BBMRI-ERIC
Biobanking and
BioMolecular resources
Research Infrastructure

RDA Data Fabric IG (DFIG): BBMRI-ERIC IT

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This document has been written as a BBMRI-ERIC use case description for Research Data Alliance (RDA) Data Fabric IG (DFIG). References to existing RDA work are minimized on purpose, as it focuses on description of the use case itself. The structure of section complies with the RDA DFIG. The document is intended to be published by RDA among other use cases.

Document Overview

1 Scientific Motivation and Outcomes

Biobanks have become a major source of biosamples as well as data for the biomedical and bioinformatics research. Biobanks are used by the researcher not only to request samples and data, but also to provide the researchers with long-term sample and data repositories for material used in their research. Data collection, harmonization and processing has been part of the biobanks since their inception, as biosamples without the data is of little use. The data collection started with the phenotype, clinical, and lifestyle data (with focus on specific data types given by the type of the biobanks, such as population biobanks or clinical biobanks). Unprecedented growth of omics data generation in recent 15 years have brought biobanks into the domain of big data, processing and storing genomics, proteomics, metabolomics and other types of data.

After about ten years of preparations, BBMRI-ERIC has become one of the first European Research Infrastructure Consortia, with the mission of providing high-quality samples, data, and biomolecular resources from biobanks to support healthcare advancement in Europe and beyond. The major goals of BBMRI-ERIC are:

- to *increase use of material and data* stored in European biobanks, while adhering to strong *privacy protection* of patients and donors contributing the material and data,
- to *improve quality and traceability* of the material and data in European biobanks, referring to the infamous recent publications demonstrating that large portions of biomedical research are not reproducible [1, 2, 3, 4, 5] and this has been even demonstrated specifically for the process of generating data from samples [6],
- to *improve data harmonization* and contribute to the standardization processes,
- to *contribute to the ethical, legal, and social issues*, with particular focus on cross-border exchanges of human biological resources and data attached for research use.

Although biomedical, bioinformatics researchers (coming from both academia and industry), and biobankers are mostly seen as the primary users of BBMRI-ERIC, other users are also embraced and supported, such as patients/donors and their organizations, data protection agencies and research funding agencies are also part of the target users. Furthermore, even for the researchers, the use cases go beyond well-known sample/data request use case: recent investigations by BBMRI.uk[1] have shown that sample/data storage and curation requests may be as frequent, and industry is specifically known for joint prospective studies with biobanks instead of requesting existing samples[2].

The IT infrastructure of BBMRI-ERIC will be developed and operated using the Common Service IT instrument, to which all the full-member countries of BBMRI-ERIC contribute. It follows up on experience from the BBMRI Preparatory Phase[3] as well as collaboration within other projects in the BBMRI ecosystem, such as BBMRI-LPC[4], BioSHaRE[5], BioMedBridges[6], or BiobankCloud[7].

[1] Results have not been published yet.

[2] The reasons for this range from the informed consent signed by the patients/donors to tighter control over the sample collection/processing/storage requirements.

[3] Material from BBMRI Preparatory Phase can be found at `http://bbmri-eric.eu/reports`

[4] `http://www.bbmri-lpc.org/`

[5] `https://www.bioshare.eu/`

[6] `http://www.biomedbridges.eu/`

[7] `http://www.biobankcloud.com/`

2 Functional Description

BBMRI-ERIC relies on a component-based software stack with well-defined components of reasonable size (preferably not excessively large), interconnected using well-defined and well-documented APIs. The component diagram is shown in Figure 1 and the components are described in further detail in Sections 3 and 4. Architecture of the system is fully distributed, following distributed architecture of BBMRI-ERIC itself, where it is called "hub and spokes" with central level, National Nodes level, and individual biobanks level. This architecture is applied to all the aspects including the long-term data storage and curation, querying data, migration of computations to data, etc. The architecture, however, must support temporary data caching for performance reasons. From this perspective, BBMRI-ERIC has no ambition to setup large central storage facilities, although some members or specific BBMRI-ERIC-related projects may opt for aggregation of data into highly secure storage systems.

