Université de Paris

Master Bio-Informatique
In Silico Drug Design

**University of Paris**
**(2021-2025)**

**DETAILED LIST OF ECU's of the MASTER 2**

**BIOINFORMATIQUE - ISDD: In silico Drug design**

Two tracks are offered in the BI-ISDD master's degree, a track "ISDD-Macromolecule Modeling" in research (initial training, FI) or in alternating training (alternating training FA) and a track "ISDD-Bioactive Molecules" in research. Each of these two courses offers the possibility of obtaining a double degree (French-Russian or French-Italian).

The main blocks of teaching units "*Unité d'enseignements*" (UE ) include one module (ECUE) of project or application. The aim of these different projects is to analyze (in structure and flexibility) a protein target and to select candidate molecules for the binding of this target, and in fine, to model and simulate their interaction and molecular docking. These projects correspond to the ECUE: "BQ2CY060 Application in Drug Design & QSAR + BQ2CY080 Structural and dynamic modeling + BQ2CY190 Application of high-throughput screening", in connection with the other ECUE (BQ2CY090 Structural exploration of proteins, BQ2CY130 Ligand-based, ...).
In the ECUE "BQ2CY170 3-projects in Drug Design", students will then have to analyze in a combined way the results of these different complementary projects in an integrated (individual) project of Drug Design in Silico.

The summary then the detailed content of the UEs is presented.

# SUMMARY OF THE MASTER BIOINFORMATICS-ISDD (2021-2025)
## University of Paris - Bioactive Molecules course
## ISDD - Design of Bioactive Molecules

(French diploma or French-Italian double diploma for students who have completed the M1 in the Universities of Strasbourg and degli studi di Milano)

## MASTER 1 - SEMESTER 1 (30 ECTS) University of Strasbourg

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|---|---|
| **BQ1AY010** Methodology (10 ECTS)<br>Operating systems and networks<br>Statistical methods<br>Organic chemistry | G. Marcou, J.O. Dalbavie, N. Giuseppone |
| **BQ1AY020** Molecular Modeling (8 ECTS)<br>Basics of electronic structure calculations<br>Molecular modelling<br>Drug discovery | Rachel Schurhammer |
| **BQ1AY030** Chemoinformatics (10 ECTS)<br>Chemoinformatics 1<br>Chemoinformatics 2<br>Chemoinformatics 3 | A.Varnek |
| **BQ1AU040** Communication (2 ECTS) | Faculty of Languages |

## MASTER 1 - SEMESTER 2 (30 ECTS) Università Degli Studi di Milano

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|---|---|
| **BQ1BY010** Programming in C (6 ECTS) | C. Lorenzo |
| **BQ1BY020** Structural Biology and enzymology (6 ECTS) | Mr. Vanoni |
| **BQ1BY030** Medicinal chemistry (6 ECTS) | L. Belvisi |
| **BQ1BY040** Simulation, Modelling and Biomolecules (6 ECTS) | S. Pieraccini |
| **BQ1BU050** Bioactive molecules or equivalent module (6 ECTS)<br>**BQ1BY050** Synthetic Methods in Biotechnology or CHIM06 races<br>Or **BQ1BE060** Bioinformatics & language (if Erasmus semester - French degree) | L. Belvisi |

## MASTER 1 - SEMESTER 1 (30 ECTS) Università Degli Studi di Milano

| Master 1 at UNIMI | | |
|---|---|---|
| CHIM/02 | Physics Chemistry A | 9 |
| CHIM/02 or CHIM/06 | Physics Chemistry B or Organic Chemistry A | 9 |
| CHIM/01 or CHIM/12<br><br>(6ECTS from the courses listed below) | - Environmental Analytical Chemistry (CHIM/01)<br>- Advanced Electro-analytical Chemistry (CHIM/01)<br>- Application of photoluminescence and magnetic resonance in inorganic and metal-organic chemistry (CHIM/01)<br>- Environmental Chemistry (CHIM/12) | 6 |
| | Free choice (the student must obtain 6 ECTS by choosing courses proposed by the university and in coherence with the educational project) | 6 |
| INF/01 | Programming in C | 6 |
| BIO/10 | Structural Biology and Enzymology | 6 |
| CHIM/08 | Medicinal Chemistry | 6 |
| CHIM/02 | Simulation, Modeling and Biomolecules | 6 |
| | English | 3 |
| | Master thesis (prova) final | 3 |

