

# Introduction to QTL mapping in model organisms

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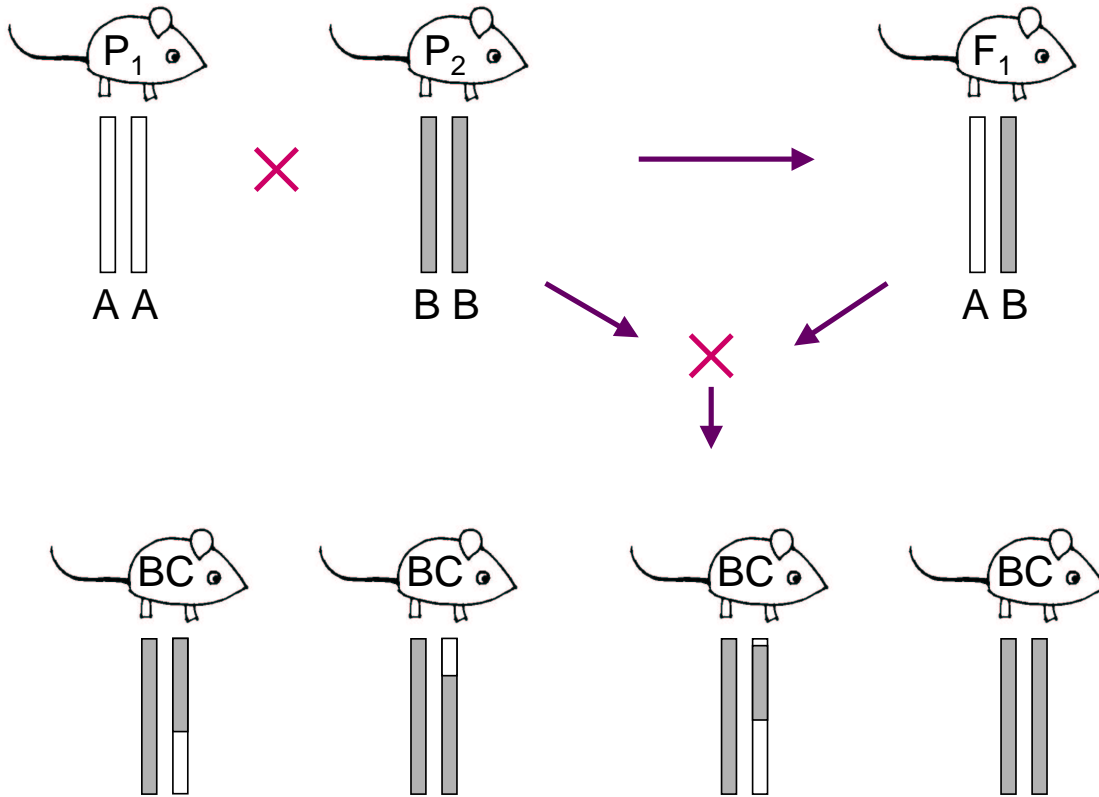
## Outline

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- Experiments and data
- Models
- ANOVA at marker loci
- Interval mapping
- Epistasis
- LOD thresholds
- CIs for QTL location
- Selection bias
- The X chromosome
- Selective genotyping
- Covariates
- Non-normal traits
- The need for good data

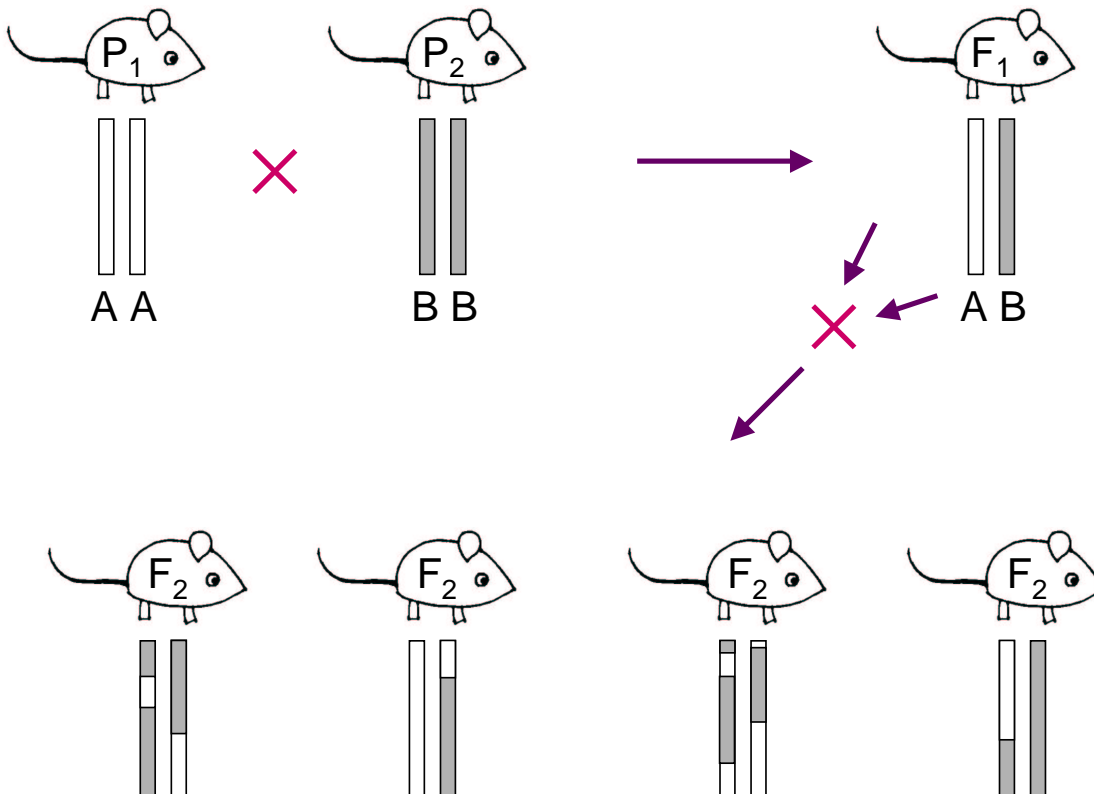
## Backcross experiment

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## Intercross experiment

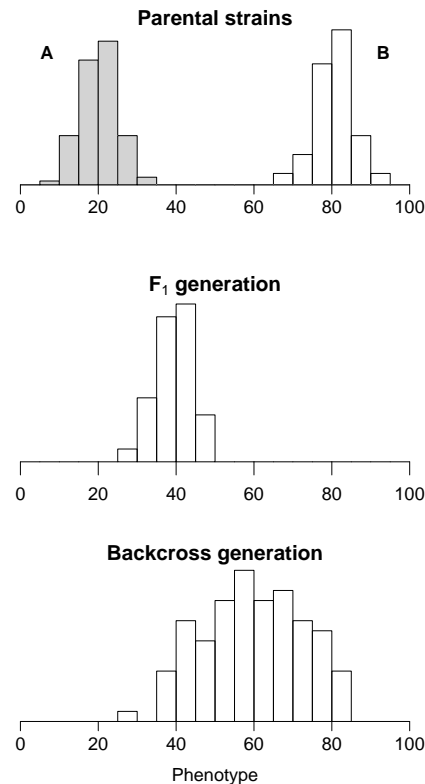
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# Phenotype distributions

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- Within each of the parental and F<sub>1</sub> strains, individuals are genetically identical.
- Environmental variation may or may not be constant with genotype.
- The backcross generation exhibits genetic as well as environmental variation.



