iMEAN

DIGITAL BIOFOUNDRY

PRODUCTS & SERVICES

2026

ABOUT US

Since 2018, iMEAN has pioneered modelling of living organisms and biological systems, turning complex biology into quantitative insight for faster R&D decision-making in biotech.

By turning complex biological data into high-quality in silico models and predictive tools, we help our clients cut the number of wet-lab experiments, shorten time-to-decision and focus resources on the most promising scenarios first. With deep biomodelling expertise, iMEAN supports the transition toward digital biofoundries that run more efficient, lower-risk development cycles.

WHAT MAKES US UNIQUE

Custom Digital Organisms For Your Biology

Tailor-made in silico models that capture the complexity of your organism and deliver high-confidence predictions for your R&D decisions.

High-quality Models, Delivered Fast by Experts

We combine mechanistic modelling with expert manual curation to turn your data into well-validated models, so your projects move from data to decisions much faster.

Your Digital Partner From Cell To Product

We team up with you and our partners to link strain design, upstream and downstream with digital twins - so you can optimise end-to-end bioprocesses before costly lab work.

46 CLIENTS TRUST US

138 PROJECTS DELIVERED

Leveraging Biological Complexity

for Smart Decision-Making

CONTENT

iMEAN

Looking for a precise solution for your biofoundry

Let's discuss how we can tailor it to your needs

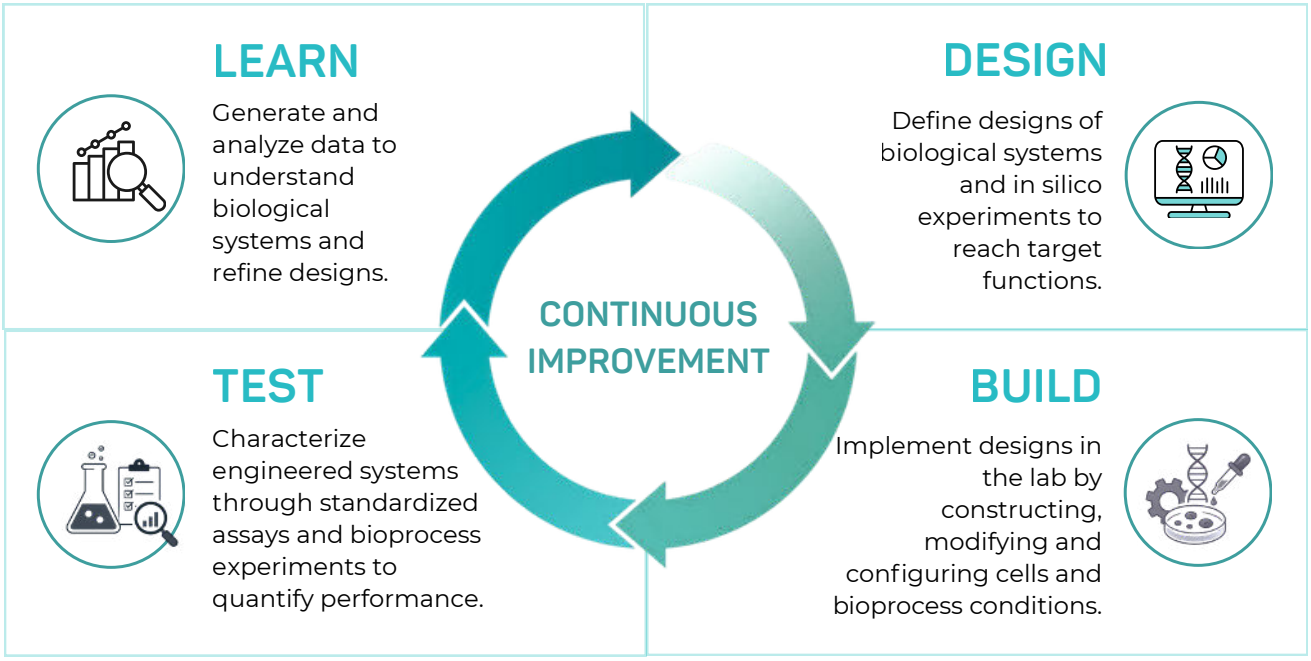
https://imean-biotech.com/

WHAT IS A BIOFOUNDRY ?

A biofoundry is a laboratory infrastructure which provides automation and analytics to support the engineering of biological systems. It is used in the field of biotechnology to accelerate the design and optimisation of industrial processes. Hence, it allows us to build physically new cells, by genetic modifications or evolution experiments, and to quickly test their performance at high-throughput and to iteratively implement **Design–Build–Test–Learn (DBTL) cycles.**

Design-Build-Test-Learn (DBTL) cycles

These DBTL cycles structure how a biofoundry engineers biological systems.



Biofoundry enables

Automated DBTL execution

High-throughput engineering of biological systems

Faster design-to-performance cycles

Typical applications

- Strain engineering
- Pathway optimisation
- Bioprocess development
- Industrial enzyme, biochemical, and bio-based materials production
- Biocatalytic process design and optimisation

4 HIDDEN BOTTLENECKS

What Really Slows Bioprocess Development

In practice, most biofoundries have focused on the **BUILD** and **TEST** phases of DBTL, using automation and high-throughput platforms to accelerate experimentation. However, the **DESIGN** and **LEARN** phases often remain fragmented, with data, models and decisions not fully integrated into a coherent cycle. As a result, even with automated **BUILD** and **TEST** capabilities, strain and bioprocess development still face significant practical bottlenecks.

From data-poor to data-overloaded

Early projects often start with very limited data, making it hard to choose the right strain and process direction. As development progresses, teams quickly move to an overload of heterogeneous data that is difficult to interpret and translate into clear, actionable decisions.

Uncertainty when moving from lab strain to process performance

Strains that perform well in screening assays or simple lab conditions frequently lose performance when tested under more process-like lab settings (e.g. production media, controlled bioreactors). Without reliable predictive tools, teams struggle to anticipate how strains will behave across different media and operating conditions.

Scale-up and tech-transfer risk

Changes in oxygen transfer, mixing, shear and gradients between lab, pilot and production scales can significantly impact titer, yield and quality. Without robust predictive models, scale-up and tech-transfer decisions remain risky and still rely heavily on empirical experience.

Fragmented workflows and siloed expertise

Strain engineers, bioprocess engineers and data scientists typically work in separate tools and speak different “data languages”. This fragmentation makes it hard to build a unified view from strain design to manufacturing-ready processes and to reuse knowledge efficiently across projects and sites.

Addressing these challenges requires mechanistic, model-driven in silico approaches embedded within the DBTL cycle.

With iMEAN, unlock the full potential of your microbial manufacturing.

HOW IMEAN POWERS
THE DIGITAL BIOFOUNDRY

From Biological Data to Integrated Design-Build-Test-Learn Cycle

1 SMART MODELLING PLATFORM

Full-stack platform including mathematical models and softwares that curate biological data and build mechanistic models across the DBTL cycles.

2 IN SILICO BIOANALYSIS

A comprehensive portfolio of in silico bioanalysis services, from long-term strategic partnerships to targeted projects, translating biological data into concrete strain and smart bioprocess decisions.

> **We offer a comprehensive digital biofoundry for strain and bioprocess development,** combining curated biological knowledge, proprietary modelling algorithms and virtual experimentation to support smarter, faster decisions from strain design to bioprocess optimisation.

3 DIGITAL TWIN SOFTWARE

Virtual replica of your bioprocess that enables in silico experimentation, design-space exploration and scale-up/tech-transfer scenario testing before running costly wet-lab campaigns.

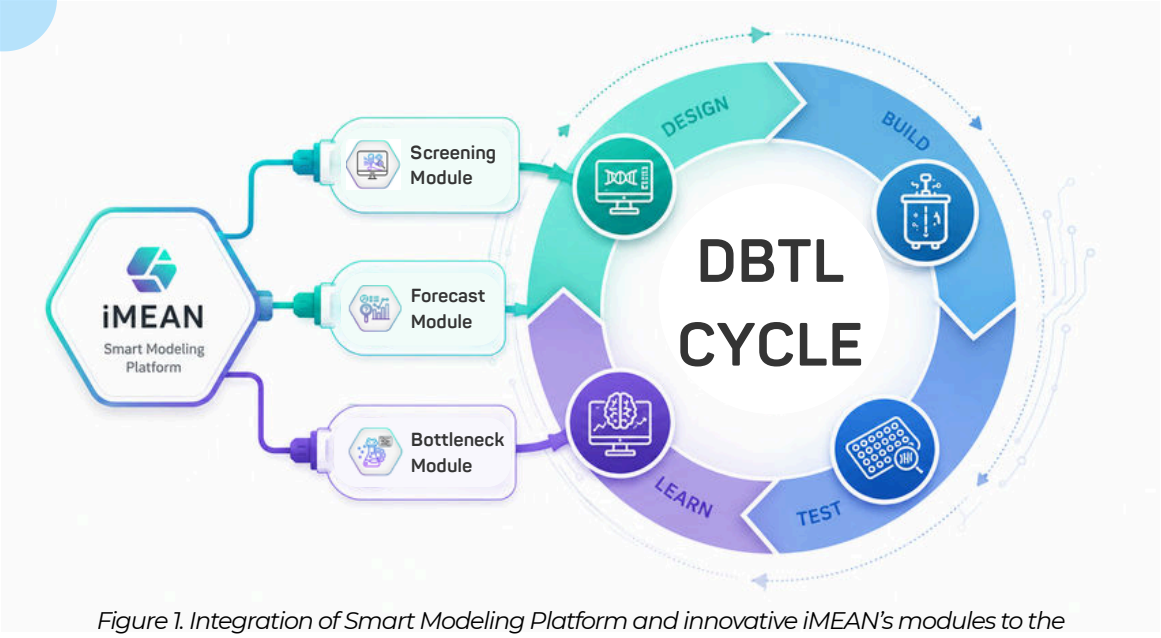


Figure 1. Integration of Smart Modeling Platform and innovative iMEAN's modules to the DESIGN-BUILD-TEST-LEARN cycle run in Biofoundry.

iMEAN

SMART MODELLING PLATFORM

1

We offer a smart modelling platform that brings together mechanistic models, biological data and simulation tools into predictive workflows,

allowing you to plug advanced modelling into existing DBTL cycles without disrupting how your teams work.

SMART

MODELLING PLATFORM

One integrated predictive platform for industrial biotechnology

Our Smart Modeling Platform brings together mechanistic models with intuitive software to support decision-making across the whole biotech lifecycle, from strain design to bioprocess scale-up. The platform is tailored to each project's objectives, adapting to the specific strain genotype and target molecule. Each model can be configured to meet your needs, and multiple models can be seamlessly combined into a unified, interruption-free workflow fully aligned with your DBTL processes.