**Parcours Molécules Bioactives**
**ISDD - Design des Molécules Bioactives**

## MASTER 2 - SEMESTER 3 (30 ECTS)
## University of Paris

***Block UE0 - Refresher course*** *(A-C. Camproux)*

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| ***BQAAY010*** *Unix and R Basics (Upgrade) (L. Regad)* |
| ***BQ2CY021*** *Toxicology -Methodology upgrade (A-C Camproux)* |

***Block UE1*** **- Data analysis in drug design (8 ECTS)** (A-C. Camproux)

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| **BQAAY070** (Python1 programming (Fuchs & P. Poulain) (3 ECTS)<br>Or **BQAAY080** Python programming 2 or **BQAAY030** Python project (S. Murail) (3 ECTS) |
| **BQ2CY050** Data analysis in Drug Design (A-C Camproux & L. Regad) (3 ECTS) |
| **BQ2CY060** Application in Drug Design & QSAR (O. Taboureau & L. Regad) (1 ECTS) |
| **BQ2CY070** Seminars and R&D (A-C Camproux) (1 ECTS) |

***Block UE2*** **- Molecular analysis and dynamics & drug design (7 ECTS)** (D. Flatters)

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| **BQ2CY090** Structural exploration of proteins (L. Regad) (3 ECTS) |
| **BQ2CY100** Dynamic Target Analysis I (D. Flatters) (2 ECTS) or According to level or path<br>**BQ2CY110** Dynamic analysis of targets II (G. Moroy) (2 ECTS) |
| **BQ2CY080** Structural and dynamic modeling (G. Moroy & D. Flatters) (2 ECTS) |

***Block UE3*** **- High-throughput screening: structure & ligand-based (5 ECTS)** (G. Moroy)

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| **BQ2CY120** Structure-based (G. Moroy) (3 ECTS) |
| **BQ2CY130** Ligand-based (O. Taboureau) (1 ECTS) |
| **BQ2CY140** Hits to lead (O. Taboureau) (1 ECTS) |

***Block UE4*** **- Space analysis of macromolecules (4 ECTS) (**A. Badel)

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| BQ1CY150 Data Analysis I (A. Badel & A-C Camproux) |
| BQ1CY160 Understanding macromolecules (D. Flatters) |

***Block UE5*** **- Preparation for research in Drug Design (6 ECTS)** (L. Regad)

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| **BQ2CY170** 3-projects in Drug Design (L. Regad & O. Taboureau) (2 ECTS) |
| **BQ2CY180** Tutored research project design (A-C Camproux) (2 ECTS) |
| **BQ2CY190** Application of high throughput screening (G. Moroy) (2 ECTS) |

## MASTER 2 - SEMESTER 4 (30 ECTS)

**INTERNSHIP (30 ECTS) (A-C. Camproux)**

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| ***UE6-*** **BQ2DY010** Preparation of a tutored research project (A-C Camproux & S. Murail) (3 ECTS) |
| ***UE7-*** **BQ2DT020** International research internship (A-C Camproux) (27 ECTS) |

*The M2 is mainly conducted in English. The Franco-Italian double degree involves the M1 validated in the Universities of Strasbourg and/or degli studi di Milano*

# MASTER 2 - SEMESTER 3 (30 ECTS)

## Block UE 0 : REFRESHER COURSE
**Persons in charge: A-C Camproux**

### ECUE 001- BQAAY000- Basics of Unix and R
**Persons in charge: L. Regad & G. Moroy**

**Title : Unix and R base (Upgrade)**
**Teachers: L. Regad, O. Taboureau, K. Audouze, S. Murail**

**Program**
Fundamental concepts of the Unix operating system and R software.
Acquire the basics of using the Unix operating system and the R software.