## Data

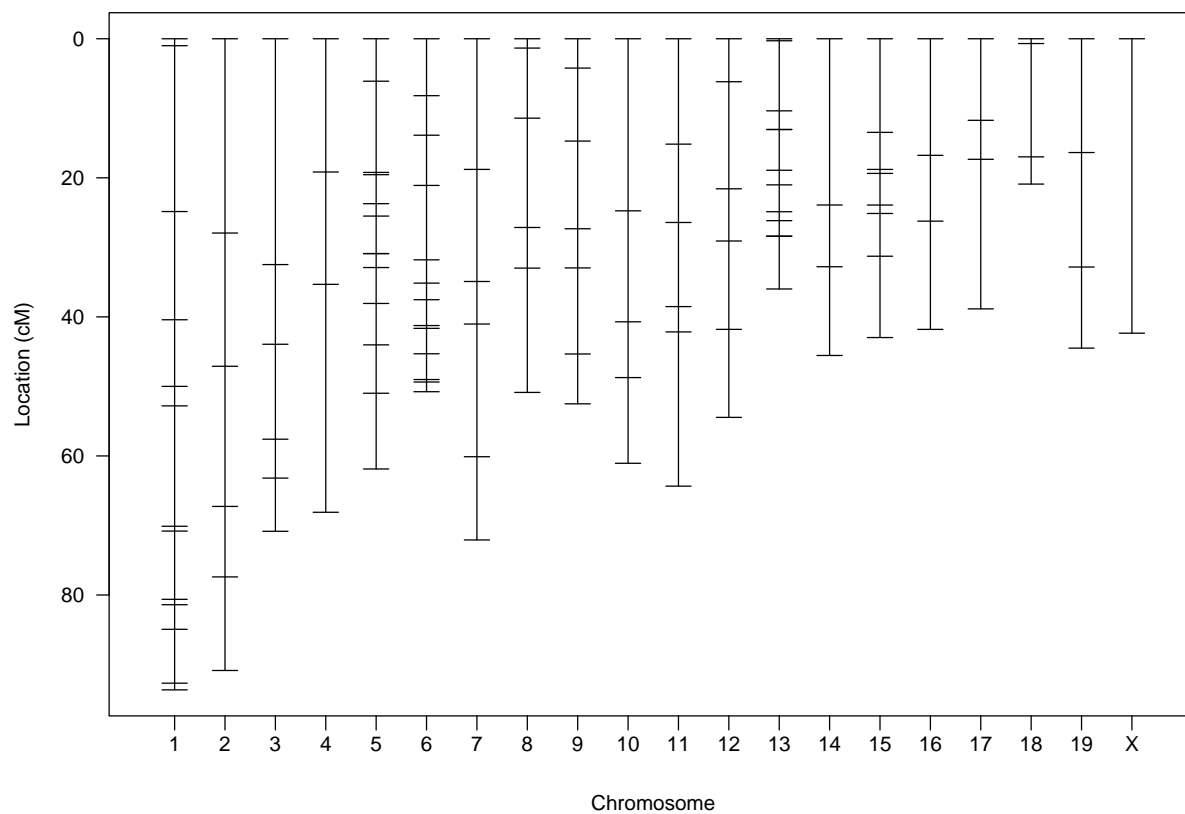
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**Phenotypes:**  $y_i$  = trait value for individual  $i$

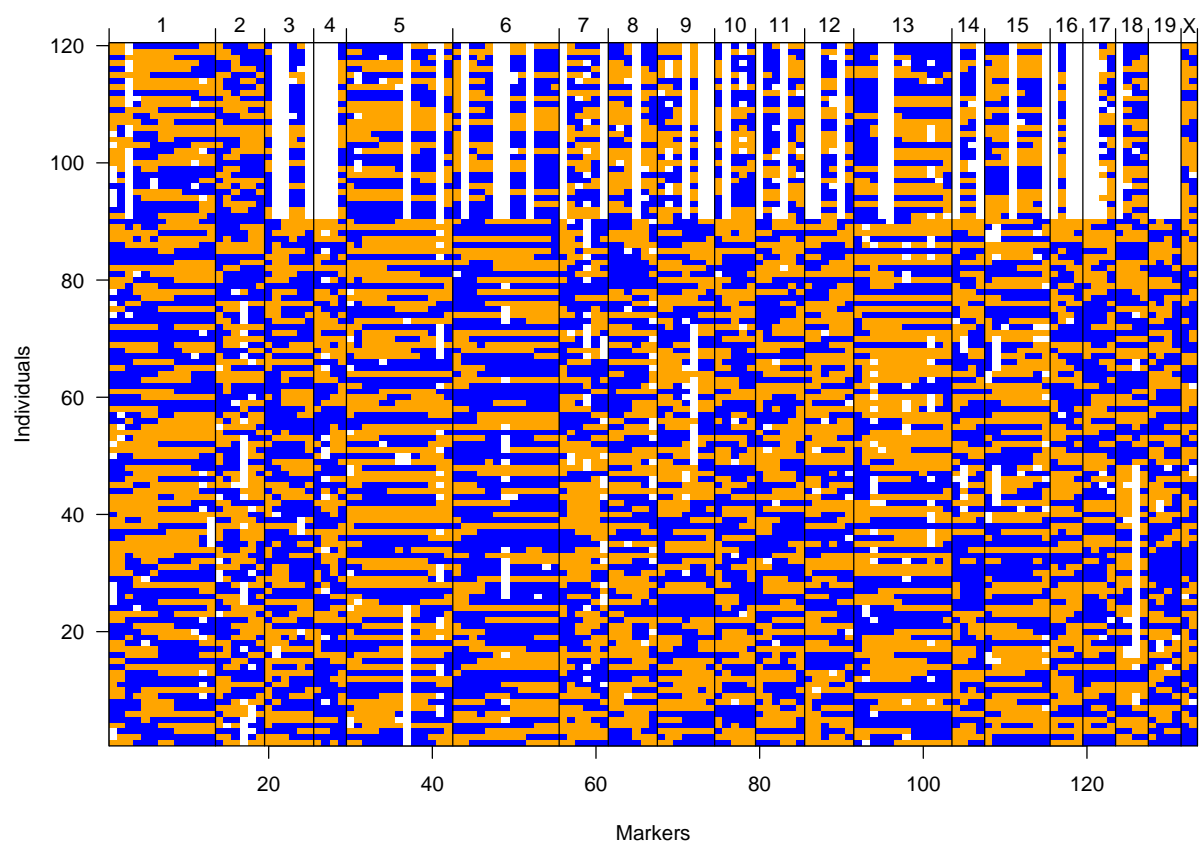
**Genotypes:**  $x_{ij}$  = 0/1 if mouse  $i$  is BB/AB at marker  $j$   
(or 0/1/2, in an intercross)

**Genetic map:** Locations of markers

## Genetic map



## Genotype data



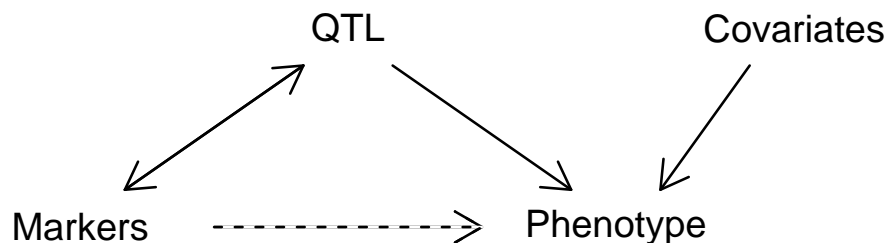
# Goals

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- Detect QTLs (and interactions between QTLs)
- Confidence intervals for QTL location
- Estimate QTL effects (effects of allelic substitution)

## Statistical structure

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The missing data problem:

Markers  $\longleftrightarrow$  QTL

The model selection problem:

QTL, covariates  $\longrightarrow$  phenotype

# Models: Recombination

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We assume no crossover interference.

