PRactical Implementation of Coexistence in Europe

Estimating Adventitious Presence and its Uncertainty

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GMCC15 – 19 November 2015

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EU coexistence framework

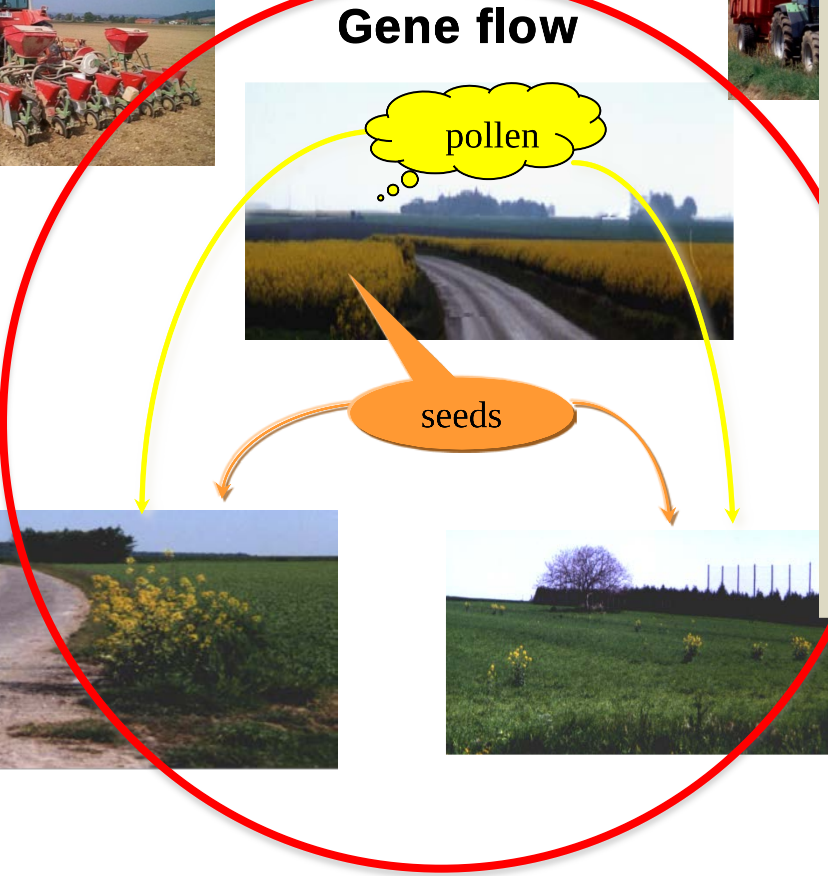
- In principle, farmers should be able to cultivate the types of agricultural crops they choose - be it GM crops, conventional or organic crops;
- The adventitious presence of GMOs above 0.9% triggers labelling « as containing GMOs »;
- The presence of traces of GMOs in particular food crops - **even at a level below 0,9%** - may cause economic damages to operators;
- Many of the influencing factors are specific to national, regional and local conditions;

