10

Split-Plot Designs

Experimental units

homogeneous

inhomogeneous

CRD

Block Designs

one block f.

two (more)

block size

block size

large

small

large

small

one-way ANOVA

One treatment factor

fixed effects, global test, contrasts, …

random effects, variance components, ...

RCB

(B)IBD

Latin Squares

Youden Squares

factorial treatment structure (fixed effects), two-way ANOVA (or more factors), concept of interaction, 2^k-designs, …

random effects, mixed effects models, nested factor structure, …

RCB with factorial treatment structure, ….

Multiple treatment factors

Multiple treatment factors, varied / randomized on different “scales”

split-plot, split-split plot designs, different models on whole- and subplots, …

Similar to Lawson (2015)

What is a Split-Plot Design? (Oehlert, 2010, Chapter 16.1)

- A split-plot design is a **special case** of a design with **factorial treatment structure**.
- It is used when some factors are **harder** (or more expensive) to **vary** than others.
- Basically, the standard split-plot design consists of two experiments with **different experimental units** of different “sizes”.
- E.g., in agronomic field trials certain factors require “large” experimental units, whereas other factors can be easily applied to “smaller” plots of land.
- Let us have a look at an example …

Example I: Irrigation and Corn Variety (Oehlert, 2010)

- Consider the following factorial problem:
  - 3 different **irrigation levels**
  - 4 different **corn varieties**
  - Response: **Biomass**
  - Available resources: **6 plots of land**
- By definition, we **cannot** vary the irrigation level on a too small scale.
- We are “forced” to use “large” experimental units for the irrigation level factor.
- Assume that we can use one specific irrigation level on each of the 6 plots.

Example I: Irrigation and Corn Variety

- We randomly assign each irrigation level to 2 of the plots, the so called **whole plots** or **main plots**.
- In each of the plots, we randomly assign the 4 different corn varieties to the so called **split plots** (or sub plots).

4	4	1	3	2	2
2	1	4	1	4	1
3	3	2	2	1	4
1	2	3	4	3	3

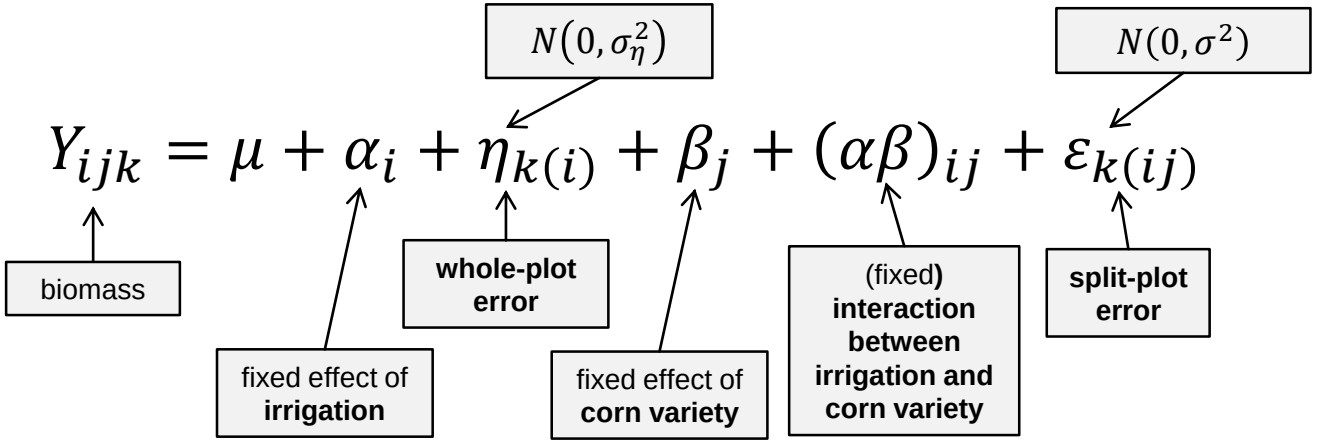
- **Two independent randomizations** are being performed!
- We also call irrigation level the **whole-plot factor** and corn variety the **split-plot factor**.