The platform can be deployed offline, ensuring flexibility, data security, and accessibility in diverse operational settings. However, depending on your experimental facilities, we can setup autonomous control of the biofoundry by our **Digital Twin.**

Key features

Gold standard

We structure data using the best standard and deliver models in SBML, ensuring compatibility across tools, interoperability, long-term maintainability, and seamless integration into your existing modelling infrastructure.

Prediction accuracy

Expert-curated mathematical models developed by a multidisciplinary team of microbiologists, biophysicists, biochemists, and molecular biologists, enabling the integration of diverse biological and physical parameters to accurately capture system and process complexity.

Data & IP protection

Secure workflows and clear IP frameworks so you keep ownership of your data, models, and project outcomes, enabling safe collaboration, compliant knowledge transfer, and sustainable internal reuse of the generated assets.

Who benefits

R&D manager

Strain & bioprocess engineers

Upstream lead

Academic researcher

What you can do

Strain design and optimisation

Target molecule production strategy

Media, feeding and operating-condition optimisation

Fermentation scale-up and robustness assessment

In the following pages, we introduce the core models and software components of the Smart Modeling Platform and illustrate how they can be assembled for your specific industrial biotechnology use cases.

GENOME-SCALE METABOLIC NETWORK MODEL

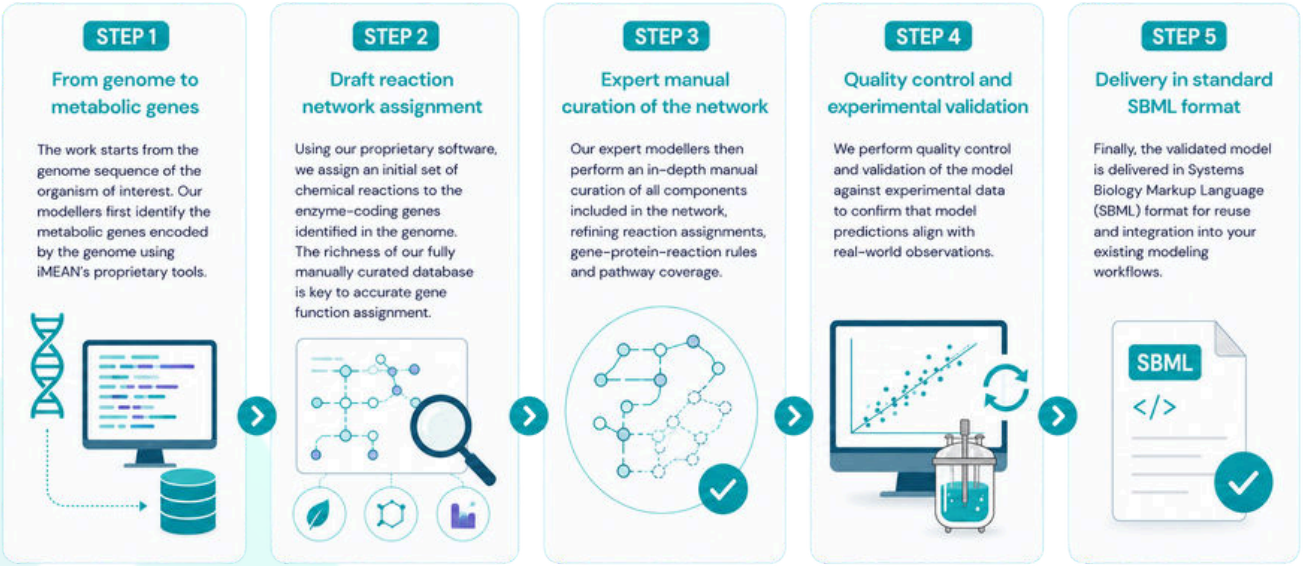
Model description

The Genome-Scale Metabolic Network Model (GEM) is a stoichiometric representation of cellular metabolism that **quantifies the relationships between all metabolic reactions.** This type of model allows to calculate the mass balance, respecting the thermodynamics, between the nutrients consumed by the cell and the cell phenotypes like growth or metabolite production.

These models enable simulations using methods like Flux Balance Analysis to predict metabolic flux distributions and optimise specific cellular objectives such as biomass production, under given process-relevant constraints (e.g. substrate uptake, DO limitation, maintenance energy).

Overview of the model reconstruction

The reconstruction of a genome-scale metabolic network model requires a complex combination of computational and experimental techniques. iMEAN has invested in and developed high-end tools and methodologies to reconstruct these models. **We follow a gold-standard protocol for building high-quality models**, based on the method described by Thiele and Palsson in 2010. We have enhanced this protocol, and our reconstruction process is outlined below:



Why high-quality reconstruction matters ?

Without rigorous reconstruction and curation, model-based predictions about yield, bottlenecks or process changes are simply not trustworthy enough for industrial decisions.

The reconstruction of the metabolic network at genome-scale of a living organism usually encompasses:

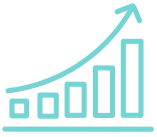
- **Central Metabolism** (energy and carbon distribution)
- **Primary Metabolism** (biomass biosynthesis pathways)
- **Secondary Metabolism** (all metabolic pathways to synthesize other components such as hormones, signals, antibiotics, toxins, etc)

GENOME-SCALE METABOLIC NETWORK MODEL

What problem it solves

Limited visibility on metabolic fluxes

GEMs provide a system-level view of intracellular flux distributions, showing how carbon and reducing equivalents are allocated between biomass production, by-product secretion and target product synthesis under defined culture conditions.



Unclear production burden on cell growth

GEMs quantify how recombinant protein expression or metabolite overproduction perturbs precursor availability, ATP demand, redox balance and growth robustness, providing an estimate of protein production costs on overall cell growth.

Uncertain yield and production limits

Using constraint-based simulations, GEMs estimate realistic and theoretical yield limits under process-relevant constraints, revealing the remaining potential for yield improvement.

Metabolic shifts during scale-up

GEMs can predict how fermentation process alterations (DO, pH, agitation, feeding) redistribute metabolic fluxes, helping you define operating windows that optimise cellular behaviour for productivity.

What Makes iMEAN's GEM Models Unique?

High-quality, manually curated reconstructions by experts

Every model is built and refined by experienced modelers, ensuring biological accuracy, consistency and reliability.

A curated knowledge base

Built on a rich, manually curated reaction and annotation database, continuously updated and quality-controlled.

Extended modelling of secretion and macromolecule production

We go beyond core metabolism to accurately represent macromolecule production and secretion network modules, such as proteins and exopolysaccharides, which are critical for real-world bioprocesses.

Most current GEMs are mainly built around central and primary metabolism, with secretion and macromolecule production often represented only by simplified or lumped reactions. This limits their ability to quantify production burden and product-associated fluxes under realistic bioprocess conditions.

Building on this foundation, **iMEAN has developed a dedicated macromolecule production and secretion network module** that is tightly integrated with the core metabolic network and leverages both a rich, manually curated reaction and annotation database and a systematic, expert-driven curation workflow. As a result, iMEAN's models more accurately capture the metabolic cost of producing and secreting target molecules and support a more reliable assessment of trade-offs between growth, robustness, and productivity, enabling your team to make better-informed strain design and upstream process optimisation decisions.

GENOME-SCALE METABOLIC NETWORK (GEM)

Flexible modelling depth. Built to match your goals.

From rapid exploratory models to genome-scale reconstructions built for industrial relevance, we are delivering **three levels of curation quality** to adapt your project needs, organism complexity and decision-making stage.

EXPLORATORY
Fast insights

DISCOVERY
Targeted understanding

INDUSTRIAL
Decision-ready performance

Level 1

MINIMAL CURATION

A minimal model focusing on essential curation for simulation. Ideal for rapid microbiome analysis, providing insights into microbiota organisation and interactions.

Level 2

STANDARD CURATION

Curated coverage of central metabolism, biomass composition, and three pathways of interest.

Level 3

HIGH-QUALITY CURATION

Entire genome associated with metabolism, expert-driven curation including central, primary and secondary metabolism, plus secreted macromolecules for industrial applications

Delivery Timeline and Pricing

PRODUCT	QUALITY	DELIVERY TIME	PRICE
Genome Scale Metabolic Network	Minimal	0 to 1 week	2 000 €
	Standard	0 to 1 month	5 000 €
	High-quality	0 to 6 month	5 000 € to 50 000 €
GEMs package: 1 microbiota community (>25 organisms)	Minimal	0 to 6 month	50 000 €

Data requirements

Mandatory for model reconstruction

Annotated genome of the organism of interest from one of these resources:

- Proprietary sequencing data
- Public database (NCBI GenBank,...)
- Publications

Recommended for higher predictive performance

At least one dataset of culture/fermentation with mesured phenotypes

Final pricing and delivery timelines depend on organism complexity, data availability and project objectives.
Contact us for a tailored proposal.

GENOME-SCALE METABOLIC NETWORK MODEL

Reconstructed models across key organism classes

iMEAN's Gaïa Database is a **constantly expanding** library of high- and standard-quality GEMs, curated by experts and built for industrial relevance. It currently contains **91 high-quality and 700 standard-quality organism models.**

Our digital organism library spans eukaryotic and prokaryotic microbes, mammalian and plant cells, as well as natural and engineered organisms – we model whatever matters to your process.

TYPE OF ORGANISM	ORGANISM	QUALITY	PRICE
Bacteria	• *Bacillus subtilis* 168	High-quality	5 000 €
	• *Echerichia coli k12*	High-quality	5 000 €
	• *Lactococcus lactis*	Standard	5 000 €
Algae	• *Chlamydomonas reinhardtii*	Standard	5 000 €
Probiotics	• *Lactobacillus acidophilus*	High-quality	30 000 €
	• *Limosilactobacillus reuteri*	Standard	5 000 €
	• *Sporolactobacillus putidus*	Standard	5 000 €
Yeasts	• *Pichia pastoris*	High-quality	5 000 €
	• *Saccharomyces cerevisiae*	High-quality	5 000 €
	• *Yarrowia lipolytica*	High-quality	5 000 €
Filamentous fungi	• *Aspergillus niger*	High-quality	10 000 €

Full organism list available on request

Additional species can be reconstructed on demand to meet your specific project needs.

REGULATORY NETWORK MODEL

Model description

A Regulatory Network Model describes the molecular components and their interactions in signalling cascades that regulate cell behaviour. This model integrates the reprogramming of gene expression, following the sequence of molecular events from signal transduction through gene transcription and translation. This type of model helps simulate and analyse the intricate regulatory processes that govern gene expression in response to environmental stimuli (e.g. stress signals, cell-cycle regulatory networks).

Key features include the ability to incorporate environmental signals such as temperature, pH, quorum sensing, nutrient availability and to simulate how these factors trigger changes in gene expression. The model also captures the detailed activation of regulatory proteins and transcription factors, reflecting molecular events such as phosphorylation and protein degradation.

What problem it solves

Condition-dependent cellular responses

Explains why the same organism can exhibit different phenotypes under different environmental or process conditions, by capturing the regulatory mechanisms that drive context-specific gene expression responses.

