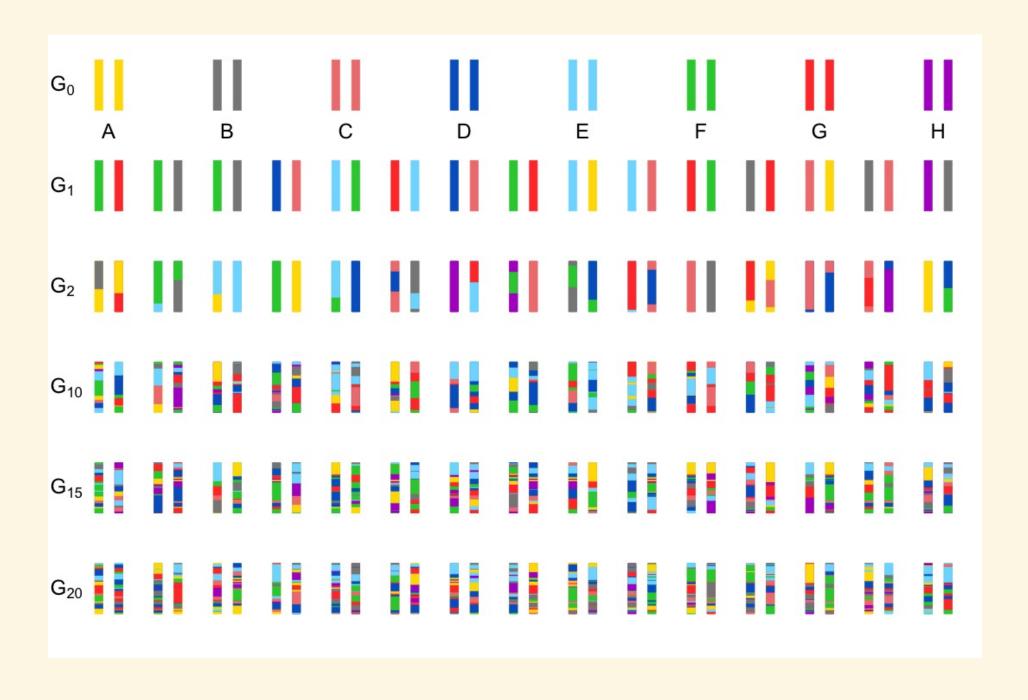
## Testing pleiotropy in multiparental populations

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#### Multiparental populations



### Background

- 10,000+ traits with RNA sequencing and mass spectrometry
- Quantitative trait locus mapping identifies genetic loci that affect measurable traits
- Multiparental populations offer high-resolution QTL mapping
- New analysis tools, such as a pleiotropy test for multiparental populations, are needed

### Benefits of a new pleiotropy test

- Insights into genetic architecture
- Tool for expression trait hotspot dissection
- Complements mediation analysis

## Jiang and Zeng (1995) test

- Two-parent crosses
- Applies to two traits that co-map
- \(H\_0\): Pleiotropy
- \(H\_A\): Two separate QTL

### Jiang and Zeng (1995) test

- Perform a two-dimensional two-QTL scan
  - $\circ \quad \backslash (\text{vec}(Y) = \text{Xvec}(B) + \text{vec}(E) \backslash)$
  - Calculate likelihood at each ordered pair of positions
- Calculate likelihood ratio test statistic

### Challenges in multiparental populations

Complex patterns of relatedness

#### Multivariate random effects

Multiple founder lines

#### Fixed effect for each founder allele



Photo by UNC Computational Genetics

### Test procedure

- Perform a two-dimensional two-QTL scan
  - $\circ \quad \backslash (\text{vec}(Y) = \text{Xvec}(B) + \text{vec}(G) + \text{vec}(E) \backslash)$
  - Calculate likelihood at each ordered pair of positions
- Calculate likelihood ratio test statistic

