Data files and GenStat analysis programs for the following publication:

van der Voet H, Goedhart PW, Lazebnik J, Kessel GJT, Mullins E, van Loon JA & Arpaia, S. Equivalence analysis to support environmental safety assessment: using non-target organism count data from field trials with cisgenically modified potato.

**Data files in subdirectory Data**

The original data files given in the table below are read by four GenStat programs to give four data files which are structured in the same way.

|  |  |  |  |
| --- | --- | --- | --- |
| **Original data files** | **Date** | **Time** | **Size** |
| Design Potato Ireland 2014.xlsx | 29-02-2016 | 20:38 | 16,852 |
| Ireland\_Pitfall\_2013\_carabidaepooled.xlsx | 20-04-2016 | 11:51 | 30,089 |
| Ireland\_Pitfall\_2014\_carabidaepooled.xlsx | 20-04-2016 | 12:20 | 30,790 |
| Metadata\_Ireland2013.xlsx | 29-02-2016 | 18:05 | 9,865 |
| Valthermond\_Pitfall\_2013\_carabidaepooled.xlsx | 20-04-2016 | 12:21 | 81,559 |
| Valthermond\_Pitfall\_2014\_carabidaepooled.xlsx | 20-04-2016 | 12:21 | 38,038 |
| Valthermond\_Visual\_2014.xlsx | 29-02-2016 | 21:26 | 19,760 |
| **Structured data files** | **Date** | **Time** | **Size** |
| IR-Pitfall-2013.xlsx | 06-08-2018 | 12:27 | 119,545 |
| IR-Pitfall-2014.xlsx | 06-08-2018 | 12:28 | 105,080 |
| NL-Pitfall-2013.xlsx | 06-08-2018 | 12:28 | 149,457 |
| NL-Pitfall-2014.xlsx | 06-08-2018 | 12:45 | 135,117 |

**GenStat procedures in subdirectory Procs**

In addition to the procedures in the Biometris GenStat Procedure Library 19ed, four GenStat procedures (D3interval, Dfold, Dinterval and Meta) are used in the statistical analysis. The GenStat code of these four procedures is given in subdirectory Procs.

**Statistical analysis and graphical display programs in subdirectory Analysis**

Statistical analysis of the four separate trial is performed by means of GenStat programs “*01‑IR‑2013.gen*”, “*02‑IR‑2014.gen*”, “*03‑NL‑2013.gen*” and “*04‑NL‑2014.gen*” and the results to be used for graphical display are exported to accompanying Excel files. These four programs only differ in their first lines. The programs basically loop over all endpoints to determine the level of interaction between *Genotype* and *Spraying­,* and to calculate the associated difference between the GMO and the CMP. Program “*05-MetaAnalysis.gen*” employs the results to perform a functional group meta-analysis for the separate trials.

Graphical display of the results are then produced by the 11-15 GenStat programs.