

# Creating a bibliome



## Filling knowledge gaps in a metabolic model of cod liver

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Poster nr. 7

### Background:

Imagine that you are working on a model of a system, but it is not complete yet. You need to know what others have discovered in this field to fill the gaps. Then imagine somebody has gathered all relevant publications, so you just need to pick the ones you need. A bibliome is a complete collection of biological texts and publications within a topic or field<sup>1,2</sup>. That is what I am creating for the dCod 1.0 project.

### About the dCod 1.0 project:

- dCod 1.0: Decoding the systems toxicology of Atlantic cod project, is an interdisciplinary collaboration between environmental toxicologists, biologists, mathematicians and bioinformaticians.
- They are working on a metabolic model<sup>3</sup> of cod liver. The provisional model has some unknown or incomplete processes and signaling pathways. To be able to fill these gaps, knowledge about biochemical processes in teleost's is needed.
- Therefore, I am creating an archive with relevant publications. The resulting library will also be useful for other parts of the project and further research on cod and other fish species.

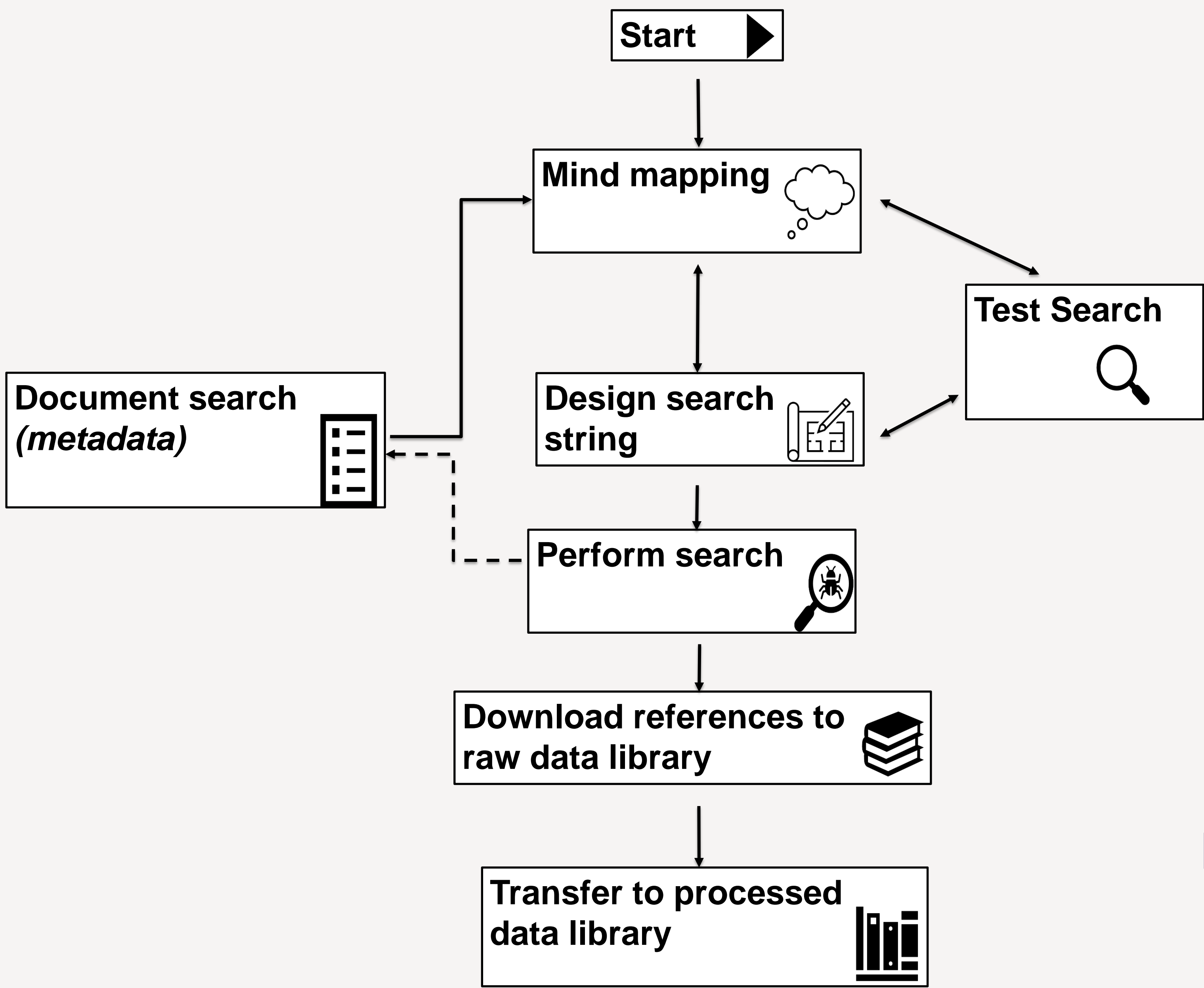


Figure 1: Flowchart overview of the work process.

### How to create a bibliome:

- Mind mapping:** used to map the relevant subjects, organize search terms and visualize hits.
