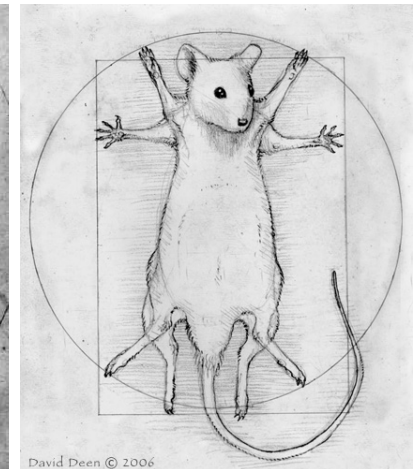
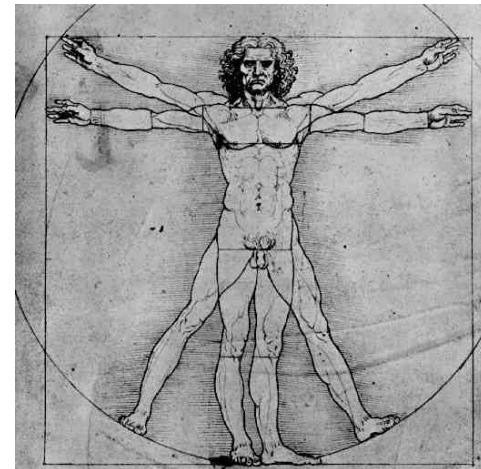


Mapping multiple QTL in experimental crosses

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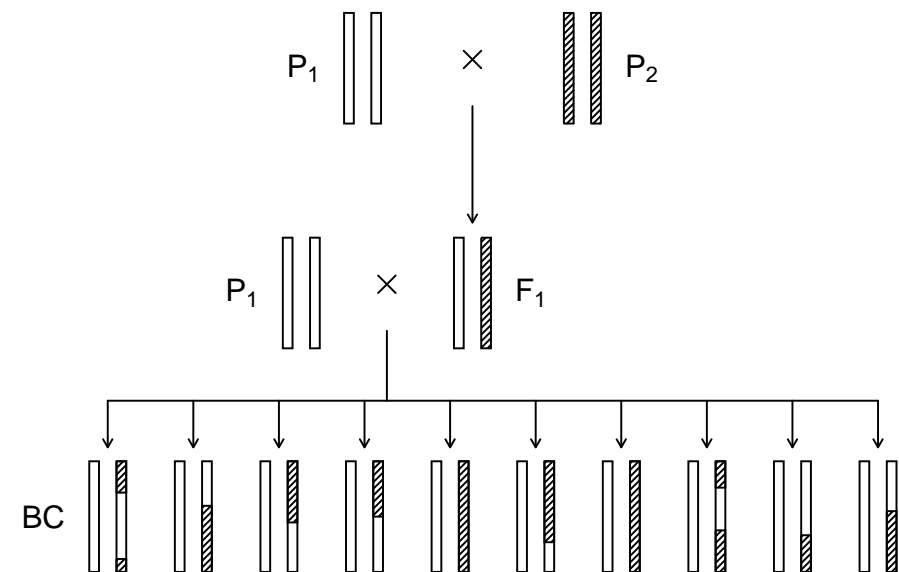