- ⇒ Points of exchange (crossovers) are according to a Poisson process.
- ⇒ The  $\{x_{ij}\}$  (marker genotypes) form a Markov chain

## Crossover locations

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Crossover locations follow a Poisson process

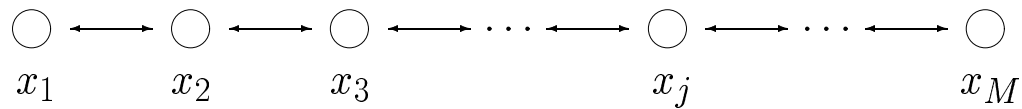
1. Number of XOs  $\sim$  Poisson(  $L / 100$  )  
Locations of XOs (given number)  $\sim$  iid uniform
2. Inter-XO distances are iid exponential( mean = 100 cM )

**Note:** In reality, crossovers are more spread out, but this no interference (NI) model is extremely convenient.

# Marker genotypes

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Under the no interference model,  
the marker genotypes follow a **Markov chain**.

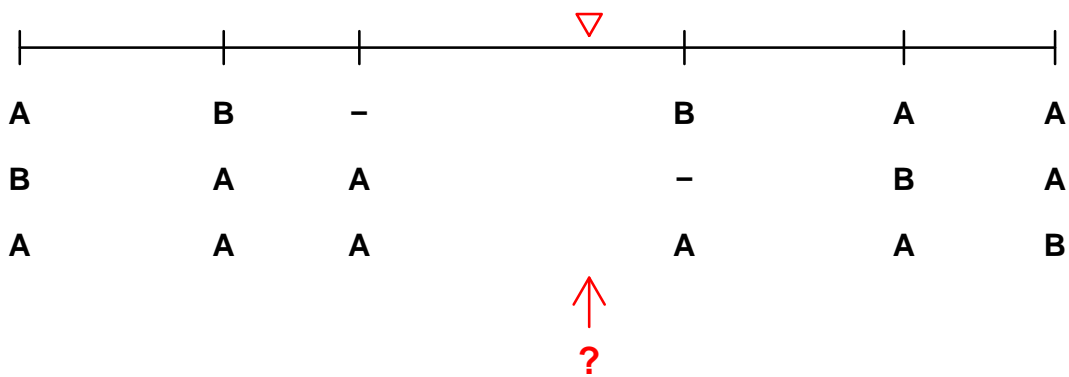


$$\Pr(x_{j+1} \mid x_j, x_{j-1}, \dots, x_1) = \Pr(x_{j+1} \mid x_j)$$

The **past** and **future** are **conditionally independent**,  
given the **present**.

## Example

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## Models: Genotype $\longleftrightarrow$ Phenotype

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Let  $y$  = phenotype  
 $g$  = whole genome genotype

Imagine a small number of QTLs with genotypes  $g_1, \dots, g_p$ .  
( $2^p$  distinct genotypes)

$$E(y|g) = \mu_{g_1, \dots, g_p} \quad \text{var}(y|g) = \sigma_{g_1, \dots, g_p}^2$$

## Models: Genotype $\longleftrightarrow$ Phenotype

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**Homoscedasticity** (constant variance):  $\sigma_g^2 \equiv \sigma^2$

**Normally distributed residual variation:**  $y|g \sim N(\mu_g, \sigma^2)$ .

**Additivity:**  $\mu_{g_1, \dots, g_p} = \mu + \sum_{j=1}^p \Delta_j g_j$  ( $g_j = 1$  or  $0$ )

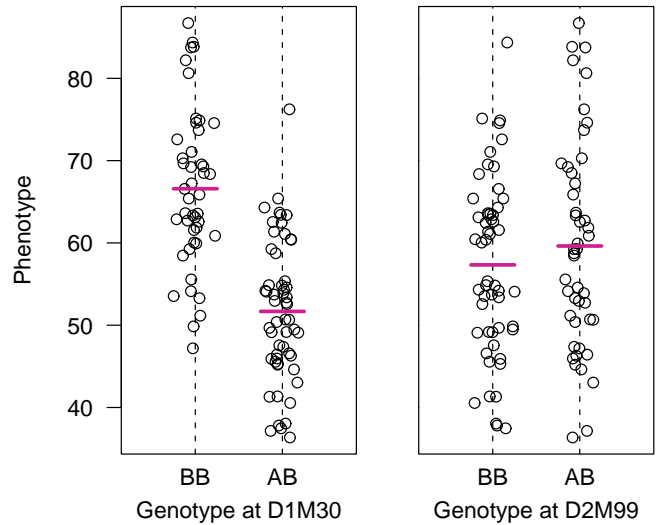
**Epistasis:** Any deviations from additivity.



# The simplest method: ANOVA

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



## Effect at a marker

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Consider the case of a **single QTL** with effect  $\Delta = \mu_{BB} - \mu_{AB}$ .

Consider a marker linked to the QTL, with  $r =$  recomb. frac.

Of individuals with marker genotype BB, mean phenotype is:

$$\mu_{BB}(1 - r) + \mu_{AB}r = \mu_{BB} - r\Delta$$

Of individuals with marker genotype AB, mean phenotype is:

$$\mu_{AB}(1 - r) + \mu_{BB}r = \mu_{AB} + r\Delta$$

**Difference:**  $(\mu_{BB} - r\Delta) - (\mu_{AB} + r\Delta) = \Delta(1 - 2r)$

# ANOVA at marker loci

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## Advantages

- Simple.
- Easily incorporates covariates.
- Easily extended to more complex models.
- Doesn't require a genetic map.

