Promoting use of biobanks through increased visibility of collections in biobank catalogues and directories

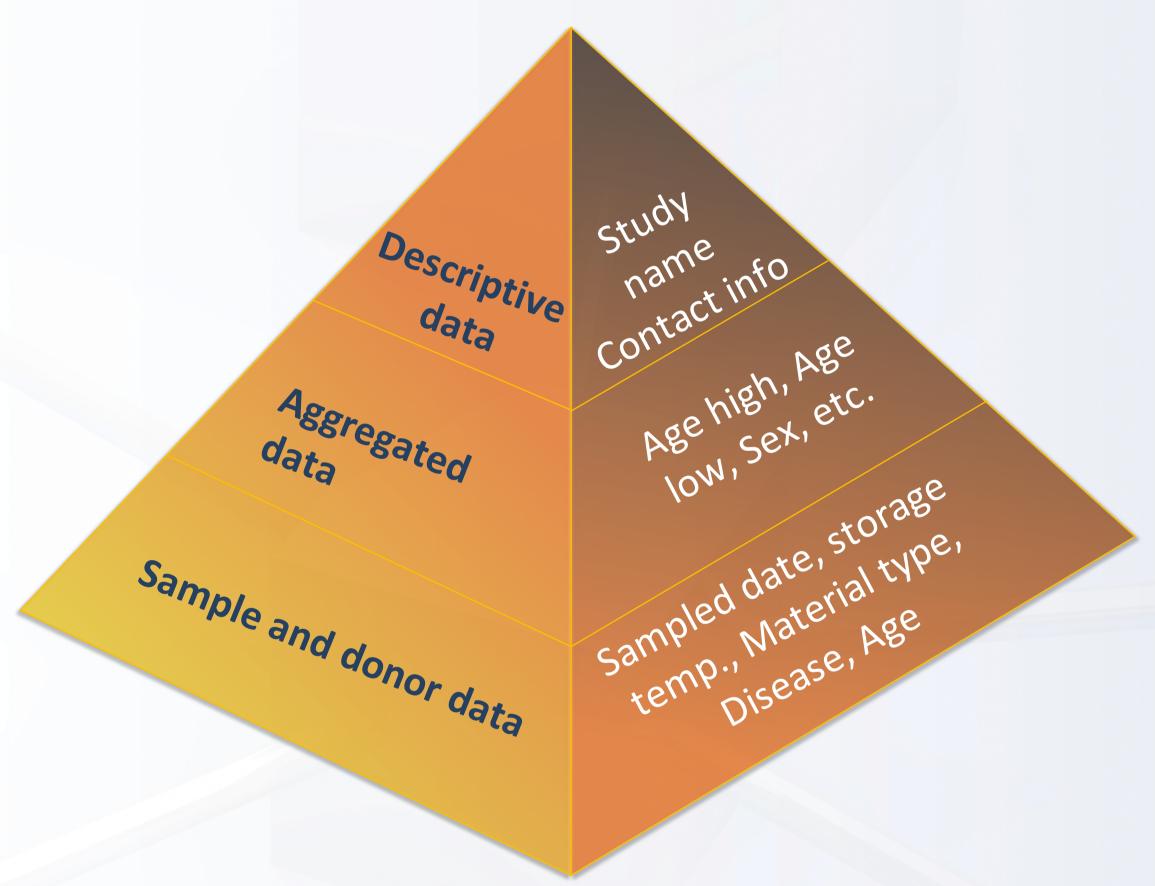
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Background

Biobanks are an important resource for biomedical research and contain large collections of biological samples and accompaning clinical data. So far biobanks have been underutilized because it is often difficult for researchers to find the collections that have relevant samples and data. To promote the discoverability and use of biobanks we have developed easy to access and query catalogues of the biobanks and their collections.



Material & Methods

Different levels of catalogues have been developed in the different biobank catalogue work packages or working groups ranging from only summaries per collection down to persample information. We used MIABIS as a common minimal information model to describe biobanks and collections in the different projects and we used MOLGENIS open source software to allow rapid development/configuration of new catalogue websites in a standardized and modular way (http://github.com/molgenis/molgenis).