**Targeted skills: To** become familiar with Unix and R and to be as autonomous as possible during the practical sessions of computer science, bioinformatics and statistics.

### ECUE 002- BQ2CY020 - Upgrading in Toxicology (Biochemistry) -Methodology
**Person in charge : A-C CAMPROUX**

**Title : Toxicology (Biochemistry)-Methodology upgrade**
**Teachers:** J. Dairou, V Arluison, F. Rodrigues, N. Triballeau, A. Badel, A-C Camproux

**Program :**
The aim of the course is to introduce students to different experimental methods to detect and characterize molecular interactions, to introduce them to biochemical tools necessary to understand drug design: The drug designer is generally at the interface between the biologist, the clinician and the chemist. He must therefore have an initiation to the biophysical methods used in drug design projects. For in silico modeling in drug design, basic biostatistics is a crucial prerequisite.

**Necessary in Toxicology and Biochemistry (**J. Dairou, V Arluison, F. Rodrigues)
The drug designer must have an initiation to certain biophysical methods frequently used in drug design projects. There is a wide range of biophysical methods that allow the study of protein/protein or protein/ligand interactions by defining the contact zone or characterizing the thermodynamic and/or kinetic constants that govern the interaction.
Methods to understand the basic principles of thermodynamics, scattering, and optical methods will be covered. In particular, some physico-chemical techniques such as light scattering, optical methods, linear and circular dichroism, fluorescence and UV-visible spectroscopies. In addition, the course will introduce three other experimental methods for the identification and characterization of biomolecule interactions in vitro: Nuclear Magnetic Resonance, Isothermal Titration Calorimetry (ITC), FRET, acronym of "Fluorescence Resonance Energy Transfer", and BRET, acronym of "Bioluminescence Resonance Energy Transfer
Papers using other fundamental approaches for drug design such as Surface Plasmon Resonance (SPR) and immunological methods (ELISA, GST pulldown assays) will be analyzed and presented by the students. The course will include enzymology lessons focusing on the study of interactions between enzymes and ligands (substrates, inhibitors, allosteric effectors...).

*** Reminder of Biostatistics, R and basic biostatistics (**A. Badel, A-C Camproux)

Training in R and Biostatistics for students to manipulate and analyze data. At the end of the training, the goal is that students are able to determine the statistical analysis that can answer the biological question posed and implement that analysis. Interpret and conclude on the statistical and biological results of their study

Reminder of probability, introduction to biostatistics

- Estimation and statistical inference
- Classical tests, Student's t test, Chi2 test,
- Pearson correlation coefficient test and simple linear regression

Fundamentals+of+Biostatistics (Chapters [1,13]) in English (available on the internet) is a suitable medium: https://collegelearners.com/ebooks/fundamentals-of-biostatistics-8th-edition-pdf-free/

*** Chemistry kit for drug design: (**N. Triballeau)

The aim of the course is to introduce students to different tools in chemistry, necessary for the understanding of drug design methods and the characterization of molecular interactions

The drug designer is generally at the interface between the biologist, the clinician and the chemist. He/she must therefore have an introduction to biophysical methods and chemical chemistry concepts used in drug design projects.

Pharmacophore, Chemical chemistry toolbox,

"Atoms useful for drugs, hybridization, chemical functions, heteroaromatics, families of drugs IUPAC names & nomenclatures Isomers, Tautomers Stereochemistry, pseudo stereochemistry pKa of common groups, Most reactive groupsPreferred

conformations of important groups (3, 4, 5 and 6 saturated rings, amide, sulphonamide, biphenyls)- Introduction to matched molecular pair analysis - Elements of IP (Intellectual Property), SciFinder (CAS database query software) "