## Disadvantages

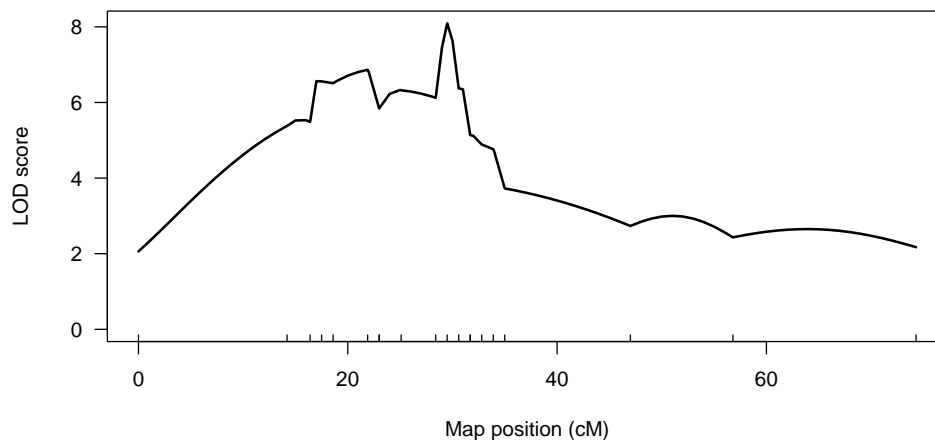
- Must exclude individuals with missing genotype data.
- Imperfect information about QTL location.
- Suffers in low density scans.
- Only considers one QTL at a time.

# Interval mapping (IM)

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## Lander & Botstein (1989)

- Take account of missing genotype data
- Interpolate between markers
- Maximum likelihood under a mixture model



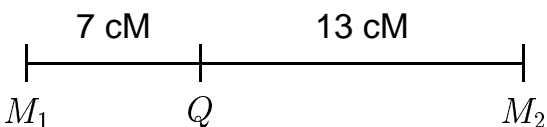
# Interval mapping (IM)

## Lander & Botstein (1989)

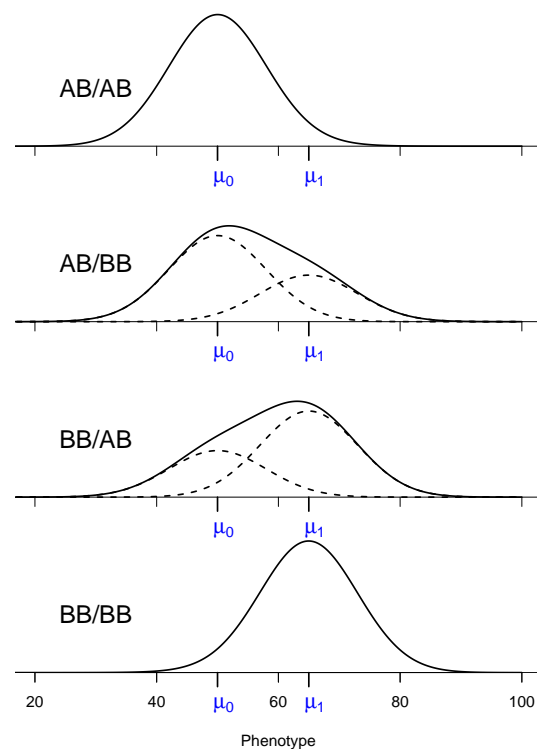
- Assume a **single** QTL model.
- Each position in the genome, one at a time, is posited as the putative QTL.
- Let  $z = 1/0$  if the (unobserved) QTL genotype is BB/AB.  
Assume  $y \sim N(\mu_z, \sigma)$
- Given genotypes at linked markers,  $y \sim$  mixture of normal dist'ns with mixing proportion  $\Pr(z = 1|\text{marker data})$ :

		QTL genotype	
$M_1$	$M_2$	BB	AB
BB	BB	$(1 - r_L)(1 - r_R)/(1 - r)$	$r_L r_R/(1 - r)$
BB	AB	$(1 - r_L)r_R/r$	$r_L(1 - r_R)/r$
AB	BB	$r_L(1 - r_R)/r$	$(1 - r_L)r_R/r$
AB	AB	$r_L r_R/(1 - r)$	$(1 - r_L)(1 - r_R)/(1 - r)$

## The normal mixtures



- Two markers separated by 20 cM, with the QTL closer to the left marker.
- The figure at right show the distributions of the phenotype conditional on the genotypes at the two markers.
- The dashed curves correspond to the components of the mixtures.



## Interval mapping (continued)

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Let  $p_i = \Pr(z_i = 1 | \text{marker data})$

$$y_i | z_i \sim N(\mu_{z_i}, \sigma^2)$$

$$\Pr(y_i | \text{marker data}, \mu_0, \mu_1, \sigma) = p_i f(y_i; \mu_1, \sigma) + (1 - p_i) f(y_i; \mu_0, \sigma)$$

$$\text{where } f(y; \mu, \sigma) = \exp[-(y - \mu)^2 / (2\sigma^2)] / \sqrt{2\pi\sigma^2}$$

**Log likelihood:**  $l(\mu_0, \mu_1, \sigma) = \sum_i \log \Pr(y_i | \text{marker data}, \mu_0, \mu_1, \sigma)$

Maximum likelihood estimates (**MLEs**) of  $\mu_0, \mu_1, \sigma$ :

values for which  $l(\mu_0, \mu_1, \sigma)$  is maximized.

## EM algorithm

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Dempster et al. (1977)

**E step:**

$$\begin{aligned} \text{Let } w^{(k+1)} &= \Pr(z_i = 1 | y_i, \text{marker data}, \hat{\mu}_0^{(k)}, \hat{\mu}_1^{(k)}, \hat{\sigma}^{(k)}) \\ &= \frac{p_i f(y_i; \hat{\mu}_1^{(k)}, \hat{\sigma}^{(k)})}{p_i f(y_i; \hat{\mu}_1^{(k)}, \hat{\sigma}^{(k)}) + (1 - p_i) f(y_i; \hat{\mu}_0^{(k)}, \hat{\sigma}^{(k)})} \end{aligned}$$

**M step:**

$$\begin{aligned} \text{Let } \hat{\mu}_1^{(k+1)} &= \sum_i y_i w_i^{(k+1)} / \sum_i w_i^{(k+1)} \\ \hat{\mu}_0^{(k+1)} &= \sum_i y_i (1 - w_i^{(k+1)}) / \sum_i (1 - w_i^{(k+1)}) \\ \hat{\sigma}^{(k+1)} &= [\text{not worth writing down}] \end{aligned}$$

**The algorithm:**

Start with  $w_i^{(1)} = p_i$ ; iterate the E & M steps until convergence.

# Example

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Iteration	$\hat{\mu}_0$	$\hat{\mu}_1$	$\hat{\sigma}$	log likelihood
1	5.903	6.492	1.668	-770.752
2	5.835	6.562	1.654	-770.291
3	5.818	6.579	1.651	-770.264
4	5.815	6.583	1.650	-770.262
⋮	⋮	⋮	⋮	⋮
∞	5.813	6.584	1.649	-770.262

