The genomic medicine revolution brings new hope in the fight against Cancer. Thousands of tumours from different cancer types have been sequenced and genomically characterised, confirming the complexity of cancer genomes and providing a new perspective in tackling cancer. Computational approaches have the capability to decipher cancer genome marks but there are still many challenges to be faced in order to translate cancer genome discoveries into clinical medicine.

The Translational Bioinformatics Unit uses computational methodologies to perform genomic analysis of cancer patients’ data, in order to identify new biomarkers and mechanisms of drug response. Our main goal is to translate this knowledge into effective treatments for cancer patients.

“The Translational Bioinformatics Unit has established a new collaboration with the Hospital Universitario de Sanchinarro in order to provide its expertise in computational cancer genomics analysis as well as to guide the diagnosis and treatment decision making process for cancer patients using next-generation sequencing data.”

**OVERVIEW**

The Translational Bioinformatics Unit was established in February 2012. During this second year, our major research activity was focused on the development of novel computational techniques for the integration of cancer genomic data with clinical and pathological features, and to apply these new methodologies to detect therapeutic targets and biomarkers of response to therapy.

**Research Highlights**

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**Pharmacogenomics**

Two international projects – Genomics of Drug Sensitivity in Cancer, from the Wellcome Trust Sanger Institute, and Cancer Cell line Encyclopaedia, from the Broad Institute of MIT and Harvard – are underway with the aim of conducting a detailed genetic and pharmacological characterisation of a large collection of cancer cell lines. This data can be used to better the optimal clinical application of cancer drugs, as well as the design of clinical trials of investigational compounds being developed for the clinic.

**Personalised medicine**

In 2013, we established a new collaboration with the Hospital de Madrid. During this period, we implemented a new pipeline for the interpretation of next-generation sequencing data from patients’ tumours. This computational module allows us to categorise patients’ tumours and match them to effective drugs or treatments based on their genomic alterations. The output result is a ranked list of genetic variants that could serve as potential therapeutic targets and thereby also help guide treatment decisions for patients. So far we have analysed more than 50 patients and this new pipeline has facilitated the identification of actionable mutations in nearly half of those patients.

**Publications at other institutions**


During 2013, the Translational Bioinformatics Unit developed a new bioinformatics methodology to match patients’ tumours with the existing information from these resources, in order to extrapolate drug response using gene expression signatures. With this method, we are able to extend the set of known genetic markers and to use oncogenic signatures as new predictive biomarkers that could help to guide therapeutic decisions.

**Clustering and correlation matrix of anti-cancer drugs based on oncogenic transcriptional states associated with drug response.**

**Figure:** Cluster and correlation matrix of anti-cancer drugs based on oncogenic transcriptional states associated with drug response.