The Quarterly Newsletter of OMIC-ENGINE

Q2 2020

In this issue

Editorial

Advances of Synthetic Biology in the Plant World

by Kalliope K. Papadopoulou, Nikolaos Delkis, Constantine Garagounis

Synthetic Biology funnels the efforts of fundamentally different disciplines into finding solutions to modern problems, of which a major one is **food security**. The human population is expected to surpass 9 billion by 2030, while current agricultural practices struggle to meet the demand [1]. It is evident that new approaches to plant breeding and plant manipulation are needed, if wish to address these issues. Plant Synthetic Biology aims to achieve that using DNA technology, engineering principles and computational tools to enable the design of new life processes and the repurposing of old ones. Plant SynBio embodies the efforts to apply engineering principles like standardization, abstraction and modularity and integrate the Design-Build-Test-Learn cycle, aiming to accelerate plant research, engineering, and applications. For example, machine-learning algorithms can develop innovative biosystem designs [2], universal assembly standards enable automated plant genetic circuit assembly [3] while high-throughput plant phenotyping allows for rapid screening of improved variants [4]. In addition, the availability of "omic" data from different plant species and different environmental conditions, can unlock exciting new possibilities in plant bioengineering.

Admittedly, when one thinks of SynBio, plants do not spring in mind, unlike bacteria and yeast, which constitute commonly utilized chassis. Despite their great diversity, their ability to withstand extreme biotic and abiotic stresses and the fact that they keep the world's population alive – directly or indirectly – plants are hard to work with. They are multicellular, polyploids and many of their genetic traits are redundant – exactly what a Synthetic Biologist would not want to start a project with! Nevertheless, plants and their complexity have inspired the development of a common Plant SynBio syntax, termed **"PhytoBricks"** [5]. Phytobricks are libraries of basic characterized bioparts – plant promoters, signal peptides, coding sequences, terminators - that can be assembled into expression vectors and transformed into any plant species. Embracing initiatives like this in a community-level can accelerate research many-fold, since both time and labor are saved in the process.

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Co-financed by Greece and the European Union

These important advances have laid the foundation for applications with much bigger impact and today Plant SynBio research is evolving in many different areas, one of them being the acceleration of precision plant breeding using CRISPR/Cas genome editing tools [6]. Researchers have surpassed the threshold of knock-outs and knock-ins of important genes, and focus on base editing – altering single nucleotide polymorphisms (SNPs) to provide beneficial traits to plants while minimizing the risks of cruder genetic modifications. Why insert a viral promoter to overexpress a plant protein, when one can alter the native promoter sequence to increase its transcriptional output?

Another body of research is oriented in improving plant processes like photosynthesis [7]. The intrinsic motive is that plant evolution has not yet explored the most efficient alternatives when it comes to photosynthesis, which leads to photorespiration and energy loss. Proposed solutions generally use genomic data to identify more efficient alternatives for central enzymes like RUBISCO and optimize them for plant use [8]. This requires both bacterial directed evolution systems to drive the optimization step, as well as sophisticated assembly methods to create libraries of mutants and assess their functionality *in planta*.

Considerable interest lies in the application of plant secondary metabolites to commercial and medicinal use. It is remarkable that a large proportion of common drugs (aspirin, the anti-cancer drug Taxol, the medicinal hormone precursor diosgenin) are derived from, or are, plant metabolites. Along this line, **our lab is using several SynBio approaches to understand the role of triterpenes, a huge class of secondary metabolites, in plant-microbe interactions**. These approaches are divided in three sub-projects:

- a platform for design, construction and optimization of triterpene biosensors to provide sensitive, specific and high-resolution spatiotemporal imaging of any desired triterpene in real time;
- a CRISPR/Cas-based genetic manipulation system for model and non-model legumes;
- a toolkit for genome editing of non-model endophytic beneficial fungi based on the CRISPR/Cas9 system.

Another major goal in our lab is to provide robust, standardized, and modular tools to make plants easier to engineer[9]. This is aligned with the efforts of OMIC-ENGINE to enhance SynBio efforts in the agro-food sector in Greece, by providing new tools to solve old problems.

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Meet iGEM Thessaly 2020-2021

iGEM Thessaly 2020-2021 is the new interdisciplinary team, which will take part in the international iGEM Competition, a competition dedicated to Synthetic biology. Goal of the project is to **design a diagnostic tool that will contribute to the treatment of IBD (Inflammatory Bowel Disease).** The iGEM competition (International Genetically Engineered Machine) was launched in 2003 by MIT (Massachusetts Institute of Technology) and is organized every year in Boston by the nonprofit organization iGEM Foundation. Each year, more than 340 research teams from universities and schools around the world travel to Boston to present their research work. Its purpose is to find solutions for modern-day problems by applying the fundamentals of Synthetic Biology and creating innovative and original research projects that will have a positive impact on everyday life. This year, due to the

COVID19 we are experiencing, it will take place in two phases, enabling the teams to submit some of their research proposals in November 2020, in Boston, in order to improve and complete them in November 2021, in Paris. The team consists of thirteen undergraduate and postgraduate students from different scientific backgrounds such as Biology, Architecture, Computing and Economics.

