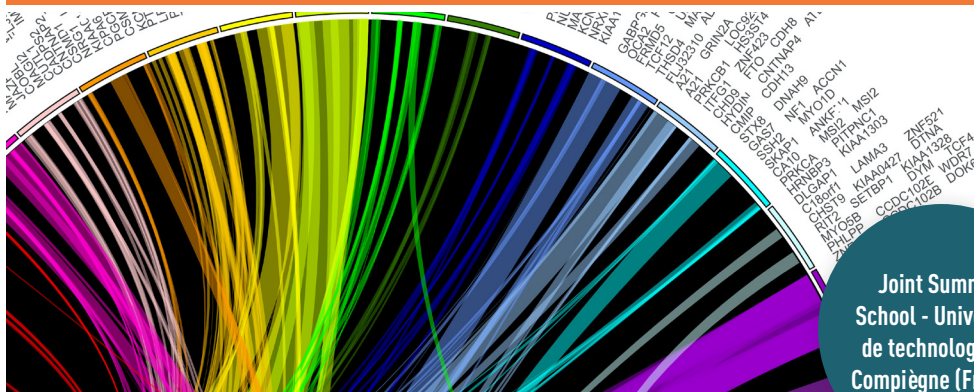




Joint Summer
School - Université
de technologie de
Compiègne (France)

18 to 29 January 2027
at the universit  de technologie de Compi gne

DURATION	DELIVERY	LOCATION	OPTIONAL CREDIT
Two-week intensive course and cultural visits	Face-to-face teaching and computer practicals	Université de technologie de Compiègne	4 ECTS after passing the assignment

WHY STUDY THIS COURSE?

In the era of big data biology, Next Generation Sequencing (NGS) is revolutionising the way we study genomes, transcriptomes, and genetic variation. From unlocking the secrets of human disease to tracking pathogens, decoding microbial communities, and shaping precision agriculture, NGS has become the bedrock of modern bioscience.

This course is designed for researchers and professionals who want to gain practical and conceptual expertise in the fast-evolving field of NGS bioinformatics. You'll gain hands-on skills in real-world NGS analysis pipelines and critically understand the software, algorithms, and data quality issues that underpin discoveries in genomics and transcriptomics.

Whether you're entering the field or looking to sharpen your analytical toolkit, this course offers a high-impact, immersive experience. Participants who complete the optional take-home assignment will be eligible for 4 academic credits (ECTS or equivalent).

COURSE OVERVIEW

Next Generation Sequencing is central to modern work on genomes, transcriptomes and genetic variation. It supports research into human disease, pathogen tracking, microbial communities and precision agriculture. This course develops the conceptual understanding and practical bioinformatics skills needed to work with real sequencing data and to interpret the results responsibly.

Participants follow the analytical pathway from sequencing and raw-read quality control to alignment, quantification, variant calling and biological interpretation. The course also examines the software, algorithms, data-quality issues and analytical choices that influence scientific conclusions.

MODULE DESCRIPTOR

Module Title	Next Generation Sequencing Informatics
Credit Rating	4 Credits (ECTS or equivalent)
Duration	2-weeks intensive course (Theory lectures and hands-on computer practicals) + assignment period
Delivery Mode	Face-to-face interactive teaching with computer-based practicals. Assignment submitted online.
Site(s) of Delivery	Université de technologie de Compiègne (UTC)

MODULE AIMS

To introduce the fundamental technologies, data types, and analytical approaches used in modern genomic and transcriptomic studies. The course combines theory and practice to:

- Understand key NGS workflows from sequencing to biological interpretation.
- Build familiarity with software for quality control, alignment, quantification and variant calling.
- Develop critical insight into best practice, limitations and result interpretation in NGS studies.

WHO THE COURSE IS FOR?

