BIOINFORMATICS

Prof. Elisa Ficarra
DAUIN, Politecnico di Torino

Team

@ DAUIN (D. Automatica e Informatica)

- Prof. Elisa Ficarra (ph. 7180) 4° floor

Bioinformatics & bioimaging

- Prof. Santa Di Cataldo (ph. 7020) 3° floor

Bioimaging

@ DAUIN: 2° floor Lab 4

- Eng. Francesco Ponzio

Bioimaging

- Eng Emanuele Parisi

Python language & Bioinformatics

- Eng. Marta Lovino

Bioinformatics

mail: <name>dot<surname>@polito.it

Course organisation

- Materials
  - Lectures slides and Recordings (previous year or, occasionally, current year)
  - Additional docs/links uploaded on the site (occasionally)
- Labs
  - Labs will take place in the room
  - Bring your own laptop
- Exam
  - Choice between
    1) Written test (theory + coding part)

       OR

    1) Project (implementation + discussion with presentation & theory related to the project) – 3 to 4 students per group

Course Content Overview (1)

- **Introduction to biology and bioinformatics**
- **Introduction to Python language**
  - Theory and exercices for common applications
  - Exercises for biological data and image analysis
- **DNA and RNA Sequencing:**
  - Description of Next Generation Sequencing (NGS) and Third Generation Sequencing technologies,
  - Algorithms and tools for Sequence alignment: *global* and *local* alignment

Course Content Overview (2A)
BIOMEDICAL ENG. class

- **Concepts of informatics/programming for bioinformaticians:**
  - Data format & Databases and web tools for genome data visualization
  - Concepts of bash scripting,
- **Genetic aberration analysis from NGS data:**
  - Algorithms and tools for gene fusion identification, and fusion functional prediction
  - Algorithms for non-coding RNA identification
  - Algorithms for mutations and CNVs detection
- **Deep Learning algorithms:**
  - Neural Networks
  - Deep Learning: e.g. CNNs, RNNs, LSTM, GNNs
    - Applications in bioinformatics (e.g. RNA sequences, bioimages)
- **Labs:** Hands on NGS data analysis tools, design of a NGS pipeline, machine learning/deep learning applications.

Course Content Overview (2B)
ICT & Math Eng. class

- **Concepts of informatics/programming for bioinformaticians:**
  - Data format & Databases and web tools for genome data visualization
  - Object-oriented Python language
- **Pattern Recognition and Learning algorithms:**
  - Machine Learning:
    - Evaluating classification and prediction performance
    - The classification paradigm: methods for feature extraction - feature selection – categorization – class balancing
    - Supervised learning vs unsupervised learning
    - Applications in bioinformatics
  - Neural Networks
  - Deep Learning: e.g. CNNs, RNNs, LSTM, GNNs, SNNs for temporal series and classification
    - Applications in bioinformatics (e.g. RNA sequences, bioimages)
- **Labs:** Hands on NGS data analysis tools, design of a NGS pipeline, machine learning/deep learning applications.

First 2 weeks

- Introduction to Bioinformatics
  - Sequencing data processing tools
  - Gene regulation analysis tools
  - Applications: personalized and precision medicine, drug design
- Introduction to Python language
  - Theory and exercices for common applications
  - Object-oriented programming (introduction)

Virtual Lessons

- For the scheduling of the lessons in the current and next few weeks please refer to introductive recordings and Readme material that will be uploaded soon in the Materiale page