Team members

Grigoriadis Antonios; Andronikidis Georgios; Lange Marios; Delkis Nikolaos; Koroxenidou Magdalini; Tsapadikou Asteria; Papadaki Foteini; Michelioudakis Venetios; Stergiou Vasileios; Messis Anastasios; Apocha Lemonia; Daskalaki Ifigeneia and Stylianakis Emmanouil

Join their journey by following their social media accounts on Facebook, Instagram, Twitter & YouTube and also by visiting their website.

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Interviewing Researchers of OMIC-Engine

In this section we will present you the researchers of the OMIC-Engine Research Infrastructure

Dr Efthymios (Makis) Ladoukakis holds a degree in Chemical Engineering, from the National Technical University of Athens (NTUA) and was awarded a PhD in Bioinformatics, focusing on the metagenomic screening for novel enzymes of industrial interest, also from NTUA. During his PhD thesis he has worked for the FP7, EU-funded multi-institutional project HotZyme, and for the EU-funded multi-institutional project COVERALL. Since then he has worked as a post-doctoral researcher for the epigenomic project "Environmental Health" of National Hellenic Research Foundation and was recruited by Omic-Engine as a post-doctoral researcher to develop the web platform for bioinformatic analyses of –omics data for Synthetic Biology.

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Makis, describe briefly your research work.

I guess the briefest explanation about my work would be "developing a web portal for anyone who wants to perform bioinformatic analyses for Synthetic Biology". That means creating an interactive, user-friendly and most importantly customizable platform with tools and databases for analysing data from different –omics technologies for Synthetic Biology purposes. A large variety of open-source tools and customized algorithms was chosen for integration based on discussions with the partners of the consortium as well as with researchers outside the project who expressed interest on the services. The latest version of the web platform comprises tools handling, among others, metagenomic (whole metagenome and 16s), transcriptomic, taxonomic and metabolic pathway analysis.

Which opportunities did your secondment offer you in terms of training, networking and personal growth?

Since Omic-Engine is a multi-institutional collaboration, it gave me the chance of interacting with some of the most

experienced people in the field of Synthetic Biology, discuss about their projects and exchange ideas on how bioinformatics could be used more efficiently to help them. Most of the fine-tuning of the web platform and the development of new algorithms for it, was based on these interactions as they helped me better comprehend the actual needs of each research field. With each new query from a researcher, a new challenge arose computationally speaking. Dealing with them was not only an opportunity for me to enhance my programming skills but also to deepen my knowledge on Synthetic Biology and Biology in general.

What do you think will be the impact in your future career?

During the different issues that we had to address for each research field, I found myself gaining, almost unknowingly, new experience about new tools that exist out there, new biological concepts and how they are translated computationally, as well as new programming tricks. I consider all these to be now part of my updated skill set which I can exploit in different projects in Synthetic Biology as well as in other fields. The great networking of the project also brought me in touch with many different research teams from all over Greece and broadened my awareness about their field of expertise. This can prove very useful for future projects and collaborations that require a multi-disciplinary approach.

Has this secondment experience matched your expectations?

The truth is that honing my programming skills for future projects was the number one, and probably only, expectation that I had from this secondment. However, at the end of my collaboration with Omic-Engine I also found myself having gained a deeper understanding about the biological meaning behind all these numbers, graphs and statistics. Getting a much better grasp at the biological problem is what I consider the most important takeaway from this endeavour. I am pretty sure this will help me in the future to better combine my bioinformatic skills with the knowledge of people from different research fields to effectively overcome any challenges.

Three words that sum up your experience within the OMIC-Engine infrastructure.

Insightful, challenging, rewarding. If I had a fourth one, I would choose “friendly”.

Meeting the OMIC-Engine Research Groups – National Technical University of Athens (NTUA) Hub

In this section we will present each time a different hub of OMIC-Engine. The second one presented will be the research groups of the Hub of Athens participating in OMIC-Engine

