level

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3 Examples of citations, figures, tables, references

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The documentation for **natbib** may be found at

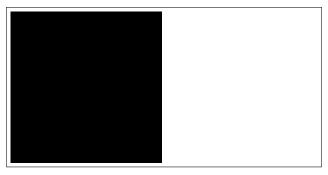


Figure 1: Sample figure caption.

http://mirrors.ctan.org/macros/latex/contrib/natbib/natnotes.pdf

Of note is the command \citet, which produces citations appropriate for use in inline text. For example,

\citet{hasselmo} investigated\dots

produces

Hasselmo, et al. (1995) investigated...

https://www.ctan.org/pkg/booktabs

3.1 Figures

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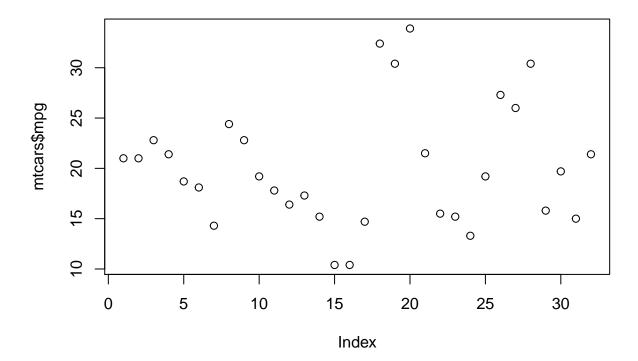
See Figure 1. Here is how you add footnotes. [^Sample of the first footnote.]

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plot(mtcars\$mpg)

Table 1: Sample table title

	Part	
Name	Description	Size (μm)
Dendrite Axon Soma	Input terminal Output terminal Cell body	$ \sim 100 \\ \sim 10 \\ up to 10^6 $



3.2 Tables

Etiam euismod. Fusce facilisis lacinia dui. Suspendisse potenti. In mi erat, cursus id, nonummy sed, ullamcorper eget, sapien. Praesent pretium, magna in eleifend egestas, pede pede pretium lorem, quis consectetuer tortor sapien facilisis magna. Mauris quis magna varius nulla scelerisque imperdiet. Aliquam non quam. Aliquam porttitor quam a lacus. Praesent vel arcu ut tortor cursus volutpat. In vitae pede quis diam bibendum placerat. Fusce elementum convallis neque. Sed dolor orci, scelerisque ac, dapibus nec, ultricies ut, mi. Duis nec dui quis leo sagittis commodo.

See a we some Table ~ 1 .

3.3 Lists

- Lorem ipsum dolor sit amet
- consectetur adipiscing elit.
- Aliquam dignissim blandit est, in dictum tortor gravida eget. In ac rutrum magna.

Hadash, Guy, Einat Kermany, Boaz Carmeli, Ofer Lavi, George Kour, and Alon Jacovi. 2018. "Estimate and Replace: A Novel Approach to Integrating Deep Neural Networks with Existing Applications." arXiv Preprint arXiv:1804.09028.

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