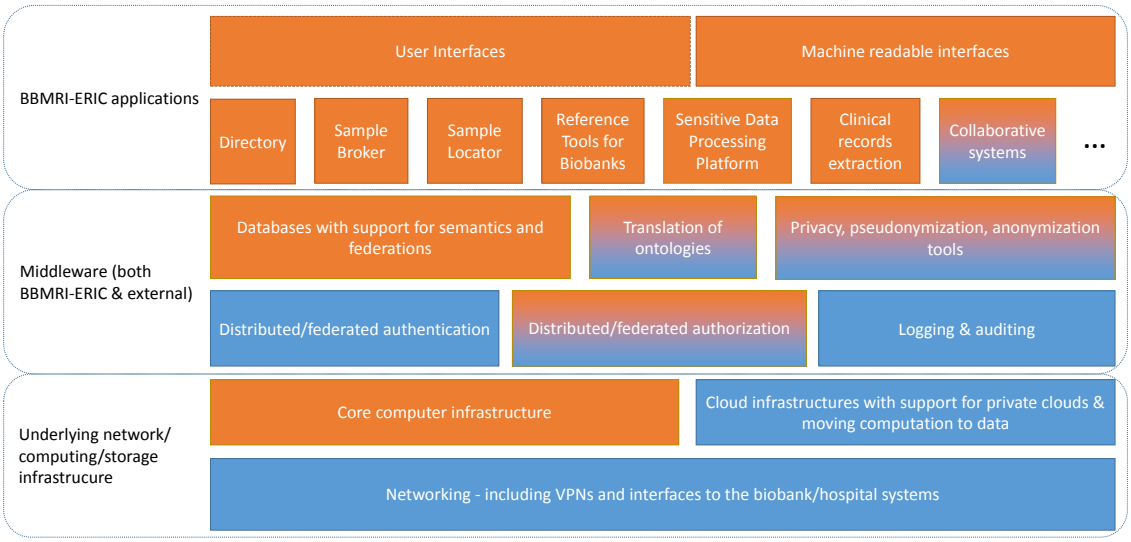

Figure 1: Software stack of BBMRI-ERIC IT system. Orange components are assumed to be build by BBMRI-ERIC, blue components are expected from other e-Infrastructures. Orange-blue components are assumed to be developed jointly with other e-Infrastructures.

From the data exchange perspective, BBMRI-ERIC is committed to FAIR principles[8] (Findable, Accessible, Interoperable, Reusable), with accessibility the limited by privacy protection of patients and donors given the nature of data in BBMRI-ERIC infrastructure. This implies that access is only provided to the authorized people, i.e., typically researchers who work on research projects that have been reviewed by a competent ethical review board.

First step toward these goals is identifiability and traceability, which requires identifiers with time-stamping support for both data and samples, as well as ability to identify subsets generated by queries on data in specific time. This is well aligned with one of the major lines of RDA focus.

[8] Data FAIRport, `http://datafairport.org/`

Typical workflow for the user starts with authenticated user[9] searching for the samples and/or data, or trying to identify biobanks to start collaboration with (see the Directory and Sample Broker/Locator components described in Section 3). Before accessing samples and/or actual data, the user must submit a project that undergoes ethical evaluation, and only users with approved projects may be allowed any further. The users then request the samples and/or data and negotiates with biobankers. At this step, the user's request may still be rejected for several reasons: the samples or data may not be fit for the intended purposes, the sample may be reserved for another project with higher priority or for another purpose (e.g., biobanks make certain samples reserved for quality management purposes including verification of previous experiments in case of dispute). Once user's request is approved, the user signs Material Transfer Agreement (MTA) and the sample/data is given to the user.

When processing data, the sensitive nature of the data may require that raw data never leaves biobank and only the aggregate anonymized data is sent out, as has been previously described and demonstrated, e.g., using DataSHIELD[10] [7, 8, 9]. Both size of the data and its nature will be helped by the moving computations to data paradigm that has been promoted in last 10 years and that has been strongly pushed forward by the availability of clouds that can be deployed also within the perimeter of a biobank; use of private clouds for processing of biobank data has been developed and demonstrated by the BiobankCloud project[11]. An extended version of this scenario is targeted by the Sensitive Data Processing Platform component in the software stack diagram.

