

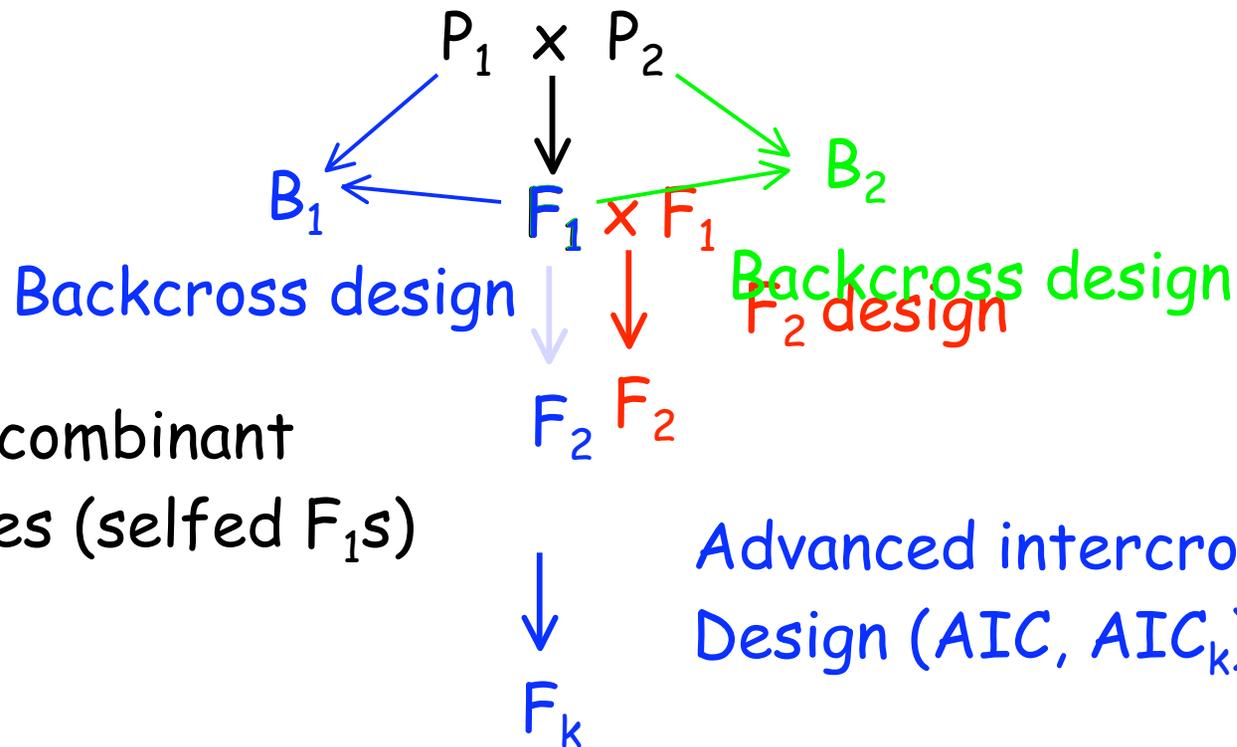
QTL Mapping I: Overview and using Inbred Lines

Key idea: Looking for marker-trait associations in collections of relatives

If (say) the mean trait value for marker genotype MM is statistically different from that for genotype mm , then the M/m marker is linked to a QTL

One can use a random collection of such markers spanning a genome (a genomic scan) to search for QTLs

Experimental Design: Crosses



RILs = Recombinant
inbred lines (selfed F_1 s)

Experimental Designs: Marker Analysis

Single marker analysis

Flanking marker analysis (interval mapping)

Composite interval mapping

Interval mapping plus additional markers

Multipoint mapping

Uses all markers on a chromosome simultaneously

Conditional Probabilities of QTL Genotypes

The basic building block for all QTL methods is $\Pr(Q_k | M_j)$ --- the probability of QTL genotype Q_k given the marker genotype is M_j .

$$\Pr(Q_k | M_j) = \frac{\Pr(Q_k M_j)}{\Pr(M_j)}$$

Consider a QTL linked to a marker (recombination Fraction = c). Cross $MMQQ \times mmqq$. In the F_1 , all gametes are MQ and mq

