

1 Initialization

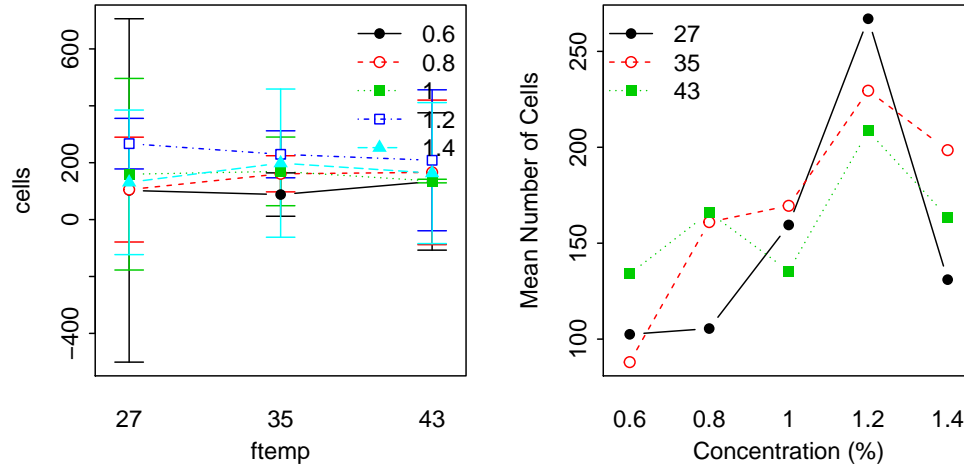
```
> library(NCStats)
> library(multcomp) # for glht()
```

2 Bacteria Example

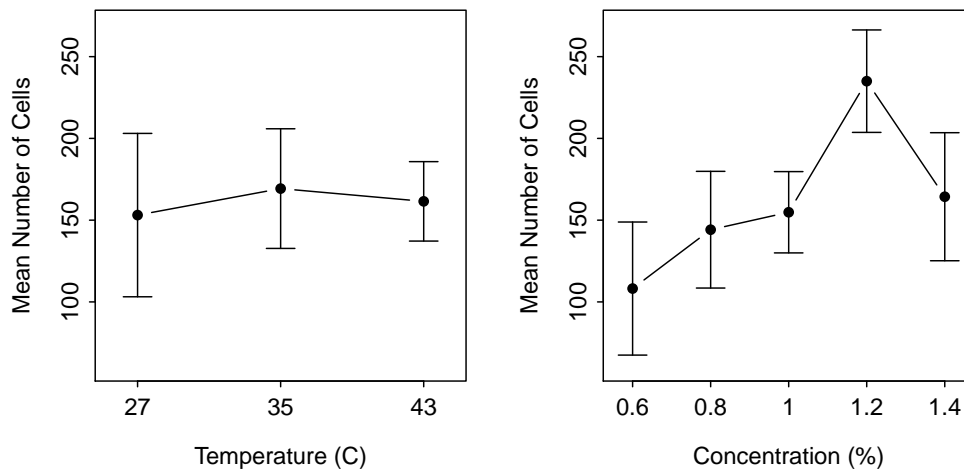
```
> bact <- read.csv("https://raw.githubusercontent.com/droglenc/NCData/master/Bacteria.csv")
> str(bact)
'data.frame': 30 obs. of 3 variables:
 $ temp : int 27 27 27 27 27 35 35 35 35 35 ...
 $ conc : num 0.6 0.8 1 1.2 1.4 0.6 0.8 1 1.2 1.4 ...
 $ cells: int 55 120 186 260 151 82 166 179 223 178 ...
> bact$ftemp <- factor(bact$temp)
> bact$fconc <- factor(bact$conc)
> str(bact)
'data.frame': 30 obs. of 5 variables:
 $ temp : int 27 27 27 27 27 35 35 35 35 35 ...
 $ conc : num 0.6 0.8 1 1.2 1.4 0.6 0.8 1 1.2 1.4 ...
 $ cells: int 55 120 186 260 151 82 166 179 223 178 ...
 $ ftemp: Factor w/ 3 levels "27","35","43": 1 1 1 1 1 2 2 2 2 2 ...
 $ fconc: Factor w/ 5 levels "0.6","0.8","1",...: 1 2 3 4 5 1 2 3 4 5 ...
> sumTable(cells~ftemp*fconc,data=bact,FUN=length)
      0.6 0.8 1 1.2 1.4
27      2  2  2  2  2
35      2  2  2  2  2
43      2  2  2  2  2
> sumTable(cells~ftemp*fconc,data=bact,FUN=mean,digits=0)
      0.6 0.8 1 1.2 1.4
27 102 106 160 267 131
35  88 161 170 230 198
43 134 166 136 208 164
> sumTable(cells~ftemp*fconc,data=bact,FUN=sd,digits=1)
      0.6 0.8 1 1.2 1.4
27 67.2 20.5 37.5  9.9 28.3
35  8.5  7.1 13.4  9.2 29.0
43 26.9 28.3  0.7 27.6 27.6
> lm1 <- lm(cells~ftemp*fconc,data=bact)
> anova(lm1)

          Df Sum Sq Mean Sq F value    Pr(>F)
ftemp      2   1313    656.4   0.8557  0.44473
fconc      4  51596  12899.1  16.8154 2.041e-05
ftemp:fconc 8  14703   1837.8   2.3958  0.06886
Residuals 15  11507    767.1
Total     29  79118

> fitPlot(lm1, main="") # left
> fitPlot(lm1,interval=FALSE,change.order=TRUE,xlab="Concentration (%)",
  ylab="Mean Number of Cells",legend="topleft", main="") # right
```



