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Fitting the model (balanced design)

example: ENZYME LEVEL \sim LITTER_R + day length

$$Y_{ij} = \mu + L_i + d_j + \varepsilon_{ij} \quad \text{with } L_i \sim N(0, \sigma_L^2)$$

$$\varepsilon_{ij} \sim N(0, \sigma)$$

litter $i=1, \dots, 6$
 day length $j=1, 2$
 for (sh, lo)

Estimates for the balanced scenario:

Grand mean $\hat{\mu} = \bar{Y}_{..} = \frac{\sum_i \sum_j Y_{ij}}{12}$

litter i effect $\hat{L}_i = \text{litter mean} - \text{grand mean} = \bar{Y}_{i.} - \bar{Y}_{..} = \frac{\sum_{j=1}^2 Y_{ij}}{2} - \bar{Y}_{..}$

day length level j effect $\hat{d}_j = \text{day length mean} - \text{grand mean} = \bar{Y}_{.j} - \bar{Y}_{..} = \frac{\sum_{i=1}^6 Y_{ij}}{6} - \bar{Y}_{..}$

Residual estimate $\hat{\varepsilon}_{ij} = Y_{ij} - \hat{Y}_{ij} = Y_{ij} - (\hat{\mu} + \hat{L}_i + \hat{d}_j)$

we can think of $\hat{\varepsilon}_{ij}$ as the result of aligning the data for all of the effects in the model, including the mean.

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Litter	ENZYM LEVEL		\hat{L}_i Same for both S & L	\hat{d}_j		$\hat{Y}_{ij} = \hat{\mu} + \hat{L}_i + \hat{d}_j$		$\hat{\epsilon}_{ij} = \hat{Y}_{ij} - Y_{ij}$	
	S	L		S	L	S	L	S	L
1	2.1	2.6	+0.275	-0.275	+0.275	2.075	2.625	.025	-.025
2	1.8	2.2	-0.075	-0.275	+0.275	1.725	2.275	.075	-.075
3	1.4	2.4	-0.175	-0.275	+0.275	1.625	2.175	-.225	.225
4	1.2	1.7	-0.625	-0.275	+0.275	1.175	1.725	.025	-.025
5	1.9	2.9	+0.325	-0.275	+0.275	2.125	2.675	-.225	.225
6	2.4	2.3	+0.275	-0.275	+0.275	2.075	2.625	.325	-.325
mean	1.8	2.35							

$\hat{\mu} = 2.075$

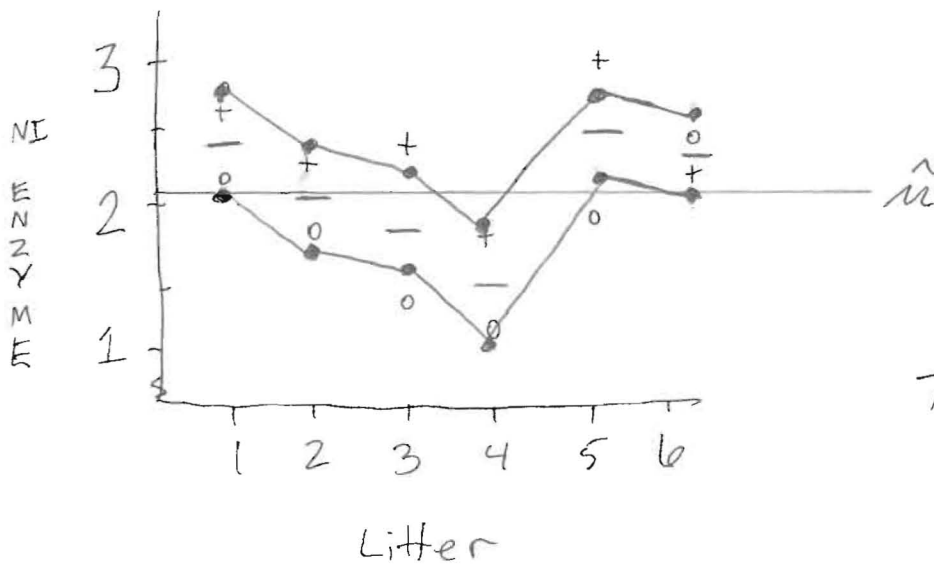
$\bar{Y}_{.1} = 1.8$

$\bar{Y}_{.2} = 2.35$

So, for Y_{11} :

$Y_{11} = \hat{\mu} + \hat{L}_1 + \hat{d}_1 + \hat{\epsilon}_{11}$

$= 2.075 + 0.275 + (-0.275) + 0.025$
 $= 2.1$



• = fitted value
 + = Long } observed
 o = short }
 - = litter mean

The fitted model is an "additive model", with no interaction.