In the F_2 , $\text{freq}(MQ) = \text{freq}(mq) = (1-c)/2$,
 $\text{freq}(mQ) = \text{freq}(Mq) = c/2$

Hence, $\Pr(MMQQ) = \Pr(MQ)\Pr(MQ) = (1-c)^2/4$

$\Pr(MMQq) = 2\Pr(MQ)\Pr(Mq) = 2c(1-c)/4$

$\Pr(MMqq) = \Pr(Mq)\Pr(Mq) = c^2/4$

Why the 2? MQ from father, Mq from mother, OR
MQ from mother, Mq from father

Since $\Pr(MM) = 1/4$, the conditional probabilities become

$\Pr(QQ \mid MM) = \Pr(MMQQ)/\Pr(MM) = (1-c)^2$

$\Pr(Qq \mid MM) = \Pr(MMQq)/\Pr(MM) = 2c(1-c)$

$\Pr(qq \mid MM) = \Pr(MMqq)/\Pr(MM) = c^2$

How do we use these?

Expected Marker Means

The expected trait mean for marker genotype M_j is just

$$\mu_{M_j} = \sum_{k=1}^N \mu_{Q_k} \Pr(Q_k | M_j)$$

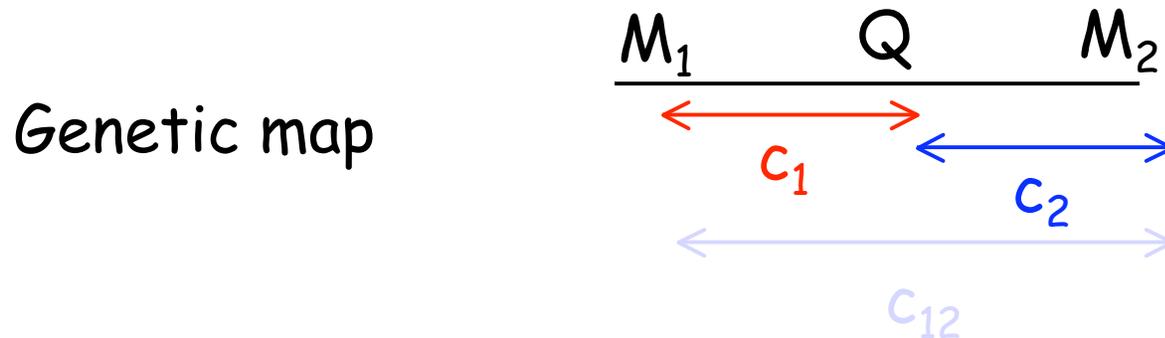
For example, if $QQ = 2a$, $Qq = a(1+k)$, $qq = 0$, then in the F2 of an $MMQQ/mmqq$ cross,

$$(\mu_{MM} - \mu_{mm})/2 = a(1 - 2c)$$

- If the trait mean is significantly different for the genotypes at a marker locus, it is linked to a QTL
- A small MM - mm difference could be (i) a tightly-linked QTL of small effect or (ii) loose linkage to a large QTL

2 Marker loci

Suppose the cross is $M_1M_1QQM_2M_2 \times m_1m_1qqm_2m_2$



No interference: $c_{12} = c_1 + c_2 - 2c_1c_2$

Complete interference: $c_{12} = c_1 + c_2$

In F_2 , $\Pr(M_1QM_2) = (1-c_1)(1-c_2)$

$\Pr(M_1Qm_2) = (1-c_1)c_2$ $\Pr(m_1QM_2) = (1-c_1)c_2$

Likewise, $\Pr(M_1M_2) = 1-c_{12} = 1-c_1+c_2$

A little bookkeeping gives

$$\Pr(QQ | M_1M_1M_2M_2) = \frac{(1 - c_1)^2(1 - c_2)^2}{(1 - c_{12})^2}$$

$$\Pr(Qq | M_1M_1M_2M_2) = \frac{2c_1c_2(1 - c_1)(1 - c_2)}{(1 - c_{12})^2}$$

$$\Pr(qq | M_1M_1M_2M_2) = \frac{c_1^2c_2^2}{(1 - c_{12})^2}$$

$$\frac{\mu_{M_1M_1M_2M_2} - \mu_{m_1m_1m_2m_2}}{2} = a - \left(\frac{1 - c_1 - c_2}{1 - c_1 - c_2 + 2c_1c_2} \right)$$

$$\simeq a(1 - 2c_1c_2)$$

This is essentially a for
even modest linkage

$$c_1 = \frac{1}{2} \left(1 - \frac{\mu_{M_1 M_1} - \mu_{m_1 m_1}}{2a} \right)$$

$$\approx \frac{1}{2} \left(1 - \frac{\mu_{M_1 M_1} - \mu_{m_1 m_1}}{\mu_{M_1 M_1 M_2 M_2} - \mu_{m_1 m_1 m_2 m_2}} \right)$$