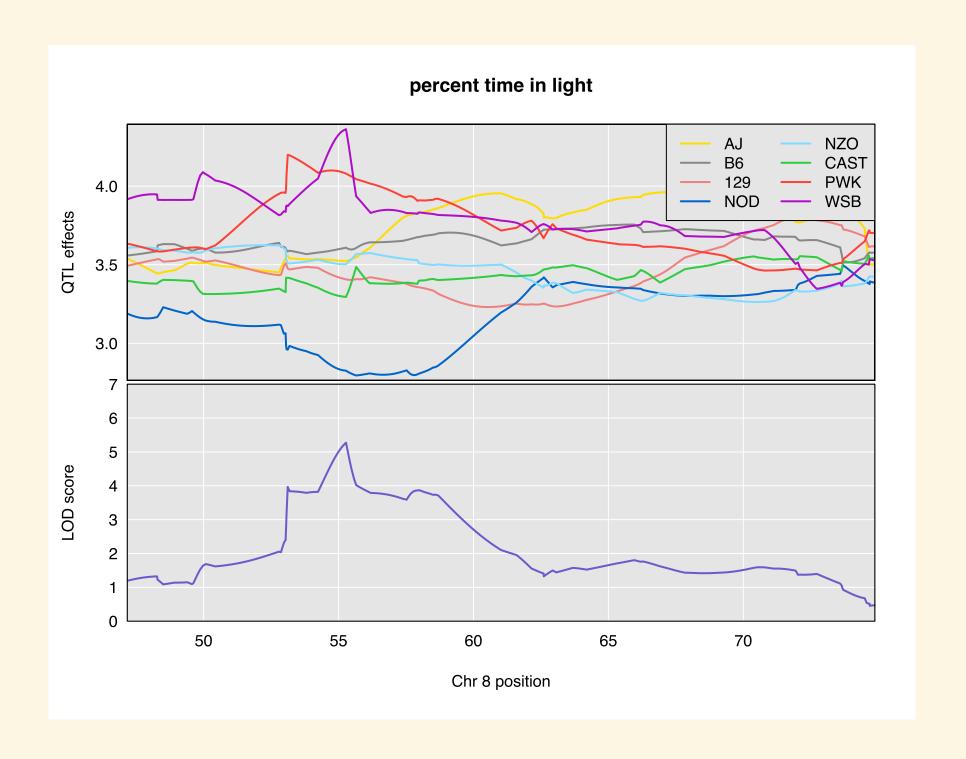
### Test procedure

- Test statistic: \$\$-\log\_{10} \frac{\max} (\text{likelihood under pleiotropy})}{\max} (\text{likelihood for separate QTL})}\$\$
- Parametric bootstrap to get a \((p\))-value

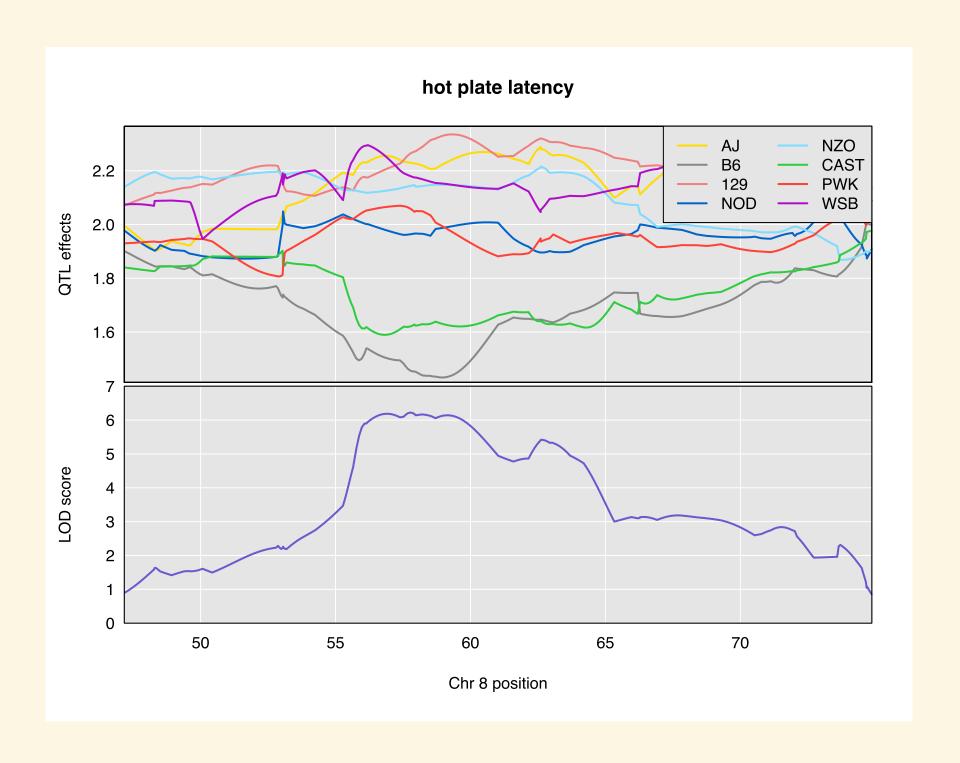
### **Application**

- Logan, et al. (2013) and Recla, et al. (2014) studied 261 Diversity Outbred mice
- Measured about two dozen behavioral traits
- Two traits map to Chr 8:
  - "hot plate latency" (57 cM)
  - "percent time in light" (55 cM)