www.daviddeen.com

3

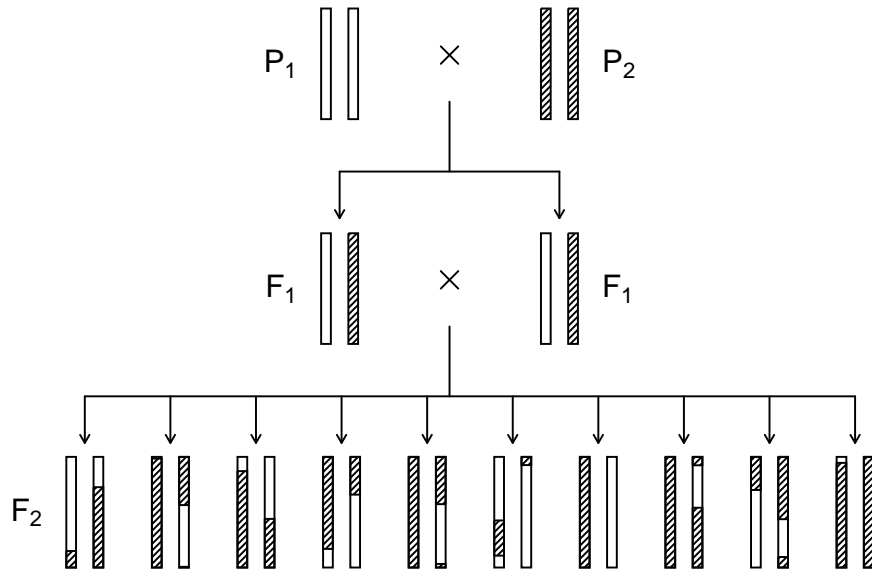


Backcross



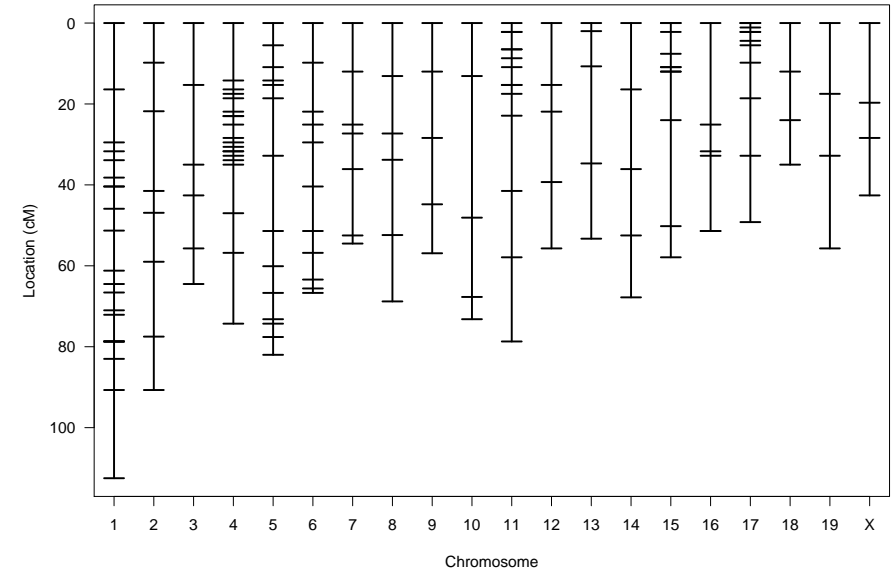
4

Intercross



5

Genetic map



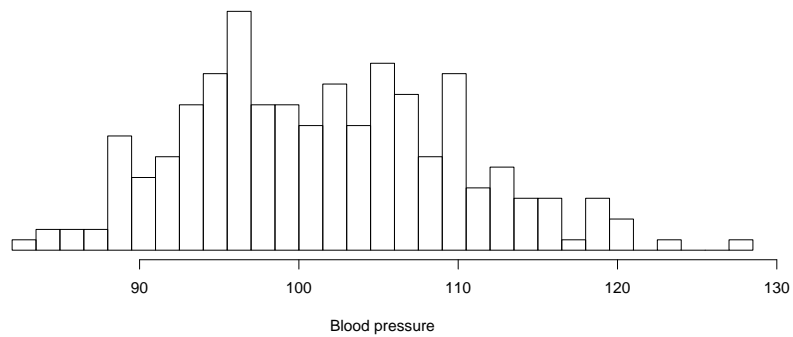
7

Phenotype data

Sugiyama et al. Genomics 71:70-77, 2001

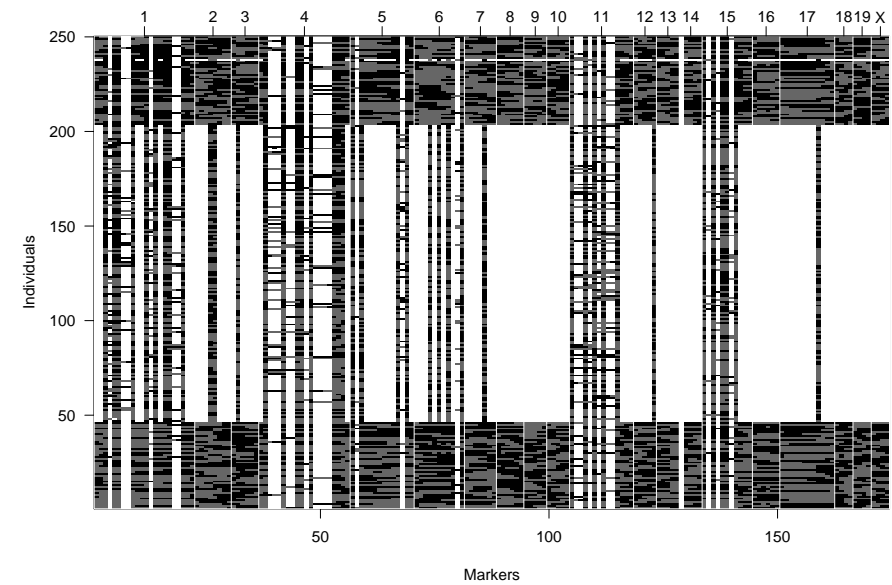
250 male mice from the backcross (A × B) × B