Hence, a and c can be estimated from the mean values of flanking marker genotypes

Linear Models for QTL Detection

The use of differences in the mean trait value for different marker genotypes to detect a QTL and estimate its effects is a use of **linear models**.

One-way ANOVA.

Value of trait in kth
individual of marker
genotype type i



$$z_{ik} = \mu + b_i + e_{ik}$$



Effect of marker
genotype i on trait
value

$$z_{ik} = \mu + b_i + e_{ik}$$

Detection: a QTL is linked to the marker if at least one of the b_i is significantly different from zero

Estimation: (QTL effect and position): This requires relating the b_i to the QTL effects and map position

Detecting epistasis

One major advantage of linear models is their flexibility. To test for epistasis between two QTLs, used an ANOVA with an interaction term

$$z = \mu + a_i + b_k + d_{ik} + e$$

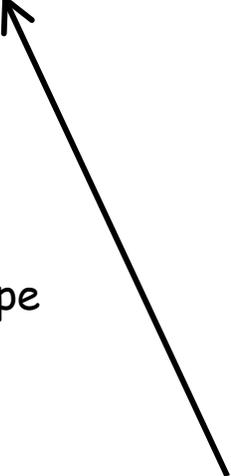
Effect from marker genotype
at first marker set (can be > 1 loci)



Effect from marker genotype
at second marker set



Interaction between marker genotypes i in 1st
marker set and k in 2nd marker set



Detecting epistasis

$$z = \mu + a_i + b_k + d_{ik} + e$$

- At least one of the a_i significantly different from 0
---- QTL linked to first marker set
- At least one of the b_k significantly different from 0
---- QTL linked to second marker set
- At least one of the d_{ik} significantly different from 0
---- interactions between QTL in sets 1 and two

Problem: Huge number of potential interaction terms
(order m^2 , where m = number of markers)

Maximum Likelihood Methods

ML methods use the entire distribution of the data, not just the marker genotype means.

More powerful than linear models, but not as flexible in extending solutions (new analysis required for each model)

Basic likelihood function:

Trait value given
marker genotype is
type j

$$\ell(z | M_j) = \sum_{k=1}^N \varphi(z, \mu_{Q_k}, \sigma^2) \Pr(Q_k | M_j)$$

This is a mixture model

Maximum Likelihood Methods

Sum over the N possible
linked QTL genotypes

Probability of QTL genotype
k given marker genotype
j --- genetic map and linkage
phase entire **here**

$$\ell(z | M_j) = \sum_{k=1}^N \varphi(z, \mu_{Q_k}, \sigma^2) \Pr(Q_k | M_j)$$

Distribution of trait value given
QTL genotype is k
is normal with mean μ_{Q_k} . (QTL
effects enter here)

ML methods combine both detection and estimation of QTL effects/position.

