Chapter 5 – Trial analysis (single-site)

Quiz block 1:

Overall, this is a good trial design for the field. The blocks are essentially squares as plots are long and thin, the rep structure captures a bit of both dimensions of the field.

Including the discard plots in the design/trial may have increased our understanding of the field fertility effects. We could have added more controls with those extra plots, or more varieties. Although this would make things more expensive.

Quiz block 2:

Read in data using:

```
beet.data<-read.csv("sugar_beet_data.csv",header=T)
```

Quiz block 3:

The standard errors are different due to the differences in replication between varieties.

Quiz block 4:

The standard error of difference between means is a quantification of uncertainty of the difference between variety mean. Therefore, if you reduce this you improve the model. Also useful to determine statistically significant differences between varieties in ad hoc way (i.e. 2 x SED).

Quiz block 5:

Each rep is an identical perfect set of all varieties (give or take a very small amount of missing data) so it makes little difference whether it is fixed or random (this might not be the case with blocks which have different vars in each).

Quiz block 6:

We are fitting row and column, but both nested within rep. We use (1|rep/row), which means fit rep and rep:row. We then fit (1|rep:column), which is just a call to fit only column nested within rep, we can't use rep/column as this would fit rep individually again.

Quiz block 7:

Run the analysis with row and column:

```
randc<-lmer(sugar.content~variety+(1|rep/row)+(1|rep:column), data= beet.d
ata)

randc.lmer.vars<-predictmeans(randc ,"variety",plot=F)

randc.lmer.vars$`Standard Error of Differences`
```

I got:

Max.SED Min.SED Aveg.SED

0.1403752 0.1012157 0.1087824

Quiz block 8:

The F tests show that the Alpha design did not fully capture the true genetic variation. Row and column were better at controlling the field fertility effects. You could also test with block included in the model with row and column:

(1|rep/column) + (1|rep:row) + (1|rep:row:block)

Note the structure of the model above, as block is actually nested within row (half a row within a rep forms a block) it needs to be included as rep:row:block. If we were to block without nesting in row, we would be double dipping the row information.

Chapter 6 - Trial analysis (cross-sites).

Block 1:

Means highly correlated but clearly distinct. SE of weighted average slightly lower. Most SEs very similar but for few outlier lines. Outlier mostly have lower SE in weighted analyses. These are probably lines with missing data – the (lower) weights will have accounted for this.

Block 2:

From the first table, NIAB_2010 and LGE_2010 have a lower correlation between the shrunken variety effects and the individual site analysis. These were the two trials with the lowest average standard errors (i.e. the better trials) so were shrunk less The BLUEs are less correlated between sites than the BLUPs, as might be expected since the BLUE estimates are not sharing information between sites. Note LGE10 is poorly correlated with the UK trials and the other German trial (LG11) for BLUEs but the difference is reduced for BLUPs.

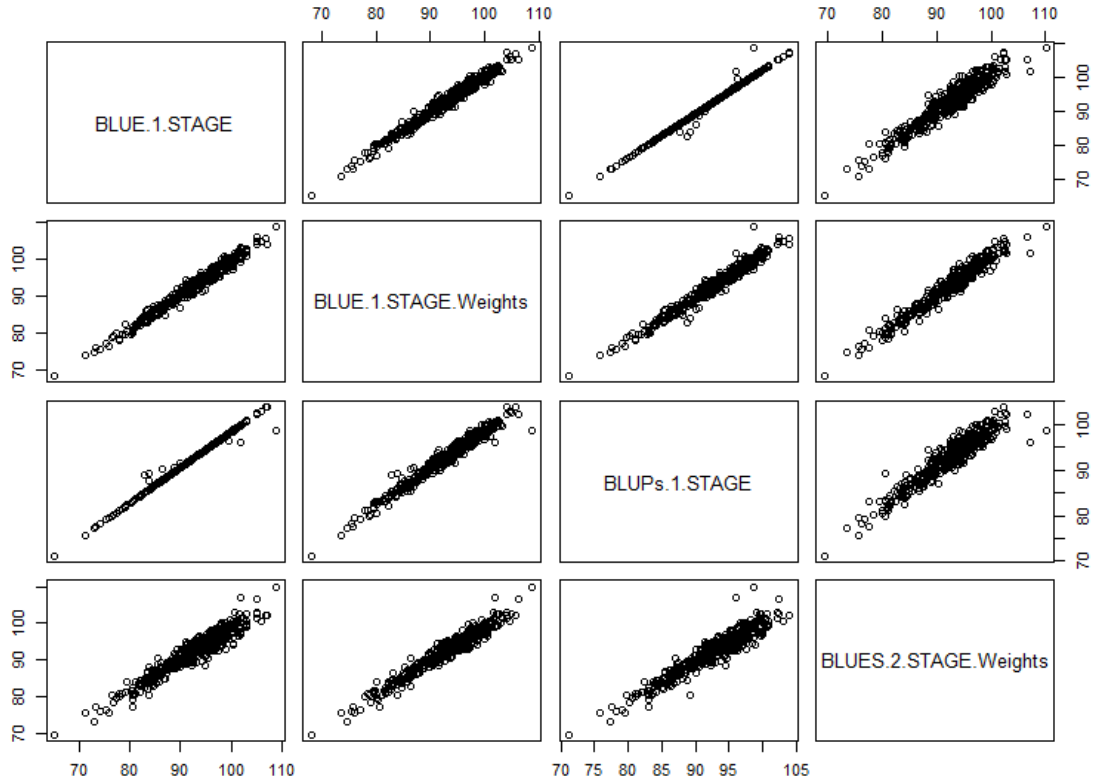
Block 3:

You should definitely not use variety mean on your farm as it was only one year of data. Srunken estimates are also generally better as they take GxE effects into account and incorporate information across sites.

Block 4:

You could run something like this:

```
combined<-data.frame(BLUE.1.STAGE=data.frame(TG.BLUE)[, 2],
           BLUE.1.STAGE.Weights = data.frame(TG.BLUE_w)[, 2],
           BLUPs.1.STAGE = TG.BLUP[, 1],
           BLUES.2.STAGE.Weights = data.frame(TG2.BLUE)[, 2] )
pairs(combined)
```



Most correlations high (>0.95) but do differ. Lower correlations are between 1-stage and 2-stage analyses, although 2-stage x weighted one stage correlations are intermediate (0.97).

Block 5:

Are big diffs. FRA2010 – no significant diffs, LGE2010 = weaker than others.

Block 6:

0-20% between country, mostly 5-10%. 20% is quite large.