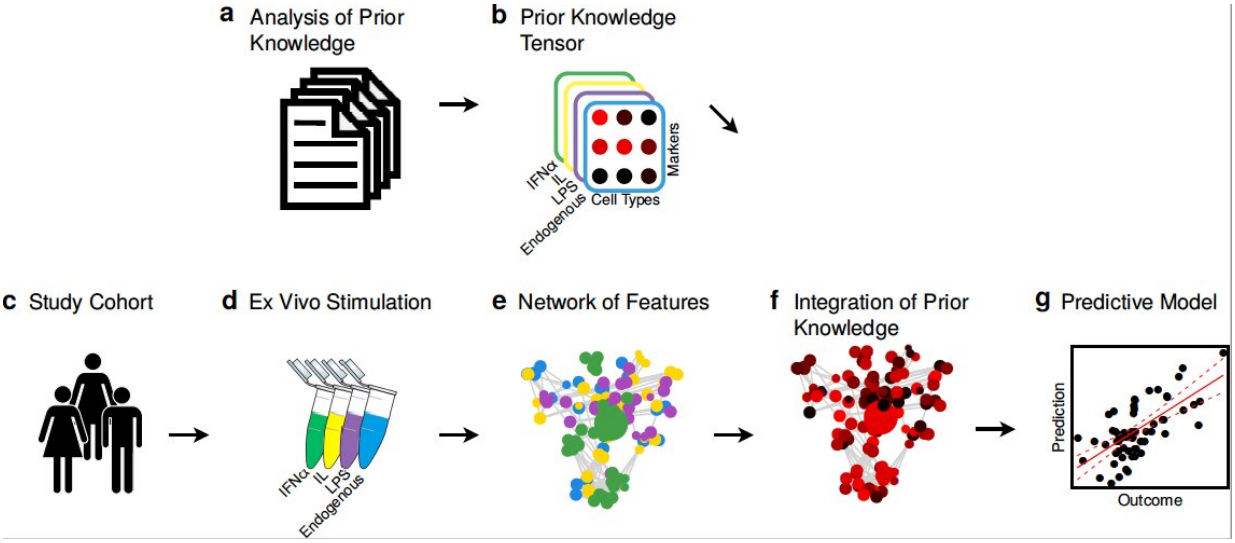
A machine leaning model that incorporates immunological knowledge

October 28 2020, by Ingrid Fadelli



The immunological Elastic-Net analysis pipeline. Credit: Culos et al

The complex network of interconnected cellular signals produced in response to changes in the human body offers a vast amount of interesting and valuable insight that could inform the development of more effective medical treatments. In peripheral immune cells, these signals can be observed and quantified using a number of tools, including cell profiling techniques.