Another specific aspect of BBMRI-ERIC infrastructure is the heterogeneity of data that are coming into the biobanks and that need to be harmonized into consistent data sets. Therefore BBMRI-ERIC works with the federated databases with semantic data support (triple store systems) and translation of ontologies, which has been being worked upon, e.g., in the BioMedBridges project[12]. Specific issue for the clinical biobanks is the unstructured clinical records that are on one hand one of the most valuable sources of information, but on the other hand that in many cases require reliable extraction from unstructured records written in the natural language.

3 Describe Essential Components and Their Services

BBMRI-ERIC Directory A distributed tool to provide highly aggregated information about biobanks, biobank networks, sample and data collections, and studies. This tool is primarily intended for the researchers to identify biobanks that might potentially have samples/data of their interest. The data is typically collected from the local biobanks via national nodes to the central level of BBMRI-ERIC, while national nodes utilize this structure to also run their national directories. This tool is used to assign identifiers to all the entities (biobanks, biobank networks, sample and data collections, studies), which can be further used not only for reproducibility and traceability, but also to assess their impact[13].

[9] Strong authentication is needed, preferably multi-factor, because of the privacy and security aspects.
[10] http://www.p3g.org/biobank-toolkit/datashaper
[11] http://www.biobankcloud.com/
[12] http://www.biomedbridges.eu/
[13] See, e.g., BioResource Impact Factor (BRIF)[14] [10, 11].

Sample Broker This tool is intended for the researchers who already have their research intent/project and need samples or data to implement it. Inquiries by the researchers for the samples often span multiple biobanks and they are subject to iterative refinement. As a part of this process, the biobankers must understand various aspects of the expected methods to be used in the planned research, in order to evaluate whether their samples are fit for the particular purpose (e.g., analytical method). This is by its nature a M:N communication between researchers and biobankers, generating large overhead that can be simplified by employing efficient tools for group communication.

Sample Locator If there were no privacy concerns (e.g., in case of non-human biosamples), the researchers could easily look up individual samples of their interest based on parametric search. For BBMRI-ERIC, the situation is, however, more complicated because and various strategies related to differential privacy [12, 13, 14] need to be in place. Approaches such as k-anonymity, l-diversity, and t-closeness together with generalization and suppression may result in substantial "hidden black matter" because in practice the high-dimensional data is sparse [15]. An alternative solution to avoid too much suppression is by reducing dimensionality, which may in turn result in users being unable to ask as specific queries as they need. Another aspect is competing interests of biobankers and researchers, which results in biobankers being reluctant to put all of their samples into a system that can identify individual samples. Despite the fact that only subset of samples and data is assumed to be available through this tool, it will still be part of the overall system because of its unique capability to support generation of novel research ideas.

Ontology Translation Service With distributed nature of BBMRI-ERIC, the data come in many different ontologies even in a single domain[15]. As data harmonization and ontology translation is an extremely important service for many other tools, we define it as a separate component with well-defined interface to be incorporated into other applications.

Sensitive Data Processing and Sharing Platform This component is composed of two parts: one is the private cloud-based tools for biobanks and the other is a platform where sensitive data can be collected and shared, such as TSD[16] or MOSLER[17].

4 Describe Optional/Discipline-Specific Components and Their Services

Clinical Records Extraction Clinical records are valuable source of information especially for the clinical biobanks, which take biosamples from the clinical practice. Typical clinical records, however, contain only limited structured information and large portions are written as free text in natural language, often with some particular domain specifics. In many cases, there is further complication for the biobanks that they are detached from the hospital information systems and may not access this data online. While very important and characteristic for BBMRI-ERIC, reliable extraction from the unstructured clinical records is still an open basic research problem to a large extent and therefore it is in the optional components list.

[15] A nice illustration is simple diagnosis coding, where not all the European countries use standard ICD-10 system and some use nationally customized variants of it of or customized variants of SNOMED CT.