→ Principles of subsidiarity and of proportionality

Various sources of adventitious presence

Seeds

Sowing

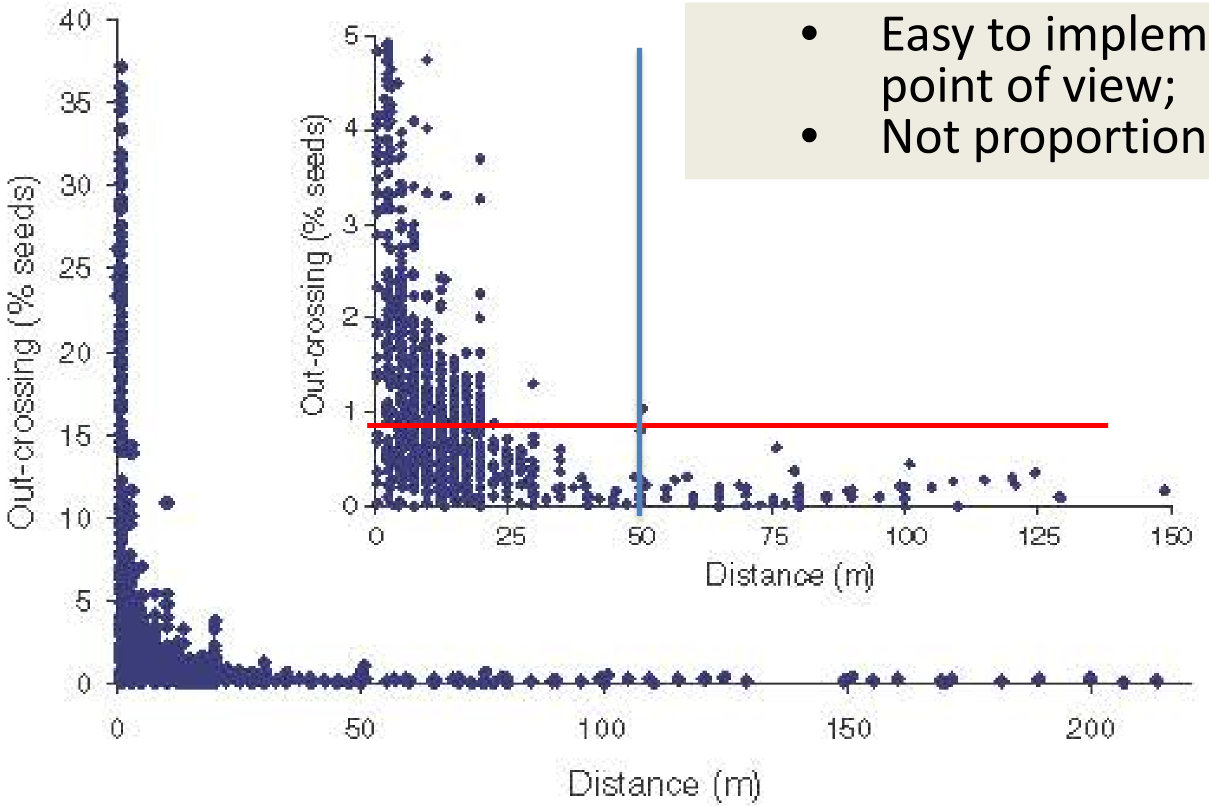


Factors affecting gene flow

- Landscape patterns
  - Distance between donor and recipient fields
  - Field sizes and shapes
  - Topology
- Wind direction and speed
- Flowering time-lag
  - Sowing dates, earliness of varieties and climate
- Crop management practices
- Genetics
  - Pollen, persistence

Uniform coexistence measures are not uniform

A statistical approach which takes advantage of gene flow studies and which determines adequate isolation distances



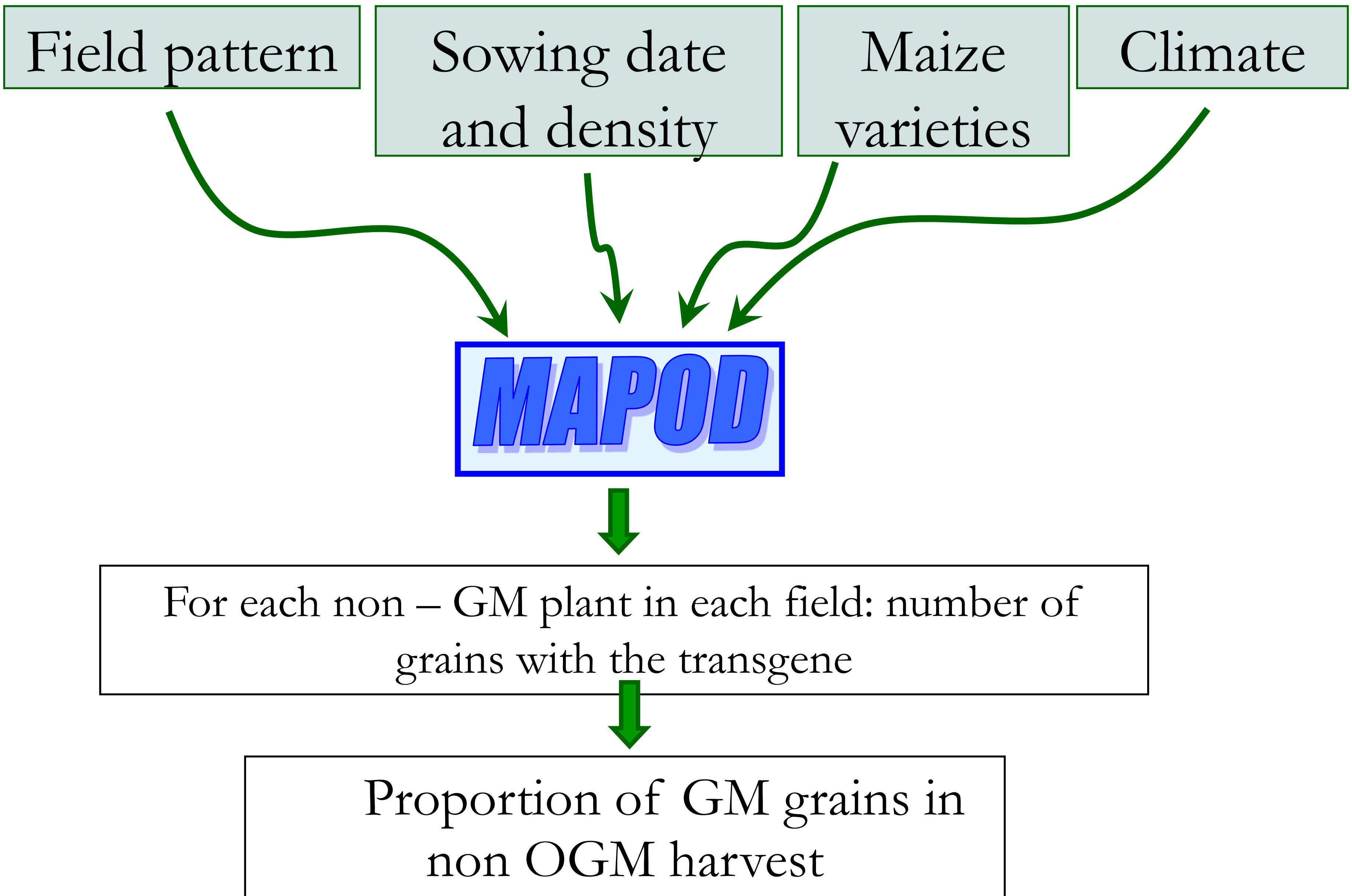
- Easy to implement from a regulatory point of view;
- Not proportional to the actual risk

