

Testing pleiotropy vs. separate QTL in multiparental populations

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Abstract

- High-dimensional phenotypes & multiparental populations inform complex trait architecture
- New analysis tools needed
- Developed a test of pleiotropy vs. separate QTL for multiparental populations
- Evidence for two separate QTL affecting three behavioral traits in a 3 cM region
- Shared methods in an R package, `qtl2pleio`
<<https://github.com/fboehm/qtl2pleio>>

Introduction

- Experimentalists measure thousands of phenotypes with RNA sequencing and mass spectrometry
- Multiparental populations enable high-resolution QTL mapping
- Together, they inform complex trait genetics
- New analysis tools, such as our test of pleiotropy vs. separate QTL, are needed

Background

- Jiang and Zeng (1995) developed a pleiotropy vs. separate QTL test for two-parent crosses
- Applies to two traits that map to a single genomic region
- Null hypothesis: pleiotropy
- Alternative: presence of two separate QTL
- Perform a two-dimensional QTL scan
- Calculate likelihood ratio test statistic

Challenges

- Relatedness: *Multivariate polygenic random effects*
- Eight founder lines: *8 fixed effects*
- Test statistic calibration: *Parametric bootstrap test*

Test procedure

- Fit the model:

$$Y = XB + G + E$$

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$$G \sim MN(0, K, V_g)$$

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$$E \sim MN(0, I, V_e)$$

- X contains allele probabilities
- B contains allele effects
- Calculate likelihood for each model fit
- Test statistic:

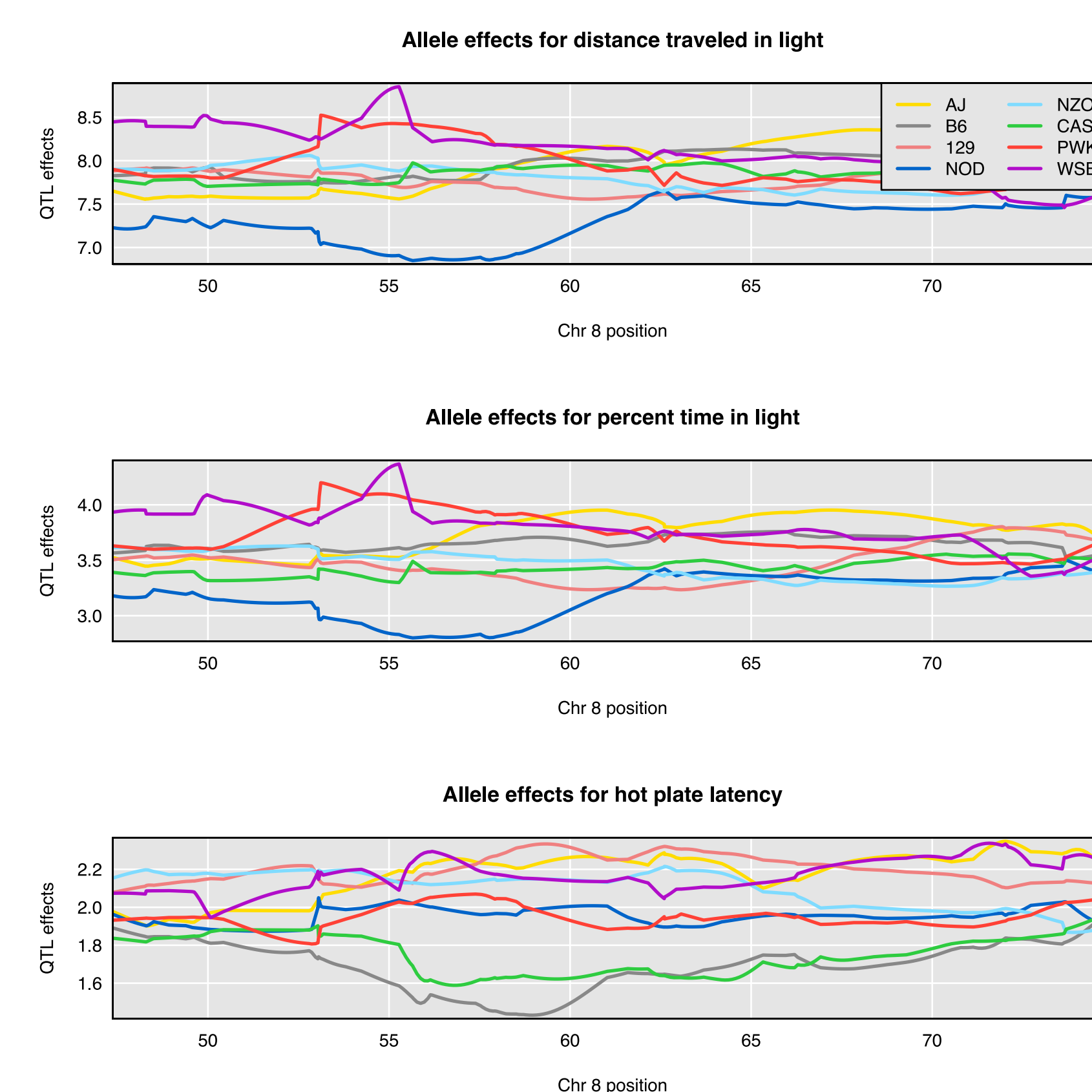
$$-\log_{10} \frac{\max L_0(B, \Sigma, \omega_1)}{\max L_A(B, \Sigma, \omega_1, \omega_2)}$$

