France ROSE, Ph.D. (she/her)
Junior Group Leader
Emmy Noether Fellow
Schaafenstrasse 7, 50676 Köln
personal webpage
france.rose@uni-bonn.de

Research and professional experience

Oct 2021 - now	Bozek Lab. Data Science of Images. *Center of Molecular Medicine Cologne (CMMC), University of Cologne*, Germany. Post-doctoral researcher : **Deep learning analysis of rodent behavior through 3D motion-tracking data and of spatial interaction of immune and cancer cells with mass spectrometry imaging**
Oct - Dec 2023	Neuronal Rhythms in Movement Unit (PI : Marylka Yoe Uusisaari). *Okinawa Institute of Science and Technology (OIST)*, Japan. Visiting researcher
Nov 2019 - Sept 2021	*MyndBlue*. Start-up incubator *X-Novation - Ecole Polytechnique*, Palaiseau, France. Biomedical data scientist : **Development of machine learning platform for Major Depression and PTSD prediction and prognosis.**
Sept 2016 - Oct 2019	Computational BioImaging & Bioinformatic. Group of Auguste Genovesio. *Institut de Biologie de l'ENS (IBENS)*, Paris, France. Doctoral researcher : **Analysis of cell phenotypical and spatial heterogeneity from microscopy images in the context of High-Content Screening.**
Aug - Nov 2018	Spatial Metabolomics. Group of Theodore Alexandrov. *European Molecular Biology (EMBL)*, Heidelberg, Germany. Short-term collaboration : Statistical spatial analysis of combined microscopy images and spatial metabolomics data, published in the form of a *Python* package, **PySpacell : A Python package for spatial analysis of cell images**
Feb - Jun 2016	*KeenEye Technologies*. Start-up incubator *Institut de la Vision*, Paris, France. Supervision : Sylvain Berlemont and Leandro Almeda. R&D project : **Developement of an image analysis pipeline to detect colocalization on mouse brain slices.**
Jul - Dec 2015	Center for Discovery and Innovation in Parasitic Diseases. Group of Jim McKerrow. Supervision : Jair Lage de Siqueira Neto. *University of California San Diego, Skaags School of Pharmacy and Pharmaceutical Sciences, USA*. **Development of a robust method to access host cell and parasites counting, and their morphological properties as a part of a high throughput screening facility.**
Feb - Jun 2014	Computational Biology & Bioinformatic Platform. Group of Auguste Genovesio. *Institut de Biologie de l'ENS (IBENS), Paris, France*. Master 2 research student : **Development of a system to perform a fully automated analysis of image sequences of cell division generated by live microscopy (detection of the mitosis from 2 to 3 cells).**

Jun - Jul 2013 Molecular Adaptation and Genome evolution. Group of Dmitri Petrov.
Stanford University, USA.
Using positive selection measurement to detect co-adaptation during Mammalian evolution.

Feb - Jun 2013 Single Molecule Nanometry. Group of Taekjip Ha.
University of Illinois at Urbana-Champaign, USA.
Master 1 research student : **Study of the looping of small double-stranded DNA molecules (around 80bp) with a smFRET technic.**

Jun - Jul 2012 Biophotonic of Molecular Interactions (Biology and Applied Pharmacology). Group of Eric Deprez.
École Normale Supérieure (ENS) Cachan, France.
Bachelor research student : **Testing properties of a new designed inhibitor of Nitric Oxid Synthase with fluorescence microscopy.**

Education

2016 - 2019 **PhD in Bioinformatics and System Biology**
Institute of Biology of ENS (IBENS)
Université Pierre et Marie Curie (Paris 6)
Doctorate school *Life Complexity* (Complexité du Vivant)

2011 - 2016 **École Normale Supérieure end of study Diploma**
Major : Biology – minor : Physics

2012 - 2014 **Master in Bioinformatics**
Courses taken include : Image treatment and pattern recognition.
ENS Ulm - Université Pierre et Marie Curie (Paris 6)

2011 - 2012 **Licence in Biology (French bachelor's degree)**
ENS Ulm - Université Pierre et Marie Curie (Paris 6)

2009 - 2011 **Classe préparatoire aux grandes écoles (CPGE)**
CPGE is a two-year intensive course preparing for highly competitive national entrance examinations to French "Grandes Écoles", including engineering schools and the ENS. It is equivalent to the first 2 years of a Bachelor degree.
"BCPST" option : specialized in Biology, including courses of Physics, Chemistry and Mathematics.
Lycée Henri 4 (highschool), Paris.

