Course unit English denomination	Emerging Infectious diseases: pathogenesis, treatment and prevention
SS	MEDS-26/A
Teacher in charge (if defined)	Luisa Barzon
Teaching Hours	10
Number of ECTS credits allocated	2
Course period	Second Semester
Course delivery method	☒ In presence ☐ Remotely ☐ Blended
Language of instruction	English
Mandatory attendance	☒ Yes (70% minimum of presence) ☐ No
Course unit contents	In this course, the main characteristics and genetic and molecular bases of the pathogenesis of emerging and re-emerging viral infections will be explored in depth, with particular reference to those caused by pathogens identified as priorities by the WHO, such as Ebola virus, SARS-CoV-2, dengue virus, Zika virus, West Nile virus, and monkeypox virus. Additionally, the drivers determining the emergence of new pathogens (including climate change), epidemiological aspects, and methods of surveillance and early warning will be considered. The course will also cover prevention and control strategies, laboratory diagnosis, drugs, and vaccines in development. Case studies will be presented and discussed interactively.
Learning goals	English
Teaching methods	The aim of this course is to provide an in-depth understanding of the characteristics, genetic and molecular bases, epidemiology, and control strategies of emerging and re-emerging viral infections prioritized by the WHO, including interactive discussions of case studies.
Course on transversal, interdisciplinary, transdisciplinary skills	☒ Yes ☐ No

Available for PhD students from other courses	☒ Yes ☐ No
Prerequisites (not mandatory)	None
Examination methods (if applicable)	Not applicable
Suggested readings	Teaching materials provided by the instructor
Additional information	

Course unit English denomination	Big data analysis and bioinformatics
SS	IBIO-01/A
Teacher in charge (if defined)	Silvio Bicciato
Teaching Hours	15
Number of ECTS credits allocated	3
Course period	03/2026
Course delivery method	☒ In presence ☐ Remotely ☐ Blended
Language of instruction	English
Mandatory attendance	☒ Yes 100% minimum of presence) ☐ No
Course unit contents	1. Introduction to the analysis of genomic data from high-throughput technologies high-throughput technologies for the analysis of genomic profiles - online resources and databases for integrative genomics - experimental design in the acquisition of genomic data with high-throughput technologies - management of metadata and clinical information related to biological samples 2. Computational methods for the analysis of RNA-seq data - quality control of raw data (raw reads), sequence alignment, and visualization of sequence alignments - algorithms to quantify gene expression levels - supervised analysis methods to identify phenotype markers of cells and tissues in different physiological states - computational methods to infer cell fractions from bulk gene expression profiles (deconvolution methods - computational strategies for the annotation and the functional interpretation of genomic data

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Learning goals

The course aims to provide the knowledge and skills necessary for the integrative analysis of genomic data and phenotypic traits of biological samples. Specific attention will be dedicated to computational methods for the analysis of genomic profiles obtained with high-throughput technologies and their integration with the sample bio- molecular characteristics to evaluate the function of genes, regulatory sequences, and molecular interaction networks.
The expected learning outcomes of the class are as follows:

1. Knowledge and understanding
    a) apply mathematical, statistical, and computer methods to the analysis of genomic data and phenotypic traits
    b) use computational methods for genomic and post-genomic data analysis
2. Ability to apply
    a) logical-mathematical, statistical, and informatic tools
    b) bioinformatics knowledge
    c) bioinformatics techniques for the analysis, managemer and interpretation of genomic and bio-molecular data
3. Autonomy of judgment
    a) plan and interpret experimental data generated with high-throughput technologies
    b) critically evaluate the computational and experimental methodologies for the integrated analysis of genomic data and molecular characteristics of biological samples
    c) interpret the results of the analysis of genomic data in the light of the sample bio-molecular traits

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Teaching methods

The teaching is delivered through face-to-face lectures which are carried out with the aid of IT supports (Power Point presentations and data analysis in the R computational environment and in the Unix shell). Students are expected to learn the theoretical and applicative aspects of algorithms and IT tools essential for the integrative analysis of genomic profiles and bio-molecular data. The practical activities involve the application of methods for genomic data analysis on case studies

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Course on transversal, interdisciplinary, transdisciplinary skills

☒ Yes
☐ No

Available for PhD students from other courses

☒ Yes
☐ No

Prerequisites (not mandatory)	
Examination methods (if applicable)	
Suggested readings	● Lecture notes, bibliographic material, R scripts, and example genomic data ● B. Tijs, F. van der Kloet, M. Galland. RNA-seq lesson. Version 2020.04 (https://scienceparkstudygroup.github.io/rna-seq-lesson/index.html) ● A. Akalin. Computational genomics with R (https://compgenomr.github.io/book/) ● S. Holmes, W. Huber. Modern statistics for modern biology (https://web.stanford.edu/class/bios221/book/index.html)
Additional information	

