Mapping scientific communities at scale

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January 2025

Keywords: open access, open science, open data, open source

1. Motivation

Analysing and mapping scientific communities provides an insight into the structure and evolution of academic disciplines. This involves providing an analytical and visual representation of the relationships between entities (e.g. researchers, research laboratories, research themes), with the aim, in particular, of understanding the networks and dynamics of scientific collaboration, and identifying collaborative groups and their influences. From the point of view of decision-makers, this type of tool is useful for strategic decision-making with a view to public policy and funding.

These maps are generally deduced from data in bibliographic databases (open or proprietary), based on co-publication or citation information. In the case of co-publications, two entities (authors, for example) will be linked if they have collaborated (co-published) on a piece of research. These links are then symmetrical. In the case of citation links, two authors will be linked if one cites the research work of another, in the list of references. This is a directed link, as one author may cite another without this being reciprocal. A lot of recent work uses this second approach, for example by trying to calculate composite indicators of novelty (or innovation) based on citation links.

The quality and completeness of the bibliographic metadata used are, of course, essential if we are to produce a relevant map. Today, the quality of open citation data still needs to be improved, cf (Alperin et al. 2024). On the other hand, it is possible to obtain quality metadata on publications (and therefore links to co-publications). For example, the French Open Science Monitor (BSO) has compiled a corpus of French publications with good coverage cf (Chaignon and Egret 2022). This corpus is exposed in the French research portal scanR (Jeangirard 2024). This is a corpus containing about 4 millions publications in all disciplines. These publications have been enriched with disambuation persistent identifier (PID) on authors, affiliations and topics. For authors and affiliations, French-specific PID have been used (idref for authors and RNSR for laboratories) because they have the best coverage, even if not perfect. For topics, wikidata identifiers has been used cf (Foppiano and Romary 2020). Other enrichments, like software detection are also present, and thus usable as entities to map.

1.1 Previous limits of the scanR application

Launched in 2016, the scanR portal used to be a search engine. Its scope first focused on research entities (institutions, laboratories and private companies) and was extended in 2020 to cover fundings, publications, patents and authors. Two main use cases were covered. Firstly, the ability to generate a list of search results corresponding to a user query. A list of laboratories, authors, funding or publications could be generated. Secondly, for each institution (or laboratory), a unified view of all the

data concerning it was grouped together on a dedicated page in scanR (administrative information, list of publications, list of funding, main partners, etc.).

However, these functions only gave a flat view of the different dimensions, without providing any insights into the interactions between laboratories or authors. For a user interested in a research theme, for example, the list of the main contributors (those who have co-authored the most publications) does not give a clear idea of which research communities are at work and how they interact with each other. A network analysis tool to describe these interactions and attempt to detect research communities could therefore enable us to go further in creating tools to help explore fields of research and innovation.

1.2 Network analysis limits

Network analysis tools for bibliographic studies are used to study the relationships between entities in a corpus. In general, the size of this corpus is limited because the calculations to determine the nodes, links and their positions for very large networks require too many resources, in addition to being very difficult to interpret. As a result, tools such as VOSViewer offer options for limiting the size of networks. The first option is to filter publications with too many authors. This is particularly true of publications in particle physics, which can list several thousand authors. As well as generating very large networks, this hyperauthorship can also be seen as reducing the relevance of the information conveyed by the co-authorship links. The second option offered by VOSViewer is to set thresholds to limit the number of nodes directly (minimum number of publications or minimum number of citations for a node). However, this approach of retaining only the largest nodes in the network can be an obstacle to scaling up to very large corpora of several million documents. Indeed, if we wish to concentrate on a few hundred nodes, the threshold will be very high and the resulting network risks being just a constellation of single nodes with no links between them, the other nodes with which they are linked being in fact made insignificant by the threshold set in terms of the number of publications (or citations) per node. In addition, the processing time for a very large corpus of publications can be very long, making such a tool unusable in a web application where the user expects rapid interaction with the application.

2. Network analysis at scale

We propose a method for overcoming the limitations set out above. We also use a filtering technique to reduce the size of the network, but with a dual approach: instead of filtering the nodes, we filter the links.