## LOD scores

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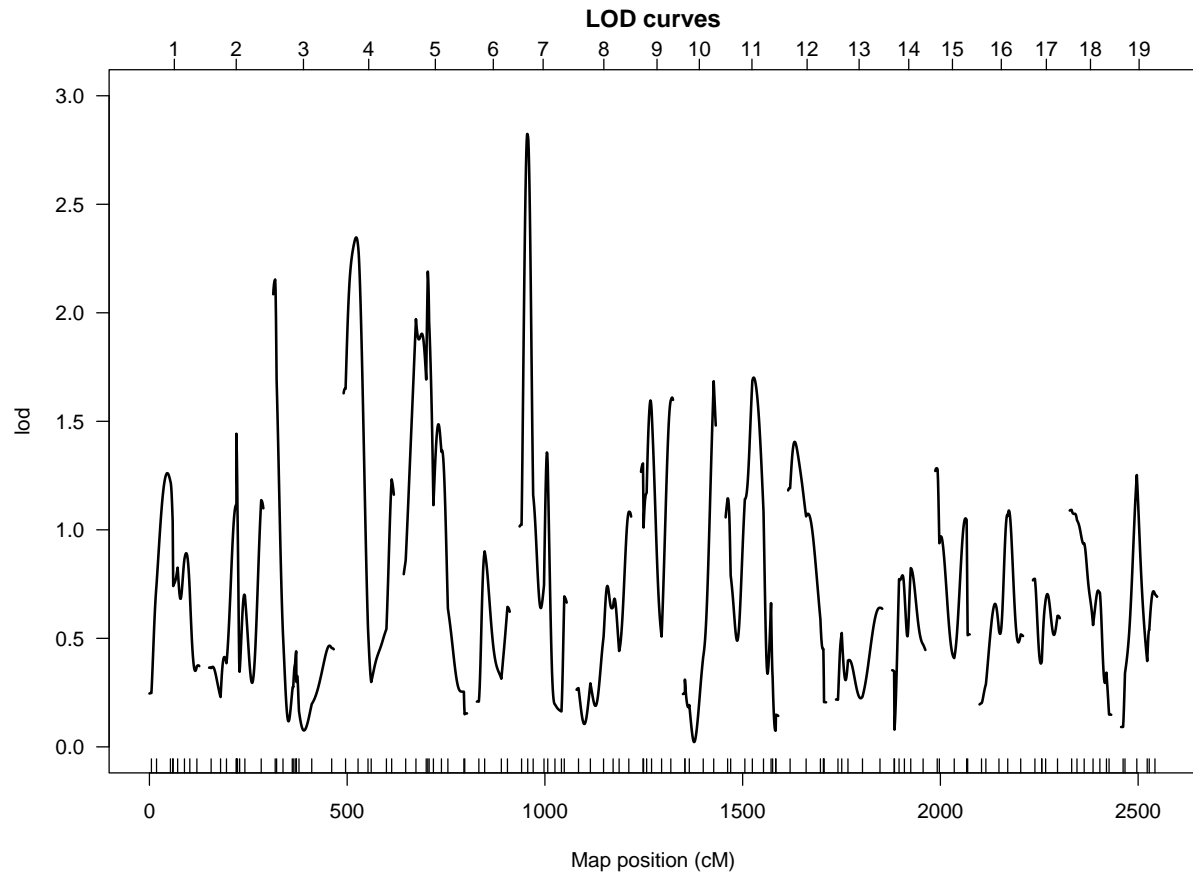
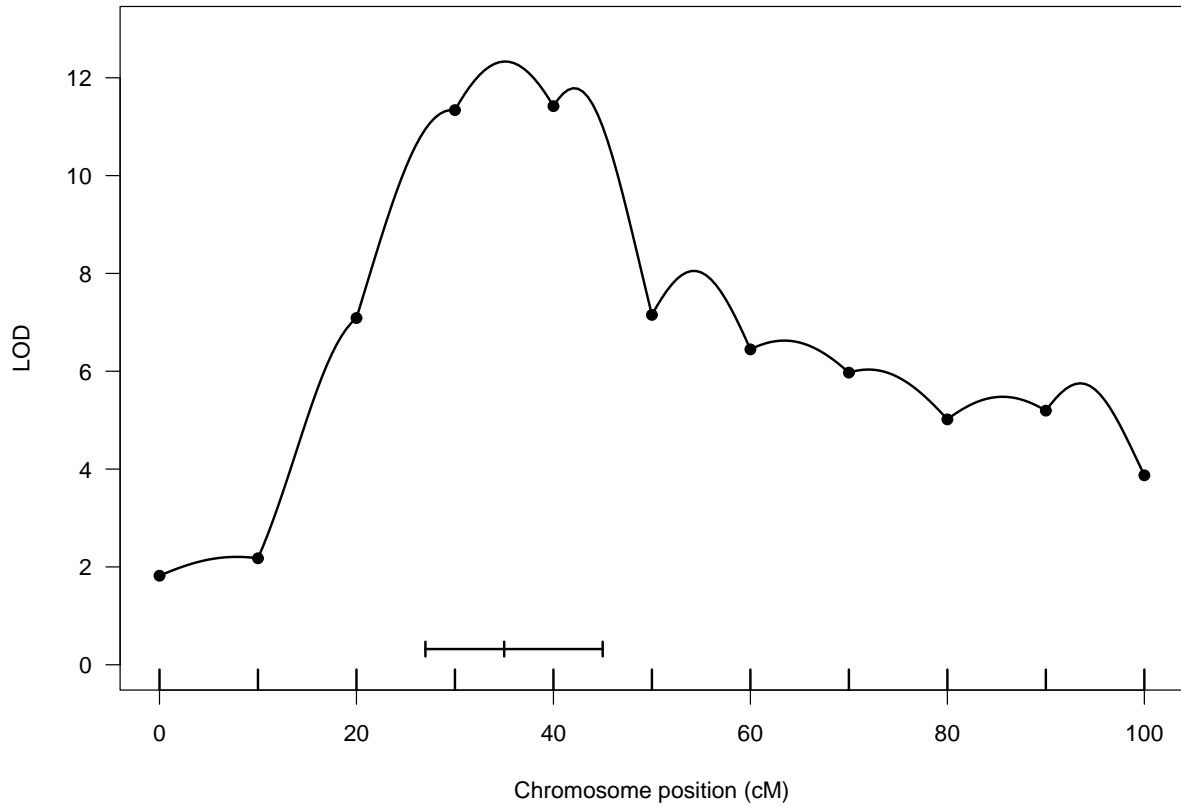
The LOD score is a measure of the **strength of evidence** for the presence of a QTL at a particular location.

$$\begin{aligned}\text{LOD}(z) &= \log_{10} \text{likelihood ratio comparing the hypothesis of a} \\ &\quad \text{QTL at position } z \text{ versus that of no QTL} \\ &= \log_{10} \left\{ \frac{\Pr(y|\text{QTL at } z, \hat{\mu}_{0z}, \hat{\mu}_{1z}, \hat{\sigma}_z)}{\Pr(y|\text{no QTL}, \hat{\mu}, \hat{\sigma})} \right\}\end{aligned}$$

$\hat{\mu}_{0z}, \hat{\mu}_{1z}, \hat{\sigma}_z$  are the MLEs, assuming a single QTL at position  $z$ .

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

# An example LOD curve



# Interval mapping

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## Advantages

- Takes proper account of missing data.
- Allows examination of positions between markers.
- Gives improved estimates of QTL effects.
- Provides pretty graphs.

## Disadvantages

- Increased computation time.
- Requires specialized software.
- Difficult to generalize.
- Only considers one QTL at a time.

# Multiple QTL methods

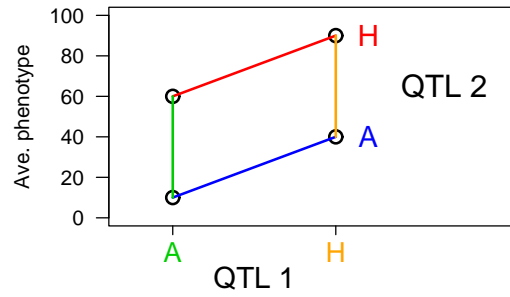
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## Why consider multiple QTLs at once?

