

## W05 - Maximum Likelihood - least squares - linear regressions

Sivia ch3, 5 ..

Lander and Botstein 1988

bio problem: Ding et al. 2015

### Maximum Likelihood (ML)

D - data

H - hypothesis

X - parameters of H

$$P(D | X, H)$$

$$P(X | D, H) = \frac{P(D | X, H) P(X | H)}{P(D)}$$

posterior:

$$P(X | D, H) \propto P(D | X, H) \cdot P(X | H)$$

if we assume an uninformative prior  $P(X | H) = \text{constant}$

$$\underset{X}{\operatorname{argmax}} P(X | D, H) = \underset{X}{\operatorname{argmax}} P(D | X, H)$$

$$= \underset{X}{\operatorname{argmax}} \log P(D | X, H)$$

$X^*$  ML fit data is also  $X$  at which

posterior of  $X$  given  $D$  is also maximal.

(uninformative prior).

$$L(X) = \log P(D | X, H), \quad \frac{\delta L}{\delta X} \Big|_{X^*} = 0$$

$$L(x) = \log P(D|X, H)$$

$$\frac{\delta L(x)}{\delta x} \Big|_{x^*} = 0 \quad \frac{\delta^2 L}{\delta x^2} \Big|_{x^*} = -\frac{1}{\sigma_2^2}$$

Distribution	$P(D X, H)$	$X^*$	$\sigma^*$
exponential $\lambda$ $D = \{t_1, \dots, t_N\}$	$\frac{e^{-\sum t_i/\lambda}}{\lambda^N}$	$\hat{\lambda} = \frac{\sum t_i}{N}$	$\hat{\lambda}/\sqrt{N}$
binomial ( $p$ ) $n, N$	$\binom{N}{n} p^n (1-p)^{N-n}$	$\hat{p} = \frac{n}{N}$	$\sqrt{p(1-p)/N}$
Gaussian $\mu, \sigma$ $D = \{t_1, \dots, t_N\}$	$\frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(t-\mu)^2}{2\sigma^2}}$	$\hat{\mu} = \frac{\sum t_i}{N}$	$\hat{\sigma} = \sqrt{\frac{\sum (t_i - \mu)^2}{N}}$

$$P(D|\mu, \sigma) = \left( \frac{1}{\sqrt{2\pi}\sigma} \right)^N e^{-\frac{\sum_i(t_i-\mu)^2}{2\sigma^2}}$$

$$\log P(D|\mu, \sigma) = -N \log \sqrt{2\pi} - N \log \sigma - \frac{\sum_i(t_i-\mu)^2}{2\sigma^2}$$

$$\frac{\delta L(\mu, \sigma)}{\delta \mu} = -\frac{1}{2\sigma^2} \cdot 2 \sum_i (t_i - \mu) \cdot (-1) = +\frac{1}{\sigma^2} \sum_i (t_i - \mu)$$

$$\frac{\delta L(\mu, \sigma)}{\delta \sigma} = -\frac{N}{\sigma} - (-2) \frac{\sum_i (t_i - \mu)^2}{2\sigma^3} = -\frac{1}{\sigma} \left[ N - \frac{\sum_i (t_i - \mu)^2}{\sigma^2} \right]$$

$$\left. \frac{\delta L}{\delta \mu} \right|_0 \quad \left\{ \begin{array}{l} \mu^* = \frac{1}{N} \sum_i t_i \end{array} \right.$$

$$\left. \frac{\delta L}{\delta \sigma} \right|_0 \quad \left\{ \begin{array}{l} \sigma^2 = \frac{\sum_i (t_i - \mu)^2}{N} \end{array} \right.$$

$$\frac{\delta^2 L}{\delta \mu^2} = -\frac{N}{\sigma^2} \quad \left. \begin{array}{l} = -\frac{N}{\sigma_x^2} \Rightarrow \end{array} \right\} \sigma_{\mu}^2 = \frac{\sigma_x^2}{N}$$

$$\left. \frac{\delta^2 L}{\delta \sigma^2} = +\frac{N}{\sigma^2} - 3 \frac{\sum_i (t_i - \mu)^2}{\sigma^4} \right\} = \frac{N}{\sigma_x^2} - 3 \frac{N \sigma_x^2}{\sigma_x^4} = -2 \frac{N}{\sigma_x^2} \Rightarrow \left\} \sigma_{\sigma}^2 = \frac{\sigma_x^2}{2N} \right.$$

