CORE TRAINING | BIOMEDICAL SCIENCES

- 10 credits must be obtained from Core training (out of your total 20 ECTS required)
- You need to choose a **minimum of 3 modules** (each worth 1.5 or 2 ECTS) and **9 'Chapitres choisis'** (0.5 ECTS each).
- There is no upper limit to the number of credits that can be obtained from Core training. Other credits obtained from conferences, from courses and workshops, from volunteering, and from attending PhD retreats are all capped at 3 ECTS.

Modules and "Chapitres choisis"

- See below for further details regarding the available modules and "Chapitres choisis"
- Registration to a module or chapitre choisi is opened 1-2 months prior to its start date
 - An email to announce the registration and deadline will be sent by Dylan Walser (Dylan.walser@unige.ch)
- The Chapitres choisis are part of the Faculty seminar series:
 - <u>https://www.unige.ch/medecine/fr/recherche/seminaires-facultaires-et-de-departement/jeudis-de-la-faculte-chapitres-choisis-5/</u>

FACULTÉ DE MÉDECINE FACULTÉ DES SCIENCES



LIFE SCIENC

PhD SCHO



Teaching activities

- The doctoral school does not currently provide a list of teaching activities and interested students should look for opportunities independently. Public announcements to recruit tutors are made on regular basis within the University.
- Before starting a teaching activity, we recommend contacting your program coordinator to confirm the number of ECTS that can be gained.

Supervision of an intern

- PhD students are strongly encouraged to supervise interns. However, PhD students should first contact the doctoral school prior to the supervision and provide the following documents:
 - A letter of motivation, detailing the proposed project (context, aim, strategies, duration...) and how it is distinct from the PhD (the intern should have their own project and cannot be used as a "technician" for the PhD student).
 - A letter of support signed by the PI where they agree to the supervision.
- At the end of the internship, the intern should send the doctoral school both:
 - A scientific report which includes a short introduction, results section and discussion (various lengths and format accepted; PhD student can correct report prior to submission). In the report, the name of the PhD student should be mentioned as a supervisor.
 - Their evaluation of the supervision by the PhD student (confidential and to be sent independently by the intern).
- As a general guideline, a 2-month student supervision will equate to 1 ECTS (up to a maximum of 3 ECTS total).





Modules:

2024-2025



HISTO-PATHOLOGY (MBM1) 2.5 ECTS

Dates: September 16, 17, 19, 23, 24, 26, and 30. Examination October 3 and 4, 2024

Contact: Marie-Luce Bochaton-Piallat Dpt of Pathology and Immunology

Priscilla Soulié Dpt of Cellular Physiology and Metabolism Jackie Perrin-Simonnot Dpt of Cellular Physiology and Metabolism Jean-Christophe Tille Dpt of Clinical Pathology Sophie Clément Dpt of Microbiologiy and Molecular Medicine Virgine Hamel Dpt of Molecular and Cellular Biology, FacSci

This module is not opened to MD-PhD students. PhD students are required to attend all sessions. Number of students : 12

INTRODUCTION (1 session) Monday September 16, 10h00-12h00

HISTOLOGY (2 sessions)

Tuesday September 17, 9h00-13h00, and Thursday September 19, 13h00-17h00

Study of primary tissues (epithelium, connective tissue, muscles, vessels, nervous tissue, lymphoid tissue) and some typical organs.

HISTOPATHOLOGY (2 sessions)

Monday September 23 and Thursday September 26, 9h00-13h00

Study of the main concepts of general pathology (cell death: necrosis and apoptosis, inflammation, tissue repair, tumor) and some organs with typical pathological alterations.

RESEARCH APPLICATIONS (2 sessions)

Tuesday September 24, 9h00-12h00 and Monday September 30, 9h00-11h00

Study of different microscopic approaches (optical, immuno-fluorescence, confocal, electron and expansion microscopy) and their applications in research (immunogold, immunohisto/cytochemistry, live imaging).

ORAL EXAM

Thursday October 3 and Friday October 4, time to be determined

Description of slides at the microscope & discussion on research application





CELL INTERACTION (MBM2) 1.5 ECTS



Dates: TBA ORAL EXAM :

The number of participants is limited to 8 students

« Introduction; Cell-Cell Adhesion, Actin Cytoskeleton », Dr. B. Wehrle-Haller

« Integrin adhesion & signalling », Dr. Michael Bachmann

« Using informatics tool to study 3D proteins structures », Dr. B. Wehrle-Haller

« Hyaluronic-acid -binding cell surface receptors », Dr. Pietro Cacialli

« Bacterial-adhesion and host Interactions », Dr William Kelley

«Direct Communication via Gap Junctions », Dr. Filippo Molica

The course aims to introduce students to the biology of cell-cell and cell-matrix interaction, from pathogen-host to cell-cell communication, and from molecular and genetic factors to tissue function and disease. The course involves attending 6 sessions held in a three –week period, guided by experts in their respective fields.

