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The feasibility of co-existence between conventional and genetically modified crops: Using machine learning to analyse the output of simulation models

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ABSTRACT

Simulation models are a commonly used tool for the study of the co-existence of conventional and genetically modified (GM) crops. Among other things, they allow us to investigate the effects of using different crop varieties, cropping systems and farming practices on the levels of adventitious presence of GM material in conventional crops. We propose to use machine learning methods to analyse the output of simulation models to learn co-existence rules that directly link the above mentioned causes and effects. The outputs of the GENESYS model, designed to study the co-existence of conventional and GM oilseed rape crops, were analysed by using the machine learning methods of regression tree induction and relational decision tree induction. Co-existence and adventitious presence of GM material were studied in several contexts, including gene flow between pairs of fields, the interactions of this process with farming practices (cropping systems), and gene flow in the context of an entire field plan. Accurate models were learned, which also make use of the relational aspects of a field plan, using information on the neighboring fields of a field, and the farming practices applied in it. The use of relational decision tree induction to analyse the results of simulation models is a novel approach and holds the promise of learning more general co-existence rules by allowing us to vary the target field within a chosen field plan, as well as to consider completely different field plans at the same time.

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1. introduction

Crop varieties developed by genetic engineering were first introduced for commercial production in 1996. Today, these crops are planted on more than 167 million acres worldwide. Genetically modified (GM) crops are usually engineered to tolerate herbicides and/or resist pests. Crops carrying genes coding for herbicide tolerance were developed so that farmers could spray their fields with non-selective herbicides to

eliminate weeds irrespective of species and stage without damaging the crop. Likewise, pest-resistant crops have been engineered to contain a gene for a protein from the soil bacterium, *Bacillus thuringiensis*, which is toxic to certain pests. This protein, referred to as Bt, is produced by the plant, thereby making it resistant to insect pests like the European Corn Borer (*Ostrinia nubilalis*) or Cotton Boll Worm (*Helicoverpa zea*). Other pest-resistant GM crops on the market today have been engineered to contain genes that confer resistance to specific plant

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viruses. So the main purpose of growing genetically modified crops in a developed European agriculture is not to achieve higher yields, but to reduce producers' inputs and operating costs.

However, genetically modified crops were not primarily developed with environmental benefit in mind and the introduction of transgenic crops and foods into the existing food production system has generated a number of questions about possible negative consequences. These concern the co-existence issue, i.e., the economic damage caused by GM contamination of conventional crops; the unwanted ecological influences of GM crops on habitats in natural and agricultural environments; the consequences of exposure of humans to transgenic proteins.

The possible unwanted influence of consuming GM crops on the human health and the influence of growing GM crops on the habitats in natural and agricultural environments are topics of ongoing research. The main concern in this paper is the co-existence issue, i.e., the possibility of GM plants mixing with conventional or organic crops. GM crops can contaminate other crops simply by pollen being transported from one field to another. In addition, for species such as oilseed rape, seeds lost before or during the harvest survive in the soil and give rise to volunteers in subsequent crops. If these volunteers emerge in later non-GM oilseed rape crops, they lead to the adventitious presence of GM seeds in non-GM harvests.

Corn (maize) and oilseed rape (OSR) are the most important transgenic crops in Europe. EU regulations allow 0.9% of adventitious presence of GM material in conventional harvests and the co-existence is concerned with achieving the prescribed level of adventitious presence in regions with both conventional and transgenic cultivars. Therefore, there is a need to find appropriate measures at the farm and regional levels to minimize gene flow from GM crops.

To study the co-existence issue for the above two crops, computer simulation models have been developed (e.g., GENESYS—for oilseed rape, MAPOD—for corn) (Colbach et al., 2001a, b; Messéan et al., 2006). Given a specific situation, e.g., a specific field plan and a set of chosen farming practices, the simulation models give predictions for the levels of adventitious presence in the fields under study. By analysing and aggregating the results of many such simulations, one can gain insight about the conditions under which co-existence is possible. For example, a JRC (Joint Research Center of the European Commission) study (Messéan et al., 2006) gives some recommendations regarding co-existence of conventional and GM corn, produced by analysing the results of MAPOD simulations.

In this study we propose the use of machine learning methods to analyse the results/outputs of the simulation model GENESYS to gain insight into co-existence issues. Machine learning methods derive general knowledge from specific examples. By applying machine learning methods, we would generalize over the specific outputs of individual simulations and derive more general rules concerning the co-existence of conventional and GM crops.

We use machine learning to analyse the outputs of two sets of GENESYS simulations. The first studies the effects of relative size and position of fields on gene flow (via pollen or seed) between pairs of fields. The second examines the adventitious

presence of GM seeds in the central field of a high-risk field pattern. To the outputs of each set of simulations, we apply suitable machine learning techniques: we use regression trees for the first and relational decision trees for the second.

2. The GENESYS simulation model

The computer model GENESYS was used to assess probable effects of changing farming practices on contamination rates. GENESYS (Colbach et al., 2001a, b) was developed by INRA (French National Institute for Agronomy Research) to rank cropping systems according to their probability of gene flow from herbicide-tolerant winter oilseed rape to rape volunteers and neighbor crops, both in time via seeds and in space via pollen and seeds. The model works for seed as well as crop production. GENESYS integrates various input variables (Fig. 1):

- The field plan of the region, comprising cultivated fields as well as uncultivated field- and road-margins (hence "borders"). Borders consist of strips of spontaneous vegetation where rape volunteers can appear, produce pollen and seeds that are dispersed to fields and other borders.
- The crop rotation of each field.
- The cultivation techniques applied to each crop (summer tillage, primary tillage and tillage for seed bed preparation, sowing date and density, herbicide applications, cutting dates and seed loss at rape harvest) as well as the management of the borders (herbicides and/or cutting).
- The type of the simulated gene (dominant A or recessive a), as well as the genotype of the rapeseed varieties.

The model is based on the life-cycle of oilseed rape, and includes both cropped and volunteer plants, starting with the seed bank at harvest and continuing with seedling emergence. Some of these seedlings become adults, flower and produce new seeds, part of which replenish the seed bank at the end of the season. The model calculates for each stage of the annual rapeseed life-cycle and for each field or border the number of individuals per m² (number of seeds in the seed bank, of seedlings, etc.) and the proportions of these individuals with and without transgenes (e.g., contamination with GM seeds).

GENESYS has already been evaluated using independent data collected on farmers' fields and on the GMO field trials set up and managed by INRA and CETIOM (Centre Technique

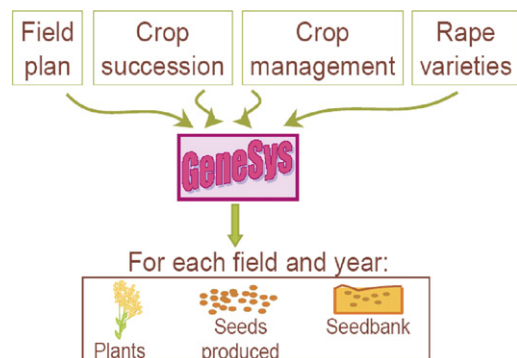


Fig. 1 – GENESYS: input and output (Colbach et al., 1999)

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