

Data Mining tools for Biomedical Discovery: a framework application in a Biotech Pharma Industry.

A case report of a working group

Gualtieri F., Colace F., Garofalo P., Rovati LC.
Rottapharm Biotech, Monza (Italy)





Data Mining – Introduction and Aims

In the era of *big data*, Text Mining (TM) represents an essential tool to automate the process of the information retrieval, extraction, interpretation and analysis.

This study provides a practical example of using the TM tool in drug discovery and hypothesis generation.

We compared **Knime** and **R**, two web based open source and free tools, as useful methods in improving the workflow of information search in the Rheumatology field.

We performed the following search query:

Osteoarthritis, Knee [MeSH] AND Humans [MeSH] AND Pain
in both systems, to search for new valuable target(s) in Knee OA.



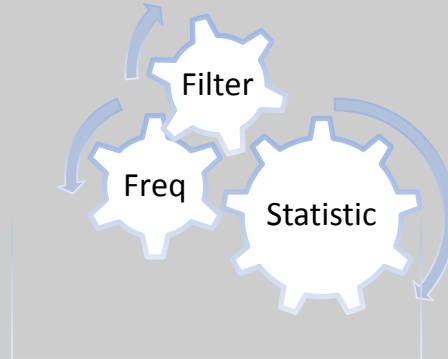
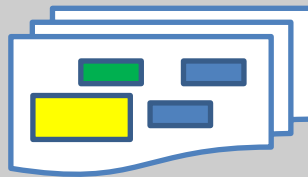
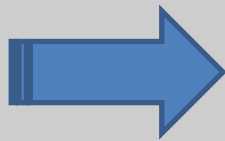
General Text Mining Plan and Workflow



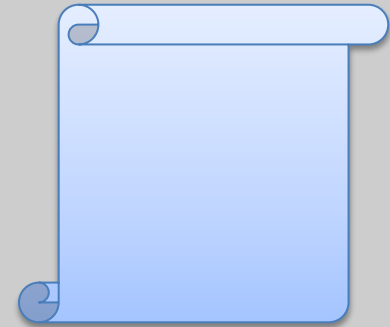
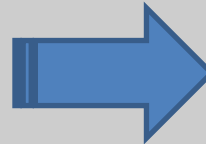
- Prepare and verify the search query
- Launch the query (PubMed)
- Create a **DB** and retrieve documents or import documents from a repository



- Organize documents
- Filter and preprocess to keep only important results for analysis

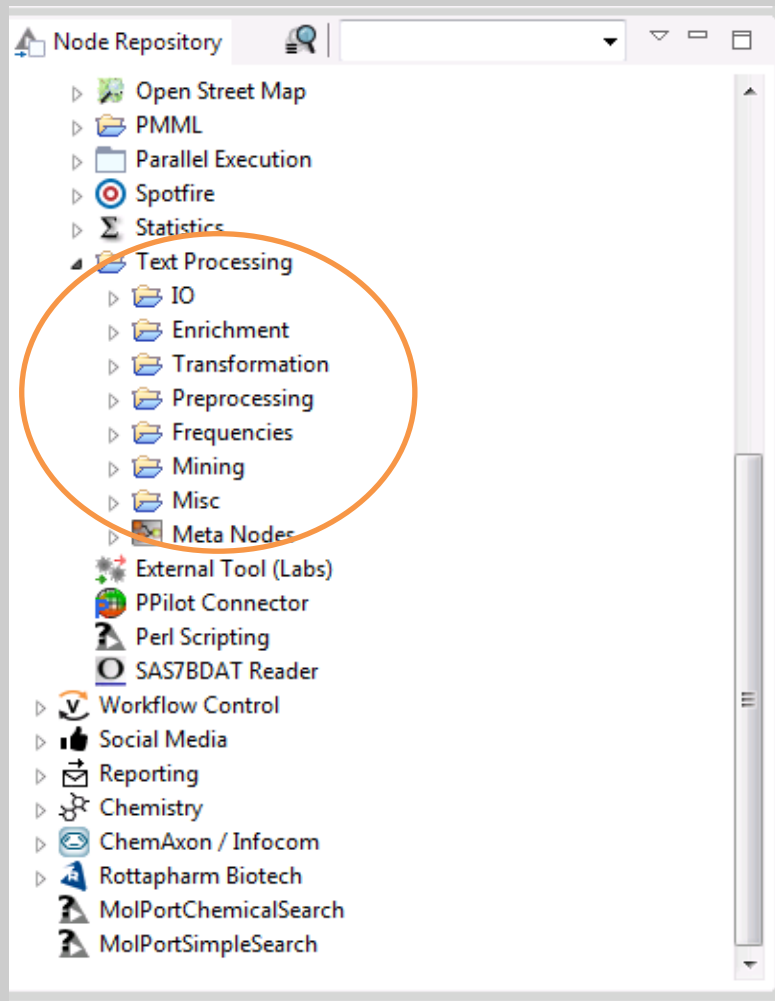


- Tag terms (Abner), filter, analyze for occurrence and classify documents or extract relevant terms