Each session lasts about 2 hours and is focused on discussing current knowledge and techniques used in studying cell interactions, using as reference pre-assigned research articles relevant to the chosen topics. It is important for students to read the material before class and to actively engage in the discussions. Student evaluation is achieved through a 30 minutes oral examination on one out of 6 papers associated with the course subjects.





Module in Metabolism (MBM3)

- Human and mouse anatomy in context of metabolism; October 2024 7 Sessions, 2.5 ECTS
- Importance of gut microbiota;
- Fat metabolism;
- Pancreas and mechanisms of insulin secretion;
- Glucose homeostasis;
- Muscle physiology
- Lipids
- Clinical overview on the metabolic diseases

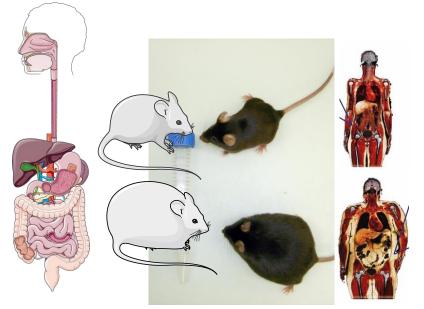
Lectures by leading experts in the respective areas :

P. Maechler, A-C. Gavin Perrin, M., V. Schwitzgebel Luscher, T. Brun, S. Konig, C. Veyrat-Durebex and M. Trajkovski

Practical work – Mouse anatomy, dissection/surgery, overview on the metabolic facilities

Organisers: Mirko Trajkovski and Pierre Maechler





2/2

Module in metabolism 2024 (MBM3) 2.5 ECTS

Session

1. Monday 07.10 / 9-12.30am	Mirko Trajkovski	
2. Monday 07.10 / 1.30-5pm	Mirko Trajkovski + lab	
3. Thursday 10.10 / 9-12am	Pierre Maechler and Thierry Brun	
4. Tuesday 15.10 / 9-11am	Valerie Schwitzgebel Luscher	
5. Wednesday 16.10 / 9-11am	Anne-Claude Gavin Perrin	
6. Friday 18.10 / 9-11am	Christelle Veyrat-Durebex (Overview on the metabolic facilities)	
7. Friday 18.10 – 2-4pm	Stéphane Konig	

Exam Tuesday 29.10. (or 05.11.) – 1-5pm Mirko Trajkovski and Pierre Maechler

Organizers: Mirko Trajkovski and Pierre Maechler

The module will have eight sessions and will include lectures given by the PIs; practical (hands on) work by the students; overview on the most important literature in this area; and overview on the clinical aspects in diagnosis and treatment of several metabolic diseases. The main goal is to familiarise the students with the basic principles governing regulation of the energy homeostasis and metabolism in health and disease, and will be accomplished by addressing the following specific subjects:

- Human and mouse anatomy in context of metabolism; emphasis on the main metabolic organs;
- Importance of gut microbiota in regulation of energy homeostasis;
- Fat metabolism different shades of fat, characteristics and importance;
- Function of the pancreas with emphasis on the insulin secretion;
- Importance of the brain in regulating the energy homeostasis;
- Clinical overview on the metabolic diseases





Introduction to applied statistics for health data analysis (MBM4) 2 ECTS



9 Sessions (from 2:15 to 5:00 pm, weekday: Monday), focusing on:

- · Descriptive statistics and introduction to statistical software
- Statistical hypothesis testing and inference and confidence intervals
- Parametric and non-parametric tests
- · Correlation and principle of linear regression models
- Statistical power and sample size
- · Interpretation of results, bias and how to mitigate them
- Reporting statistical analyses

Professeure Delphine COURVOISIER, Service qualité des soins, Direction médicale et qualité, HUG

Contact : Delphine COURVOISIER (delphine.courvoisier@unige.ch)

Number of course participants: minimum 6, no maximum.

The aim of this course is to provide basic knowledge of statistical inference, methods to describe data, to test hypotheses and to characterize associations between variables. This aim includes a correct interpretation of the results of the analysis. The course has about 1/3 of theory and 2/3 of practice with statistical software. Students are encouraged to bring their own laptops to the course.



Current topics in applied statistics for health data (MBM5) 2 ECTS

9 Sessions (from 2:15 to 5:00 pm, weekday: Tuesday), focusing on:

- Reproducibility of statistical analysis
- Regression models (logistic and gaussian)
- Non linear regression
- Missing data and imputation
- Confounding and multivariable models for adjustment
- Effect modification and mediation

Professeure Delphine COURVOISIER, Service qualité des soins, Direction médicale et qualité, HUG

Contact : Delphine COURVOISIER (delphine.courvoisier@unige.ch)

Number of course participants: minimum 6, maximum 28.

