Directors
Hervé Monod
Carole Caranta

Project manager
Marjorie Domergue

Steering Committee
Hugues Berry (INRIA)
Julien Chiquet
Pauline Ezanno
Anne Goelzer
Olivier Hamant
Fabien Joudan
Matthieu Jules
Gabriel Krouk (CNRS)
Marie-Laure Martin-Magniette
Christele Robert-Granie
Leopoldo Sanchez-Rodriguez
Thierry Simonneau
Masoomeh Taghipoor
Isabelle Maillet (National Metaprogramme Coordination unit)

Metaprogram DIGIT-BIO

Digital biology to explore and predict living organisms in their environment

The quantitative and qualitative boom of data in biology, combined with the development of new tools for processing and analysing these data, is revolutionising research in the life sciences. This development opens up new perspectives for better understanding the functioning of biological systems and predicting their behaviour.

The life sciences have undergone a fundamental paradigm shift at the end of the 20th century, with living organisms being considered as dynamic, complex and evolving systems whose overall behavior cannot be deduced from the properties of their individual components.

Systems biology now seeks to integrate different levels of information in order to understand the functioning of a biological system and predict its behaviour, via the use of methods and computer tools for modelling and simulating biological processes. The specific properties and dynamic interactions between the components of these systems are being formalised and it makes it possible to observe emerging properties and to integrate them at different spatial and temporal scales.

© sheep : Jose Llamas - Unsplash, landscape : freestocks - Unsplash, organoid : Kjparjeter - Freepik, montage : Comscience

These *in silico* approaches now benefit from new technologies, including the massive integration of data and knowledge, intensive computing, new models and meta-models, machine learning algorithms, etc. These modelling and simulation methods have opened up unprecedented possibilities for better understanding biological processes, predicting their responses to different stresses and, more broadly, for designing and better driving these systems.

The metaprogramme was launched in 2021 and its aim is to support research at the interface between computational / engineering sciences and life sciences (biology, physics, chemistry or environmental sciences), in order to:

- **Understand the functioning and predict the behaviour of biological systems**
- **Anticipate the impact of stresses on these systems, reason out their management and develop levers for action. In the medium term, the ambition is to develop a small number of projects for *in silico* monitoring of biological systems, based on the concept of the "digital twin".**

DIGIT-BIO in figures (2022)

- A community of **over 900 members** participating in the scientific activities (projects, events) of the metaprogramme
- **14 projects** and **5 consortia** funded since 2021, involving more than 200 researchers and engineers
- **9 interdisciplinary doctoral theses cofunded**

Metaprogramme
DIGIT-BIO

Contact : digitbio@inrae.fr

www.inrae.fr/digitbio/

The metaprogram is structured around 4 research axes

DIGIT-BIO addresses the behaviour of biological systems **from the molecular scale to that of the organism and the population** within their surrounding environments (biotic, abiotic, practices and management methods). At the moment, it does not address larger scales, for example populations or species interactions within ecosystems.

Axis 1: Understand

© kjpargeter, CS - Freepik

Understanding biological processes, their regulation and how these processes interact or cooperate.

This axis concerns all levels of organisation of living organisms: from the molecule to the organism and the population.

The aim is to **describe, understand and model biological systems**, to establish links within and between biological scales, by integrating systemic effects, such as stochastic or feedback, as determinants of the dynamics and evolution of the system.

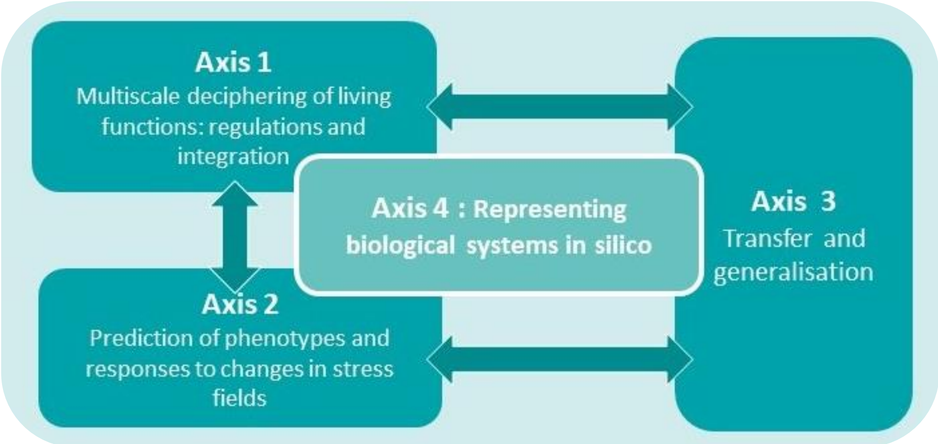
Axis 2: Predict

© INRAE

Predicting phenotypes *from the cell to the individual and the population,* ***their functionalities*** *and* ***responses to changes in stress fields*** *(biotic and abiotic environment, management methods, practices).*

One of the challenges of digital biology is to develop, compare and improve learning methods, adapting them to integrate multi-source data (omics, sensors, environment, data from participatory approaches). The modelling of biological and physiological processes to develop predictive approaches and the simulation of complex biological systems are also major challenges. In particular, the robustness of the models built in axis 1 must be tested by subjecting them to fluctuating conditions (internal or external).

Biological systems
from the cell to the individual and the population in their environment(s)



Axis 3: Transfer

© rawpixel.com - Freepik

Generalise and transfer the results and knowledge acquired towards scales, organisms, species or systems*, that have been less studied or only partially observed.*

This axis also aims to **develop more robust comparative approaches** that better evaluate the generic scope of the data.

Axis 4: Toward the digital twin?

Digital biology offers the possibility of experimenting and monitoring biological systems in silico, based on their computer representations and their regular updates from data collected in real time.

The concept of "**digital twin**", a true *in silico* copy of its real counterpart, is a promising tool for monitoring and steering systems, which the metaprogramme aims to explore.

Metaprogramme
DIGIT-BIO

Contact : digitbio@inrae.fr

www.inrae.fr/digitbio/