- Report and Visualization
- Knowledge Discovery (*Known or hypothesis*)

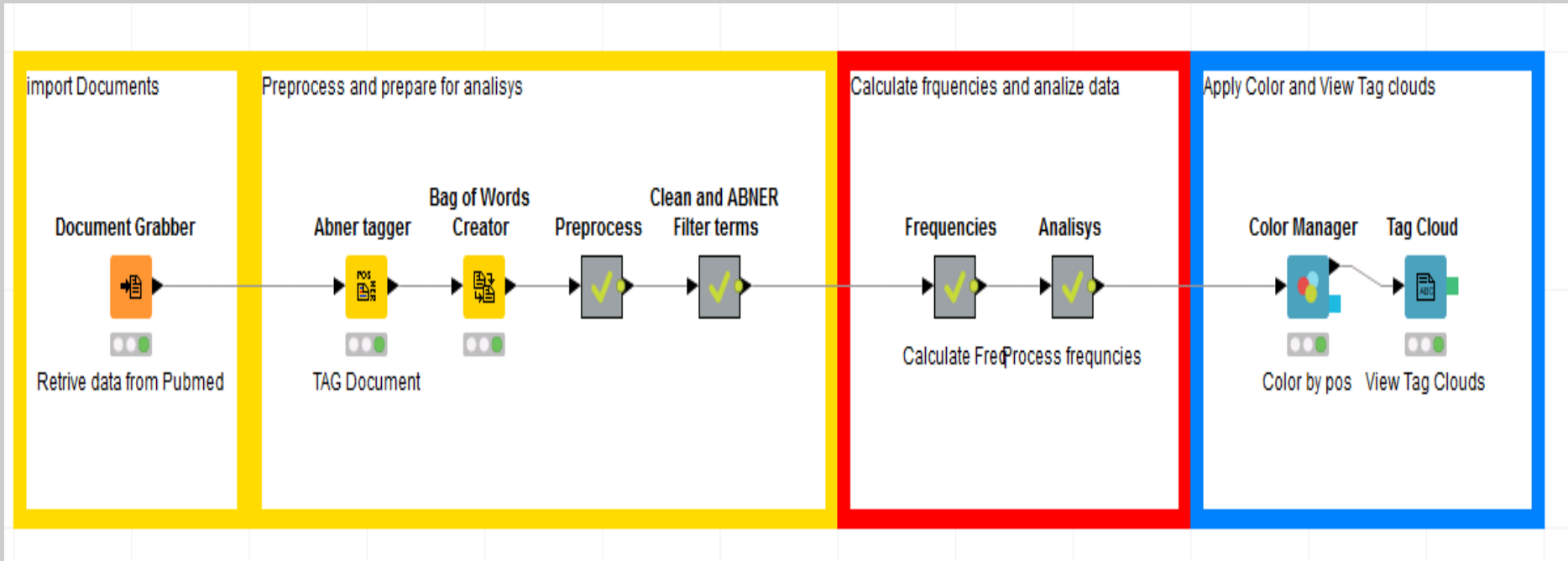
Knime plugin



- **IO** = Several Nodes are available for Query/Read documents
- **Enrichment** = assign Tags
- **Preprocess** = clean the «bag of words»
- **Frequencies** = Statistic analysis of frequency or co-occurrence of Terms
- **Mining** = extract important terms to report



