

## Bayes posterior vs. maximum likelihood

- classical approach maximizes likelihood
- Bayesian posterior averages over other parameters

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

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

$$\text{pr}(y | m, \mu, \lambda) = \sum_q \text{pr}(y | q, \mu) \text{pr}(q | m, \lambda)$$

## comparing genetic architectures

- compare  $H_1$  vs  $H_2$ 
  - with ( $H_2$ ) or without ( $H_1$ ) QTL at  $\lambda_2$ 
    - preserve model hierarchy (e.g. drop any epistasis with QTL at  $\lambda_2$ )
  - with ( $H_2$ ) or without ( $H_1$ ) epistasis at  $\lambda_2$
  - allow for QTL at all other loci  $\lambda_1$  in architecture  $H_1$
- use conditional LPD or other conditional diagnostic
  - conditional posterior or conditional Bayes factor
  - conditional heritability

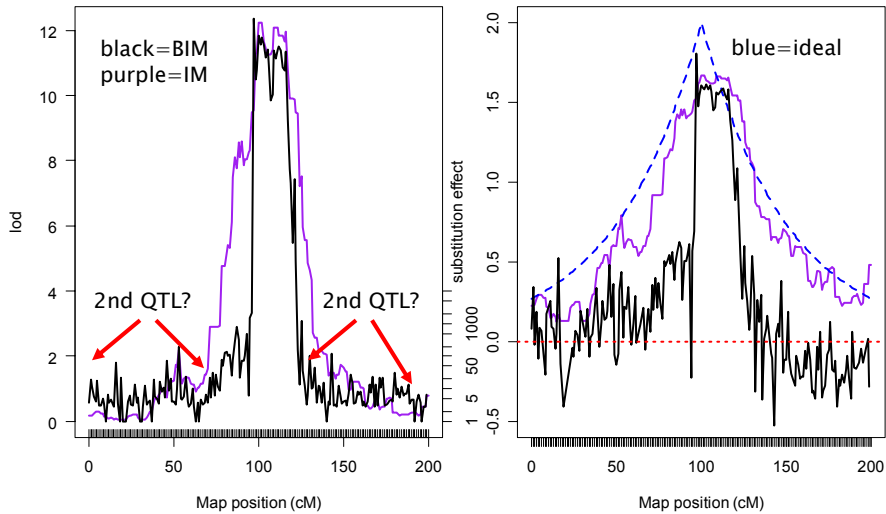
$$\text{LOD}(\lambda_1, \lambda_2 | H_1) - \text{LOD}(\lambda_1 | H_1)$$

$$\text{LPD}(\lambda_1, \lambda_2 | H_1) - \text{LPD}(\lambda_1 | H_1)$$

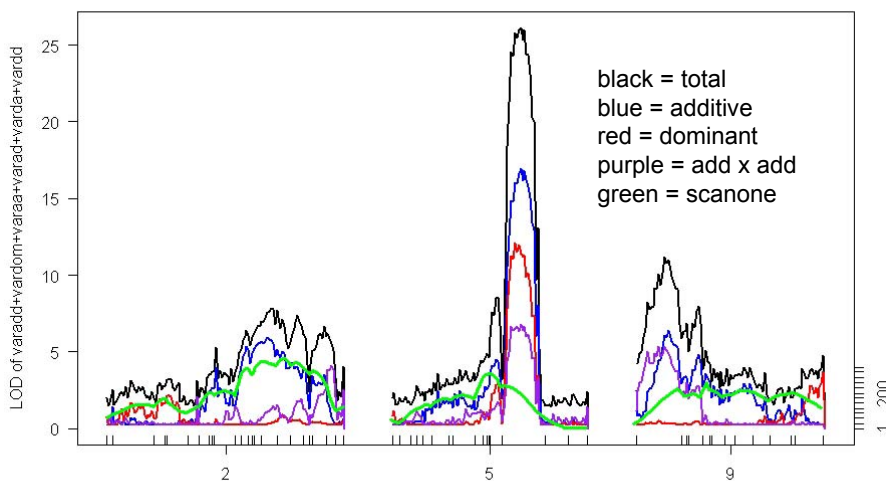
# BC with 1 QTL: IM vs. BIM

LOD and LPD: QTL at 100

substitution effect



# marginal LOD by locus



QTL 2: Bayes

Seattle SISG: Yandell © 2006

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