Seattle Summer Institute 2008
Advanced QTL
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- overview: multiple QTL approaches
- Bayesian QTL mapping & model selection
- data examples in detail
- software demos: R/qtl and R/qtlbim

Real knowledge is to know the extent of one's ignorance.
Confucius (on a bench in Seattle)

Overview of Multiple QTL

1. what is the goal of multiple QTL study?
2. gene action and epistasis
3. Bayesian vs. classical QTL
4. QTL model selection
5. QTL software options

1. what is the goal of QTL study?

- uncover underlying biochemistry
  - identify how networks function, break down
  - find useful candidates for (medical) intervention
  - epistasis may play key role
  - statistical goal: maximize number of correctly identified QTL
- basic science/evolution
  - how is the genome organized?
  - identify units of natural selection
  - additive effects may be most important (Wright/Fisher debate)
  - statistical goal: maximize number of correctly identified QTL
- select "elite" individuals
  - predict phenotype (breeding value) using suite of characteristics (phenotypes) translated into a few QTL
  - statistical goal: mimimize prediction error

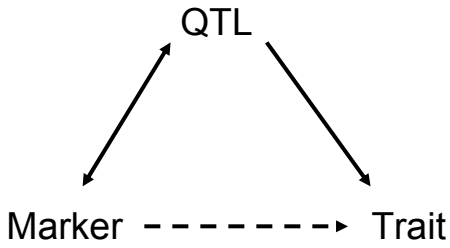
cross two inbred lines

→ linkage disequilibrium

→ associations

→ linked segregating QTL

(after Gary Churchill)



problems of single QTL approach

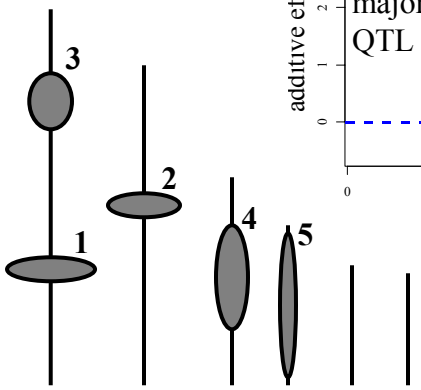
- wrong model: biased view
  - fool yourself: bad guess at locations, effects
  - detect ghost QTL between linked loci
  - miss epistasis completely
- low power
- bad science
  - use best tools for the job
  - maximize scarce research resources
  - leverage already big investment in experiment

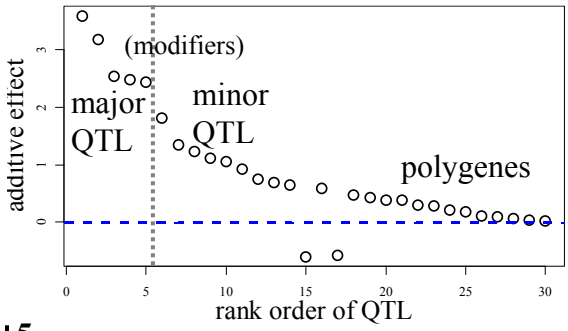
advantages of multiple QTL approach

- improve statistical power, precision
  - increase number of QTL detected
  - better estimates of loci: less bias, smaller intervals
- improve inference of complex genetic architecture
  - patterns and individual elements of epistasis
  - appropriate estimates of means, variances, covariances
    - asymptotically unbiased, efficient
  - assess relative contributions of different QTL
- improve estimates of genotypic values
  - less bias (more accurate) and smaller variance (more precise)
  - mean squared error = MSE = $(\text{bias})^2$ + variance