Case 1: Knime Abner tagger node



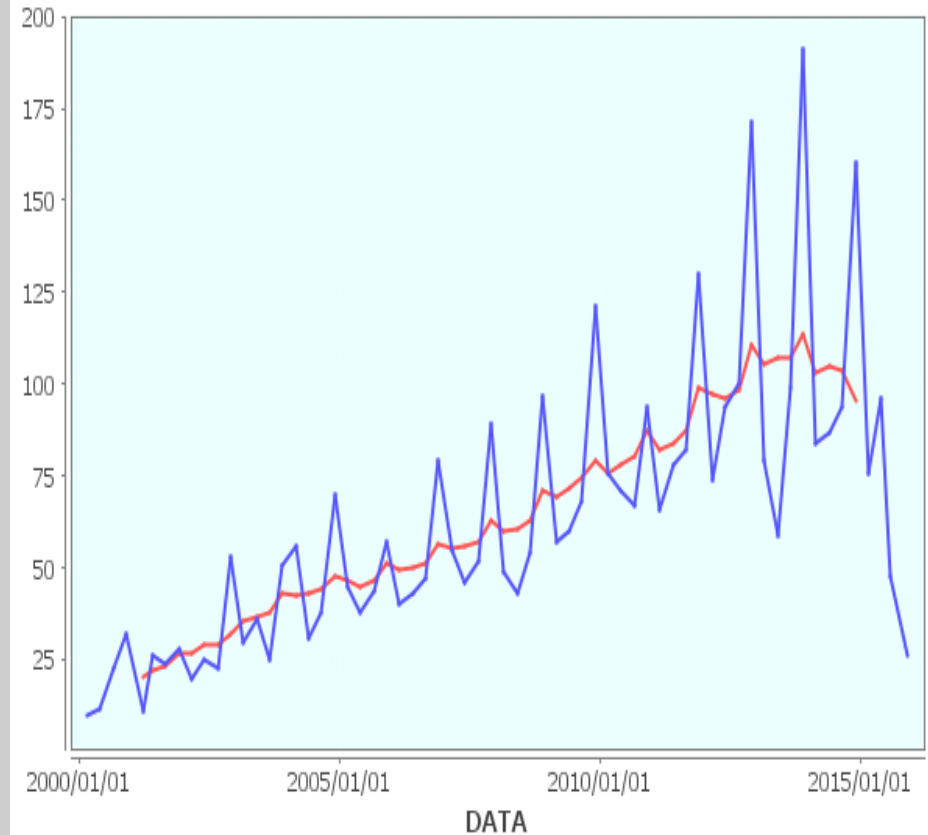
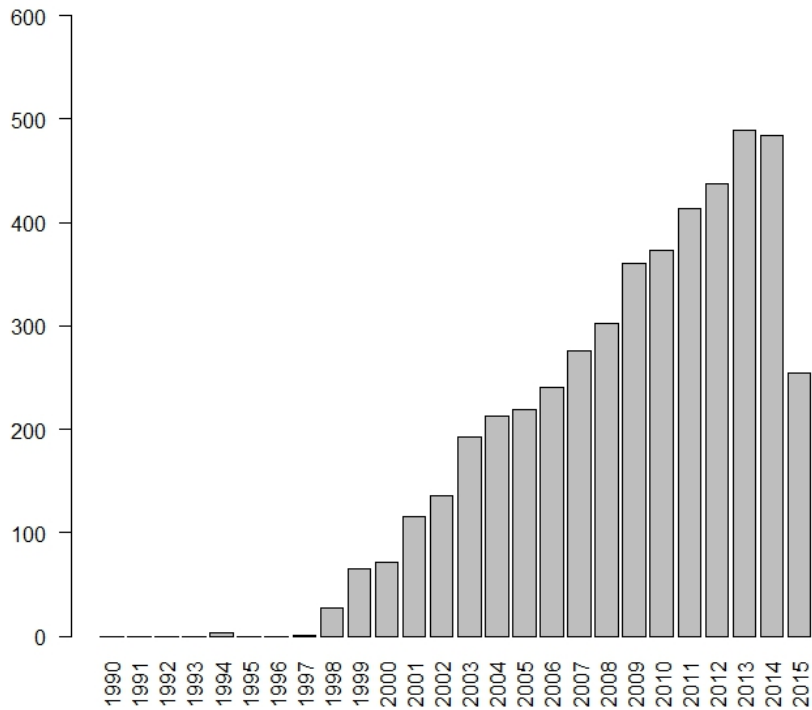


Case 2(a): temporal tendency in query

R:

