# SPAGNA

| Riferimento | EURES Svizzera - rif. 85/2019 |
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| **Mansione** | Computational Systems Biologist - EURES Svizzera - rif. 85/2019 |
| | STALICLA is expanding on its R&D effort by launching a dedicated computational systems biology unit in Barcelona. The research and development unit of STALICLA in Spain embarks on the identification of subgroups of patients based on genetic, phenotypic and clinical factors, integrating molecular, anatomical and medical data. Through big biomedical data analysis, the research unit aims to exploit compounds that are already on the market or in the advanced stages of clinical trials to offer treatments tailored to patients in each subgroup. The fundamental elements of the project are the computational analysis of omics data (proteomics, genomics, transcriptomics, metabolomics, etc.) and personalized systems medicine. This analysis involves statistical modeling and machine learning centered on the biology of diseases, comorbidities and pharmacology. <br> Position <br> Title: Computational Systems Biologist Location: Barcelona Work type: Permanent <br> Salary: Competitive - depending on experience and profile- Participation in the company's option plan <br> Candidates living Barcelona or EU and able to relocate rapidly would be preferable. <br> The Role <br> The computational systems biologist will work closely with the other members of the unit and contribute to the design, implementation and the analysis of computational models and algorithmic approaches towards the characterization of "targetable" molecular, genetic and clinical features in neurodevelopmental disorders. <br> The Person <br> The ideal candidate will have outstanding track record on computational biology and systems medicine, coupled with practical experience in machine learning, translational bioinformatics and drug repurposing in neurodevelopmental disorders or a related field. S/he is expected to track record in the analysis and visualization of omics data with an emphasis on the systems-level understanding of disease pathology. <br> Desired skills & software: <br> - Scripting languages (and relevant packages): R, Python <br> - Biological and network data visualization: Cytoscape, Gephi <br> - Database: MySQL, Neo4j, MongoDB or equivalent <br> - Other: Linux, Git, Inkscape, Photoshop, (Libre)Office tools <br> Desired capabilities: <br> - Build computational pipelines to process, integrate, analyze, summarize and visualize large scale interconnected biomedical data including but not limited to genomics, transcriptomics, proteomics, metabolomics, clinical, and pharmacological data. <br> - Contribute to the strategical planning and development of new and existing projects and generate high quality documentation of materials, methods, software and analysis results. <br> - Have a solid understanding of molecular data analysis (i.e. quality control, normalization, clustering, differential expression, pathway enrichment), feature engineering and prediction model validation. <br> - Knowledge on widely used biological data resources (such as UniProt, GWAS catalog, Reactome, UMLS) and disease ontologies. <br> - Previous experience on pharmacological data analysis and drug repurposing is a plus. <br> In addition, the candidate is expected to have: <br> - A high comfort level working in a high paced start-up environment, where a pragmatic, resourceful, well organized and effective approach is required with limited resources <br> - A hands-on, decisive approach and a proven ability to work independently and as a team player <br> - Excellent communication skills <br> - A passionate, energetic and enthusiastic personality that will ensure commitment to the company and its vision <br> Contact: info@stalicla.com and cc: eures@afolmet.it |
| **Sede** | Barcellona |
| **Email:** | **info@stalicla.com and cc: eures@afolmet.it** |
| **Scadenza:** | 30/04/2019 |

Le offerte sono consultabili online al seguente link