Pareto diagram of QTL effects

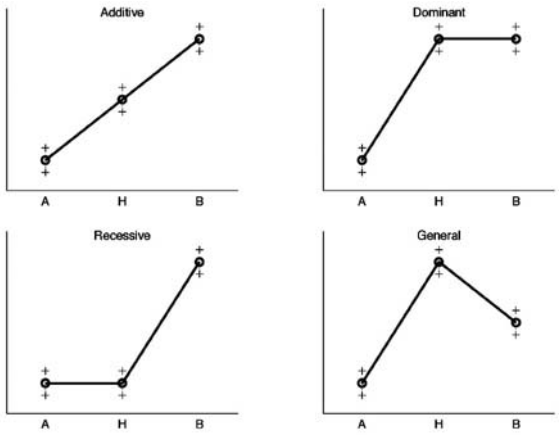
major QTL on linkage map





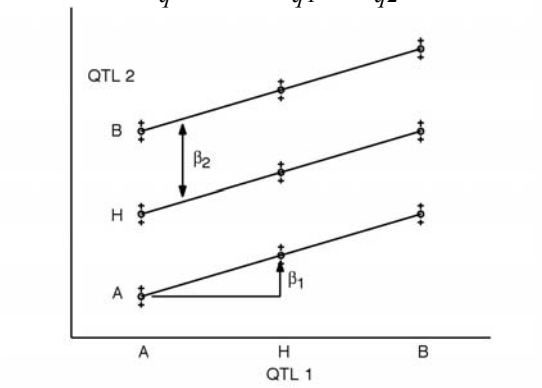
2. Gene Action and Epistasis

additive, dominant, recessive, general effects of a single QTL (Gary Churchill)



additive effects of two QTL (Gary Churchill)

$$\mu_q = \mu + \beta_{q1} + \beta_{q2}$$



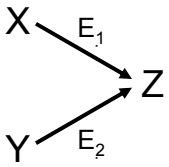
Epistasis (Gary Churchill)

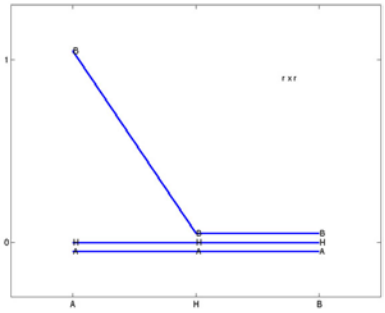
The allelic state at one locus can mask or uncover the effects of allelic variation at another.

- W. Bateson, 1907.

epistasis in parallel pathways (GAC)

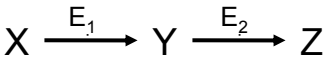
- Z keeps trait value low
- neither E_1 nor E_2 is rate limiting
- loss of function alleles are segregating from parent A at E_1 and from parent B at E_2

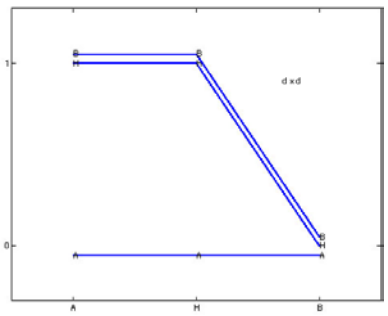




epistasis in a serial pathway (GAC)

- Z keeps trait value high
- neither E_1 nor E_2 is rate limiting
- loss of function alleles are segregating from parent B at E_1 and from parent A at E_2





epistatic interactions

- model space issues
  - 2-QTL interactions only?
    - or general interactions among multiple QTL?
  - partition of effects
    - Fisher-Cockerham or tree-structured or ?
- model search issues
  - epistasis between significant QTL
    - check all possible pairs when QTL included?
    - allow higher order epistasis?
  - epistasis with non-significant QTL
    - whole genome paired with each significant QTL?
    - pairs of non-significant QTL?
- see papers of Nengjun Yi (2000-7) in *Genetics*

limits of epistatic inference

- power to detect effects
  - epistatic model sizes grow quickly
    - $|A| = 3^{n.qtl}$ for general interactions
  - power tradeoff
    - depends sample size *vs.* model size
    - want $n / |A|$ to be fairly large (say > 5)
    - 3 QTL, $n = 100$ F2: $n / |A| \approx 4$
- rare genotypes may not be observed
  - *aa/BB & AA/bb* rare for linked loci
  - empty cells mess up balance
    - adjusted tests (type III) are wrong
  - confounds main effects & interactions

2 linked QTL empty cell with $n = 100$

	bb	*bB*	*BB*
aa	6	15	0
aA	15	25	15
AA	3	15	6

limits of multiple QTL?

- limits of statistical inference
  - power depends on sample size, heritability, environmental variation
  - "best" model balances fit to data and complexity (model size)
  - genetic linkage = correlated estimates of gene effects
- limits of biological utility
  - sampling: only see some patterns with many QTL
  - marker assisted selection (Bernardo 2001 *Crop Sci*)
    - 10 QTL ok, 50 QTL are too many
    - phenotype better predictor than genotype when too many QTL
    - increasing sample size may not give multiple QTL any advantage
  - hard to select many QTL simultaneously
    - 3^m possible genotypes to choose from

QTL below detection level?