How to engineer the Omics' engine – The role of NTUA

by Frangiskos Kolisis

In our days with the increasing demand to produce chemicals, pharmaceuticals, even energy in a sustainable and stable manner, bioprocessing offers an attractive alternative to traditional chemical production by using microbial – and not only- cells as a factory for chemical synthesis. The recent advances in biology, genetics and genome sequencing as well as the application of engineering principles to the design and development of biological systems has enabled researchers not only to understand living organisms at the individual molecules and at the system level but also to design and construct synthetic ones. To transform microbes into "cell factories" is necessary to rewire microbial metabolism in order to reroute metabolic flux towards chemical production, a process which may include installation of heterologous genes and deregulation of native pathways, based on the Metabolic Engineering approach. Subsequently, the modified cells have to be cultured into big bioreactors or fermentors. A successfully designed Bioprocess is the one that can produce chemicals at large scale and ideally at low cost. Those two parameters namely the engineering of the microorganism or cell – via genetic engineering and/or synthetic biology- in order to reach to a maximum production level and the use of cheap row materials as growth media are crucial for a prosperous industrial process. In addition to be sustainable, bioprocessing is also a "green" approach, considering that, renewable feedstock can be used as the initial energy source instead of burning fossil fuels. Furthermore, chemicals produced using bio-based methods are regarded as cleaner in comparison to their fossil-based equivalents, helping to reduce greenhouse gas emission and the effects on global warming. In the design of the scaling up of Bioprocessing an important parameter that has to be taken into account is the culture volume of the "cell factories". Metabolic engineering efforts begin by using cultures within Erlenmeyer shake and then in chemostats to simulate industrial bioreactor conditions. However, larger culture vessels can create problems as heterogeneity into the local environment during microbial fermentation, leading thus to a poor cell performance. In addition to the synthesis/production of fine chemicals and drugs a big market has also to do with the production of biopharmaceutical proteins such as antibodies, vaccines, blood factors, and hormones (e.g. insulin). In these bioprocesses we have to think of using mammalian cells, *E. coli* and *S. cerevisiae,* as the predominant host organisms for their production. Therefore, the necessity to develop cells with novel properties able to maximize their synthetic abilities and to consume renewable and cheap substrates is obvious. All these targets have to be taken into account in the design of the novel "synthetic cell factories".

Systems and Synthetic Biology in Bioprocessing

The systems and synthetic biology techniques are incorporated in many biotechnological processes including bioprocessing.

- **Systems biology (-omics technologies)** studies complex natural biological systems as integrated wholes, using tools of modeling, simulation, and comparison to experiment. "Model" is the representation of the essential aspects of a system under construction or of an existing one and applies knowledge of that system derived from its analysis. The efficient design of complex systems is based on the engineering approach rooted in mathematical modeling, model analysis and systems design and control. A model can be used to answer to specific demands, as for instance to design a gene regulation system that produces specific proteins or to engineer a metabolic pathway allowing *E. coli b*acteria to produce as much ethanol as possible from a cheap carbon source.
- **Synthetic biology** studies how to build artificial biological systems, using many of the same as System's Biology tools and experimental techniques. The focus is to take parts of natural biological systems, characterize and simplify them, and using them as components of an engineered biological system. The two basic concepts for engineer biological systems in Synthetic Biology are: how information flows and how this information flow is controlled. Based on these we can apply engineering principles to the design and constructing new biological systems using tools which involve computational modeling, modular parts and standardized measurements (identification and catalog of standardized genomic parts that can be used as bricks to build novel biological systems). These principles are completely novel in the field of reprogramming cellular systems at the genetic level for desired functional outputs. The concept of modularity is the ability to reduce a device or a system to a number of its component parts, while, each of the parts has to be characterized in detail. This is known as the *Parts, Devices* and *Systems approach to synthetic biology*, and they can be defined as follows:
  (i) ***Parts*** (bioparts) encoding biological functions (in principle, to construct a simple gene circuit comprising a promoter, ribosome binding site, protein coding sequence and terminator would consist of joining four sections of DNA)
  (ii) ***Devices*** made from a collection of parts (bioparts)
  (iii) ***Systems*** (of devices) which perform tasks, such as counting and intracellular control functions.

Designing biological systems from already constructed bioparts and modules it is important to address their crosstalk, the "orthogonality", which means that the modules and bioparts should not interfere with existing parts and modules in the designed biological systems as well as the genetic background circuit of the host. The toolkit of Synthetic Biology in our days contains a small repertoire of orthogonal regulatory elements and this area needs further investigation to avoid unexpected interactions. The design of microbial chassis or minimal cells seems to be a constructive attempt in order to follow the principle of orthogonality.

