From July 25th till August 24nd, 2014 I visited the group of Prof. Stefano Volinia from University of Ferrara, Italy. My visit was coordinated under the twinning agreement between the Medical University of Warsaw and the University of Ferrara in Italy within WP1 (Task 1.6).

Prof. Stefano Volinia is an expert in computational biology. He has been involved in developing bioinformatics applications since 1988 (identification of statistically anomalous oligonucleotides in DNA databases). Lately he has been responsible for developing in-house protocols for DNA microarrays and next-generation sequencing analysis.

During my stay, Prof. Volinia and I have had the great opportunity to discuss the details of our current collaborative projects, and future plans of cooperation. We both are especially interested in genome-wide analysis of miRnome in human cancers. We were working together on novel ways of analysis of the next-generation sequencing data, and combining them with publicly available data from different platforms. We focused on single nucleotide mutations in microRNA genes, and the ways to prove their functional relevance. First, we went through the detection and annotation process of all known and yet unidentified miRs and their isoforms in pairs of cancer and unaffected tissue from the same individual, and in normal tissue from cancer-free controls. As result we obtained a complete dataset of RNA molecules and their changes as normal tissue develops into cancer. Then, we correlated the deregulated miRs with the results of mRNA decay analysis. Finally, we worked on using the obtained data for the analysis of genetic background of an individual patient, identification of various factors implicated in clinical outcome of the disease and the ways to use it for tailoring of potential targeted therapies.