Test for a linked QTL given from the LR test

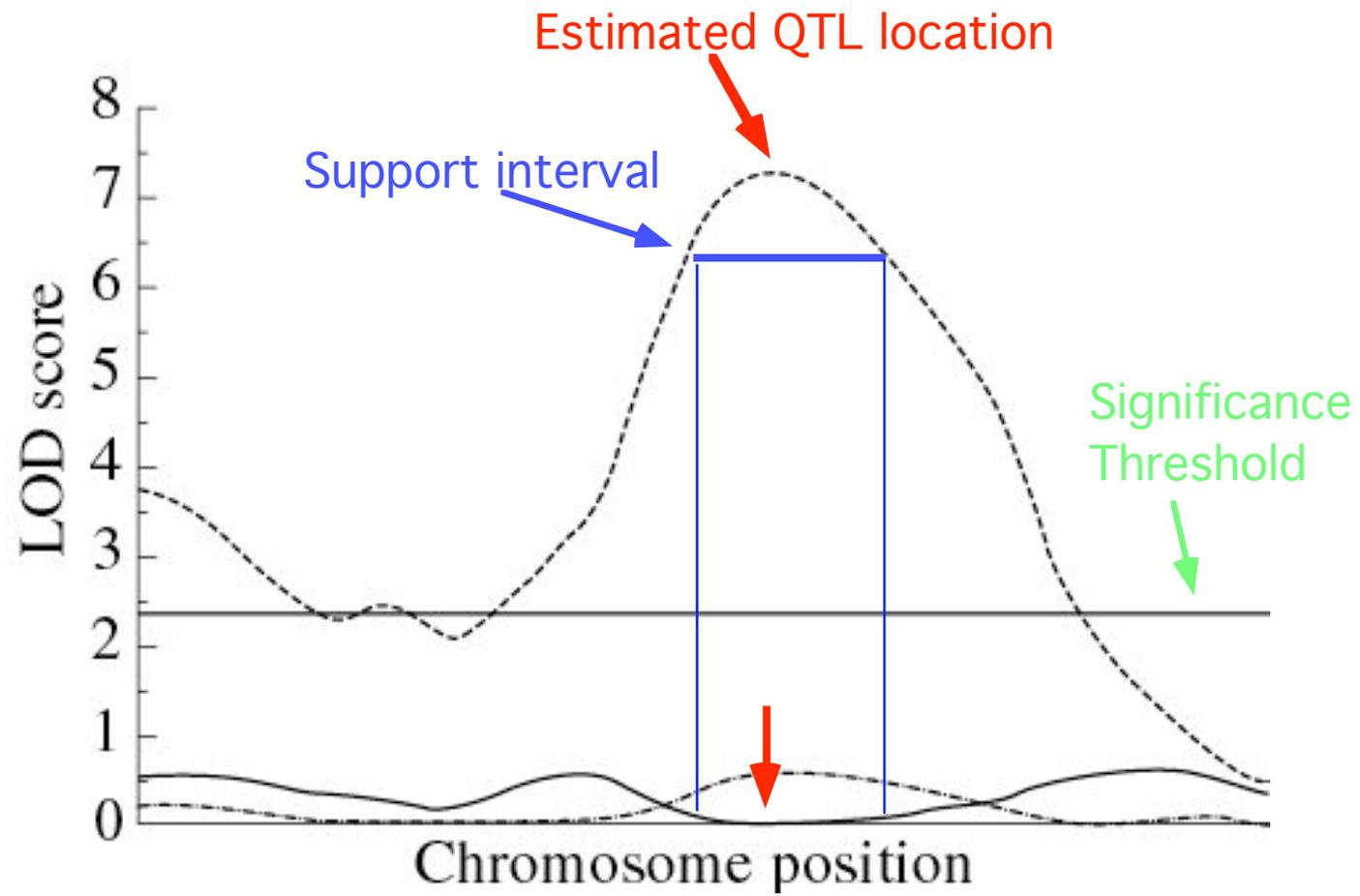
Maximum of the likelihood under a no-linked QTL model

$$LR = -2 \ln \frac{\max \ell_r(\mathbf{z})}{\max \ell(\mathbf{z})}$$

Maximum of the full likelihood

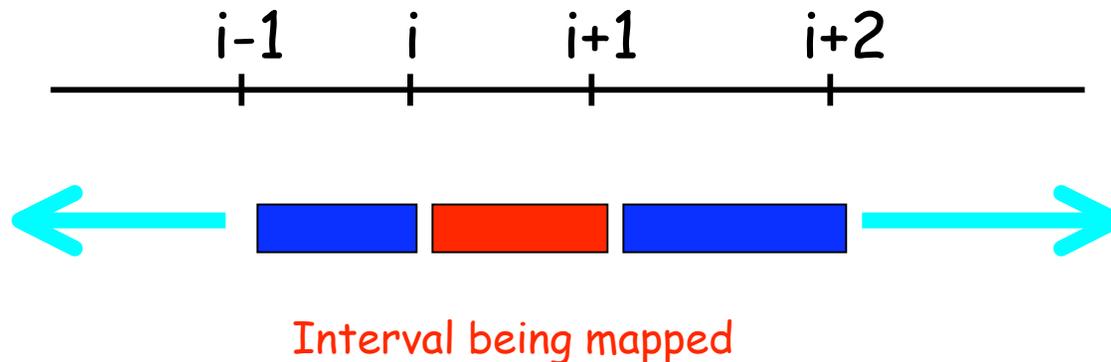
The LR score is often plotted by trying different locations for the QTL (i.e., values of c) and computing a LOD score for each

