## Software engineer in bioimage analysis (H/F)

Keywords. Image processing and analysis ; spatial statistics ; C++ programming.



**Mission.** You will develop original image analysis methods and algorithms for the quantification and modeling of spatial organizations in 3D images of biological systems. You will build upon the spatial statistical analysis methodology developed in the team [1,2,3]. You will integrate your algorithms in <u>software developed in our group</u> (such as Free-D [4] or our new BIP software). You will apply the developed methods to 3D images of plant cells.

Salary before taxes between 2 104,92€ and 2 526,87€ ; contribution to additional healthcare cover. Telework. Initial contract 12 months, extensible. Starting as soon as possible.

**Environnement.** The <u>Modeling and Digital Imaging</u> team of <u>Institut Jean-Pierre Bourgin</u> (INRAE Versailles) conducts original research in image processing, applied mathematics and computational modeling with applications to plant functioning and development [e.g., 5,6,7,8]. You will benefit from a human-sized interdisciplinary working environment and from the exceptional and green surroundings of the Versailles Royal Palace gardens, at less than 45 minutes from Paris.

**Profile.** Master, engineer or equivalent in applied mathematics, computer science, or computational biology. Background or experience in image processing and analysis. Good knowledge in object-oriented programming (C++ or Java). Curiosity and motivation for working within an inter-disciplinary environment.

How to apply ? Send CV, motivation letter and 2-3 references to philippe.andrey@inrae.fr.

## References

**1.** Keller D, Stinus S, Umlauf D, Gourbeyre E, Biot E, Olivier N, Mahou P, Beaurepaire E, Andrey P and Crabbe L. (2024) <u>Non-random spatial organization of telomeres varies during the cell cycle and requires LAP2 and BAF</u>. IScience. 27, 109343.

**2.** Arpòn J, Sakai K, Gaudin V and Andrey P (2021). Spatial modeling of biological patterns shows multiscale organization of Arabidopsis thaliana heterochromatin. Scientific Reports, 11, 323.

**3.** Andrey P et al (2010). <u>Statistical analysis of 3D images detects regular spatial distributions of centromeres and chromocenters in animal and plant nuclei</u>. PLoS Computational Biology, 6, e1000853.

**4.** Biot E, Crowell E, Burguet J, Höfte H, Vernhettes S and Andrey P (2016). <u>Strategy and software for the statistical spatial analysis of 3D intracellular distributions</u>. Plant Journal, 87, 230-242.

**5.** Legland D, Arganda-Carreras I and Andrey P (2016). <u>MorphoLibJ: integrated library and plugins for mathematical</u> <u>morphology with ImageJ</u>. Bioinformatics, 32, 3532-3534.

**6.** Moukhtar J, Trubuil A, Belcram K, Legland D, Khadir Z, Urbain A, Palauqui J-C and Andrey P (2019). <u>Cell geometry</u> <u>determines symmetric and asymmetric division plane selection in Arabidopsis early embryos</u>. PLoS Computational Biology, 15, e1006771.

**7.** Laruelle E, Belcram K, Trubuil A, Palauqui JC and Andrey P (2022). L<u>arge-scale analysis and computer modeling reveal hidden regularities behind variability of cell division patterns in Arabidopsis thaliana embryogenesis</u>. ELife, 11, e79224.

**8.** Oughou M, Biot E, Arnaud N, Maugarny-Calès A, Laufs P, Andrey P and Burguet J (2023). <u>Model-based reconstruction</u> <u>of whole organ growth dynamics reveals invariant patterns in leaf morphogenesis</u>. Quantitative Plant Biology, 4, 1-11.