Regulatory bottlenecks and control points

Identifies key transcription factors, regulatory proteins and signaling nodes that constrain or control cellular behaviour, including stress response pathways, helping prioritise intervention points for strain engineering or functional analysis.

Process and design decision support

Predicts how regulatory networks will respond to different stimuli and offers systems-level analysis to understand the interplay between multiple regulatory pathways, providing insights into the organism's overall regulatory architecture.

Delivery Timeline and Pricing

Delivery Timeline : From 0 to 2 months

Price: From 5 000 € to 20 000 €

Why metabolism alone could not be enough ?

Metabolic capacity alone is not always sufficient to predict cellular behavior. A cell may possess the metabolic potential to perform a function, yet fail to activate the necessary genes under specific conditions. In such cases, regulatory network models help address a key limitation of GEMs by capturing gene expression control and condition-dependent response.

Data requirements

Mandatory for model reconstruction

Annotated genome of the organism of interest of one of these resources:

- Proprietary sequencing data
- Public database (NCBI GenBank,...)
- Publications

Recommended for higher predictive performance

At least one gene expression data sets in a specific condition

KINETIC MODELS

Model description

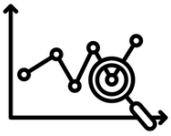
Kinetic Models are mathematical descriptions of biochemical reaction networks that use reaction rate laws and kinetic parameters to predict how metabolites, proteins and other intracellular states change over time under different genetic or process conditions.

By explicitly capturing enzyme capacity, saturation and regulation, they provide a dynamic view of pathway and protein-production behaviour, enabling the identification of rate-limiting steps and quantitative assessment of the impact of genetic edits or process changes on strain performance and process robustness.

Why stoichiometric models may not be enough ?

Static models are valuable for analysing network structure and steady-state behaviour, but they do not capture time-dependent responses, transient dynamics or rate-limiting kinetic effects across metabolic pathways and protein production machinery. This motivates the use of kinetic models when dynamic behaviour and quantitative prediction of pathway performance, from precursor supply to protein synthesis and secretion, are required.

Unlock Valuable Insights with Kinetic Models



Predict time-resolved metabolic and protein-production responses

Identify bottlenecks and rate-limiting steps with precision

Forecast pathway and protein-production performance in silico before experimental validation

Tailor-made Kinetic Modules for Your R&D Projects

Our Smart Modeling Platform is designed with a modular architecture, allowing each model to be built and adapted to your biological question, specific problem and available data.

Depending on your needs, we can develop dedicated kinetic modules to explore metabolic pathways, protein translation and secretion machinery, biomass formation, regulatory, and other process-specific mechanisms. **The next pages highlight specific kinetic modules in practice.**

Build your own kinetic model

Work with us to design a customized module tailored to your project scope and data availability.

https://imean-biotech.com/

KINETIC MODELS

Kinetic modules

Kinetics Model of Metabolic Pathway

Kinetic Model of Metabolic Pathway unlock capacity to predict rates of production of metabolites, *in vivo* enzymology, or even enzyme inhibition mechanisms.

This model integrates kinetics enzyme parameters such as Km, Kcat, Ki, optimum pH, and temperature as well as well as the enzyme concentration inside the cell. It can accurately predict metabolic fluxes and metabolites concentration in the cell or subcompartments.

What this model reveals:

- bottlenecks in the metabolic pathway like limiting substrate or enzyme in a metabolic pathway
- key parameters controlling performances of the pathway, like Kcat of pathway
- potential competition between pathways and enzymatic inhibition

Delivery Timeline and Pricing

Delivery Timeline : From 0 to 3 weeks

Price: From 4 000 € to 10 000 €

Data requirements

Mandatory to build the model

- Minimal information if proprietary enzymes are involved

Recommended for higher predictive performance

- Kinetics properties of proprietary enzyme
- One data set of culture/fermentation with quantification of metabolites of interest

What problem it solves

Unpredictable pathway performance

Identifying bottlenecks helps explain why metabolic pathways fail to reach expected yields or drift toward suboptimal pathway routes, by analysing enzyme kinetics to reveal rate-limiting reactions, limiting substrates, and critical enzyme activities

Uncertain metabolic phenotypes

Predicts how pathway fluxes and metabolite pools will repond to gene edits or changes in process conditions, improving phenotype prediction beyond stoichiometric models alone.

Overflow metabolism

Forecasts overflow and by-product formation under different feeding or process conditions, so you can anticipate when flux will leak into undesired branches and adjust the process before performance drops.

KINETIC MODELS

Kinetic modules

Kinetic Models of Translation and Secretion Machinery for Protein Production

Kinetic Models of Translation Machinery for Protein Production unlock capacity to predict rate of production of general protein or for a specific protein of interest.

This model includes gene sequence structures, RNA transcription and protein translation rates, and secretion machinery parameters predicting the functioning of ribosome, protein maturation, secretion system, codon usage,... It allows you to determine the concentration of the protein in the cell or in the supernatant.

What this model reveals:

- Bottlenecks in the protein production like codon usage, gene expression, or ribosome availability
- Key parameters controlling performances of the pathway, like mRNA concentration of the protein of interest
- Potential competition between general cellular needs and the resources required for its production

Delivery Timeline and Pricing

Delivery Timeline : From 0 to 3 weeks

Price: 8 000 €

Data requirements

Mandatory to build the model

- Sequence of the gene of the specific protein of interest

Recommended for higher predictive performance

- Quantitative proteomics or transcriptomics data
- One data set of culture/fermentation with measurement of the protein of interest quantity

What problem it solves

Low and unstable protein titers

Identifies bottlenecks in translation and secretion, such as codon usage, mRNA levels, ribosome availability or secretion capacity, that cap protein productivity and cause batch-to-batch variability.

Imbalanced production vs. cell fitness

Helps identify production conditions where high protein expression imposes excessive metabolic burden on the production host cell, compromising growth, viability or secretion quality, and predicts balanced operating windows.

Trial-and-error strain and process optimisation

Moves from static, trial-and-error optimisation to mechanistic, dynamic predictions of pathway and protein-production behavior under different genetic and process scenarios.

CELLULAR RESOURCE ALLOCATION MODELS

Model description

Cellular Resource Allocation Models (Burden module) are mechanistic extensions of GEMs that incorporate enzyme catalytic properties and constraints on enzyme expression capacity, improving quantitative predictions such as feasible growth rates and substrate uptake rates.

Metabolic burden is particularly pronounced when cells are engineered to produce heterologous proteins or strongly overexpress pathway enzymes, diverting limited cellular resources away from growth and native functions. Hence, Burden module is very helpful to de-risk bioprocess scale-up by addressing the bottleneck observed at this stage.

What problem it solves

Hidden cost of heterologous expression

Engineered strains often lose growth and productivity because the resource cost of expressing non-native pathways and recombinant proteins is not quantified.

Unpredictable impact on growth and productivity

Without explicit resource constraints, additional expression can overload cells in ways that are only discovered late in development or at scale-up.

No integrated view of metabolism and resources

Classical GEMs miss proteome and expression limits, making it hard to optimize metabolism and burden together.

Delivery Timeline and Pricing

Delivery Timeline : From 1 to 2 months

Price: From 8 000 € to 10 000 €

Data requirements

Mandatory to build the model

- Genome-Scale Metabolic Network Model

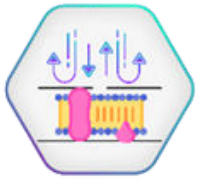
Recommended for higher predictive performance

- Kinetics properties of enzymes (Kcat, Km, Keq, quantity of protein)
- Quantitative proteomics data sets
- One data set of culture/fermentation

Why Burden module matters ?

Cells have limited space. This fundamental constraint in biological systems has a strong impact on cellular capacity and physiology. The Burden module explicitly accounts for this limitation. Understanding and managing burden metabolism is crucial for optimizing organism performance, especially in engineered strains.

CELLULAR MEMBRANE BIOPHYSICAL MODELS



Model description

Cellular Membrane Biophysical Models describe key biophysical properties of biological membranes, such as membrane shape and the diffusion of molecules across it. It integrates underlying physical phenomena, including mechanical properties, to describe how cells generate forces and maintain their structural integrity. It also captures passive and active transport processes through the spatial organisation and compartmentalisation of the cell.

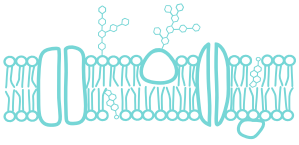
What this model reveals:

- Active and passive diffusion of small molecules across the cellular membrane, as well as their accumulation within the membrane.
- Small-molecule concentrations inside cellular compartments.
- Membrane integrity and shape as a function of membrane composition, such as lipid types and content.

What problem it solves

Unpredictable small-molecule transport across membranes

Makes it possible to quantitatively predict how small molecules cross and accumulate in cellular membranes and compartments, instead of relying only on empirical permeability measurements.



How composition affects membrane robustness is unclear

Reveals how changes in lipid types and composition impact membrane integrity, mechanics and shape, helping explain loss of robustness under stress or formulation changes.

Lack of mechanistic insight into membrane-generated forces

By explicitly representing membrane mechanics, curvature and tension, the model explains how cells generate and sustain forces at their membranes, which cannot be captured by purely phenomenological descriptions.

Delivery Timeline and Pricing

Delivery Timeline: From 1 to 2 months

Price: around 8 000 €

Data requirements

Mandatory to build the model

- In case of small molecules diffusion through the membrane, the structure of the molecule has to be known to predict its chemical properties

Recommended for higher predictive performance

- Quantitative measurement of the cell membrane composition such as lipid types

Why Cellular Membrane Biophysical Models matter ?

Cell membranes control which molecules can enter, leave or accumulate inside cells, and their composition strongly affects integrity under process conditions. Cellular membrane biophysical models make these effects quantifiable, enabling more reliable prediction of small-molecule transport and membrane robustness across conditions.

SEE HOW FAR
YOUR STRAIN CAN REALLY GO

Multi-layer models that reveal metabolic, regulatory and biophysical limits before you spend months in the lab.

MODEL LAYERS	WHAT IT ADDS	BEST USED WHEN
 Genome-Scale Metabolic Network	Metabolic feasibility and system-level flux analysis to identify what the cell can in principle produce and the trade-offs between growth and productivity.	When you need fast strain or pathway feasibility assessment and high-level metabolic flux distribution analysis.
 Regulatory Network	Captures condition-specific gene regulation, stress response, quorum sensing, cell cycle and conserved regulatory mechanisms	Need to understand phenotype or production changes that strongly depend on regulatory control.
 Kinetic Model	Describes time-dependent behavior and reveals rate-limiting steps and bottlenecks, enabling dynamic optimisation of pathways and processes.	Need dynamic simulation to identify rate-limiting steps and bottlenecks in your strain under different process conditions.
 Cellular Resource Allocation Model	Represents host resource allocation and the burden caused by heterologous pathways, circuits or protein expression competing for resources.	When improving pathway design no longer increases titer, suggesting host burden rather than pathway stoichiometry is the bottleneck.
 Cellular Membrane Biophysical Model	Models transport, permeability, diffusion, accumulation and membrane integrity, capturing how lipid composition shapes membrane behaviour.	Need to understand whether uptake, secretion, accumulation or membrane integrity, influenced by lipid composition, are limiting performance.