- problem of selection bias
  - QTL of modest effect only detected sometimes
  - effects overestimated when detected
  - repeat studies may fail to detect these QTL
- think of probability of detecting QTL
  - avoids sharp in/out dichotomy
  - avoid pitfalls of one "best" model
  - examine "better" models with more probable QTL
- rethink formal approach for QTL
  - directly allow uncertainty in genetic architecture
  - QTL model selection over genetic architecture

3. Bayesian vs. classical QTL study

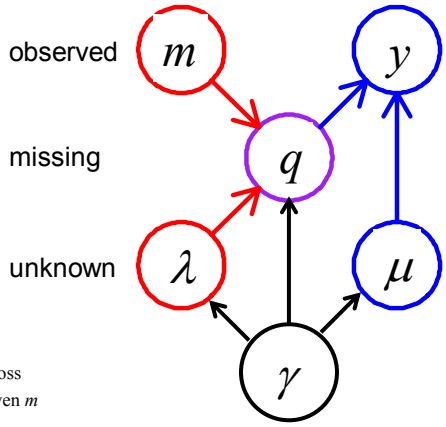
- classical study
  - ***maximize*** over unknown effects
  - ***test*** for detection of QTL at loci
  - model selection in stepwise fashion
- Bayesian study
  - ***average*** over unknown effects
  - ***estimate*** chance of detecting QTL
  - sample all possible models
- both approaches
  - average over missing QTL genotypes
  - scan over possible loci

Bayesian idea

- Reverend Thomas Bayes (1702-1761)
  - part-time mathematician
  - buried in Bunhill Cemetary, Moongate, London
  - famous paper in 1763 *Phil Trans Roy Soc London*
  - was Bayes the first with this idea? (Laplace?)
- basic idea (from Bayes' original example)
  - two billiard balls tossed at random (uniform) on table
  - where is first ball if the second is to its left?
    - prior: anywhere on the table
    - posterior: more likely toward right end of table

QTL model selection: key players

- observed measurements
  - y = phenotypic trait
  - m = markers & linkage map
  - i = individual index (1,…,n)
- missing data
  - missing marker data
  - q = QT genotypes
    - alleles QQ, Qq, or qq at locus
- unknown quantities
  - λ = QT locus (or loci)
  - μ = phenotype model parameters
  - γ = QTL model/genetic architecture
- pr($q|m,\lambda,\gamma$) genotype model
  - grounded by linkage map, experimental cross
  - recombination yields multinomial for q given m
- pr($y|q,\mu,\gamma$) phenotype model
  - distribution shape (assumed normal here)
  - unknown parameters μ (could be non-parametric)



after
Sen Churchill (2001)

Bayes posterior vs. maximum likelihood

- LOD: classical Log ODds
  - maximize likelihood over effects μ
  - `R/qtl scanone/scantwo: method = "em"`
- *LPD*: Bayesian *L*og *P*osterior *D*ensity
  - average posterior over effects μ
  - `R/qtl scanone/scantwo: method = "imp"`

$$\mathrm{LOD}(\lambda) = \log_{10}\{\max_{\mu} \mathrm{pr}(y \mid m,\mu,\lambda)\} + c$$

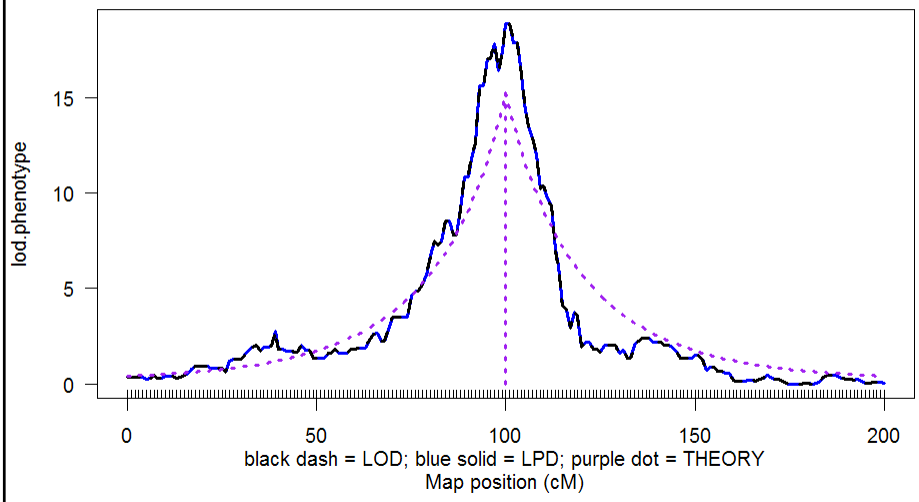
$$\mathrm{LPD}(\lambda) = \log_{10}\{\mathrm{pr}(\lambda \mid m)\int \mathrm{pr}(y \mid m,\mu,\lambda)\mathrm{pr}(\mu)d\mu\} + C$$

