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MEETING ABSTRACT

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MOLGENIS catalogue

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Characterisation
Tool, biobanking, meta-data, data, miabis, open source.

Description
MOLGENIS/catalogue is a generic toolbox for building biobank and study catalogues and is used in BBMRI-NL, EU-BioSHaRE, EU-BioMedBridges, LifeLines, CTMM/ TraIT, Durrer Center, PALGA NL pathology network. The catalogue can host four levels of information:

1) Biobank/study descriptions using custom or MIA-BIS standard of BBMRI-ERIC format;
2) Data schema/data dictionary of data elements;
3) Aggregate data/sample availability counts and;
4) Individual level data ready for analysis.
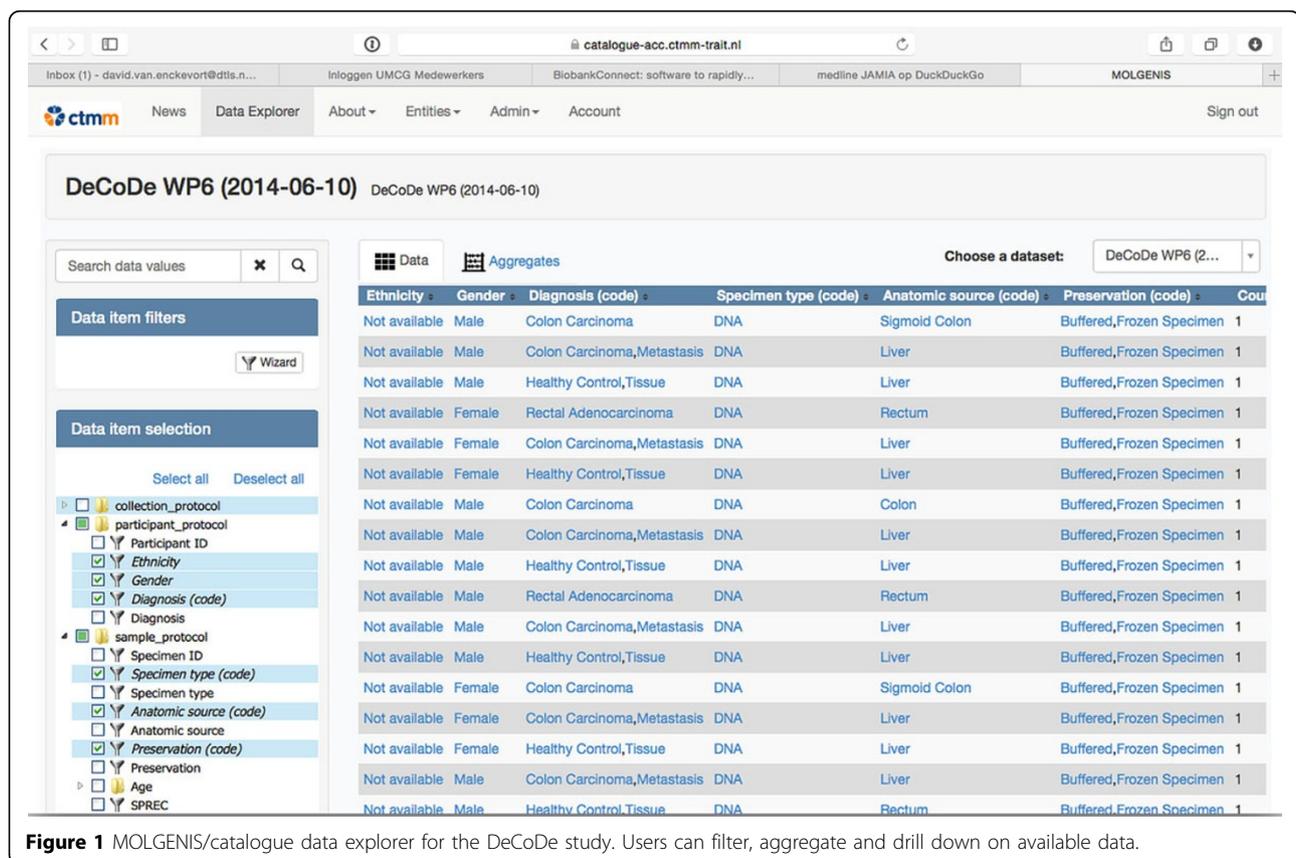
Figure 1 MOLGENIS/catalogue data explorer for the DeCoDe study. Users can filter, aggregate and drill down on available data.

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Increasingly bigger datasets are required for epidemiological and genetic analysis; hence it has become important to enable pooling of data from multiple biobanks. Therefore, the catalogue also comes with BiobankConnect, a tool to rapidly match data elements across studies and biobanks based on lexical matching and ontologies [1]. MOLGENIS/catalogue is build on the open source MOLGENIS platform [2] and offers pre-build components that allow users to upload data in a simple Excel format and supports any data model through a meta-data definition in the Excel file; to visualize the data in aggregated or tabular form; to share securely data through a comprehensive security model and to integrate data from different domains (Figure 1).

Status of development
Stable/production ready; version 1.2.0.

Users
10 known installations.

Links
http://github.com/molgenis/molgenis, http://www.molgenis.org, https://www.dropbox.com/s/bez1r4lq5q69o9e/Swertz%20ECRIN%20Dussseldorf%20catalogue%202014_05_26.pptx.pdf.pdf

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References
1. Pang C, Hendriksen D, Dijkstra M, van der Velde KJ, Kuiper J, Hillege H, Swertz MA: BiobankConnect: software to rapidly connect data elements for pooled analysis across biobanks using ontological and lexical indexing. *J Am Med Inform Assoc* 2014, epub ahead of print. doi: 10.1136/amiajnl-2013-002577.
2. Swertz MA, Dijkstra M, Adamusiak T, van der Velde JK, Kanterakis A, Roos ET, *et al*: The MOLGENIS toolkit: rapid prototyping of biosoftware at the push of a button. *BMC Bioinformatics* 2010, **11**(Suppl 12):S12.