Pillow Example: BIBD treating blocks as fixed

A key feature of the Balanced Incomplete Block Design (BIBD) is that the SE is the same for each treatment combination (or pair of trts). This can be seen from the emmeans output.

In this example we treat blocks as fixed. We will consider treating blocks as random in the Random2 notes.

```r
library(dplyr)
library(car)
library(emmeans)
Pillow <- read.csv("C:/hess/STAT512/RNotes/ExpDesign3/ED3_PillowBIBD.csv")
str(Pillow)
```

```
## 'data.frame':    36 obs. of  3 variables:
##  $ blk     : int  1 1 1 2 2 2 3 3 3 4 ...
##  $ pillow  : Factor w/ 9 levels "A","B","C","D",..: 1 2 3 4 5 6 7 8 9 1 ...
##  $ firmness: int  59 26 38 85 92 69 74 52 27 62 ...
```

```r
#Important: Need to define blk as.factor!!!!
Pillow$blk<-as.factor(Pillow$blk)
str(Pillow)
```

```
## 'data.frame':    36 obs. of  3 variables:
##  $ blk     : Factor w/ 12 levels "1","2","3","4",..: 1 1 1 2 2 2 3 3 3 4 ...
##  $ pillow  : Factor w/ 9 levels "A","B","C","D",..: 1 2 3 4 5 6 7 8 9 1 ...
##  $ firmness: int  59 26 38 85 92 69 74 52 27 62 ...
```

```r
SumStats <- summarize(group_by(Pillow, pillow),
              n = n(),
              mean = mean(firmness),
              sd   = sd(firmness),
              SE   = sd/sqrt(n))
SumStats
```

```
## # A tibble: 9 x 5
##   pillow     n  mean    sd    SE
##   <fct>  <int> <dbl> <dbl> <dbl>
## 1 A          4  59    4.97  2.48
## 2 B          4  23.2  4.11  2.06
## 3 C          4  38.8  5.91  2.95
## 4 D          4  77    6.48  3.24
## 5 E          4  89.8  6.55  3.28
## 6 F          4  69.5  6.95  3.48
## 7 G          4  74.5  5.32  2.66
## 8 H          4  51.2  6.55  3.28
## 9 I          4  33.2  6.13  3.07
```

```r
Model <- lm (firmness ~ pillow + blk, data = Pillow)
Anova(Model, type = 3)
```

```
## Anova Table (Type III tests)
##
## Response: firmness
##              Sum Sq Df  F value     Pr(>F)
## (Intercept)  6927.5  1 218.2198 9.609e-11 ***
## pillow      11930.1  8  46.9756 1.142e-09 ***
```

```
## blk             447.8 11   1.2824      0.3163
## Residuals       507.9 16
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
emmout <- emmeans(Model, pairwise ~ pillow)
CLD(emmout$emmeans)
```

```
##  pillow emmean   SE df lower.CL upper.CL .group
##  B        20.0 3.21 16     13.2     26.8  1
##  I        35.6 3.21 16     28.8     42.4  12
##  C        39.6 3.21 16     32.8     46.4  2
##  H        50.4 3.21 16     43.6     57.2  23
##  A        61.4 3.21 16     54.6     68.2   34
##  F        70.8 3.21 16     64.0     77.6    45
##  G        75.7 3.21 16     68.9     82.5    45
##  D        76.2 3.21 16     69.5     83.0    45
##  E        86.6 3.21 16     79.8     93.4     5
##
## Results are averaged over the levels of: blk
## Confidence level used: 0.95
## P value adjustment: tukey method for comparing a family of 9 estimates
## significance level used: alpha = 0.05
```

```
emmout$contrasts
```

```
##  contrast estimate  SE df t.ratio p.value
##  A - B      41.333 4.6 16   8.985 <.0001
##  A - C      21.778 4.6 16   4.734 0.0052
##  A - D     -14.889 4.6 16  -3.236 0.0899
##  A - E     -25.222 4.6 16  -5.483 0.0013
##  A - F      -9.444 4.6 16  -2.053 0.5325
##  A - G     -14.333 4.6 16  -3.116 0.1112
##  A - H      11.000 4.6 16   2.391 0.3500
##  A - I      25.778 4.6 16   5.603 0.0010
##  B - C     -19.556 4.6 16  -4.251 0.0133
##  B - D     -56.222 4.6 16 -12.221 <.0001
##  B - E     -66.556 4.6 16 -14.467 <.0001
##  B - F     -50.778 4.6 16 -11.038 <.0001
##  B - G     -55.667 4.6 16 -12.100 <.0001
##  B - H     -30.333 4.6 16  -6.594 0.0002
##  B - I     -15.556 4.6 16  -3.381 0.0692
##  C - D     -36.667 4.6 16  -7.970 <.0001
##  C - E     -47.000 4.6 16 -10.217 <.0001
##  C - F     -31.222 4.6 16  -6.787 0.0001
##  C - G     -36.111 4.6 16  -7.850 <.0001
##  C - H     -10.778 4.6 16  -2.343 0.3737
##  C - I       4.000 4.6 16   0.869 0.9918
##  D - E     -10.333 4.6 16  -2.246 0.4238
##  D - F       5.444 4.6 16   1.183 0.9490
##  D - G       0.556 4.6 16   0.121 1.0000
##  D - H      25.889 4.6 16   5.628 0.0010
##  D - I      40.667 4.6 16   8.840 <.0001
##  E - F      15.778 4.6 16   3.430 0.0633
##  E - G      10.889 4.6 16   2.367 0.3618
##  E - H      36.222 4.6 16   7.874 <.0001
```

```
##  E - I      51.000 4.6 16  11.086 <.0001
##  F - G      -4.889 4.6 16  -1.063 0.9720
##  F - H      20.444 4.6 16   4.444 0.0092
##  F - I      35.222 4.6 16   7.656 <.0001
##  G - H      25.333 4.6 16   5.507 0.0012
##  G - I      40.111 4.6 16   8.719 <.0001
##  H - I      14.778 4.6 16   3.212 0.0938
##
## Results are averaged over the levels of: blk
## P value adjustment: tukey method for comparing a family of 9 estimates
```