YOU DON'T NEED THE FULL STACK FOR EVERY PROJECT

Start at the layer that matches your current bottleneck, and expand as your decisions require deeper biological insight.

MIXED-CULTURE FERMENTATION

Advanced mechanistic model for mixed-culture bioprocess optimisation

Model description

The complexity of interactions within mixed microbial communities makes it difficult to systematically design and optimize mixed-culture processes in industrial biotechnology, so they remain largely empirical and underexploited.

Our Mixed-Culture Fermentation Model has been developed to advance these processes by providing tools to manage and engineer the underlying biological complexity. It simulates complex biological systems by explicitly capturing interactions between multiple organisms within a bioprocess, enabling rational design and optimisation of microbial consortia and opening new opportunities for innovative mixed-culture bioprocesses.

What you get

Quantitative insight into community interactions
Simulate competition, cross-feeding, and functional niche partitioning, linking these mechanisms to process KPIs such as titer, yield, and productivity.

Faster and more focused process development
Narrow the experimental design space, prioritize impactful conditions, and reduce empirical trial-and-error in mixed-culture projects.

Decision support across R&D and operations
Provide a shared, quantitative framework that aligns scientists, engineers, and managers around the same set of simulations, assumptions, and performance projections.

Model architecture

1/ Genome-Scale Metabolic Network Models

This first layer of the model aggregates the genome-scale metabolic models of each microorganism in the system. For mixed cultures with naturally occurring and not fully controlled microbial communities – such as contaminated feedstocks or open fermentation processes – a subset of representative microorganisms can be selected based on their prevalence, abundance, and metabolic functions*. This approach ensures that the primary activities of the biological system are realistically captured.

2/ Interaction Model

This second layer represents the biotic interactions between organisms. It captures the dynamic relationships and signal exchanges between the different microorganisms within the system.

3/ Process Parameters - Ecological Niche

The last layer includes medium (e.g., feedstock characteristics, and nutrient feed) and physical (e.g., temperature, pH, oxygen levels,...) parameters of the bioprocess. These parameters are modelled to establish the constraints applied to the mixed-culture model, ensuring a realistic and accurate representation of the biological system.

Delivery Timeline and Pricing

The prices for the mixed-culture fermentation model depend on the number of GEM organisms, the level of curation quality, and the complexity of the bioprocess. For your reference, a model including **at least 2 micro-organisms** is priced below:

Delivery Timeline: a minimum of 3 months to develop

Price: starts at around 20 000 €

Data requirements

Mandatory to build the model

Annotated genome of the organism of interest of one of these resources:

- Proprietary sequencing data
- Public database (NCBI GenBank,...)
- Publications

Recommended for higher predictive performance

- At least one data set of culture/fermentation where phenotypes are mesured
- A description of the bioprocess parameters and monitoring

**Micro-organism selection to define the minimal mixed culture model would need an additional study, not include in this module.*

IN SILICO BIOANALYSIS

2

We offer a In silico Bioanalysis service that combines iMEAN's modelling, simulation and bioinformatics expertise into adaptive DBTL support, giving you flexible, end-to-end bioreactor bundles, from early feasibility to full process characterization so your team can move faster without expanding internal infrastructure.

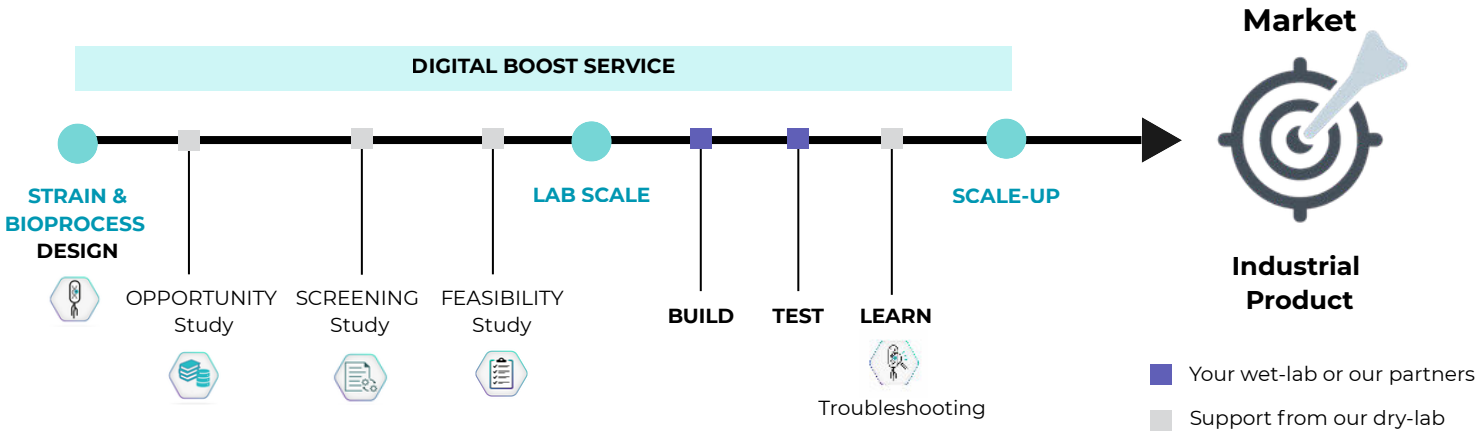
IN SILICO BIOANALYSIS

From Design to Learn: powering your entire DBTL cycle with in-silico insight

Many biotechnology teams already have strong scientific and process expertise, but internal resources are often stretched across multiple priorities. As a result, there is limited time to structure data, build modelling workflows or fully exploit advanced digital tools in day-to-day projects. In other cases, teams may not have in-house expertise in computational modelling or in the effective use of specialised software, making it difficult to know where to start, how to interpret outputs or how to translate model results into actionable decisions.

iMEAN provides a combination of modelling expertise, software and workflow design that plugs directly into your existing biofoundry, R&D and process activities. Instead of asking your teams to become full-time modellers or software specialists, we help them leverage advanced models and digital tools through our **In Silico Bioanalysis service** in a pragmatic, project-driven way.

Our In silico Bioanalysis Supports Your Project at Every Stage



YOUR INPUTS

- OMICS DATA
- BIOPROCESS DATA
- HISTORICAL DATA
- CONSTRAINTS & GOALS

YOUR RESULTS

- OPTIMIZED STRAIN PERFORMANCE
- OPTIMIZED BIOPROCESSES
- HIGHER YIELD & PRODUCTIVITY
- SHORTER TIME TO MARKET

DIGITAL BOOST SERVICE

Continuous Support for Your Bioprocess Optimisation

Accelerate and empower your innovation, research, and development bioprocesses with **iMEAN's Digital Boost service.** This service is designed to provide continuous support throughout the Design, Build, Test, and Learn phases, enabling you to continuously **LEARN** from your data, **DESIGN** the most efficient experiments, and improve your bioprocess.

What you get

YEAR-LONG SUPPORT

Continuous digital guidance throughout your DBTL cycle, so your teams are never alone when making critical design and process decisions.

COST & RISK REDUCTION

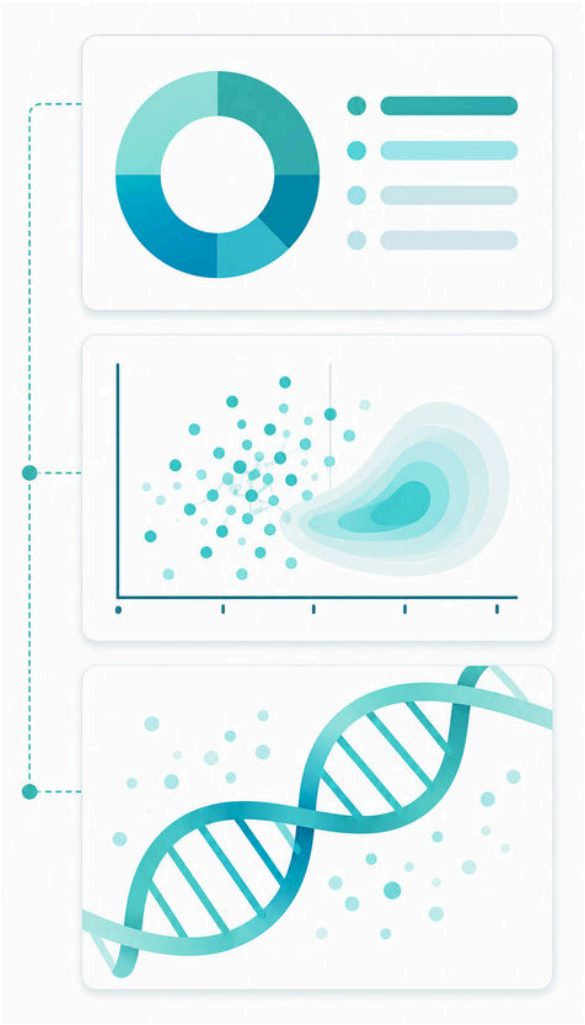
Reduce R&D expenses and failure rates by focusing experiments on the most promising designs and operating conditions identified in silico.

BOTTLENECK RESOLUTION

Identify key biological and process bottlenecks, explore targeted solutions, and minimize experimental bias in how you test them.

INSIGHTFUL INTERPRETATION

Turn complex, noisy experimental data into clear, actionable insights, avoiding unnecessary experiments and wasted resources.



BEFORE GETTING STARTED

Before deploying our **Digital Boost service**, it is essential to set up the **Smart Modeling Platform**, encompassing models of both the organism and its process environment. Once this is in place, the Digital Boost service comes into action by continuously integrating your results throughout the R&D process, as presented in the following pages.

***Your modelling platform is continuously updated:** Data and knowledge generated from each TEST and LEARN phase will be integrated into the models, which are refined over time rather than remaining a one-off snapshot.*

DESIGN PHASE

The DESIGN phase focuses on defining new cells or processes to be tested and on planning the experiments that will probe them. It delivers clear specifications for the BUILD and TEST phases while addressing critical points and bottlenecks by exploring innovative solutions. By combining biological insight with advanced technical tools, this phase reframes the scientific roadmap, bioprocess strategy, and experimental plans so R&D teams can aim higher and deliver breakthroughs in efficiency and optimisation. iMEAN further empowers this phase with its **Forecast and Screening modules.**

Process and Strain Design

Designing high-performing strains and robust processes is challenging because every genetic change can propagate through complex metabolic networks and behave differently under industrial conditions. Without an integrated view, it is difficult to anticipate trade-offs, de-risk scale-up and systematically reach the targeted yield, productivity and robustness.