The aim of this course is to provide a hands-on approach to regression, especially in the context of observational studies. This includes theoretical and practical lectures on (non-)linear associations, missing data, and how to impute them, and confounding. In addition, tests for mediation and effect modification (eg. Gene x environment effect) will be presented and applied.

The course has about 1/3 of theory and 2/3 of practice with statistical software (R software). Students must bring their own laptops to the course.





Protein purification and identification by Mass Spectrometry (MBM6)

2 ECTS



 Dates:
 November 5
 13h00 - 14h00

 November 12, 13, 19, 20, 26
 13h00 - 17h00

Organizers/ Supervisors: Oscar Vadas, Alexandre Hainard, Rémy Visentin

Session comprises both : 1) Theoretical presentations by students and tutors

2) Hands-on experimental part

Methodologies:

- 1) Cell lysis, centrifugation / Protein purification by affinity chromatography / Enzymatic activity test and SDS-PAGE analysis
- 2) In-gel protein digestion for Mass Spectrometry data generation and analysis

Theoretical part:

- 1) Protein engineering and purification strategies
- 2) Principles of a mass spectrometer analyzer and mass spectrometry applications

Evaluation: Student individual presentations and preparation of a scientific report

Participation is limited to 8 people



IMMUNITY (MBM7) 2.0 ECTS



Monday October 28, 2024 at 2 - 5.30 pm; (xxxxxx CMU) : Paul WALKER : Cancer and the Immune System: From immunosurveillance to immunotherapy.

Monday November 4, 2024 at 2 - 5.30 pm; xxxxxx CMU) : Simone BECATTINI: Role of the Microbiota in Immunity.

Monday November 11, 2024 at 2-5.30pm (xxxxx CMU): **<u>Gisella PUGA YUNG</u>**: NK cell biology, Xenotransplantation, Immunodeficiency, immunosuppression/biologicals/immunoglobulins as treatment for autoimmune diseases

Monday November 18, 2024 at 2 – 5.30 pm; (xxxxxx CMU) : Denis Migliorini: Engineered immune cells as cancer therapeutics

Monday November 25, 2024 at 2 – 5.30 pm; xxxxxx CMU) : Christoph SCHEIERMANN: The circadian immune system - a new paradigm

Monday December 2, 2024 at 2 – 5.30 pm; (xxxxxxxx CMU) : Federico Simonetta: Transplantation (allogeneic HSCT, GvHD, GvT); Immunoregulatory cellular therapies; Tregs; Peripheral tolerance

Monday December 9, 2024 at 2 - 5.30 pm; (xxxxxxx CMU) : Examination

The course will take place with a minimum of 6 and a maximum of 12 participants. Exact times and rooms are subject to confirmation. The aim of the course will be to present selected areas of basic and applied immunology over 5 themed sessions. The interdependence of innate and adaptive immune interactions will be stressed, and a selection of protective and pathologic immune processes will be discussed. Students are expected to attend all sessions and to actively participate. Assessment will be made both during the courses (some reading will be required beforehand) and in a final exam.



Communicating your science: how to make the message stick! (MBM8) 1.5 ECTS

Dates:

First full course (Mondays 25.11and 2.12): 8.45 am to 6.15 pm (1 hour lunch break), Monica Gotta and Miriam Stoeber Second full course (dates to be announced): 8.45 am to 6.15 pm (1 hour lunch break), Monica Gotta and Sofia Barbieri Participation is limited to 8 people

Organizers: Monica Gotta, Sofia Barbieri and Miriam Stoeber

Goals of the course:

- Communicate persuasively your work in an oral presentation.
- Create slides that respect fundamental design and principles and present data appropriately.
- Experiment strategies to continue improving your presentation skills.
- Write a title and a concise abstract that tells your scientific story.
- The participants will bring a 5 minutes presentation of their research project to the first day of the course.



GENEV



Effective scientific writing (MBM9) 1.5 ECTS

Dates: TBA

Organizers: Patrick Meraldi and Intidhar Labidi-Galy

The course will be limited to 8 students maximum and 3 minimum.

The aim of the course is to give PhD students the basics of effective scientific English writing. The course will focus on the redaction of abstracts based on prominent cancer biology papers. The course will also study how to use and not to use ChatGPT when writing scientific documents. Prior knowledge in cancer biology is not required.



Effective Scientific writing (MBM9)



BEFORE:

The DNA replication is an error prone process in which DNA mismatch repair (MMR) plays a crucial role in maintaining the genome stability. The dimeric MutS protein found in E.coli is able to bound to DNA strand and initiate the repair mismatch with a mechanism that is still partial unclear.

In this study, we define the dimeric crystal structure of the MutS protein from E.coli using a multiwavelength anomalous dispersion experiment. We used the protein crystal structure to elucidate the mechanisms of DNA binding, scanning and repair in MMR.