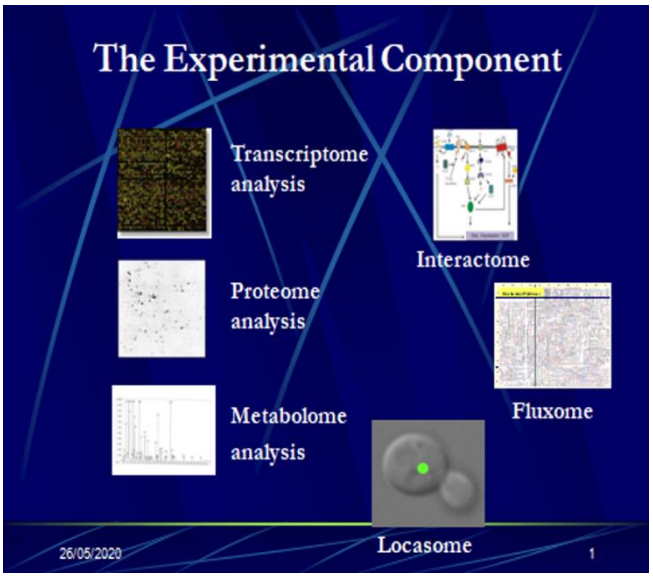

Figure 1. The different omics layers

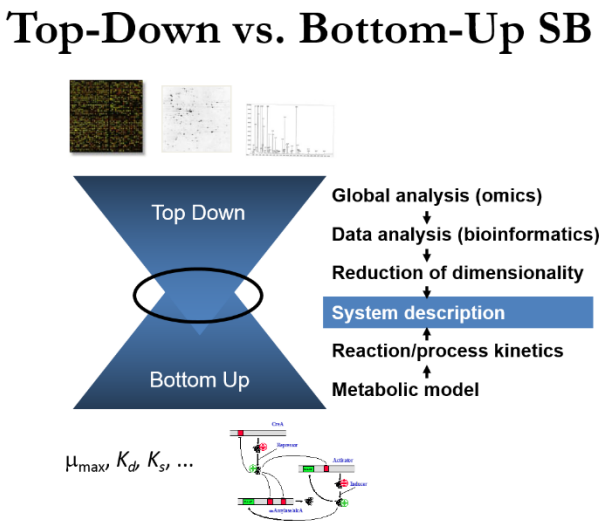

Figure 2. The two primary strategies for constructing a microbial chassis

Concluding, the –omics' and synthetic biology's tools use data-driven approaches to get a comprehensive and holistic understanding of cell metabolism and to characterize cell physiology by measuring different components of a cell as mRNA, proteins, and metabolites. Computational models then can be used for integrating these genome-wide datasets representing cellular metabolism entirely in *silico*. These models designed with the use of quantitative and comprehensive datasets from different omic layers (genome, transcriptome, metabolome, fluxomics etc, Figure 1) allow a large number of combinatorial gene changes to be tested without extended experimental tests in the laboratory and offer the predictions of the best metabolic routes for the synthesis e.g of new antibiotics and pharmaceuticals, or of a promising cell factory for biofuel production. Also, systems/synthetic biology may be used to optimize the bioprocessing approach for a given cell factory, reducing thus the cost of microbial fermentation by utilizing low-cost sources of carbon for feedstock. Another way in which systems/synthetic biology can enhance the function of cell factories is by generating the metabolic "chassis". Engineering and modifying synthetic microbial chassis is one of the best ways to enhance applications in the health, medicine, agricultural, veterinary, and food industries. The two primary strategies for constructing a microbial chassis are the top-down approach (genome reduction) and the bottom-up approach (genome synthesis) (Figure 2).

Cell modeling

In a living cell take place hundreds of coupled (bio)chemical reactions, which constitute its metabolic network, as well as, transportation of numerous components amongst its various micro compartments. All these elements define the holistic functionality of the cell which can be analyses as a "state machine" (a behavior model) consisting of a finite number of states following a time depending low under a given input. Under these controlled conditions the machine can performs state transitions and produces outputs. This dynamic system can be approached as a system of differential equations or/and as a distinctive network of automata. In the description of the functionality of the model is necessary to consider also the operation by the metabolic network of the data derived at every instant from the genomic activity of the state under investigation. This

approach is fundamental for the simulation of the cell activity towards the design of an “artificial cell” and requires the analysis of big –omics data. The use of genome-scale models can provide the necessary scaffold for such data integration. In addition to their bioinformatic handling there is a need for storing the part data and the metadata in electronic database the commonly known as a web-based information system.

Scaling up

Currently, bioprocessing requires heavy investment in time and money to develop cell factories because of the difficulties in their optimization. Optimal titer (chemical concentration), rate (chemical production over time), and yield (chemical synthesized relative to raw material consumed), need an extensive study with the implementation of faster and novel technologies in order to be achieved. The commercialization of a bioprocess to the industrial scale is an essential step. Industrial scale fermentations typically involve medium volumes greater than 1000 l (and exceeding 100 000 l for commodity chemicals and biofuels), necessitating constant mixing to obtain a homogenous environment. A bad mixing can result in spatial fluctuations of medium composition, translating to temporal variation in the environment to which cells are exposed. Such delays in mass and heat transfer lead to gradient formations within the bioreactor for a variety of components including substrates, products, byproducts, dissolved oxygen, temperature, pH, and carbon dioxide. Therefore microbes/cells fermenting at the industrial scale undergo constant changes in their microenvironment resulting in dynamic metabolic behavior and heterogeneity in biomass. The bottlenecks can be overcome (a) by multi-omic characterization which can address the various phenotypic changes due to scaling differences comparing transcriptomic, proteomic, and metabolomic data from the same fermentation in order to understand how extracellular conditions affect cell phenotype and (b) integrating fluid dynamics and cell metabolism kinetics. Other parameters that need to be studied are oxygenation conditions, substrate usage, and cofactor generation, enabling cell activity to be more precisely characterized.