Example I: Irrigation and Corn Variety

- **Whole plots** (plots of land) are the experimental units for the **whole-plot factor** (irrigation level).
- **Split plots** (subplots of land) are the experimental units for the **split-plot factor** (corn variety).
- In the split-plot “world”, whole plots act as **blocks**.
- Basically, we are performing **two different experiments in one**:
  - each experiment has its own **randomization**,
  - each experiment has its own idea of **experimental unit**.

Example I: Irrigation and Corn Variety

- How can we model this type of data?
- We use a **mixed model** formulation with **two different errors**:



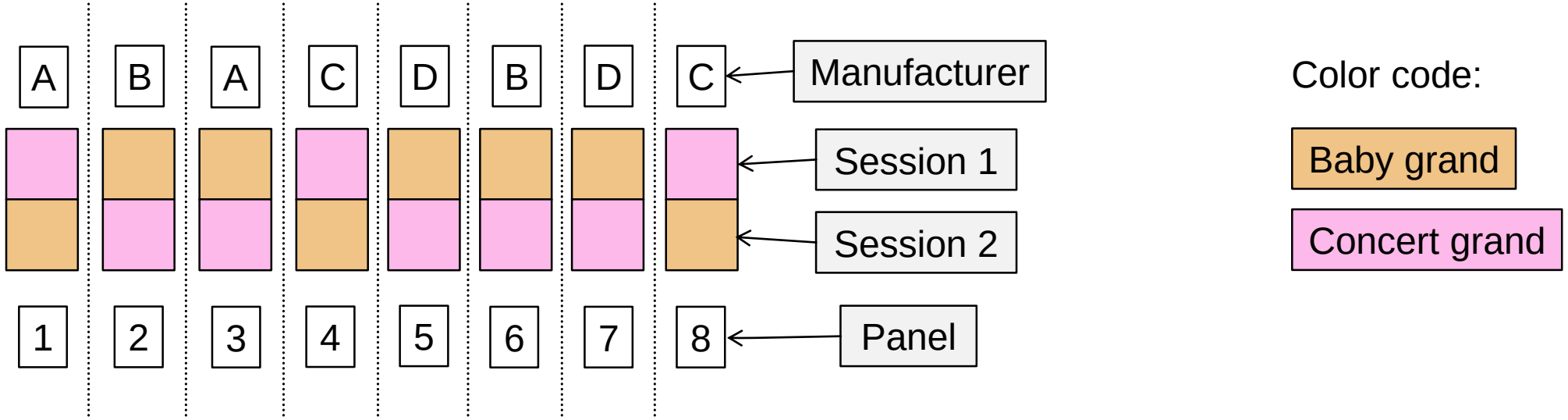
- This means: Observations in the same whole plot share the same whole-plot error $\eta_{k(i)}$ and are therefore **not independent**.
- In R, this model can be easily fitted using `lmer` with a **random effect** (better terminology here: **error**) of the form `(1|whole.plot)`.

Example II: Pianos (Oehlert, 2010)

- **2 piano types** (“baby grand” & “concert grand”) from each of **4 manufacturers** (A, B, C, D).
- 40 music students are divided at random into **8 groups (“panels”)** of 5 students each.
- 2 panels are assigned at random to each manufacturer (= 2 panels per manufacturer).
- Each panel goes to the concert hall and hears (blindfolded) the sound of **both pianos** (in random order).
- **Response**: Average rating of the 5 students in the panel (hence, a student is “only” a measurement unit here).