$$LOD(c) = -\log_{10} \left[\frac{\max \ell_r(\mathbf{z})}{\max \ell(\mathbf{z}, c)} \right] = \frac{LR(c)}{2 \ln 10} \approx \frac{LR(c)}{4.61}$$

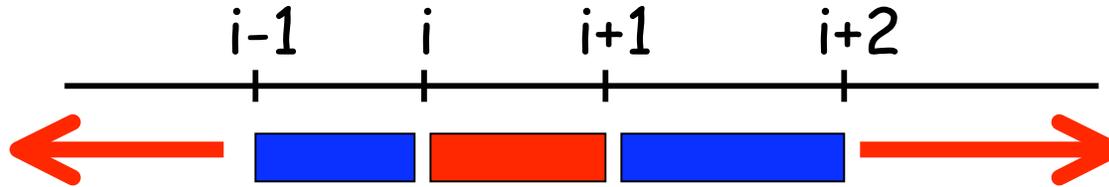


Interval Mapping with Marker Cofactors

Consider interval mapping using the markers i and $i+1$. QTLs linked to these markers, but outside this interval, can contribute (falsely) to estimation of QTL position and effect



Now suppose we also add the two markers flanking the interval ($i-1$ and $i+2$)



Inclusion of markers $i-1$ and $i+2$ fully account for any linked QTLs to the left of $i-1$ and the right of $i+2$

Interval mapping + marker cofactors is called **Composite Interval Mapping (CIM)**

CIM works by adding an additional term to the linear model ,

$$\sum_{k \neq i, i+1} b_k x_{kj}$$

CIM also (potentially) includes unlinked markers to account for QTL on other chromosomes.

Power and Precision

While modest sample sizes are sufficient to **detect** a QTL of modest effect (power), large sample sizes are required to **map it** with some precision

With 200-300 F_2 , a QTL accounting for 5% of total variation can be mapped to a 40cM interval

