Flavio Mignone

Curriculum vitae

BIO AND EDUCATION

Associate Professor in Molecular Biology at the Department of Science and Innovation Technology (DISIT) University of Piemonte Orientale. He has a degree in Biology a bachelor degree in Computer Engineering and a PhD in Molecular and Cell Biology. He worked as Marie Curie fellow at the European Bioinformatics Institute (EBI).

Since 2006 he is interested in high throughput data analysis and in high performance computing. He works to the development of tools for the storage, analysis and exploration of data obtained from microarrays and NGS techniques (mainly RNASeq, exome sequencing and metagenomics). He is also interested in the characterization of mRNA untranslated regions (UTRs) focusing on regulatory regions controlling mRNA stability, sub-cellular localization and translation efficiency.

UNIVERSITY CAREER

2016-	Associate Professor , Università del Piemonte Orientale
2011-2016	Assistant Professor, Università del Piemonte Orientale
2006-2011	Assistant Professor, Università degli Studi di Milano
2004-2006	Research fellow, Università degli Studi di Milano

UNIVERSITY POSITIONS

2014-	Coordinator of "attività formative Laurea in Scienze Biologiche e LM Biologia"
2014-	Member of "gruppo di gestione AQ dei corsi di Laurea in Scienze Biologiche e LM Biologia"
2016-	Member of "gruppo del riesame per la ricerca" of Department

MAIN FIELDS OF INTEREST

1. Bioinformatics
2. Next Generation Sequencing

CURRENT ISSUES OF RESEARCH

1. **High throughput analysis systems**

Main research interest is focused on the development of automatic systems for management, presentation and analysis of data obtained from High throughput technologies (such as microarray and NGS). The main goal is the setup of bioinformatics analysis systems devised to support systems biology and molecular medicine.

2. **UTRs and alternative splicing**

Study of involvement of Untranslated regions (UTR) in regulation of gene expression and in-silico prediction of alternative splicing.

3. **Algorithms for bioinformatics**

Development of algorithms for de-novo transcriptome assembly from NGS data.

TOP FIVE PAPERS

1: Patrucco L, Peano C, Chiesa A, Guida F, Luisi I, Boria I, Mignone F, De Bellis G, Zucchelli S, Gustincich S, Santoro C, Sblattero D, Cotella D. Identification of novel proteins binding the AU-rich element of α-prothymosin mRNA through the selection of open reading frames (RIDome). RNA Biol. 2015;12(12):1289-300. doi: 10.1080/15476286.2015.1107702. PubMed PMID: 26512911; PubMed Central PMCID: PMC4829324.

2: Minucci A, Scambia G, Santonocito C, Concolino P, Canu G, Mignone F, Saggese I, Guarino D, Costella A, Molinario R, De Bonis M, Ferrandina G, Petrillo M, Scaglione GL, Capoluongo E. Clinical impact on ovarian cancer patients of massive parallel sequencing for BRCA mutation detection: the experience at Gemelli hospital and a literature review. Expert Rev Mol Diagn. 2015;15(10):1383-403. doi: 10.1586/14737159.2015.1081059. Epub 2015 Aug 26. PubMed PMID: 26306726.

3: Landini MM, Borgogna C, Peretti A, Doorbar J, Griffin H, Mignone F, Lai A, Urbinati L, Matteelli A, Gariglio M, De Andrea M. Identification of the skin virome in a boy with widespread human papillomavirus-2-positive warts that completely regressed after administration of tetravalent human papillomavirus vaccine. Br J Dermatol. 2015 Aug;173(2):597-600. doi: 10.1111/bjd.13707. Epub 2015 Jun 25. PubMed PMID: 25639663.

4: Boria I, Boatti L, Saggese I, Mignone F. NGS-Trex: an automatic analysis workflow for RNA-Seq data. Methods Mol Biol. 2015;1269:243-56. doi: 10.1007/978-1-4939-2291-8_15. PubMed PMID: 25577383.

5: Boria I, Boatti L, Pesole G, Mignone F. NGS-Trex: Next Generation Sequencing Transcriptome profile explorer. BMC Bioinformatics. 2013;14 Suppl 7:S10. doi: 10.1186/1471-2105-14-S7-S10. Epub 2013 Apr 22. PubMed PMID: 23815181; PubMed Central PMCID: PMC3633008.