# Percent time in light



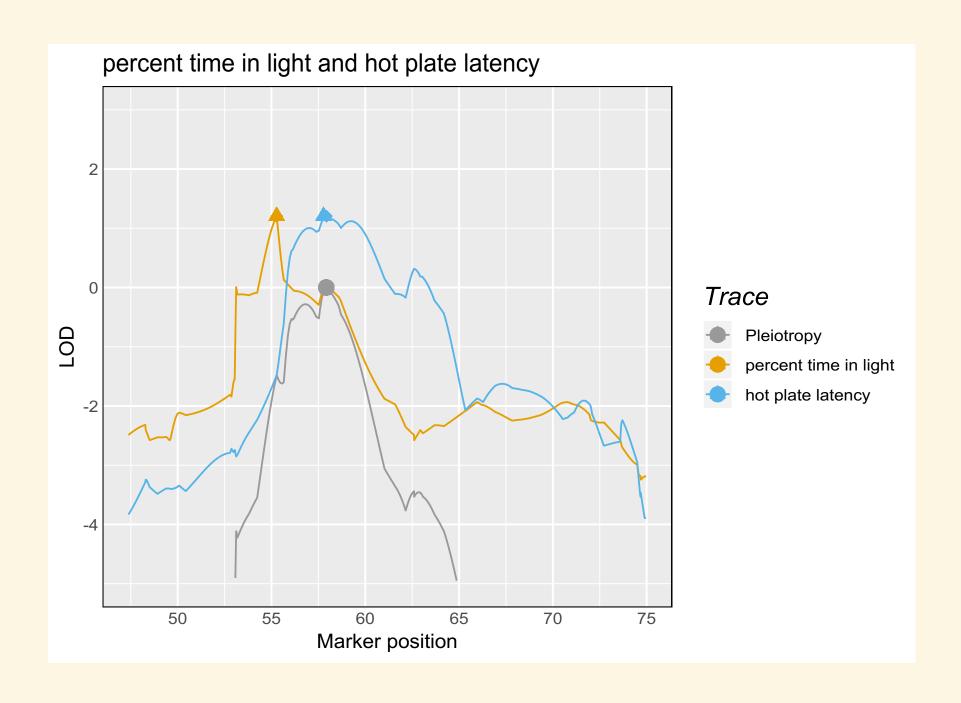
# Hot plate latency



#### LOD definitions

- \$\$LOD(\lambda\_1, \lambda\_2) = ll\_{10}
  (\lambda\_1, \lambda\_2) \max\_{\lambda} ll\_{10}
  (\lambda, \lambda)\$\$
- \$\text{profile LOD}\_{\text{trait 1}}(\lambda\_1) = \max\_{\lambda\_2}LOD(\lambda\_1, \lambda\_2)\$\$
- \$\$LOD\_p(\lambda) = ll\_{10}(\lambda, \lambda) \max\_{\lambda} ll\_{10}(\lambda, \lambda) \$\$

#### Profile LOD



#### Test results

- $(\log_{10} \Lambda = 1.2)$
- (p = 0.11) (1000 bootstrap samples)

