Emma Rousseau

 emmarousseau | emmarousseau1 | emmarou1@icloud.com | +32 470.133.971

EDUCATION

MSc Bioinformatics, *KU Leuven* — Expected graduation June 2025

Relevant Coursework:

Mathematics and Statistics: Biological Data Analysis, Longitudinal Data Analysis, Fundamentals of Artificial Intelligence, Statistical Methods for Bioinformatics, Dynamical Systems, Bayesian Modeling for Biological Data Analysis, Machine Learning and Inductive Inference, Applied Multivariate Statistical Analysis, Artificial Neural Networks and Deep Learning.

Computer Science: Management of Large-Scale Omics Data, Structural Bioinformatics, Comparative and Regulatory Genomics, Evolutionary and Quantitative Genetics.

BSc Computer Science and Biology, *McGill University*

Awards and Bursaries:

IRCM Foundation Scholarship for Young Researchers (2020)
Scholarship for Women in Technology (2020-2021)

Relevant Coursework:

Mathematics and Statistics: Calculus 3, Discrete Structure, Linear Algebra, Probability, Ordinary Differential Equations, Statistics, Applied Regression.

Computer Science: Algorithms and Data Structures, Programming Languages and Paradigms, Computational Biology Methods and Research, Computational Methods in Biomolecular Engineering, Applied Machine Learning.

WORK AND RESEARCH

Graduate Researcher - Laboratory for Translational Breast Cancer Research
September 2024 - June 2025

- Developed analysis pipelines to study the resistance mechanisms of lobular triple-negative metastatic breast cancer to antibody-drug conjugate treatment.
- Leveraged high-performance computing clusters, workflow management software (Nextflow), NGS data analysis and phylogenetic analysis tools to uncover relevant variants from whole genome and whole exome sequencing data.
- Developed a custom suite of visualization dashboards using R-shiny patients' for analysis of clinical data and information sharing between researchers and pathologists.

Student developer - Data-Intuitive
March 2024 - October 2024

- Contributed to open-source repositories of modular pipeline components for RNA-seq data analysis (Viash Hub - Biobox).
- Wrote wrappers for most commonly used packages within the Viash framework using Docker containers and YAML, R, Python, and bash scripts.
- Collaborated on projects while adhering to code quality standards and version control procedures.

Data science and web development freelancer - Sight Consulting   June 2023 - December 2024

- Collaborated with clients to define project requirements and deliver tailored solutions.
- Designed and developed responsive, user-friendly dashboards using the Flask framework, HTML, CSS, and JavaScript.

Undergraduate Researcher - Vogel Lab, McGill University   May 2021 - August 2023

- Studied yeast protein conformation using Monte-Carlo simulations.
- Developed mass-spectrometry data analysis pipelines using KNIME and bash scripting to investigate the dynamics of spindle pole proteins in yeast.
- Contributed to super-resolution microscopy imaging of live yeast samples and computational image analysis using Fiji to investigate mitosis and cell growth dynamics.

Bioinformatics intern - Coté Lab, Clinical Research Institute of Montreal   Summer 2020

- Developed a pipeline for tandem mass-spectrometry data analysis to reduce computational costs and improve the sensitivity of MS-based experiments.
- Efficiently used high-performance computing (HPC) clusters, batch processing and bash scripting to study protein-protein interactions in pathways linked to cancer progression.

Skills

Programming	Python, Java, R, bash, SQL, high-performance computing (HPC) clusters, workflow management (Snakemake, Nextflow), dashboard and web development (R-shiny, Flask), containerization (Docker, Singularity), version control.
Bioinformatics	Next-Generation Sequencing (NGS) data analysis, statistical analysis and modeling, machine learning applications, data visualization, RNA-seq data analysis, mass-spectrometry (MS) data analysis.
Research	Scientific writing and research communication, cellular biology laboratory methods, experimental design.