

Engineer job opportunity in Bioinformatics (M/F): Development of tools for the analysis of single-cell RNA-seq data

<u>1 year position (extendable up to 2 years) @ SysFate / UMR8030 Genoscope; France.</u>

The team SysFate, driven by Marco Antonio MENDOZA (PhD / HDR; permanent CNRS researcher), is interested on understanding cell fate decisions from the reorganization of complex gene regulatory programs that are defining their biological state. SysFate is currently located within the French National Sequencing Center, Genoscope, in the city of Evry at the South of Paris – France.

<u>The engineer position falls within an EU funded collaborative project T-Fitness</u>, to develop more resistant CAR-T cells in the context of solid tumors.

Specifically, you will (i) develop novel tools for processing single-cell multiomics data, allowing to reveal major gene programs; (ii) participate at the analysis of the various NGS generated data within the EU consortium, as well as within the team SysFate. <u>The engineer position is expected to start in</u> <u>October 2023.</u>

Competitive salary package for international standards (> 2,600 euros gross salary/month including French social insurance, and according to the experience of the candidate).

Candidate profile:

The candidate must hold a master degree in bioinformatics, computer science, or related. Essential qualifications include excellent programming skills in languages as Python, Java, Perl and/or R. Experience in next-generation sequencing and related functional genomic data analysis (transcriptomics, ChIP-sequencing, etc) is a strong asset. Furthermore, experience in single cell transcriptomics and / or gene regulatory networks reconstruction is a plus for this application.

The successful applicant is expected to be an enthusiastic and self-motivated person.

Interested candidates might submit (i) a detailed CV, (ii) a list of publications, (iii) letter of support of their previous institution(s). Please submit your application by email to Marco Antonio Mendoza: **mmendoza at genoscope.cns.fr** and via de <u>web-portal of CNRS</u>.

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