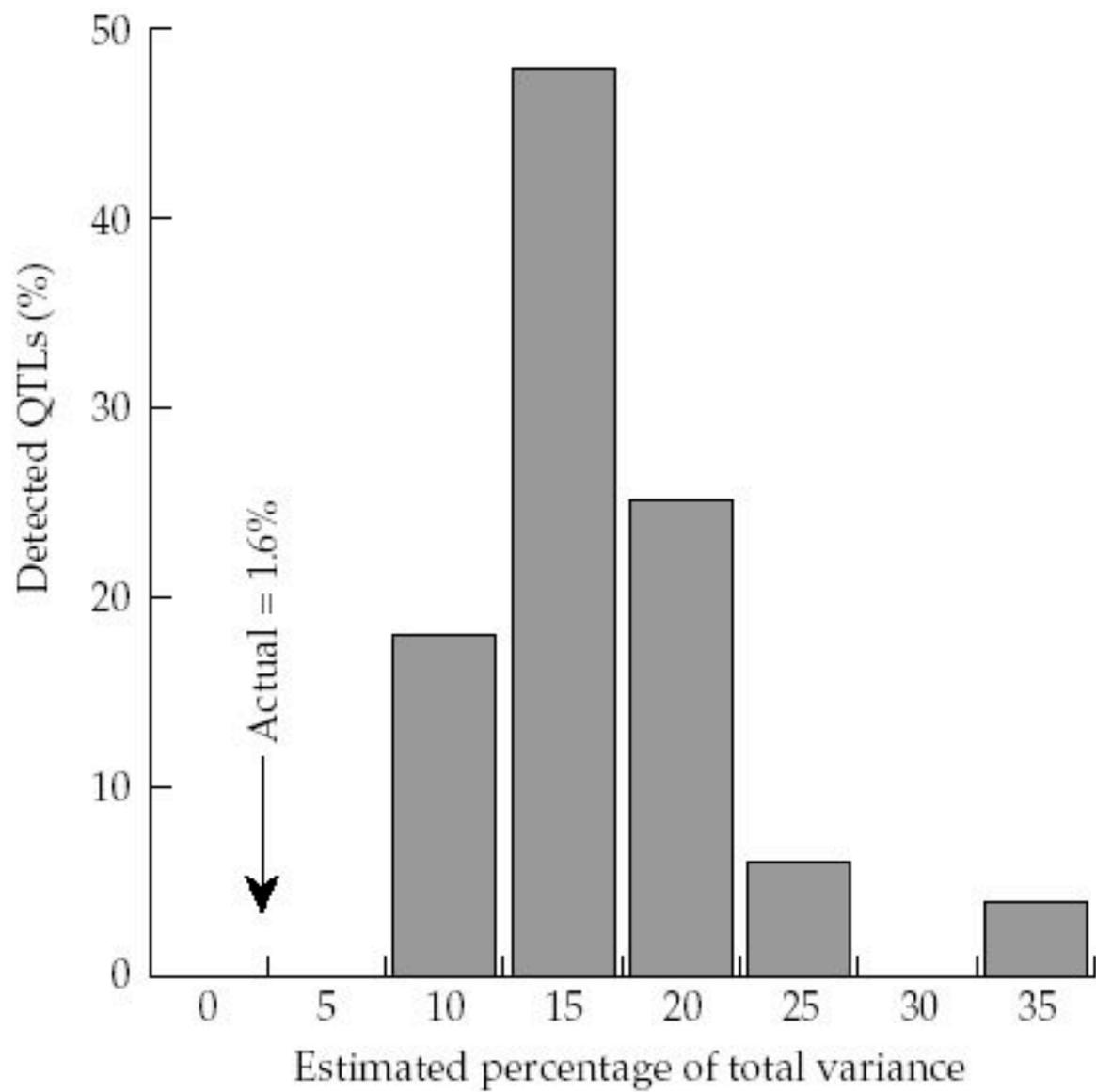
Over 10,000 F_2 individuals are required to map this QTL to a 1cM interval

Power and Repeatability: The Beavis Effect

QTLs with low power of detection tend to have their effects overestimated, often very dramatically

As power of detection increases, the overestimation of detected QTLs becomes far less serious

This is often called the **Beavis Effect**, after Bill Beavis who first noticed this in simulation studies



Model selection

- With (say) 300 markers, we have (potentially) 300 single-marker terms and $300 \times 299 / 2 = 44,850$ epistatic terms
 - Hence, a model with up to $p = 45,150$ possible parameters
 - 2^p possible submodels = $10^{13,600}$ ouch!
- The issue of **Model selection** becomes very important.
- How do we find the best model?
 - Stepwise regression approaches
 - Forward selection (add terms one at a time)
 - Backwards selection (delete terms one at a time)
 - Try all models, assess best fit
 - Mixed-model approaches (SSVS)

Model Selection

Model Selection: Use some criteria to choose among a number of candidate models. Weight goodness-of-fit (L , value of the likelihood at the MLEs) vs. number of estimated parameters (k)

AIC = Akaike's information criterion

$$AIC = 2k - 2 \ln(L)$$

BIC = Bayesian information criterion (Schwarz criterion)

$$BIC = k \cdot \ln(n)/n - 2 \ln(L)/n$$

BIC penalizes free parameters more strongly than AIC

Other measures. Smaller is better

Model averaging

Model averaging: Generate a composite model by weighting (averaging) the various models, using AIC, BIC, or other

Idea: Perhaps no "best" model, but several models all extremely close. Better to report this "distribution" rather than the best one

One approach is to average the coefficients on the "best-fitting" models using some scheme to return a composite model

Stochastic search variable selection (SSVS)