likelihood mixes over missing QTL genotypes:

$$\mathrm{pr}(y \mid m,\mu,\lambda) = \sum_q \mathrm{pr}(y \mid q,\mu)\mathrm{pr}(q \mid m,\lambda)$$

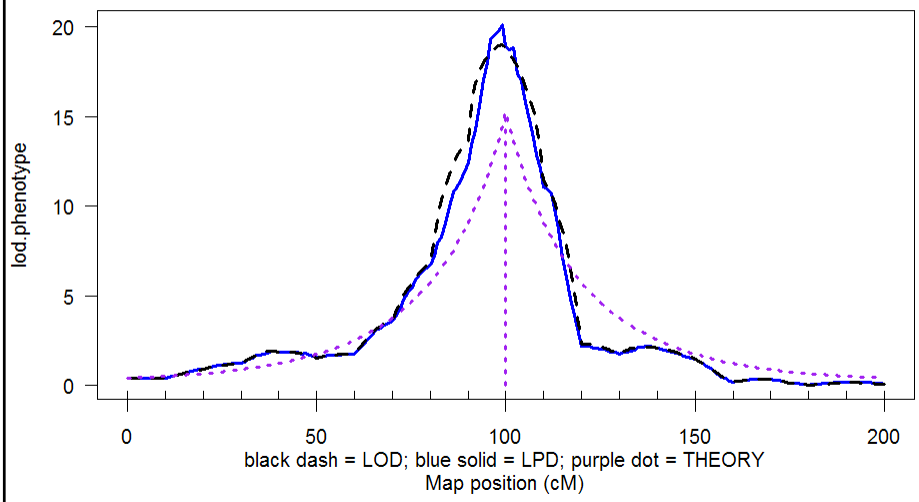
LOD & LPD: 1 QTL

n.ind = 100, 1 cM marker spacing



LOD & LPD: 1 QTL

n.ind = 100, 10 cM marker spacing



marginal LOD or LPD

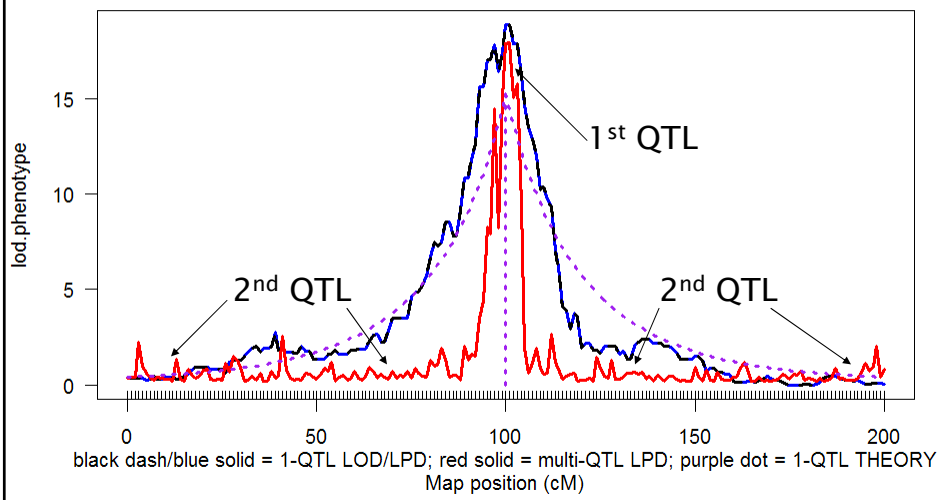
- compare two genetic architectures (γ_2,γ_1) at each locus
  - with (γ_2) or without (γ_1) another QTL at locus λ
    - preserve model hierarchy (e.g. drop any epistasis with QTL at λ)
  - with (γ_2) or without (γ_1) epistasis with QTL at locus λ
  - γ_2 contains γ_1 as a sub-architecture
- allow for multiple QTL besides locus being scanned
  - architectures γ_1 and γ_2 may have QTL at several other loci
  - use marginal LOD, LPD or other diagnostic
  - posterior, Bayes factor, heritability

