All questions are 1 point, with 1 free point.

1. Barley-Fungus studies

   (a) e.u.=chamber, o.u.=trays

Source	DF	denominator MS for F test
fungus	1	MS_chamber
barley	2	MS_chamber
fungus*barley	2	MS_chamber
chamber	12	
tray	36	

   (b) block=repetition, e.u.=chamber, o.u.=trays

Source	DF	denominator MS for F test
repetition	2	
fungus	1	MS_chamber
barley	2	MS_chamber
fungus*barley	2	MS_chamber
chamber	10	
trays	36	

   Note: chamber could also be written repetition*barley*fungus, since the combination of repetition, barkey and fungus uniquely identifies each chamber and time of use.

   (c) block=repetition, whole plot e.u.=chamber, split plot e.u.=trays

Source	DF	denominator MS for F test
repetition	2	
fungus	1	MS_chamber
chamber	2	
barley	2	MS_tray
fungus*barley	2	MS_tray
trays	8	

   Note: chamber could also be written repetition*fungus

   (d) whole plot e.u.=chamber, split plot e.u.=trays

Source	DF	denominator MS for F test
fungus	1	no F test
chamber	0	
barley	2	MS_tray
fungus*barley	2	MS_tray
trays	12	

   (e) No F test for fungus can be provided in design(d)

2. Pigs:

   (a) $Var(\bar{y}_{i.}) = \sigma_\alpha^2 + \frac{\sigma_e^2}{n_j}$ MSLitter=$\frac{n}{I}\sigma_\alpha^2 + \sigma_e^2$ so $\sigma_\alpha^2 = 0.10175$ and $\sigma_e^2 = 0.35761$

   (b) $\sigma_\alpha^2 = 0.10464$ and $\sigma_e^2 = 0.35698$

   (c) they are not the same because this is not a balanced design

   (d) correlation=$\frac{\sigma_\alpha^2}{\sigma_e^2+\sigma_\alpha^2} = 0.227$

   (e) both are 2.676

   (f) prediction for birth weight born to female 1 $\hat{y}_{1.} = \frac{\sigma_\alpha^2}{\sigma_e^2/10+\sigma_\alpha^2}\bar{y}_{1.} + \frac{\sigma_e^2/10}{\sigma_e^2/10+\sigma_\alpha^2}\bar{y}_{..} = 2.798$
   This is the same as the value of coef() reported by lmer.

   (g) prediction for the mean of 20 birth weights born to female 1 $\hat{y}_{1.} = \frac{\sigma_\alpha^2}{\sigma_e^2/20+\sigma_\alpha^2}\bar{y}_{1.} + \frac{\sigma_e^2}{\sigma_e^2/20+\sigma_\alpha^2}\bar{y}_{..} =$ 2.816
   Note: I didn't ask this question as carefully as I might have. I intended to ask about predicting the mean for litter if it were calculated from 20 piglets. This is the same value no matter whether you are predicting the mean of 1 new piglet, the mean of 10 new piglets, or the mean of 20 new piglets. What matters is how precisely estimated is the sample average for litter 1 and the variability among litters.

   (h) $P(Y_{1j} < 2.5) = P(\mu+\alpha_1+\epsilon_{1j} < 2.5) = P(\epsilon_{1j} < 2.5-\mu-\alpha_1) = 0.31$, where $\epsilon_{1j} \sim N(0, \sigma_e^2)$

   (i) $P(Y_{ij} < 2.5) = P(\mu + \alpha_i + \epsilon_{ij} < 2.5) = P(\epsilon_{ij} + \alpha_i < 2.5 - \mu) = 0.40$, where $\epsilon_{ij} + \alpha_i \sim N(0, \sigma_e^2 + \sigma_\alpha^2)$

3. Fungus

   (a) estimates are 1.16 and -1096 with s.e. 0.1283 and 377.6

   (b) 95% confidence interval for the mean slope is (-1838,-353)

   (c) -2.125

   (d) 0.294

   (e) same as (c)