Blood pressure after two weeks drinking water with 1% NaCl



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Genotype data



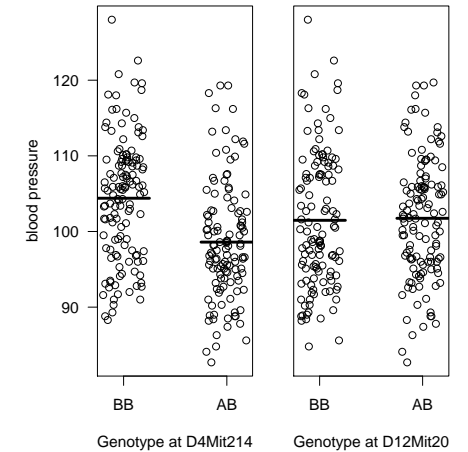
8

Goals

- Identify quantitative trait loci (QTL) (and interactions among QTL)
- Interval estimates of QTL location
- Estimated QTL effects

ANOVA at marker loci

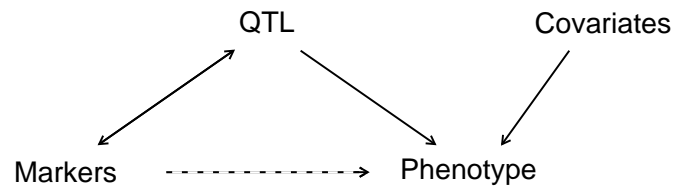
- Split mice into groups according to genotype at a marker.
- Do a t-test / ANOVA.
- Repeat for each marker.



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Statistical structure



Interval mapping

Lander & Botstein (1989)

- Assume a single QTL model.
- Consider each position in the genome, one at a time, as the location of the putative QTL.
- Let $q = 0/1$ if the (unobserved) QTL genotype is BB/AB. (Or $0/1/2$ if the QTL genotype is AA/AB/BB in an intercross.)

Assume $y | q \sim N(\mu_q, \sigma)$

- Calculate $p_q = \Pr(q | \text{marker data})$.

$y | \text{marker data} \sim \sum_q p_q \phi(y | \mu_q, \sigma)$

The missing data problem:

Markers \longleftrightarrow QTL

The model selection problem:

QTL, covariates \longrightarrow phenotype

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LOD scores

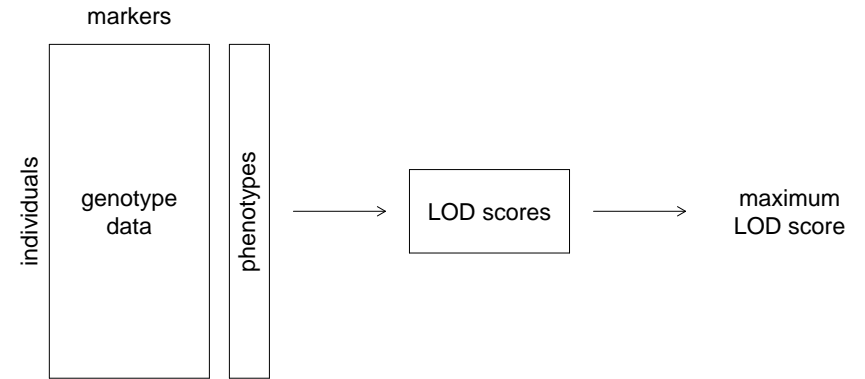
$\text{LOD}(\lambda) = \log_{10}$ likelihood ratio comparing the hypothesis of a QTL at position λ versus that of no QTL

$$= \log_{10} \left\{ \frac{\Pr(y|\text{QTL at } \lambda, \hat{\mu}_{q\lambda}, \hat{\sigma}_\lambda)}{\Pr(y|\text{no QTL}, \hat{\mu}, \hat{\sigma})} \right\}$$

$\hat{\mu}_{q\lambda}, \hat{\sigma}_\lambda$ are the MLEs, assuming a single QTL at position λ .

No QTL model: The phenotypes are iid $N(\mu, \sigma^2)$.