Role of the Laboratory of Biotechnology, School of Chemical Engineering, NTUA in Omic-Engine Infrastructure: the contribution of NTUA consist of

(a) Bioprocess Scaling up

(b) Storage and handling of big –omics data, and

(c) metabolic modeling of microorganisms and chassis.

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Scale-up of fermentation processes

by Dimitris Kekos

The contribution of Biotechnology laboratory of NTUA to Omic-Engine infrastructure in the scale-up of fermentation processes. Fermentation scale up is aimed at the manufacture of larger product quantities, if possible, with a simultaneous increase or at least consistency of specific yields and product quality. The factors affected by scale are the number of generations, the mutation probability, medium sterilization, the quality of temperature and pH regulations, agitation, aeration and pressure. Biotechnology Laboratory is equipped with a wide range of different working volume bioreactors, thus enable conducting scale-up studies (Figure 3).

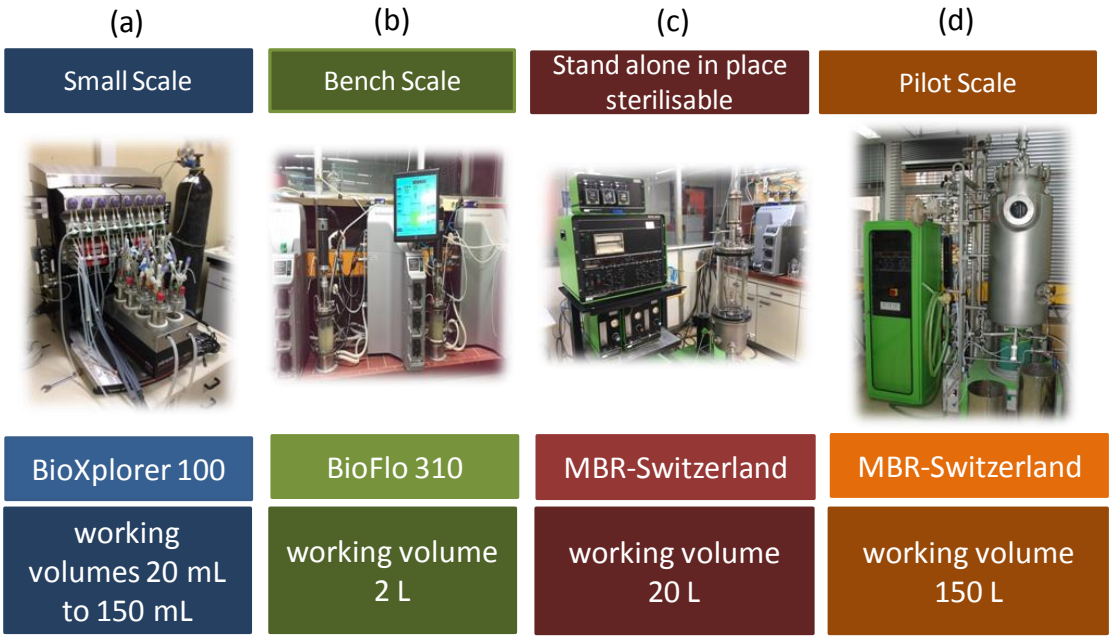

Figure 3. Fermentation systems, (a) small scale, (b) bench scale, (c) stand alone 20L and (d) pilot scale, available in Biotechnology Laboratory, NTUA.

More specifically the following bioreactors are available in BL: (a) multi-parallel microscale bioreactors system (BioXplorer 100, acquired through funding of OMIC-Engine infrastructure) designed for fermentation working volumes of just 20 ml to 150 ml in blocks of 8 parallel reactors totally independent in temperature, stirring and all other process conditions (Figure 3a). The 8 vessels are made of glass and/or stainless steel and have a cover plate made of stainless steel. Stirrers are fitted with a magnet that couples with the powerful magnetic drive system integrated into the base of the unit. Agitation speed is monitored and controlled by the software, with a speed range of 50 to 1300 rpm. The impeller configuration comprising of a Rushton turbine (radial flow impeller). Heating control for each reactor is attained through individual heating mantle, controlled individually for each reactor. The temperature probes monitor temperature inside each bioreactor. Temperature is computer controlled by adjustment of heating through the heating mantle surrounding each reactor. The unit has pH sensors for independent real time monitoring of pH in each bioreactor and the pH control can be achieved through use of variable speed peristaltic pumps. Mass flow controllers (MFC) are integrated and software controlled. MFC integration also enables control of partial pressure through feedback loop from DO

