Postdoctoral researcher position in Computational Biology

A postdoctoral position is available in the SPARKS team at the I3S laboratory, Université Côte d'Azur, France (see https://www.i3s.unice.fr/ for more information on the lab).

The bioinformatics group focuses on using network approaches to analyze and integrate large-scale 'omic data, and on developing computational tools to model how perturbations in gene regulation can affect biological processes.

Within the framework of a project whose objective is to develop a new test capable of detecting and quantifying the risk linked to non-genotoxic carcinogenic substances (NGTxC), we plan to take a holistic approach to better understand the processes at work at the scale of the biological system. By integrating public data and genomic data generated by our biologist partners (including coding but also non-coding genes), we will model the data as networks. In systems biology, a network maps molecular entities (e.g. genes, transcripts, proteins) via their functional interconnections (which can be physical interactions, transcriptional inductions, enzymatic activation, etc). This modeling, taking into account the individual components and their interactions, will allow us to identify subparts of the networks that are particularly active in NGTxC-induced deregulations. Efficient algorithms to discover these active modules in complex networks have been proposed [1] and are being studied by the SPARKS team [2-3].

The mission

The aim is to extend current network analysis methods along several axes by (1) enabling the processing of data obtained from Single-cell RNA sequencing and Long-Read RNA Sequencing, (2) integrating other data into the analysis pipeline, wether new types of high-throughput biological data or other knowledge represented as networks, (3) taking into account the temporal aspect of the data by including measurements made at several time points.

For this, the candidate will have to rely on recent developments concerning community detection in temporal networks [4], community detection in attributed networks [5], multi-view clustering [6] and of course machine learning applied to single cell data analysis [7].

Key responsabilities

The person recruited will be in charge of the following:

- Literature review of software solutions to apprehend the underlying strategies for extracting knowledge from complex network structures,
- Practical tests to evaluate the efficiency and ease of use of selected tools in the context of high-throughput analyses,
- Determination and implementation of optimal strategies for data extraction,
- analysis of the findings in collaboration with biologists.

Profile

- PhD in computational biology, biostatistics or computer science
- Experience with analysis of high-throughput 'omics data
- Proficiency in programming (experience with Python and its ecosystem is preferred)
- Knowledge in single cell transcriptomics, gene regulation and network biology is desirable
- Experience with high performance computing is a plus
- Ability to think and work independently, set goals and meet deadlines
- Professional proficiency in English
- Good communication and writing skills
- Willingness to work in a multidisciplinary environment, sharing skills and ideas

Work environment

Located in the Sophia Antipolis technology park, between Nice and Cannes, the I3S laboratory (Computer Science, Signals and Systems of Sophia Antipolis - CNRS UMR 7271) employs 230 people, including about 100 researchers and professors and about 80 PhD students. The SPARKS team (Scalable and Pervasive softwARe and Knowledge Systems) is the largest team at I3S with a staff of 104, including 44 permanent staff.

The team studies the organization, representation and distributed processing of knowledge, as well as its extraction from data and its semantic formalization, with a particular focus on scaling up and designing adaptive knowledge-centric and human-centric software systems. The team is structured around four themes: "knowledge extraction and learning" (machine learning, data mining, artificial intelligence), "formalization and reasoning between users and models" (multidisciplinary approaches to multi-criteria analysis and modeling, reasoning about these models using graph-oriented approaches of the Semantic Web), "scalable software systems" (adapting and composing systems, data and workflows at different scales, from local loop to massive distribution), "computer science and biology" (knowledge extraction, modeling and simulation of dynamic biological systems, formal proofs of the behavior of biological systems and computer-aided model-based reasoning).

The work will be carried out within the framework of the NewgenTOXiv project financed by the 4th Future Investment Programme (AIP 4) of the French government. The project involves 3 public research laboratories (I3S, IPMC and ICN) and two industrial companies (ImmunoSearch and MyDataModels).

Information and application

Type of contract : fixed-term contract, full-time position

Contract duration: 24 months

Desired hiring date : 1st june 2022

Place of work: I3S laboratory in Sophia Antipolis

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Adresse postale : Laboratoire I3S - CS 40121 - 06903 Sophia Anitpolis CEDEX

Gross salary: from 2500€ to 3800€, depending on experience

Applications should include the following documents in electronic format:

- a cover letter, stating your motivation, scientific background, and research interests,
- a detailed CV with a list of publications,
- 2-3 references (name, institution, e-mail, telephone number, and relation to the candidate).

Send all these documents by email to claude.pasquier@univ-cotedazur.fr

Références

1. Nguyen, H., Shrestha, S., Tran, D., Shafi, A., Draghici, S., & Nguyen, T. (2019). A comprehensive survey of tools and software for active subnetwork identification. Frontiers in genetics, 10, 155.

2, Corrêa, L., Pallez, D., Tichit, L., Soriani, O., & Pasquier, C. (2019, December). Population-based meta-heuristic for active modules identification. In Proceedings of the Tenth International Conference on Computational Systems-Biology and Bioinformatics (pp. 1-8).

3, Pasquier, C., Guerlais, V., Pallez, D., Rapetti-Mauss, R., & Soriani, O. (2021). Identification of active modules in interaction networks using node2vec network embedding. BioRxiv.

4, Rossetti, G., & Cazabet, R. (2018). Community discovery in dynamic networks: a survey. ACM computing surveys (CSUR), 51(2), 1-37.

5, Chunaev, P. (2020). Community detection in node-attributed social networks: a survey. Computer Science Review, 37, 100286.

6. Fu, L., Lin, P., Vasilakos, A. V., & Wang, S. (2020). An overview of recent multi-view clustering. Neurocomputing, 402, 148-161.

7, Ji, Y., Lotfollahi, M., Wolf, F. A., & Theis, F. J. (2021). Machine learning for perturbational single-cell omics. Cell Systems, 12(6), 522-537.