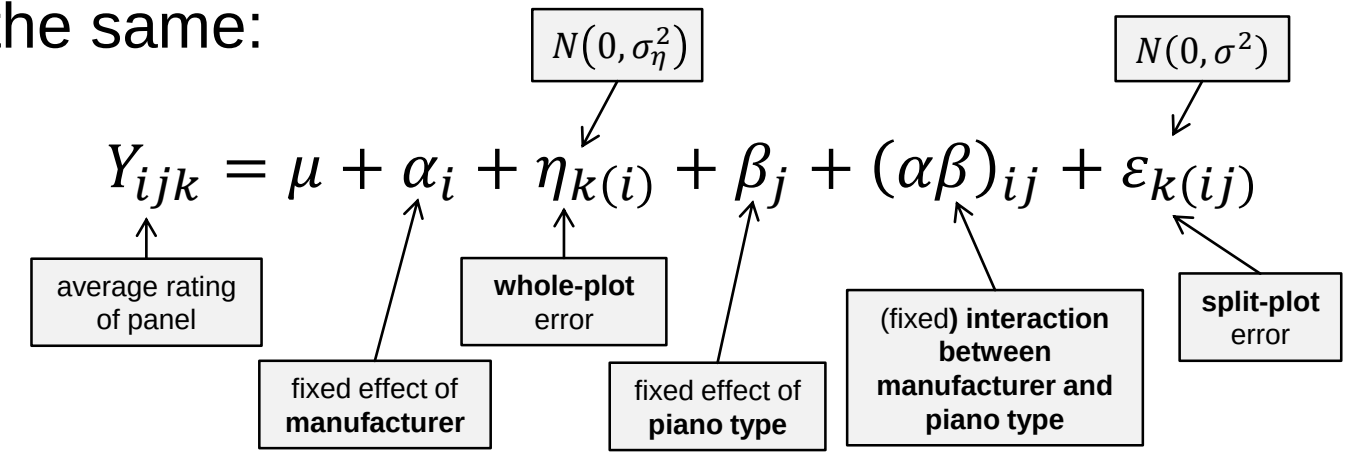
Example II: Pianos

- The **whole plots** are the 8 **panels**.
- The **whole-plot factor** is the **manufacturer**.
- The **split plots** are the **2 session time-slots**.
- The **split-plot factor** is the **piano type** (baby vs. concert grand).



Example II: Pianos

- The model is the same:



- Again: This means that observations in the same whole-plot share the same whole-plot error $\eta_{k(i)}$ and are therefore **not independent**.

