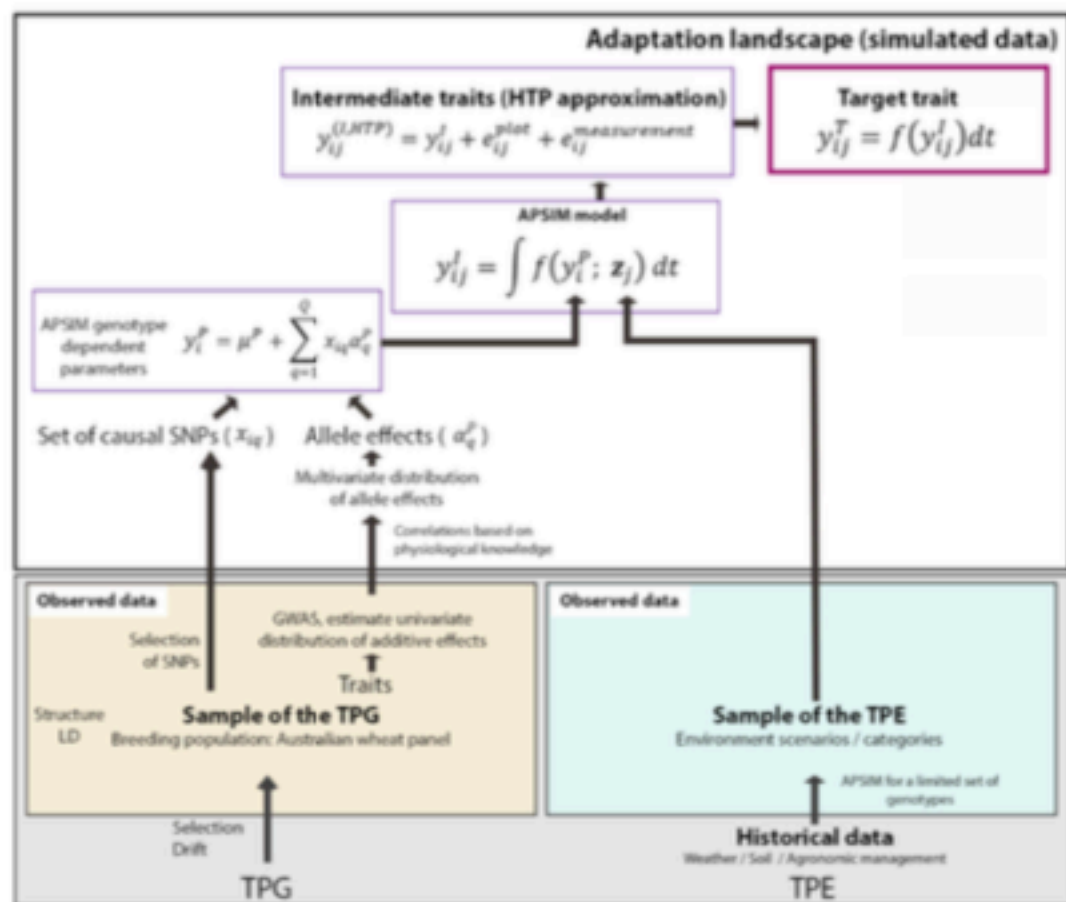


Using statistical and crop growth models to characterize genotype by environment interaction (GxE) over time

Daniela Bustos-Korts¹, Karine Chenu², Scott Chapman², Martin P. Boer¹, Willem Kruijer¹, Fred van Eeuwijk¹



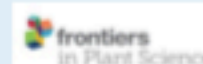
- **GxE for yield** arises because of the interplay between underlying traits and the environment over time.
- We provide a framework to **study the performance of genotype to phenotype (G2P)** modelling approaches.
- We use the crop growth model **APSIM-wheat** with genotype-dependent parameters to simulate **non-linear trait responses** over time with complex trait dependencies and apply it to wheat crops in Australia.



Application 1: Evaluation of phenotyping strategies

How often and how precise do we need to phenotype for secondary traits to help breeders improving yield prediction accuracy?

We assess the effectiveness of parametric and spline models to remove part of the measurement error.



We extract curve characteristics and use them in a multi-trait genomic prediction model.

Combining Crop Growth Modeling and Statistical Genetic Modeling to Evaluate Phenotyping Strategies

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Application 2: Multi-environment genomic prediction

We use the simulated landscape to classify environments based on water deficit patterns.

Environment classification and indices of environment quality were used to assess multi-environment genomic prediction models.



We conclude that prediction models that predict yield predicted per environment type, or that explicitly model the gradient in water deficit let to much higher prediction accuracy than those without explicit variable selection.

From QTLs to Adaptation Landscapes: Using Genotype-To-Phenotype Models to Characterize GxE Over Time

Daniela Bustos-Korts¹, Marcos Malvar¹, Karine Chenu², Scott Chapman², Martin P. Boer¹, Bangqiu Zhang² and Fred A. van Eeuwijk¹

Application 3: Identification of adaptive traits with network reconstruction methods

Genetic variance of a phenotypic trait can originate from direct genetic effects, or from indirect effects

We propose an alternative strategy, where genetic effects are formally included in the graph.

Advantages:

- (1) genetic effects can be directly incorporated in causal inference, implemented via our PCgen algorithm.
- (2) we can test the existence of direct genetic effects, and improve the orientation of edges between traits.



Reconstruction of Networks with Direct and Indirect Genetic Effects

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