The iMEAN Digital Boost service enables:

- In-silico screening of candidate solutions (enzymes, pathways, organisms)
- Genetic modifications (codon optimisation, Knock-Out, Knock-IN, expression tuning)
- Bioprocess optimisation (batch, fed-batch, continuous modes)

What you get:

- Faster convergence towards higher yield and operational success
- Better alignment between strain engineering and process development, maximising the impact of both
- **Stronger IP potential** by enabling rational design of novel pathways, chassis configurations and process strategies

Design of Experiment (DoE)

Experimental phases are often expensive and time-consuming, with too many conditions to test and limited capacity to explore the design space systematically. This can lead to under-optimised protocols, inconclusive results and missed productivity gains.

The iMEAN Digital Boost service enables:

- Expert consulting on experiment design
- In-silico predictions of expected outcomes (e.g., productivity increases)
- Development of optimized experimental protocols targeting your performance parameters

What you get:

- Fewer, more informative experiments, reducing wet-lab workload and costs
- Higher probability of reaching targeted performance (e.g. productivity, yield, robustness)
- More robust protocols with reduced experimental bias and better use of existing data

DNA Sequence and Protein Engineering

**These modules can be conducted as an option.*

Fine-tuning gene expression and protein properties is often handled late in the project, through trial-and-error mutagenesis, leading to long optimisation cycles and uncertain impact on process performance.

The iMEAN Digital Boost service enables:

- **DNA Sequence Engineering**: in-depth design and optimisation of DNA sequences (coding and regulatory regions) to fine-tune gene expression, including promoter/RBS selection, codon optimisation, vector construction, and regulatory element engineering.
- **Protein Engineering**: in-depth exploration and design of protein sequences and structures to optimize key properties such as substrate specificity and affinity, active and binding sites, catalytic efficiency, secretion and folding pathways, and thermal and formulation stability.

What you get:

- Shorter cycles to reach target activity and robustness at enzyme or protein level
- Better alignment between molecular design and process requirements, increasing the chances of success in downstream development
- **Stronger IP potential**

DESIGN PHASE

Forecast Module

Scaling a strain and process from lab to industrial conditions is risky because real performance limits, bottlenecks and constraints are often unknown. Teams lack reliable forecasts of productivity, yield, robustness and feasibility at scale, making it hard to prioritise investments and design a realistic R&D roadmap.

The iMEAN Digital Boost service enables:

- Predictive modelling of synthetic or natural organism behaviour under industrial conditions
- Estimation of theoretical performance ceilings (productivity, titer, yield, robustness)
- In-depth bottleneck analysis at industrial scale, including expected bottlenecks, process constraints and scale-up challenges
- Continuous updates of predictions as new data are collected throughout the project

What you get:

- De-risked scale-up and tech-transfer decisions
- Clear performance targets and benchmarks to steer optimisation efforts and investment choices
- Faster time to industrial readiness by focusing R&D on the most impactful levers and eliminating critical bottlenecks earlier

In Silico Screening Module

R&D teams often face huge design spaces: too many enzymes, pathways, feedstocks or chassis combinations to test experimentally. Without a way to virtually explore these options, resources are spread thin across low-value experiments and promising candidates are easily missed.

iMEAN In-Silico Screening module includes:

- **Molecular Docking:** in-silico ligand-based screening platform that enables the selection of candidate molecules based on their binding interaction capabilities.
- **Enzymatic Screening:** exploring native enzyme diversity within a family and leveraging enzyme promiscuity to identify optimal biocatalysts for a target reaction, under realistic bioprocess constraints.
- **Metabolic Pathways Screening:** exploring metabolic pathway diversity to identify the most suitable routes for endowing a host with new metabolic capabilities, while accounting for host specificity.
- **Chassis Screening:** identifies the most suitable host chassis using genome-scale metabolic network models, under realistic bioprocess constraints.

The iMEAN Digital Boost service enables:

- In silico evaluation of large candidate spaces, including combinatorial screening
- In-silico predictions of expected outcomes (e.g., increase and robustness of activity)
- Use of advanced simulation algorithms and high-quality models to predict performance of each candidate under relevant conditions
- Integration of proprietary and public datasets to broaden the search space while staying aligned with your constraints and objectives
- Generation of a prioritised shortlist of top candidates, together with strategic recommendations on what to test in the lab next

What you get:

- Strong reduction in wet-lab screening effort
- Higher probability of identifying high-performing candidates early in the programme
- Shorter time from concept to validated solution

LEARN PHASE

The LEARN phase focuses on extracting maximum value from your experimental data through systematic integration and comprehensive analysis. By refining data interpretation, it clarifies complex biological and biochemical interactions and turns them into actionable insights. iMEAN further enriches this phase with the **Bottlenecks and Troubleshooting Investigation module.**

Data Integration and Optimisation

Experimental and process data are often scattered across instruments, files and teams. Cleaning, matching and merging these datasets for the LEARN phase can be slow, manual and error-prone, delaying insights and making it hard to reuse past results.

The iMEAN Digital Boost service enables:

- Audit of your data workflows
- Design of digital tools (pipelines, interfaces) to accelerate data processing
- Recommendations for workflow improvements

What you get:

- Less time spent on manual data and report preparation.
- Faster, more reliable access to integrated datasets for modelling and decision-making.
- Improved traceability and reusability of project data across teams and cycles.

Bioinformatics Data Treatment

Omics datasets are often large, heterogeneous and generated with different tools and formats. Many teams lack the time or specific bioinformatics expertise to process these data consistently, compare conditions or extract clear, decision-ready insights for strain and process engineering.

The iMEAN Digital Boost service enables:

- End-to-end omics support, including genome assembly and annotation, transcriptomics, metabolomics and mass-spectrometry data analysis
- Comparative and sensitivity analyses on your datasets

What you get:

- Turn complex omics data into a small set of clear, prioritised biological hypotheses.
- Accelerate the LEARN phase by linking omics signals to actionable changes in strain selection.

Bottlenecks and Troubleshooting Investigation

When a strain or process underperforms, teams often see symptoms (low titer, unexpected by-products, instability) but lack a clear, ranked view of the underlying bottlenecks. Root-cause analysis relies on manual interpretation and trial-and-error troubleshooting, which consumes time, materials and budget without guaranteeing that the real blocking points are addressed.

The iMEAN Digital Boost service enables:

- In-silico simulations to detect pathway constraints relevant to the strain and identify factors limiting production of the compound of interest.
- Hierarchical prioritisation of bottlenecks based on their impact on activity and performance.
- Strategic recommendations on resolution paths to unlock and/or enhance strain activity and increase production.

What you get:

- Faster, more systematic identification of the real factors limiting performance (e.g. nutrient deficiencies, limiting metabolic pathways, metabolic burden, variability in experimental setup).
- Reduced trial-and-error in troubleshooting campaigns, saving experiments and capacity.

> *Addressing cellular bottlenecks* ***before they become process failures.***

DIGITAL BOOST SERVICE – PACKAGE FEATURE OVERVIEW

Package Deals for 1 year support	**Essential**	**Premium**	**Ultimate**	**All-in**
LEARN Services	✓	✓	✓	✓
Data Integration	✓	✓	✓	✓
Bottlenecks Identification & Troubleshooting	✓	✓	✓	✓
Experimental Support	✓	✓	✓	✓
Forecast Module	✓	✓	✓	✓
In-Silico Screening	-	✓	✓	✓
DESIGN Services	-	-	✓	✓
Organism Design	(10 000€)	(10 000€)	(10 000€)	✓
DNA Engineering	(10 000€)	(10 000€)	(10 000€)	✓
Protein Engineering	(10 000€)	(10 000 €)	(10 000€)	✓
Price	**25 000€**	**30 000€**	**40 000€**	**60 000€**
Advance High-throughput option	**+ 20 000€**	**+ 20 000€**	**+ 20 000€**	**+ 20 000€**

Explore what a Digital Boost could look like for your process.

Discuss your use case with our experts and design a customised Digital Boost package.
Contact us.

https://imean-biotech.com/

DIGITAL SPRINT SERVICE

One-shot in silico bioanalysis for your specific needs

Besides the Digital Boost service, iMEAN also offers a set of standalone services that help clients move from opportunity identification to feasibility assessment and solution design.

OPPORTUNITY Study

The Opportunity Study supports early-stage project evaluation by assessing the scientific, technical and economic potential of a new R&D programme for producing a molecule or macromolecule. It helps teams make an informed first decision before entering deeper feasibility or design work.

What it includes:

- **Background review**: what has already been done on the project
- **Scientific review:** state-of-the-art knowledge supporting the project's feasibility
- **Roadmap drafting:** key steps required to reach industrial production

What you get:

- Faster and more objective assessment of project potential at ideation stage
- Earlier visibility on scientific, IP and economic risk factors for the project
- Clearer prioritisation and roadmap for industrial development

Delivery Timeline and Price: 1 month for 8 000€

Deliverables: completed study report

Optional analyses:

- **IP landscape:** we perform an in-depth screening of the patent space to identify potential overlaps and patents closely related to your project. This analysis helps quantify IP density and assess the strength of the technological barrier around your innovations. However, it does not replace a formal prior art study conducted by an IP jurist or lawyer.
- **Cost metrics:** we perform a market study to collect information on the actual cost of the target molecule or macromolecule, when available. We also assess feedstock costs and provide a first estimate of the expected economic performance.
- **Expense and timeline estimation study:** we provide a preliminary assessment of the required expenses (scientific and technological resources, specific skills, and time commitments) to support better planning and resource allocation.

FEASIBILITY Study

The Feasibility Study explores the space of possibilities for developing a new bioprocess or biobased molecule by assessing its scientific, technological and industrial feasibility. By stress-testing the project under industrial scenarios, it helps anticipate performance, quantify key constraints and shape a realistic R&D strategy before major resources are committed.

What it includes:

- **Bibliography review:** a comprehensive review of the state-of-the-art, including recent advances, similar technologies and existing solutions
- **Forecast:** preliminary simulation of your future bioprocess to investigate different scenarios and crash-test your project idea
- **Bottleneck identification:** using bibliographic data, preliminary simulation results, and our expertise, we identify key bottlenecks that may hinder progress, slow production, or increase costs.
- **Troubleshooting and debottlenecking strategies:** once bottlenecks are identified, we design and test solutions to remove them, addressing potential hurdles early to minimize downtime and improve project efficiency.

What you get:

- A clearer view of the project's potential performance, critical barriers and possible setbacks under industrial conditions
- Early visibility on investment-related implications, including CAPEX, OPEX, timelines and resource requirements
- A de-risked R&D roadmap with realistic benchmarks, targeted troubleshooting priorities and stronger decision-making before development scale-up

Delivery Timeline and Price: 2 months for 15 000€

Deliverables: a complete analysis report with recommendations and a productivity optimisation roadmap, enabling you to allocate resources strategically and make informed decisions.

