

**Position Profile:**

MSc or BSc in Software Engineering, Bioinformatics, Data Science, Statistics, Mathematics or related fields. Experience in transcriptomics, gene regulatory networks and machine learning will be valued. Strong skills in programming with Python is necessary. Proficiency in English is required.

**Description of Work:**

The successful candidate will work at Computational Intelligence Group (<http://cig.fi.upm.es/>) at the School of Computer Science of the Technical University of Madrid in Madrid, Spain.

Main objective: develop a genetic atlas toolbox (Neurogenpy) with a stand-alone web interface (Neurosuites) and basic functionality plugin in the interactive atlas viewer of the HBP project. Neurogenpy will be a Python software library for analysis of gene expression and cytogenetic data. Users will be able to introduce their own data or interface with the atlas viewer to extract data, analyse it and return the models which will be visualised using Neurosuites, a web-interface for the analysis software, or an integrated viewer on top of the atlas. The models will include gene regulatory networks using simple correlation or regression methods and Bayesian networks and probabilistic clustering. Everything will be available at [neurosuites.com](http://neurosuites.com).

This project is part of the European Union's Horizon 2020 Flagship Human Brain Project (Specific Grant Agreement SGA3).

**Duration of contract:**

12 months. From June 1, 2020 to May 31, 2021 (that can be extended by a further 24 months).

**(gross) Salary:**

Up to €24000 per annum (full time), depending on skills and experience.

**Start date:**

June 1, 2020.

**Application deadline:**

May 18, 2020.

**Contact:**

Interested candidates should send their CV to Concha Bielza ([mcbielza@fi.upm.es](mailto:mcbielza@fi.upm.es)) and Pedro Larrañaga ([pedro.larranaga@fi.upm.es](mailto:pedro.larranaga@fi.upm.es)).