

Computational Postdoc position – Pancreatic cancer

Gioacchino Natoli lab

A postdoctoral position is immediately available for a bioinformatician in the context of a long-term project that aims at understanding the **molecular bases** and **therapeutic implications of cellular heterogeneity in human pancreatic cancer**.

Pancreatic ductal adenocarcinoma (PDAC) is predicted to become the major cause of cancer cell deaths in the western world by 2030. It is nearly always an incurable disease, with a median survival time after diagnosis of four months. The causes of this extremely aggressive behavior are both the advanced stage of the disease at diagnosis and the peculiar biological properties of this tumor type, notably the co-occurrence within the same tumor of completely different and morphologically identifiable components: well-differentiated (low-grade) epithelial structures and nests of poorly differentiated (high-grade) quasi-mesenchymal tumor cells, whose coexistence reflects distinct underlying gene regulatory networks and transcriptional outputs. This project is the continuation of a long-term research effort motivated by the assumption that the extreme heterogeneity of human PDACs is a critical determinant of the aggressive clinical behavior of these tumors. Our overall aim is to obtain a molecular characterization and mechanistic understanding of the transcriptional bases of cellular variability, eventually leading to the identification of novel mechanism-aware therapeutic options.

The project is highly integrative, making use of complementary cutting-edge technologies, including **sequencing-** and **imaging-based spatial transcriptomics** and epigenomics.

Your role will be to lead, develop and apply advanced computational methods for genomics research, large-scale data integration and analysis of sequencing data from complementary genomic technologies applied to primary human pancreatic cancer samples and to samples from experimental models developed in the lab. Applicants should have a PhD in bioinformatics or related disciplines, excellent programming skills, a documented research background and excellent interpersonal and communication skills.

Interested candidates should submit their curriculum vitae, a motivation letter and contact information for referees to Gioacchino Natoli (gioacchino.natoli@ieo.it).

Selected recent publications from the lab

- 1) FOXA2 controls the cis-regulatory networks of pancreatic cancer cells in a differentiation grade-specific manner (M. Milan...G. Natoli) *EMBO Journal* 15, 38(20):e102161 (2019).
- 2) Dissection of acute stimulus-induced nucleosome remodeling in mammalian cells (F. Comoglio... G. Natoli) *Genes & Development* 33: 1159-1174 (2019).
- 3) Cooptation of tandem DNA repeats for the maintenance of mesenchymal identity (C. Balestrieri...G. Natoli). *Cell* 173:1150-1164 (2018).
- 4) Opposing macrophage polarization programs show extensive epigenomic and transcriptional cross-talk (V. Piccolo ...G. Natoli). *Nature Immunology* 18, 530-540. PMID 28288101 (2017).
- 5) High constitutive activity of a broad panel of housekeeping and tissue-specific cis-regulatory elements depends on a subset of ETS proteins (A. Curina A...G. Natoli) *Genes & Development* 31,399-412. PMID 28275002. (2017).
- 6) Dissection of transcriptional and cis-regulatory control of differentiation in human pancreatic cancer (G. Diaferia...G. Natoli). *EMBO Journal* 35, 596-617 PMID: 26769127 (2016).
- 7) Transcription of mammalian cis-regulatory elements is restrained by actively enforced early termination (L.M.I. Austenaa...G. Natoli). *Molecular Cell* 60, 460-474. PMID: 26593720 (2015).
- 8) A dual cis-regulatory code links IRF8 to constitutive and inducible gene expression in macrophages (A. Mancino...G. Natoli) *Genes & Development* 29, 394-408. PMID: 25637355. (2015).
- 9) Co-regulation of transcription factor binding and nucleosome occupancy through DNA features of mammalian enhancers (I. Barozzi...G. Natoli) *Molecular Cell* 54, 844-857. PMID: 24813947. (2014).
- 10) Latent enhancers activated by stimulation in differentiated cells (R. Ostuni...G. Natoli) *Cell*. 152: 157-71 (2013).