

Sixth International Conference on Sensitivity Analysis of Model Output

# Global Sensitivity Analysis of the Process-Based Wheat Simulation Model *SiriusQuality1* Identifies Key Genotypic Parameters and Unravels Parameters Interactions

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## Abstract

Improving crop performance to satisfy an increasing demand for agricultural products is a constant challenge to plant scientists. The recent improvements of process-based simulation models offer new avenues to explore variations of genetic traits on crop performance. In this study, global sensitivity analyses were performed using the Morris and Sobol' methods sequentially to identify influential parameters of the *SiriusQuality1* wheat simulation model. Twenty three influential parameters were identified. The response of the model outputs to these parameters was analyzed. A genetic algorithm with self-adaptation was then developed to optimize these parameters for 16 genotypes of wheat and to define the minimum set of parameters needed to simulate genetic differences in grain yield under diverse environments.

**Keywords:** Crop simulation model; genetic algorithm; genotypic parameter; parameter optimisation.

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## 1. Main text

Improving crop performance to satisfy an increasing demand for agricultural products is a constant challenge to plant scientists. Plant breeders approach this challenge by searching the genetic space for superior genotypes that have improved performance in target environments, while agronomists optimize crop management for the cohort of elite genotypes developed by plant breeding (Messina et al., 2009). Prior to releasing a new cultivar to the public, plant breeders must identify superior cultivars through many stages of testing. These tests must be conducted over several seasons and multiple locations, since crop performance is determined by the combined effects of genotype, environmental conditions, and crop management. This process usually consumes a great deal of time, labor, and resources. The recent improvements of Process-Based Simulation Model (PBSM) offers new avenues to assess the value of genetic traits on crop performance under differing environments and management (Bertin et al., 2010). In

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PBSM differences between genotypes are described through genotypic parameters, which are mathematical constructs designed to mimic the phenotypic outcome of genes under different conditions. These parameters represent a sub-set of the total number of parameters. Modelers and model users are faced with difficulties trying to identify the minimum set of parameters that can be used to describe the differences between genotypes. Therefore, the aim of this study was (i) to identify the most influential parameters of the wheat PBSM *SiriusQuality1* (Martre et al., 2006) through a global sensitivity analysis (GSA); (ii) to identify among these influential parameters the minimum set needed to simulate contrasted wheat genotypes under different pedo-climatic conditions.

A GSA was first conducted using Morris method (Morris, 1991) to identify the most sensitive parameters. The full space of possible values of all of the 76 parameters of the model, which was defined by uniform distributions with maximum and minimum of  $\pm 50\%$  of default values, was explored using 10 trajectories and 8 factor levels in a simulation experiment conducted for 40 years at two contrasted sites in France and UK with two nitrogen application levels and two wheat cultivars. A subset of parameters was selected according to their values of elementary effect with respect to relevant model outputs. Then a second GSA was conducted for the subset of parameters selected above using the Sobol' method (Sobol', 1993). Multiple sets of parameters were created using Monte Carlo random sampling from the parameter distributions by coupling the sensitivity analysis software SimLab (Saltelli et al., 2004) with *SiriusQuality1*. The variances of response variables were decomposed into the contributions from the various input parameter variations over their ranges of uncertainties and interactive SI were computed based on the variability associated with the main effect of parameters. The main effect indices for each parameter along with the total sensitivity to each parameter were then computed considering its interactive effects with other parameters. These analyses identified 23 parameters with a significant SI. These parameters were distributed over the seven sub-models of *SiriusQuality1*. Model outputs responded non-linearly to variations in about half of these parameters.

In order to define the minimum set of parameters to describe the genetic variability of grain yield under different environments, the short list of 23 most sensitive parameters defined above was optimized for 16 wheat genotypes using experimental results from multi-environment replicated field trials in France and UK under optimal and low nitrogen fertilizer levels for the 16 genotypes. A genetic algorithm with self-adaption (GA-SA, Marseguerra et al., 2003) was developed and implemented in *SiriusQuality1*. The different sub-models were then optimized iteratively for each genotype. This study demonstrates the efficiency of GA-SA algorithms to optimize complex PBSM and further restricted the number of genetic parameters that can be used for genetic analysis.

## 2. References

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