[16] `https://www.uio.no/tjenester/it/forskning/sensitiv/`

[17] `https://wiki.bils.se/wiki/Mosler_user_documentation`

Reference Tools for National Nodes and Biobanks Because biobanks and BBMRI-ERIC national nodes have often very limited IT personnel capacity, BBMRI-ERIC is committed to provide reference tools for both of these levels. These tools are assumed to be distributed either as software packages or even as pre-installed and mostly pre-configured virtual machines.

An important aspect of the reference tools will be documentation of APIs and file formats used for the data exchange, as biobanks and national nodes will be free to replace any of the components of the reference tool set by the tools of their preference, only retaining the API interoperability.

5 Describe Essentials of the Underlying Data Organization

The schema below tries to provide an overview of data organization. Please note there are two major types of biobanks that differ in how they store and access data in most cases: (a) population biobanks, which typically store all the relevant data inside the biobank together with the biosamples, (b) clinical biobanks, which rely on their connection to the clinical source of biosamples/data (hospital or other healthcare provider) and which typically need to query that source for more detailed data beyond very basic data structure that is transferred initially together with the biosample.

(1) **Data stored inside a biobank.**

This is data that is stored within physical or at least logical perimeter of the biobank. Typically comprises several subtypes:

(2a) **Data generated inside a biobank.**

Typically operational data related to the biosamples, such as their position in storage systems. In some cases, biobanks also perform further biosample analysis on their own, such as sequencing.

Example data: location information of biosamples (in storage system).

(2b) **Data received together with the biosample and stored in a biobank.**

This is the data the comes into the biobank as a part of ingestion of the biosample into the biobank storage system. For clinical biobanks, it may consist of a subset of structured clinical data, while for population biobanks it may contain complete data set collected in the research/study about the donor.

Example data: (a) description of the sample (information on how and when the sample was taken and processed), (b) excerpt of structured patient's clinical data (pre-approved structure – typical for the clinical biobanks), (c) donor-related information related to the purpose of the research or biobank, such as life-style data, phenotype data, etc. (typical for the population biobanks).

(3c) **Data generated outside biobank and stored in a biobank.**

Example data: omics data generated by a user of a biobank, which is returned back to the biobank.

(2) **Data used by biobanks but stored outside the biobank.**

This category is typical for clinical biobanks detached from the hospital on technical or administrative basis[18]. For any data access that is not part of the initial data transfer with the biosample (Item (2b)), the biobank needs to apply for the data to the hospital information system managers.

Example data: clinical records of patients.

(3) **Data stored at national level.**

Amount and types of the data stored on this level varies largely based on the type of the national node. Typically consists of administrative/operational data and data linking to the biobanks. For some (typically smaller) national nodes, it may also store some data on behalf of the biobanks.

Example data: (a) Lists of interfaces to the biobanks, (b) authorization data for the services on the national level, (c) access/usage logs, (d) data query caches, (e) registry data on behalf of biobanks (if there is no on-line interface for the biobank).

(4) **Data stored at central BBMRI-ERIC level.**

This typically consists of administrative/operational data and data linking national nodes to the central BBMRI-ERIC level. BBMRI-ERIC intentionally avoid storing any privacy-sensitive data on the central level.

Example data: (a) Lists of interfaces to the national node services and service discovery, (b) authorization data for the services on the central BBMRI-ERIC level, (c) access/usage logs, (d) data query caches.

(5) **Data stored outside of EU.**

This data may consist of any of the previously described data types (Items (1)–(4)), but regulations of other countries as well as European Union apply, if integrated into BBMRI-ERIC.

As one can see from the list above, BBMRI-ERIC features fully federated distributed architecture with distributed databases in autonomous organizations and organizational units (working under same umbrella of BBMRI-ERIC allowing for the federated operations) and distributed querying.

Data life cycle and traceability. An important aspect for traceability is data modifications/updates, which are an inherent part of the data life cycle in the BBMRI-ERIC ecosystem. This aspect is particularly critical for the clinical biobanks, where the data coming from the clinical practice may come in largely varying quality and may require several rounds of refinement before they become usable for further research. The issue of data improvements and fixes should not be underestimated, however, even for other types of biobanks. The primary data can be only edited on the level where they are stored, see the Items (1)–(5). All the changes must result in a traceable and identifiable changes that can be used, e.g., in the provenance graphs [16, 17].