DESIGN Study

The Design Study delivers in-silico bioprocess conception with a **focus on both genetic strain engineering and process engineering**, providing a ranked **Top 100 solutions** with key performance metrics to select the most promising options for industrial compliance. It accounts for product- and facility-specific constraints to design options that overcome bottlenecks, troubleshoot issues and strengthen robustness and reliability.

Our approach targets various metabolic and genetic components, including codon optimisation, gene deletion, gene integration or modification, genetic expression systems and strategies (inducible or constitutive promoters, etc.), host strain, feedstock, and bioproduction modes, alongside process strategies and monitoring, to enhance efficiency and productivity. Our screening algorithms can also be used to further improve the performance of our designs.

Key areas of focus:

- Improving natural pathway or designing new to nature metabolic pathways
- Metabolic Pathway Regulation
- Directing and Redirecting Metabolic Flux to achieve targeted performance
- Chassi primary metabolism optimisation
- Process Improvement and Reshaping, such as transitioning between Batch, Fed-Batch, and Continuous fermentation, solid state fermentation, etc

The Design Study enables:

- In-silico exploration of metabolic and genetic design options, including codon optimisation, gene deletion, gene integration and genetic expression systems/strategies (induction, constitutive, promoter, etc.)
- Joint optimisation of cell host, feedstock and bioprocess modes (Batch, Fed-Batch, Continuous, solid-state fermentation, etc.) to enhance efficiency and productivity
- Use of in-silico screening algorithms to score and rank design scenarios
- Definition of a Design Study roadmap aligned with Feasibility Study outcomes and industrial performance objectives
- Optional historical data analysis

What you get:

Faster convergence towards robust strain and process designs

Stronger industrial relevance, robustness and productivity potential

Clearer R&D decisions through quantitative metrics

Delivery Timeline and Price: 2 months, starting from 20 000 € (optional historical data analysis available from 10 000 €).

Deliverables: a complete report detailling the simulation results and the final optimised design, along with strategic recommendations.

SIMULATION AND PREDICTION STRATEGIES

for Molecules & Macromolecules

iMEAN

	Ask yourself	Are you assessing ideas or identifying opportunities?	Are you evaluating option's potential to identify best solution available in biodiversity?	Do you have a concept and need to validate its feasibility (technically and economically) ?	Are you focused on detailed design, optimization or implantation strategies ?
	Stage of idea/project	Exploration stage (uncertain concept)	Benchmark stage	Evaluation stage focused on 1 option	Advanced stage (ready for industrialisation)
		Opportunity study	**Screening study**	**Feasibility study**	**Design study**
Molecule(s)	Bibliography Review & Current state of knowledge	✓	-	✓	✓
	Several similar molecules	-	(Opt) -5k€ +1week	(Opt) -5k€ +1week	(Opt) -10k€ +2weeks
Pathway(s)	Pathway screening (biodiversity)	-	✓	(Opt) +5k€/pathway +1week	✓
	New to nature pathway design (genetics eng.)	-	-	-	✓ IP
Chassis & Process	Chassis screening (biodiversity)	-	✓	(Opt) +5k€/chassi +1week	(Opt) +15k€ +1month
	Process screening	-	-	(Opt) +2k€/process +1week	(Opt) +5k€ +1week
	Substrate screening	-	-	(Opt) +2k€/matrix +1week	(Opt) +5k€ +1week
	Chassis & process optimisation (genetics eng.)	-	-	-	✓ IP
Metrics for industrialisation - Need model(s) -	FORECAST performance	-	-	✓	✓
	BOTTLENECK Identification	-	-	✓	✓
Economic data publicly available	IP landscape	(Opt) +4k€ +1week	(Opt) +4k€ +1week	(Opt) +4k€ +1week	✓
	Cost metrics	(Opt) +5k€ +1week	(Opt) +5k€ +1week	(Opt) +5k€ +1week	(Opt) +5k€ +1week
	Fee & Duration	**8k€, 1 month**	**10k€, 1 month**	**15k€, 2 months**	**20k€, 2 months (+3x success fees)**

Design Natural Evolution Experiments

Today, laboratory equipment allows biofoundries to run directed evolution experiments. The results can be very impressive, but these campaigns often take months or even a year and leave operators and scientists blind to the underlying genetic trajectories, the time required, and the maximum performance that can realistically be achieved. Moreover, they often lack insight into which genetic modifications have occurred and whether these changes could negatively impact other performance criteria that are critical for developing an optimal bioprocess.

What we do:
We have developed **an algorithm that mimics natural evolution in silico**, which we use to accelerate these experiments by:

- Designing natural evolution experiments (selection pressure, population size, campaign design).
- Predicting experiment duration and expected evolutionary trajectories.
- Anticipating key bottlenecks such as epistatic effects and loss of fitness.

Why it matters:
In natural evolution, microorganisms are constantly exposed to environmental pressures (such as pH, temperature, or toxic compounds) that drive natural selection and the acquisition or loss of traits. These dynamics are particularly relevant for assessing strain robustness and the evolution potential of GMO and non-GMO strains.

Our in-silico algorithm mimics these evolutionary dynamics, allowing you to explore how strains may adapt under process-relevant conditions, anticipate potential loss of fitness, and focus experimental efforts on the most promising evolutionary trajectories.

What you get:

- Theoretical maximal performance expected before and after evolution experiments.
- Prioritised bottlenecks with quantified performance gains for each.
- Gene candidates potentially involved in strain fitness, to guide DNA sequencing during the evolution experiment.
- Number of genetic events, their probability, and expected timing for each evolutionary trajectory.
- The solution space of plausible evolutionary trajectories that may occur during the experiment.
- Estimated time required to run the experiments and to monitor them effectively.

Delivery Timeline and Pricing

Delivery Timeline and Price: to be defined according to the project scope, with a minimum duration of 2 months and fees starting from 20 000 €.

Deliverables: a comprehensive report detailing simulations of evolutionary trajectories and their associated output data, along with strategic recommendations

Data requirements

Mandatory to carry out the evolution study

- High-quality GEM of the micro-organism

Recommended for higher predictive performance

- Some data sets in a specific condition

BIOINFORMATICS SERVICES

iMEAN offers a large range of bioinformatics services, providing high-quality and expertise to help you advance your R&D needs.

Genome Assembly and Annotation

iMEAN has developed an efficient and robust end-to-end pipeline designed to transform your raw DNA sequence data into fully assembled and functionally annotated genomes. Our pipeline is optimized to handle data from various Next-Generation Sequencing (NGS) technologies, including short-read, long-read, and Sanger sequencing.

Our end-to-end workflow covers every step from raw FASTQ to QC report to sequence trimming, filtering and optimized reference-based or de novo assembly, delivering high-quality genomes. We then perform comprehensive structural annotation (gene prediction and feature identification) and functional annotation (pathways, functions and biological roles), providing accurate and biologically relevant genomic models.

Price starts from*:

- 850€ per genome for assembly
- 450€ per genome for structural annotation
- 450€ per genome for functional annotation

**for small projects (1–10 genomes). Volume discounts are available for larger studies.*

Multi-OMICS Analysis & Exploration

Unlock the full potential of your multi-omics (Genomics, Transcriptomics, Proteomics, Metabolomics, fluxomics...) dataset based with our in silico cutting-edge pipeline and know-how to provide to your biological systems models the most holistic complex mechanisms understanding and forecasting capabilities.

Using advanced data science approaches, we are able to explore and analysed any omics data come from extract key information from transcriptomics, proteomics, metabolomics, and fluxomics. Essential for a better understanding of the driving cell behaviour.

Custom pricing available on request.

Transcriptomics analysis

We offer a comprehensive RNA-Seq versatile pipeline set to fit with all transcriptomics analyses. Our RNA-seq data analysis services is designed to address the unique challenges and requirements according to specific needs of your project.

Ours pipeline includes rigorous quality control process, accurate read alignment, quantification of gene and transcript level, differential gene expression, alternative splicing, functional analysis, gene fusion detection and eQTL mapping...

All these transcriptomics analysis could be fully integrated to our digital twin models to strengthen their prediction accuracy high-throughput RNA sequencing using Illumina technology to analyse the transcriptome of your samples. Our service includes the preparation of high-quality RNA libraries, precise sequencing on Illumina platforms, and robust data analysis to quantify gene expression and transcripts.

Price: starts at around 500€

Genome-Wide Association Studies (GWAS) Analysis

Leveraging iMEAN's biostatistical expertise, we identify genes responsible for the determinism of traits of interest. Our experts analyze genetic variation across the genome, examining correlations between alleles at specific loci and observed phenotypic values, giving you a deeper understanding of complex traits

With iMEAN's biostatistical GWAS analysis, we identify genes responsible for the determinism of traits of interest. Our experts analyse the genetic variations across the entire genome and study the correlations between alleles at a specific loci and observed phenotypic values, providing you with a deeper understanding of complex traits.

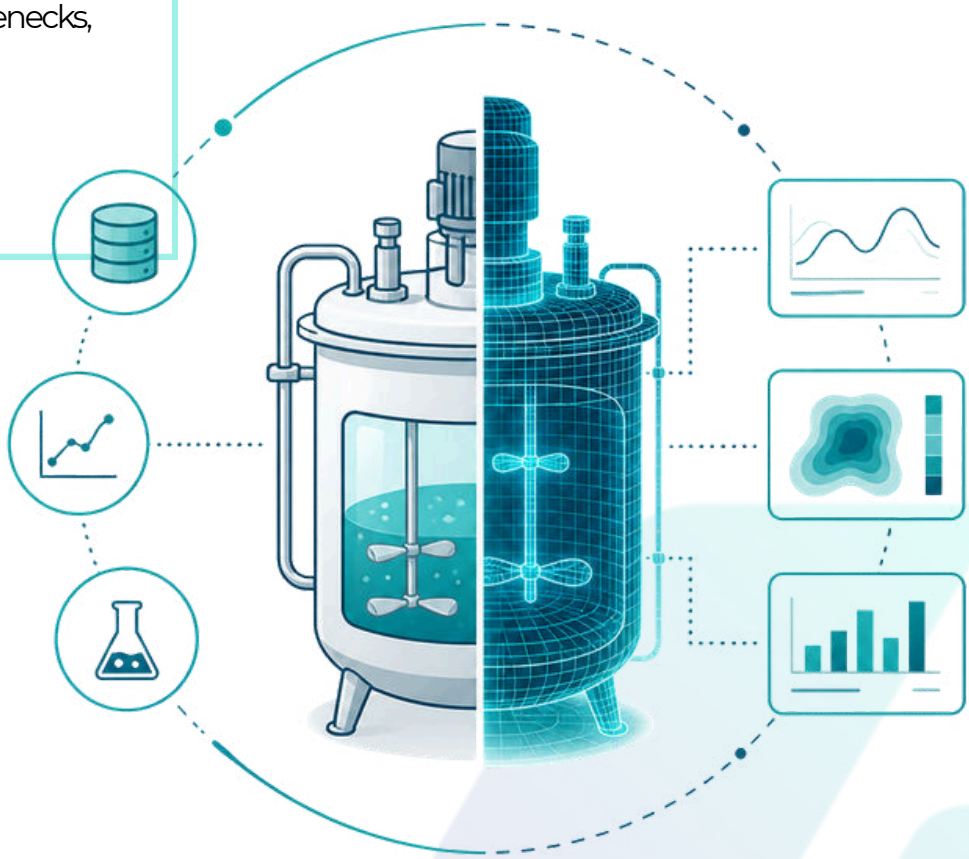
Price: starts at around 1 500€

iMEAN

DIGITAL TWIN SOFTWARE

3

> **We offer a digital twin solution that connects directly to your existing automation workflows,** creating a continuously evolving predictive environment that pinpoints bottlenecks, suggests adaptive next steps and accelerates upstream bioprocess development through real-time, remote bioreactor monitoring.