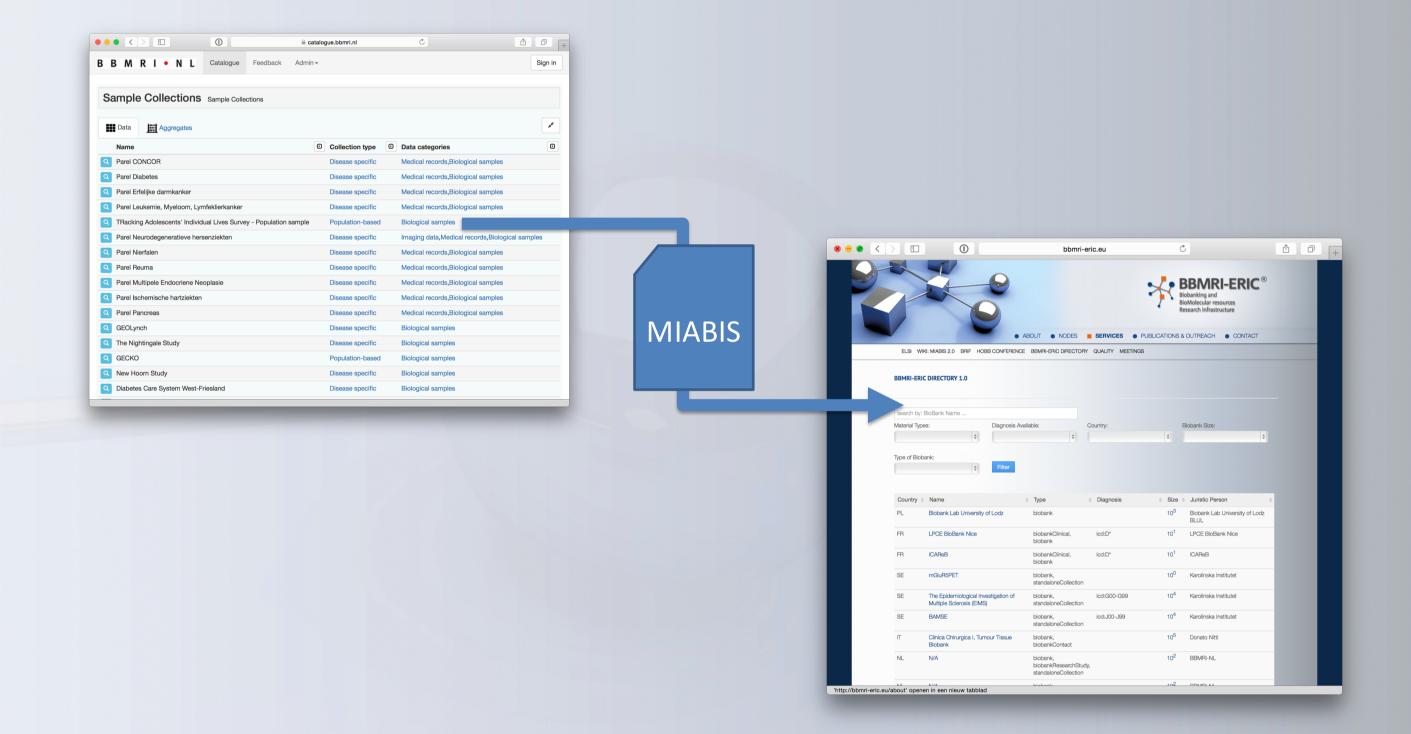
Level	Type of information
1	Sample/study collection meta-data
2	Data and sample elements
3	Availability and counts
4	Access to the individual level data

Find examples at

https://catalogue.bbmri.nl
http://www.palgaopenbaredatabank.nl/
https://catalogue.lifelines.nl
http://directory-molgenis.bbmri-eric.eu/

Results

Within the different projects we have identified the biobanks that are of interest to the project and published these in a biobank catalogue or directory, including BBMRI-NL, BBMRI-ERIC, CTMM TraIT biobank catalogue, RD-Connect sample catalogue, PALGA open database, LifeLines data catalogue. To enable data sharing, between the BBMRI-NL catalogue and the BBMRI-ERIC directory we established a data exchange so the biobanks can be found at both the national and the ERIC level with just a single data entry. In the BBMRI-NL catalogue almost 200 biobanks are listed, while the BBMRI-ERIC directory lists over 500 biobanks.



Discussion

Further development of the software should address open issues to improve accessiblity of the biobanks, and further integrate their data. Semantic search could enable relating collections that have similar data, but use different code systems (e.g. SNOMED-CT vs. ICD-10). A federative querying model will allow more in-depth searches of the biobank data, while leaving the biobank in control of potentially sensative data.