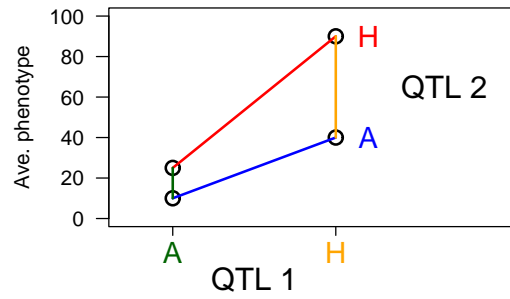
- Reduce residual variation.
- Separate linked QTLs.
- Investigate interactions between QTLs (epistasis).

# Epistasis in a backcross

Additive QTLs

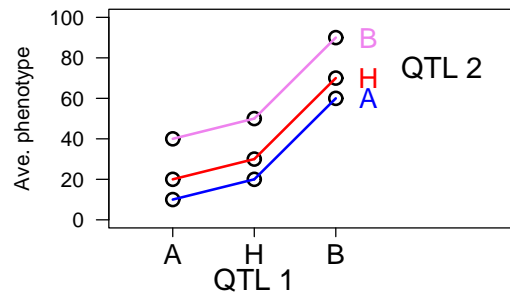


Interacting QTLs

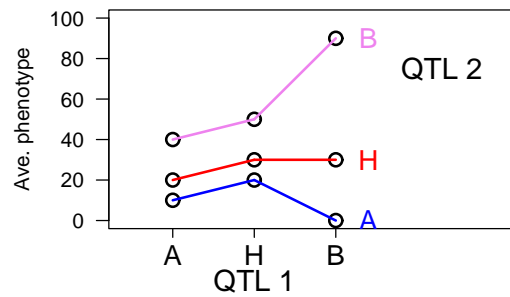


# Epistasis in an intercross

Additive QTLs



Interacting QTLs





# LOD thresholds

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Large LOD scores indicate evidence for the presence of a QTL.

**Q: How large is large?**

→ We consider the distribution of the LOD score under the null hypothesis of no QTL.

**Key point:** We must make some adjustment for our examination of multiple putative QTL locations.

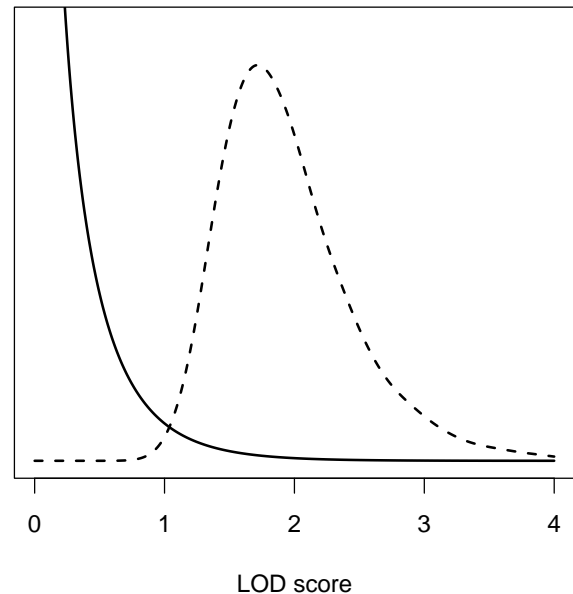
→ We seek the distribution of the *maximum* LOD score, genome-wide. The 95th %ile of this distribution serves as a **genome-wide LOD threshold**.

Estimating the threshold: simulations, analytical calculations, permutation (randomization) tests.

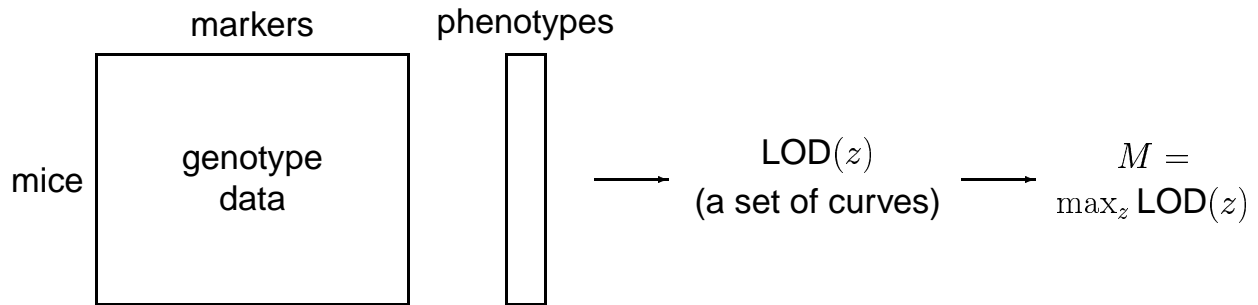
## Null distribution of the LOD score

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- Null distribution derived by computer simulation of backcross with genome of typical size.
- Solid curve: distribution of LOD score at any one point.
- Dashed curve: distribution of maximum LOD score, genome-wide.

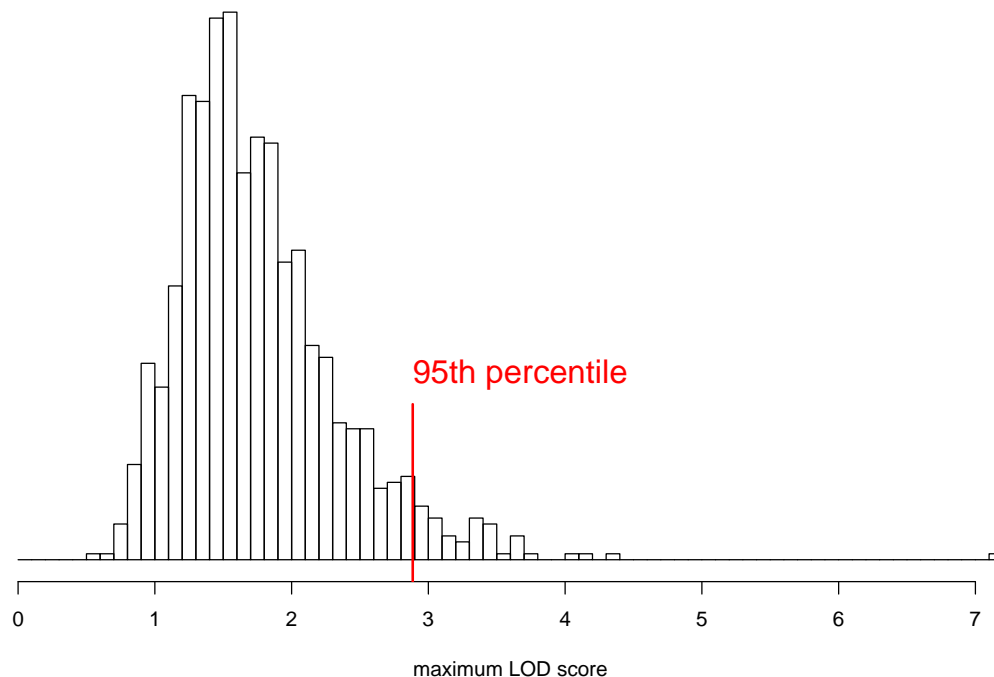


# Permutation tests



- Permute/shuffle the phenotypes; keep the genotype data intact.
- Calculate  $\text{LOD}^*(z) \rightarrow M^* = \max_z \text{LOD}^*(z)$
- We wish to compare the observed  $M$  to the distribution of  $M^*$ .
- $\Pr(M^* \geq M)$  is a genome-wide P-value.
- The 95th %ile of  $M^*$  is a genome-wide LOD threshold.
- We can't look at all  $n!$  possible permutations, but a random set of 1000 is feasible and provides reasonable estimates of P-values and thresholds.
- **Value:** conditions on observed phenotypes, marker density, and pattern of missing data; doesn't rely on normality assumptions or asymptotics.