## Least-squares fit

$$D = \{d_i\}_{i=1}^N$$

$$P(D|XH) = \prod_{i=1}^N P(d_i|XH)$$

Assume we know how ideal data behaves except for a noise

$$d_i = f_i(x)$$

$$d_i - f_i(x) \sim \mathcal{N}(0, \sigma_i)$$

Gaussian noise  
• symmetric  
• not too large

$$\sigma_i \approx \sigma$$

$$P(D|XH) = \left( \frac{1}{\sqrt{2\pi}\sigma} \right)^N e^{-\frac{\sum_i (d_i - f_i(x))^2}{2\sigma^2}}$$

$$\log P(D|XH) \propto -N \log \sigma - \frac{\sum_i (d_i - f_i(x))^2}{2\sigma^2}$$

$$\chi^2 = \sum_i (d_i - f_i(x))^2$$

least

$$\arg \max_X \log P(D|XH) = \arg \min_X \chi^2$$

least square fit  
 $L^2$ -norm.

Particular case fit to a line

$$d_i = \{x_i, y_i\}_{i=1}^N$$

$$y_i - (a + b x_i) \sim N(0, \sigma)$$

$$P(D|a, b) = \left(\frac{1}{\sqrt{2\pi}\sigma}\right)^N e^{-\frac{\sum_i (y_i - a - b x_i)^2}{2\sigma^2}}$$

$$\left. \arg\max_{a, b} P(D|a, b) \right) = \arg\min_{a, b} \sum_i (y_i - (a + b x_i))^2$$

linear regression

## QTL analysis

crossable  $S_1$   $S_2$   $\rightarrow$  have a phenotypic difference  
Which genomic region is responsible for it?  
noisy: many loci  
 $\sim$  large environmental variation.

To identify the loci responsible for a particular trait.

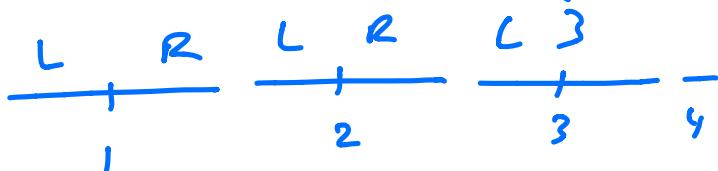
Ding et al 2016

$\times$  ( $Drosophila Simulans$  ( $Dsim$ ))  $\mu_{sim} \approx 176$  Hz  
 $Drosophila mauritiana$  ( $Dmav$ )  $\mu_{mav} = 186$  Hz

male courtship song

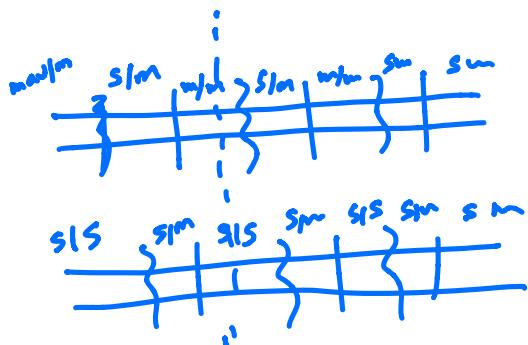
Where does the difference come from?

$Dsim, Dmav \sim 98\%$  similarity of genomes



$\frac{Sam}{gen}$   $\equiv$   $Dsim \text{ ♂} \times Dmav \text{ ♂} \equiv \frac{mav}{mav}$   
 $\downarrow$   
 $F_1 \equiv \frac{sim}{mav}$

## Back crosses



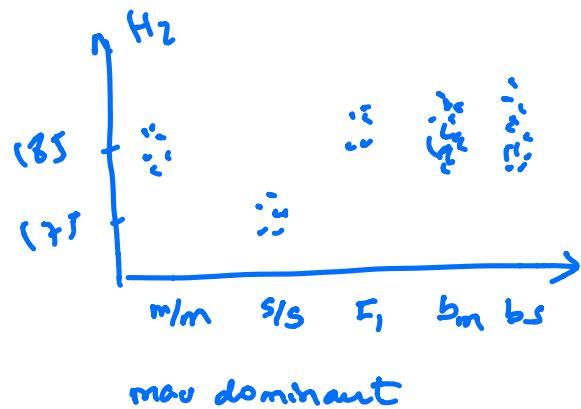
~1 breakpoint average

From backcrosses collect information across c'

+ pheno type  $\{p_i\}_{i=1}^L$

+ genotype  $\{g_i\}_{i=1}^L$

$$g_i = \begin{cases} 1 & \text{if } m/m \\ 0 & \text{if } s/s \end{cases}$$



notice: how to get the haplotype assignment is another computational question in itself flat we will study in WOF/WOT using hidden marker models (HMMs)