Meta-analysis of maize gene flow datasets
(Riesgo et al., 2010)

How to set up coexistence measures

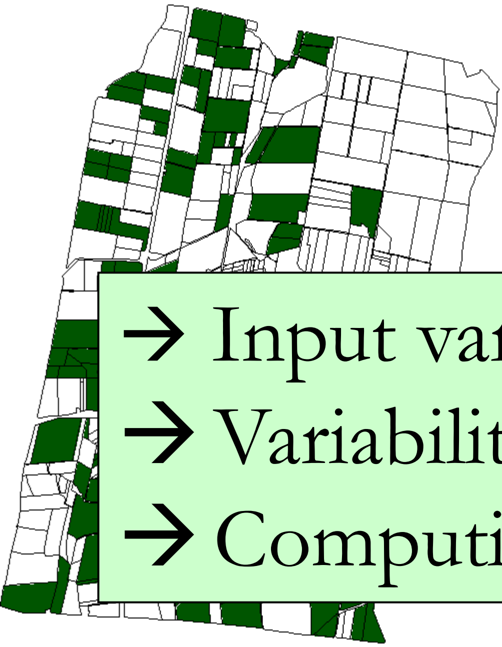
1. A statistical approach which takes advantage of gene flow studies and which determines adequate isolation distances
   – Easy to implement from a regulatory point of view;
   – Not proportional to the risk;
2. A mechanistic approach which aims at considering the effects of landscapes, climate and agricultural practices on gene flow at the landscape level
   – Adaptation to regional contexts
   – Flexible coexistence measures (may change from field to field);
   – More difficult to implement under a regulatory framework;

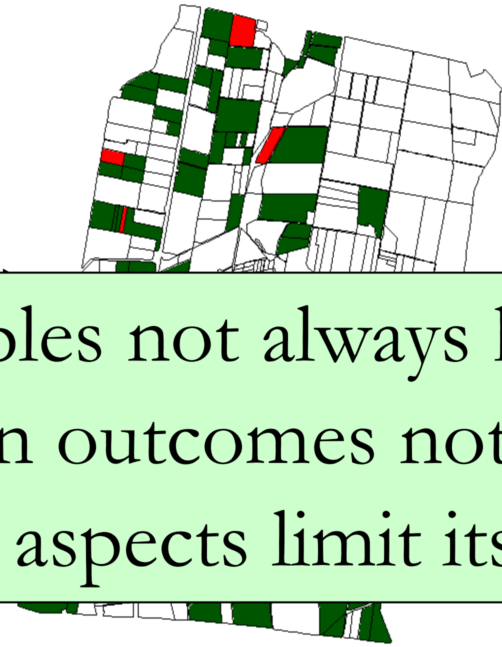
Adaptation to local conditions are necessary to meet the proportionality principle → gene flow models can help



(Angevin et al., 2008)

Assessment of Agronomic Scenarios with MAPOD





Effect of climate

→ Input variables not always known

→ Variability in outcomes not explicitly expressed

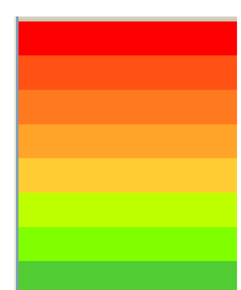
→ Computing aspects limit its practical use

sowing dates

Typical agricultural landscape where maize fields are represented in 'green'

Users decide where they would like to grow GM maize (in 'red')

MAPOD estimates the subsequent AP in non-GM fields



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→Three major steps forward

- Develop a dynamic and operational decision-support tool to help secure compliance with given thresholds
  - Development of a web-based prototype
- Associate confidence intervals to AP predictions by taking into consideration uncertainty/variability
  - Design of a Bayesian framework
- Develop cost-effective sampling strategies
  - Use of predictive models to optimize sampling

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Scenarios for the DST

Ex ante
- GM maize fields location (if registered)
- Hypotheses on allocation of non GM fields
- Historical climatic data

Sowing

Discussion between neighbouring farmers, could result in changes in GM allocation

Ex post 1
- Actual spatial location of GM and non GM fields
- Sowing dates and estimation of flowering
- More precise climate

Flowering

Estimation of AP risk, can trigger the need for additional observations and/or field sampling

Ex post 2
- Observed flowering dates;
- Climatic data for the whole growing season

