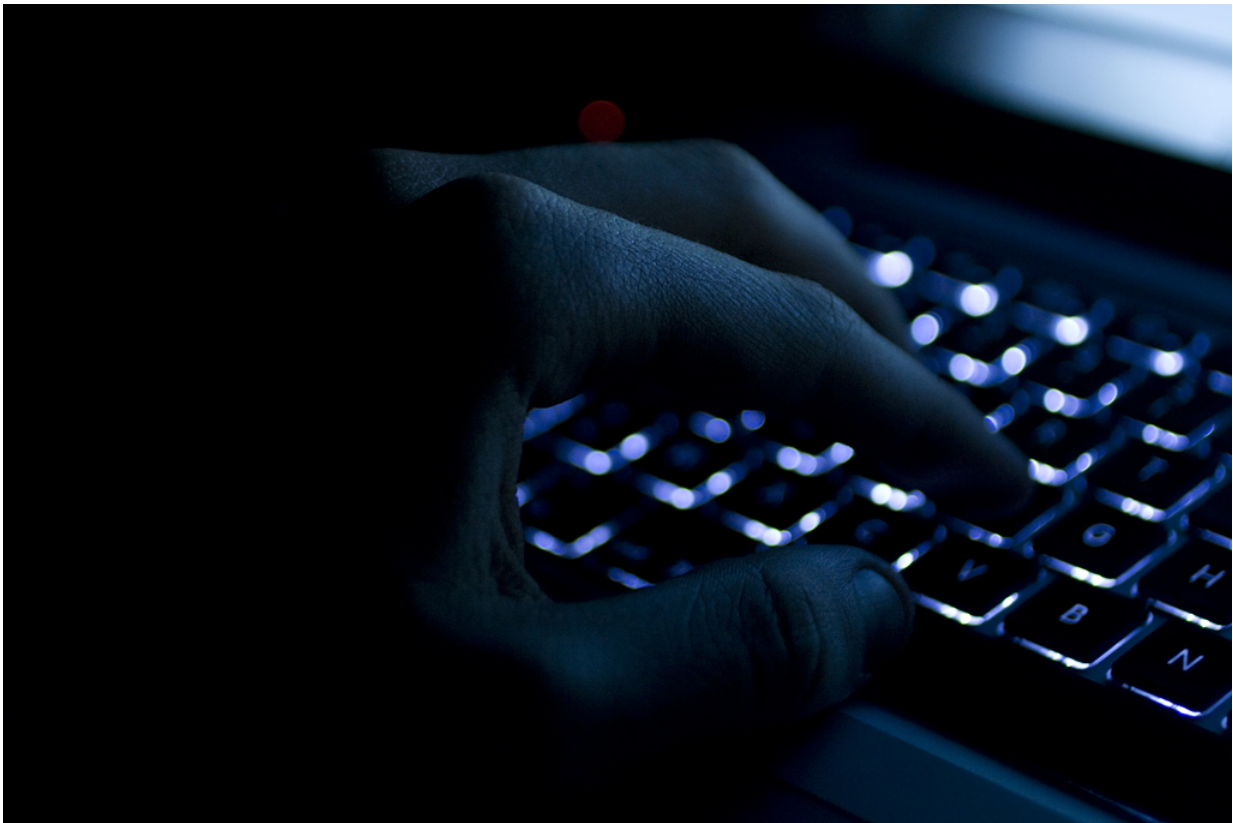


Easy integration of biological knowledge improves understanding of diseases

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Researchers have improved the integration of disparate sources and types of data which will advance scientists' understanding of disease using Wikipathways. This study, published in *PLOS Computational Biology*, will help other scientists better utilize open data and will aid the discovery of new therapeutic targets for disease. Credit: Thomas Heylen / Flickr

Researchers have improved the integration of disparate sources and types of data which will advance scientists' understanding of disease using Wikipathways. This study, published in *PLOS Computational Biology*, will help other scientists better utilize open data and will aid the discovery of new therapeutic targets for disease.

These scientists from Maastricht University and the Gladstone Institutes have been working to address the data problem that hinders everyday research. Despite the fact that innovative new technologies have exponentially advanced biomedical research - which makes it easier than ever to collect essential information about human health and disease - there are still many diseases that scientists do not understand in enough detail to develop effective treatments for them.

This problem is in part due to the difficulty of aggregating different types of experimental data. The amount of information that needs integration is overwhelming and the databases that contain this information are typically targeted towards a specific problem and store the data in ways that make it hard to reuse in another context. "There is a wealth of information available to us, but we need a better way to bring it all together," says co-senior author Alex Pico, PhD, interim director of the Gladstone Bioinformatics Core.

To solve this problem, the researchers converted WikiPathways - an open source knowledgebase of biological pathways - into a modern linkable format. They applied semantic web and ontology approaches to greatly simplify the integration of the data contained in WikiPathways with other knowledge bases. This allowed the scientists to combined information from WikiPathways with two other databases, DisGeNET and the EBI Expression Atlas, which contain information about the relation between genes and diseases, and the expression of genes under different conditions, respectively. The integration of these resources gives scientists greater insight into the biological processes behind

diseases like diabetes mellitus and asthma.

The authors also worked with the Open PHACTS Foundation, the outcome of a project funded by the European Innovative Medicines Initiative aimed at facilitating drug discovery. Nick Lynch at Open PHACTS, says: "Twenty-five percent of the current requests to our programmable database include information from WikiPathways. Therefore, being able to integrate data from different pathways adds valuable, complementary [information](#) to our services in support of drug discovery."

"There is tremendous potential for this technology to spur new connections and foster new collaborations," adds co-senior author Prof. Chris Evelo, PhD, head of the Department of Bioinformatics (BiGCaT) at Maastricht University.

WikiPathways is a community-curated, wiki-based, open database that was started in 2008, initiated by a collaboration between Maastricht University and the Gladstone Institutes. It is frequently used to analyze high-throughput studies involving gene expression and metabolism. All knowledge collected in this database is compatible with the European Open Science Cloud. WikiPathways collaborates with external projects, such as WormBase, through research portals, and has been cited more than 600 times.

More information: Waagmeester A, Kutmon M, Riutta A, Miller R, Willighagen EL, Evelo CT, et al. (2016) Using the Semantic Web for Rapid Integration of WikiPathways with Other Biological Online Data Resources. *PLoS Comput Biol* 12(6): e1004989. [DOI: 10.1371/journal.pcbi.1004989](https://doi.org/10.1371/journal.pcbi.1004989)

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