The MutS dimer is the physiologically relevant form but we founded that only one of the monomer is able to bind to GT mismatch and to ADP. The DNA interaction mainly occurs by nonspecific major groove DNA-binding. We observed that only one of the monomer has specific mismatch-binding domains located on the minor groove side of DNA.

We hypothesized that after the binding to the mismatch site, the MutS dimer is retained on the DNA strand until a strand-discrimination signal is found. This signal is mainly lead by different charges interactions mechanisms.

We already know that in human two homologs of the MutS dimer exist: MHS2/MHS3 or MHS2/MHS6. The MSH3 or the MSH6 monomers of the MutSa protein are responsible for the mismatch discrimination.

Furthermore, the crystal structure of the protein that we provide made possible to localize the mutations in those domains that could be associated to cancer predispositions such as HNPCC (hereditary non-polyposis colorectal cancer).

247 Words

AFTER:

DNA replication is an error prone process that requires mismatch repair to maintain genomic stability. The dimeric E. coli protein MutS binds to DNA and initiates mismatch repair via an unknown molecular mechanism. Here, we defined the dimeric crystal structure of MutS to elucidate the DNA binding, scanning and repair mechanisms. We find that in the MutS dimer, only one monomer binds to GT mismatches and ADP via the minor groove side, while the other monomer forms nonspecific major groove DNA-interactions. We hypothesize that after binding to the mismatch site, the MutS dimer is retained on the DNA strand until a strand-discrimination signal is found. These findings fit with the existence equivalent MutS heterodimers in humans: MHS2/MHS3 or MHS2/MHS6. The crystal structure of the protein also reveals the location of mutations associated to cancer predispositions such as hereditary non-polyposis colorectal cancer.

141 words



PROJECT DEVELOPMENT in GENE EXPRESSION REGULATION (MBM 10) 2.5 ECTS

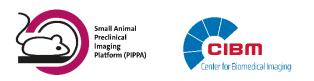


- Monitors: Prof. Martine Collart (MIMOL), Prof. Guillaume Andrey (GEDEV), Prof. Simon Braun (GEDEV), Prof. Pei-Hsuan Wu (GEDEV)
- The module comprises one introductory and three 4-hours sessions.
- Before each session: A research problem related to gene expression regulation is proposed to the students. Each group of students will **prepare a project proposal** to tackle the presented problem.
- During the session: each group will be given 20 minutes to present their proposal (in English), which should include:
 - 1) An introduction followed by an outline of the steps needed to reach the objective,
 - 2) The experimental approach(es) used and the reasons behind choosing these approaches
 - 3) Expected results, possible pitfalls and impact of the project
 - The presentations will be interactively discussed in a <u>critical and detailed</u> manner.
- This module aims at helping the students in **designing and interpreting research projects** that address important questions in the field of gene expression regulation. General knowledge of the mechanisms underlying gene expression will be taught, yet, the module is not meant to be exhaustive but rather focuses on a few key questions in the field.
- The introductory meeting will be held on <u>Friday 13th December 2024</u> from 10h00 to 12h.
- The sessions will take place on Thursday: 23rd January, Friday 14th February and Friday 7th March 2025 from 14h00-18h
- ATTENDANCE AT ALL SESSIONS IS MANDATORY
- The course will only take place with a minimum of 9 participants and a maximum of 16



Preclinical Imaging Course 2024 (MBM11) 1.5 ECTs

Dates: February 17th - 19th (Days 1-3) & February 21st (Day 4-MCQ) Organizers: Dr Didier Colin (PIPPA), Olivia Bejuy (CIBM) Participants: maximum 10 Evaluation: MCQ



GENEVA

Location: Small Animal Preclinical Imaging Platform (PIPPA) & Center for Biomedical Imaging (CIBM), HUG, Bâtiment des Laboratoires, 6th floor.

There is no prerequisite to follow this module.

This module will provide principles and advanced concepts in state-of-the-art techniques used in animal preclinical imaging. Students will learn proper practices in animal imaging and image analyses in Computed Tomography (CT), Magnetic Resonance Imaging (MRI), Positron Emission Tomography (PET), Single-Photon Emission Computerized Tomography (SPECT) and Luminescence/Fluorescence Optical Imaging. Multimodal imaging methods will also be discussed. Theory will be supported by hands-on sessions on the equipment.