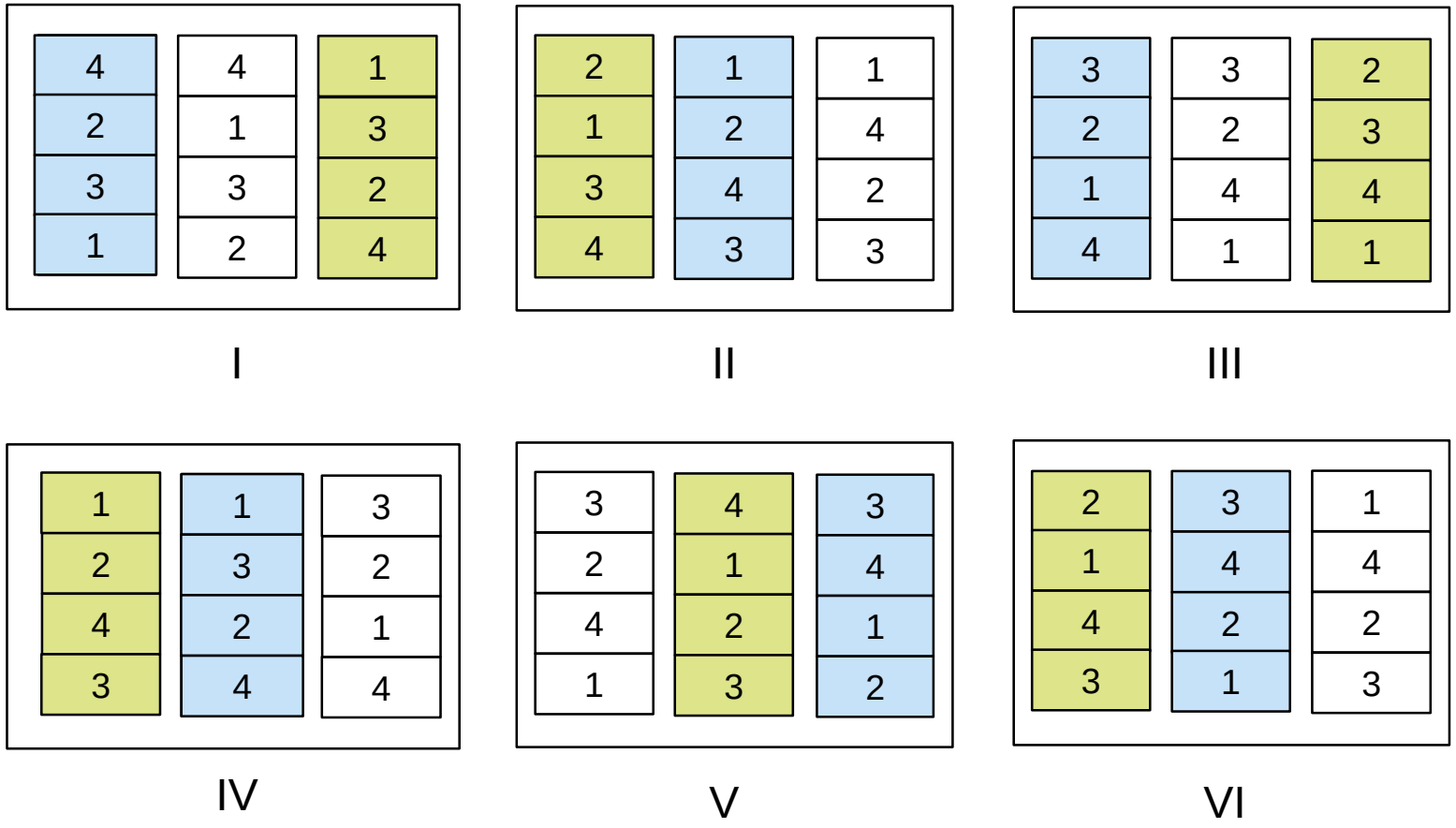
Example III: Oats

- Dataset `oats` from R-package `MASS`.
- As stated in the help file:

  *The yield of oats from a **split-plot field trial** using 3 varieties and 4 levels of manurial treatment. The experiment was laid out in 6 blocks of 3 main plots, each split into 4 sub-plots. The varieties were applied to the main plots and the manurial treatments to the sub-plots.*

- Overview of data:
  - 6 different **blocks (B)**
  - 3 different **varieties (V)**
  - 4 different **nitrogen treatments (N)**
  - **Response (Y):** Yields (in ¼ lbs per sub-plot, each of area $\frac{1}{80}$ acre).
- Let us first have a **graphical overview** of the experimental design.