Fellowships and programs

2025 - 2031 6-year Emmy Noether starting grant (∼€1,500,000 – DFG, Germany).
2023 - 2025 2-year Künstliche Intelligenz (Artificial Intelligence)-starter grant for young researchers (∼€200,000, Nordrhein-Westfalen, Germany).
2022 1-year IFS-Mentoring : Mentoring Program for International Female Scholars (University of Cologne).
2022 5-week Quantitative Biology Summer Course at KITP, "Neurophysics of Locomotion" (UC Santa Barbara). (Equivalent of ∼€3,500)
2018 4-month DAAD (Deutsche Akademischer Austauschdienst) fellowship for PhD students for a collaboration with a laboratory in Germany. (∼€6,000)
2016 - 2019 3-year Doctoral fellowship. Ecole Normale Supérieure, Paris. (3 year Ph.D. student salary)

Teaching experience

2025 **Teaching Assistant for Computer Vision, Master level**
Professor : Katarzyna Bozek. University of Cologne, Germany.
30 hours — Creating content for practical sessions and 1-2 month research projects. Animating in-person sessions, mentoring students during the projects and evaluating written reports and oral presentations.

2020 - 2023 **Founder of the Coding Sisters association and volunteer tutor, high-school level**
Association *Coding Sisters*, free programming courses for high school girls (on site and online).
40 hours — Creating content for Python practical sessions for beginners and advanced students. Animating in-person and online sessions in small groups during three years. Finding new volunteers and supervising the volunteer team for managing the student application, creating more exercises, and animating the sessions.

2019 **Teaching Assistant in Programming, 1st year of Bachelor**
Professor : Virginie Gabrel-Willemin
Paris Science Lettres (PSL) University, Paris.
Teaching the computer practical sessions in Python on defined curriculum.

2017 - 2017 **Examiner of projects in Biology, 2nd year of Bachelor**
Prof. Jean-François Allemand. Paris Science Lettres (PSL) University.
6 hours — Evaluating written reports and oral defense of 1 to 2 months project in research teams.

2016 - 2018 **Teaching Assistant in Cell and Molecular Biology, 2nd year of Bachelor**
Professor : Zsolt Lenkei
Paris Science Lettres (PSL) University, Paris.
35 hours — Creating teaching content covering the basis of cellular and molecular biology including historical experiments, experimental data results, textbook content and original published documents.

2016 - 2018 **Teaching Assistant in Developmental Biology, 2nd year of Bachelor**
Professor : Xavier Morin
Paris Science Lettres (PSL) University, Paris.
35 hours — Creating entire curriculum for the the class, specifically content based on key publications in the field, to guide the students in acquiring proper methodology for literature search, reading, and reviewing as well as critical thinking.

2017 **Tutor of high-school students in the lab as an initiation to research**
Apprentis Chercheurs program organized by *L'arbre des connaissances* association.
15 hours — Two students coming twice a month to work on image and high-throughput screening data. Introduction to the use of computer vision for biological research questions, production of research results and presentation of the subject and obtained results.

2014 - 2015 **Oral examinator in Mathematics and Informatics, 1st year of CPGE BCPST (equivalent 1st year Bachelor)**
Teacher : Martine Ginestet at Lycée Fénelon (highschool), Paris.
Teacher : Mlle Launay at Lycée Saint Louis (highschool), Paris.
30 hours — Evaluating students individually based on exercises and interactive questions.

2011 - 2012 **Volunteer tutoring for highschool students in Biology.**
Association *TalENS*, Paris.
20 hours — Creating original content inspired from current research and adapting it to high-school level. The goal of the initiative is to interest students to a topic in-depth and prepare them in terms of methodology to post-high-school studies.