**Block UE1 - DATA ANALYSIS IN DRUG DESIGN (8 ECTS)**
**Person in charge : A-C. CAMPROUX**

**3 Python modules to choose from depending on level: EC101 or EC102 or EC 103**

## EC 101 - BQAAY070- Python I programming (3 ECTS)
## Persons in charge: P. FUCHS & P. POULAIN

**Title :** Python I programming
**Teachers : P. Fuchs, P. Poulain, S. Murail**

**Program :**

- Main data types (integers, floats, lists, strings, dictionaries, tuples)
- Loops, comparisons, tests
- Modules
- Input/output management with files
- Functions
- Regular expressions
- Notion of classes in Python

**Targeted Skills:**
Training bioinformaticians in Python programming
Know the main concepts related to Python programming.
Be able to write programs (i) analyzing large amounts of data, (ii) producing data (e.g. simulation of a system).
Be able to develop/debug a program in Python.

## Or EC 102 - BQAAY080-Python 2 programming (3 ECTS)
## Persons in charge: P. FUCHS & P. POULAIN

**Title : Programming python 2**
**Teachers : P. Fuchs, P. Poulain, S. Murail**

**Objectives in terms of knowledge:** Train bioinformaticians in Python programming. Acquire autonomy in the development of a Python program. Python is the most widely used programming language in bioinformatics today, especially for data analysis. It is very much in demand in laboratories, but also in private companies.

**Targeted skills:** Know the main concepts related to Python programming.
Be able to write programs (i) analyzing large amounts of data, (ii) producing data (e.g. simulation of a system).
Be able to develop/debug a program in Python.

**Program :**
Main data types (integers, floats, lists, strings, dictionaries, tuples)

- Loops, comparisons, tests
- Modules
- Input/output management with files
- Functions
- Regular expressions

Notion of classes in Python

## Or EC 103 - BQ2CY030-Python project (3 ECTS)
## Person in charge: S. Murail

**Title : Python project**
**Teachers : S. Murail**

Objectives in terms of knowledge: a) Training in Python programming or/and b) Carrying out projects in Python (advanced level in the context of drug design or structural bioinformatics projects).
**Program :**

a. Know the main concepts related to Python programming.

Be able to write programs (i) analyzing large amounts of data, (ii) producing data (e.g. simulation of a system). Be able to develop/debug a program in Python.

b. Be able to develop a project in Python in the context of drug design or structural bioinformatics projects.

## EC 103- BQ2CY050- Data Analysis and Drug Design (3 ECTS)
## Persons in charge: A-C CAMPROUX & L. REGAD

**Title : Data analysis and Drug Design**
**Teachers: A-C Camproux & L. Regad, O. Taboureau, F. Guyon**

**Program:** Optimize and combine different learning methods on drug design datasets Example on molecule space

- Unsupervised methods: descriptive or exploratory methods that propose groupings into object classes following algorithmic calculations

Factorial methods (Principal Component Analysis) and Classification methods (hierarchical or partitioning)

- Supervised methods: explanatory and/or predictive:

Cross-validation protocol, optimization criteria.
Linear and PLS model, knn, CART, Logistic regression
Presentation of SVMs and opening towards deep learning

**Knowledge objectives: To** teach students to combine and optimize different unsupervised and supervised learning methods to analyze drug design data. Both in the target space (structure-based application) and in the molecule space (ligand-based application) with the particular problems associated, descriptor selection and selection criteria, optimization, comparison and robustness of models in cross-validation.
Applications and projects will be done with different packages of the statistical software R.
Evaluation : Comparative reports on unsupervised methods on the one hand and supervised methods on the other hand + a presentation of articles or book chapters

## EC 104 - BQ2CY060 - Application in Drug Design & QSAR (1 ECTS)
## Persons in charge: O. TABOUREAU & L. REGAD

**Title: Application in Drug Design & QSAR**
**Teachers: O. Taboureau & L. Regad**

**Program :**
The goal of this course is to apply the various unsupervised and supervised techniques seen in class to develop a QSAR model to predict the activity of small molecules for a given target. These models will then be used to develop chemical library filters from the supervised methods. Application of these filters to the search for new inhibitors of a given target This project will be carried out with the statistical software R.