Example III: Oats

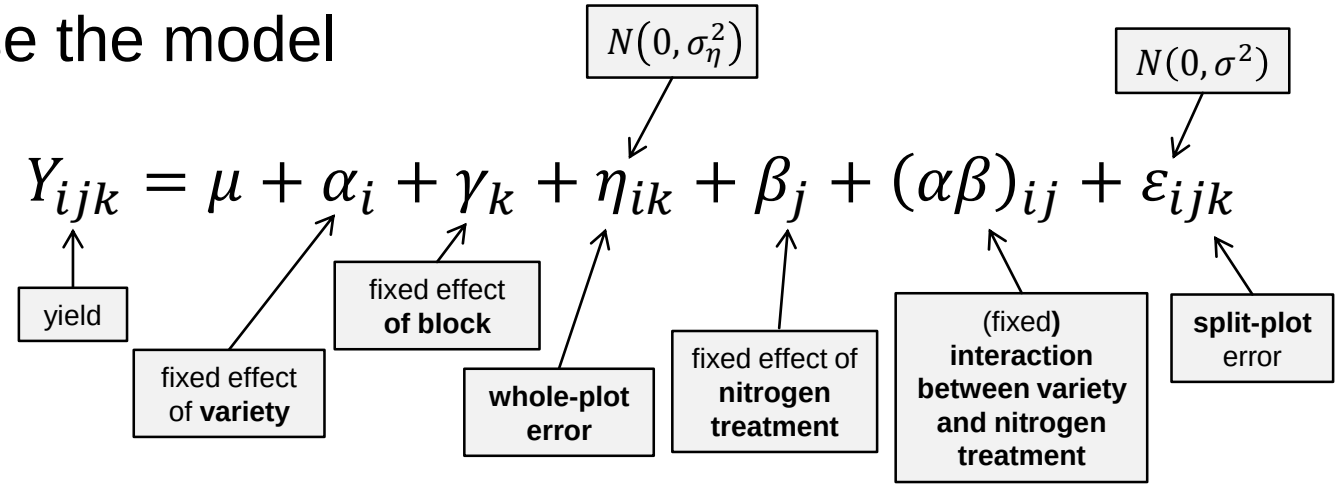


Example III: Oats

- This is a more complicated design as before as we have an additional **block factor**.
- A **whole plot** is given by a plot of land in a block.
- The **whole-plot factor** is variety.
- A **block design (RCB)** was used at the whole-plot level.
- A **split plot** is given by a **subplot of land**.
- The **split-plot factor** is given by **nitrogen treatment**.

Example III: Oats

- We have a **RCBD** for the whole-plot factor.
- An **experimental unit** on the whole-plot level is given by the **combination of block and variety**.
- We therefore use the model



Example III: Oats

- In R we use the `lmer` function with an extra random effect (better terminology here: **error**) per **combination** of **block** and **variety**.
- We get the following output:

```
> fit.lme <- lmer(Y ~ B + V * N + (1 | B:V), data = oats)
> anova(fit.lme)
Analysis of Variance Table of type III  with  Satterthwaite
approximation for degrees of freedom
     Sum Sq Mean Sq NumDF DenDF F.value    Pr(>F)
B    4675.0   935.0     5    10   5.280   0.01244 *
V     526.1   263.0     2    10   1.485   0.27239
N   20020.5  6673.5     3    45  37.686 2.458e-12 ***
V:N   321.8    53.6     6    45   0.303   0.93220
```

- Observe that the test for variety uses 2 and 10 degrees of freedom, respectively.
- Why? Let us have a closer look at the potential ANOVA table on the whole-plot level.

Example III: Oats

- On the whole-plot level we have the following ANOVA table:

Source	*df*
Block	5
Variety	2
Error (whole-plot)	$10\ (= 17 - 7)$
Total	$17\ (= 18 - 1)$

- Think of “averaging away” the nitrogen factor, hence we have **one observation** per **combination of block and variety**.
- Technically speaking, variety is tested against the **interaction** of block and variety.

Example III: Oats

- This also reveals a problem: We don't have too many error df's left to test the main effect of the whole-plot factor (only 10).
- In contrast, we test everything involving the **split-plot** factor against the **residual error**, which has 45 df's.
- Remember:

```
> fit.lme <- lmer(Y ~ B + V * N + (1 | B:V), data = oats)
> anova(fit.lme)
Analysis of Variance Table of type III  with  Satterthwaite
approximation for degrees of freedom
     Sum Sq Mean Sq NumDF DenDF F.value    Pr(>F)
B    4675.0   935.0     5    10   5.280   0.01244 *
V     526.1   263.0     2    10   1.485   0.27239
N   20020.5  6673.5     3    45  37.686 2.458e-12 ***
V:N   321.8    53.6     6    45   0.303   0.93220
```

- Hence, the main effect of the whole-plot factor is estimated **less precisely** and the test is **less powerful** (compared to the split-plot level).

  → "Prize" for "laziness" on the whole-plot level (only a few observations).

General Situation

- Split-plot designs can also arise in (much) **more complicated** forms.
- There can be **more than one whole-plot factor**. E.g., think of a two-way factorial on the whole-plot level.
- In addition, there can be **more than one factor on the split-plot** level.
- To get the correct model we “only” have to **follow “the path of randomization”**.
- For each “level” (whole plot / split plot) of the experiment we have to introduce a corresponding random effect (better terminology here: **error**) which acts as the experimental error on that level.

General Situation

- This means:
  - Start on the whole-plot level and forget about the split plots.
  - Write down the corresponding model equation (incl. random effect / error).
  - Move on to the next level, expand equation with new terms (the upper level is now a block).
  - Etc.
- In R we just have to make sure that we tell `lmer` the correct random effects.
- In R it is sometimes useful to **define new variables** which identify the different experimental units on the different levels in order to specify the random effect structure.