- A Bayesian approach approach to search through a space of possible models
 - Fit the model $y_i = \mu + \mathbf{x}_i^T \beta + e$, including ALL possible covariates of the full model, $\mathbf{X} = (\mathbf{x}_1^T \dots \mathbf{x}_n^T)$
 - Idea: Assume model parameters fall into two classes: those with values very near zero and those with larger values
 - We use the latent (unobservable) variable γ_i , which determines into which class the covariate falls
 - $\beta_i \sim (1 - \gamma_i) \mathcal{N}(0, \tau_i^2) + \gamma_i \mathcal{N}(0, c_i^2 \tau_i^2)$
 - τ_i^2 small, hence values near zero
 - $c_i^2 \tau_i^2$ large, hence values can deviate substantially from zero
 - Posterior probability of (γ_i) is the probability that the parameter is included in the final model

- $\beta_i \sim (1 - \gamma_i)N(0, \tau_i^2) + \gamma_i N(0, c_i^2 \tau_i^2)$
- While τ and c can vary over covariates (model variables), typically they are assigned the same values over all i (e.g., $\tau_i^2 = 0.001, c_i^2 \tau_i^2 = 10$)
- Let γ be the vector of indicator random variables, with a value of one if in the model, zero otherwise
- Given a current γ vector, the conditional prior of the β values is MVN with mean zero and covariance matrix $\mathbf{D}_\gamma \mathbf{R} \mathbf{D}_\gamma$
 - Where \mathbf{R} is the prior correlation matrix, either taken as $\mathbf{R} = \mathbf{I}$ or $\mathbf{R} = (\mathbf{X}^T \mathbf{X})^{-1}$
 - And \mathbf{D} is a diagonal matrix whose i th element is 1 if $\gamma_i = 0$ and c_i if $\gamma_i = 1$.

- The idea is that with a current estimate of μ , σ_e^2 , and γ in hand, we can update β , which is drawn from a MVN distribution
 - Mean = $(\mathbf{X}^T \mathbf{X} + \sigma_e^2 (\mathbf{D}_\gamma \mathbf{R} \mathbf{D}_\gamma)^{-1})^{-1} \mathbf{X}^T (\mathbf{y} - \mu \mathbf{I})$
 - Variance = $(\mathbf{X}^T \mathbf{X} + \sigma_e^2 (\mathbf{D}_\gamma \mathbf{R} \mathbf{D}_\gamma)^{-1})^{-1}$
- With an updated β vector in hand, we update the γ vector

$$\Pr(\gamma_i | \gamma_{(-i)}, \mu, \beta, \sigma_e^2) = \frac{p(\beta | \gamma_{(-i)}, \gamma_i = 1) \Pr(\gamma_i = 1)}{p(\beta | \gamma_{(-i)}, \gamma_i = 1) \Pr(\gamma_i = 1) + p(\beta | \gamma_{(-i)}, \gamma_i = 0) \Pr(\gamma_i = 0)}$$

Usually, the prior on the γ_i is independent of i and taken to be $p_i = 1/2$

Supersaturated Models

A problem with many QTL approaches is that there are far more parameters (p) to estimate than there are independent samples (n).

Case in point: epistasis

Such supersaturated models arise commonly in Genomics. How do we deal with them?

Again, an approach like SSVS, where all parameters are included, but some are shrunk back (regressed) towards zero by assigning them a very small posterior variance

Shrinkage estimators

Shrinkage estimates: Rather than adding interaction terms one at a time, a shrinkage method starts **with all interactions included**, and then shrinks most back to zero.

Under a Bayesian analysis, any effect is *random*. One can assume the effect for (say) interaction ij is drawn from a normal with mean zero and variance σ^2_{ij}

Further, the interaction-specific variances are themselves random variables drawn from a hyperparameter distribution, such as an inverse chi-square.

One then estimates the hyperparameters and uses these to predict the variances, with effects with small variances shrinking back to zero, and effects with large variances remaining in the model.

Key ideas in QTL mapping

Look for marker-trait associations

- Many difference crossing designs (F2, BC, RIL)
- Many difference methods of analysis:
Linear models, MLE, Bayesian
- Most studies UNDERPOWERED, esp. for
"fine" mapping

What is a "QTL"

- A detected "QTL" in a mapping experiment is a region of a chromosome detected by linkage.
- Usually large (typically 10-40 cM)
- When further examined, most "large" QTLs turn out to be a linked collection of locations with increasingly smaller effects
- The more one localizes, the more subregions that are found, and the smaller their effect