The Models " assume one loci

+ QTL model

$$f_i = a + b g_i + \epsilon_i$$

$\uparrow f_{\text{fly}}$        $\uparrow g_i$

$$P(D|a, b, \text{QTL}) = \left( \frac{1}{\sqrt{2\pi} \sigma} \right)^N e^{-\frac{\sum_i (f_i - a - b g_i)^2}{2\sigma^2}}$$

+ NQTL model

$$f_i = c + \epsilon_i$$

$$P(D|c, \text{NQTL}) = \left( \frac{1}{\sqrt{2\pi} \sigma} \right)^N e^{-\frac{\sum_i (f_i - c)^2}{2\sigma^2}}$$

QTL  $\rightarrow$  2 parameters  $a, b$

(if  $a=c$  and  $b=0$ )

NQTL  $\rightarrow$  1 " "  $c$

$$\frac{P(\text{QTL|ID})}{P(\text{NQTL|ID})} = \frac{P(D|\text{QTL}) \cdot P(\text{QTL})}{P(D|\text{NQTL}) \cdot P(\text{NQTL})} = \frac{P(D|\text{QTL})}{P(D|\text{NQTL})}$$

equal prior

$$P(D|\text{QTL}) = \int_{-\infty}^{+\infty} da \int_{-\infty}^{+\infty} db P(D|a, b) P(a, b|\text{QTL})$$

$$P(D|\text{NQTL}) = \int_{-\infty}^{+\infty} dc P(D|c) P(c|\text{NQTL})$$

## priors for parameters

$$P(a, b | QTL) = P(a | QTL) \cdot P(b | QTL)$$

$$P(a | QTL) = \begin{cases} \frac{1}{a^+ - a^-} = \frac{1}{\sigma_a} & a^- < a < a^+ \\ 0 & \text{otherwise} \end{cases}$$

$$P(b | QTL) = \begin{cases} \frac{1}{b^+ - b^-} = \frac{1}{\sigma_b} & b^- < b < b^+ \\ 0 & \text{otherwise} \end{cases}$$

$$P(c | NQTL) = \begin{cases} \frac{1}{c^+ - c^-} = \frac{1}{\sigma_c} & c^- < c < c^+ \\ 0 & \text{otherwise} \end{cases}$$

Laplace approximation: for  $P(D|a, b, QTL)$

$$P(D \mid c \sim N QTL)$$

$$L^Q(a, b) =: \log P(D|a, b, QTL)$$

$$L^N(c) =: \log P(D \mid c \sim N QTL)$$

Taylor expand around ML vals  $a^*, b^*, c^*$

$$L^Q(a, b) \approx L^Q(a^*, b^*) + \frac{1}{2} \left. \frac{\partial^2 L^Q}{\partial a^2} \right|_{*} (a - a^*)^2$$

$$\left. \frac{\partial L^Q}{\partial a} \right|_{a^* b^*} = 0 + \frac{1}{2} \left. \frac{\partial^2 L^Q}{\partial b^2} \right|_{*} (b - b^*)^2$$

$$\left. \frac{\partial L^Q}{\partial b} \right|_{a^* b^*} = 0 + \left. \frac{\partial L^Q}{\partial a \partial b} \right|_{*} (a - a^*)(b - b^*)$$

$$L^N(c) \approx L^N(c^*) + \frac{1}{2} \left. \frac{\partial^2 L^N}{\partial c^2} \right|_{*} (c - c^*)^2$$

$$\left. \frac{\partial L^N}{\partial c} \right|_{c^*} = 0$$

## ML values of QTL/NQTL parameters

$$L^Q_{OC} = \frac{\sum_i (f_i - a - bg_i)^2}{2\sigma^2}$$

$$L^N_{OC} = \frac{\sum_i (f_i - c)^2}{2\sigma^2}$$

$$\frac{\delta L^Q}{\delta a} = -\frac{2}{2\sigma^2} \sum_i (f_i - a - bg_i) (-1) = \frac{1}{\sigma^2} \sum_i (f_i - a - bg_i)$$

$$\frac{\delta L^Q}{\delta b} = -\frac{2}{2\sigma^2} \sum_i (f_i - a - bg_i) (-g_i) = \frac{1}{\sigma^2} \sum_i (f_i - a - bg_i) g_i$$

$$= \frac{1}{\sigma^2} (\bar{x}_i f_i g_i - a \bar{x}_i g_i - b \bar{x}_i g_i^2)$$

