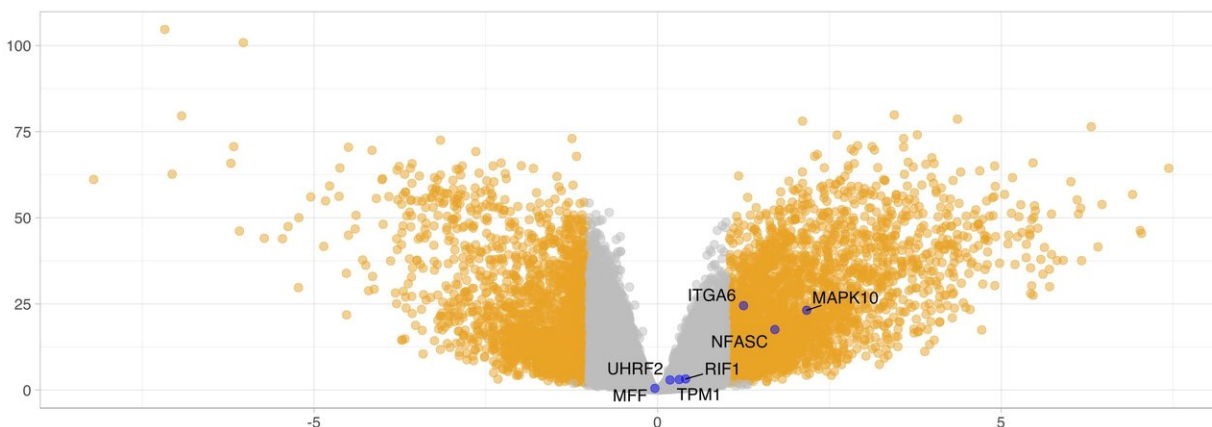


# New approach on the use of big data in clinical decision support

October 4 2018



Graph resulting from analysis of the expression of different genes Credit: Nuno Agostinho, iMM.

A new computational approach that allows the identification of molecular alterations associated with prognosis and resistance to therapy of different types of cancer was developed by the research group led by Nuno Barbosa Morais at Instituto de Medicina Molecular João Lobo Antunes (iMM; Portugal). It has been published in *Nucleic Acids Research*.

Cancer cells are characterised by perturbations in the regulation of genes, and in particular, by alterations in [alternative splicing](#), a process by which the same gene can originate different proteins. Some of those

alterations are associated with different malignant features of cancer and its resistance to treatment, but vary from tumour to tumour. "Each patient hosts a different cancer, so scientists and clinicians need molecular information about many individuals to understand disease mechanisms, assess prognosis and make predictions on the best treatment for each patient based on their tumour's molecular profile," explains Nuno Barbosa Morais.

"We have created software that analyses large databases with clinical and splicing information for thousands of tumours, detects patterns of similarities between different cases, and allows us to identify the relation of each molecular alteration with patient survival for more than 30 types of cancer. In practice, the program quickly converts a lot of genome-wide data into biological information with clinical potential," explains Nuno Saraiva Agostinho, first author of the study and student of the Ph.D. programme CAML (Centro Académico de Medicina de Lisboa, da Faculdade de Medicina da Universidade Lisboa).

"Thanks to this approach, we have already identified a possible mechanism of resistance to chemotherapy in colorectal cancer that we are now investigating in an international collaboration that we are leading. We have also identified a new prognostic marker in breast [cancer](#) that we will now study, teaming up with other iMM colleagues," says Nuno Barbosa Morais, who leads the lab and has supervised the study.

**More information:** Nuno Saraiva-Agostinho et al, psichomics: graphical application for alternative splicing quantification and analysis, *Nucleic Acids Research* (2018). [DOI: 10.1093/nar/gky888](https://doi.org/10.1093/nar/gky888)

Provided by Instituto de Medicina Molecular

Citation: New approach on the use of big data in clinical decision support (2018, October 4)  
retrieved 22 September 2023 from

<https://phys.org/news/2018-10-approach-big-clinical-decision.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.