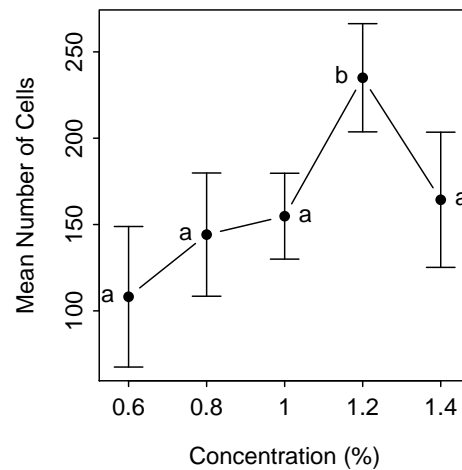
```
> fitPlot(lm1, which="ftemp", ylim=c(60, 270), xlab="Temperature (C)",
  ylab="Mean Number of Cells", main="") # left
> fitPlot(lm1, which="fconc", ylim=c(60, 270), xlab="Concentration (%)",
  ylab="Mean Number of Cells", main="") # right
```



```
> bact.mc1 <- glht(lm1, mcp(fconc="Tukey"))
Warning in mcp2matrix(model, linfct = linfct): covariate interactions found -- default contrast
might be inappropriate
> summary(bact.mc1)
```

	Estimate	Std. Error	t value	Pr(> t)
0.8 - 0.6 == 0	3.0	27.7	0.108	0.999965
1 - 0.6 == 0	57.0	27.7	2.058	0.287137
1.2 - 0.6 == 0	164.5	27.7	5.939	0.000232
1.4 - 0.6 == 0	28.5	27.7	1.029	0.838163
1 - 0.8 == 0	54.0	27.7	1.950	0.334982
1.2 - 0.8 == 0	161.5	27.7	5.831	0.000288
1.4 - 0.8 == 0	25.5	27.7	0.921	0.884518
1.2 - 1 == 0	107.5	27.7	3.881	0.010953
1.4 - 1 == 0	-28.5	27.7	-1.029	0.838175
1.4 - 1.2 == 0	-136.0	27.7	-4.910	0.001492

```
> fitPlot(lm1,which="fconc",xlab="Concentration (%)",ylab="Mean Number of Cells",main="")
> addSigLetters(lm1,which="fconc",lets=c("a","a","a","b","a"),pos=c(2,2,4,2,4))
```



3 Soil Phosphorous Example

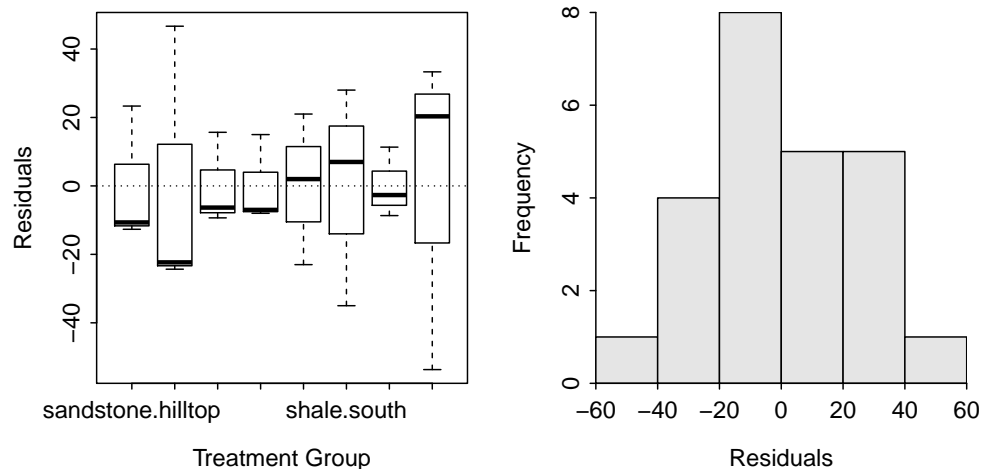
```
> sp <- read.csv("https://raw.githubusercontent.com/droglenc/NCData/master/SoilPhosphorous.csv")
> str(sp)

'data.frame': 24 obs. of 3 variables:
 $ soil: Factor w/ 2 levels "sandstone","shale": 2 2 2 2 2 2 2 2 2 2 ...
 $ topo: Factor w/ 4 levels "hilltop","north",...: 4 4 4 2 2 2 3 3 3 1 ...
 $ phos: int 98 172 185 78 77 100 117 54 96 83 ...

> lm1 <- lm(phos~soil*topo,data=sp)
> leveneTest(lm1)

      Df F value Pr(>F)
group  7  0.3741 0.9043
      16

> residPlot(lm1)
```



```

> adTest(lm1$residuals)
Anderson-Darling normality test with lm1$residuals
A = 0.2126, p-value = 0.8351
> outlierTest(lm1)

No Studentized residuals with Bonferonni p < 0.05
Largest |rstudent|:
      rstudent unadjusted p-value Bonferonni p
1 -2.824098      0.012821      0.30769
> anova(lm1)
      Df Sum Sq Mean Sq F value    Pr(>F)
soil    1  17876  17876.0  22.9818 0.0001988
topo    3   9694   3231.3   4.1542 0.0235128
soil:topo 3  11391   3796.9   4.8814 0.0134826
Residuals 16  12445    777.8
Total    23  51406

