Model assisted phenomics and phenotype modeling

Pierre Martre, Shouyang Liu
Outline

1. Dynamics models for phenotype modeling
   - Process-based models
   - Functional structural plant models
2. Role of crop modeling in genetics and breeding
3. Interpretation of high-throughput phenotyping data
4. Model assisted phenotyping
5. High-throughput phenotyping data assimilation (parameter estimation)
6. Conclusions
Functional Structural Plant Model (FSPM)

- Individual based models (behavior of individual plants determine canopies properties)
- Plant architecture is represented in 3D
- Explicit feedback between plant growth and environmental drivers
- Only few functional processes considered

Robert et al., 2017
Garin et al., 2017
Fournier et al., 2003
Process-Based Model (PBM)

- **Focus on functional processes and feedbacks (explicit or implicit {emerging properties})**
- **Canopy architecture not explicitly considered (canopy = 1D turbid medium)**

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**Crop Management**
- Sowing date
- N fertilization
- Irrigation

**Soil**
- Hydraulic characteristics
- % organic matter
- pH

**Weather**
- Temperature
- Radiation
- Precipitation

**Cultivar**
- Radiation use efficiency
- Phyllochron
- Potential grain size
- Fruiting efficiency

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**Yin et al., 2010**

**Crop model**

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21 June 2018
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**Inputs**
- Crop Management
  - Sowing date
  - N fertilization
  - Irrigation

**Simulations**
- Grain yield
- % Proteins
- GPD
- NUE
- WUE

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**Plant**

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**Crop model**
- **Potential transpiration**
- **Photosynthesis**
  - C assimilates
  - Growth
  - Respiration

**Development stage**
- **N assimilates**
  - Use

**Partitioning**
- N uptake
- N demand
- N fixation

**Sink strength**
- Leaf N
- Leaves
- Stems
- Seeds
- Remobilization

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**Crop model**

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Phenotyping distance and prediction

Crossing scales of biological organization confounds prediction

- Crop model by integrating traits effect reduce the phenotypic distance
- Genetic analysis should be carried on simple traits and crop model allow scaling to the crop

Hammer et al., 2016
Role of crop modeling in genetics and breeding

Predict – Trait evaluation in target environments to unravel G x E interactions
Dissect – Understand and simplify complex traits (use of NILs, mutants)
Detect – Inform phenotyping for QTL detection
Connect – Link QTL/genes to crop attributes/processes

Hammer et al., 2016
Integration of modeling in a breeding program

New Traits and methods

Crop Model

Sélection des meilleurs combinaisons alléliques

Harrison et al., 2014

Novel germplasm

Caractérisation environnementale pour comprendre les interactions G x E x M

Hammer et al., 2005

Climate, Management

Tester la valeur de traits

Sinclair et al., 2010

Parental pool

Selection of best

High-throughput phenotyping

Crop Model

Biomass LAI Cover Zadoks

Chapman et al., 2014

Crop Model

Phénotypage assisté par modèle

Chapman et al., 2014

Industry output New cultivars

Crop Model

Integration of modeling in a breeding program
QTL/gene-based modeling

Phénotypage haut-débit

Réseau d’essais

Model assisted phenotyping

Genetic Analysis of model parameters

Genotype to phenotype model

Which allele where?

Phenotype modeling

Genetic model (GWAS, GS)

Hammer et al., 2006

Pierre Martre
high-throughput phenotyping data assimilation

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High-throughput Phenotyping starts from big data

Phenotyping data interpretation is the key
- to transform big data to phenomics
- and finally contribute to the crop improvement

Slide from S. Liu
Levels of Phenotyping data interpretation

- Sensor
  - Empirical model
    - L0: Raw signal
  - Physics-based model
    - L1: Physical quantities
    - L2: State variables
  - Process-based crop model
    - L3: Functioning traits

Traits level/Heritability

Slide from S. Liu
Phenotyping data interpretation:

**Goal**: maximize the traits’ outcome with satisfactory accuracy

**Strategy**: Optimize the information use from measurements and prior knowledge
# Levels in phenotyping data interpretation

<table>
<thead>
<tr>
<th>Level</th>
<th>Sensor</th>
<th>Traits</th>
<th>Method</th>
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<tbody>
<tr>
<td>L1</td>
<td>RGB</td>
<td>Plant distribution</td>
<td>Statistic model</td>
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<td>Plant density</td>
<td>Machine learning</td>
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<td>Ear density</td>
<td>Deep learning (Simon Madec)</td>
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<td>L2</td>
<td>LiDAR</td>
<td>GAI</td>
<td>Digital Plant Phenotyping Platform (D3P)</td>
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<td>Multispectral</td>
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<td>Chlorophyll content</td>
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<td>L3</td>
<td>RGB</td>
<td>3D canopy structure</td>
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<td>Light interception</td>
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*Slide from S. Liu*
Model assisted field phenotyping

Estimating wheat green area index from ground-based LiDAR measurement using a 3D canopy structure model

Shouyang Liu\textsuperscript{a,a}, Fred Baret\textsuperscript{a}, Mariem Abichou\textsuperscript{b}, Fred Boudon\textsuperscript{c}, Samuel Thomas\textsuperscript{d}, Kaiguang Zhao\textsuperscript{a}, Christian Fournier\textsuperscript{d}, Bruno Andrieu\textsuperscript{b}, Kamran Irfan\textsuperscript{a}, Matthieu Hemmerlé\textsuperscript{a}, Benoit de Solan\textsuperscript{d}
Model assisted platform phenotyping

HPT assay -> Plant Images -> Binarization -> 3D-Reconstruction

Leaf area and biomass

RATP light model

3D virtual canopy

Canopy light interception

Alvarez Prado et al., 2017

Sinoquet et al., 2001
High-throughput data assimilation

Prediction of wheat flowering time

Phenotyping

Trait distinction

- Emerged leaf number
- Vernalization rate
- Day length

Genetic material: 100 RIIs of O. berottiana x Cappelli

Vernalization at 4°C for 8 weeks

Plants grown until anthesis in a greenhouse or outside

Measurements:
- Karn stage
- Final leaf number
- Anthesis date

QTL-based parameters

Phenotype prediction (in new environments)

Genetic analysis

Data assimilation

\[ y_j = \mu + \sum_{i=1}^{n} a_i QTL_j \]

Martre et al., 2018
Conclusions et perspectives

- Phenotyping-oriented crop model are required (biological/physical coherence).
- Phenomics is renewing model development, improvement, and testing.
- To retrieve functional traits Integration of D3P with process-based model is required.
- To develop real time data assimilation for precision agriculture emulators (meta-models) will probably be required (computation time).

Liu, 2016
Thank you for your time

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