$$\bar{f} = \frac{1}{N} \sum_i f_i \quad \bar{f}^2 = \frac{1}{N} \sum_i f_i^2$$

$$\bar{g} = \frac{1}{N} \sum_i g_i \quad \bar{g}^2 = \bar{gg} = \frac{1}{N} \sum_i g_i^2$$

$$\bar{fg} = \bar{f}\bar{g} = \frac{1}{N} \sum_i f_i g_i$$

$$\frac{\delta L^Q}{\delta a} = \frac{N}{\sigma^2} (\bar{f} - a - b \bar{g}) \quad | = 0 \quad \bar{f} = a + b \bar{g}$$

$$\frac{\delta L^Q}{\delta b} = \frac{N}{\sigma^2} (\bar{f}\bar{g} - a\bar{g} - b\bar{g}\bar{g}) \quad | = 0 \quad \begin{aligned} \bar{fg} &= a\bar{g} + b\bar{g}\bar{g} \\ a' &= \bar{f} - b\bar{g} \end{aligned}$$

$$\frac{\delta L^N}{\delta c} = \frac{N}{\sigma^2} (\bar{f} - c) \quad | = 0 \Rightarrow \boxed{c = \bar{f}}$$

$\bar{fg} = (\bar{f} - b\bar{g})\bar{g} + b\bar{g}\bar{g}$

$b[\bar{gg} - \bar{g}^2] = \bar{fg} - \bar{f}\bar{g}$

$$\left. \begin{array}{l} b^* = \frac{\bar{f}\bar{g} - \bar{f}\bar{g}}{\bar{g}\bar{g} - \bar{g}^2} \\ a^* = \bar{f} - b^* \bar{g} \end{array} \right\} \text{QTL}$$

$$\text{NQTL} \quad \left. \begin{array}{l} c^* = \bar{f} \end{array} \right\}$$

$$\frac{\delta L^Q}{\delta a} = \frac{N}{\sigma^2} (\bar{f} - a - b \bar{g})$$

$$\frac{\delta L^Q}{\delta b} = \frac{N}{\sigma^2} (\bar{f}\bar{g} - a\bar{g} - b\bar{g}\bar{g})$$

$$\frac{\delta L^N}{\delta c} = \frac{N}{\sigma^2} (\bar{f} - c)$$

$$\frac{\delta^2 L^Q}{\delta a^2} = -\frac{N}{\sigma^2}$$

$$\frac{\delta^2 L^Q}{\delta a \delta b} = -\frac{N}{\sigma^2} \bar{g}$$

$$\frac{\delta^2 L^Q}{\delta b^2} = -\frac{N}{\sigma^2} \bar{g}\bar{g}$$

$$\frac{\delta^2 L^N}{\delta c^2} = -\frac{N}{\sigma^2}$$

$$P(D|a \neq b \text{ QTL}) \approx P(D|a^* \neq b^* \text{ QTL})$$

$$\times \exp \left[ -\frac{n}{2\sigma^2} (a-a^*)^2 - \frac{n}{2\sigma^2} \bar{g}_g (b-b^*)^2 - \frac{n}{\sigma^2} \bar{f}(a-a^*)(b-b^*) \right]$$

$$P(D|c \neq b \text{ QTL}) \approx P(D|c^* \neq b^* \text{ QTL})$$

$$\exp \left[ -\frac{1}{2} \frac{n}{\sigma^2} (c-c^*)^2 \right]$$

$$P(D|a \neq b \text{ QTL}) \approx P(D|a^* \neq b^* \text{ QTL}) \exp \left[ \text{etc...} \left[ \begin{array}{cc} 1 & \bar{g}_g \\ \bar{g}_g & \bar{g}_g \end{array} \right] \left[ \begin{array}{c} c-c^* \\ b-b^* \end{array} \right] \frac{n}{\sigma^2} \right]$$

$$P(D|a \text{ QTL}) = P(D|a^* \neq b^* \text{ QTL}) \cdot \int_{-\infty}^{+\infty} \int_{-\infty}^{+\infty} e^{-\frac{1}{2} (c-a^*, b-b^*)^T Q (c-a^*, b-b^*)} \times \frac{1}{\sigma_a} \frac{1}{\sigma_b}$$

$$Q = \frac{n}{\sigma^2} \begin{bmatrix} 1 & \bar{g}_g \\ \bar{g}_g & \bar{g}_g \end{bmatrix} \approx P(D|a^* \text{ QTL}) \frac{1}{\sigma_a} \frac{1}{\sigma_b} \frac{2\pi}{\Gamma_{\text{det Q}}}.$$