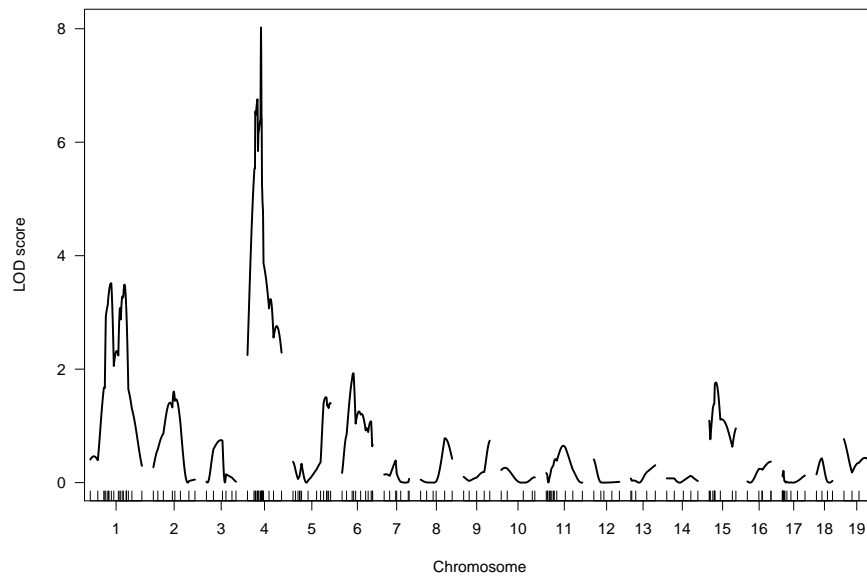
Permutation test



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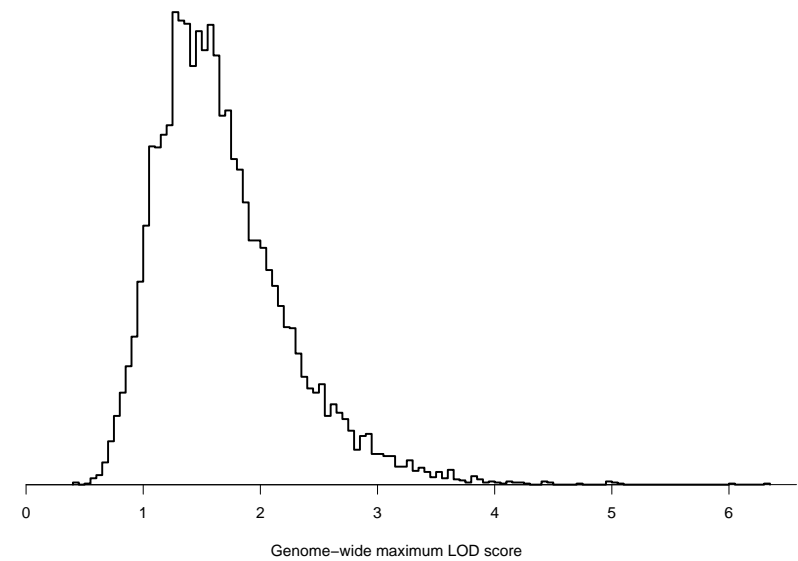
15