- Researchers using high-throughput sequencing data in research or clinical settings
- Early-stage researchers planning to add NGS to experimental workflows
- Genomics, molecular biology or computational biology professionals moving into NGS analysis
- Industry professionals in genomics, diagnostics or biotechnology research and development

COURSE LEADER

Professor Fady Mohareb

Professor of Bioinformatics and Artificial Intelligence at UTC



COURSE DETAIL

LEARNING OUTCOMES AND COURSE CONTENT

On successful completion of the module, participants will be able to :

- 1 Critically evaluate** the operation of NGS technologies and their bioinformatics workflows.
- 2 Perform data quality control** and apply techniques to clean, filter and normalise sequencing data.
- 3 Execute transcriptomic analysis** and differential gene-expression workflows.
- 4 Interpret outputs** from alignment, assembly and variant-calling tools.
- 5 Compare analytical pipelines** and evaluate their impact on scientific conclusions.

INDICATIVE COURSE CONTENT

TOPIC	WHAT PARTICIPANTS COVER
NGS overview	Principles of next-generation sequencing platforms, data types and the route from sequencing to biological interpretation.
Data acquisition and quality control	Quality assessment of raw reads using FastQC, followed by trimming, filtering and normalisation.
Genome assembly and alignment	Short-read mapping, indexing, assembly outputs and visualisation.
Transcriptomics	Gene-expression quantification and differential-expression analysis.
Variant analysis	Genotyping, SNP and indel calling, and variant-annotation pipelines
Comparative practices	Microarrays compared with RNA-Seq, bulk compared with single-cell analysis, and the consequences of pipeline choice.

LEARNING METHODS

Lectures	Concept teaching in sessions of one to two hours
Practicals	Step-by-step computer exercises
Discussion	Group work and real-world case studies
Assignment	Applied analysis and report writing

TEACHING SCHEDULE

INDICATIVE TWO-WEEK TIMETABLE

The timetable arranges the module topics into a progressive sequence from technology and data quality to transcriptomics, variant analysis and integrated interpretation. Session order may be adjusted to support practical progress.

Week 1

Monday 18th	Tuesday 19th	Wednesday 20th	Thursday 21th	Friday 22th
09:30-10:30 Module Introduction - 11:00-13:00 Lecture 01 Genomics, Microarrays and Gene Expression	09:30-10:30 Next Generation Sequencing Platforms - 11:00-13:00 Lecture 02 Sequencing Technologies	09:30-13:00 NGS Quality Control and Data Pre- processing	09:30-13:00 Lecture 04 Genome Informatics	09:30-13:00 Lecture 05 Alignment-Free RNA-Seq
Lunch	Lunch	Lunch	Lunch	Lunch
14:00-17:15 Practical Gene Expression Analysis for Cancer Treatment	14:00-15:15 Lecture 03 Data Outputs - 15:30-17:15 Practical NGS Quality Control and Data Pre- processing	14:00-17:15 Free for Cultural Visit	14:00-17:15 Practical RNA-Seq Informatics	14:00-16:30 Practical Alignment-Free RNA-Seq - 16:30 onward Free for Dinner

MORNING BREAK
Usually 10:30-11:00
LUNCH
Usually 13:00-14:00

Week 2

Monday 25th	Tuesday 26th	Wednesday 27th	Thursday 28th	Friday 29th
09:30-13:00 Lecture 05 Variant Calling	09:30-10:30 Lecture 06 NGS Applications in Pathogen Identification - 11:00-12:15 Lecture 07 NGS Applications in Crop Genomics - 12:15-13:00 Assignment Briefing	09:30-13:00 NGS Project Assignment	09:30-13:00 NGS Project Assignment	09:30-13:00 NGS Project Assignment
Lunch	Lunch	Lunch	Lunch	Lunch
14:00-17:15 Practical Variant Calling	14:00-17:15 NGS Project Assignment	14:00-17:15 NGS Project Assignment	14:00-17:15 NGS Project Assignment	14:00-15:30 Assignment Debrief and Discussion - 15:30-17:15 NGS Project Assignment