2.1 Focusing on strongest interactions

One of the added values of mapping with a network view is to show the interactions between entities, i.e. the links between the nodes in the graph. These links provide crucial information that can be used to structure communities. If the size of the network needs to be reduced (for reasons of computation, speed, legibility and interpretability), it is vital to preserve the links that carry the most information, i.e. the strongest interactions. With this reasoning, it seems logical to reduce the size of the network by only affecting the strongest links.

Thus, from a given corpus, however large, we seek to extract the pairs of entities with the strongest interactions, for example the most co-signatures per pair of authors. From this list of pairs, we can naturally find the nodes of the graph and deduce a new graph. If the graph has several independent components, i.e. several unconnected sub-graphs, we can decide to keep only the main component(s).

2.2 Elasticsearch implementation

To identify the strongest links, it would be too costly to go through the entire corpus. We have pre-calculated the links at the level of each publication. So, if a publication is linked to 3 themes, T1,

T2 and T3, a pre-calculated field, at publication level, contains all T1-T2, T1-T3 and T2-T3 pairs. This co_topics field represents the co-appearance links within the publication. We then use elasticsearch's aggregation functionality to list the most present links, very efficiently.

In practice, a PID is also stored (the wikidata for topics, for example) to disambiguate entities. In practice, for a given query, elasticsearch returns a response containing the strongest links, for example:

```
{
    "key": "Q15305550###carbon sequestration---Q7942###climate change",
    "doc_count": 17,
},
{
    "key": "Q15305550###carbon sequestration---Q623###carbon",
    "doc_count": 14,
},
{
    "key": "Q15305550###Carbon sequestration---Q7942###Climate change",
    "doc_count": 13,
},
{
    "key": "Q15305550###Carbon sequestration---Q898653###Climate change mitigation",
    "doc_count": 10,
},
{
    "key": "Q397350###agroforestry---Q8486###coffee",
    "doc_count": 10,
},
{
    "key": "Q15305550###Carbon sequestration---Q1997###CO2",
    "doc_count": 9,
},
{
    "key": "Q623###carbon---Q627###nitrogen",
    "doc_count": 9,
},
{
    "key": "Q15305550###Carbon sequestration---Q623###carbon",
    "doc_count": 7,
},
```

2.3 Network creation

The network creation process involves several key steps: transforming Elasticsearch results into a graph using Graphology, filtering the network to focus on the most interesting nodes, applying spatialization algorithms for visualization, and detecting communities within the network. Below, we detail each of these steps.

The network creation process begins with the results obtained from Elasticsearch, utilizing the open-source JavaScript library Graphology https://github.com/graphology/graphology to construct and manipulate the network. Each link result from Elasticsearch is transformed into nodes and edges, with the edge strength corresponding to the interaction intensity derived from the Elasticsearch aggregations.

To ensure that the network remains manageable and focuses on the most interesting nodes, we employ a strategy that prioritizes the best-connected nodes rather than the largest nodes. By default, the

maximum number of nodes is set to 300. This threshold helps in maintaining the computational efficiency and interpretability of the network.

In graph theory, a component refers to a subgraph in which any two nodes are connected to each other by paths, and which is connected to no additional nodes in the larger graph. Using Graphology, we filter the network components by iteratively removing the smallest components until the number of nodes falls below the threshold or only one component remains. This largest component is then subjected to further filtering if it still exceeds the node threshold. In this second filtering step, we utilize the betweenness centrality metric to retain the best-connected nodes. Betweenness centrality measures the extent to which a node lies on the shortest path between other nodes, thereby identifying nodes that act as bridges within the network.