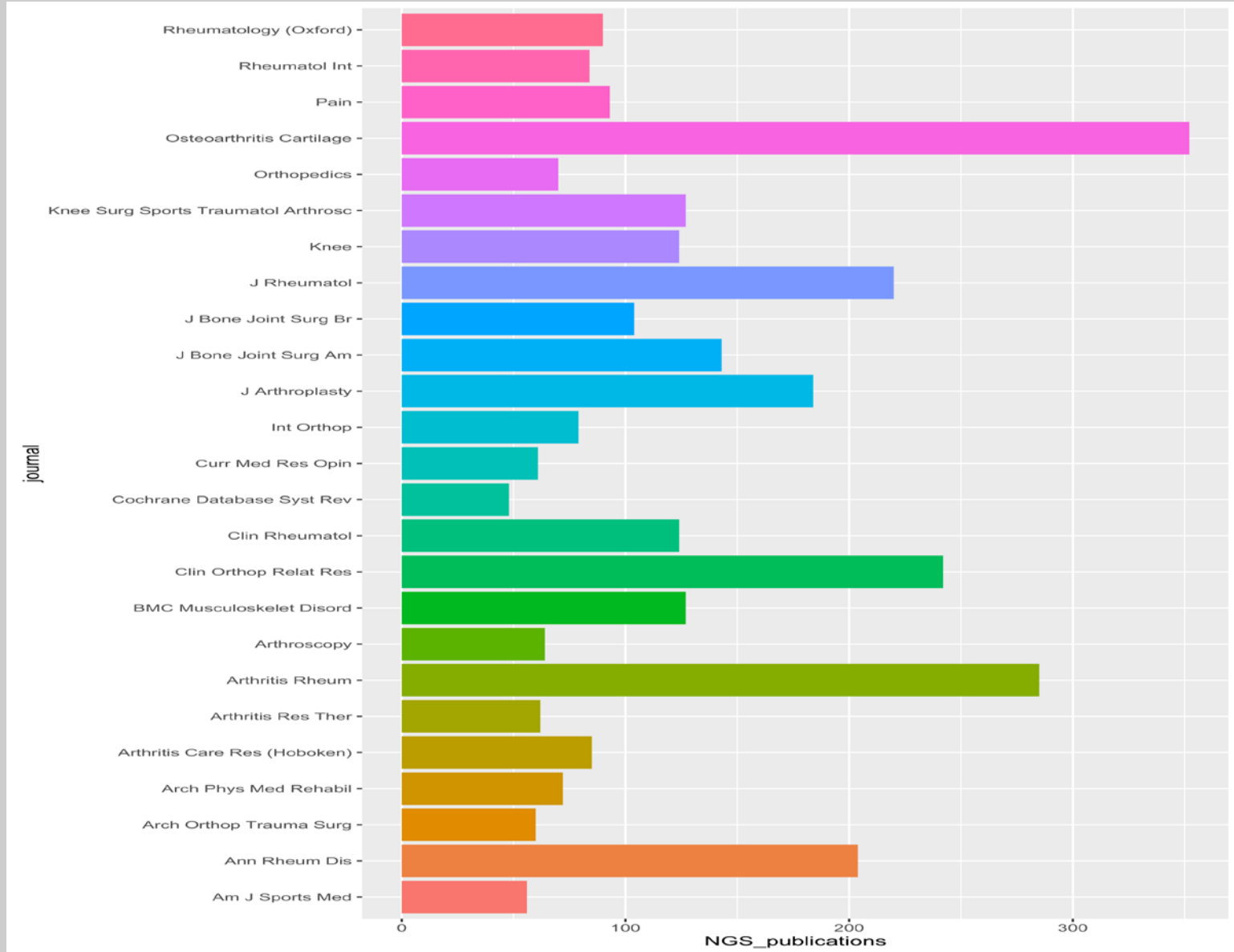
Knime

Number of PubMed articles containing Osteoarthritis, Knee and pain



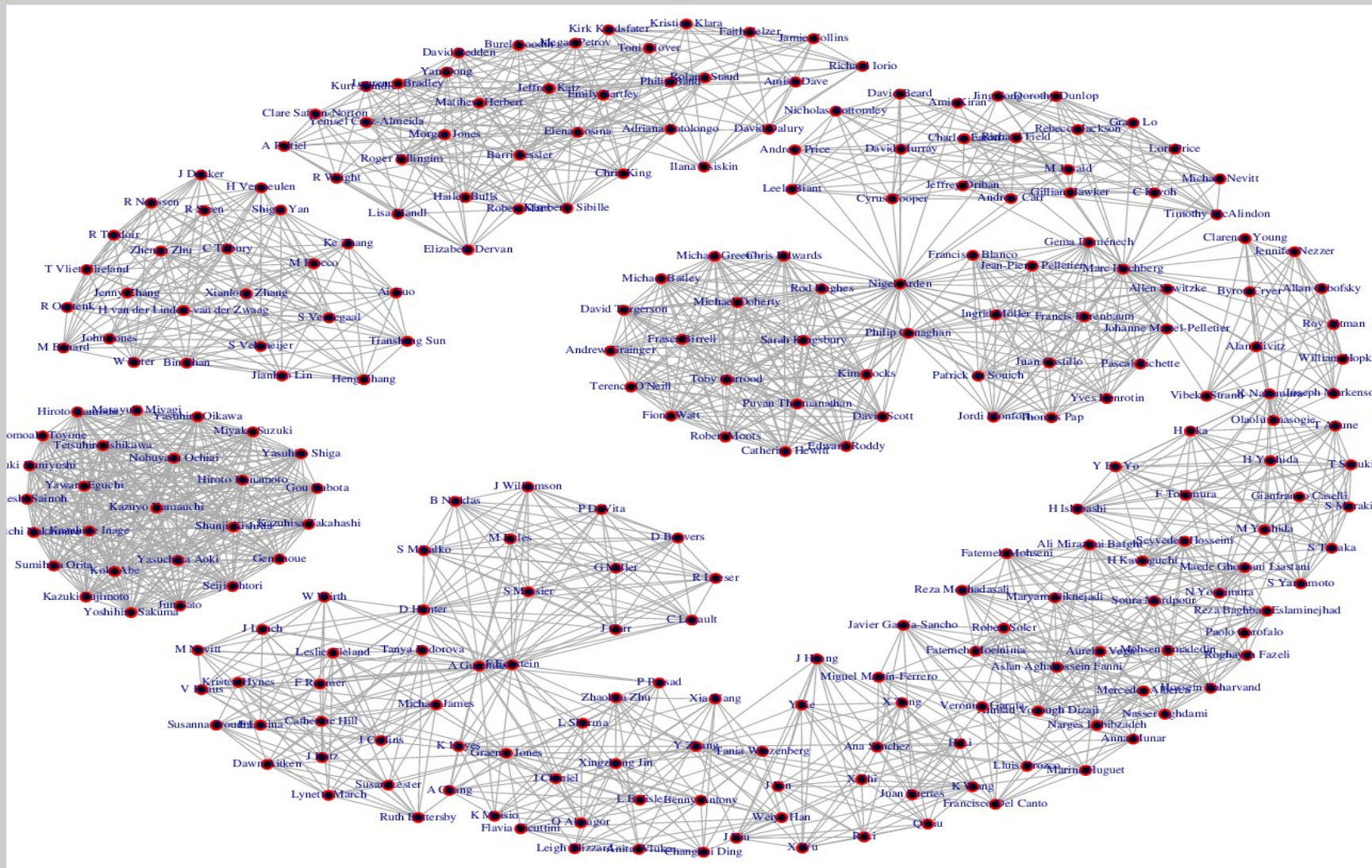


Case 2(a1): R - number of publications per journal





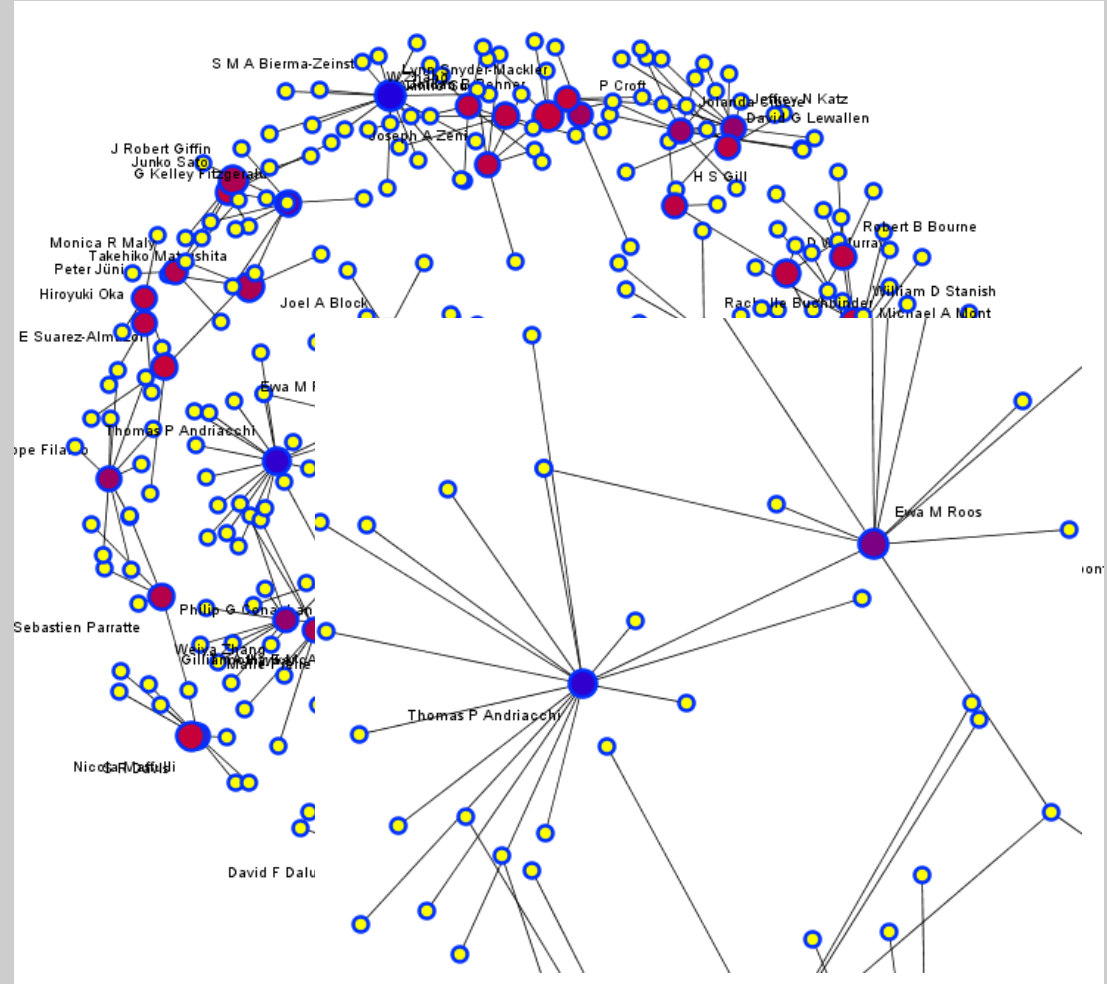
Case 2(b): R - Author network