[18] This happens often that biobanks are considered research infrastructures and as a part of their institutionalization, they become detached from the clinical network in the hospital and from the hospital information systems, even though they may still reside in the same hospital premise.

6 Indicate the Type of APIs behind Used

The most common interfaces in the BBMRI-ERIC community are REST interfaces. For linked data, JSON-LD and less frequently RDF is being used with Virtuoso[19] used as triple store database.

Other interfaces are used as appropriate for given applications. For example Directory 1.0 relies on hierarchy of LDAP servers (national nodes can run their own LDAP servers, or can upload LDIF/JSON data directly to the central server) and LDIF data format for distributed data queries and JSON translators are available in/out for the LDAP.

When dealing with the clinical data, hospital information systems rely on HL7 (Health Level 7)[20] as well as custom interfaces. Data often utilize PACS formats (if relevant for given data type, e.g., imaging). There is ongoing work on harmonization of Electronic Health Records (EHR) within HL7 called Fast Healthcare Interoperability Resources (FHIR)[21], which in turn relies again on REST.

National nodes and local biobanks run variety of systems and APIs and it is one of the major goals of BBMRI-ERIC to simplify the situation by providing reference tools for the national nodes and biobanks.

As a part of the efforts to improve quality and interoperability of APIs and data formats, BBMRI-ERIC actively participates in ISO TC 276[22] Working Group 5 (WG5) "Data processing and integration", which aims at (a) definition of data and model formats and their interfaces; (b) definition of metadata and relations of data and models; (c) quality management of processed data and models. In order to provide consistent input, BBMRI-ERIC also participates in ISO TC 276 WG1 (terminology) and WG2 (biobanking).

7 Achieved Results

At the time of writing, BBMRI-ERIC is running collaborative tools to support interaction of its community, released Directory 1.0 covering more than 500 biobanks and standalone collections with overall estimated size between 34,000,000 and 46,000,000 samples[23] and Common Service IT is under setup process with expected start in Fall 2015. National nodes are running their own infrastructures of highly varying extent and quality, as do also local biobanks. BBMRI-ERIC also benefits from other related activities such as operation Catalogue of BBMRI-LPC providing data warehouse capabilities.

[19] http://virtuoso.openlinksw.com/

[20] http://www.hl7.org/

[21] Pronounced "fire", http://hl7.org/implement/standards/fhir/ .

[22] http://www.iso.org/iso/home/standards_development/list_of_iso_technical_committees/iso_technical_committee.htm?commid=4514241

[23] Only an order of magnitude of biobanks and standalone collections has been collected for the first release of Directory (1.0), in order to avoid frequent data updates on the biobankers side, as for many biobanks the amount of samples is constantly changing and there is so far no automatic link between the biobank and the national/central levels of the Directory.

8 (Frequently) Asked Questions

Q-1 *You make the distinction between "sample" and "data". Isn't a sample not just data as well? What is the difference? Samples for me were always the following: make an experiment or extract blood etc. and that would be stored as a sample. Sometimes I get the idea that samples in your terminology are also collections.*

Answer:

- First of all, it is important to distinguish between *(a)* the physical samples, *(b)* meta-data about the samples (e.g., information how the sample was retrieved, where it is stored, what are its properties such as size), *(c)* data accompanying the sample (e.g., the information about the patient/donor, about the treatment the patient is undergoing), *(d)* data generated from the samples (e.g., genomic, proteomic, transcriptomic data, collectively known as omics data).
- There are important distinction on the legal basis between physical samples and data, especially when it comes to cross-border sharing. Sharing data is generally easier than sharing samples. For more detailed discussion see answer to **Q-2**.
- A part of the ongoing BBMRI-ERIC IT effort is to define policies for long-term preservation of both samples and data. This is of particular interest for data generated from the samples: the data preservation incurs non-trivial cost as well as storage of samples does. Therefore, we are searching for balance between reasonable cost of the infrastructure and the reproducibility of results.
  If the data is not used and can be re-generated in the future at fraction of the cost and better quality compared to the state of the art today, it may be more efficient to delete the data after some inactivity threshold and generate a fresh data once it is needed again (or when the sample is going to be depleted).
  However, once the data is used for producing scientific results, it needs to be retained at least for some period, to allow for identification of potential problems when assessing reproducibility of results.
- Biobanks should keep some samples as a reserve for quality evaluation and reproducibility assessment. Currently, the behavior of biobanks is largely varying in this respect and BBMRI-ERIC will try to facilitate harmonization of the field.
- Collections of samples are tools to organize samples. Their use ranges from defining arbitrary subsets of samples, e.g., based on material types, but in many cases this also includes consistent goals of sample collections and/or standard operating procedures (SOPs) that were used to collect and process the samples. As a part of MIABIS 2.0 [18], we recommend that collections are implemented as partitioning of parent set (a biobank or another collection), in order to allow for easy aggregation of collections.