Once the filtering process is complete, we apply a spatialization algorithm to position the nodes in a 2D space. For this purpose, we use the ForceAtlas2 algorithm, which is designed to produce aesthetically pleasing and informative layouts by simulating a physical system where nodes repel each other and edges act as springs pulling connected nodes together. This results in a clear and intuitive visual representation of the network (Jacomy 2014).
Thanks to Graphology the settings of the ForceAtlas2 algorithm are automatically infered from our network order (number of nodes) as below:

```
barnesHutOptimize: order > 2000,
strongGravityMode: true,
gravity: 0.05,
scalingRatio: 10,
slowDown: 1 + Math.log(order)
```

In graph theory, a community corresponds to a set of nodes in a graph that are strongly interconnected with each other, while being less connected with nodes outside this community. Communities can be identified in order to understand the underlying structure and patterns of the graph, as well as to analyze the relationships and interactions between the entities that make it up. To identify and visualize communities within the network, we apply the Louvain algorithm using Graphology. This algorithm works by optimizing a modularity measure that evaluates the strength of communities in a graph (Blondel et al. 2008). More precisely, Louvain seeks to maximize modularity by progressively moving the nodes of a graph into different communities, in an iterative fashion. At each stage, he merges neighboring communities if this leads to an improvement in the overall modularity of the graph. This iterative process continues until no further moves can increase modularity.
This step helps in revealing the underlying structure and communities within the scientific network, providing valuable insights into the interactions and collaborations within the bibliometric data.

2.4 VOSviewer implementation

To display the network within our application, we use the open source VOSviewer online tool for network visualization https://github.com/neesjanvaneck/VOSviewer-Online. It is based on the VOSviewer software which is very popular for network analysis in bibliometric studies (Waltman, Eck, and Noyons 2010).

VOSviewer accepts JSON files formatted according to a specific template https://app.vosviewer.com/docs/file-types/json-file-type. This template includes essential attributes for nodes and edges, such as the node ID, name, position, and additional metadata. To ensure compatibility, we transform our Graphology object into a JSON file that adheres to VOSviewer's required format.

Once the JSON file is generated, VOSviewer renders the network, displaying nodes and edges in an interactive and visually appealing manner. The nodes are colorized based on the communities identified through the clustering process performed using the Louvain algorithm. This colorization helps in

visually distinguishing different communities within the network, making it easier to analyze and interpret the underlying structure and interactions.

VOSviewer includes its own spatialization algorithm and parameters for layout customization. However, after testing these options, we found them to be visually less intuitive and informative. Consequently, we chose to use the ForceAtlas2 algorithm for spatialization, as described in the previous section, which offers a more aesthetically pleasing and informative layout by being automatically set for our network.
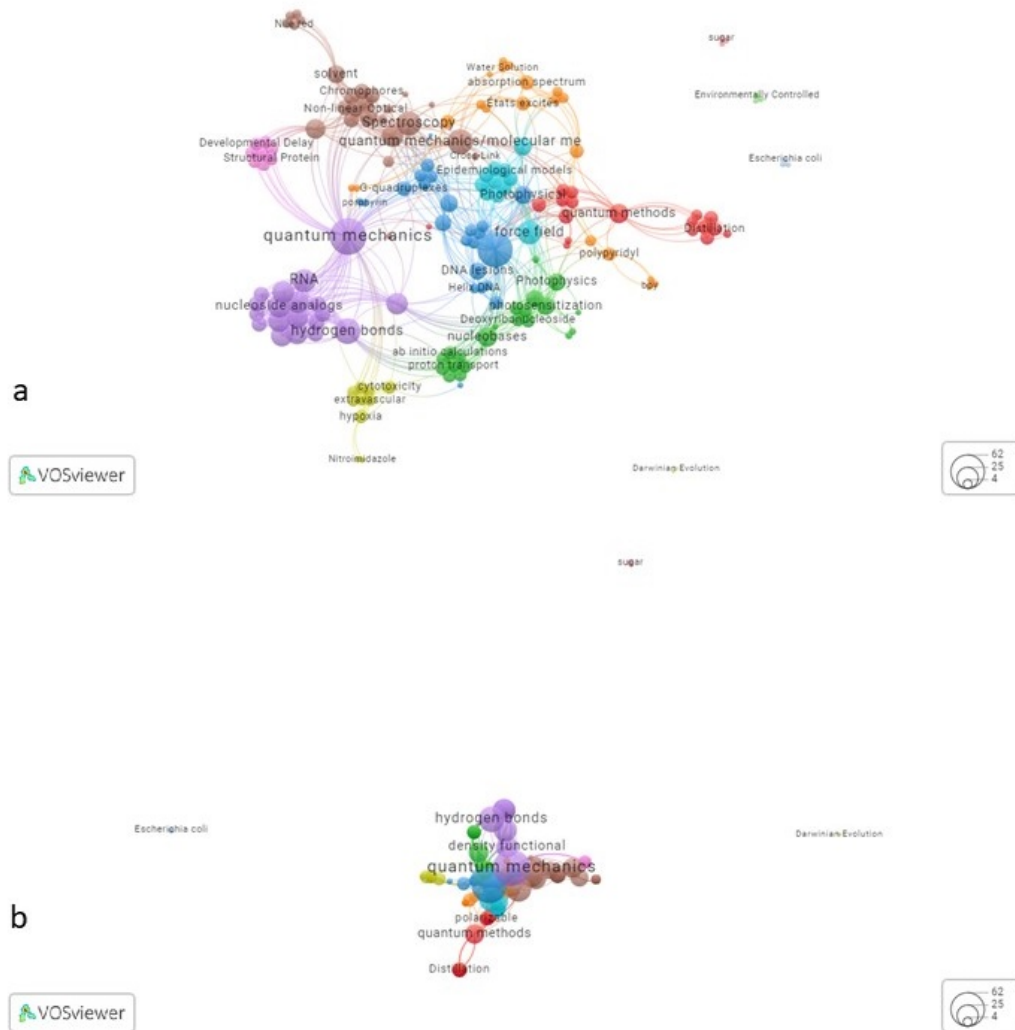