DIGITAL TWIN

iMEAN

Industrial biotechnology workflows are increasingly complex, while experimental iteration remains time-consuming and costly. In practice, strain, process and scale-up decisions are often made using fragmented data and disconnected models, limiting predictability and slowing development. Digital Twin addresses this gap by connecting data, models, simulation softwares and decision workflows in a single environment to support faster and more reliable optimisation.

Description

Digital Twin provides a virtual representation of a real biological system or process – such as a strain, a bioreactor or an entire fermentation – that is continuously informed by experimental and process data. It combines mechanistic models, data-driven components and integration with lab data to mirror the behaviour of the physical system, confront incoming fermentation data in real time, detect deviations from expected performance, explore "what-if" scenarios and support decision-making across design, development and scale-up.

Digital Twin modules

Digital Twin of Bioreactors

Digital Twin of Strain Construction

Delivery Timeline and Pricing

We have **2 modalities for the software access:**

- **As product**: permanent licence for 10 000 € per module per equipment
- **As services**: one year subscription for 2 500 € per module per equipment

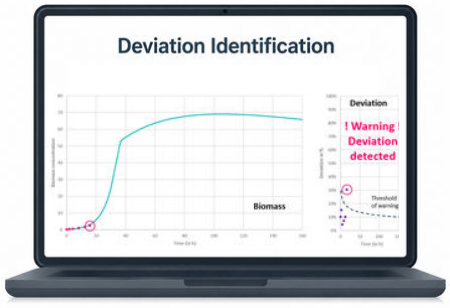
Delivery Timeline: less than 1 week if no software adaptation is needed and all required mathematical models of the organism already exist.

From deviation detection to advanced model-advanced process control

LEVEL 1

Deviation Identification

The Digital Twin simulate the expected output of the experiments (fermentation, strain construction, etc) depending of the experimental setup. The prediction are visualised on graphical interface mimicking expected cultivation process. Then, the online data generated during the experiment will be treated, visualised graphically and then compared to the prediction. Then, simulation will be perfomed to generate hypothesis of mechanisms explaining the deviation. The hypothesis will be ranked based on their likelihood and then displayed to the operators.



Key outputs

- **Highly accurate predictions** about the expected performance
- **Ranked hypotheses** based on their likelihood, explaining the deviation
- **Insightful warning messages** when significant deviations arise

DIGITAL TWIN

From deviation detection to advanced model-based process control

LEVEL 2

Troubleshooting Exploration

With this additional brick, the Digital Twin will be able to launch exploratory analysis to identified the risk in performance due to the observed deviation. Simulations will be performed to predict the new expectation of the final process performance. Then, the Digital Twin will explore thousands of troubleshooting strategies based on the hypothesis behind the deviation. The troubleshooting strategies will be benchmarked and top strategies will be recommended with the expected gain.

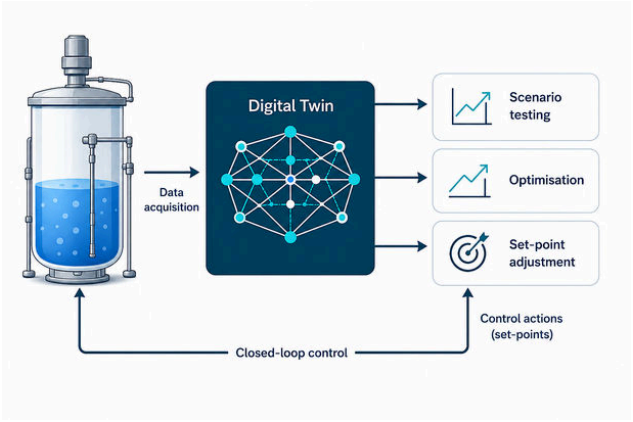
Key outputs

- **Performance loss quantification** and likelihood assessment
- **List of troubleshooting strategies** to help recover performance
- **Performance gain and likelihood** of achieving this performance gain

LEVEL 3

Advanced Control

With this last level, the Digital Twin will be able to control the bioreactor. During deployment, we will adapt the module to the control system of your specific bioreactor. The Digital Twin will launch the troubleshooting strategies by changing the bioreactor parameters and then monitor if the strategy applied lead to the recovery of performance. For labs with high level or robotisation with analytics for instance, the Digital Twin can launch sampling measurement in order to collect the information required for better identification of the source of performance loss.



Key outputs

- **Automatic troubleshooting commands** for robotised equipment
- **Analysis of troubleshooting success** based on process measurements

Customisation to a new equipment

We can adapt the Digital Twin to any new type of equipment and ensure a smooth plug-in to your infrastructure and workflows.

Contact us to discuss your specific setup.

Digital Twin is just one part of a broader iMEAN's software suite for industrial biotechnology.

iMEAN offers your team several options for data and tailor-made software to power your Digital Biofoundry. Our modules cover the full digital pipeline, from data processing and experimental data management to strain library management and the exploration of mathematical models. Within your Digital Biofoundry, the data integration and simulation software is configured as a custom module, adapted to your datasets, workflows, and modelling needs.

Data Storage and Management

Organize and store your data and metadata in optimized formats to maximize their value for future analysis. iMEAN designs databases tailored to your specifications, standardises and harmonises your historical data, ensuring reliable and accurate analysis.

Database contents are built according to agreed specifications and including, in particular:

- **Genomic data for each strain:** whole-genome sequences, gene/protein sequences and annotations, quality control information
- **Metadata for each strain:** unique identifier, taxonomic information, isolation origin, data quality information, bibliographic sources, experimental data, etc.
- **Metabolic models for each strain:** genome-scale metabolic network, model quality information, bibliographic sources, etc.

Database format
Choose one of the following:

- Unstructured "data lake"
- Structured Query Language (SQL)

Documentation: comprehensive user manual included

Price: starts at 10 000 €

Delivery Timeline: from 2 months

Graphical User Interface (GUI) Development

iMEAN offers customized GUI development services tailored to the specific needs of your project.

Key features

Configure the GUI with the modules you need:

- Interface for visualising and exploring your **strain database (Genome Browser, BLAST,...)**
- Interface for analysing and exploring your **experimental data**
- Interface for exploring **mathematical models and simulations**
- **Core data management functions** enabling users to import, query, visualise, explore, edit, delete and download data
- Multi-user access (standard version for up to 5 users)

Additional features can be added upon request.

We also create predictive algorithms and bioinformatics analysis tools, for instance comparative genomics analysis, that can be integrated into the developed GUI.

The interface can be delivered either as a web application or as stand alone software.

Price: starts at 15 000 € per module*
Delivery Timeline: from 3 months*

**to be refined with the specifications*

iMEAN tools to Explore, Simulate, and Optimize your Bioprocesses

Network Explorer Interface (NetExpl)

Network Explorer is a **web-based visualization interface** for your genome-scale metabolic networks. It gives project teams an intuitive way to explore the full content of their models (reactions, genes, metabolites, pathways, ...) while keeping reconstruction and analysis reports directly at hand. This helps scientists quickly understand model structure, trace design decisions, and align on next experimental steps.

Key features

- **An easy-to-use model exploration interface**, allowing you to navigate complex networks without scripting.
- **Your centralized model library**, ensuring consistent access to curated versions across projects.
- **Project workspaces with shared data and deliverables**, supporting collaboration between modelers and experimental teams.

Key outputs

- **For reaction tab,** it provides reaction metadata, the reaction equation, and links to the corresponding pathways.
- **For gene tab,** it provides its nucleotide and protein sequences together with the associated reactions.
- **For metabolites tab,** you can overview its information and all reactions and pathways it is involved in.
- **For pathways tab,** it displays interactive metabolic pathway maps with direct access to the underlying reaction list.

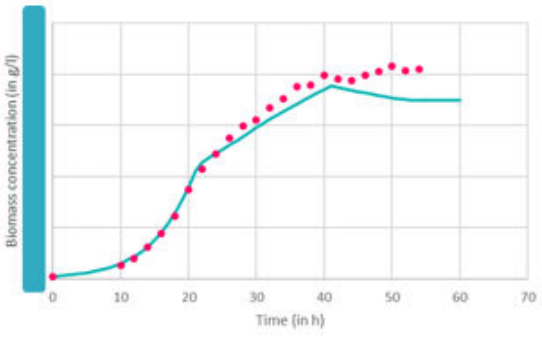
Example of a pathway map as visualized in NETEXPL, showing interactive nodes and reactions for trehalose degradation.

Bioprocess Simulation (DynPop)

To better support our clients, iMEAN provides **DynPop**, a simulation software that extends your model exploration beyond NetExpl into full bioprocess behavior. DynPop takes your strain model and a set of process parameters (medium, volume, feed strategy, inoculation and induction times, etc.) and simulates how the bioprocess will evolve over time.

Key features

- **Generates time-course profiles for key variables such as biomass, volume, metabolites and fluxes,** allowing you to compare multiple in silico scenarios before going to the lab.
- **Generates new parameter files directly from simulation results,** making it easy to capture promising conditions and reuse or refine them in subsequent runs.



MAPE (Mean absolute percentage error) : 11%

Key outputs

An intuitive time-course view of biomass, volume, metabolites, and fluxes, along with model validation against experimental data.

Price: starts at 10 000 €

LICENSE & INTELLECTUAL PROPERTY

Your Questions Answered

What license do I get for iMEAN's digital products?

Clients retain full control of their models when choosing iMEAN. Our perpetual model license ensures that you can continue to use and build on your scientific innovations over time.

What can I do with iMEAN's digital products?

Clients are granted the rights to:

- Use the digital products.
- Reproduce them (unless limited by the Quotation).
- Modify them, except where a no-source-code license applies.

What restrictions apply to my digital product license?

Unless otherwise agreed in the Quotation, Clients may not:

- Publish or make the digital products publicly available.
- Sell, rent, lend, or transfer the digital products or their modified versions to third parties.
- Use the digital products to reverse engineer iMEAN's technologies.

(The possibility to subcontract the license can be negotiated.)