Q-2 *What is the difference between sharing samples and sharing data across borders?*

Answer: Within the context of heterogeneous ethical and legal national and/or regional frameworks across Europe, cross-border sharing of samples and data faces constant challenges [19, 20]. Biobanking in Europe has made major steps towards harmonization and shared standards for the collection and processing of data and samples stored in biobanks. Still, biobanks and researchers face substantial legal difficulties in the field of data protection and sample management. One of the main complications is that, although the field of data protection is harmonized through the EC directives,

the collection, storage and sharing of samples is not. Whereas data protection law was harmonized in 1995 in the European interest of a common market, samples fall under the competency of each individual EU Member States as subjected to the health domain. Although some countries have introduced even special biobank acts, it is not always clear where the borderline lies. There seems to be a trend to break down the sample/data dichotomy and to subsume under "database" both the physical sample and the information derived from it [21]. Nonetheless an international agreement is still lacking to date and many biobanks adhere to soft law and regulations such as the Oviedo Convention (ETS 164), the Helsinki Declaration, the OECD Guidelines for Human Biobanks and Genetic Research Databases (HBGRD) 64, the Recommendation Rec(2006) 4 of the Committee of Ministers to Member States on research on biological materials of human origin.

Internationally agreed key principles relevant to the operation of BBMRI-ERIC are that research on human biological samples and identifiable medical data require informed consent from the sample and data donor, and approval by an ethical review board. Both HBGRD and the Helsinki Declaration foresee that in case informed consent cannot be obtained for practical or scientific reasons, ethical review boards can provide a waiver for informed consent. Despite several harmonization efforts, there are no common regulatory frameworks internationally and in the EU for sample exchanges for research and research biobanking operations. Each Country has its own legislations and no specific EU level legislation applies. For the ethical aspects of biobanking, the role and work of different national authorities and research ethics committees are strong elements and mandatory procedures exist in each Country that need to be respected [22, 23].

Q-3 *What would curation requests typically include?*

Answer:

- Fixes of incorrect data (e.g., data coming from clinical practice, which is put manually by the clinicians into the hospital information systems).
- Input of additional data obtained. This covers both acquisition of new data accompanying the samples (e.g., progress of treatment of a patient) and retrieving data generated from the samples analyses back into the biobanks (e.g., various omics data).
- Dealing with changes in formats and vocabularies (ontologies) of data. For instance, change from ICD-9 to ICD-10 vocabulary with need for harmonization of both old and new data.
- Increasing level of detail when the community redefines the standards and when more detailed information can be obtained from the original sources.

Q-4 *Central aggregation is said to be an option. Does that mean that you offer distributed search and/or data mining on banks? If so we would be interested to understand details and you refer to DataSHIELD. On the other hand you state the user receives the sample/data which actually means a transfer which could be infeasible if it is about omics data etc.*

Answer:

- BBMRI-ERIC architecture generally presumes distributed search, with optional support for centralized data warehouse. For performance and user experience reasons, caching needs to be supported wherever applicable.

- What the user actually receives depends on what is allowed to do with the given samples/data. He/she may: *(a)* receive physical samples, *(b)* receive a copy of data, *(c)* receive only remote access to the data that must not leave the biobank. This depends on informed consent, and on the ethical and legal frameworks in a given country.
- BBMRI-ERIC assumes that the user may not be allowed to extract the data from the biobank and only aggregated information can be sent out; hence reference to DataSHIELD[24] [7, 8, 9] and generalized linear models.