Oral presentations

"From Flies to Squirrels : How AI Helps Us Decode the Secrets of Animal Movement"
- *Soapbox Science Rheinland*, dissemination talk. Düsseldorf, Germany. June 28th, 2025

"Deep Learning Imputation for SKeleton data (DISK)"
- *MLinPL conference*, Warsaw, Poland. Nov 7th-11th 2024. (Talk – video available)
- *MOTOR CRC "Motor Mastery" symposium*, Cologne, Germany. Sept 5th-6th 2024. (Talk)
- *DataNinja sAIOnARA 2024 conference*, Bielefeld, Germany. June 25th-27th 2024. (Short talk)
- *Measuring Behavior*, Aberdeen, Scotland. May 15th-17th 2024. (Tutorial)
- *MOTOR CRC "Key Mechanisms of Motor Control in Health and Disease" lecture series*, Cologne, Germany. April 15th 2024. (Talk)

"Imaging Mass Spectrometry Analysis"
- *"Integration and analysis of multiplex imaging technologies" workshop, Center of Molecular Medicine Cologne Annual Retreat*, Cologne, Germany. March 2nd-3rd 2023.

"Spatial heterogeneity of cell responses in drug treatment"
- *Young Researchers in Life Science Conference*. Paris, France. June 4th-6th 1019.
- *Quantitative BioImaging conference*, Göttingen, Germany. January 4th-6th 2018.

Posters

"Deep Learning Imputation for SKeleton data (DISK)"
- *Machine Learning Workshop*, OIST, Japan. March 3rd-5th 2025.
- *Society for Neuroscience 2024 conference*, Chicago, USA. Oct 5th-9th 2024.
- *MOTOR CRC "Motor Mastery" symposium*, Cologne, Germany. Sept 5th-6th 2024.

"Studying spatial heterogeneity of cell responses to cancer drugs"
- *2018 SLAS Advanced 3D Human Models and High-Content Analysis Conference.* Leiden, Netherlands. October 17th-19th 2018.

"Quantifying the heterogeneity of cell responses to cancer drugs"
- *Young Researchers in Life Science Conference*. Paris, France. May 15th-17th 1017.
- *France BioImaging meeting*. Paris, France. April 14th 2017.
- *StatLearn meeting*, French Society of Statistics (SFDS). Lyon, France. April 6th-7th 2017.

Other

Languages

Native French speaker
Fluent English (TOEFL 107/120)
German B2 level

Computer skills

Highly proficient $Python$ and python deep learning libraries $Keras$, $Tensorflow$ and $PyTorch$.
Good programming in $bash$, $Matlab$, $C++$ and R
Extensive experience with cluster job scheduler ($condor$, $slurm$), git versioning and $Linux$ operating system.

Publications

All following publications are published in or submitted to peer-reviewed journals and consist in original research papers.

Most important publications

- **Rose, F.**, Michaluk M., Blindauer T., Ignatowska-Jankowska B., O'Shaughnessy L., Stephens G., Pereira T., Uusisaari M., Bozek K. (2025). Deep Imputation for Skeleton Data (DISK) in Behavioral Science. *Nature methods* `https://doi.org/10.1038/s41592-025-02893-y`

  This publication is the result of my current work on animal behavior data. DISK consists in a proof-of-concept of self-supervised learning in kinematics time series. It is, to our knowledge, the first deep learning method to tackle the problem of missing data in animal behavior recordings, agnostic to the defined animal skeleton. With the rise of a posteriori tracking methods such as DeepLabCut and motion capture systems, the quantity of tracked motion data is exponentially rising, making DISK a fundamental tool. Furthermore, the exploration of DISK embeddings shows promises in its encoding capacities, which will be further investigated in the proposed research project. I suggested the main research concept of using deep learning and masking task to impute missing data in recordings. I wrote most of the code and ran trainings and tests, with some help from M. Michaluk and T. Blindauer.

- **Rose, F.*** , Ibruli, O.* , Lichius, L., Kiljan, M., Gozum, G., Caiaffa, M.I., Cai, J., Niu, L.N., Herter, J.M., Grüll, H., Büttner, R., Beleggia, F., Bosco, G., George, J., Herter-Sprie, G.S., Reinhardt, H.C., & Bozek, K. Imaging mass cytometry dataset of small-cell lung cancer tumors and tumor microenvironments. BMC Res Notes. 2025 18(1) :385. PMID : 40922010 ; PMCID : PMC12418687. `https://doi:10.1186/s13104-025-07460-4`

- **Rose, F.**, Rappez, L., Triana, S. H., Stadler, M., Heikewalder, M., Alexandrov, T., & Auguste Genovesio. (2020) PySpacell : A Python package for spatial analysis of cell images. Cytometry Part A (open access) `https://doi.org/10.1002/cyto.a.23955`

