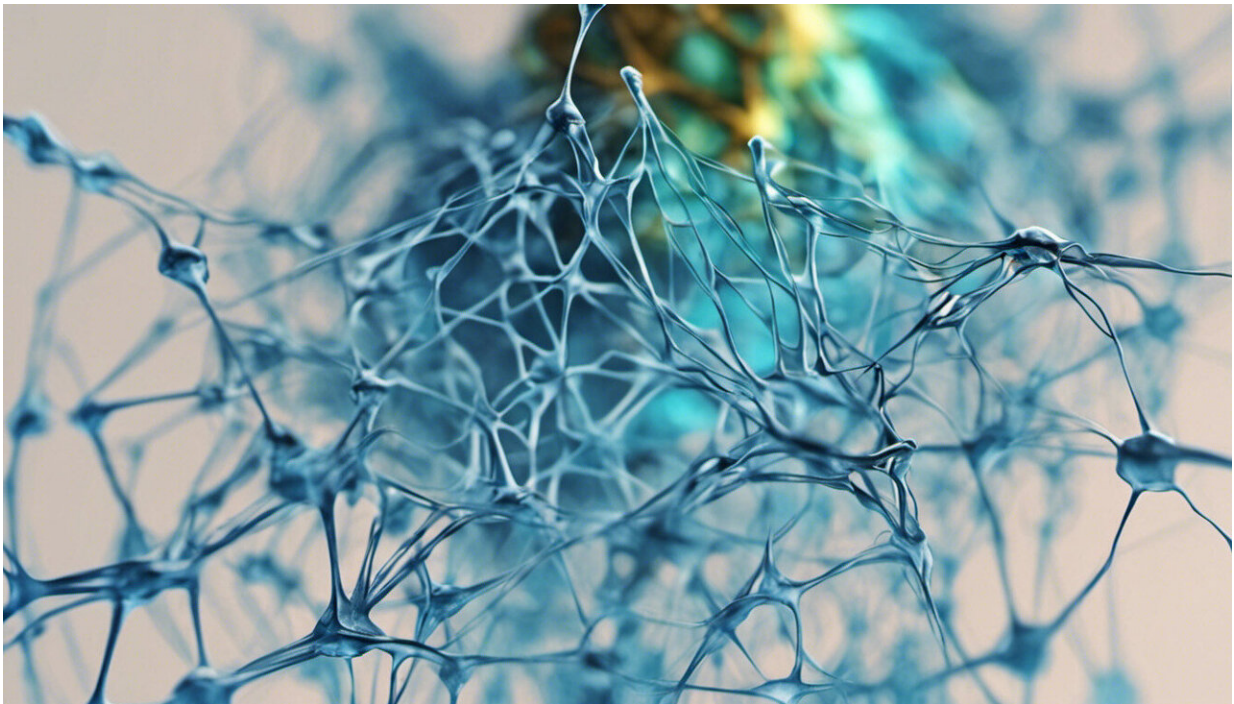# Beyond genetics: Mining biological networks for new treatments for disease

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Credit: AI-generated image (disclaimer)

Our genes define us and every other living organism. They hold essential information to build and maintain an organism's cells and pass genetic traits to offspring - everything from eye and hair colour to susceptibility or resistance to disease.

But genes are not the only source of biological information: proteins, metabolic networks, and gene and protein interaction networks, to name a few, hold the potential to tell us so much more. Combined, this data could lead to key advances in biomedical research and new treatments for disease.

The EU project BIONET ('Network topology complements genome as a source of biological information') is using graph theory - a branch of mathematics - to model biological network interactions and develop advanced algorithms to analyse these complex data.

Take baker's yeast, for example. A single cell contains around 6000 proteins and approximately 50 000 interactions between them. While genetic information is important because it contains the cell's blueprint, these interactions between proteins forming the network are no less significant as they specify how the cell functions.

"Just as we build single family homes different from schools or shopping malls, natural selection has 'selected' the structure of biological networks to best perform a particular biological function," explains Dr Nata?a Pr?ulj of Imperial College London in the United Kingdom, which received a European Research Council (ERC) Starting Grant worth EUR 1.6 million to work on the BIONET project.

Dr Pr?ulj and her colleagues are using advanced mathematics, parallel computing and data mining techniques to uncover information buried in the structure of genetic interaction networks, protein-protein interaction networks, metabolic networks, protein structure networks and brain functional networks, among others.

It's a huge challenge involving large and complex data sets, computational problems that require enormous amounts of computer time to analyse. The team is drawing on expertise and technology from

fields as diverse as mathematics, parallel computing, scientific computing and data mining, as well as biology and medicine.

"Deciphering these large networks is not easy as it involves many computationally intractable problems," Dr Pr?ulj says. "These biological networks are very large, containing for example, all proteins and their known interactions in a cell, and we are extracting information from a different type of biological data, the topology of biological networks. This is important, because no single source of biological data can fully explain biological processes and we need to extract information from each of them before we can combine them to get the full picture about complex biological systems."

The payoff is potentially huge, however. Understanding how biological networks function and the interactions within and between them could, among other things, lead to revolutionary treatments for a wide variety of diseases.

In that vein, the BIONET team is collaborating with Prof. Charles Coombes from the Faculty of Medicine at Imperial College London, Prof. Djordje Radak from the Institute for Cardiovascular Disease at the University of Belgrade, Serbia, and Prof. Anand Ganesan from the Dermatology Department of the University of California, Irvine, in the USA, in order to study the biological processes involved in skin cancer, breast cancer and cardiovascular disease.

"We have been working with medical doctors and researchers on exploiting the information hidden in network topology that our new computational techniques have uncovered," Dr Pr?ulj says.

For example, from the topology of the human protein-protein interaction network, the team has computationally identified new proteins involved in melanin production and obtained biological validations of their

results.

It is particularly significant for skin cancer research, since some of these new proteins could be potential targets for new drugs that would help cure this complex disease.

Similarly, the BIONET researchers have also identified proteins that are involved in the onset and progression of many other complex diseases, including cancers and cardiovascular problems.

But the impact of BIONET does not end in the biology and biomedical research domains. The computational techniques developed by the team for mining network data could also be applied in many other fields, from economics and demographics to disaster response.

Dr Pr?ulj notes, for example, that the team has also been working with economists to apply the computational techniques to the world trade network in order to search for the causes of economic crises and uncover potential recovery processes.

The BIONET project is due to be completed in December 2016.

 More information: BIONET www.doc.ic.ac.uk/~natasha/erc-project.html

Provided by CORDIS

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