1st INFOGUT TRAINING SCHOOL, 22-24 September 2025,
Campus of Food Science – *Alma Mater Studiorum*-University of Bologna, Cesena (FC), Italy
DRAFT PROGRAM

INFOGUT TRAINING SCHOOL

Basics of main in vitro GM models and the whole experimental pipeline: from fermentation process technologies to data capture and data analysis.

Cesena, 22-24/09/2025

- Hybrid Event: Face to Face at University of Bologna, **in Cesena** (70 Km far from Bologna; trains to Bologna every 30 min) Campus of Food Science, Piazza Goidanich, 60 and Online on Teams (invitation required)

1st INFOGUT TRAINING SCHOOL, 22-24 September 2025,

Campus of Food Science – *Alma Mater Studiorum*-University of Bologna, Cesena (FC), Italy

DRAFT PROGRAM

22/09	Topic	Trainer	Form	*Objectives*
13.15	Welcome by UNIBO Authorities			
13:30	State of the art of the INFOGUT Project	Andrea Gianotti (UNIBO)	FtoF	*At the conclusion of this session, students will be expected to: i) provide an overview of the INFOGUT platform and its foundational purpose; ii) Outline the organizational structure, including key leaders and partner networks; iii) Explore the main activities carried out and potential future developments, including STSM and other grant opportunities.*
14:30	Reviewing Batch GM Models.	Harsh Mathur (TEAGASC)	FtoF	*i) To give new students and researchers an introduction to the batch GM models, especially those who are unfamiliar with the system; ii) In addition, to supplement training for researchers who are already using batch models in their research institutes. iii) Finally, to have a Question and Answer session where any specific questions and troubleshooting steps can be discussed in detail e.g. issues relating to microbial blooms in batch model faecal fermentation experiments using the microMatrix system as an example.*
16:00	In vitro dynamic models of colon fermentation	Edoardo Capuano (Uni Wageningen)	FtoF	*In this contribution, a number of widely used in vitro dynamic models of colon fermentation are presented and discussed. This contribution will include general information on the fundamental operational principles of a dynamic model of colon fermentation, the main characteristics of each model, the difference in key parameters and settings, strength and limitations of each model and how this knowledge can be used to select the appropriate model depending on the research question. Specific examples will be presented on the use of (some) of the models, taken from the relevant scientific literature or the research work of the presenter.*
23/09				
09:00	Reviewing Animal GM Models	Jurgen Zentek (Freie Uni Berlin)	FtoF	*By the end of the lesson, students will be able to: i) Understand the principles behind Animal GM Models; ii) Summarize the history and evolution of these models; iii) Recognize the main types of Animal GM Models currently in use; iv) Describe applications of Animal GM Models across substrates and animal species.*
10:30	Coffe break			
10:45	Models with GM and the Small Intestine	Ludovica Marinelli (Uni GHENT)	Remote	*Upon completing this session, students will be able to: i) Explain the fundamental principles of host–gut microbiota (GM) interactions in the human small intestine; ii) Describe experimental approaches used to study these interactions; iii) Identify the types of cells, tissues, and organoids applied in these models; iv) Understand how the gut microbiota is introduced and how host–GM interaction stability is assessed; v) Recognize the main host–GM models used to mimic the human small intestine.*
12:15	Parameters & Sample Processing of Batch GM Models	Lorenzo Nissen (UNIBO)	FtoF	*By the end of the lesson, students will be able to: i) Understand key terms related to Batch GM Models; ii) Describe volunteer recruitment and inoculum preparation steps; iii) Identify main components of a Batch GM Model; iv) Outline sampling and sample processing for omics analyses; v) Explain how to mount, set up and operate a Batch GM Model.*
13:30	Lunch time			
14:15	Synthetic Communities: The creation and use of SynComs to study the gut microbiota	Tom Hitch (Uni ACHEN)	Remote	*The lecture will introduce the concept of SynComs, why they exist, their history, and their complexity. Then, the major methods by which SynComs are created, and the limitations of each approach, as well as their benefits, will be discussed. Use-cases of existing SynComs will be made throughout to highlight their application in research.* *As a case study, a variety of strains, as well as a specific ecosystem will be provided. The students will aim to create a suitable SynCom for the ecosystem based on the information provided. We will go over which strains were selected, and why.*
15:45	Applied Genomics to GM Models	Sabrina Tamburini (Ca' Foscari)	FtoF	*Upon completing this session, students will be able to: i) Understand the core principles of genomics as applied to gut microbiota (GM) models; ii) Describe key methods for microbial detection and quantification, including qPCR, RT-PCR, and preparative steps; iii) Compare major sequencing strategies such as 16S rDNA, metataxonomics, metagenomics, and shotgun approaches; iv) Interpret essential data outputs from genomic analyses relevant to GM models.*
24/09				

1st INFOGUT TRAINING SCHOOL, 22-24 September 2025,

Campus of Food Science – *Alma Mater Studiorum*-University of Bologna, Cesena (FC), Italy

DRAFT PROGRAM

09:00	MICRO-B: a gut microenvironment-mimicking bioreactor for the human gut microbiota in vitro culture	Irene Chiesa (UNIPI)	FtoF	*The objective of our lecture is to instruct the participants on the main requirements and operational steps to develop a dynamic bioreactor for relevant in vitro cultures in tissue engineering and regenerative medicine. As a case study, MICRO-B bioreactor's development steps and its use in the human gut microbiota and the intestinal epithelium contexts will be shown.*
10:30	Coffe break			
10:45	Using nuclear magnetic resonance to extract metabolomic information from biological samples for fecal metabotype classification	Francesco Capozzi (UNIBO)	FtoF	*The training will provide insights into the usefulness of metabolomic tools in understanding the physiological phenomena underlying digestion in the colonic tract of the intestine and has the objectives to have training on (i) sample preparation and the effect of sample nature on spectroscopic data quality, (ii) spectrum interpretation and metabolite identification, and (iii) data preparation for multivariate analysis*
12:15	Basics of Bioinformatics Applied to GM Models	Alise Ponsero (Quadram)	Remote	*Upon completing this session, students will be able to: i) Introduce participants to the fundamental concepts of metagenomic analysis in the context of gut microbiome research; ii) Introduce participants to bioinformatics tools and workflows for metagenomic data processing; iii) Enable participants to critically evaluate and interpret metagenomic results from colon fermentation experiments; iv) Demonstrate best practices for quality control and statistical analysis of microbiome compositional data*