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MODELLING EPISTASIS BETWEEN QUANTITATIVE TRAIT LOCI ON SWINE CHROMOSOME SIX

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MATERIAL

ANIMALS: 305 F2 individuals from a commercial cross

TRAIT: intramuscular fat content

MARKERS: SSC6, 24 markers, analysis between 40-70 and 80-100cM

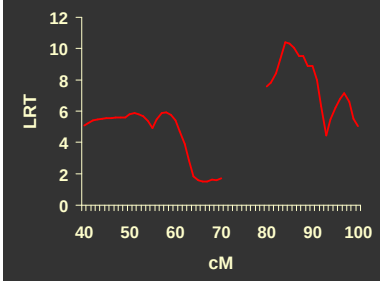
CONCLUSIONS

- evidence for 2 QTL (P_N=0.00005, $P_{BONFERRONI}$=0.072) at 84 cM (SW1473 - LPIN2) and 96 cM (ADCYAP - S0003)
- variances: $\hat{\sigma}^2_{\alpha} = 0.24$ $\hat{\sigma}^2_{q1} = 0.62$ $\hat{\sigma}^2_{q2} = 0.54$ $\hat{\sigma}_{q1q2} = 0.09$ $\hat{\sigma}^2_{e} = 0.77$
- result highly consistent with previous analysis with fixed QTL
- epistatic relationship between QTL at 49 and 59 cM was not confirmed
- allowing for covariance between QTL did not influence estimates of QTL position and variances -> a too simple covariance model

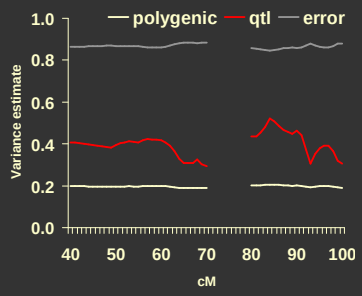
RESULTS and MODELS

1 QTL

$$y = \mu + Z_{\alpha}\alpha + Z_q q + e$$



LRT profile
no QTL vs. 1 QTL



estimated variance components

α additive polygenic $\sim N\left(0, A\sigma^2_{\alpha}\right)$

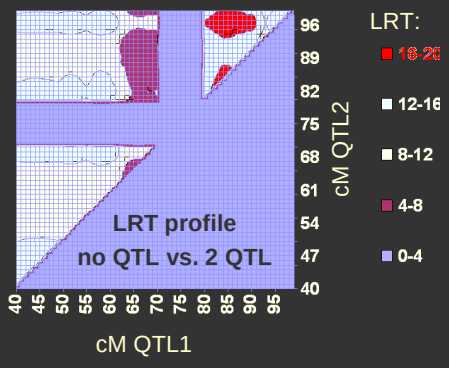
q QTL $\sim N\left(0, IBD\sigma^2_{q}\right)$

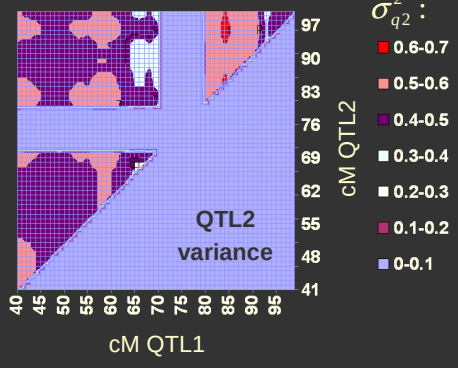
e residual $\sim N\left(0, I\sigma^2_{e}\right)$

$$G = \begin{bmatrix} A\sigma^2_{\alpha} & 0 \\ 0 & IBD\sigma^2_{q} \end{bmatrix}$$

2 QTL without covariance

$$y = \mu + Z_{\alpha}\alpha + Z_{q1}q_1 + Z_{q2}q_2 + e$$





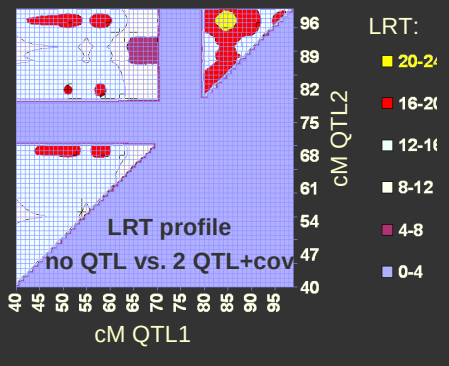
q_1 QTL 1 $\sim N\left(0, IBD_1\sigma^2_{q1}\right)$

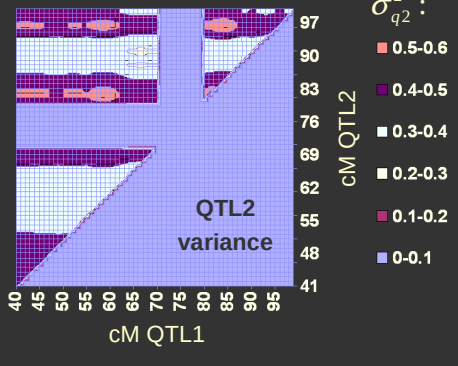
q_2 QTL 2 $\sim N\left(0, IBD_2\sigma^2_{q2}\right)$

$$G = \begin{bmatrix} A\sigma^2_{\alpha} & 0 & 0 \\ 0 & IBD_1\sigma^2_{q1} & 0 \\ 0 & 0 & IBD_2\sigma^2_{q2} \end{bmatrix}$$

2 QTL with covariance

$$y = \mu + Z_{\alpha}\alpha + Z_{q1}q_1 + Z_{q2}q_2 + e$$





$$G = \begin{bmatrix} A\sigma^2_{\alpha} & 0 & 0 \\ 0 & IBD_1\sigma^2_{q1} & I\sigma_{q1q2} \\ 0 & I\sigma_{q1q2} & IBD_2\sigma^2_{q2} \end{bmatrix}$$