**Targeted competences : Implementation of** a protocol to identify the best QSAR model to predict the activity of a molecule.
Development of chemical library filtering as part of a *drug design* project.
R script development for supervised model development and optimization

## EC 105 - BQ2CY070 - Seminars and R&D (1 ECTS)
## Person in charge : A-C CAMPROUX

**Title : Seminars and R&D**
**Teacher: A-C Camproux, ISDD Master alumni, future colleagues ...**

Program: This module aims to enable students to understand the functioning and networks of research in ISDD, whether at the academic level or in companies (start-ups and large pharmaceutical companies). Meetings will allow students to exchange and discuss with people from the private and academic sectors, who are confronted with current research problems in drug design. These seminars will include presentations from recognized laboratories in drug design, structural bioinformatics and chemoinformatics, both national and international, and depending on the year, presentations from platforms (RPBS, Orphanet), PhD students and former students of the Master's program, participation in a conference in the field, and company visits.

Part 1: How to network: presentation of linkedIn, ISDD Master Group, create a linkedIn CV, learned societies of chemoinformatics and bioinformatics...
Preparation for the post-Master's period: information on the functioning of research in France and abroad. Operation of doctoral schools. National (doctoral schools), European and international (DIM, ANR) thesis funding.
Part 2: Seminars and communication: ISDD alumni will come to present their profession and career (Examples of obtaining a ministerial grant by ISDD Masters students), students will meet professional speakers (Sanofi or Servier start-up or DassaultSystems) who will present their company and its operations, and/or participation in a scientific conference (2021: SFCI and GGM conference)

**Evaluation methods**: Attendance and summary of seminars, registration and CV on linkedIn,

## Block UE2 - MOLECULAR ANALYSIS AND DYNAMICS & DRUG (7 ECTS)
## Person in charge : D. FLATTERS

### EC 203 - BQ2CY090- Structural exploration of proteins (3 ECTS)
### Person in charge: L. REGAD

**Title : Structural exploration of proteins**
**Teachers: L. Regad, Delphine Flatters, AC Camproux, F. Pierruccini, M.Bonomi**

**Program :**
Structural analysis of the target 3D- STRUCTURE-BASED PREPARATION
Optimize a therapeutic target, model the loops of a target. Analysis of protein structure and variability at the global, local and pocket levels. Search for druggable pockets and the effect of mutations.
Targeted Skills: To provide students with the basis for advanced exploration of protein structure in preparation for the search for active compounds

**3D Macromolecule Analysis**

1) Construction of 3D protein models by homology modeling and advanced sequence alignment (modeller, pymol), loop optimization
2) Study of mutations and structural variability, (SA-Conf )
3) Identification-estimation of pockets and their druggability (Pockdrug )
4) Metadynamics and accelerated dynamics
5) MMPBSA

### CHOICE OF EC 202 or EC 203 depending on the level

### EC 201 - BQ2CY100- Dynamic analysis of targets I (2 ECTS)
### Person in charge : D. FLATTERS

**Title : Dynamic analysis of targets I**
**Teachers: D. Flatters, C. Etchesbest**

**Program:** Understand the theoretical concepts governing molecular modeling techniques (force field, minimization, molecular dynamics)
- Semi-empirical force field and molecular mechanics: description of the basic forces (Harmonic and torsional potentials, electrostatic interactions, van der Waals interactions)
- Optimization of molecular geometry (energy minimization)
- Molecular Dynamics (MD) Simulation and Trajectory Analysis (algorithm & conformational property calculations)

Each theme will be approached in a theoretical way in CM and in a practical way in TP (modeling of a biomolecule in water with the GROMACS software)

**Targeted competences:** Model a basic molecular system (a biomolecule in water). Know how to apply these notions to biomolecules (peptides, proteins, etc.)
Critical reading of a publication using molecular modeling. Be able to do an internship in a laboratory using molecular dynamics.

## EC 203 - BQ2CY110- Dynamic analysis of targets II (2 ECTS)
## Person in charge : G. MOROY

**Title: Dynamic analysis of targets II**
**Teachers: G. Moroy**

**Program:** Know how to select the appropriate bioinformatics tools to study the flexibility of a protein.
Study of the flexibility of proteins.
Analysis of molecular dynamics simulation results.