$$\mathrm{LOD}(\lambda \mid \gamma_2) - \mathrm{LOD}(\lambda \mid \gamma_1)$$

$$\mathrm{LPD}(\lambda \mid \gamma_2) - \mathrm{LPD}(\lambda \mid \gamma_1)$$

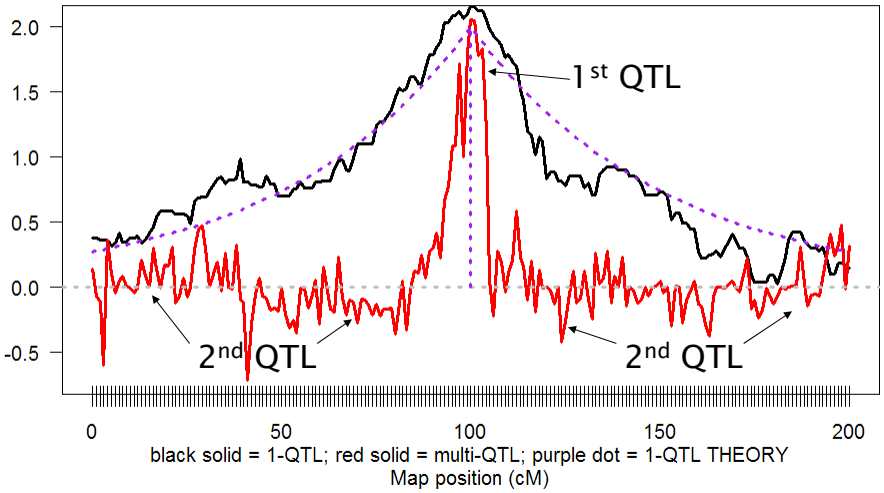
LPD: 1 QTL vs. multi-QTL

marginal contribution to LPD from QTL at λ



substitution effect: 1 QTL vs. multi-QTL

single QTL effect vs. marginal effect from QTL at λ



why use a Bayesian approach?

- first, do *both* classical and Bayesian
  - always nice to have a separate validation
  - each approach has its strengths and weaknesses
- classical approach works quite well
  - selects large effect QTL easily
  - directly builds on regression ideas for model selection
- Bayesian approach is comprehensive
  - samples most probable genetic architectures
  - formalizes model selection within one framework
  - readily (!) extends to more complicated problems

4. QTL model selection

- select class of models
  - see earlier slides above
- decide how to compare models
  - (Bayesian interval mapping talk later)
- search model space
  - (Bayesian interval mapping talk later)
- assess performance of procedure
  - see Kao (2000), Broman and Speed (2002)
  - Manichaukul, Moon, Yandell, Broman (in prep)
  - be wary of HK regression assessments

pragmatics of multiple QTL

- evaluate some objective for model given data
  - classical likelihood
  - Bayesian posterior
- search over possible genetic architectures (models)
  - number and positions of loci
  - gene action: additive, dominance, epistasis
- estimate "features" of model
  - means, variances & covariances, confidence regions
  - marginal or conditional distributions
- art of model selection
  - how select "best" or "better" model(s)?
  - how to search over useful subset of possible models?

comparing models

- balance model fit against model complexity
  - want to fit data well (maximum likelihood)
  - without getting too complicated a model

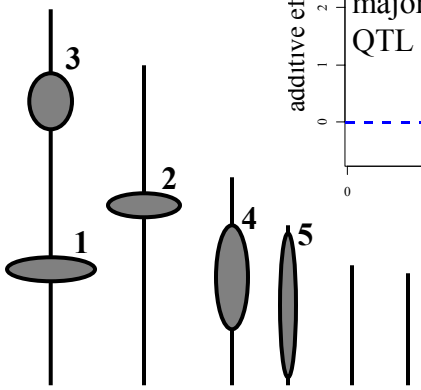
	smaller model	**bigger model**
fit model	miss key features	fits better
estimate phenotype	may be biased	no bias
predict new data	may be biased	no bias
interpret model	easier	more complicated
estimate effects	low variance	high variance

