ESR 15 – DEVELOPMENT OF A BIOINFORMATICS SOFTWARE SUITE FOR SINGLE CELL GENOMICS DATA ANALYSIS

Research project	Generating automatic bioinformatics pipelines for obtaining quality results from huge data packages from Single Cell Next-Generation Sequencing (NGS) data has become key for the advance of biological discoveries. The main objectives of the Early Stage Researcher (ESR15) are: I. Generate a set of automatic bioinformatics pipelines that will allow all the research community to analyze single-cell genomics, transcriptomics and metabolomics data with very little computational biology knowledge. II. Create a visual framework and back-end database in order to link the most well-known and curate databases with the NGS data results, and allow the researchers to interact and generate downstream discoveries. III. Deploy and maintain a bioinformatics suit Software as a Service (SaaS) for Singe Cell Genomics. We expect that generating a robust and scientifically validated automatic bioinformatics system for analysing, organizing and visualizing single-cell genomics, transcriptomics and metabolomics will help the research community to increase the usage and adoption of single-cell high-throughput genomic studies.
Supervisor	Name: Albert Mascarell Email: amascarell@ascidea.com Website: www.ascidea.com/
Host institution	aScidea Barcelona, Spain
PhD program	The Early Stage Researcher in this case will not be asked to get a PhD after the 3 years.
Expected results	A set of automatic bioinformatics tools for the analysis of single-cell NGS data. Database structures and a front-end implementation for NGS data analysis, organisation and visualisation allowing a workspace framework for researchers.
Planned secondments	CRG-CNAG - Month 19 (3 m) - Bioinformatics on single gene genomics CNRS-R - Month 28 (3 m) - Bioinformatic analysis and databases for SCG and metagenomics CSIC-IBE - Month 36 (3 m) - SAG databases and tools for genome screening
Required profile	- Software engineer with strong programming background and previous experience using: o LAMP: Linux, Apache, MySQL, PHP o Object oriented programming o Design patterns o MVC software architecture o Version control, GiT, Subversion o Symphony, Laravel, Zend o Web deployment (Capistrano) o Microframeworks (Silex) and Ansible. - Valuable previous experience in Bioinformatics software development. - Valuable background in NGS and NGS data analysis and/or in Biology/Molecular Biology.