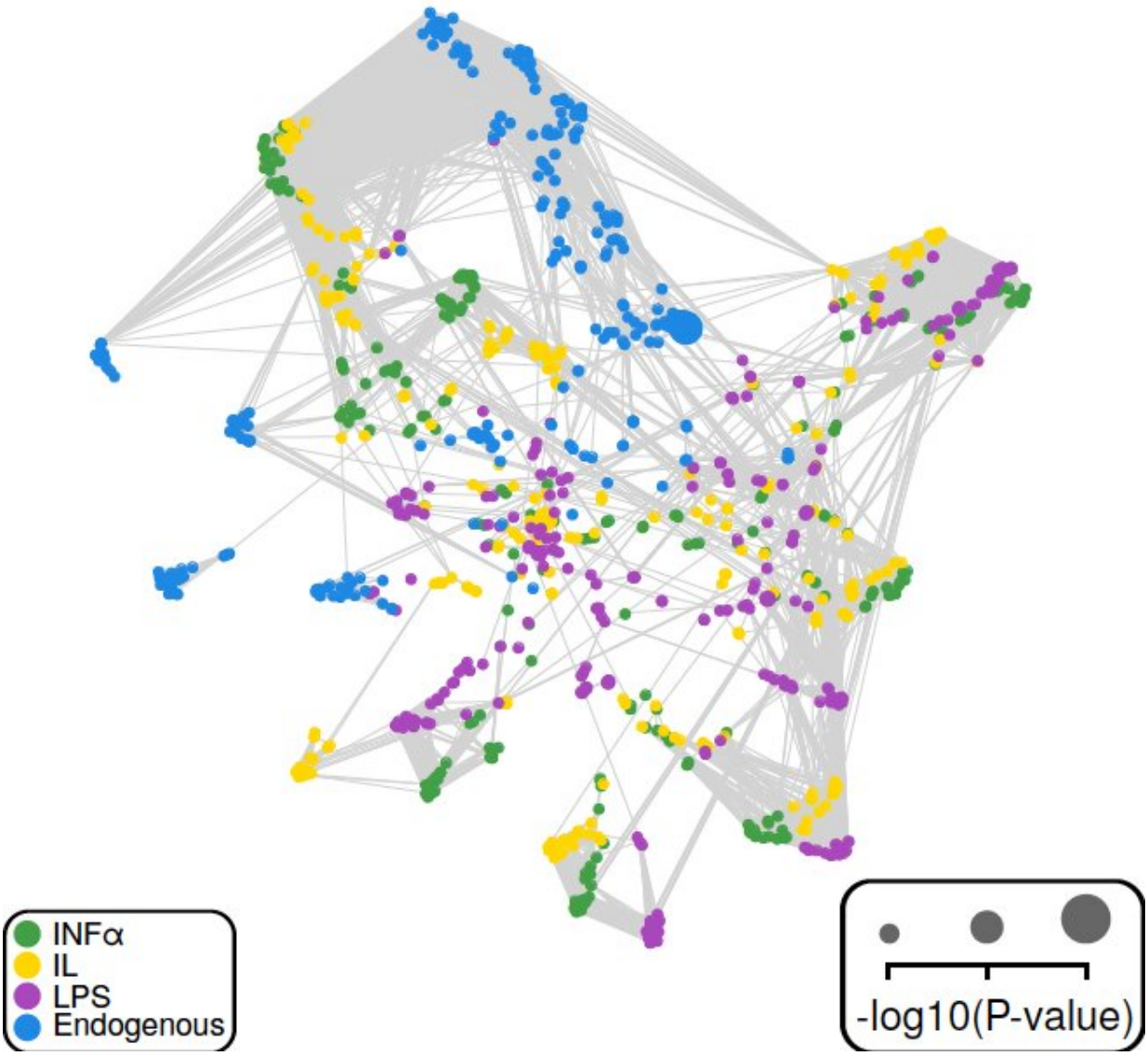
Single-cell profiling techniques such as polychromatic flow and mass cytometry have improved significantly over the past few years and they

could now theoretically be used to obtain detailed immune profiles of patients presenting a number of symptoms. Nonetheless, the limited sample sizes of past studies and the high dimensionality of the patient data collected so far increase the chances of false-positive discoveries, which in turn lead to unreliable immune profiles.

Conducting studies on larger groups of patients could improve the effectiveness of these cell-profiling techniques, allowing medical researchers to gain a better understanding of the patterns associated with medical conditions. Gathering data from many patients, however, can be both expensive and time consuming.

Researchers at Stanford University School of Medicine have recently developed immunological Elastic-Net (iEN), a machine-learning model that predicts cellular responses based on mechanistic immunological knowledge. In a paper published in *Nature Machine Intelligence*, they demonstrated that incorporating this immunological knowledge into their model's prediction processes increased its predictive power on both small and large patient datasets.

"Our methodology allows us to leverage previous studies to increase our models' accuracy without enrolling additional patients," Nima Aghaeepour, one of the researchers who led the study, together with Anthony Culos, Martin Angst, and Brice Gaudilliere, told TechXplore. "A key advantage of our method is that it does not limit the data-driven nature of the models. In cases where the collected data disagrees with prior knowledge, our algorithm is allowed to reduce the importance of prior knowledge and instead focus on raw data if that proves to be the stronger solution."



Overview of the LTP study. A correlation network of intracellular signalling responses, measured in peripheral immune cells and coloured by ex vivo stimulation status, is visualized. Edges represent significant (P

Citation: A machine leaning model that incorporates immunological knowledge (2020, October 28) retrieved 20 March 2024 from https://techxplore.com/news/2020-10-machine-incorporates-immunological-knowledge.html

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