Case 2(b): Author network

Authors' network related to No. of papers on Knee OA



Legend Color

 High n° publications

 Medium n° publications



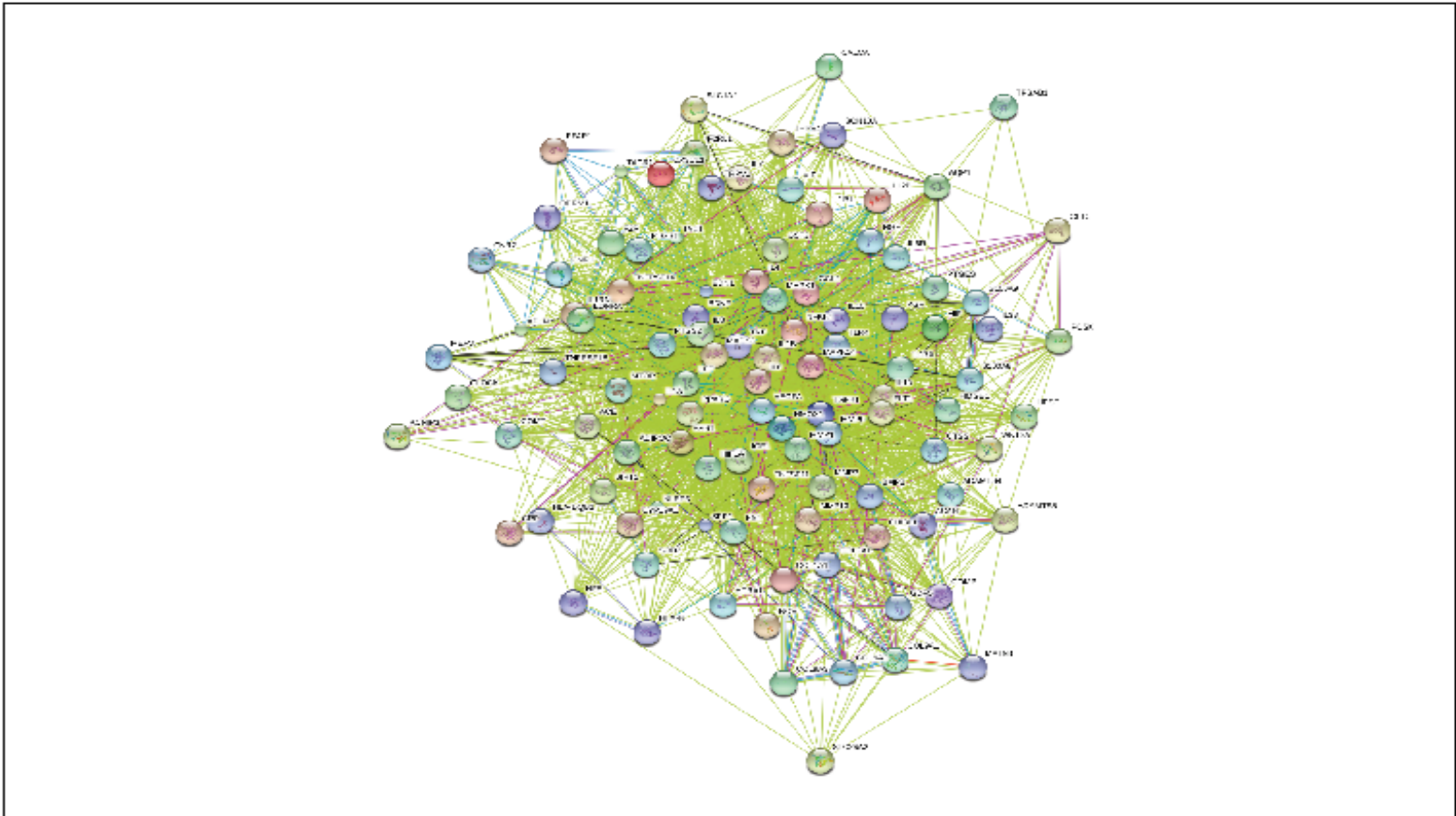
Case 4: target discovery PP-interaction network

- Workflow can extract Protein-gene and Protein-Protein Interaction from literature.
- based on a custom dictionary of terms of interaction.
 - It is important to find out and extract the right Interactions
- The most «interesting» protein lists are sent to iHOP to investigate and compare the results