probes. DO probes are Clarke-Type Dissolved Oxygen probes. The airflow is controlled through a manual rotameter. Each reactor is equipped with a stainless-steel condenser in order to reduce the effects of evaporation. Condensers are cooled with miniature “click in place” electrical, peltier cooling units. Finally, each bioreactor is equipped with a sterilizable turbidity probe, allowing on line measurement of total cell density inside each vessel. (b) a bench-scale bioreactor system (BioFlo® 310) of 2L working volume. It features a totally integrated control station with a color touchscreen interface, built-in pumps, gas flow controllers, pH/DO, foam/level controllers (Figure 3b). (c) Stand alone in place sterilisable bioreactor (MBR-Switzerland) of 20 L working volume (Figure 3c), (d) Pilot scale bioreactor (MBR-Switzerland) of 150 L working volume (Figure 3d). Systems (c) and (d) feature a control station, built-in pumps, gas flow controllers, pH/DO, foam/level controllers. The above systems were used in (a) the development of high cell density cultures in batch mode, for the production of human membrane protein BR2 by a recombinant E. coli strain (E. coli SuptoxD). Scaling BR2 production from Erlenmeyer flasks to 2L bioreactor resulted in increase in the protein production and reduction of induction time, (b) lycopene production, using also a recombinant E. coli strain. In this case high lycopene production was achieved in 2L bioreactor operating in fed-batch mode, (c) two thermostabe enzymes namely β-glycosidase and β-xylosidase.

Dr. Dimitris Kekos is professor in the School of Chemical Engineering, NTUA). He has long experience in the area of bioconversion of lignocellulosic materials to fuel ethanol, microbial enzyme production, enzyme biocatalysis and process development. He has been the coordinator in 26 R&D National and European projects and in 37 was the principle investigator. He has authored over 130 publications in international peer-reviewed journals and according to Scopus analysis his publications were cited 3500 (h-index 36).

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Contribution of Bioinformatics Unit in the National Infrastructure OMIC-Engine

A web platform of bioinformatic tools and databases for Synthetic Biology analyses

by Efthymios Ladoukakis

The Bioinformatics Unit of the Laboratory of Biotechnology, NTUA, is the principal contributor in the Digital Unification objective of the Omic-Engine infrastructure providing a web platform of numerous bioinformatic tools and databases for Synthetic Biology analyses based on the Galaxy [1] and ANASTASIA [2] paradigms. This web platform has been developed on one of NTUA’s servers (motherbox.chemeng.ntua.gr) of high computational capacity (64 CPUs, 512GB RAM, ~7.2 TB disk space) and provides access (via an intuitive graphic user interface) to all its integrated tools (with their corresponding databases) and in-house customized scripts that tackle a broad range of bioinformatic tasks for–omic data analysis:

1. Quality Control of NGS reads (Trimmomatic, FASTQC, FASTX, CD-HIT , EMBOSS, RSeQC)
2. Assembly of NGS reads (Velvet, Megahit, Bowtie2)
3. Detection of open reading frames and coding gene sequences (Getorf, Prodigal)
4. Sequence annotation (BLAST, DIAMOND, HMMER, PROKKA, EFICAz)

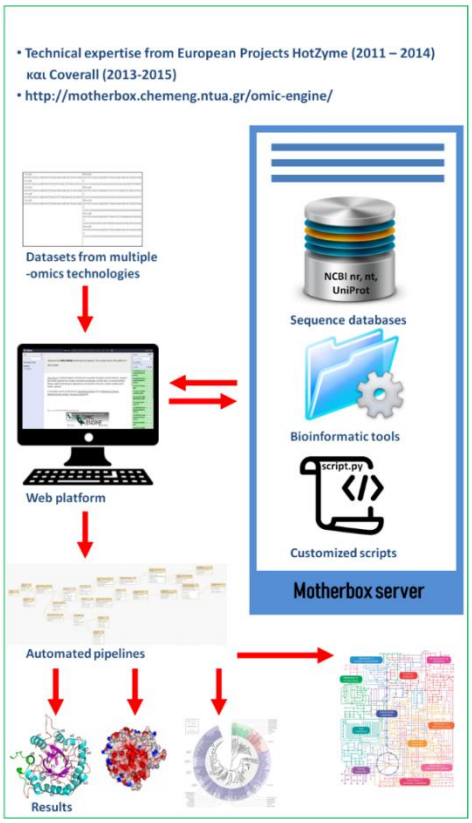

Figure 4. Schematic illustration of the bioinformatics web platform

5. Differential gene expression analysis (edgeR, HISAT2, DESeq2, txtimport, Kallisto, Salmon, HTSeq-count, featureCounts, SAMSA2, MetaTrans)
6. Taxonomic and metabolic pathway analysis (MEGAN5)
7. Supplementary tools for data handling and statistical analysis (Picard tools, limma)
8. Essential databases for analysis (NCBI-nr/nt, UniProt/SwissProt, Pfam)