Are the digital products exclusive or confidential?

Exclusive licenses can be granted when digital products are generated from the Client's confidential information.

- **Types of exclusivity**
  - Temporary exclusivity: duration negotiated and specified in the Quotation.
  - Confidential exclusivity: remains in force as long as the Client's confidential data used to generate the digital products remains confidential.
- **Lifting of exclusivity may occur if:**
  - The exclusivity period expires.
  - The digital products enter the public domain without iMEAN's liability.
  - The underlying confidential information loses its confidential status.
- **Exclusivity** can be extended upon request and mutual agreement.

Can I access or modify the source code?

Clients may optionally obtain a licence to access the application source code, typically at twice the standard application licence fee. This option grants the right to modify the source code under the applicable usage and confidentiality terms.

LICENSE & INTELLECTUAL PROPERTY

Your Questions Answered

What study results do I own?

All study results generated by iMEAN on behalf of the Client, including final reports and project-specific deliverables, are transferred to the Client upon delivery of the Services. The Client is entitled to use and exploit these results for its own research, development, and business activities. Any results generated from the Client's confidential information remain the exclusive property of the Client.

What intellectual property rights may arise from iMEAN's study results?

The Client may seek intellectual property protection in its own name for inventions, patents, copyrights, trade secrets, trademarks, or other rights arising from the results of the Services, at its own expense. Where needed, iMEAN may support the Client in preparing the documentation required for IP protection. iMEAN also ensures that individuals involved in the provision of the Services assign any relevant rights related to their contributions in accordance with the applicable contractual terms.

If a patent application includes an inventive contribution from iMEAN personnel, the relevant inventors from iMEAN shall be named in accordance with applicable legal requirements.

Which technologies remain owned by iMEAN after delivery?

Unless otherwise agreed, iMEAN retains all intellectual property rights to its underlying technologies, methods, software applications, algorithms, mathematical models, prototypes, and other background materials used or developed independently of the Client's specific project. The transfer of study results to the Client does not include any transfer of ownership of iMEAN's background technology. Accordingly, the Client may not reproduce, transfer, disclose, or reverse engineer such technologies or materials without iMEAN's prior written consent, which may be subject to separate commercial terms.

In which cases do I need to pay a success fee?

Our success-fee model applies only to Design service that have the potential to generate innovative, protectable results (e.g. patentable inventions, pilot plants or commercial applications). In such cases, we apply the following conditional success fees:

- 10 000 € after filing the first patent based on the study results.
- 1X the project price (typically around 20 000 €) upon construction of a pilot plant.
- 2X the project price (typically around 40 000 €) upon commercialization or licensing of the patents.

Success fees are payable by the entity that exploits the study results when the corresponding milestones are reached. If the licence is transferred to a third party before pilot plant construction or commercialization, the third party responsible for the pilot plant and/or commercialization will be liable for the success fees.

These conditions are open to negotiation regarding their modalities.

CASE STUDY

Biobased Molecules Productivity **at Scale**

Background

PILI is a pioneering company in the field of biobased pigment production. They develop innovative bioprocesses to produce aromatic molecules using engineered microorganisms. Achieving industrial success for bulk products depends on robust and efficient bioprocesses, optimized operational expenditures (OPEX), and above all, high productivity.

However, for Deeptech startups like PILI, the path to industrial scale is often challenged by long development timelines and significant cash burn. Balancing technological innovation with economic viability is key to reaching industrial objectives.

How we helped

iMEAN reconstructed the organism's Genome-Scale Metabolic Network and implemented a kinetic metabolic pathway module tailored to their bioprocess. We then simulated the production process, and our bottleneck analysis revealed two major limitations affecting productivity. Then, PILI's team validated experimentally the predictions.

Based on these insights, we provided strategic recommendations for both culture process optimisation and strain engineering. PILI subsequently involved us in exploration studies to overcome the identified bottlenecks and reach their key industrial productivity objectives.

pili
carbon
conscious
color
company

"Thanks to iMEAN we improved the understanding of our process limitations and turns it into actionable decisions "

Guillaume Boissonnat-Wu,
Managing Director and PILI's cofounder

Benefits

FAQ

Frequently Asked Questions

iMEAN

WHAT'S AN SBML FILE ? HOW CAN WE USE IT ?

An SBML (Systems Biology Markup Language) file is an XML-based format for representing computational models in systems biology. It is a standardized way to exchange and share stored models of biological processes, particularly those related to cellular and molecular biology, such as metabolic networks, signal transduction pathways, and gene regulatory networks.

There are various software tools and libraries available for creating, editing, simulating, and analyzing SBML models, such as COPASI and CellDesigner. You can also choose to use iMEAN's Network Explorer Platform.

HOW ACCURATE ARE THE PREDICTIONS FROM IMEAN'S GENOME-SCALE METABOLIC MODELS?

Even though the accuracy of the predictions will depend on the data quality and model complexity, we've conducted various comparison of data generated by our predictive models and the data measured in real wet lab experiments, we've been able to evaluate a prediction accuracy of our High-Quality models being around 90%.

OUR DATA ARE INCOMPLETE OR HETEROGENEOUS, CAN WE STILL WORK WITH IMEAN?

Yes. Many projects start from incomplete or heterogeneous datasets, and our workflows are designed to handle exactly that situation.

However, we do require a minimum level of data, typically at least a sequenced genome (partial or complete) for the strain(s) of interest, so that we can build a consistent and biologically grounded model.

We first assess the data you already have, identify the most critical gaps for modelling, and then focus on standardising and cleaning the information that can be reliably reused. Where appropriate, additional information can also be sourced from the literature or predicted using our deep learning algorithms (AI), so that you do not need to generate everything experimentally from scratch. Our modelers also verify the accuracy and biological consistency of key data inputs (e.g. genes, enzymes, metabolites and their interactions in biochemical pathways), to ensure that models are built on a robust foundation.

CAN IMEAN ALSO ORGANISE THE EXPERIMENTAL WORK, OR DO WE NEED TO RUN ALL WET-LAB ACTIVITIES OURSELVES?

For projects that require both modelling and experiments, iMEAN can team up with our wet-lab partners – including upstream and downstream processing experts – to design and execute targeted experiments, generate the missing data, and iterate DBTL cycles, without requiring additional internal lab capacity on your side.

WE DO NOT HAVE IN-HOUSE EXPERTISE IN MODELLING AND IN-SILICO TOOLS. DOES IMEAN PROVIDE TRAINING?

Yes. We can organise tailored, fee-based training sessions that combine a concise theoretical refresher with hands-on exercises on your own use cases, so that your team can confidently reuse and adapt the delivered models and tools.

Still have questions?

Our team is here to help you.

https://imean-biotech.com/

MAXIMIZE THE IMPACT

OF YOUR R&D WITH IMEAN

**average value measured with our past customers*

De-risk projects by 32%*

to strengthen your R&D program

Save up to 48%*

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neoplants

SUNRISE

ALTAR

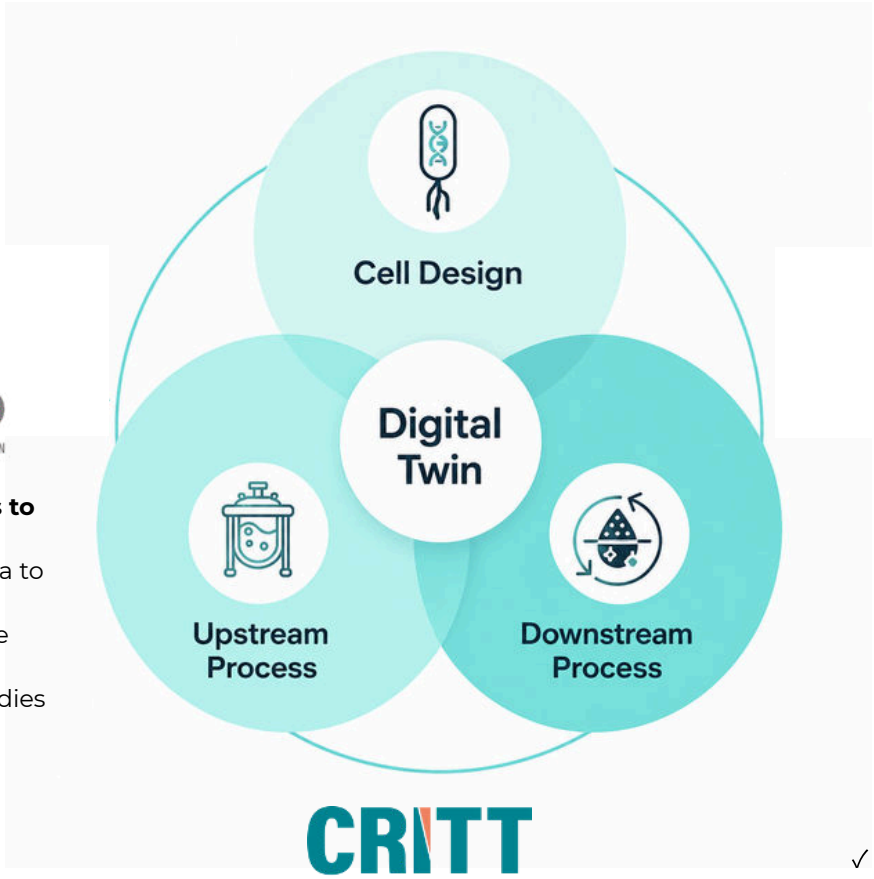
EUROGERM

pili carbon conscious food company

lipme

ALREADY
ESTABLISHED PARTNERS

Partners across the industrial biotech value chain



From Lab Experiments to First Pilot Scale-Up
✓ R&D catalyst from idea to market
✓ Lab- and pilot-scale demonstrator
✓ Techno-economic studies

Industrial Bioprocess Scale-Up and Pre-Production
✓ Pilot-scale fermentation
✓ Downstream processing
✓ Pre-industrial batches and process validation

Bioprocess Foresight
✓ In-house hybrid models (AI & Mechanistic)
✓ Techno-Economic Analysis
✓ LIfe Cycle Assessment

We are always open to **collaborating** with other industrial biotech leaders – from wet-lab and DSP partners to CDMOs – **to scale model-driven processes together.**

LET'S CONNECT

CONTACT

OUR TEAM

Share your challenges in industrial biotechnology with our team and discover how our modelling capabilities can support your projects.

Rémi PEYRAUD, PhD
CEO - Co-founder

+33 7 86 83 39 45
remi.peyraud@imean-biotech.com

Yasmine JERAD
Business Developer

+33 6 83 88 28 69
yasmine.jerad@imean-biotech.com

Damien MICHELON
Business Developer

+33 5 25 63 16 87
damien.michelon@imean-biotech.com

Website

Linkedin

iMEAN - 135 avenue de Rangueil - INSA bâtiment 50 - 31077 Toulouse Cedex 4

+33 7 86 83 39 45

contact@imean-biotech.com