Integrative analysis of molecular factors influencing overall survival of patients diagnosed with different types of cancer.

DIPARTIMENTO DI MORFOLOGIA, CHIRURGIA E MEDICINA SPERIMENTALE
SEZIONE DI ANATOMIA E ISTOLOGIA
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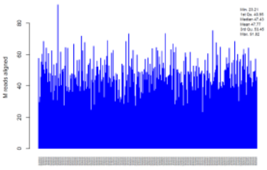
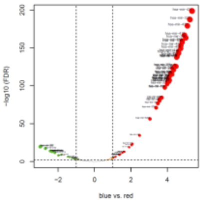
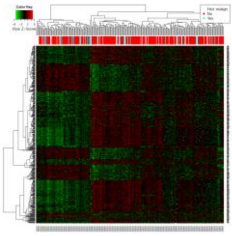
Pawel Gaj PhD has visited the rearch group of Professor Stefano Volinia at the University of Ferrara, Italy. During his two month stay in Italy Dr Gaj was working in the field of bioinformatics carrying out a study focused on discovery contribution of different kinds of molecular determinants to differential survival rates in cancer patients. He paid especial attention to the interplay between genetic molecules of different types and those exhibiting different functions on the regulation of transcriptome of the human cells. During the first month of his stay in Italy he was developing his own scientific approaches whereas during the second month Dr Gaj has been working on a very promising collaborative project focusing on the genomic data of patients diagnosed with the acute myeloid leukemia. This part of the research will be continued in the future at the Medical University of Warsaw and/or in collaboration with other institutions giving it a great chance to sustain the international collaboration between the institutional and personal partners participating in the Twining Programme.

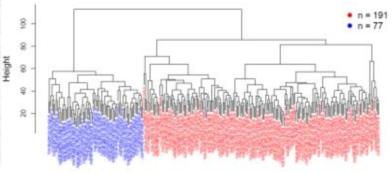
Dr Pawel Gaj (third from the left) discussing approaches relevant for his study during a laboratory meeting of Professor Stefano Volinia's (most right) scientific group at the University of Ferrara.

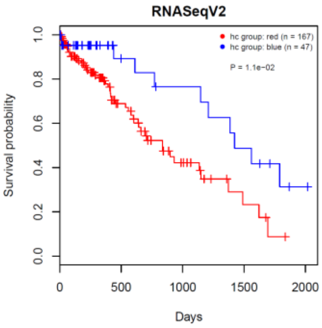
During his stay at the Laboratory of Professor Stefano Volinia Dr Gaj has had opportunity to use various cutting-edge bioinformatics tools to run analysis of the Next Generation Sequencing (NGS) data carrying out statistical analyses on various different levels i.e. starting from using low level data processing procedures and then further progressing with higher level statistical algorithms used for the NGS data normalization, differential gene expression between classes of samples selected in unsupervised analyses. Finally Dr Gaj investigated the influence of differential expression of genes on survival rates characterizing identified groups of cancer patients. As a validation measure for the differential gene expression results obtained for the transcriptomics part of Dr Gaj's study he performed a Geneset Enrichment Analysis (GSEA) for the terms included in the Gene Ontology (GO) data base.

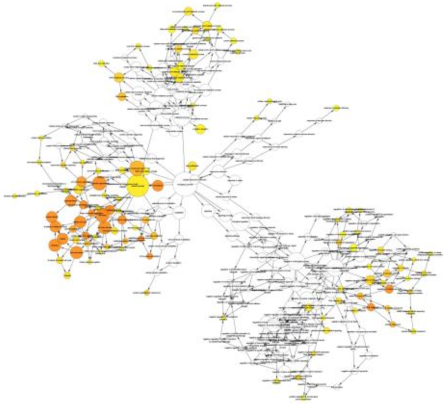












Dr Gaj has also contributed to the assembly and installation of a high performance workstation used to carry out complex and computationally intensive calculations which are nowadays an essential element of the modern approaches in bioinformatics. The server presently available under the deepseq.unife.it web address will be very useful for the planned scientific collaboration in the future.