$$\Delta t Q = \left( \frac{n}{\sigma^2} \right)^2 (\bar{g}_g - \bar{g}^2) \approx P(D|a^* \text{ QTL}) \frac{2\pi\sigma^2}{\sigma_a \sigma_b} \frac{1/N}{\bar{g}_g - \bar{g}^2}$$

$$\approx P(D|a^* \text{ QTL}) \frac{2\pi/N}{\bar{g}_g - \bar{g}^2} \cdot \frac{\sigma_a}{\sigma_a} \frac{\sigma_b}{\sigma_b}$$

$$P(D|c \neq b \text{ QTL}) \approx P(D|c^* \neq b^* \text{ QTL}) \frac{1}{\sigma_c} \int_{-\infty}^{+\infty} e^{-\frac{1}{2\sigma_c^2} (c-c^*)^2} dc$$

$$\approx P(D|c^* \text{ QTL}) \frac{\sqrt{2\pi}\sigma/\sqrt{N}}{\sigma_c}$$

$$\frac{P(D|Q \text{ QTL})}{P(D|N \text{ QTL})} = \frac{P(D|a^* \neq b^* \text{ QTL})}{P(D|c^* \neq b^* \text{ QTL})} \underbrace{\sqrt{\frac{2\pi/N}{\bar{g}_g - \bar{g}^2}}}_{\text{occam's razor}} \frac{\sigma/\sigma_a \sigma/\sigma_b}{\sigma/\sigma_c}$$

## LOD scores

Daly et al were not bayesian's, but they used  
a method similar to Lander's.

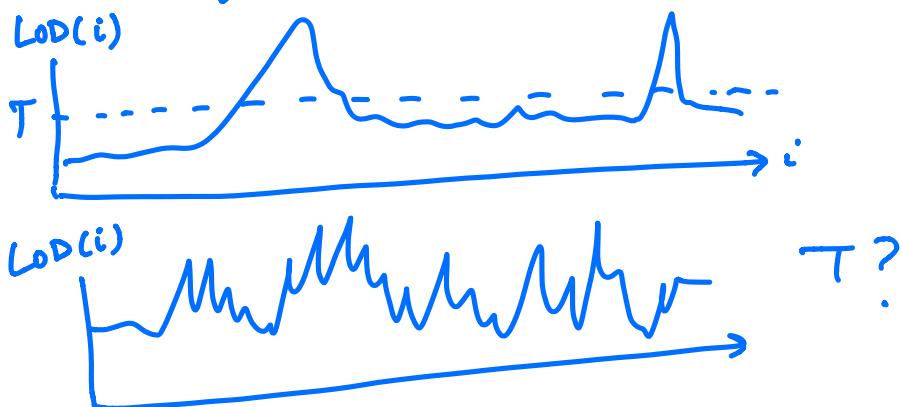
$$\text{LOD} = \log \frac{P(D|a^* b^* \& T_L)}{P(D|c^* N\& T_L)}$$
$$= \log P(D|a^* b^* \& T_L) - \log P(D|c^* N\& T_L) \geq 0$$

"Important issue"

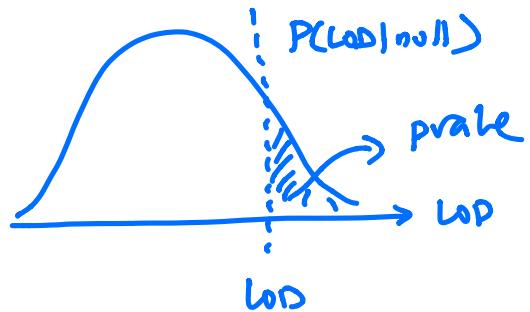
nested hypotheses

"What LOD threshold  $T$  should be used in order  
to maintain an acceptable low positive rate?"

Lander Fig 2,3



+ Take a collection of pairs  $(f_i, s_i)$  known to be non-associated  $\sim H_0$



$$\text{expected \#FP} \approx P(\text{LOD} > \text{LOD}(i) | \text{null}) \times N$$

↑  
number of loci tested

## Generalization

1 phenotype - 1 loci  $f_i = a + b g_i$

1-phenotype -  $K$  loci  
 $f_i = a + \sum_{k=1}^K b_k g_i^k + \epsilon_i$

## Assumptions

1- linear fit b/w  $f_i \sim g_i^K$

2- Gaussian noise

3- all loci have same noise  
all individuals

4-  $\sigma$  is known.