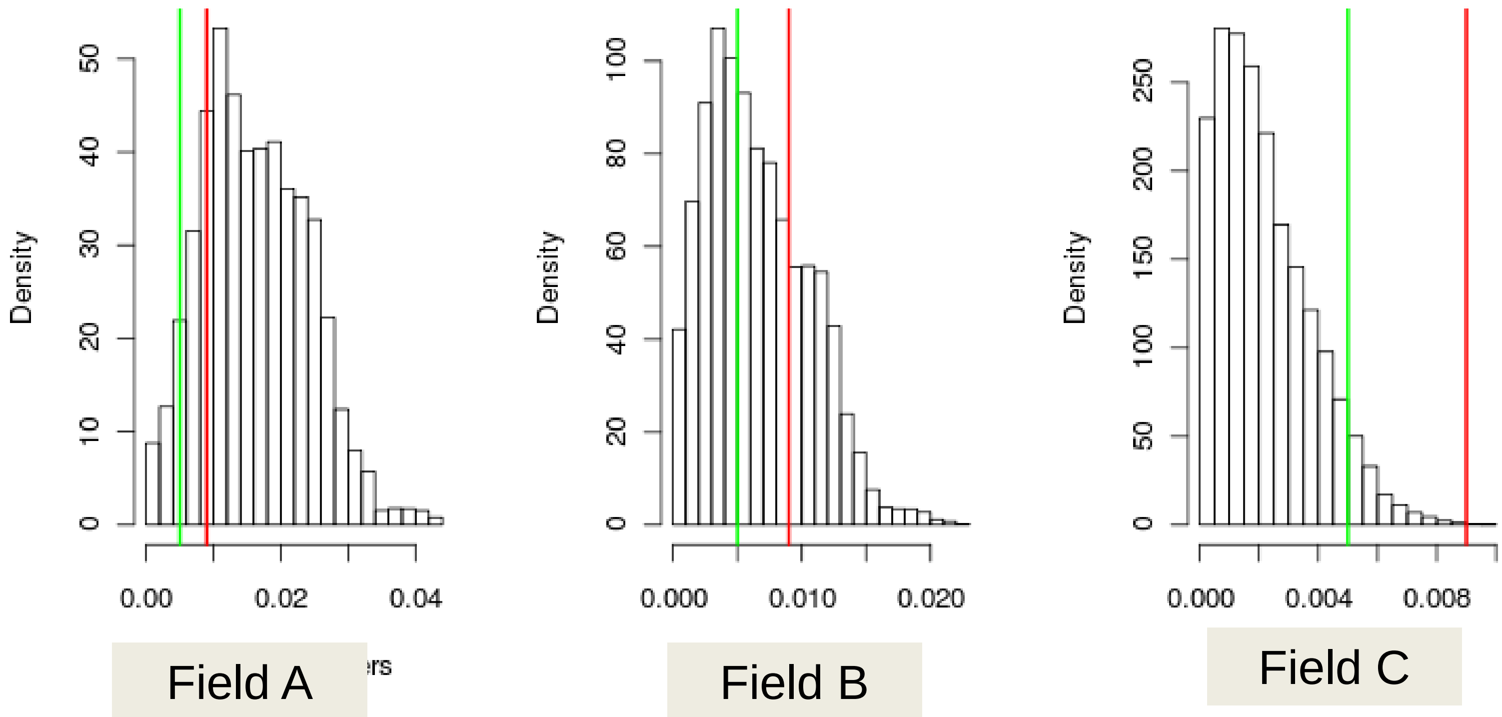
Harvesting

Harvest allotment to meet specific thresholds

Time

→ Can useful information on AP be delivered all along the growing season and whatever is the level of information?

Distribution of GM AP in every non-GM field of the landscape rather than one single value



→ End-users have to make decisions knowing the uncertainty → more difficult but more accurate

Bayesian models

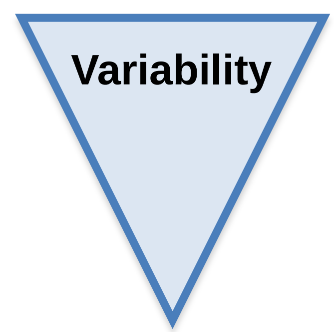
- Observation model → Zero-inflated Poisson

$$Y_s \sim ZI\mathcal{P}(1 - q_s, \mu'_s)$$

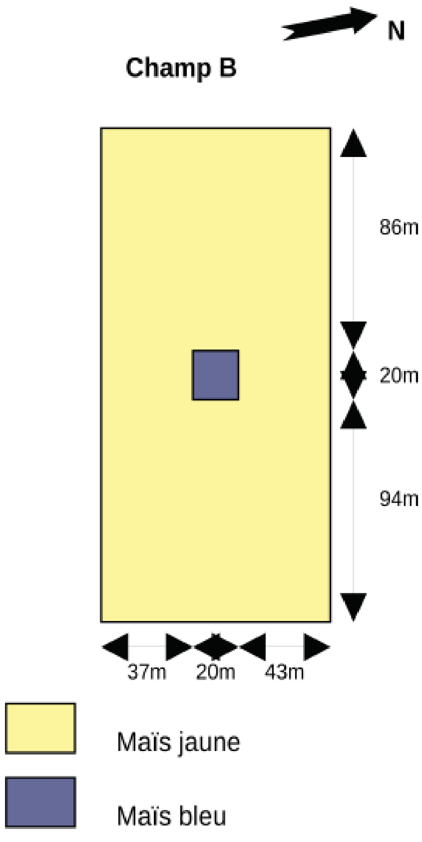
$$\mu'_s = \mu_s \times \mathrm{FD}$$

or $$\ln(\mu'_s) \sim \mathcal{N}(\ln(\mu_s \times \mathrm{FD}), \sigma^2)$$

- 3 pollen dispersal models: exponential, 2Dt, NIG
- 3 « co-variate » models
  - Distance
  - Distance + Wind
  - Distance + Wind + Flowering