Figure 1: Visualization of a network with VOSviewer.
(a) Using ForceAltlas2 spatialization
(b) Using VOSviewer default spatialization

3. Making insightful maps

This scanR feature is designed to help users gain a better understanding of the underlying structures via thematic or co-publication maps. To help the user, it's important to be able to characterize each of the communities automatically identified. It is therefore important to label each community before

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describing them.

3.1 LLM trick

To name the communities we use generative AI from Mistral AI ('open-mistral-nemo' model). The names are obtained from the main themes of the publications collected for each community. For the time being, we limit ourselves to the 2000 most relevant publications (in relation to the user's search) for each community. The following prompt is used:

> You have been tasked with naming distinct fields of study for several communities of research publications. Below are lists of topics and their weights representing each community. Your goal is to provide a unique and descriptive name for each field of study that best encapsulates the essence of the topics within that community. Each should be unique and as short as possible. If the list of topic is empty, output a empty string. Output as JSON object with the list number and the single unique generated name. "'

3.1 Citation / hot topics

A citation score is estimated for each cluster. This score relates the number of recent citations (over the last two years) to the number of total publications in the cluster. This score is intended to help detect hotspots in the communities identified in the corpus. We use citations data from OpenAlex, which is as of today one of the best open source datasource. However, citations metadata from OpenAlex remains incomplete and must therefore be interpreted with caution (Alperin et al. 2024).

3.2 Custom perimeter

scanR offers this mapping tool for the entire indexed corpus, but it is also possible to adapt the tool to a restricted perimeter, at the user's discretion. For example, an institution or laboratory can define its own corpus (based on a list of publications) and a mapping tool dedicated to this perimeter is automatically created. Technically, elasticsearch queries are the same, with just an additional filter to query only the publications within the perimeter. The tool can be embedded in any website using an iframe. It's the same principle as the local barometer. This approach eliminates the need for automatic alignment of affiliations, which remains a highly complex task. Automation is possible to a certain extent (L'Hôte and Jeangirard 2021), but human curation remains necessary in the majority of cases (Jeangirard, Bracco, and L'Hôte 2024). In this way, users retain control over the definition of their perimeter, and can, if they wish, have several distinct perimeters.

4. Code availibility

The code developed for the scanR web application is open source and available online on GitHub https://github.com/dataesr/scanr-ui

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