- Structuring of searches:** important for making forms and structure which searches that have been done and organize how the searches stand in context to each other.
- Download relevant publications:** when the amount of hits are low (around 500) and the resulting publications relevant, the references are downloaded to a raw data library in Endnote. All references of one search is filed in their own folder, then it's possible to link each references back to the search.
- Sort and categorize Endnote library:** The hits from the raw data library are transferred to a library where the publication is checked for duplicates and categorized.

### Results:

- Two search strings were created.
- General search string:** This shows the number of hits by using different terms. This shall visualize/map how many publications there are in the different fields. Figure 2 shows this in form of a mind map.
  - Specific search string:** Those are specific designed searches with relevant fish taxonomy, see figure 3. These hits are downloaded and processed in Endnote.
  - An Endnote library with relevant publications**

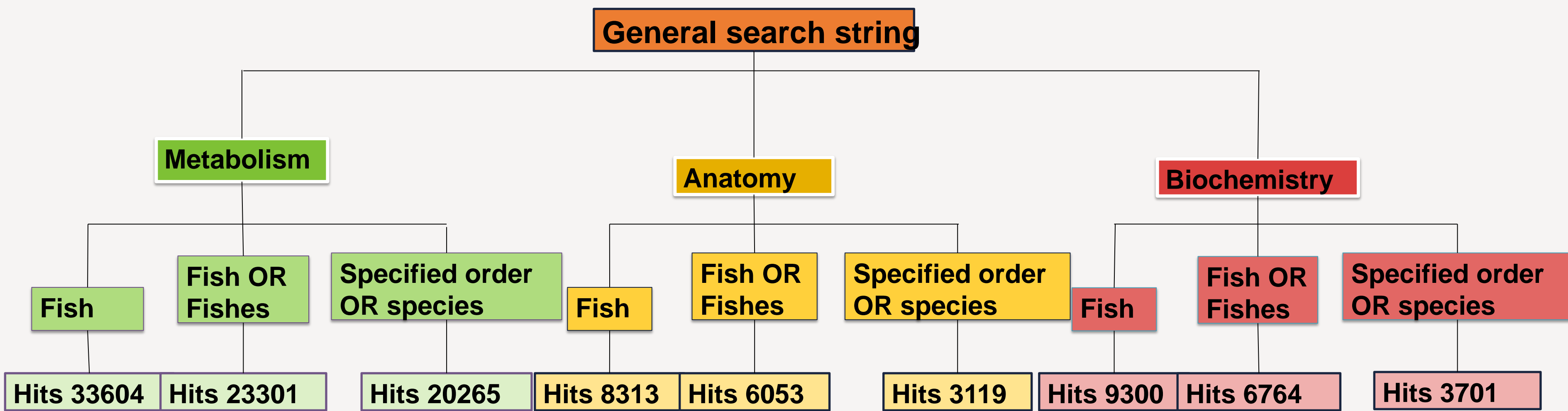


Figure 2: Part of the general search string. At the beginning of each branch stands the search term there was used. At next level, the term is combined with type of organisms there were used in the search: "Fish", "Fishes" OR "Fish" and lastly, the specified fish orders and species. The number at the end of the branch shows number of hits from each search.