Course outline: 3 sessions of 1 day each. Morning (10h-12h): theory sessions; afternoon (13h30-17h): hands-on sessions with imaging scanners and image analyses. 1 exam session of 1h. Total duration: **4 days**

- Day 1: General introduction on preclinical imaging, Computed Tomography (CT) and Optical Imaging
- Day 2: Magnetic Resonance Imaging (MRI)
- Day 3: Positron Emission Tomography (PET) & Single-Photon Emission Computerized Tomography (SPECT)
- Day 4: MCQ Evaluation (1h)





Medical Genetic (MBM12) 1.5 ECTS

From 14pm to 4pm room E09.2753.A

Prof. E. Zdobnov (Département de Médecine Génétique et Développement)

- Thursday 28 février 2025: Introduction by Prof. T. Frayling / Prof. E. Zdobnov
- Monday 4 march 2025: Genetic Variation by Dre E. Kriventseva
- Thursday 7 march 2025: Mendelian Disorders by Prof. T. Frayling
- Monday 11 march 2025: Cytogenetics by Dre F. Bena
- Thursday 14 march 2025: Technology by Prof. E. Zdobnov
- Monday 18 march 2025: Complex Disorders /Traits by Prof. E. Zdobnov
- Thursday 21 march 2025: Comparative Genomics by Dre E. Kriventseva
- Monday 25 march 2025: Epigenetics by Prof. Guillaume Andrey
- Thursday 28 march 2025: Exam by Prof. E. Zdobnov



VIROLOGY (MBM13) 2 ECTS

Organizers: Manel Essaidi-Laziosi and Sophie Clément



Rooms : TBA Students : 6 minimum, 10 maximum

DATE	TIME	COURSE	SPEAKER
Tuesday, 15 th of April 2025	1:30pm-4:30pm	Presentation of the course General introduction to virology Virus detection tools	Manel Essaidi-Laziosi Sophie Clément
	4:30pm-5:30pm	Practical part: BSL3 lab visit	
Tuesday, 6 th of April 2025	1:30pm-3:30pm	Quasispecies	Manuel Schibler
	3:30pm-5:30pm	Influenza virus and emergence of antiviral resistance	Manel Essaidi-Laziosi and Sophie Clément
Tuesday, 13 th of May 2025	1:30pm-3:30pm	Emerging viruses	Isabella Eckerle
	3:30pm-5:30pm	Emergence of SARS-CoV-2 VOCs	Manel Essaidi-Laziosi and Sophie Clément
Tuesday, 20 th of May 2025	1:30pm-3:30pm	Anti-viral immunity	Mirco Schmolke
	3:30pm-5:30pm	paper presentations Graphical abstract	Manel Essaidi-Laziosi and Sophie Clément
Tuesdav. 20 th of Mav 2025	1:30pm-3:30pm		Exam



Data Management & Laboratory Information Management System (LIMS)(MBM14)



1 ECTS Dates (2025): Day 1 : Monday April 7th 9 :00 - 12:00 Day 2 : Tuesday April 8th 9 :00 - 12:00 Day 3 : Wednesday April 9th 9 :00 - 12:00 Day 4 : Thursday April 10th 9 :00 - 12:00 Room: CMU tbd

Exam: MCQ & practical exercice + participation to all sessions is mandatory

Participants number: Minimum 4 & maximum 12 students

This course aims to introduce students to the data management as it is asked by the FNS. In addition, a specific training to the Laboratory Information Management System (LIMS), eLabNext, implemented at the Medical Faculty, as well as the YARETA repository, will be provided.

Day 1: General presentation about data management

Day 2: Introduction to YARETA & the LIMS systems

Day 3: eLabNext & YARETA training hands-on session (please bring your own laptop)*

Day 4: Feedback discussion & Exam (please bring your own laptop)*

Responsible <u>Coralie Fournier</u>, <u>SmartLab</u> project manager.

Speakers : Floriane Muller, Jean-Blaise Claivaz, Hugues Cazeaux

*We have two computers available for loan. If you need it, do not hesitate to contact Coralie Fournier.



Developmental Biology (MBM15) 1.5 ECTS

Every Wednesday of _May (7,14,21 & 28 May 2025); room CMU E09.2753.A, from 2pm to 5pm. (4 sessions) + 20 min ORAL EXAM (4 of June)

Prof. P. Herrera, Dr. F. Thorel (dépt. de médecine génétique & développement CMU).

Optional: see and practice with mouse embryo injections to generate transgenic mice (@transgenic core facility)

- The course will only take place with a minimum of 6 and a maximum of 8 students.
- Attendance at all sessions is mandatory

Topics:

- Transgenics and mouse molecular genetics
- Limb development
- Regenerative medicine : ES and IPS cells; cell reprogramming
- Pancreas development and regeneration





Immuno & Metabolic Aspects of Cardiovascular Disease (MBM16) 2.5 ECTS



Dates: from April 29th to June 10th, from 2pm to 5pm

Contact: Dr. Sandrine Morel, Dr. Filippo Molica. Dept. of Pathology and Immunology

PhD students are required to attend all sessions. For some sessions, students will have to read articles. Number of students : 5-10.

Session 1 (Tuesday April 29th): Vascular Physiology and Atherosclerotic Diseases (Dr. Filippo Molica and Dr. Sandrine Morel).