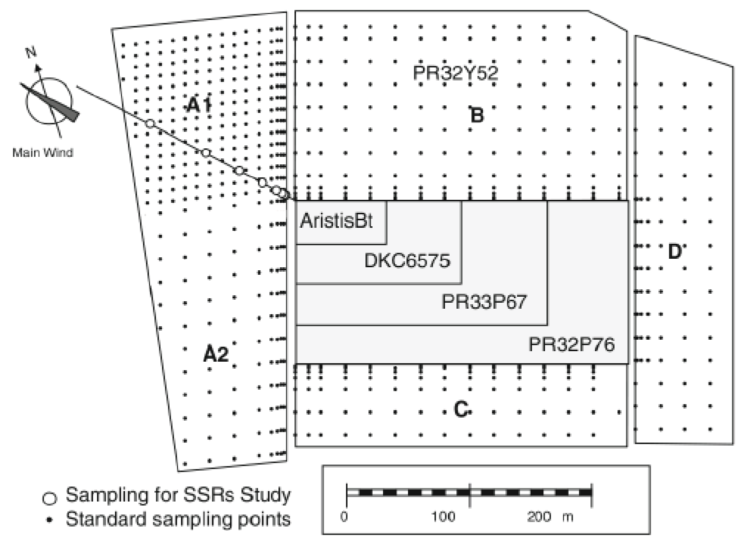


Datasets used

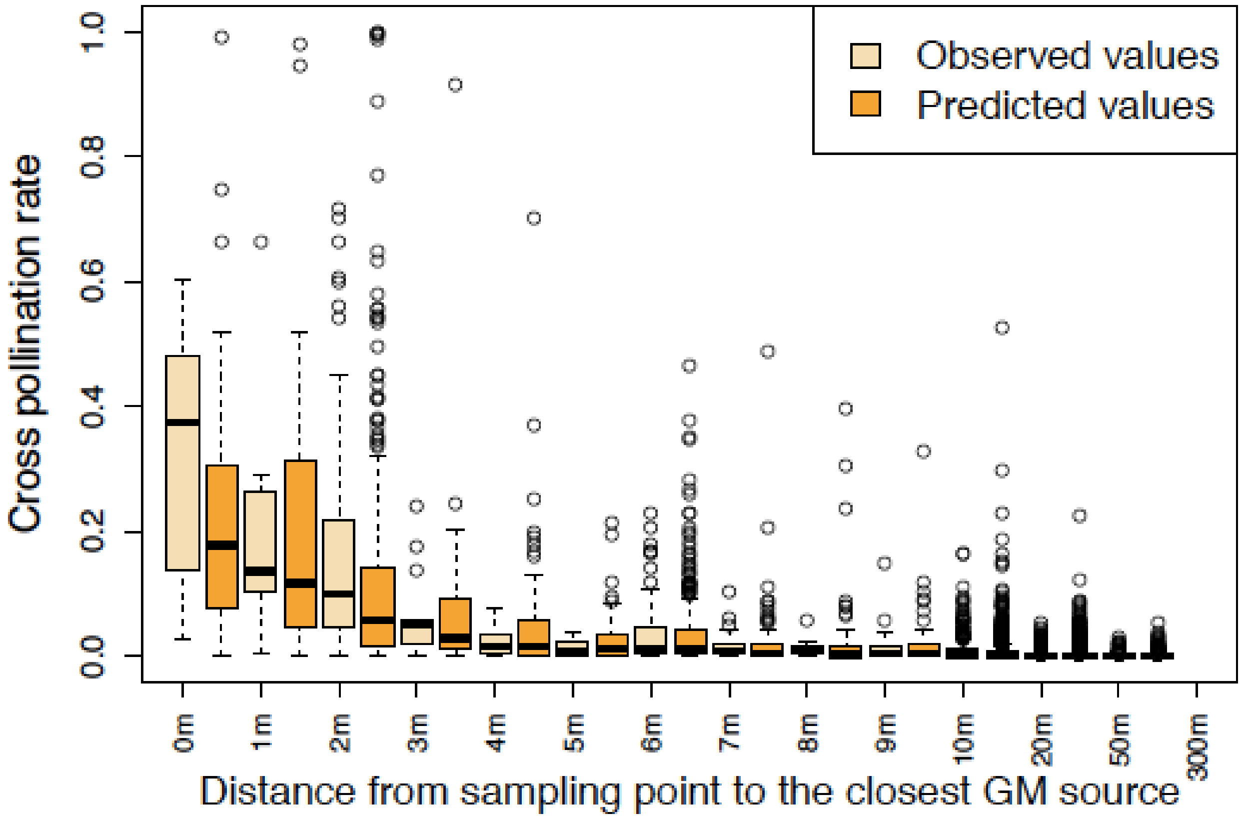


Montargis, France, 98/99
(Klein et al., 2003)

Mas Cebria, 2006
(Palaudelmas, 2012)



