MARGAUX HAERING

CONTACT

🎂 July 12, 1997
Cannes, France

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📍 Monaco

🪪 Permis A, B, Bateau

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SKILLS

INFORMATICS :
Python - R - Bash
JavaScript - PHP - MySQL
HTML - CSS - Office

LANGUAGES :
Anglais (courant)
Allemand (scolaire)

ACTIVITIES

SPORT :
Horse Riding - Amateur competiting
Scuba diving - Level 2
Skydiving- BPA

ARTS :
Photography, piano,
drums, saxophone

EXPERIENCE

2024
2021
Bioinformatics PhD
Development of a platform for sc-RNA-seq exploration and analysis of cerebelar ataxias
IBDM - Habermann Team
Fullstack development with database, preprocessing pipelines
Teaching R, MySQL Licence & Master, AMU

2021
2020
Biological data procesing engineer
NGS, -omics, IBDM - Habermann Team
Analysis pipelines sc/bulk, proteomics, HyperTRIBE, microRNA, ATAC-seq, DamID, vizualisation

2020
Master 2 internship   -
Development of a R-shiny app for NGS, -omics data analysis and integration
IBDM - Habermann Team
Bulk analysis, data integration, vizualisation

2019
Master 1 internship -
Adhesion analysis of leukemic molecules by videonanoscopy
CRCM, Marseille
Molecular path tracing and characterization, MATLAB

FORMATION

2024
2021
Bioinformatics PhD

2020
2018
Bioinformatics Master (DLAD)
Software development and data analysis
AMU

2018
2015
Biology Bachelor (BCB)
Biochemistry and Biopharmaceutical Chemistry
AMU

2015
Scientifi Baccalaureat
École de Provence, Marseille

PUBLICATIONS

2025
Haering M, Del Bondio A, Puccio H, Habermann B. ataxiaXplorer, the first ataxia interactome and its exploration and analysis platform. In progress...

2024
Haering M, Del Bondio A, Puccio H, Habermann B. mitoXplorer 3.0 for exploring mitochondrial dynamics in single-cell RNA-seq data. 2024, doi:https://doi.org/10.1101/2024.12.17.628870

2022
Marchiano F, **Haering M**, Haberman BH. The mitoXplorer 2.0 update: integrating and interpreting mitochondrial expression dynamics within a cellular context. 2022 Feb 7;
doi: https://doi.org/10.1101/2022.01.31.478461

2021
Meiler A, Marchiano F, **Haering M**, Weitkunat M, Schnorrer F, Habermann BH. AnnoMiner is a new web-tool to integrate epigenetics, transcription factor occupancy and transcriptomics data to predict transcriptional regulators. Sci Rep.
2021 Jul 29;11(1):15463. doi: 10.1038/s41598-021-94805-1. PMID: 34326396; PMCID: PMC8322331.

Haering M, Habermann BH. RNfuzzyApp: an R shiny RNA-seq data analysis app for visualisation, differential expression analysis, time-series clustering and enrichment analysis. F1000Res. 2021 Jul 26;10:654. doi: 10.12688/f1000research.54533.2. PMID: 35186266; PMCID: PMC8825645.