

## Bioinformatic analysis of vitamin D receptor (VDR).

Roland Amir, Centre de Santé des Fagnes. Nuclear Medicine Department,  
Boulevard Louise, 18 - 6460 Chimay. Belgium.

Email: roland.amir@outlook.com

### **Introduction.**

One of the goals of bioinformatics is to reveal novel biological understanding. The premise for such analyses is that the comprehensive analyses of biological data, free from a bias as to what are the major biological drivers of a given phenotype, will reveal organizational insight that is neither obvious nor intuitive.

In this respect, analyses that has no assumptions what are the biological drivers of a given phenotype can be achieved by applying algorithmic approaches that depend on discrete mathematics and information theory associated with a central role for the statistical sciences.

### **Background.**

With the emergence of genomic profiling technologies and selection molecular targeted therapies, biomarkers play an increasing by important role in the clinical management of cancer patients. Genome-based prognostic biomarkers are also available for several cancer types. With the recent emergence of highly selective molecular targeted agents and high throughput genomic characterization technologies, accurate and well validated cancers biomarkers are increasingly needed. It is well known that an important amount of oncological drugs that enter clinical development will not reach market approval due to failure of clinical trials to demonstrate therapeutic benefit, contributing to costly and slow cancer drug development <sup>(1)</sup>.

As acknowledged by the USA Food and Drug Administration (FDA), the judicious use of biomarkers is expected to play an important role in minimizing risk of clinical trial failure by enriching the trial populations with specific molecular subtypes responding better to tested therapies. A biomarker is any substance, structure or process that can, be measured in the body or its products and influence or predict the incidence of outcome or disease <sup>(2-3)</sup>.

### **Conclusion.**

Using combination and integration of omic data sets, the altered expression of VDR target genes associated with more aggressive disease and suggests that analyses of genes that are regulated by VDR, and other transcription factors, may offer an opportunity to understand how VDR signalling rather than the VDR itself, impacts cancer phenotypes.

### **References.**

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