



Bioinformatics job offer

The Genomics Unit of the Institute of Biomedical Technologies of the National Research Council (ITB-CNR), under the scientific supervision of Dr. Gianluca De Bellis has been focusing for several years on many projects aimed to the employment of high-throughput sequencing technologies.

- Sequencing and annotation of bacterial genomes and transcriptomes
- Characterization of complex microbial communities
- Sequencing and annotation of hypervariable regions in viruses
- Sequencing and functional annotation of plant transcriptomes
- Transcriptomics analysis in tumors
- Mutation detection in nuclear and mitochondrial DNA
- Ancient DNA sequencing

The laboratory is equipped with state-of-the-art sequencing platforms, such as an Illumina GAIIx plus a Roche GS-FLX and a Roche GS Junior instruments. Moreover, the laboratory possesses a computational infrastructure made of a local 5-node cluster (20 cores total, 20 Gb RAM, 3 Tb HDD) and a high-performance server (48 cores total, 128 Gb RAM, 40 TB HDD)

In the context of a new cooperative project for resequencing and mutation detection in genes involved in myelodysplastic syndromes we are looking for:

1 Bioinformatician

Requisites:

- Strong Linux/Unix programming skills
- Knowledge of at least one scripting language (Perl, Python, Ruby,...)
- Experience in the data analysis of next-generation sequencing (NGS) data

Other skills:

- Previous experience in the field of mutation detection and SNP analysis in human pathologies
- Experience in the implementation of computational pipelines/scripts for NGS data analysis
- Knowledge of relational databases (MySQL, PostgreSQL,...)

All candidates should apply sending their personal CV (with, if available, the name of a contact person) to:

Dr. Marco Severgnini: marco [dot] severgnini [at] itb [dot] cnr [dot] it

or

Dr. Gianluca de Bellis: gianluca [dot] debellis [at] itb [dot] cnr [dot] it.

Web: <http://www.itb.cnr.it/web/genomics/home>

Selected publications

Tomato Genome Consortium. The tomato genome sequence provides insights into fleshy fruit evolution. *Nature*. 2012 May 30;485(7400):635-41

Peano C, Talà A, Corti G, Pasanisi D, Durante M, Mita G, Bicciato S, De Bellis G, Alifano P. Comparative genomics and transcriptional profiles of *Saccharopolyspora erythraea* NRRL 2338 and a classically improved erythromycin over-producing strain. *Microb Cell Fact*. 2012 Mar 8;11:32

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Ermini L, Olivieri C, Rizzi E, Corti G, Bonnal R, Soares P, Luciani S, Marota I, De Bellis G, Richards MB, Rollo F. Complete mitochondrial genome sequence of the Tyrolean Iceman. *Curr Biol*. 2008 Nov 11;18(21):1687-93

Iacono M, Villa L, Fortini D, Bordoni R, Imperi F, Bonnal RJ, Sicheritz-Ponten T, De Bellis G, Visca P, Cassone A, Carattoli A. Whole-genome pyrosequencing of an epidemic multidrug-resistant *Acinetobacter baumannii* strain belonging to the European clone II group. *Antimicrob Agents Chemother*. 2008 Jul;52(7):2616-25.