Sensitivity analysis of dynamic crop models to assist crop science: assessing the impact of multiple traits on yield in Australian wheat.

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Crop functioning can be viewed as a complex system, which depends on genetic determinants, physiological processes, pedo-climatic factors and management practices. To understand this system, we must first explore it. The elements of this system (genotype, environment, management) defines a landscape that can be explored by controlling the determining parameters. The numerical exploration of crop models appears as an efficient method to deal with the large dimensionality of this landscape, assuming that the crop simulation model gives a credible description of the biological system.
Our aim is to assess the impact on crop yield of a suite of traits involved in important processes and to evaluate how the value of such traits varies across environments and in relation to other traits. The study targets wheat crops in the Australian wheatbelt, with an emphasis on drought adaptation. A large set of traits ($\sim$ 100) has been be evaluated in a wide population of environments and management practices (9000).
The Morris sensitivity analysis method [1] was used to sample the parameter space and reduce computational requirements, while keeping a realistic representation of the targeted trait x environment x management landscape ($\sim 82.10^6$ individual simulations in total). The APSIM-wheat [2] crop model was used to represent the biological system. This approach allowed us to focus on impacting parameters ($\sim$ 50% of total parameters) to identify patterns of parameter $\times$ environment $\times$ management interactions. While parameters with a high and stable impact under climate variability may have already been considered for breeding, parameters with high impact in frequently-occurring environment types may be relevant as breeding targets to further improve yield.
This work contributes to improving high-dimensional exploration and visualization methods available in cropping systems. The R software and packages *sensitivity* (sampling and analysis), *dplyr* (data manipulation), *ggplot2* (visualization) and *knitr* (reporting) allowed to easily integrate the presented steps in dynamic documents, aiming for a more open and reproducible analysis process. Its application in crop science will assist crop physiologists and breeders to

better understand G×E×M landscapes an ultimately focus on relevant traits for the targetted environments.

References

[1] Morris, M. D. (1991), 'Factorial sampling plans for preliminary computational experiments', *Technometrics* **33** (2), 161–174.

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