LOD curves



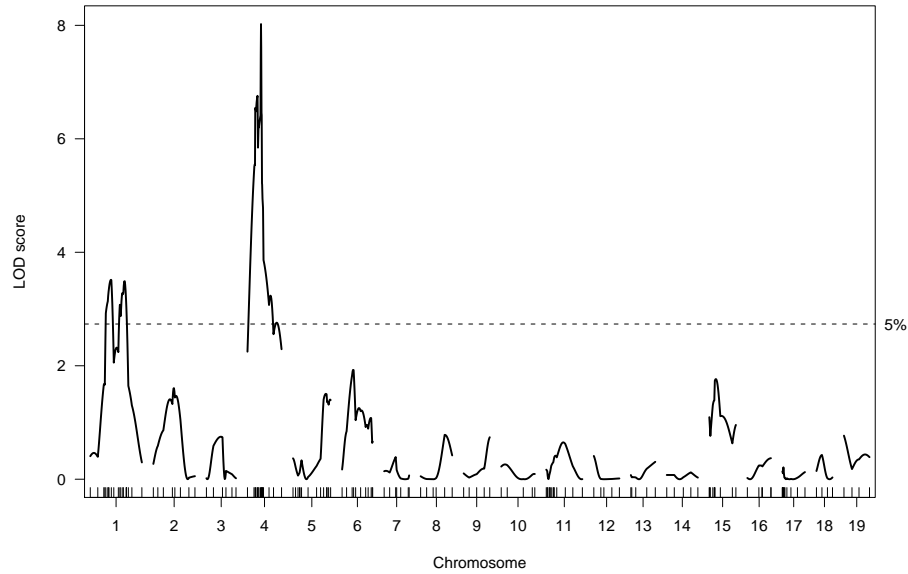
14

Permutation results



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LOD curves



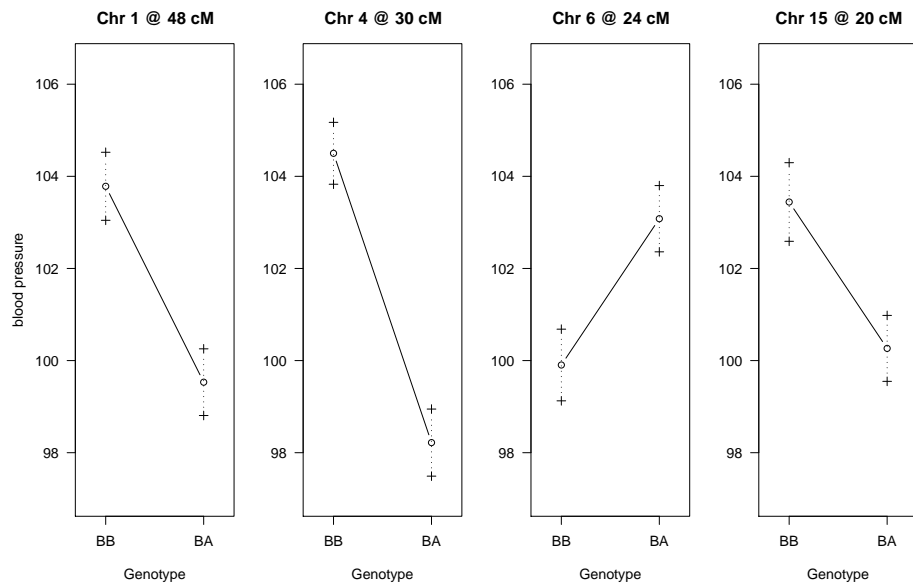
17

Modeling multiple QTL

- Reduce residual variation → increased power
- Separate linked QTL
- Identify interactions among QTL (epistasis)

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Estimated effects



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2-dim, 2-QTL scan

For each pair of positions, fit the following models:

$$H_f : y = \mu + \beta_1 q_1 + \beta_2 q_2 + \gamma q_1 q_2 + \epsilon$$

$$H_a : y = \mu + \beta_1 q_1 + \beta_2 q_2 + \epsilon$$

$$H_1 : y = \mu + \beta_1 q_1 + \epsilon$$

$$H_0 : y = \mu + \epsilon$$

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2-dim, 2-QTL scan

LOD_i and LOD_f

For each pair of positions, fit the following models:

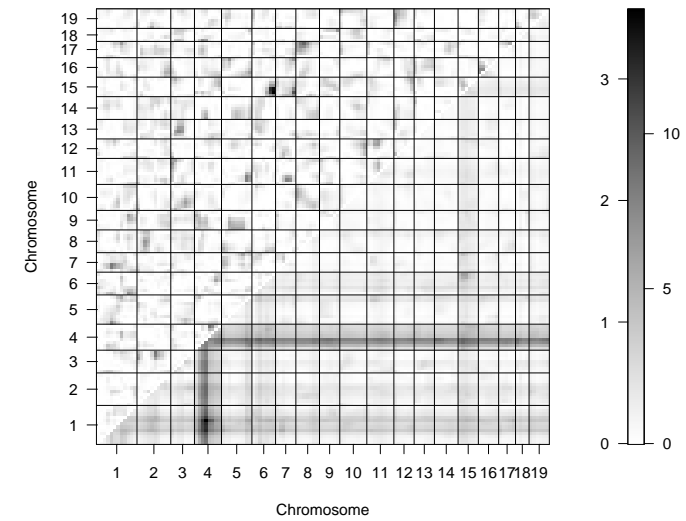
$$H_f : y = \mu + \beta_1 q_1 + \beta_2 q_2 + \gamma q_1 q_2 + \epsilon$$

$$H_a : y = \mu + \beta_1 q_1 + \beta_2 q_2 + \epsilon$$

$$H_1 : y = \mu + \beta_1 q_1 + \epsilon$$

$$H_0 : y = \mu + \epsilon$$

$$\text{LOD}_f(s, t) = \log_{10} \{ L_f(s, t) / L_0 \}$$



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2-dim, 2-QTL scan

LOD_i and LOD_f

For each pair of positions, fit the following models:

