

Francesco Iorio is a Principal Staff Scientist in the Cancer, Aging and Somatic Mutations program at the Wellcome Sanger Institute, where he leads the development of new algorithms and computational tools for integrative analyses of large-scale cancer genomics and functional genomics datasets.

The aim of his work is to identify molecular markers of drug response and new oncology therapeutic targets. To this aim, Francesco is responsible for the design of new analytical methods and software, and to deliver scientific projects toward the definition of a *Cancer Dependency Map*. This is an atlas of genetic dependencies and vulnerabilities, at individual cancer cell resolution, which could be exploited for the development of targeted and personalized cancer therapies.

Francesco completed his PhD in the Systems, Synthetic and Computational Biology Laboratory of the TeleThon Institute of Genetics and Medicine (TIGEM, Naples, Italy), focusing on computational methods for drug discovery and repositioning based on the analysis of large compendia of gene expression profiles.

Subsequently he was awarded a joint EMBL-EBI/Sanger postdoctoral (ESPOD) fellowship and he worked on integrative computational frameworks for predicting and dissecting drug susceptibility in cancer based on the analysis of data from large-scale drug screens.

Following his postdoctoral research, he was a senior computational scientist at Open Targets, a public-private initiative involving EMBL-EBI, GlaxoSmithKline, Takeda, Biogen and the Wellcome Trust Sanger Institute. His work aimed at identifying new therapeutic targets and synthetic lethalties in cancer through the analysis of data from a large-scale, genome-wide CRISPR-Cas9 knockout screen across hundreds of cancer cell lines. Within Open Targets he currently leads the CELLector project to systematically evaluate the disease relevance of novel and existing cancer *in-vitro* models.

Full CV: https://www.dropbox.com/s/90m7on0l3mepku4/cv_F_Iorio.pdf?dl=0

Selected Publications

* Equally contributing authors,
+Senior/Corresponding Author

Garcia-Alonso LM*, **Iorio F***, Matchan A, Fonseca NA, Jaaks P, Peat G, Pignatelli M, Falcone F, Benes CH, Dunham I, Bignell GR, McDade S, Garnett MJ, Saez-Rodriguez J+.

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Stransky N*, Ghandi M*, Amzallag A*, Lehár J*, Menden MP* and **Iorio F*** with the Cancer Cell Line Encyclopedia Consortium and the Genomics of Drug Sensitivity in Cancer Consortium.

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Nature. 2015 Dec 3;528(7580):84-7.

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