**Postdoctoral Position in Modeling of Drug resistant Lung Cancers Microenvironment**

The Colinge Laboratory *Cancer Bioinformatics and Systems Biology* at IRCM (Cancer Research Institute of Montpellier) is looking for a talented postdoctoral fellow.

The microenvironment of cancer cells is known to play an important role in tumor progression and resistance. We are looking for a talented post-doctoral scientist to develop models relating the response to different drugs, e.g. platinum-based, with the microenvironment of lung adenocarcinomas (LUADs). This work will integrate on-going developments to infer the cellular interactions taking place in tumor microenvironments (TMEs), both in single cell transcriptomics and bulk analyses (Cabello *et al*., 2020; Alame *et al*., 2020). We aim at establishing quantitative and predictive models of treatment outcome based on data acquired from mouse tumors following different dynamics (rapid/slow growth, spontaneous/acquired resistance, response, etc.). The project involves a consortium of expert laboratories in lung cancer and mouse models thereof, bulk and single cell transcriptomics, animal computer tomography, and 3D-imaging. The postdoc position is funded for 2 years.

**Preferred qualifications** are either a bioinformatics PhD and solid computational skills or a mathematics/physics/computer science PhD with strong interests in life science applications. The successful candidate will be appointed for one year, which will be extended by another year upon performance evaluation.

Interested applicants should e-mail their CV, a letter of motivation and the names and e-mails of 2 references to Prof Jacques Colinge ([jacques.colinge@inserm.fr](mailto:jacques.colinge@inserm.fr)). Applications will be studied immediately. Starting data from July 1, 2021, or later.

**Research topics of the Colinge laboratory** are focused on the functional analysis and modeling of interaction networks in cancer biology, with a particular interest for the TME for several new projects. The lab also develop advanced computational proteomics methods, e.g. to model protein dynamics in biofluids.

**Selected publications**

* Alame M, *et al*. The immune contexture of primary central nervous system diffuse large B cell lymphoma associates with patient survival and specific cell signaling. *Theranostics*, 2021, 11:3565-3579.
* Alame M, *et al*. The molecular and stromal landscape of salivary duct carcinoma reveals new therapeutic opportunities. *Theranostics*, 2020, 10:4383-4394.
* Cabello-Aguilar S, *et al*. SingleCellSignalR: inference of intercellular networks from single-cell transcriptomics. *Nucleic Acids Res*, 2020, 48:e55.
* Lehmann *et al*., In Vivo Large Scale Mapping Of Protein Turnover In The Human Cerebrospinal Fluid. *Anal Chem*, 2019, 91:15500-8.
* Jimenez-Dominguez G, *et al*. An R package for generic modular response analysis and its application to estrogen and retinoic acid receptor crosstalk. *Sci Rep*, 2021, 11:7272.
* Blomen *et al*. Gene essentiality and synthetic lethality in haploid human cells. *Science*, 2015, 350:1092-6.
* Huber *et al*. Proteome-wide drug and metabolite interaction mapping by thermal-stability profiling. *Nat Methods*, 2015, 12:1055-7.
* Muellner *et al*. Targeting a cell state common to triple-negative breast cancers. *Mol Syst Biol*, 2015, 11:789.