- Session 2 (Tuesday May 6th): CerebroVascular Accidents (Dr. Sandrine Morel).
- Session 3 (Thursday May 8th): Cardio-Metabolic Diseases (Dr. Christophe Montessuit).
- Session 4 (Thursday May 15th): : Lymphatic Circulation and Immunity (Prof. Stéphanie Hugues).

Session 5 (Thursday May 22nd): Circadian Rhythm, Inflammation and Cardiovascular Diseases (Prof. Christophe Scheiermann).

Session 6 (Thursday May 29th): Auto-Immune Diseases and Cardiovascular Risks (Prof. Gaby Palmer).

Session 7 (Tuesday June 3rd): Fundamental Basis of Vascular and Cardiac Anatomo-Pathology (Dr. Christophe Lamy and Prof. Marie-Luce Bochaton-Piallat)

> ORAL EXAM

June 10th. Each student will have to discuss the topic of one of the sessions. The topic of the exam will be announced to each student at the end of the last session. Active participation during all the sessions will count towards the final note.



Bioimaging Course 2025: Imaging techniques in life and biomedical sciences (MBM17) 1.5 ECTs



Dates: June 9- June 13 (4.5 days)

Organizers: Dr. F. Prodon (contact), O. Brun, Dr. B. Maco, Dr. D. Moreau, Dr, V. Mercier, Dr. D. Colin, O. Bejuy

Participants: minimum 9, maximum 30

Evaluation: MCQ

Room: TBA

This course can be an advantage for the module "Image Processing and Analysis (MBM17)", but it is not a prerequisite.

This module will focus on state-of-the-art techniques in bio-imaging and will provide underlying principles and advanced concepts in electron & light microscopy, high-content imaging and preclinical imaging, thus covering a wide range of observation scales from ångströms (molecules) to centimeters (whole animal). Multimodal and multiscale imaging methods will be discussed and two advanced microscopy techniques (FLIM and FCS) will be also introduced. Finally, a tour will be organized to show the equipment available in the different imaging core facilities of the University of Geneva.

This course will take place in 4 sessions of 1 day each (total duration of this module: **4.5 days**). Hand-on sessions will be organized in order to recess the theoretically taught content (morning: theory, afternoon: demos).

- General introduction, F. Prodon (day 1)
- Light microscopy (fluorescence microscopy) : widefield vs confocal microscopy, F. Prodon and O. Brun (day 1)
- Electron microscopy techniques (SEM, TEM, etc...), B. Maco (day 2)
- High content screening, D. Moreau and V. Mercier (day 3).
- Preclinical imaging (MRI, CT, PET, etc.), D. Colin and O. Bejuy (day 4).
- Evaluation (day 5)



Image Processing and Analysis (MBM18) 2 ECTS



Dates: Courses on June 16, 17, 18 and 19, 2025, from 13:30 to 17:30. Exam on June 20 from 13h30 to 17h30.

Room: TBA.

Limited to 15 students.

Organizers: Nicolas Liaudet and Dimitri Moreau

This module will be an introduction to image processing and analysis. Nevertheless, preliminary knowledge in microscopy and in sample preparation are an advantage (cf. Histo-pathology and Bioimaging modules). Modern imaging techniques are generating an increasing amount of data; however, switching from qualitative observations to quantitative information remains a difficult step. This is even more critical when results must be published.

Participants will be taught basic theoretical background prior to hands-on software applications:

- Fundamentals of image processing and analysis, Nicolas Liaudet and Sergei Startchik
- Electron microscopy (3D, FIB, correlative, etc.), Bohumil Maco
- Optical microscopy (IHC and fluo. analysis, nucleus detection, etc.), Nicolas Liaudet and Sergei Startchik
- High content screening (workflow, phenotypic analysis, etc.), Dimitri Moreau



Alphafold – structure prediction and visualisation using PyMol (MBM19)



Date: April 2nd 2025 : 8h30 – 12h30 (date subject to modification)

Organizer : Oscar Vadas

- **1. Theory :** Alphafold: principle, benefits and limitations with examples
- 2. Hands-on : Alphafold model analysis and figure preparation using PyMol

Summary :

This short module aims at explaining how **alphafold** protein structure prediction software works, how to use it and identify what kind of information can be obtained using this algorithm.

A practical part will introduce the **PyMoI** software, to analyse alphafold-generated models and prepare figures for illustrations

Evaluation : Preparation of a report describing and illustrating alphafold predictions

Participation is limited to 12 people Open to postdocs and PIs



CUSO Biology





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PhD course programmes

- Microbiology
- StarOmics
- Molecular Plant Sciences
- Ecology & Evolution







CUSO Biology





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- \rightarrow Courses in different locations (Geneva, Lausanne, Neuchâtel, Fribourg, Bern)



Université de Lausanne

Reimbursements for CUSO members:

 \checkmark travel expenses \checkmark accommodation (if > 1h15 from your home)



CUSO courses

(some examples)





- Introduction to R (UNIGE)
- Computer Skills for Biological Research: Intro. to GNU/Linux & Bash Scripting (UNIGE)
- First Steps with Python in Life Sciences (UNIBE)
- Teaching (and Learning) Science (UNIL)
- Research Data Management for Microbiologists (UNINE)
- Electron Microscopy (EM) and Cryo-EM Practical Course (UNIL)
- RNA in Plants, Animals, and Bacteria (UNIL)
- Genomics and society (UNIL)
- Advanced programming with R (UNIL)
- Molecular Population Genetics (UNIGE)
- Data Visualisation with R (UNIL)
- Data Analysis and Graphing Using GraphPad Prism (UNIL)

• .



