| NAME Granjeaud, Samuel | POSITION TITLE |
|-----------------------------------|--|
| BORN 21/03/1967 in Valence FRANCE | Research Engineer, Computational Biology |

EDUCATION/TRAINING

| INSTITUTION | DEGREE | YEAR(s) | FIELD OF STUDY |
|---|----------------|-----------|--|
| Centre de Recherche en Cancérologie de Marseille | Staff engineer | 2012- | Data analysis for Cytometry and Biology |
| IFR Cancérologie et Immunologie de Marseille | Staff engineer | 1999-2011 | Transcriptomics, Biological data analysis |
| Centre d'Immunologie de Marseille Luminy | R&D engineer | 1995-1998 | Micro-arrays development |
| GPEC, Université de la Méditerranée | Ph.D. | 1990-1993 | Physics, Material sciences |
| IUSPIM / Polytech Marseille | Engineer | 1989 | Informatics, Instrumentation |

PROFESSIONNAL ADDRESS

Centre de Recherche en Cancérologie de Marseille, INSERM UMR 1068 27 Bd Lei Roure, 13273 Marseille samuel.granjeaud@inserm.fr

POSITIONS

2012-present Co-head of the CRCM's Integrative Bioinformatics core facility Co-head of the Bioinformatics core facility at TAGC 1999-2011 2007-present Manager of the Bioinformatics for Marseille Proteomics Platform (IBiSA) 2008 **Research Engineer 1st class**

SCIENTIFIC EXPERTISE

Co-organizer of the "Computational Cytometry Club" within the French Cytometry Association Organizer of the annual INSERM training in Marseille called "Multi-parametric advanced tools for

cytometry analysis"

Chairman at the annual congress of the French Cytometry Association Contributor to the flowCore and hypergate Bioconductor packages

BIBLIOMETRIC PARAMETERS

>65 publications, H index: 34, average citation per year: 130, source: Google Scholar.

OVERVIEW

Samuel Granjeaud is experienced in data analysis, database development, numerical programming, Web and Linux administration. He already published three Laboratory Information Management Systems (LIMS) for the wet lab and the transcriptomic data. He is experienced in the analysis of transcriptomic and proteomic data, including the query of nucleic and protein databases and the conversion of identifiers across those databases. He is now working on the analysis of the multidimensional data from flow and mass cytometry. Currently, his goal is to ease and validate the analysis of complex dataset. He also trains scientists at the wet bench to analyze dataset on their own. He is working also in mass spectrometry at the Marseille Proteomics Platform, conducting data analyses of labelled and label free experiments.

SUPERVISION

- 2021 2 Engineers, 1 Master 2
- 2020 1 Engineer, 1 Master 2, 1 Master 1
- 2019 1 Engineer, 1 Master 2, 1 Master 12018 2 Master 2, 1 Master 1
- 2017 1 Lic. Prof
- 2016 2 Master 1, 1 Lic. Prof