```

```

> sp$comb <- sp$soil:sp$topo
> view(sp)
      soil    topo phos      comb
2    shale valley  172  shale:valley
6    shale  north  100   shale:north
10   shale hilltop   83  shale:hilltop
13 sandstone valley   19 sandstone:valley
17 sandstone  north   49 sandstone:north
18 sandstone  north   24 sandstone:north
> lm1a <- lm(phos~comb,data=sp)
> anova(lm1a)
      Df Sum Sq Mean Sq F value    Pr(>F)
comb    7  38961  5565.8   7.1555 0.0005729
Residuals 16  12445    777.8
Total    23  51406
> spint.mc <- glht(lm1a, mcp(comb="Tukey"))

```

```
> summary(spint.mc)
```

	Estimate	Std. Error	t value	Pr(> t)
sandstone:north - sandstone:hilltop == 0	1.667	22.772	0.073	1.00000
sandstone:south - sandstone:hilltop == 0	19.333	22.772	0.849	0.98685
sandstone:valley - sandstone:hilltop == 0	-4.000	22.772	-0.176	1.00000
shale:hilltop - sandstone:hilltop == 0	4.667	22.772	0.205	1.00000
shale:north - sandstone:hilltop == 0	53.333	22.772	2.342	0.33037
shale:south - sandstone:hilltop == 0	57.333	22.772	2.518	0.25508
shale:valley - sandstone:hilltop == 0	120.000	22.772	5.270	0.00161
sandstone:south - sandstone:north == 0	17.667	22.772	0.776	0.99220
sandstone:valley - sandstone:north == 0	-5.667	22.772	-0.249	1.00000
shale:hilltop - sandstone:north == 0	3.000	22.772	0.132	1.00000
shale:north - sandstone:north == 0	51.667	22.772	2.269	0.36530
shale:south - sandstone:north == 0	55.667	22.772	2.445	0.28540
shale:valley - sandstone:north == 0	118.333	22.772	5.196	0.00181
sandstone:valley - sandstone:south == 0	-23.333	22.772	-1.025	0.96343
shale:hilltop - sandstone:south == 0	-14.667	22.772	-0.644	0.99746
shale:north - sandstone:south == 0	34.000	22.772	1.493	0.80039
shale:south - sandstone:south == 0	38.000	22.772	1.669	0.70564
shale:valley - sandstone:south == 0	100.667	22.772	4.421	0.00791
shale:hilltop - sandstone:valley == 0	8.667	22.772	0.381	0.99992
shale:north - sandstone:valley == 0	57.333	22.772	2.518	0.25512
shale:south - sandstone:valley == 0	61.333	22.772	2.693	0.19373
shale:valley - sandstone:valley == 0	124.000	22.772	5.445	< 0.001
shale:north - shale:hilltop == 0	48.667	22.772	2.137	0.43375
shale:south - shale:hilltop == 0	52.667	22.772	2.313	0.34394
shale:valley - shale:hilltop == 0	115.333	22.772	5.065	0.00228
shale:south - shale:north == 0	4.000	22.772	0.176	1.00000
shale:valley - shale:north == 0	66.667	22.772	2.928	0.13094
shale:valley - shale:south == 0	62.667	22.772	2.752	0.17604

```
> glhtSig(spint.mc)
```

```
[1] "shale:valley - sandstone:hilltop" "shale:valley - sandstone:north"
[3] "shale:valley - sandstone:south"   "shale:valley - sandstone:valley"
[5] "shale:valley - shale:hilltop"
```

```
> fitPlot(lm1,change.order=TRUE,interval=FALSE,main="",ylab="Mean Phosphorous Level",
  xlab="Topographic Location",legend="topleft")
```

```
> addSigLetters(lm1,change.order=TRUE,lets=c("a","a","a","ab","a","ab","a","b"),
  pos=c(1,3,1,3,1,1,3,1))
```