Correct prediction of AP and of its within-field variability



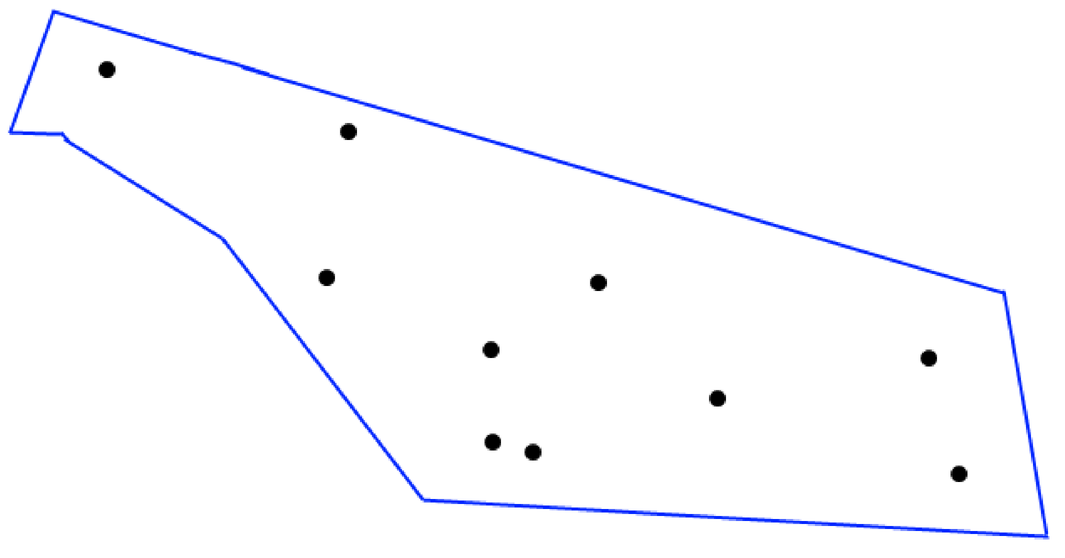
(Montargis, 1998/1999)

Model-based sampling strategies

- Simulation of the **within-field spatial distribution** of GMO AP using our Bayesian gene flow model predictions
- Calculation of mean and variance of the simulated AP values
- Possible stratification of fields (mean and variance)
- Comparison of various estimation strategies with random sampling

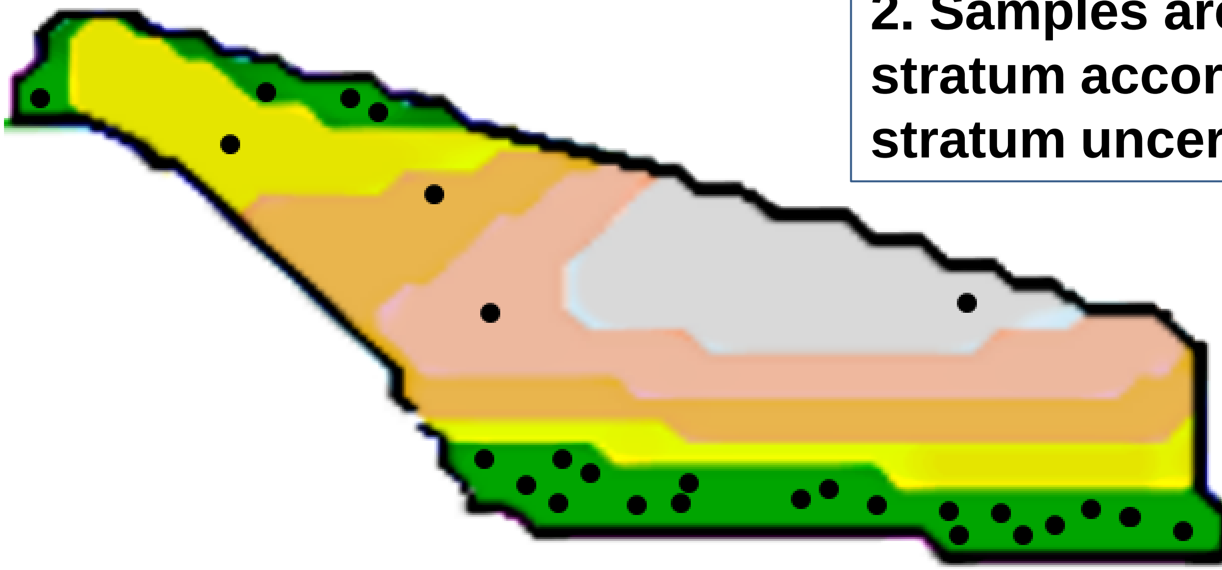
Random sampling

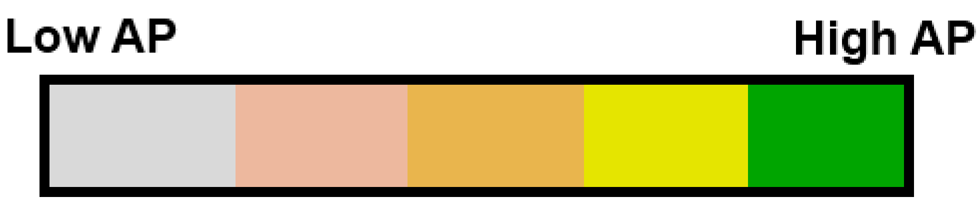
- The random sampling without replacement was used as a reference method, since it does not need any prior information. The estimator of the field AP is the sample mean.