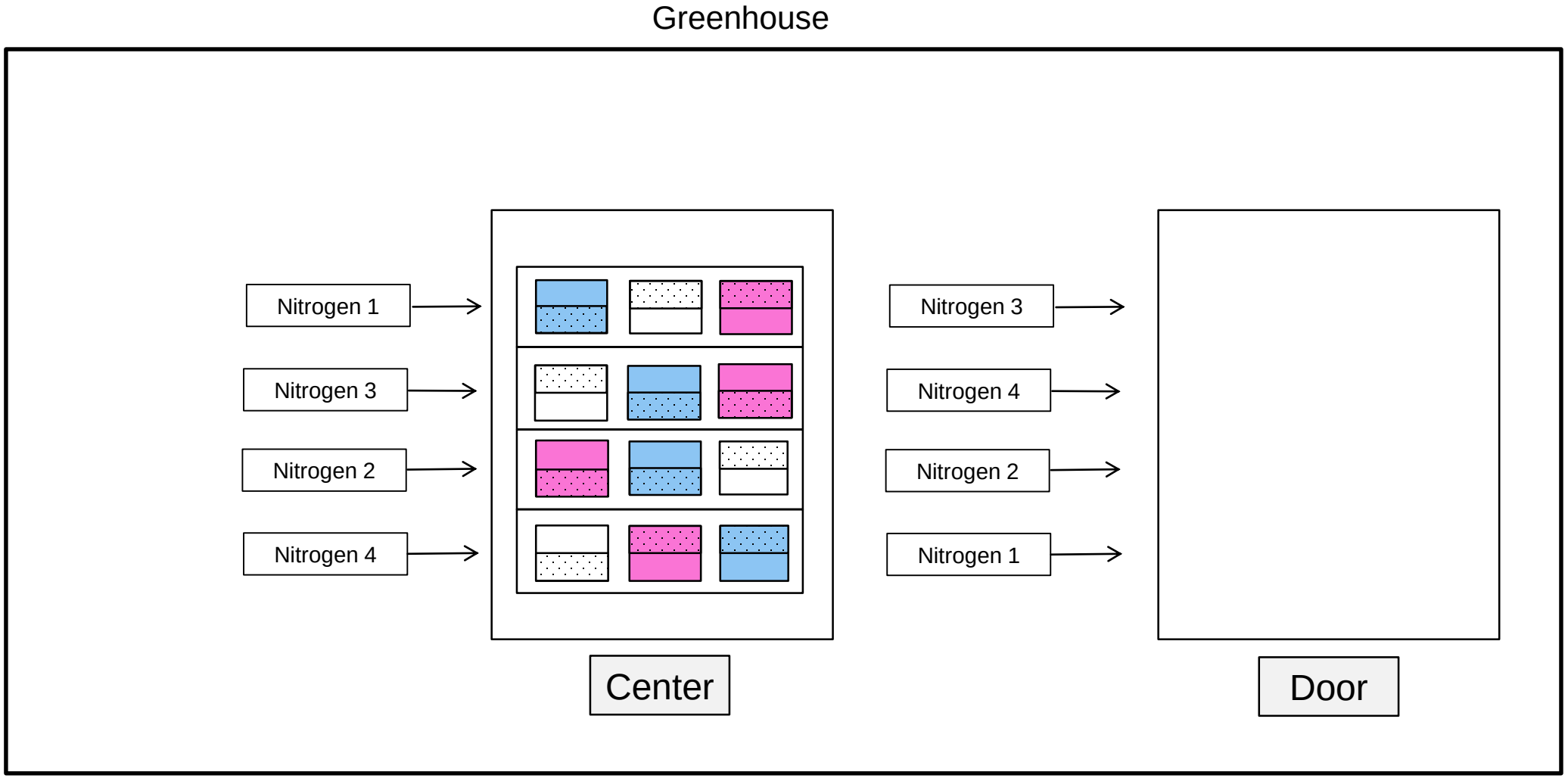
Example IV: Weed Biomass in Wetlands (Oehlert, 2010, Ex. 16.7)