Furthermore, the abovementioned tools have been seamlessly assimilated into automated pipelines in the web platform thus allowing the execution of several analyses consisting of multiple tools while minimizing the need of user interaction (Figure 4). Meanwhile the web platform also allows for the integration of additional customized tools and the creation of new automated pipelines according to its users' needs and the complexity of their data. Access to this web platform is provided to all partners of the consortium, becoming thus the computational hub for all analyses that aim to the development of high value products for the Greek Agro-Food sector.

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Metabolic Modeling

by Marianthi Logotheti

The Bioinformatics Unit develops the metabolic model of the thermophilic bacteria *Geobacillus thermoglycosidasius*, for the construction and development of a heat-resistant chassis in collaboration with the Microbial Biotechnology Unit of the Depart. of Biology, NKU of Athens. A chassis is an engineerable and reusable biological platform usually, a microorganism as *E. coli, B. subtilis*, and *P. putida*, with a genome encoding a number of basic functions for stable self-maintenance, growth and optimal operation, but with the tasks and signal processing edited for strengthening performance under pre-specified environmental conditions. The difficulty to control the behavior of the host is addressed with the design of the so-called "minimal cells," which are host cells that retain only the minimal biological functions necessary for their survival [1].

The bacterium *Geobacillus thermoglycosidasius*, seems ideal for this purpose as a heat-resistant biological chassis [2], and as a rich source of thermostable enzymes and natural products. The construction of the metabolic model is a fundamental step in the *in silico* design of the chassis and its metabolic pathways for simulating its metabolism (Figure 1). In this direction we develop the genome-scale metabolic model of the microorganism *G. thermoglycosidasius*, to help the design of important *in-silico* experiments. Initially, a draft of the model has been created that essentially concerns an initial collection of candidate metabolic functions of the organism that result directly from its annotated genome and then the improvement of the draft has followed. The next stage involved the mathematical representation of the model, in which the boundaries of the system have been determined according to experimental data concerning the metabolism of the microorganism. The model has been then transformed into a COBRA Toolbox [3] file for the performance of *in-silico* experiments and for the flux balance analysis.

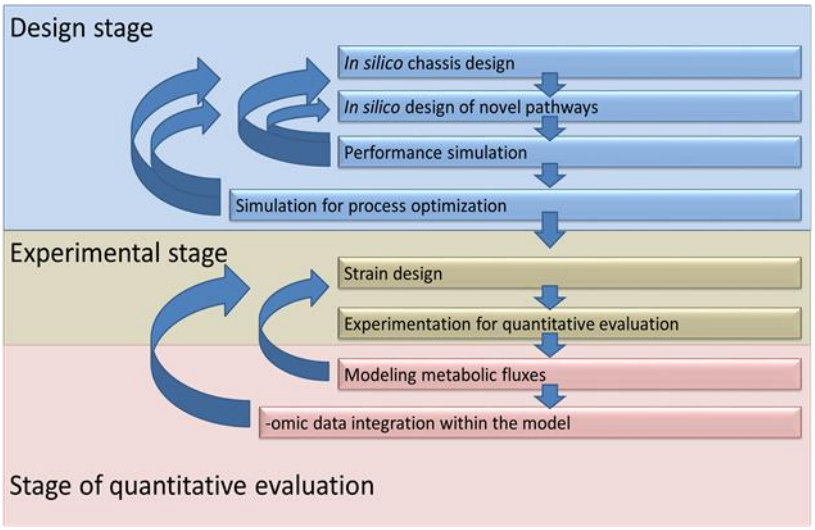

Figure 6. Design stages of a biological chassis. The construction of metabolic models is involved in the design and quantitative evaluation stages.

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Dr. Marianthi Logotheti is a post-doctoral researcher in National Technical University of Athens (NTUA), in the field of metagenomics in psychiatric disorders. She has received her degree in chemical engineering from the NTUA and has finished her PhD studies in Medical Science in Örebro University of Sweden, in collaboration with the Bioinformatics and Metabolic Engineering team of the National Hellenic Research Foundation. She has experience in the field of metabolic engineering, through her participation in research projects in collaboration with the NTUA utilizing bioinformatics tools to model the metabolism of microorganisms of biotechnological interest. She is currently working as a researcher in Omic-Engine on the development of the metabolic model of the thermophilic bacteria *Geobacillus thermoglycosidasius* for the construction and development of a heat-resistant chassis.