1.The field is divided in strata of same surface, created by ranking each ear with the model output.

2. Samples are distributed in each stratum according to the intra-stratum uncertainty of the model.





1% of the samples

96% of the samples

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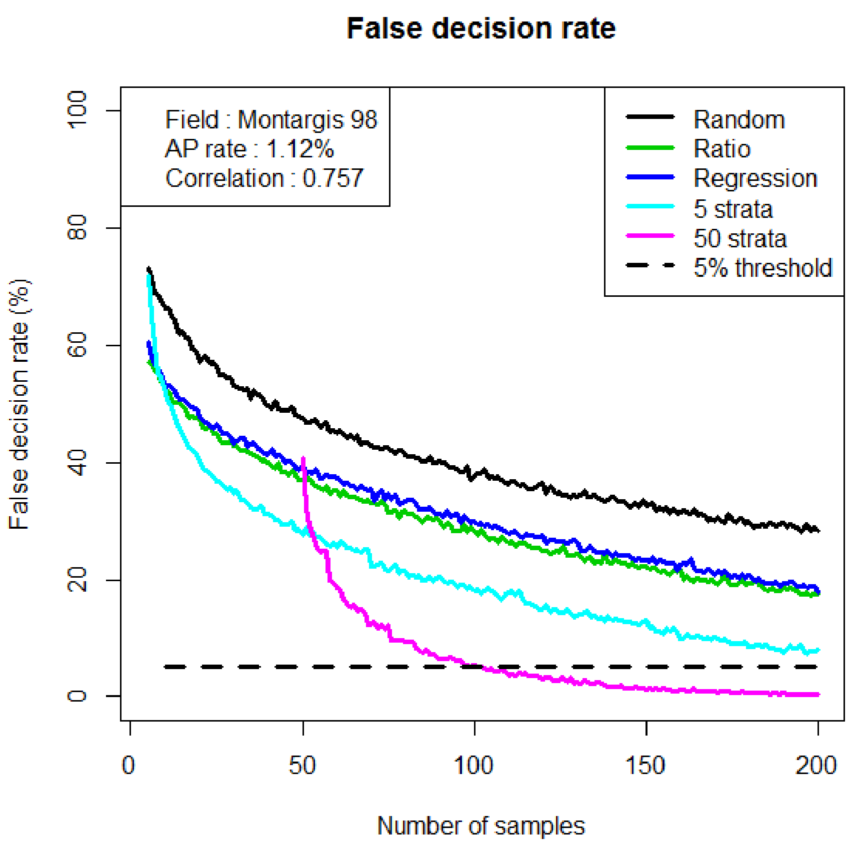
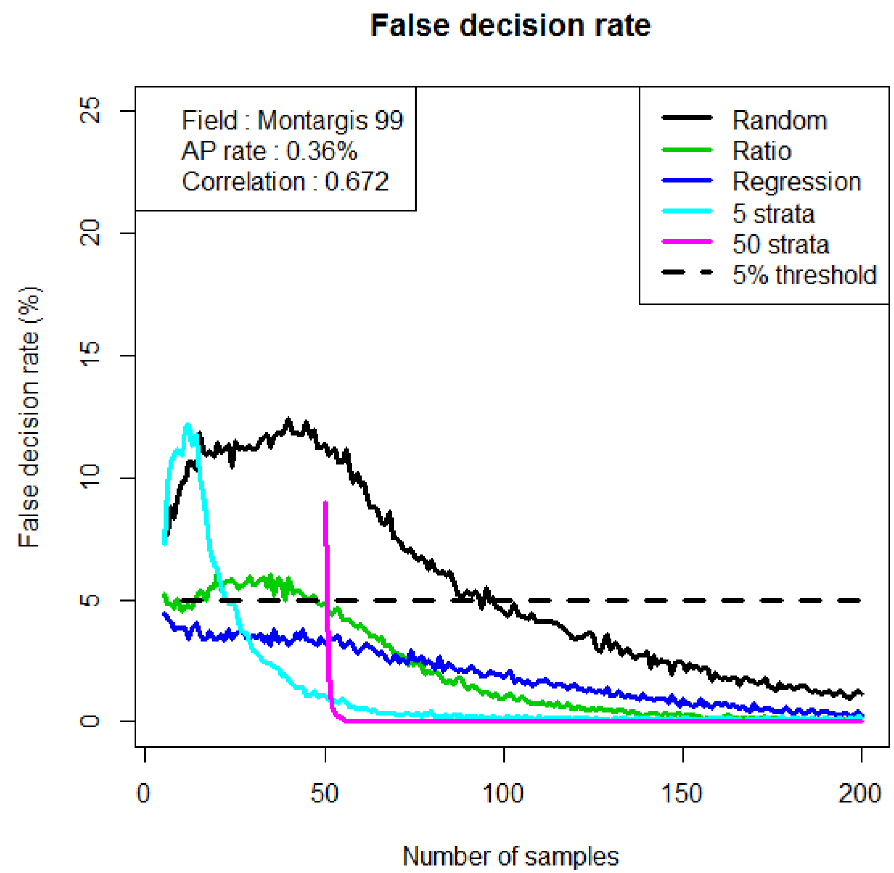
Simulation study on real datasets