CUSO courses in Geneva





Upcoming courses:

- Introduction to R Nov/Dec 2024
- Molecular Population Genetics Jan 2025
- Computer Skills for Biological Research: Intro. to GNU/Linux & Bash Scripting Feb 2025
- Advanced Computer Skills for Biological Research June/July 2025



Introduction to R (fall edition)

Dates: 21-22 November and 5-6 December 2024

Organizers: BioSC : José Manuel Nunes , Nicolas Hulo Participants: maximum 18 Credits: Presence and active participation: 1 ECTS, written report: 1 additional ECTS Location: University of Geneva – Sciences II- 4th floor – AGP computer lab

Description:

The R environment for statistical computing and graphics has become an undisputed reference for data analyses in Life Sciences, Biology and many other sciences. It combines unparalleled facilities to learn, design, explore, analyse, graph, tabulate, draft and report computational/statistical data analyses. Its simple and reliable yet powerful extensions' system (packages) makes R the environment where many new methods are developed. The RStudio interface provides an easy-to-use interface to this complete system that runs almost equally in a large number of operating systems. Furthermore, R is free software. The course includes some topics in statistics and presents some programming-related features of R but it is not intended as an introductory or refresher statistics course or an introduction to programming.

Learning objectives:

By the end of the course, the participants are expected to: be able to make basic exploratory data analyses

- Write R expressions to perform everyday tasks in data analysis
- Produce tables and graphics and make them available as files
- Be capable of reading, understanding and writing basic R scripts
- Use the help facilities available

Previous knowledge/skills: The course assumes no prior knowledge of the R system nor any specific background except being familiar with basic text editing and file manipulation (copy, move) in computer systems.

Technical requirements: You may use the computers provided by the University or bring your own laptop in which case you'll need to make a 10-minute check-up test two days prior to the course (details provided upon confirmation).





Computer Skills for Biological Research: Introduction to GNU/Linux and Bash Scripting

Dates: 10-14 February 2025

Organizers: BioSC : José Manuel Nunes Participants: minimum 6, maximum 10 Credits: Check with your programme coordinator Location: University of Geneva – Sciences II- 4th floor – AGP computer lab

Description and Learning Objectives:

This course intends to present useful computer tools and techniques for young researchers in biology that substantially extend basic computer knowledge acquired at undergraduate levels. The course concentrates on GNU/Linux environment and tools because it is powerful, free and easy to install in any kind of computer. Moreover, most of the computer clusters available for scientists run Linux.

The course is intended for beginners and for more advanced people, its level of complexity increasing through the four days. Basic knowledge in computing and programming is a plus but is not mandatory.

The first part of the course will consist in learning the basic of GNU/Linux: installation of the environment, useful shell commands to work with text files, simple command lines and the use of regular expressions, pipes, and short scripts.

The second part will consist in developing more complex scripts, as well as exercises using a computer cluster. Upon conclusion of the course the attendees are expected to be able to:

- use comfortably GNU/Linux workstations environments
- work with shells and write shell scripts,
- manipulate data files and perform file format conversions
- be able to read and write simple regular expressions
- use GNU/Linux computer clusters.

The training will provide a minimal theoretical basis in each of the topics listed below and concentrate on practical aspects through numerous applications. It will confer a working autonomy to solve problems while handling data and conducting data analyses pertinent to the researcher in biology.





Introduction to R

Dates: twice two full days — June/July 2025
Organizers: BioSC : José Manuel Nunes , Nicolas Hulo
Participants: maximum 30
Credits: Presence and active participation: 1 ECTS, written report: 1 additional ECTS
Location: University of Geneva – Sciences II- 4th floor – AGP computer lab

Description:

The R environment for statistical computing and graphics has become an undisputed reference for data analyses in Life Sciences, Biology and many other sciences. It combines unparalleled facilities to learn, design, explore, analyse, graph, tabulate, draft and report computational/statistical data analyses. Its simple and reliable yet powerful extensions' system (packages) makes R the environment where many new methods are developed. The RStudio interface provides an easy-to-use interface to this complete system that runs almost equally in a large number of operating systems. Furthermore, R is free software. The course includes some topics in statistics and presents some programming-related features of R but it is not intended as an introductory or refresher statistics course or an introduction to programming.