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New Projects coming in the OMIC-Engine Network

In this section we will update you on research activities and new project coming in the research network of the OMIC-Engine Research Infrastructure

- **H2020-MSCA-ITN project ARISTO - The European Industry - Academia Network for RevIsing and Advancing the Assessment of the Soil Microbial TOxicity of Pesticides**
  Coordinator: Prof. D. Karpouzas, University of Thessaly, Department of Biochemistry and Biotechnology, Laboratory of Plant & Environmental Biotechnology. dkarpouzas@bio.uth.gr

  ARISTO is an ETN-EID project aiming to train the next generation of soil microbial ecotoxicologists. It will provide the benchmarking research needed to facilitate the most needed revision of the regulatory framework regarding the soil microbial ecotoxicity of pesticides. It will explore toxicity of pesticides on soil microbes at different experimental scales spanning from in vitro, to in soil and finally to ecosystem level looking at toxicity levels across the soil food web and in microbial networks. The toxicity of pesticide mixtures, biopesticides and transformation products will be also determined using standardized and advanced molecular tools. ARISTO is a 4-year project (2020-2024) of 2.5 million euros coordinated by Dr D. Karpouzas, Department of Biochemistry and Biotechnology, University of Thessaly (member of OMIC-Engine). The ARISTO network comprises 7 academic and 9 industrial partners coming from France (INRAE, HYDREKA-ENOVEO, Ecole Centrale de Lyon, SATT SAYENS), Germany (UFZ, INOQ GmbH, Envipath GmbH, ECT Oekotoxicologie GmbH), Switzerland (EAWAG, Syngenta Crop Protection A.G.), Sweden (Swedish University of Agricultural Sciences), UK (NCIMB ltd), Israel (Metabolic Insights Ltd), Belgium (Universite Catholique de Louvain), Greece (University of Thessaly, Phytothreptiki S.A.) which will join forces in the training of 9 PhD students. Complementary expertise will be provided by partners from Australia (Univ. Western Sydney) and Germany (DSMZ, Bayer A.G.) The ARISTO project was ranked 1st among the ITN-EID projects submitted in the 2020 call.

- **Project ForFUN (Formulated FUNgi)**
  Coordinator: Assoc. Prof. Kalliope K. Papadopoulou, University of Thessaly, Department of Biochemistry and Biotechnology, Laboratory of Plant & Environmental Biotechnology. kalpapad@bio.uth.gr

  ForFUN (Formulated FUNgi) will develop a formulated inoculum (biostimulant) to promote and improve the capability of the endophytic beneficial fungal strain Fusarium solani K to induce increased plant resilience against abiotic stress factors. The characteristics of the entrapped endophytic fungus in terms of extended shelf-life, improved handling, targeted transfer, protection from abiotic and biotic stress factors and endophytism will be greatly improved by encapsulation systems and properties of the biopolymers. Through ForFUN, both basic and applied knowledge will be generated on inocula/biostimulants, in full coordination with the partner company's primary goals for the development of an innovative Greek microbial product that will respond to the new challenges of the primary production under the effects of climate change in the Mediterranean Basin, promote the Sustainable Development Goals and Circular Bioeconomy and allow the entrance of the participant company (ORA- Out of Ordinary Agroscience) to the emerging market of microbial inocula/biostimulants.

OMIC-Engine Open Positions

Here we will keep you updated about open positions that are available in the different hubs of OMIC-Engine

A position for a postdoc fellow in Biotechnology - Synthetic Biology - Biochemistry. The position is available for 12 months with the possibility of further extension and it is based in the Lab of Plant and Environmental Biotechnology, Department of Biochemistry and Biotechnology, Larissa, Greece. The person employed will be part of the Research Infrastructure OMIC-Engine. He or she will work on (a) the screening of metagenomic libraries for the identification and characterization of novel enzymes with advanced catabolic properties against emerging pollutants and (b) the evaluation of novel synthetic microbial communities for the effective detoxification of persistent organic pollutants. We expect the successful candidate to have a first degree in Biosciences, and a PhD in Molecular Biology, Biotechnology or Biochemistry. Experience in heterologous expression of proteins or metagenomic library construction and bioinformatics will be desirable. The successful candidate will be contracted with the University of Thessaly through scholarship.
The monthly net salary will be 1330 euro. For more information please contact Prof. Dimitrios G. Karpouzas, Tel. +302410565294, Email. dkarpouzas@uth.gr

Co-financed by Greece and the European Union

OMIC-Engine is implemented under the Action "Reinforcement of the Research and Innovation Infrastructure" funded by the Operational Programme "Competitiveness, Entrepreneurship and Innovation" (NSRF 2014-2020) and co-financed by Greece and the European Union (EU Regional Development Fund)