# Power study with local expression QTL

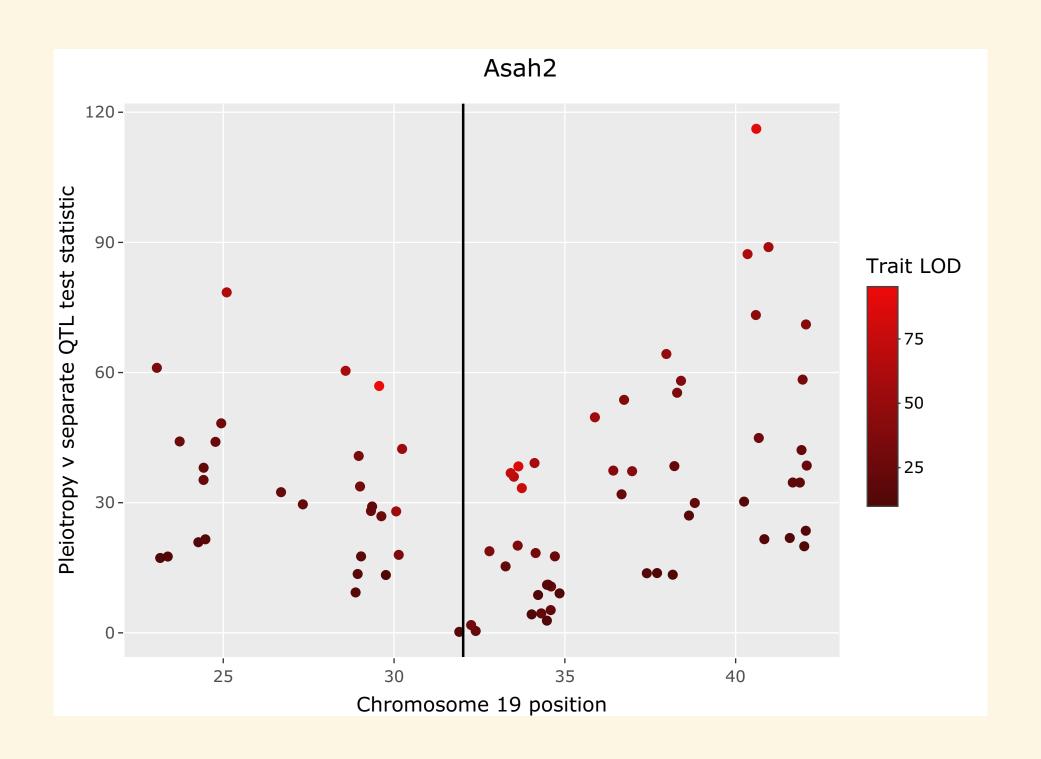
#### Data

- Keller, et al. (2018) measured pancreatic islet gene expression levels in 378 Diversity Outbred mice
- 80 local expression QTL were identified in a 20-Mb region of Chr 19
  - o local: expression trait QTL is near gene position
- Assume that a local expression QTL affects only one local expression trait

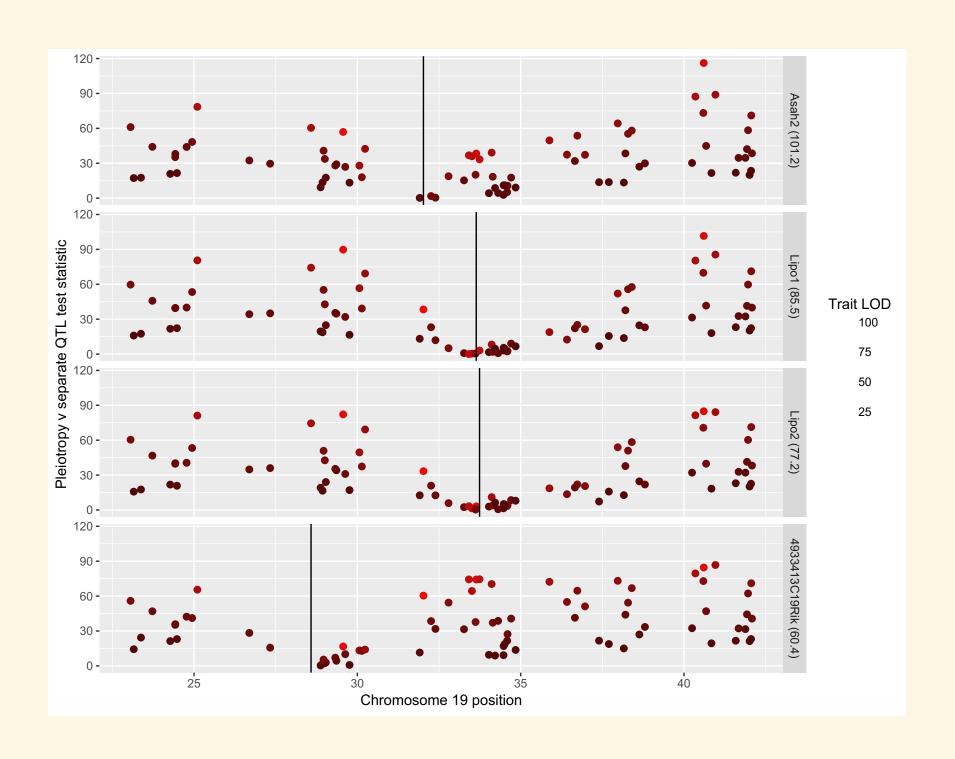
### Design

- Examine power with known expression trait QTL locations
  - Interlocus distance
  - Univariate LOD
- 4 strong, centrally located, local eQTL chosen as "anchor" traits
  - Asah2, Lipo1, Lipo2, 4933413C19Rik
- Pairwise pleiotropy tests each involving one anchor and one of 79 other traits