- The experiment studied the effect of
  - **nitrogen** (4 levels of nitrogen)
  - **weed** (3 levels)
  - **clipping treatments** (2 levels: clipping / no clipping)

  on **plant growth** in wetlands.
- The experiment was performed as follows:
  - 8 **trays**, whereof each holds 3 artificial wetlands (rectangular wire baskets)
    - 4 of the trays were placed on **a table near the door** of the greenhouse,
    - 4 of the trays on **a table in the center** of the greenhouse.
  - On **each table**, we randomly assign one of the trays to each of the 4 **nitrogen treatments**.
  - Within **each tray**, we randomly assign the 3 **weed treatments**.
  - In addition, each wetland is split in half. One half is chosen at random and will be clipped, the other half is not clipped.
  - After 8 weeks: Measure fraction of biomass that is nonweed.

Example IV: Weed Biomass in Wetlands

Experimental layout



Example IV: Weed Biomass in Wetlands

- Let us follow the path of randomization:
  - Position in the greenhouse is a **block factor** (with levels center / door).
  - **Trays** are **whole plots**, and **nitrogen level** is the **whole-plot factor**.
  - **Wetlands** are **split plots** and **weed treatment** is the **split-plot factor**.
  - **Wetland halves** are so called **split-split plots** and **clipping** is the **split-split-plot factor**.
- Hence, we have a so-called **split-split plot design**.
- Let us now try to fit a model to this data set in R.

Example IV: Weed Biomass in Wetlands

- We use the following model:

```
> fit <- lmer(pct.nonweed.biomass ~ table + (1 | tray) + weed * nitrogen * clipping + (1 | wetland),
+             data = wetland)
> anova(fit)
Type III Analysis of Variance Table with Satterthwaite's method
                       Sum Sq Mean Sq NumDF DenDF  F value    Pr(>F)
table                    0.16    0.16     1     3   0.1538   0.72113
weed                  1186.82  593.41     2     8 555.4531 2.613e-09 ***
nitrogen                36.73   12.24     3     3  11.4610   0.03765 *
clipping               125.45  125.45     1    12 117.4290 1.494e-07 ***
weed:nitrogen          157.57   26.26     6     8  24.5814 9.665e-05 ***
weed:clipping            0.25    0.12     2    12   0.1149   0.89246
nitrogen:clipping        0.74    0.25     3    12   0.2293   0.87419
weed:nitrogen:clipping   4.82    0.80     6    12   0.7514   0.62033
```

- All **main effects** and the **nitrogen** $\times$ **weed interaction** are significant.

Example IV: Weed Biomass in Wetlands

- We are here performing three experiments in one.
- On the **whole-plot level** we have the “experiment”:

Source	*df*
Table (block)	1
Nitrogen	3
Error (per tray)	$\mathbf{3}\ (= 7 - 4)$
Total	$7\ (= 8 - 1)$

- On the **split-plot level** we have the “experiment”:

Source	*df*
Block (=Tray)	7
Weed	2
Weed × Nitrogen	6
Error (per wetland)	$\mathbf{8}\ (= 23 - 15)$
Total	$23\ (= 24 - 1)$

Example IV: Weed Biomass in Wetlands

- On the **split-split-plot level** we have the “experiment”:

Source	*df*
Block (= wetland)	23
Clipping	1
Weed × Clipping	2
Nitrogen × Clipping	3
Nitrogen × Weed × Clipping	6
Error (per wetland half)	$\mathbf{12}$ $(= 47 - 35)$
Total	47 $(= 48 - 1)$

Summary

- Split-plot designs and more complicated versions thereof are useful if some factors are harder (more expensive, …) to vary than others.
- The “prize” for “laziness”: Less precision (power) on whole-plot level.
- To identify the correct design we **have to know the randomization procedure**.
- The general situation can be very complex, but by following the different randomization levels / steps, setting up a model is **easy**.
- Mixed effects software like `lmer` automatically identify the correct denominator for tests if the random effects / errors are stated correctly.