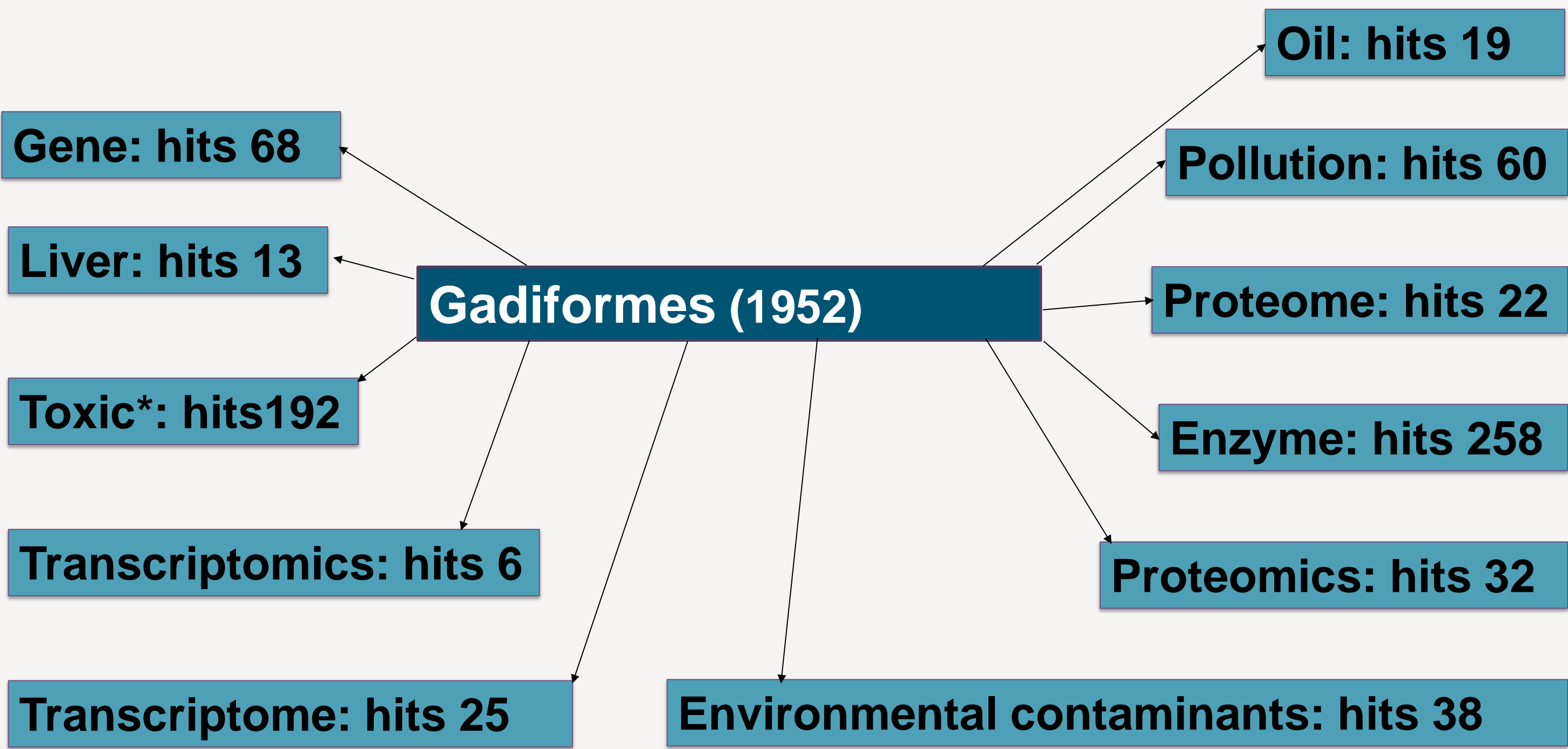


Figure 3: Visualization of number of hits from the different searches. The centre node show the fish order of interest, indicating the number of hits. The surrounding branches shows the amount of hits resulted from a search when "Gadiformes" was combined with the term in the branch.

### REFERENCES

<sup>1</sup> SEARLS, D. B. 2001. Mining the bibliome. *Pharmacogenomics J*, 1, 88-9.  
<sup>2</sup> ANDERSEN, M. R., *et al.*, 2008. Metabolic model integration of the bibliome, genome, metabolome and reactome of *Aspergillus niger*. *Mol Syst Biol*, 4, 178.  
<sup>3</sup> NORONHA *et al.*, 2018. "The Virtual Metabolic Human database: integrating human and gut microbiome metabolism with nutrition and disease", *Nucleic Acids Research*.

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SCAN ME