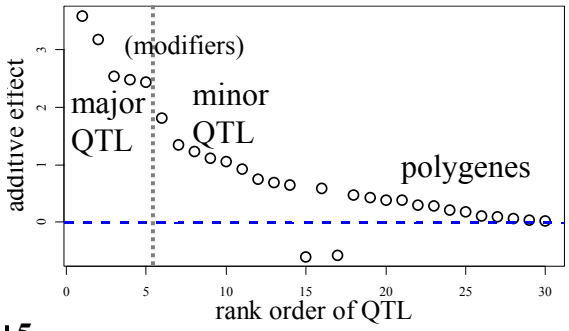
Bayesian model averaging

- average summaries over multiple architectures
- avoid selection of "best" model
- focus on "better" models
- examples in data talk later

Pareto diagram of QTL effects

major QTL on linkage map





5. QTL software options

- methods
  - approximate QTL by markers
  - exact multiple QTL interval mapping
- software platforms
  - MapMaker/QTL (obsolete)
  - QTLCart (statgen.ncsu.edu/qtlcart)
  - R/qtl (www.rqtl.org)
  - R/qtlbim (www.qtlbim.org)
  - Yandell, Bradbury (2007) book chapter

approximate QTL methods

- marker regression
  - locus & effect confounded
  - lose power with missing data
- Haley-Knott (least squares) regression
  - correct mean, wrong variance
  - biased by pattern of missing data (Kao 2000)
- extended HK regression
  - correct mean and variance
  - minimizes bias issue (R/qtl "ehk" method)
- composite interval mapping (QTLCart)
  - use markers to approximate other QTL
  - properties depend on marker spacing, missing data

exact QTL methods

- interval mapping (Lander, Botstein 1989)
  - scan whole genome for single QTL
  - bias for linked QTL, low power
- multiple interval mapping (Kao, Zeng, Teasdale 1999)
  - sequential scan of all QTL
  - stepwise model selection
- multiple imputation (Sen, Churchill 2001)
  - fill in (impute) missing genotypes along genome
  - average over multiple imputations
- Bayesian interval mapping (Yi et al. 2005)
  - sample most likely models
  - marginal scans conditional on other QTL

QTL software platforms

- QTLCart (statgen.ncsu.edu/qtlcart)
  - includes features of original MapMaker/QTL
    - not designed for building a linkage map
  - easy to use Windows version WinQTLCart
  - based on Lander-Botstein maximum likelihood LOD
    - extended to marker cofactors (CIM) and multiple QTL (MIM)
    - epistasis, some covariates (GxE)
    - stepwise model selection using information criteria
  - some multiple trait options
  - OK graphics
- R/qtl (www.rqtl.org)
  - includes functionality of classical interval mapping
  - many useful tools to check genotype data, build linkage maps
  - excellent graphics
  - several methods for 1-QTL and 2-QTL mapping
    - epistasis, covariates (GxE)
  - tools available for multiple QTL model selection

Bayesian QTL software options

- Bayesian Haley-Knott approximation: no epistasis
  - Berry C (1998)
    - R/bqtl (www.r-project.org contributed package)
- multiple imputation: epistasis, mostly 1-2 QTL but some multi-QTL
  - Sen and Churchill (2000)
    - matlab/pseudomarker (www.jax.org/staff/churchill/labsite/software)
  - Broman et al. (2003)
    - R/qtl (www.rqtl.org)
- Bayesian interval mapping via MCMC: no epistasis
  - Satagopan et al. (1996); Satagopan, Yandell (1996) Gaffney (2001)
    - R/bim (www.r-project.org contributed package)
    - WinQTLCart/bmapqtl (statgen.ncsu.edu/qtlcart)
  - Stephens & Fisch (1998): no code release
  - Sillanpää Arjas (1998)
    - multimapper (www.rni.helsinki.fi/~mjs)
- Bayesian interval mapping via MCMC: epistasis
  - Yandell et al. (2007)
    - R/qtlbim (www.qtlbim.org)
- Bayesian shrinkage: no epistasis
  - Wang et al. Xu (2005): no code release

R/qtlbim: www.qtlbim.org

- Properties
  - cross-compatible with R/qtl
  - new MCMC algorithms
    - Gibbs with loci indicators; no reversible jump
  - epistasis, fixed & random covariates, GxE
  - extensive graphics
- Software history
  - initially designed (Satagopan Yandell 1996)
  - major revision and extension (Gaffney 2001)
  - R/bim to CRAN (Wu, Gaffney, Jin, Yandell 2003)
  - R/qtlbim to CRAN (Yi, Yandell et al. 2006)
- Publications
  - Yi et al. (2005); Yandell et al. (2007); …

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