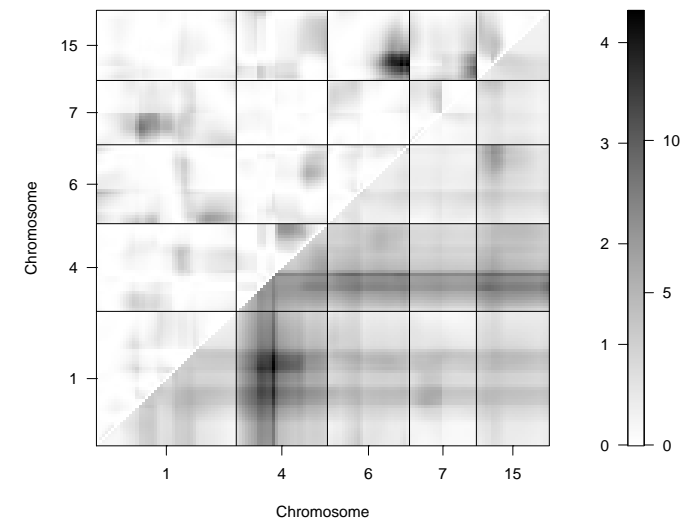
$$H_f : y = \mu + \beta_1 q_1 + \beta_2 q_2 + \gamma q_1 q_2 + \epsilon$$

$$H_a : y = \mu + \beta_1 q_1 + \beta_2 q_2 + \epsilon$$

$$H_1 : y = \mu + \beta_1 q_1 + \epsilon$$

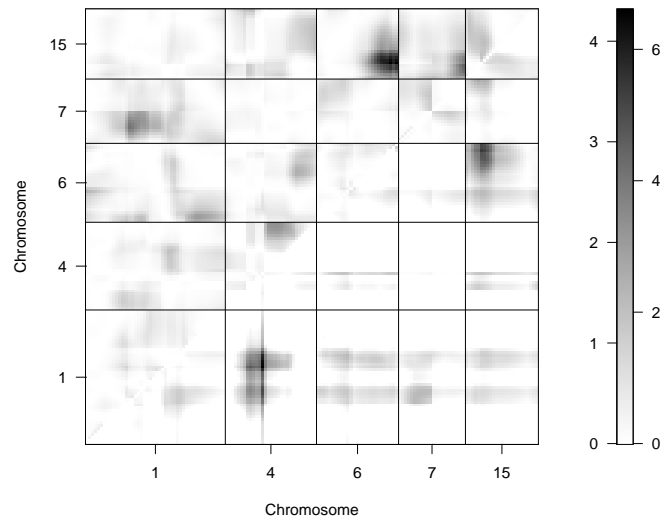
$$H_0 : y = \mu + \epsilon$$

$$\text{LOD}_i(s, t) = \log_{10} \{ L_f(s, t) / L_a(s, t) \}$$

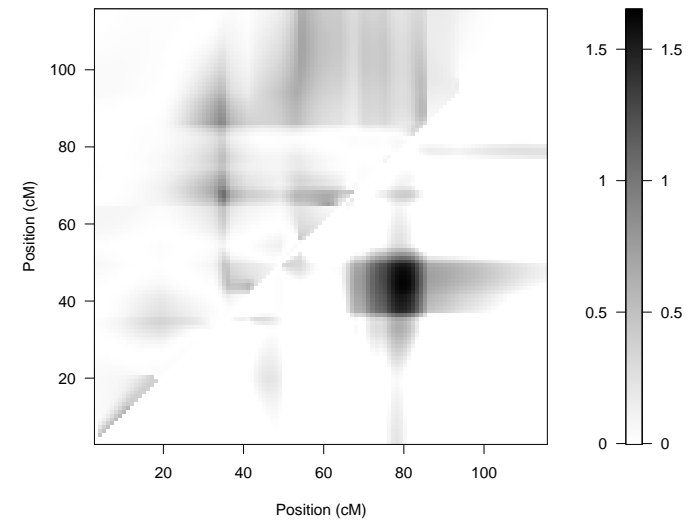


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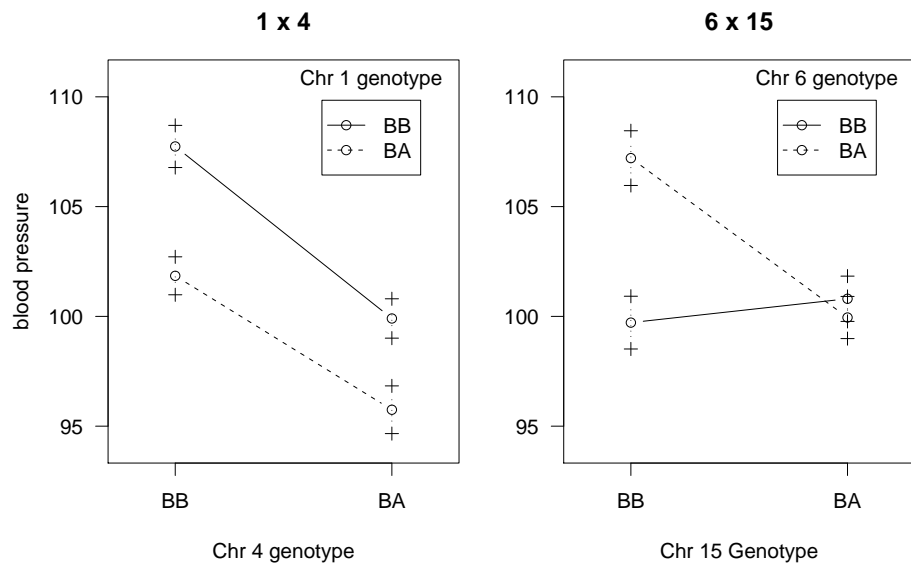
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Estimated effects

Hypothesis testing?