## Permutation distribution



# Confidence intervals for QTL location

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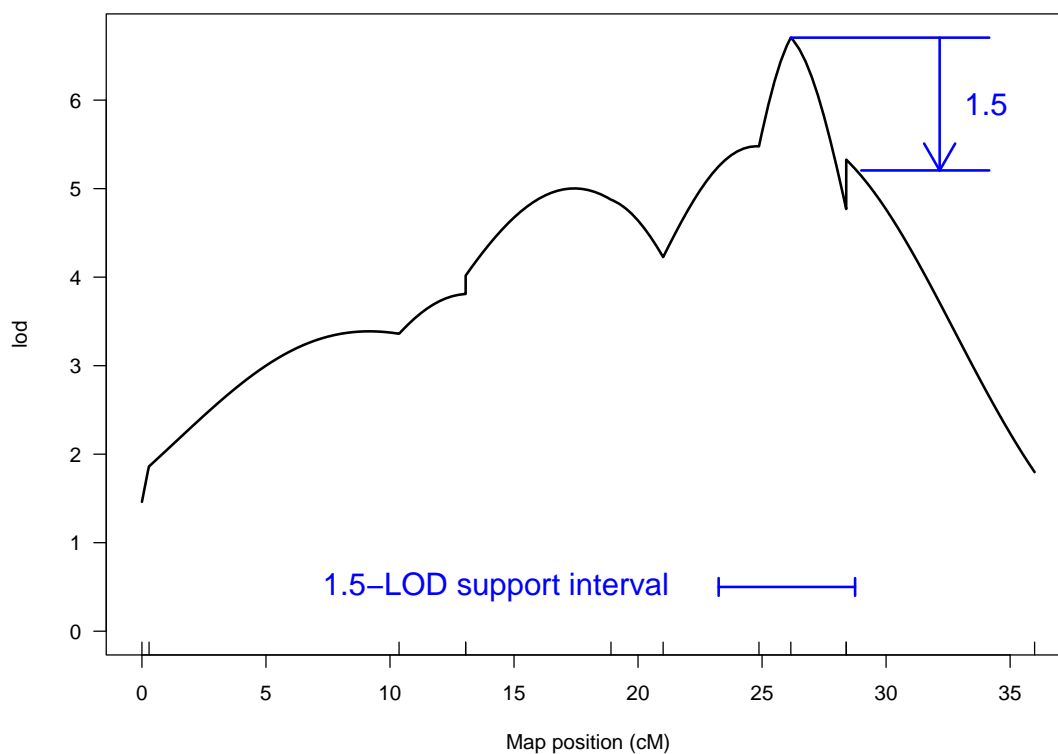
**Confidence interval** indicates plausible location of a QTL.

## Methods:

- **LOD support intervals**  
(I prefer 1.5-LOD intervals.)
- **Bootstrap**  
(Resample individuals with replacement)

## 1.5-LOD support interval

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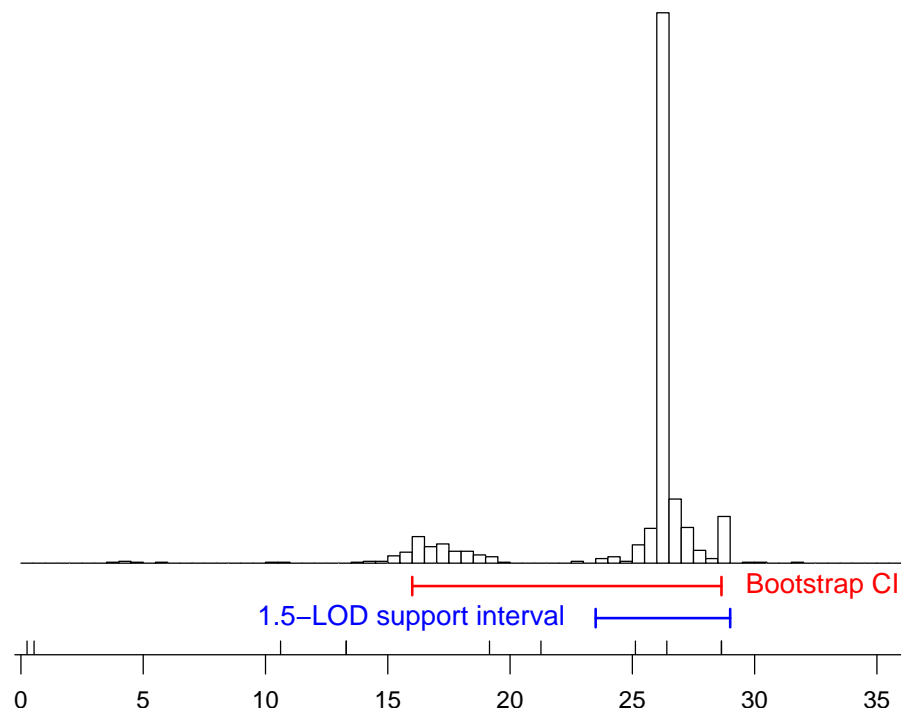
# Bootstrap-based confidence intervals

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- **Consider** a set of  $n$  individuals (e.g.,  $n = 124$ )
- **Sample, with replacement**,  $n$  individuals
  - Some individuals duplicated
  - Some individuals missing
- Using the sampled individuals, **re-calculate the LOD curve** for the chromosome of interest
- **Identify the location of the maximum LOD score**
- **Repeat many times** (e.g., 250)
- **Bootstrap CI** = (2.5 %ile to 97.5 %ile) of locations of maximum LOD.