Learning objectives:

By the end of the course, the participants are expected to: be able to make basic exploratory data analyses

- Write R expressions to perform everyday tasks in data analysis
- Produce tables and graphics and make them available as files
- Be capable of reading, understanding and writing basic R scripts
- Use the help facilities available

Previous knowledge/skills: The course assumes no prior knowledge of the R system nor any specific background except being familiar with basic text editing and file manipulation (copy, move) in computer systems.

Technical requirements: You may use the computers provided by the University or bring your own laptop in which case you'll need to make a 10-minute check-up test two days prior to the course (details provided upon confirmation).





Advanced Computer Skills for Biological Research

Dates: twice two full days — June/July 2025
Organizers: BioSC : José Manuel Nunes , Nicolas Hulo
Participants: minimum 6, maximum 10
Credits: Presence and active participation: 1 ECTS, written report: 1 additional ECTS
Location: University of Geneva – Sciences II- 4th floor – AGP computer lab



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Description:

A hands-on practical course (two times two full days) that is a continuation of <u>*Computer Skills for Biological Research*</u>, looking more deeply into regular expressions (sed and grep), the use (and misuse) of pipes, input and output redirections and the design of bash scripts for use with computer clusters (slurm based).

It starts with an introduction to the awk scripting language highlighting its simplicity for the manipulation of large files including reshaping inputs/outputs and summarising data. It concludes with computer cluster parallelisation strategies.

The course is organised as a set of exercises that involve the manipulation of large fasta files retrieved from public resources

Learning objectives:

- Write well-documented and descriptive bash scripts.
- Write effective scripts to reformat the output of one program as the input of another
- Become a conscious user of regular expressions (not too long not too short)
- Use awk scripts to handle complex data structures (such as fasta entries) in a simple and efficient way
- · Identify the best strategy to use clusters for a given work and write the appropriate scripts



Molecular Population Genetics Training Course

Dates: 6-10 January 2025

Organizers: Alicia Sanchez-Mazas, BioSC : José Manuel Nunes **Participants:** minimum 6, maximum 20 **Credits:** check with your programme coordinator **Location:** University of Geneva – Sciences II- 4th floor – AGP computer lab

Description and Learning Objectives:

This course intends to present useful computer tools and techniques for young researchers in biology that substantially extend basic computer knowledge acquired at undergraduate levels. The course concentrates on GNU/Linux environment and tools because it is powerful, free and easy to install in any kind of computer. Moreover, most of the computer clusters available for scientists run Linux.

The course is intended for beginners and for more advanced people, its level of complexity increasing through the four days. Basic knowledge in computing and programming is a plus but is not mandatory.

The first part of the course will consist in learning the basic of GNU/Linux: installation of the environment, useful shell commands to work with text files, simple command lines and the use of regular expressions, pipes, and short scripts.

The second part will consist in developing more complex scripts, as well as exercises using a computer cluster. Upon conclusion of the course the attendees are expected to be able to:

- use comfortably GNU/Linux workstations environments
- work with shells and write shell scripts,
- manipulate data files and perform file format conversions
- be able to read and write simple regular expressions
- use GNU/Linux computer clusters.

The training will provide a minimal theoretical basis in each of the topics listed below and concentrate on practical aspects through numerous applications. It will confer a working autonomy to solve problems while handling data and conducting data analyses pertinent to the researcher in biology.





RNA-seq Hands-On

Dates: October 2025

BIO SCHO GENEVA

Organizers: BioSC : José Manuel Nunes , Nicolas Hulo Participants: minimum 6, maximum 10 Credits: Presence and active participation: 1 ECTS, written report: 1 additional ECTS Location: University of Geneva – Sciences II- 4th floor – AGP computer lab

Description and Learning Objectives:

In the first session, you will learn how to connect to a remote machine, basic command lines in the Linux environment and how to launch a program on a cluster. You will use various bioinformatic tools to map reads on the genome and to calculate count tables. The hands-on will focus on the analysis of RNA-seq but you will also see the necessary tools needed for ChIP-seq/ATAC-seq and scRNA-seq. At the end of the first session, you will have a count table and various QC files

In the second session, we will go back to the scripts of the pipeline and understand more precisely what each line is doing. We will also review the QC files to identify potential problems

During the third session, we will import the count table in R

A second step of QC will be done with the Bioconductor package edgeR. With the same package we will do the statistical analysis. At the end of the session we will have:

- Various QC figures to estimate if the treatment has an effect and that there isn't too much variability between replicates.
- A list of differentially expressed genes with their P.value and fold change
- Visualisation of the output with Volcano plot and Heatmaps

The last session will be dedicated to try to give a biological meaning to the list of differentially expressed genes. For this, we will use the bioconductor package ClusterProfiler to do various pathway analyses and graphical representations of the output.