  In this publication, I suggested the exploration of different spatial statistics and to apply to microscopy images, which was still an under-studied question before 2020. Indeed, spatial information was usually overlooked by downstream data analyses, which usually consider single-cell read-out values as independent measurements for further averaging or clustering, thus disregarding spatial locations. I developed a toolbox that allows one to test for the presence of a spatial effect in microscopy images of adherent cells and estimate the spatial scale of this effect. The proposed Python module can be used for any light microscopy images of cells as well as other types of single-cell data such as in situ transcriptomics or metabolomics. I developed a python package to make the computation and statistics available to the community, and contribute to open and reproducible science.

- **Rose, F.***, Basu, S.*, Rexhepaj, E., Chauchereau, A., Del Nery , E. & Genovesio, A. (2017) Compound Functional Prediction Using Multiple Unrelated Morphological Profiling Assays. SLAS TECHNOLOGY : Translating Life Sciences Innovation. (open access) `https://doi.org/10.1177/2472630317740831`

  Morphological profiling assays or high-content screens are using automated microscopy techniques to test hundreds of pharmacological compounds directly on cells. This work led to conceptual important results to increase the efficiency of screen-based compound functional predictions, namely to reduce the number of required microscopy channels to be acquired. On a first dataset, we showed that the prediction of the function of the pharmacological compound was only slightly altered when removing microscopy channels associated with cytoskeleton proteins. On a second dataset, we showed that combining multiple cell lines only imaged with a nuclear marker improved the prediction compared to a single cell line. These two results are particularly relevant because the nuclear signal is routinely acquired for many experiments in hospital facilities for simple cell counting. Leveraging existing databases for more precise analysis of compound function can lead to new discovery at lower cost. Dr. Basu, Dr. Genovesio and I proposed the prediction tasks ; and Dr. Basu and I developed the code and ran the tests.

*. Co-first authors

- Fompeyrine, D.A., Vorm, E.S., Ricka, N., **Rose, F.**, & Pellegrin, G. (2021). Enhancing human-machine teaming for medical prognosis through neural ordinary differential equations (NODEs). Hum.-Intell. Syst. Integr., p. 1-15 (open access) https://doi.org/10.1007/s42454-021-00037-z

  Forecasting scenarios can be exploited to optimize explanability of deep learning algorithms. In this work, we explored a novel kind of neural networks, based on ordinary differential equations, to forecast with higher confidence for a longer time window in the future. We discussed how to interface this forecast with the user and design a usability study to bridge the gap between black-box performance and simple interpretable model. In this work, I performed most of the data analysis using a published NODE model on an untested dataset, including retraining and analysis of the results.

- Li, Y.*, **Rose, F.***, di Pietro, F., Morin, X., & Genovesio, A. (2016). Detection and tracking of overlapping cell nuclei for large scale mitosis analyses. BMC Bioinformatics, 17(1). (open access) http://doi.org/10.1186/s12859-016-1030-9

  Dr. di Pietro and Prof. Morin developed a genome-wide approach to screen which genes were involved in the control of cell division orientation. In front of the amount of generated data, we devised an automated technique to detect the precise moment of division from two to three cells, and calculate the angle distribution from hundreds of events. Dr. Genovesio and I suggested the core idea of the division detection method, based on gaussian mixtures, which was refined by Dr. Li.

Other publications

- Bachurski, D., Gholamipoorfard, R., Bu, Y.-J., Hoelker, P., Wessendorf, L., Jestrabek, H., Schreurs, L.D., Stahl, D., Mokhlesi, A., Gödel, P., Gaedke, F., Ranjbari, E., Seyhan, S., Resch, U., Schmidt, L.M., Tertel, T., **Rose, F.**, Pinheiro, C., Corona, M.L., von Lom, A., vom Stein, A.F., Nguyen, P.-H., Reiners, K.S., Hendrix, A., van Niel, G., Krüger, M., Bozek, K., Meder, L., Malmberg, P., Cramer, P., Eichhorst, B., Peifer, M., Ullrich, R.T., Schauss, A., Pallasch, C., Bröckelmann, P.J., Jachimowicz, R.D., Preußer, C., Giebel, B., von Strandmann, E.P., Nitz, M., Hallek, M., & Abedpour, N. Single recipient cell tracking of tellurium-labeled extracellular vesicle proteomes (TeLEV) identifies EV-driven immunomodulation. bioRxiv 20252025.11.01.685872. https://doi.org/10.1101/2025.11.01.685872