**Objectives in terms of knowledge: To** know how to apply the knowledge acquired for the study of protein dynamics to the modeling of a therapeutic target.

## EC 204 - BQ2CY080- Structural and dynamic modeling (2 ECTS)
## Persons in charge: G. MOROY & D. FLATTERS

**Title : Structural and dynamic modeling**
**Teachers: G. Moroy & D. Flatters**

**Program:** Generation and analysis of structures from molecular dynamics simulation trajectories of a protein of interest. To be able to propose and apply a protocol combining structural and dynamic studies of proteins + MMPBSA
**Targeted competences:** Understand and master the bioinformatics tools that help in the structural and dynamic study of proteins.

**Block UE3 – HIGH-THROUGHPUT SCREENING : STRUCTURE & LIGAND-BASED (5 ECTS)**
**Person in charge : G. MOROY**

## EC 302 - BQ2CY130- Ligand-based (1 ECTS)
## Person in charge: O. TABOUREAU

**Title : Ligand-based**
**Speakers: O. Spérandio, G. Moroy, S. Murail, O. Taboureau**

**Program:** This course is designed to provide hands-on learning of in silico preparation of chemical libraries for virtual screening based on the structure of reference ligands and to perform ligand-based virtual screening. The program includes parts

- Mastery of the different molecule file formats and handling of PDB, **smile**, SMARTS, mol2, MDL-sdf, 3D molecules with Pymol, Advantages, limitations and frameworks of use of different file types.
- Generation of three-dimensional molecular models for small molecules (1D/2D to 3D) and calculations of ligand descriptors and transformation from 2D to 3D format and dimensions using software (knime rdkit, frog and openbabel) (different behaviors: Smart change, isomer, tautomer).
- Descriptors visualization, molecules visualization
- Pharmacophores & main ADME/tox rules : Lipinski, Weber, Egan,...
  Notion of Frequent, Hitter, Aggregants, Toxic Fragments using FAFdrug,
- Ligand-based screening, (notion of decoys)

**Objectives in terms of knowledge:** Practical learning of in silico preparation of chemical libraries for virtual screening, based on the structure of reference ligands including a part i) generation of three-dimensional molecular models for small molecules (1D/2D to 3D), how to go from 1D-2D-3D ii) calculation of ligand descriptors, iii) pharmacokinetic aspects (ADME/tox) based on specific physicochemical criteria, iv) application of a ligand-based screening

**M1 chemoinformatics information/materials (MOE descriptors) are made available to MB students.**
Targeted skills: Generation of compound libraries and ligand-based screening

## EC 301- BQ2CY120- Structure-based screening (3 ECTS)
## Person in charge : G. MOROY

**Title : Structure-based**
**Person in charge of training : G. Moroy**

**Program:** The objective of this course is to present advanced theoretical concepts, algorithms and associated programs for the design of therapeutic molecules by approaches based on the structure of the target protein. Taking into account the flexibility of the protein and the ligand. How to dock with covalent bonds?
Molecular dynamics stability study of the protein-ligand interaction.
Presentation and use of several docking and virtual screening programs.
Autodock & Rdock, seed (fragment-based), a therapeutic target screening
using @TOME-3

**Targeted skills:** Understand and master some bioinformatics tools that help in the design of therapeutic molecules based on the structure of the target protein.