- Using the gene flow information helps reduce the sampling effort
- Stratification further reduces the effort



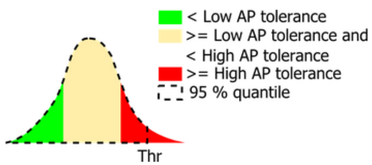


Decision support tool taking into account local conditions

Bayesian

Display

- (•) 95% probability value *Set low and high tolerance value to see fields where the quantile 95% of AP is below or above*
- ( ) Probability above threshold *Set a tolerance value and quantiles boundaries to see fields where the tolerance is below or above quantiles*



Low and high tolerances

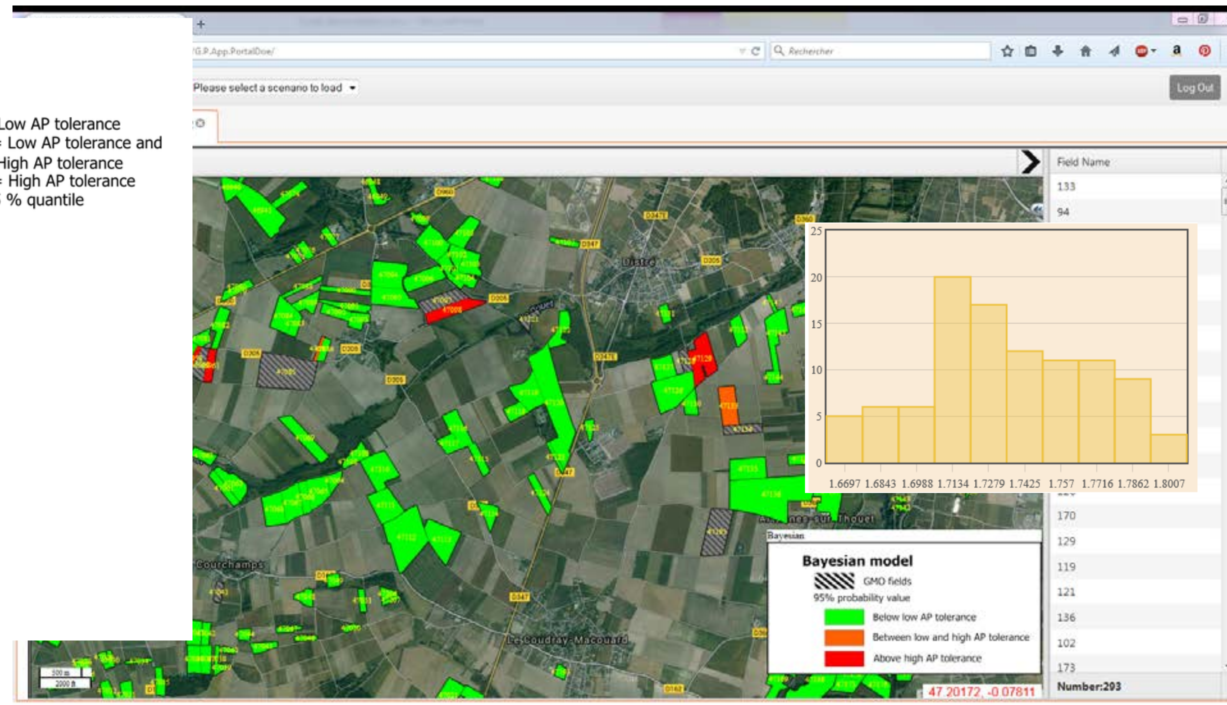
Low AP tolerance 0.1 %

High AP tolerance 0.9 %

The modeling is based on distance between fields, select an option bellow to take into account more parameters.

- [ ] Use wind in the pollen dispersal process
- [ ] Use flowering date in the pollen dispersal process

Simulate



Set inputs → Run model → Analyze results → Format outputs

Simulated Distribution of AP (%) at the Landscape Level

Conclusions

- A comprehensive Bayesian statistical approach has been successfully implemented (for the first time) to the case of gene flow and has made it possible to:
  - Give information on the uncertainty related to adventitious presence in non-GM fields;
  - Inform the decision-maker on adventitious presence whatever is the level of information available on practical situations;
  - Model the variability of adventitious presence within a field;

Conclusions (2)

- The cost-effectiveness of conventional sampling strategies is poor when the AP is close to targeted thresholds;
- More cost-effective sampling strategies can be proposed by:
  - Using the information given by the above Bayesian gene flow models to optimize sampling within fields;

Conclusions (3)

- A prototype of a web-based platform implementing decision-tools to support coexistence at the landscape level has been designed;
  - To allocate GM and non-GM fields meeting given **uniform isolation distances**, directly applicable to a wide range of crops (soybean, rapeseed) or cropping systems (seed production);
  - The Bayesian approach featuring the adaptability to available information and reflecting the level of uncertainty has been implemented for maize;
- The Bayesian approach can be extended to cover other compartments of the coexistence supply chain as well as other dispersal issues (pests)

DST available on
http://www.price.preprod.farmsat.com (User name: DemoPrice; login: PriceDemo, load scenario foixa_2004)