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- In the past, QTL mapping has been regarded as a task of hypothesis testing.

Is this a QTL?

Much of the focus has been on adjusting for test multiplicity.

- It is better to view the problem as one of model selection.

What set of QTL are well supported?

Is there evidence for QTL-QTL interactions?

Model = a defined set of QTL and QTL-QTL interactions (and possibly covariates and QTL-covariate interactions).

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Model selection

- Class of models
 - Additive models
 - + pairwise interactions
 - + higher-order interactions
 - Regression trees
- Model fit
 - Maximum likelihood
 - Haley-Knott regression
 - extended Haley-Knott
 - Multiple imputation
 - MCMC
- Model comparison
 - Estimated prediction error
 - AIC, BIC, penalized likelihood
 - Bayes
- Model search
 - Forward selection
 - Backward elimination
 - Stepwise selection
 - Randomized algorithms

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Target

- Selection of a model includes two types of errors:
 - Miss important terms (QTLs or interactions)
 - Include extraneous terms
- Unlike in hypothesis testing, we can make both errors at the same time.
- Identify as many correct terms as possible, while controlling the rate of inclusion of extraneous terms.

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What is special here?

- Goal: identify the major players
- A continuum of ordinal-valued covariates (the genetic loci)
- Association among the covariates
 - Loci on different chromosomes are independent
 - Along chromosome, a very simple (and known) correlation structure

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Exploratory methods

- Condition on a large-effect QTL
 - Reduce residual variation
 - Conditional LOD score:

$$\text{LOD}(q_2 | q_1) = \log_{10} \left\{ \frac{\Pr(\text{data} | q_1, q_2)}{\Pr(\text{data} | q_1)} \right\}$$

- Piece together the putative QTL from the 1d and 2d scans
 - Omit loci that no longer look interesting (drop-one-at-a-time analysis)
 - Study potential interactions among the identified loci
 - Scan for additional loci (perhaps allowing interactions), conditional on these

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Automation

- Assistance to the masses
- Understanding performance
- Many phenotypes

Experience

- Controls rate of inclusion of extraneous terms
- Forward selection over-selects
- Forward selection followed by backward elimination works as well as MCMC
- Need to define performance criteria
- Need large-scale simulations

Broman & Speed, JRSS B 64:641-656, 2002

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Additive QTL

Simple situation:

- Dense markers
- Complete genotype data
- No epistasis

$$y = \mu + \sum \beta_j q_j + \epsilon \quad \text{which } \beta_j \neq 0?$$

$$\text{LOD}_\delta(\gamma) = \text{LOD}(\gamma) - T |\gamma|$$

0 vs 1 QTL: $\text{LOD}_\delta(\emptyset) = 0$

$$\text{LOD}_\delta(\{\lambda\}) = \text{LOD}(\{\lambda\}) - T$$

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Epistasis

$$y = \mu + \sum \beta_j q_j + \sum \gamma_{jk} q_j q_k + \epsilon$$

$$\text{LOD}_{\delta\epsilon}(\gamma) = \text{LOD}(\gamma) - T_m |\gamma|_m + T_i |\gamma|_i$$

$T_m =$ as chosen previously

$T_i = ?$

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Idea 1

Imagine there are two additive QTL and consider a 2d, 2-QTL scan.

$$T_i = 95\text{th percentile of the distribution of } \max \text{LOD}_f(s, t) - \max \text{LOD}_a(s, t)$$

