

# Research Internship

## Image processing for bacterial communication with phages

### Topic profile

theory/math



coding



### Tags

#image processing

#communication via phages

#data analysis

#gene expression

### Supervision

**Matthias FÜGGER**

CNRS Researcher at ENS Paris-Saclay

**Thomas NOWAK**

Professor at ENS Paris-Saclay

**Alexandra LOUDIERES**

PhD candidate at ENS Paris-Saclay

### We are looking for

We are looking for a Master's student in signal processing, computer vision, biomedical engineering, or any related field, with prior experience in image analysis, ideally gained during coursework or a previous internship. The student should be familiar with Python-based image analysis, Fiji, or CellProfiler. Experience with machine learning or AI-based image segmentation and tracking is a strong plus. Basic understanding of microbiology or synthetic biology is appreciated but not mandatory. Strong communication skills are important for documenting and sharing findings.

### The team

You will be part of an interdisciplinary research team at [Laboratoire Méthodes Formelles](#) located at [ENS Paris-Saclay](#), near Paris, working at the interface between artificial intelligence, synthetic biology, distributed computing and circuit design.

### Research

In *E. coli*, horizontal gene transfer can be engineered using M13 bacteriophages, filamentous viruses that infect bacteria without killing them. These phages can encapsulate and transmit genetic material from a sender population to a receiver population. While this mechanism allows for the creation of powerful synthetic communication systems, certain key aspects remain poorly understood: the dynamics of phage diffusion between cells, as well as the timing and variability of gene expression once the receiver has been infected.

The aim of this internship is to shed light on these processes through quantitative image analysis of fluorescence. The student will apply and develop image processing workflows, likely including AI-based methods for cell segmentation and tracking, to extract features at the individual cell and population levels. These approaches will help us to better characterize phage-mediated communication between bacterial populations.

### You are interested or would like to join us?

Please mail your questions or, in case you would like to apply, a short statement of interest and a CV to Matthias FÜGGER ([mfuegger@lmf.cnrs.fr](mailto:mfuegger@lmf.cnrs.fr)), Thomas NOWAK ([thomas@thomasnowak.net](mailto:thomas@thomasnowak.net)), and Alexandra LOUDIERES ([alexandra.loudieres@ens-paris-saclay.fr](mailto:alexandra.loudieres@ens-paris-saclay.fr)).

### Literature

- [1] Pujar, Abhinav, et al. Phage-mediated intercellular CRISPRi for biocomputation in bacterial consortia. *Nucleic Acids Research* 2025. [URL](#)
- [2] Pujar, Abhinav, et al. An M13 phagemid toolbox for engineering tuneable DNA communication in bacterial consortia. *bioRxiv* 2025. [URL](#)
- [3] Cho, Da-Jung et al. Distributed computation with continual population growth. *Distributed Computing* 2022 [URL](#)