Case 4: target discovery PP-Interaction network by R

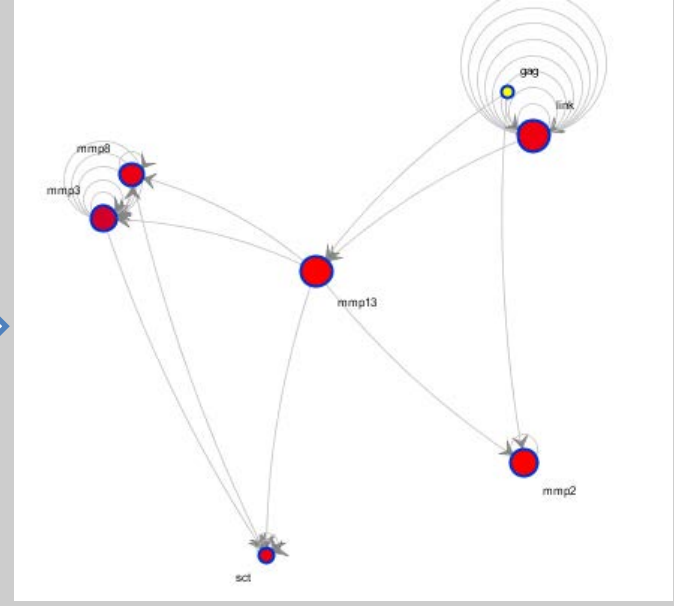
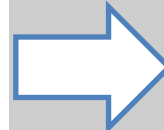
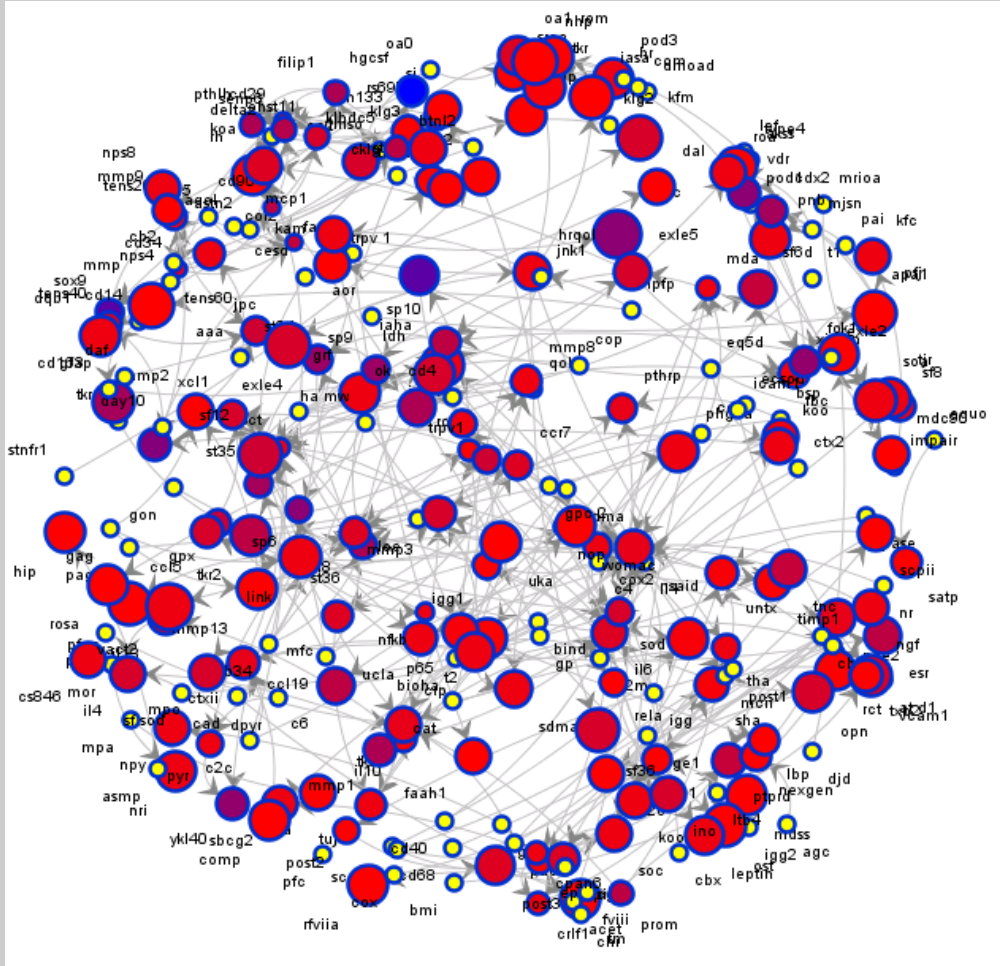
proteins: 200
Interactions: 2492
expected Interactions: 1021 (p-value: 0)



<http://string-db.org/10/p/8344194184>



Case 4: target discovery PP-Interaction network (knime)





Conclusions

- TM brings knowledge from literature to identify known and new relationship between genes, pathways, drugs and diseases.
- TM is integration of different sources even in human ware
- A collaborative team with Biologists, Chemists, Statisticians, Librarians and Computer Technicians will be a new challenge in drug discovery.
- Biomedical Librarians can play a critical role in TM process, providing researchers access to taxonomy and vocabulary use or creation, and sharing content platform.



