

## BACKGROUND

The centralized Biomaterial Bank of RWTH (RWTH cBMB) is built on top of a solid IT infrastructure, consisting of a variety of software components for a wide range of applications.

Registration of the received medical samples, managing biobank workflow, performing patients data pseudonymization and depseudonymization are just a few examples of activities that require development of specific software tools. While offering interfaces for the different tasks and being physically separated due to privacy policies, these applications are expected to be integrated to share data in special cases.

## AIM

The cBMB datawarehouse is the current solution to search for samples within the RWTH cBMB with a wide array of criteria. It incorporates data from different data sources within the biobank and University Hospital Aachen. But it is only available to selected members of the IT staff due to the high complexity of the utilized tools.

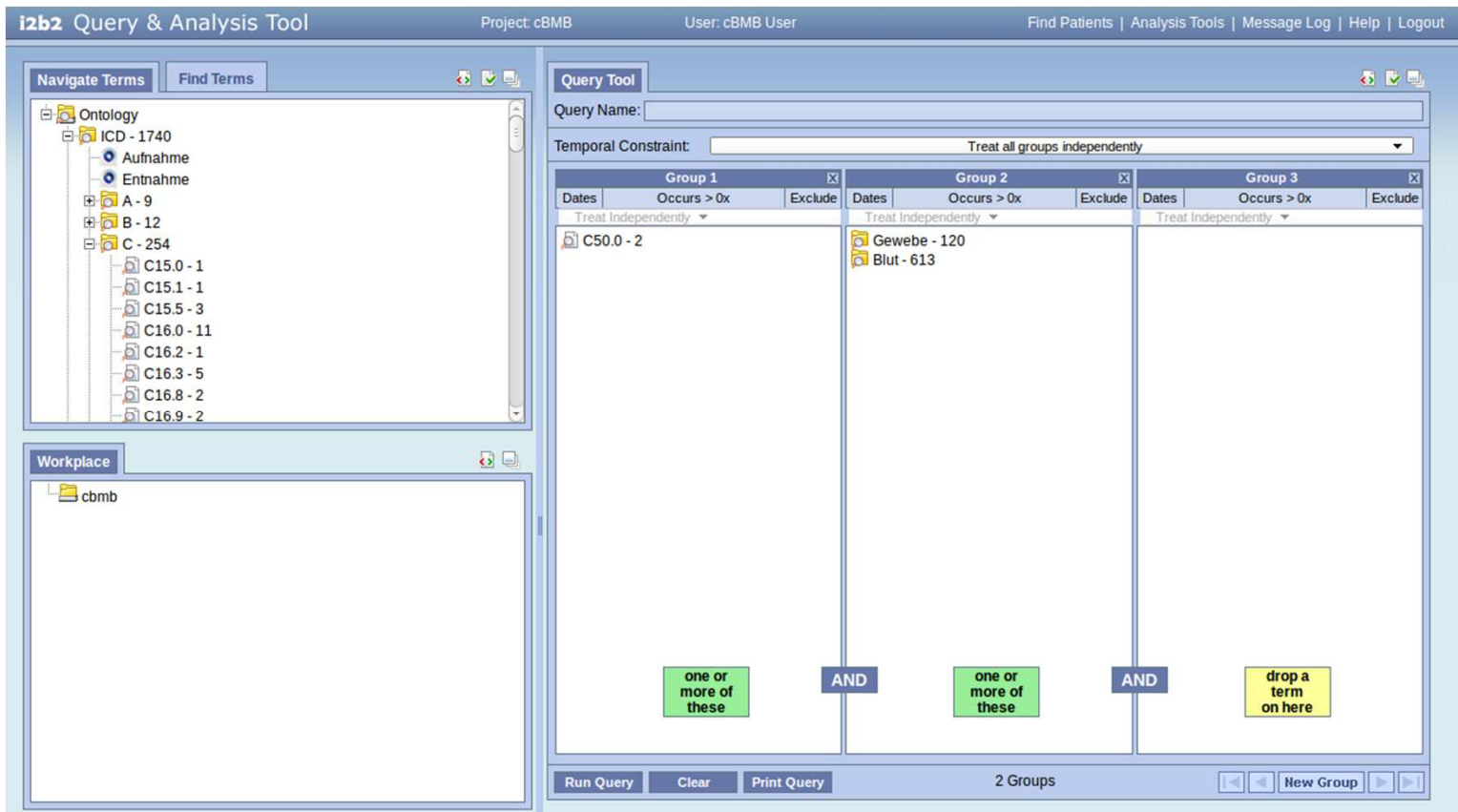
RWTH cBMB works towards making searching samples more simple, without sacrificing complexity of the query criteria. Our improved cBMB datawarehouse will offer a clean and comprehensible graphical user interface as well as a powerful search functionality to satisfy all biomaterial inquiries. This will also allow medical staff and internal clients to browse available samples with only little introduction.

## METHODS

From the point of view of a RWTH cBMB client, this tool should offer an interface for sample search by criteria like sample material and/or patient diagnosis. This tool has to provide both pseudonymized data like IDs for the later sample request, as well as access to sample metadata like diagnosis and material type. In this particular example three software systems are involved: the pseudonymization service for ID retrieval, the patient diagnosis database and the biobank organizational database for sample metadata. All these data sources have to be queried in an organized and secure way.

## RESULTS

I2b2R (Informatics for Integrating Biology and the Bedside at RWTH cBMB) is our search tool for biobank clients. I2b2R provides a software infrastructure that allows researchers to access medical data associated with samples. It constitutes a flexible database schema that can store and query almost any kind of data in an effective way by allowing user to build custom queries when search concepts are defined. It also provides knowledge organization in a clear way using an ontology tree, so search criteria selection can be made in an intuitive way. A tool prototype has been developed to populate the i2b2 database with the data collected from our systems: diagnoses are associated with the metadata from samples archivation software using sample identifiers provided by the identification tool.



**Fig. 1: Graphical user interface of I2b2R.** The “Navigate Terms” panel in the top left corner contains hierarchical organized search terms such as ICD-O codes, material types or patient metadata like age or diagnosis. These terms can be dragged over to one of the groups inside the “Query Tool” panel. Terms within groups are conjoined by a logical “OR” while entire groups are conjoined by a logical “AND”. Now the client just needs to click “Run Query” to get a list of suitable samples.

## CONCLUSIONS

Dynamically imported high-level concepts like diagnoses and material types all together form the knowledge base concepts for the i2b2 ontology and can be used as sample search query criteria. To satisfy the special needs of a biomaterial bank, a dedicated data view plugin is in development to support sample-oriented search results inspection.