## EC 303- BQ2CY140- Hits to lead (1 ECTS)
## Person in charge: O. TABOUREAU

**Title : Hits to lead**
**Speakers: O. Taboureau & H. Xhaard**

**Program:** Several experimental approaches and rational in silico design methods can be used to transform a "hit" into a "lead" (X-ray diffraction, NMR, medicinal chemistry, SAR, QSAR, rescoring, molecular simulation, ligand-based, fragment-based methods...).
Several examples of optimization will be discussed with applications in infectious diseases, cancer, cardiovascular diseases and the reproductive system.
The aim of screening is to identify molecules with biological activity of therapeutic interest with respect to a therapeutic target. High throughput, in silico or in vitro, allows the testing of several thousand molecules per week. Pharmacological screening is the first step in the drug discovery process. The molecules identified during the initial screening phase (hits) are far from being drugs yet. Their binding to their target is still too weak, so they will have to be optimized (leads). Thanks to subtle and progressive transformations of the structure of the hit, the medicinal chemist and the drug designer will allow it to bind more efficiently to its target. However, this increase in affinity alone will not be enough to make the key a drug candidate. Before being evaluated in animal efficacy models and then in humans, the product will have to satisfy several other constraints: a) specificity, b) adequate bioavailability, c) appropriate pharmacokinetic properties, d) absence of toxicity.

**Targeted skills:** Students will discover, through specific examples, the main strategies to optimize an initial touch to the drug candidate and the marketed therapeutic molecule

**Block UE4 - RECHERCHE Course – BIOACTIVES MOLECULES**
**SPACE ANALYSIS OF MACROMOLECULES (4 ECTS)**
**Person in charge : A. BADEL**

## EC 401- BQ1CY150- Data Analysis I (2 ECTS)
## Person in charge : A. Badel

**Title : Data analysis I**
**Teaching staff** : **A. Badel, A-C. Camproux**

**Program :**
Training in data analysis for the statistical exploration of biological data and the implementation of prediction methods (machine learning), using the R language.
Targeted skills: Training in R and unsupervised data analysis: classification, factorial methods (PCA), and supervised methods: logistic and linear regressions, overlearning problem and verification of the performance of a model in learning and validation
**Evaluation methods :** 2 TP report

## EC 402 - BQ1CY160- Understanding macromolecules (2 ECTS)
## Persons in charge: D. Flatters

**Title : Understanding macromolecules**
**Pedagogical coordinators: D. Flatters, G. Moroy**

**Program: Construction of** 3D protein models by homology modeling
- 3D structures of biological macromolecules and visualization with Pymol.
Alignment of sequences. Comparison of structures.
- Homology and folding conservation
- Bioinformatics methods for predicting the secondary and tertiary structure of macromolecules
- Construction of 3D protein models by homology modeling

**Targeted skills:** 3D structures of biological macromolecules and visualization with Pymol. Master the methods of protein and RNA structure prediction and comparative modeling to establish structural models of macromolecules, and evaluate the relevance of a 3D model.

## UE5. PREPARATION FOR RESEARCH IN DRUG DESIGN (6 ECTS)
**Person in charge: L. REGAD**

### EC 501-BQ2CY170 - 3-projects in Drug Design tutorial (2 ECTS)
**Persons in charge: L. Regad & O. Taboureau**

**Title : 3-projects in Drug Design tutored**
**Teachers : L**. Regad, O. Taboureau, G. Moroy, S. Murail, O. Taboureau, AC Camproux, S. Pasquali, D. Flatters,

The main UE blocks of the first semester include training modules and a project module. These different projects aim at proposing the analysis (and dynamics) of a protein target and the selection, analysis and screening of candidate molecules for the binding of this target. The molecular docking of partners on the same system is dealt with throughout the semester and in the different projects corresponding to the ECUE: "BQ2CY060 Application in Drug Design & QSAR + BQ2CY080 Structural and dynamic modeling + BQ2CY190 High-throughput screening application", in connection with other modules (BQ2CY090 Structural exploration of proteins, BQ2CY130 Ligand-based, Hits to lead EU ...).
In this ECUE3-projects in Drug Design", students (individually) will have to analyze in a combined way and synthesize the results of these different projects) in an integrated and complete project of drug design in silico.

**Program :**
An integrated analysis of the results of the different projects [combining molecular modeling on a target to assess its flexibility, selection of candidate molecules by statistical filtering approaches to create an optimized chemical library and virtual screening (ligand-based and structure-based) of the target by its molecules to predict inhibitor molecules from the optimized chemical library], will be performed by the students in order for them to gain hands-on experience on an in silico drug design project. This target and molecules are treated and analyzed in a concrete way in the form of projects or reports during different modules of the semester. The objective of this project is for the students to link the different approaches studied and projects obtained on the same system in order to understand the complementarity and the finality of these approaches for a complete in silico drug design project.