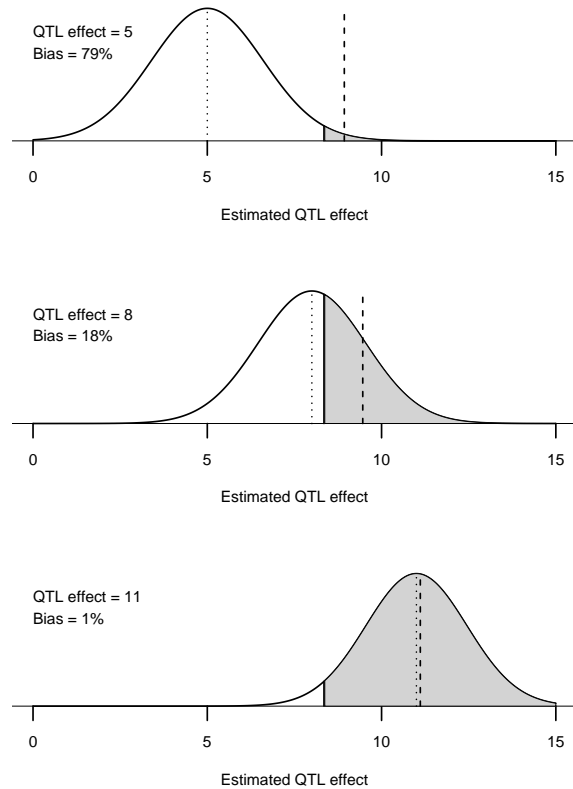
## Bootstrap confidence interval

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# Selection bias

- The estimated effect of a QTL will vary somewhat from its true effect.
- Only when the estimated effect is large will the QTL be detected.
- Among those experiments in which the QTL is detected, the estimated QTL effect will be, on average, larger than its true effect.
- This is **selection bias**.
- Selection bias is largest in QTLs with small or moderate effects.
- The true effects of QTLs that we identify are likely smaller than was observed.



## Implications of selection bias

- Estimated % variance explained by identified QTLs
- Repeating an experiment
- Congenics
- Marker-assisted selection

## The X chromosome

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In a backcross, the X chromosome may or may not be segregating.

$$(A \times B) \times A$$

Females:  $X_{A \cdot B} X_A$

Males:  $X_{A \cdot B} Y_A$

$$A \times (A \times B)$$

Females:  $X_A X_A$

Males:  $X_A Y_B$

## The X chromosome

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In an intercross, one must pay attention to the **paternal grandmother's genotype**.

$$(A \times B) \times (A \times B) \quad \text{or} \quad (B \times A) \times (A \times B)$$

Females:  $X_{A \cdot B} X_A$

Males:  $X_{A \cdot B} Y_B$

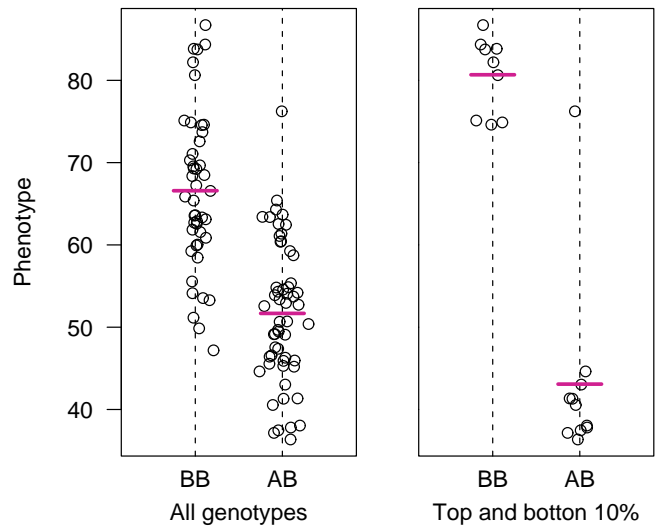
$$(A \times B) \times (B \times A) \quad \text{or} \quad (B \times A) \times (B \times A)$$

Females:  $X_{A \cdot B} X_B$

Males:  $X_{A \cdot B} Y_A$

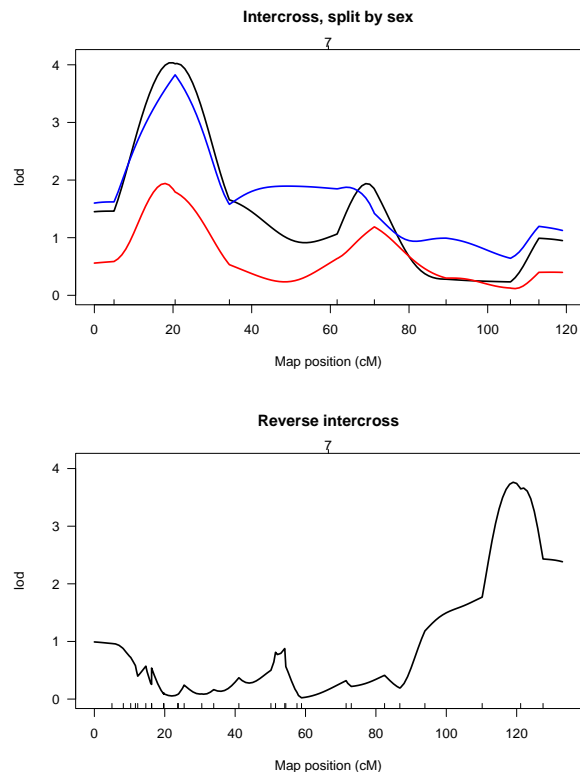
# Selective genotyping

- Save effort by only typing the most informative individuals (say, top & bottom 10%).
- Useful in context of a **single, inexpensive** trait.
- Tricky to estimate the effects of QTLs: use IM with **all** phenotypes.
- Can't get at interactions.
- Likely better to also genotype some random portion of the rest of the individuals.



# Covariates

- **Examples:** treatment, sex, litter, lab, age.
- Control residual variation.
- Avoid confounding.
- Look for QTL  $\times$  environ't interactions
- Adjust before interval mapping (IM) versus adjust within IM.



## Non-normal traits

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- Standard interval mapping assumes normally distributed residual variation. (Thus the phenotype distribution is a mixture of normals.)
- **In reality:** we see dichotomous traits, counts, skewed distributions, outliers, and all sorts of odd things.
- Interval mapping, with LOD thresholds derived from permutation tests, generally performs just fine anyway.
- Alternatives to consider:
  - Nonparametric approaches (Kruglyak & Lander 1995)
  - Transformations (e.g., log, square root)
  - Specially-tailored models (e.g., a generalized linear model, the Cox proportional hazard model, and the model in Broman et al. 2000)

## Check data integrity

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The success of QTL mapping depends crucially on the integrity of the data.

- Segregation distortion
- Genetic maps / marker positions
- Genotyping errors (tight double crossovers)
- Phenotype distribution / outliers
- Residual analysis



# Summary I

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- **ANOVA** at marker loci (aka marker regression) is simple and easily extended to include covariates or accommodate complex models.
- **Interval mapping** improves on ANOVA by allowing inference of QTLs to positions between markers and taking proper account of missing genotype data.
- ANOVA and IM consider only single-QTL models. **Multiple QTL methods** allow the better separation of linked QTLs and are necessary for the investigation of epistasis.
- Statistical significance of LOD peaks requires consideration of the maximum LOD score, genome-wide, under the null hypothesis of no QTLs. **Permutation tests** are extremely useful for this.
- **1.5-LOD support intervals** indicate the plausible location of a QTL. Alternatively, perform a **bootstrap**.
- Estimates of QTL effects are subject to **selection bias**. Such estimated effects are often too large.

# Summary II

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- The **X chromosome** must be dealt with specially, and can be tricky.
- **Study your data**. Look for errors in the genetic map, genotyping errors and phenotype outliers. But don't worry about them too much.
- **Selective genotyping** can save you time and money, but proceed with caution.
- **Study your data**. The consideration of covariates may reveal extremely interesting phenomena.
- Interval mapping works reasonably well even with **non-normal traits**. But consider transformations or specially-tailored models. If interval mapping software is not available for your preferred model, start with some version of ANOVA.

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