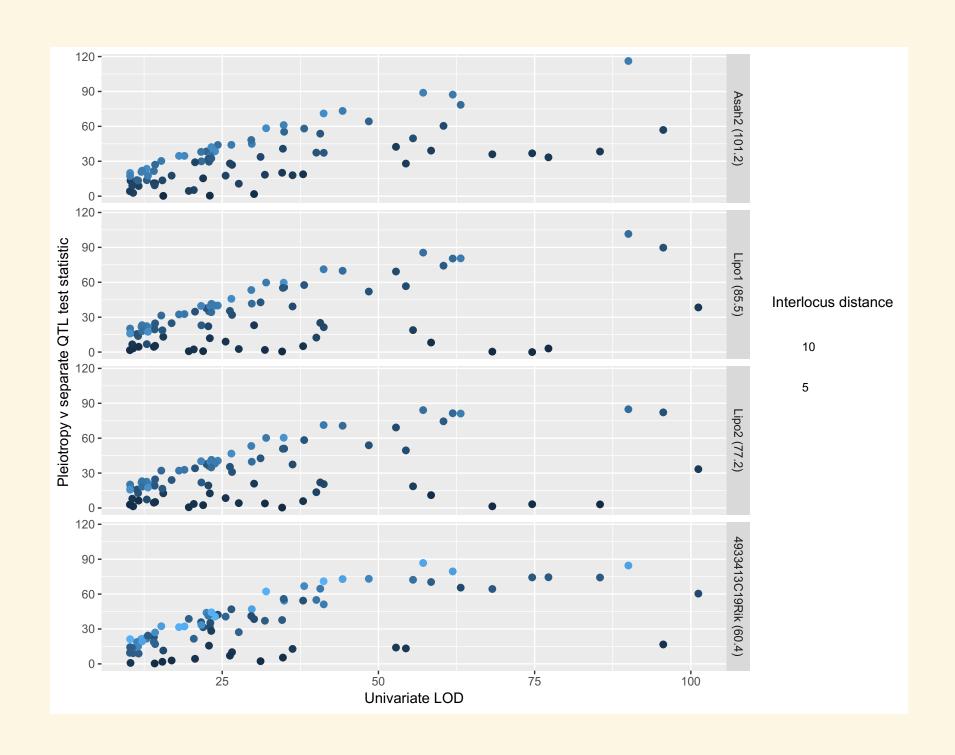
#### Interlocus distance



### Interlocus distance



# Univariate LOD



#### Conclusions

- \(\uparrow\) Pleiotropy test statistics
  - \(\uparrow\) Interlocus distance
  - \(\uparrow\) Univariate LOD

# qtl2pleio R package

### qtl2pleio R package

- Functions for \((d\))-variate, \((d\))-QTL scan & profile LOD plots
- Uses C++ for matrix calculations (via Rcpp and RcppEigen)
- Uses gemma2 R implementation of GEMMA EM algorithm for multivariate random effects
- Unit tests, vignettes, and version control

#### Summary

- 1. Background
- 2. Methods
- 3. Applications
  - a. Pleiotropy testing and mediation analysis
  - b. Power in pleiotropy testing
  - c. Microbiome case study
- 4. Software
- 5. Conclusions

#### References

Jiang, C. and Z. Zeng (1995). "Multiple trait analysis of genetic mapping for quantitative trait loci." In: *Genetics* 140.3, pp. 1111-1127.

Keller, M. P, D. M. Gatti, et al. (2018). "Genetic Drivers of Pancreatic Islet Function". In: *Genetics*, pp. genetics-300864.

Logan, R. W, R. F. Robledo, et al. (2013). "High-precision genetic mapping of behavioral traits in the diversity outbred mouse population". In: *Genes, Brain and Behavior* 12.4, pp. 424-437.