**CRD**

This example is taken from “Example 4.3” of the course material “Quantitative Methods in Biosciences (3402-420)” by Prof. Dr. Hans-Peter Piepho. It considers data published in Mead et al. (1993, p.52) from a yield trial with melons. The trial had 4 melon varieties (variety). Each variety was tested on six field plots. The allocation of treatments (varieties) to experimental units (plots) was completely at random. Thus, the experiment was laid out as a completely randomized design (CRD).

**RCBD**

This example is taken from Chapter “2 Randomized complete block design” of the course material “Mixed models for metric data (3402-451)” by Prof. Dr. Hans-Peter Piepho. It considers data published in Clewer and Scarisbrick (2001) from a yield (t/ha) trial laid out as a randomized complete block design (3 blocks) with cultivar (4 cultivars) being the only treatment factor. Thus, we have a total of 12 plots.

**Augmented**

This example is taken from Chapter “3.7 Analysis of a non-resolvable augmented design” of the course material “Mixed models for metric data (3402-451)” by Prof. Dr. Hans-Peter Piepho. It considers data published in Peterson (1994) from a yield trial laid out as an augmented design. The genotypes (gen) include 3 standards (st, ci, wa) and 30 new cultivars of interest. The trial was laid out in 6 blocks (block). The 3 standards are tested in each block, while each entry is tested in only one of the blocks. Therefore, the blocks are “incomplete blocks”.

**Augmented 2**

This example is taken from Chapter “3.9 Analysis of a resolvable design with checks” of the course material “Mixed models for metric data (3402-451)” by Prof. Dr. Hans-Peter Piepho. It considers data from an augmented design that was laid out for 90 entries and 6 checks. The block size was 10. Incomplete blocks were formed according to a 10 x 10 lattice design, in which incomplete blocks can be grouped into complete replicates. Thus, this is a resolvable design. Checks are coded as 1001 to 1006; while the 90 entries are coded as, 2 to 100 (note that there are no entries with labels 11, 21, 31, 41, 51, 61, 71, 81 and 91). Some of the checks have extra replication. We here consider the trait “yield”.

**Alpha-Design**

This example is taken from Chapter “3.8 Analysis of an α-design” of the course material “Mixed models for metric data (3402-451)” by Prof. Dr. Hans-Peter Piepho. It considers data published in John and Williams (1995) from a yield (t/ha) trial laid out as an alpha design. The trial had 24 genotypes (gen), 3 complete replicates (rep) and 6 incomplete blocks (inc.block) within each replicate. The block size was 4

**Row-Col**

This example is taken from Chapter “3.10 Analysis of a resolvable row-column design” of the course material “Mixed models for metric data (3402-451)” by Prof. Dr. Hans-Peter Piepho. It considers data published in Kempton and Fox (1997) from a yield trial laid out as a resolvable row-column design. The trial had 35 genotypes (gen), 2 complete replicates (rep) with 5 rows (row) and 7 columns (col). Thus, a complete replicate is subdivided into incomplete rows and columns.