France ROSE, Ph.D. (she/her)
Am Rosengarten 71, 50827 Köln
+33 686658597
france.rose@uk-koeln.de
www.normalesup.org/~frose/

Research and professional experience

10/2021 - now	Data Science of Bioimages lab (PI : Katarzyna Bozek). *Center of Molecular Medicine Cologne (CMMC), University of Cologne*, Germany. **Post-doctoral research** : Deep learning analysis of animal behavior through 3D motion-tracking data, and of spatial interaction of immune and cancer cells with mass spectrometry imaging
10 - 12/2023	Neuronal Rhythms in Movement Unit (PI : Marylka Yoe Uusisaari). *Okinawa Institute of Science and Technology (OIST)*, Japan. **Visiting researcher** : Deep learning analysis of animal behavior through 3D motion-tracking data
11/2019 - 09/2021	*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.
09/2016 - 10/2019	Computational BioImaging & Bioinformatic. Group of Auguste Genovesio. *Institut de Biologie de l'ENS (IBENS)*, Paris, France. **Doctoral research** : Analysis of cell phenotypical and spatial heterogeneity from microscopy images in the context of High-Content Screening.
08 - 11/2018	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.
02 - 06/2016	*KeenEye Technologies*. Start-up incubator *Institut de la Vision*, Paris, France. Supervision : Sylvain Berlemont and Leandro Almeda. **5-month R&D project** : Developement of an image analysis pipeline to detect colocalization on mouse brain slices.
07 - 12/2015	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*. **6-month voluntary internship** : 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.
02 - 06/2014	Computational Biology & Bioinformatic Platform. (PI : Auguste Genovesio). *Institut de Biologie de l'ENS (IBENS), Paris, France*. **Master 2 research** : 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).
06 - 07/2013	Molecular Adaptation and Genome evolution. (PI : Dmitri Petrov). *Stanford University, USA*. **Summer internship** : Positive selection measurement to detect co-adaptation during Mammalian evolution.

Fellowships and programs

2025 -	6-year Emmy Noether starting grant from the DFG (Germany).
08/2023 - 07/2025	2-year Künstliche Intelligenz (Artificial Intelligence)-starter grant for young researchers (Nordrhein-Westfalen, Germany).
07 - 08/2022	5-week Quantitative Biology Summer Course "Neurophysics of Locomotion" (UC Santa Barbara).
08 - 11/2018	4-month DAAD fellowship for PhD students for a collaboration with a research group in EMBL, Heidelberg.
09/2016 - 09/2019	3-year Doctoral fellowship. Ecole Normale Supérieure, Paris.

Education

09/2016 - 10/2019	**PhD in Bioinformatics and System Biology** Institute of Biology of ENS (IBENS) & Université Pierre et Marie Curie (Paris 6)
09/2011 - 06/2016	**École Normale Supérieure diploma** – major : Biology, minor : Physics
09/2012 - 06/2014	**Master in Bioinformatics** ENS Ulm & Université Pierre et Marie Curie (Paris 6)
09/2009 - 06/2012	**Licence in Biology (French bachelor's degree)** ENS Ulm & Université Pierre et Marie Curie (Paris 6)
07/2009	**High school graduation diploma** – major : Mathematics (baccalauréat général), obtained with highest honors. Lycée Louis-le-Grand (high school), Paris

Teaching experience

09/2020 - 05/2023	**Founder and volunteer tutor for high-school girls in Programming.** Association *Coding Sisters*.
01 - 06/2019	**Teaching Assistant in Programming, 1st year of Bachelor** Professor : Virginie Gabrel-Willemin. Paris Science Lettres (PSL) University.
09/2016 - 06/2018	**Teaching Assistant in Cell and Molecular Biology, and Developmental Biology, 2nd year of Bachelor** Professors : Zsolt Lenkei, Xavier Morin. Paris Science Lettres (PSL) University.
09/2014 - 05/2015	**Oral examinator in Mathematics and Informatics, 1st year Bachelor** Teacher : Martine Ginestet and Mlle Launay at Lycée Fénelon (high schools), Paris.
10/2011 - 05/2012	**Volunteer tutoring for high school students in Biology** Association *TalENS*, Paris.

Oral presentations

"Deep Learning Imputation for SKeleton data (DISK)"

11/2024	*Machine Learning in Poland (MLinPL) conference*, Warsaw, Poland.
09/2024	*CRC1451 2-days "Motor control" symposium*, Cologne, Germany.
06/2024	*DataNinja sAIOnARA 2024 conference*, Bielefeld, Germany.
05/2024	*Measuring Behavior*, Aberdeen, Scotland. (tutorial format)
04/2024	*Collaborative Research Center "Key Mechanisms of Motor Control in Health and Disease" (CRC1451) lecture series*, Cologne, Germany.

"Imaging Mass Spectrometry Analysis"

03/2023	*"Integration and analysis of multiplex imaging technologies" workshop, Center of Molecular Medicine Cologne Annual Retreat*, Cologne, Germany.

"Spatial heterogeneity of cell responses in drug treatment"

06/2019 *Young Researchers in Life Science Conference*. Paris, France.
01/2018 *Quantitative BioImaging conference*, Göttingen, Germany.

Posters

"Studying spatial heterogeneity of cell responses to cancer drugs"

10/2018 *2018 SLAS Advanced 3D Human Models and High-Content Analysis Conference.* Leiden, Netherlands.

"Quantifying the heterogeneity of cell responses to cancer drugs"

05/2017 *Young Researchers in Life Science Conference*. Paris, France.
04/2017 *France BioImaging meeting*. Paris, France.
04/2017 *StatLearn meeting*, French Society of Statistics (SFDS). Lyon, France.

"Deep Learning Imputation for SKeleton data (DISK)"

03/2025 *OIST Machine Learning workshop*. Okinawa, Japan.
10/2024 *Society for Neuroscience conference 2024*. Chicago, USA.

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. (2024). Deep Imputation for Skeleton Data (DISK) in Behavioral Science. *(bioRxiv – in review at Nature methods)* `https://doi.org/10.1101/2024.05.03.592173`

  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.**, 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. I reached out to the team of T. Alexandrov to extend the application of mass spectrometry images. 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

*. Co-first authors

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.

Other publications

- 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 *(submitted to Cell)*

  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. *(accepted in Journal of Cancer Research and Clinical Oncology)*

  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.

- 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.