Course unit English denomination	Functional interpretation of genomic data
SS	IBIO-01/A
Teacher in charge (if defined)	Silvio Bicciato
Teaching Hours	15
Number of ECTS credits allocated	3
Course period	05/2026
Course delivery method	☒ In presence ☐ Remotely ☐ Blended
Language of instruction	English
Mandatory attendance	☒ Yes (100% minimum of presence) ☐ No
Course unit contents	1. Introduction to annotation and functional interpretation of Genomic profiling experiments from high-throughput technologies 2. Gene sets for the functional annotation of genomic data - construction of gene sets - collections of molecular signatures and gene sets 3. Computational methods for annotation and functional interpretation of transcriptional and ChIP-seq profiles - gene set enrichment methods: over-representation analysis - gene set enrichment methods: functional class scoring
Learning goals	The course aims to provide the ability to use computational tools for the functional interpretation of genomic data and their analyses. The student will acquire fundamental concepts of computational methods for the functional annotation of results obtained from bioinformatic analyses of genomic data. Through its various components, the course seeks to develop the following skills: 1. Knowledge and understanding a) in the application of mathematical, statistical, and computational methods for the integrated analysis of

genomic data
   - b) in the use of computational methods for the functional interpretation of genomic data analysis
2. Ability to apply
   - a) logical-mathematical, statistical, and computational tools
   - b) bioinformatics knowledge
   - c) bioinformatics techniques for the functional interpretation of genomic data analysis
3. Independent judgment
   - a) in evaluating and functionally interpreting genomic data
   - b) in critically assessing computational and experimental methodologies that enable the integrated study of genomes and molecular characteristics of biological samples
   - c) in interpreting the results of genomic data analysis in the context of the molecular mechanisms of cellular systems

Teaching methods	The course is delivered through in-person lectures, conducted with the aid of digital tools (PowerPoint presentations and data analysis in the R computational environment and with specific applications). Students are expected to learn both the theoretical and practical aspects of algorithms and computational tools essential for the integrated analysis of genomic profiles. The practical activities involve the application of methods for the functional interpretation of genomic data analysis results on case studies. A key aspect is the use of each student's personal laptop during the lectures
Course on transversal, interdisciplinary, transdisciplinary skills	☒ Yes ☐ No
Available for PhD students from other courses	☒ Yes ☐ No
Prerequisites (not mandatory)	Big data analysis and bioinformatics
Examination methods (if applicable)	
Suggested readings	Lecture notes, bibliographic material, R scripts, and example genomic data

Additional information

Course unit English denomination	Gene editing: technologies and applications
SS	BIO/17, BIO/11
Teacher in charge (if defined)	Michelangelo Cordenonsi
Teaching Hours	10
Number of ECTS credits allocated	2
Course period	May – June 2026
Course delivery method	☒ In presence ☐ Remotely ☐ Blended
Language of instruction	English
Mandatory attendance	☒ Yes 100% minimum of presence) ☐ No
Course unit contents	Classic gene editing technologies: gene knockout and knockin in mouse embryonic stem cells. Conditional gene editing in mice: strategies and opportunities. Mouse breeding strategies to obtain complex genotypes. Gene editing technologies using CRISPR/Cas9: basic concepts. Application of CRISPR/Cas9 for gene knockout in human and murine cells: advantages and disadvantages. Targeted mutagenesis using CRISPR/Cas9. Gene knockin with CRISPR/Cas9 and its application to achieve conditional gene editing. Other conditional gene editing strategies with CRISPR/Cas9. Gene activation induced by defective-Cas9: opportunity for gain-of-function experiments. Screening using CRISPR/Cas9: loss-of-function and gain-of- function approaches.
Learning goals	Learn the basics of CRIPR/Cas9 technologies and the opportunities they create for biomedical research. Learn to design targeting specific genes
Teaching methods	The teaching is delivered through face-to-face lectures which are carried out with the aid of IT supports (Power Point presentations and online tools for planning the experiments). Students are expected to learn the theoretical and applicative aspects of gene editing via CRISPR/Cas9, and IT tools essential for planning the experiments. The practical activities involve the application of online tools for planning the experiments.