- Stahl, D., Gödel, P., Balke-Want, H., Segbers, P., Tetenborg, L. ; Gholamipoorfard, R., Bachurski, D., **Rose, F.**, Good, Z., Simon, A.G., Nill, M., Flümann, R., Riet, T., Dörr, J., Blakemore, S.J., Baurmann, H., Voltin, C., Potter, N., Schlözer, L., Wagener-Ryczek, S., Iuga, A., Heger, J., Ludwig, H., Schleifenbaum, J.K., Bröckelmann, P.J. ; Jachimowicz, R.D., Knittel, G., Borchmann, S., Merkelbach-Bruse, S., Pallasch, C., Peifer, M., Nitz, M., Brägelmann, J., Müller, W., Persigehl, T., Bozek, K., Büttner, R., Hallek, M., Kobold, S., Chmielewski, M., Reinhardt, H.C., Mackall, C., Abedpour, N., Borchmann, P. & Ullrich, R.T. (2024). High-dimensional profiling uncovers a CSF1R+ myelo-monocytic cell population mediating CAR-T cell resistance in aggressive B cell lymphoma. Blood 2024 ; 144 (Supplement 1) : 367. https://doi.org/10.1182/blood-2024-203291

  I analyzed the mass-spectrometry multiplex imaging data from control and lymphoma from mouse and human patient biopsies, treated with CAR-T cell therapy. Mass-spectrometry multiplex imaging allows to visualize up to 40 proteins in the same tissue, detecting with precision subtypes of immune cells. With this extended information, the tumor micro-environment can be probed and spatial interactions of different cell populations described. Namely in this study we describe a totally different tissue organization in the responder compared to non-responder mice. In patients, a subtype of macrophages could be described from the gene expression data, paving the way to a new stratification strategies for aggressive B cell lymphoma patient.

- Ibruli, O.*, **Rose, F.***, Beleggia, F., Schmitt, A., Cartolano M., Torres Fernandez, L., Saggau, J., Bonasera, D., Kiljan, M., Gözüm, G., Lichius, L., Cai, J., Niu, L., Iannicelli Caiaffa, M., Herter, J., Walczak, H., Liccardi, G., Grüll, H., Büttner, R., Bosco, G., George, J., Thomas, R.K., Bozek, K., Reinhardt, H.C., & Herter-Sprie, G.S. (2024) A novel mouse model recapitulating the MMR-defective SCLC subtype uncovers an actionable sensitivity to immune checkpoint blockade. J Cancer Res Clin Oncol 150, 496. https://doi.org/10.1007/s00432-024-05942-9

  We developed an MMR-deficient genetically engineered mouse model of small cell lung cancer. Genomic characteristics and preclinical therapy responses were evaluated by focusing on overall survival and

whole exome sequencing analyses. We propose the novel mouse model as a suitable system to mimic patient signature and provide in vivo evidence that DNA mismatch deficiency may enhance checkpoint inhibitor sensitivity. These findings could contribute to stratifying SCLC patients to immunotherapy, thereby improving treatment outcomes. During this work, I was involved in designing the experiments and analyzing the image data.

- Vom Stein, A.F., Rebollido-Rios, R., Lukas, A., Koch, M., von Lom, A., Reinartz, S., Bachurski, D., **Rose, F.**, Bozek, K., Abdallah, A.T. & Kohlhas, V. (2023). LYN kinase programs stromal fibroblasts to facilitate leukemic survival via regulation of c-JUN and THBS1. Nature Communications, 14(1). p. 1330 (open access) `https://doi.org/10.1038/s41467-023-36824-2`

  I analyzed the mass-spectrometry multiplex imaging data from control and CLL patient biopsies, crucial to validate the results found by in vitro and mouse experiments. Specifically I detected and segmented fibroblasts and endothelial cells, then I compared their expression of LYN kinase in different CLL and MCL human samples. Altogether, we showed that LYN kinase regulates the polarization of stromal fibroblasts which lead to a favorable environment that supports leukemic progression.