Rottapharm Biotech TM Team

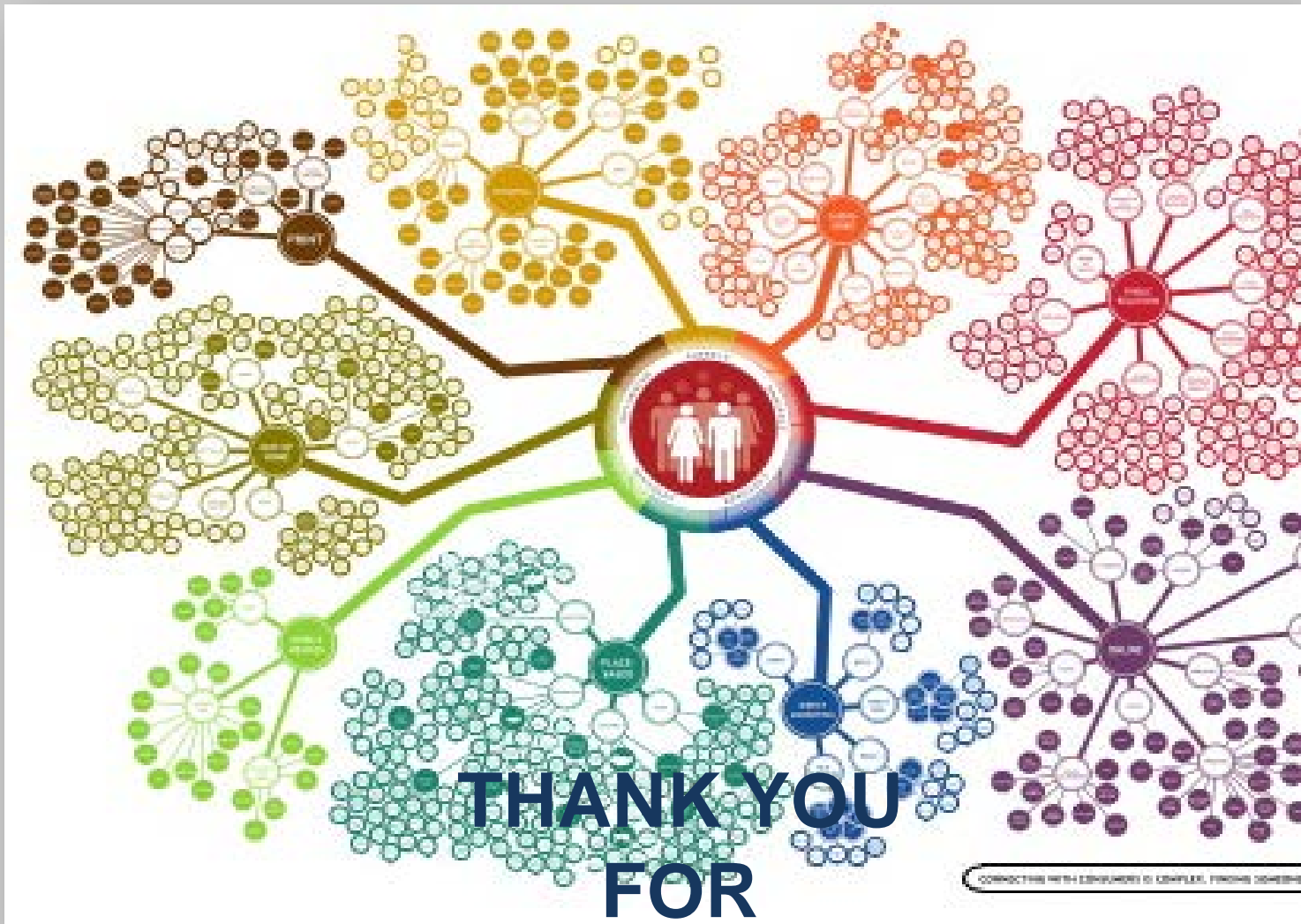
Paolo Garofalo, Biologist

Fabrizio Colace, Medicinal Chemist

Francesca Gualtieri, Biomedical Librarian

Lucio Rovati, Medical Doctor

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**THANK YOU
FOR
YOUR ATTENTION**

info @: francesca.gualtieri@rottapharmbiotech.com