Course on transversal, interdisciplinary, transdisciplinary skills	☐ Yes ☒ No
Available for PhD students from other courses	☒ Yes ☐ No
Prerequisites (not mandatory)	Basic knowledge of molecular biology methods
Examination methods (if applicable)	Not applicable
Suggested readings	
Additional information	

Course unit English denomination	Flow cytometry: from basic principles to research applications
SS	BIOS-12/A HUMAN ANATOMY
Teacher in charge (if defined)	Di Liddo Rossa
Teaching Hours	10
Number of ECTS credits allocated	2
Course period	February-June 2026
Course delivery method	☒ In presence ☐ Remotely ☐ Blended
Language of instruction	English/Italian
Mandatory attendance	☒ Yes (70% minimum of presence) ☐ No
Course unit contents	The course aims to provide the knowledge and skills of basic flow cytometry topics and applications. In detail, the teaching course will have the following educational objectives: - understanding of the basic principles of fluorescence and light-particle interactions; - learning of the general concepts related to fluidics, optics, and electronic systems of flow cytometers; - knowledge of the different aspects of flow cytometry, including the quality control of both instrument and measurable parameters; - training in biological sample preparation and detection of cell targets (membrane, cytoplasmic, and nuclear), cell proliferation, cytotoxicity, apoptosis, and signaling pathways; - data analysis and graphical representation.
Learning goals	● Learning of the basic concepts of flow cytometry; ● set up of flow cytometry analysis protocols; ● cell handling and staining; ● data acquisition and analysis

Teaching methods	The Program includes a part of frontal teaching followed by interactive exercises using different strategies for the presentation of flow cytometric data.
Course on transversal, interdisciplinary, transdisciplinary skills	☒ Yes ☐ No
Available for PhD students from other courses	☒ Yes ☐ No
Prerequisites (not mandatory)	
Examination methods (if applicable)	
Suggested readings	
Additional information	

Course unit English denomination	Computational analysis of single cell genomic data
SS	BIOS-08/A
Teacher in charge (if defined)	Mattia Forcato
Teaching Hours	20
Number of ECTS credits allocated	4
Course period	April - may
Course delivery method	☒ In presence ☐ Remotely ☐ Blended
Language of instruction	English
Mandatory attendance	☒ Yes (100% minimum of presence) ☐ No
Course unit contents	- Introduction to the analysis of single cell sequencing data: single cell technologies and biological sample preparation - experimental protocols for the acquisition of single cell genomic profiles: transcriptional (scRNA-seq), chromatin accessibility (scATAC-seq) and multimodal data - Analysis of single cell transcriptional (scRNA-seq) data: sequence alignment; quantification of the expression; identification, visualization and annotation of cell populations - Advanced methods for the analysis of single cell transcriptional profiles: integration of multiple datasets and multimodal data; study of cell-cell communications; analysis of trajectories
Learning goals	The course aims to provide the knowledge and skills necessary for the integrative analysis of single cell genomic data. Specific attention will be dedicated to computational methods for the analysis of genomic profiles obtained with single cell high-throughput technologies and their application to the reconstruction of cellular ecosystems in eukaryotic tissues.
Teaching methods	The teaching is delivered through face-to-face lectures which are carried out with the aid of IT supports (Power Point presentations and data analysis in computational environments available via web browser). Students are expected to learn the theoretical and applicative aspects of algorithms and IT tools essential for the integrative analysis of single cell

	genomic profiles. The practical activities involve the application of methods for single cell genomic data analysis on case studies
Course on transversal, interdisciplinary, transdisciplinary skills	☒ Yes ☐ No
Available for PhD students from other courses	☒ Yes ☐ No
Prerequisites (not mandatory)	
Examination methods (if applicable)	
Suggested readings	Amezquita et al. Orchestrating Single-Cell Analysis with Bioconductor (https://bioconductor.org/books/release/OSCA/)
Additional information	

Course unit English denomination	Applied Structural Bioinformatics
SS	BIOS-08/A
Teacher in charge (if defined)	Stefano Toppo
Teaching Hours	10
Number of ECTS credits allocated	2
Course period	October 2025
Course delivery method	☒ In presence ☐ Remotely ☐ Blended
Language of instruction	English
Mandatory attendance	☒ Yes (100% minimum of presence) ☐ No
Course unit contents	Topics of structural bioinformatics will be addressed with a practical approach, starting from sequence data that will be analyzed in various ways. From multiple sequence alignment to molecular phylogenetics and the construction of a protein structural model where amino acid mutations will be mapped for comparison. The practical part will be based on sequences from SARS-CoV-2 haplotypes.
Learning goals	Students will learn to use some bioinformatics techniques for the analysis of structural variants on proteins.
Teaching methods	Practical activity at the computer lab after a theoretical introduction to the topics
Course on transversal, interdisciplinary, transdisciplinary skills	☒ Yes ☐ No
Available for PhD students from other courses	☐ Yes ☒ No

Prerequisites (not mandatory)	None
Examination methods (if applicable)	
Suggested readings	Materials provided during the course unit
Additional information	