**Targeted Skills:**
- Know how to apply, analyze and combine the different steps of a drug design protocol

Know a drug design protocol to identify new inhibitors of a target of interest
At the end of the semester, students combine and analyze the results of different projects obtained on the same target system in order to understand the complementarity and the purpose of the approaches studied in the M2 core curriculum. Know how to develop an optimized pipeline to identify new inhibitors of a given target, optimize and combine the different tools needed in a drug design protocol.

As part of this module, depending on the year, if the D3R Grand Challenge is offered, students have the opportunity to participate in the D3R Grand Challenge, which is the international Drug Design Challenge hosted by the University of California, San Diego. Its goal is to predict the position of small molecules in the binding site of a given protein and to predict the affinity of small molecules for that same protein. https://drugdesigndata.org/about/grand-challenge

## EC 502 - BQ2CY180 - Tutored research project design I (2 ECTS)
## Persons in charge: A-C. Camproux

**Title : Design of a tutored research project**
**Person in charge of training: A-C Camproux**

**Program:** Preparation of the course *:
- Build your research networks: presentation of linkedIn, ISDD Master Group, create a linkedIn CV, contact alumni (linkedIn, facebook), chemoinformatics and bioinformatics companies.
*How to make an oral presentation, an internship report, structure a publication?*
- Preparation of the research internship topic, involving bibliographic work and reflection on possible collaborations. Writing of the internship topic in a 3 to 4 page format

**Targeted Skills:**
Understanding by the students of what a research project involves. Reflection, preparation of their internship research topic, requiring bibliographic work.
You can consult the Pôle de l'Orientation et de la Professionnalisation https://u-paris.fr/orientation-et-insertion/

## EC 503- BQ2CY190 - High throughput screening application (2 ETCS)
## Person in charge : G. MOROY

**Heading : High speed screening application**
**Person in charge of training : G. Moroy**

**Program :**
Application of the knowledge acquired to propose inhibiting molecules of a target protein.
Analysis and preparation of the structure of a target protein.
Preparation of an adequate chemical library.
Selection and adaptation of a virtual screening protocol.
**Targeted Skills:**
Use and selection of appropriate tools for virtual screening to propose inhibitor molecules for a given target protein.

# MASTER 2 - SEMESTER 4 (30 ECTS)

## INTERNSHIP (30 ECTS)
**Person in charge : A-C. Camproux**

### UE6 - BQ1DY010- Preparation of a tutored research project II (3 ECTS)
**Persons in charge: A-C. Camproux, S. Murail**

**Title : Preparation of a tutored research project**
**Pedagogical coordinators: A-C. Camproux, S. Murail**

**Program:** In preparation of the research internship topic, a reflection on possible collaborations and the integration of the different in silico modules followed in Master for a three-year extended research project. In preparation of the research internship topic, involving bibliographic work, reflection on possible collaborations and integration of the main in silico modules followed in Master for the research project. Budgeting of the project. Pairs of tutors guide them in this work.

**Evaluations**
Students prepare a worksheet for the interviews, a long report (maximum 10 pages) before the internship in order to prepare it as well as possible. Two tutorial meetings to discuss and advise on the preparation of this project are proposed with the tutors during semesters 1 and 2.

In addition, a report (2 to 3 pages) is requested midway through the course in March.

### UE7 - BQ1DT020- International research internship or internship in a company (27 ECTS)
**Person in charge : A-C. Camproux**

**Title: International research internship or in a company**
**Person in charge of training : A-C. Camproux**

**Program:** Laboratory internship or equivalent bibliographic work
The aim of the course is to introduce students to research in academic or private laboratories, depending on the student's international project, which is strongly recommended for the Macromolecules course

**The Master 2 is mainly conducted in English. The Franco-Italian double degree involves the Master 1 validated in the Universities of Strasbourg and/or degli studi di Milano**