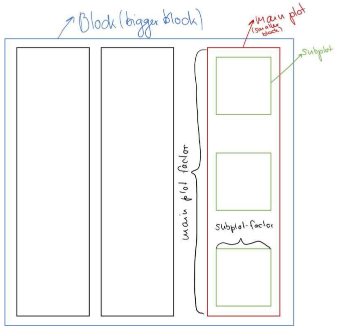
Analize design of experiment

Plot structure → Chapter 1.3
Treatment structure → Chapter 1.2
Sketch the DoE → Chapter 1.4



Look at the data

Descriptive statistics
Summaries of the data

```
with(data, tappy(count, y, x, length))
with(data, tappy(count, y, x, summary))
with(data, tappy(count, y, x, sd))
```

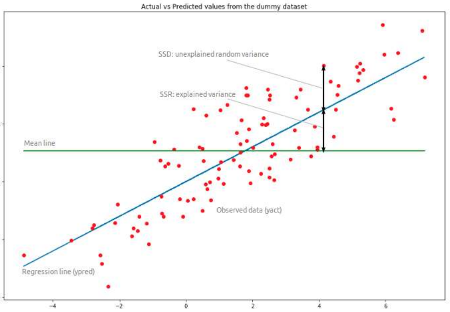
Plot the data

```
library(ggplot2)
ggplot(detergent, aes(x=treatment, y=plates))+
  geom_jitter(shape = 4, width = 0.1)
```

Y: numerical outcome
X: categorical explanatory variable
Z: categorical explanatory variable

One-way ANOVA

General idea: $SS_T = SS_B + SS_W$
mymodel.lm = lm(Y ~ X, data = data)
anova(mymodel.lm)



One-way ANOVA with blocking

mymodel = lme(Y ~ X, random = ~ 1 | block, data = data)

Anova → anova(mymodel, type = «marginal»)

Visualization of block structure

```
base = ggplot(InsectSprays, aes(x = spray, y = count)) +
  geom_point(shape = 1, position = position_jitter(width = 0.2, height = 0))
g1 = base + facet_grid(~block)
G1
```

Two-way ANOVA with repetitions: interactions

mymodel = lme(Y ~ X*Z, random = ~ 1 | block, data = data)

Interaction.plot→ with(data, interaction.plot(x, block, y))

Anova → anova(mymodel, type = «marginal»)

Visualization

```
library(ggplot2)
qplot(density, yield, data = turnip,  facets = ~block, shape = gen, size = I(2))
```

Split-plot design: hierarchical data

mymodel <- lme(Y ~ X*Z, random = ~ 1 |large.block/small.block, data = data)

Interaction.plot → with(data, interaction.plot(x, block, y))

anova(mymodel, type = «marginal»)

Visulization

Model diagnostics

Test the normality assumption:
- Graphical normality checking: qqPlot(resid(mymodel.lm)
- Testing for normality with shapiro-Wilk test: shapiro.test(resid(mymodel.lm)

Test the homoskedasticity assumption:
(do the residuals have equal variances): plot(data.lm, which = 1)
Barlett's or Levene's test: leveneTest(y~x, data = data)

#If Data is not normal then 3 options: --> one-way ANOVA which requires normality but not equal variances oneway.test(y~x, data = data)
# Transformation approach
# Abandon normal distribution methods --> nonparametric, robust, bootstrap or exact methods
# Dont care about non-normality --> in most cases not smart

If variances are not equal then 3 options: --> --> one-way ANOVA which requires normality but not equal variances oneway.test(weight~group, data = PlantGrowth)
- Transformation approach
- Use robust methods
- Perform a one-way ANOVA with adjustet degrees of freedom

Extract information

summary(mymodel)
fixef()
confint()

coef(mymodel)
ranef()
predict()

Pairwise comparisons

TukeyHSD --> HSD.test(mymodel.lm.lm, "x", group = TRUE, console = TRUE)
Multcomp --> summary(glht(mymodel.lm, mcp(y = "Dunnet")))
emmeans()

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