Q-5 *Do you automate the knowledge about ethically approved projects and their members somehow or is it all manual work? I mean whether MTAs are done every time or whether they are re-used etc.*

Answer:

- BBMRI-ERIC does *not* assume to perform project evaluation on central basis. However, it will be collecting of project information when users request samples, in order to simplify the request procedures (so that the project does not need to be verified for each sample request or query).
- Evaluation of the project priority/acceptability for given biobank may occur for every sample/data request.
  This of particular importance for physical samples, which are considered a "scarce resource". It implies the biobankers have right refuse to deliver samples for an ethically approved project, if they have reasons to do so, e.g., samples are intended for higher priority project, or sample request is not compatible with the collection purpose (e.g., creating selective holes in large cohorts that are intended to be used "as a whole"). This is part of the negotiation between biobankers and requesters.
- MTAs are generated every time the material/data is transferred out of the biobanks. As of today, biobanks are using their own custom MTAs in most cases, and BBMRI-LPC[25] project is working on generic MTAs to be reused by biobanks.
  MTAs are particularly complicated in case of cross-border transfers, where it needs to comply with both countries of sender and receiver, as well as with European regulations if at least one of the parties is in Europe. BBMRI-ERIC is working on simplifying generation of such cross-border MTAs; rudimentary work in this direction can be seen in hSERN website[26].

Q-6 *Not clear how ontologies are used and what "translation of ontologies" means – difficult topic anyhow. Does "translation of ontologies" simply mean "mapping between concepts in different ontologies"? Then it would be clear to me what you are doing, since we all have the same problems to solve. How static is conceptualization and thus mapping in your field?*

Answer:

- Life sciences in general suffer from various competing and overlapping vocabularies, which in many cases need to be harmonized for larger studies. A good relatively simple example are ontologies describing diagnoses: ICD-9, ICD-10, SNOMED CT,

[24] http://www.p3g.org/biobank-toolkit/datashaper
[25] http://www.bbmri-lpc.org/
[26] hSERN: Human Sample Exchange Regulation Navigator, http://www.hsern.eu/.

and their local variations. An important experience here is that in many cases, it is very difficult or outright impossible to translate the ontologies unambiguously.
- BBMRI-ERIC will push toward using standard or at least commonly accepted ontologies to simplify the problems.

Q-7 *Is extraction from unstructured clinical records automatic – probably not, since as you say it's in natural language.*

Answer:

- As obvious, this is very hard natural language processing (NLP) problem, with strong language and regional impact (even the same language environment may have fragmented way of annotating).
- There is a problem of reliability of the clinical records themselves even if the NLP extraction was perfect (which it is not).
- There have been relatively successful efforts on extraction of some specific information from selected languages (e.g., extraction of pathology information from German/Austrian clinical records[27]).

Q-8 *You say something about deploying software packages on clinical machines (or?) – this is often very problematic, since it requires full testing etc.*

Answer:

- It is important to distinguish among several types of computers: *(a)* "clinical computers" in the clinical practice and in the clinical laboratories, *(b)* computers residing in biobanks, which are in many cases outside of the clinical perimeter of the hospital (thus also introducing a disconnection between biobanks and hospital information systems), *(c)* other (external) computers, including infrastructure of national nodes and central infrastructure of BBMRI-ERIC.
- It is generally impossible to install software on clinical computers in general. The situation is substantially different with computers in the biobanks, though.

Q-9 *Are you aware of EPIC?*[28]

Answer: Yes and we plan to discuss with them registering our IDs (such as biobank and collection identifiers introduced in the BBMRI-ERIC Directory 1.0/2.0).

[27] See *SAAT Semi-Automated Annotation Tools*, http://sourceforge.net/p/saat/news/, and a paper on ResearchGate http://www.researchgate.net/publication/258451276_Challenges_and_solutions_in_the_setup_of_a_findings_database_for_a_large_scale_tissue_collection.

[28] http://www.pidconsortium.eu/

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