# InSoLiTo project: The research software graph-based network from OpenEBench

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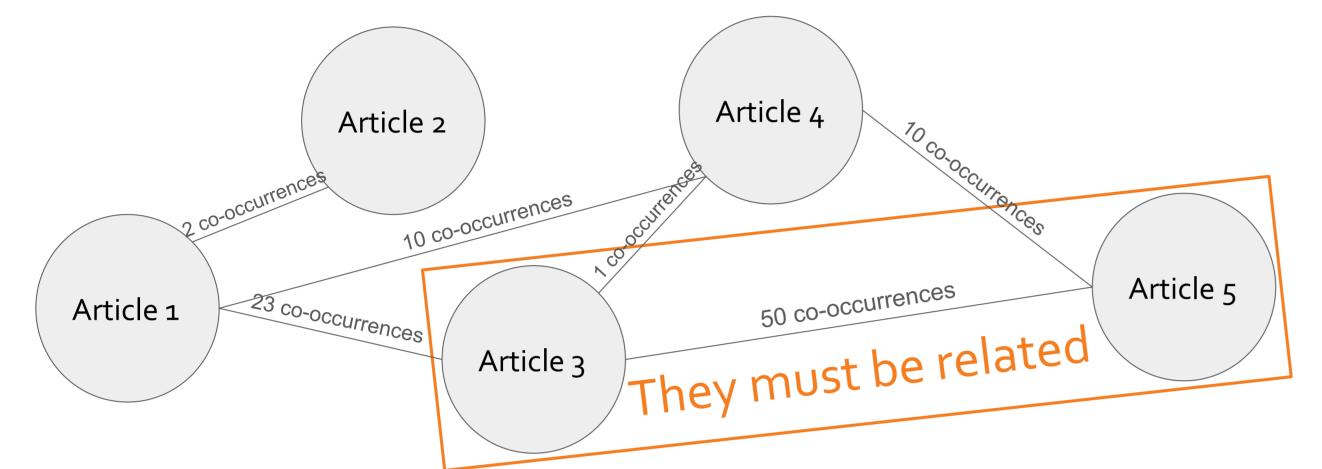




InSoLiTo is a graph-based network of the co-usage of research software from the tools collection hosted by OpenEBench. Co-usage is understood as being cited in the same scientific publications. The initial aim of the project is to identify how bioinformatics software relate to each other allowing to potentially infer analytical workflows commonly used from the literature.

# Development

Calculate the Co-occurrences: How many scientific publications two articles have been referenced together.



The most direct way of knowing how the bioinformatics community uses their software is by looking to the references in their scientific articles.

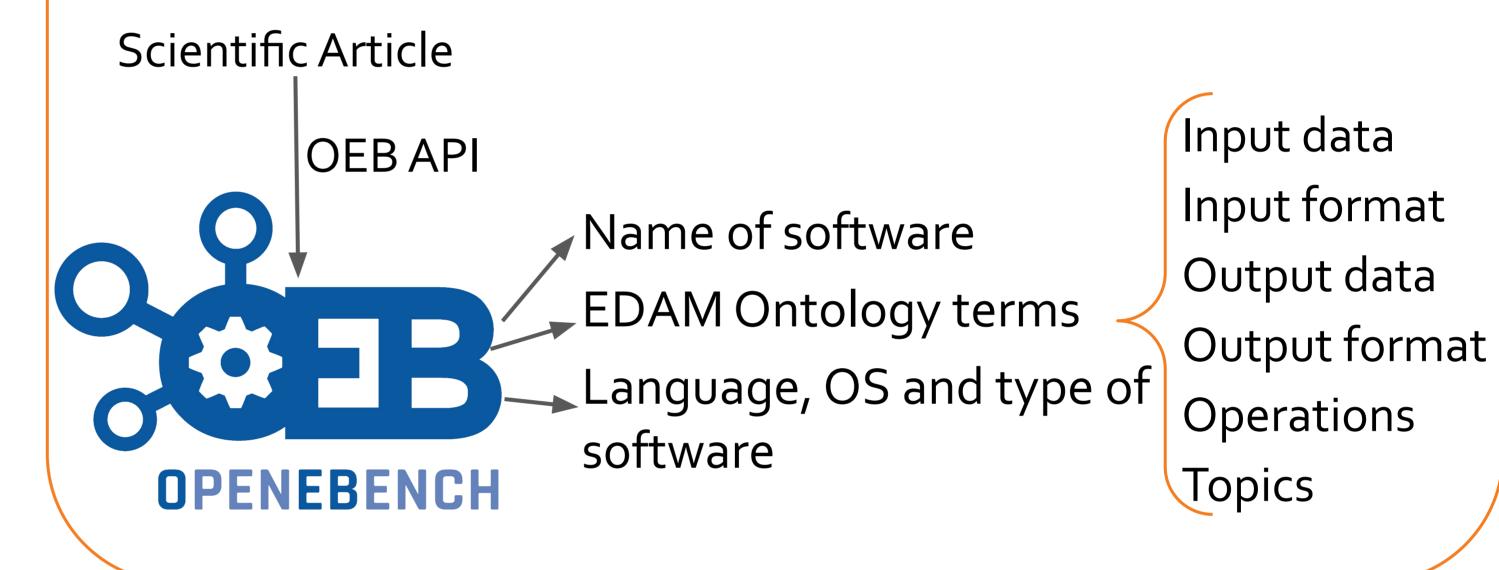
The theory is simple:

Two articles are closely related when there is high co-occurrence between them.

### **Transform Articles to Research Software**

The tools, databases and services stored in the OpenEBench Technical Monitoring database, among other information, include references to the articles associated to the software.

The OpenEBench API is used to assign the articles to the cited software and collects the additional information stored in OEB.



#### Type of OS Language Schema **SUBCLASS INPUT DATA** USE LANGUAGE USE OS **INPUT FORMAT EDAM** Software Article ontology term OPERATION **OUPUT FORMAT OUPUT DATA**

## **Graph database**

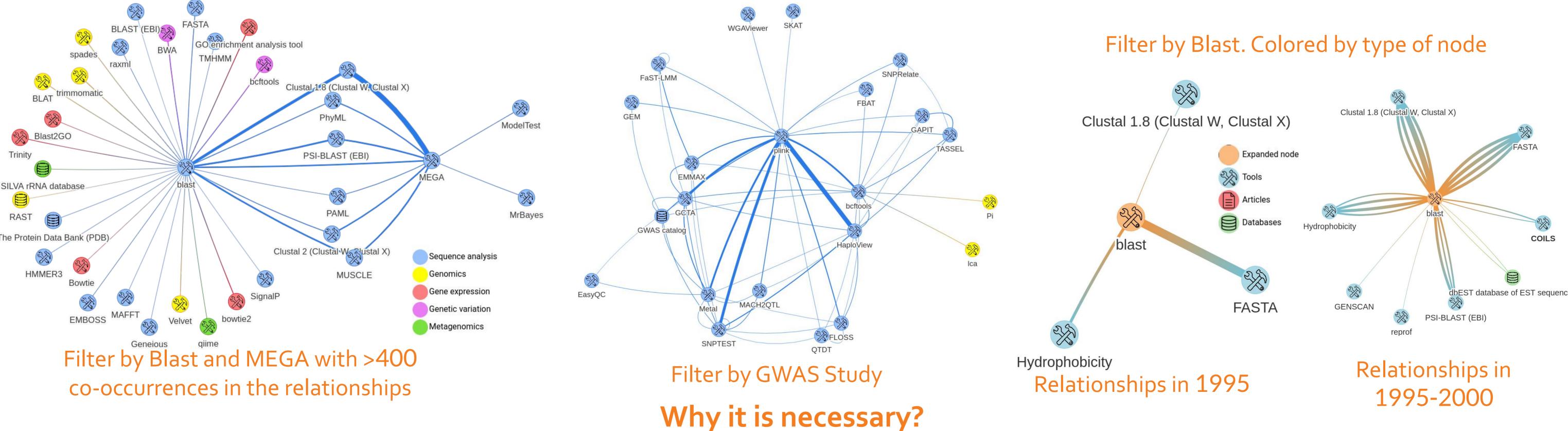
Input data is filtered by the minimum number of co-occurrences (in this case > 10co-occurrences) to remove unrelated or random relationships between the data. Data is stored in a Neo4j property graph database, and clustered with the Louvain approach.

Interestingly, clusters show a high correlation with EDAM Topic (Ex: 71% of Proteomics software is in the same cluster).

Filter by software, see common relationships and the main topic of their cluster.

# User Interaction

Filter per year to see the evolution of the usage of other software in relation to the selected tool Filter for whole bioinformatics' domain



Results can be used by research communities organizing scientific benchmarks on popular pipelines in their domains. Include widely used databases, popular articles and other relevant resources as part of those workflows.

## Contact

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