



## Coordination

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## Key words

High throughput phenotyping  
Growth curves  
Statistics for functional data: growth  
model  
Genetic-environmental interaction  
model

## INRAE units involved

[MISTEA](#)  
[MIAT](#)  
[MaIAGE](#)  
[GQE-Le Moulon](#)  
[GenPhyse](#)

# Bringing together INRAE expertise for the prediction of dynamic phenotypes

## Context and challenges

In response to the multiple challenges of climate change and multi-performance agriculture, the sciences of breeding and plants are faced with the challenge of selecting breeds or varieties on the basis of increasingly complex phenotypes. Examples include plant growth curves in the face of water stress, microbial community growth in the face of nutrient restriction, and weight gain dynamics in animal husbandry. Thanks to the popularisation of sensor technologies and the emergence of digital agriculture, INRAE researchers now have access to medium and even high-speed growth data.

This is the case, for example, thanks to the PHENOME-EMPHASIS plant phenomics infrastructure in plant science, to automated distribution methods for concentrated feeds (DAC) in animal husbandry, or to real-time monitoring methods for bacterial communities. Nevertheless, the analysis and prediction of these phenotypes and, ultimately, their use in selection schemes, raise many challenges, linked to the noisy nature of the data and their highly complex structure (response in the form of curves linked to environmental covariates).

Currently, different INRAE teams contribute to these challenges, but in a relatively individual way. This segregation is as much related to the diversity of the species studied (microbial, plant or animal), to the diversity of the biological aspects (complex phenotypes versus genetics) as to the diversity of the statistical approaches used.



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## Goals

The objective of the PhenoDyn consortium is to bring together statisticians and geneticists from the institute who are interested in the prediction of complex dynamic phenotypes, in order to compare the approaches used and decompartmentalise the fields of application. As such, the consortium includes members of four INRAE departments (MathNum, GA, AgroEcosystem and Plant Biology and Breeding). Initially, the consortium will draw up an inventory of the various methodological contributions to the study of dynamic phenotypes, which currently include a wide range of approaches: semi- or non-parametric methods of functional statistics, Markovian dynamics models, non-linear models based on more refined dynamic modelling, etc.

This first step will make it possible to enhance INRAE's contributions in the field, but also to guide future users - including private partners - on the methodological choices to be adopted according to the identified objective: measurement of a genetic index (e.g. heritability of the dynamic phenotype), prediction of the phenotype at future times, identification of characteristic phenotypic profiles, etc. Then, we will try to compare approaches, in two stages:

1. extracting some key indicators from the complex phenotype
2. plugging these indicators into a multidimensional GXE model with more integrative approaches, aiming to simultaneously model the dynamics in a complex integrated model, coupling dynamic and GXE interaction aspects.

## Research units involved and partnerships

INRAE scientific division	INRAE research units	Expertises
<b><u>Mathematics, computer and data sciences, digital technologies</u></b>	<u>MISTEA</u>	Analysis of high-throughput phenotyping data
	<u>MIAT</u>	Statistical learning
	<u>MaIAGE</u>	Mixed models, GXE analysis models
<b><u>Plant biology and breeding</u></b>	<u>GQE-Le Moulon</u>	Statistical methods in quantitative genetics
<b><u>Animal genetics</u></b>	<u>GenPhyse</u>	Phenotyping and animal genetics DAC data analysis