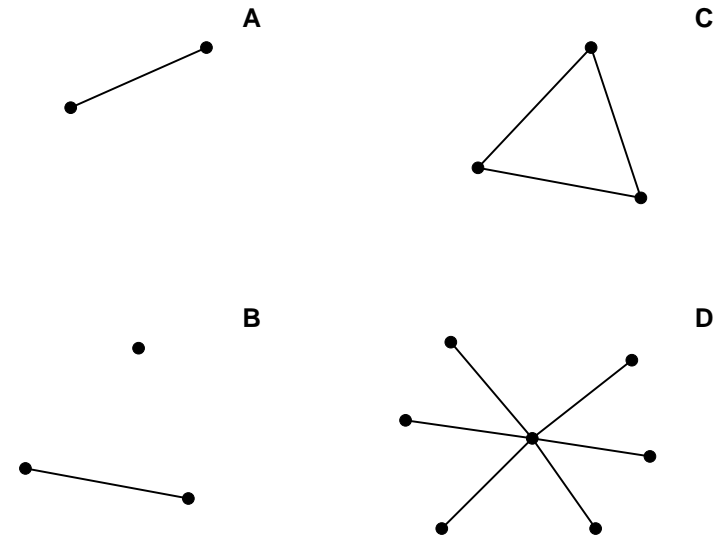
For the mouse genome:

$$T_m = 2.69 \text{ (BC) or } 3.52 \text{ (F}_2\text{)}$$

$$T_i^H = 2.62 \text{ (BC) or } 4.28 \text{ (F}_2\text{)}$$

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Models as graphs



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Idea 2

Imagine there is one QTL and consider a 2d, 2-QTL scan.

$$T_m + T_i = 95\text{th percentile of the distribution of } \max \text{LOD}_f(s, t) - \max \text{LOD}_1(s)$$

For the mouse genome:

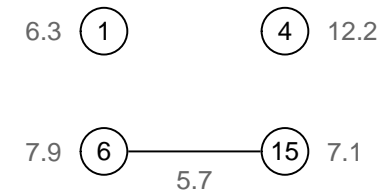
$$T_m = 2.69 \text{ (BC) or } 3.52 \text{ (F}_2\text{)}$$

$$T_i^H = 2.62 \text{ (BC) or } 4.28 \text{ (F}_2\text{)}$$

$$T_i^L = 1.19 \text{ (BC) or } 2.69 \text{ (F}_2\text{)}$$

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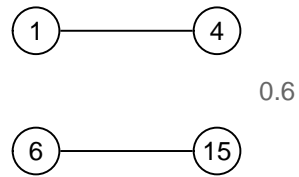
Results



$$T_m = 2.69 \quad T_i^H = 2.62 \quad T_i^L = 1.19 \quad T_m + T_i^H = 5.31 \quad T_m + T_i^L = 3.88$$

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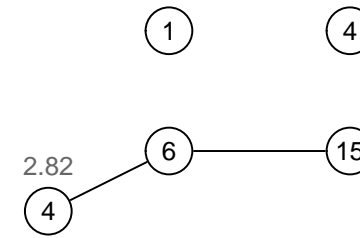
Add an interaction?



$$T_m = 2.69 \quad T_i^H = 2.62 \quad T_i^L = 1.19 \quad T_m + T_i^H = 5.31 \quad T_m + T_i^L = 3.88$$

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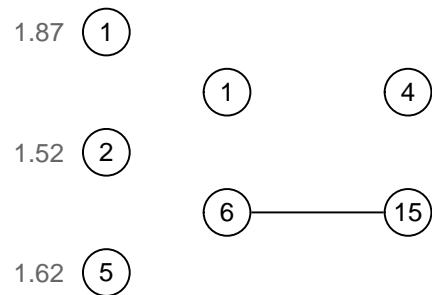
Add another QTL?



$$T_m = 2.69 \quad T_i^H = 2.62 \quad T_i^L = 1.19 \quad T_m + T_i^H = 5.31 \quad T_m + T_i^L = 3.88$$

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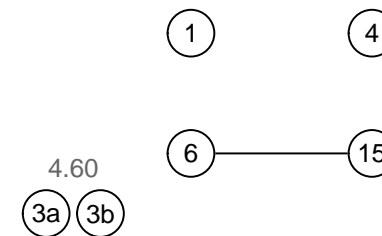
Add another QTL?



$$T_m = 2.69 \quad T_i^H = 2.62 \quad T_i^L = 1.19 \quad T_m + T_i^H = 5.31 \quad T_m + T_i^L = 3.88$$

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Add a pair of QTL?



$$T_m = 2.69 \quad T_i^H = 2.62 \quad T_i^L = 1.19 \quad T_m + T_i^H = 5.31 \quad T_m + T_i^L = 3.88$$

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To do

- Improve search procedures
- Study performance
(especially relative to other approaches)
- Measuring model uncertainty
- Measuring uncertainty in QTL location

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Summary

- QTL mapping is a model selection problem
- The criterion for comparing models is most important
- We're focusing on a penalized likelihood method
and are close to a practiceable solution

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Acknowledgments

Ani Manichaikul	Johns Hopkins University
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Bev Paigen	Jackson Laboratory

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