- Parametric bootstrap to get p-value

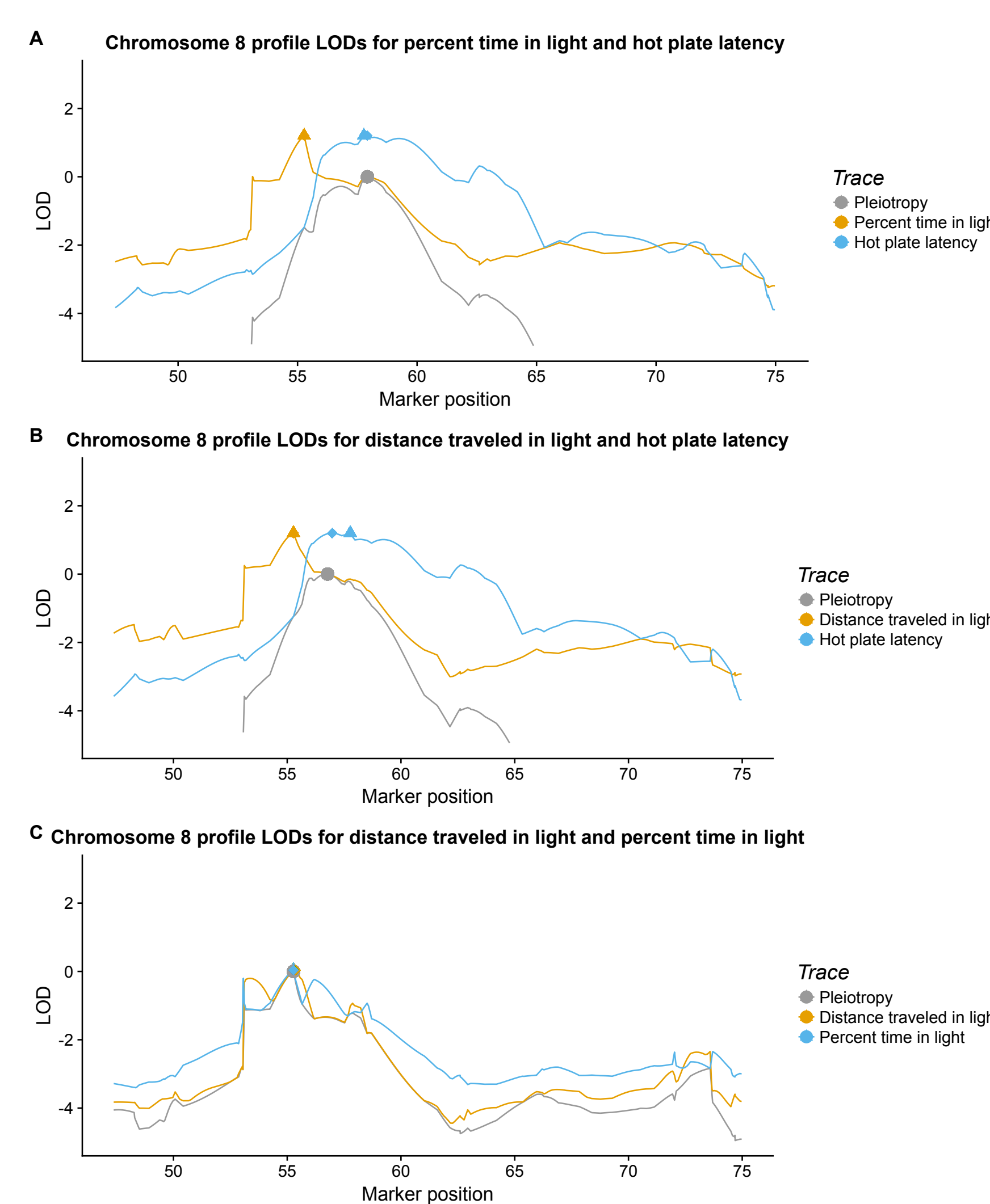
Behavioral genetics

- Logan et al. (2013) and Recla et al. (2014) genotyped and phenotyped 261 Diversity Outbred mice
- Identified *Hydin* as the Chr 8 gene affecting “hot plate latency” at 57 cM
- Identified Chr 8 QTLs for “percent time in light” and “distance traveled in light” at 55 cM
- Motivated us to ask if *Hydin* also affects “percent time in light” and “distance traveled in light”

Allele effects plots



Profile LOD plots for pairwise



3 pairwise tests

Trait1	Trait2	pvalue
pct. time in light	hot plate latency	0.109
distance traveled	hot plate latency	0.108
pct. time in light	distance traveled	0.871

Conclusions

- Evidence for two separate QTL affecting the 3 traits
- 1 QTL affects both “distance traveled in light” and “percent time in light”
- Second QTL contains *Hydin* and affects “hot plate latency”

Future directions

- Examine expression data from Keller et al. (2018)
- 378 Diversity Outbred mice
- Expression QTL hotspot dissection
- Statistical power studies
- Comparisons with mediation test results

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qtl2pleio R package:

<<https://github.com/fboehm/qtl2pleio>>

References

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