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Information Event: Open Research Data in Veterinary Medicine (ORDVET)

December 8, 2023

Vetsuisse Faculty

https://padlet.com/ORDVET/open_research_data_vetsuisse

Universität Bern | Universität Zürich
vetsuisse-fakultät
ACCREDITED BY EAEVE/FVE

Data sharing in (veterinary) genetics

Tosso Leeb

Institute of Genetics, Vetsuisse Faculty, University of Bern

Data Sharing in Genetics

Universität Bern | Universität Zürich
vetsuisse-fakultät

Tosso Leeb

```
ID   V00179; SV 1; linear; genomic DNA; STD; MAM; 1304 BP.
XX
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XX
DT   13-JUL-1983 (Rel. 03, Created)
DT   18-APR-2005 (Rel. 83, Last updated, Version 4)
XX
DE   Dog gene encoding insulin.
XX
KW   germ line; insulin; signal peptide.
XX
OS   Canis sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Laurasiatheria; Carnivora; Caniformia; Canidae; Canis;
OC   unclassified Canis.
XX
RN   [1]
RP   1-1304
RX   PUBMED; 6296142.
RA   Kwok S.C.M., Chan S.J., Steiner D.F.;
RT   "Cloning and nucleotide sequence analysis of the dog insulin gene";
RL   J Biol Chem 258(4):2357-2363(1983).
XX
DR   MD5; 3c32d256fa5e594c99f0548e36ee5b66.
XX
CC   Data kindly reviewed (13-JUN-1983) by S.C.M. Kwok
XX
FH   Key             Location/Qualifiers
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FT                   LENYCN"
FT   intron          512..775
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FT   mRNA            776..1024
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SQ   Sequence 1304 BP; 212 A; 459 C; 405 G; 228 T; 0 other;
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//
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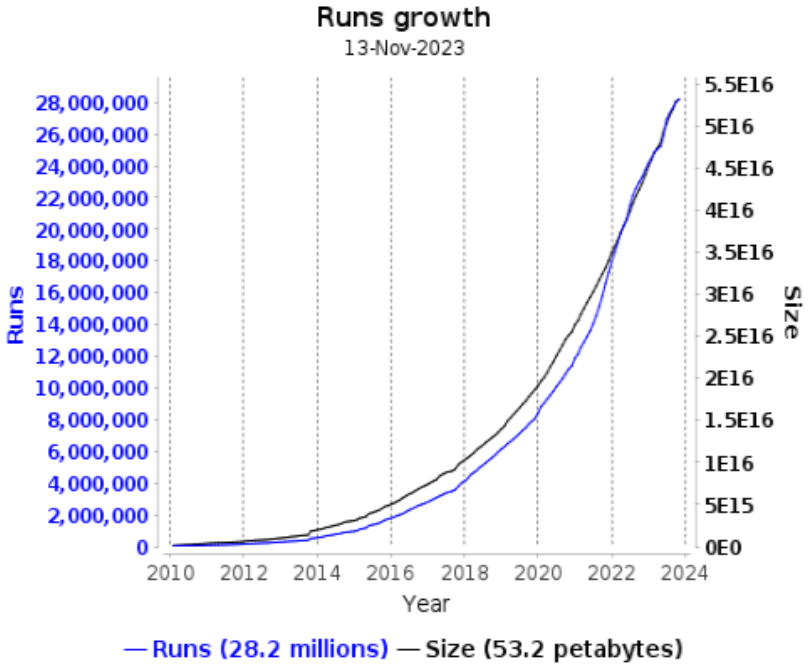
History

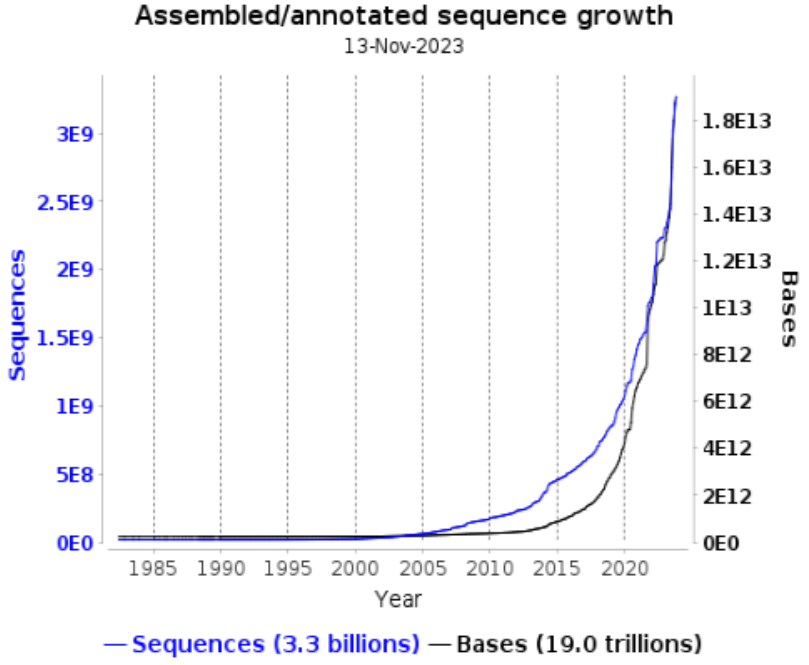
1980 EMBL Nucleotide Sequence Data Library

1988 Database submission mandatory for publication in Nucl Acids Res

2008 European Nucleotide Archive (ENA)

European Nucleotide Archive





History

1996 Bermuda Principles:

- Automatic release of sequence assemblies larger than 1 kb (preferably within 24 hours).
- Immediate publication of finished annotated sequences.
- Aim to make the entire sequence freely available in the public domain for both research and development in order to maximise benefits to society.

2003 Fort Lauderdale Agreement

Sharing Data from Large-scale Biological Research Projects:

A System of Tripartite Responsibility

Report of a meeting organized by the Wellcome Trust and held on 14–15 January 2003 at Fort Lauderdale, USA.

The Wellcome Trust

- The meeting attendees enthusiastically reaffirmed the 1996 Bermuda Principles, which expressly called for rapid release to the public international DNA sequence databases (GenBank, EMBL, and DDBJ) of sequence assemblies of 2kb or greater by large-scale sequencing efforts and recommended that that agreement be extended to apply to all sequence data, including both the raw traces submitted to the Trace Repositories at NCBI and Ensembl and whole genome shotgun assemblies.

- The attendees recommended that the principle of rapid pre-publication release should apply to other types of data from other large-scale production centers specifically established as 'community resource projects'.

- The attendees recognized that pre-publication data release might conflict with a fundamental scientific incentive – publishing the first analysis of one's own data. The attendees noted that it would not be possible to absolutely guarantee this incentive without applying restrictions that would undermine the rationale for rapid, unrestricted release of data from community resources. Nonetheless, it is essential that excellent scientists continue to be attracted to these projects. To encourage this, the scientific community should understand that pre-publication data release needs active community-wide support if it is to continue to receive widespread support from the producers. The contributions and interests of the large-scale data producers should be recognized and respected by the users of the data, and the ability of the production centres to analyse and publish their own data should be supported by their funding agencies.

Tripartite Reponsibilities

A. **Funding agencies.** Funding agencies are the major sources of support of research projects leading to community resources and projects that depend on the availability of such resources. Funding agencies have a critical role in determining the quality and breadth of community resources through the peer review evaluation system and as the sources of scientific research policies. For these reasons funding agencies should:

1. designate appropriate efforts as community resource projects, and encourage resource producers to prepare and submit Project Descriptions (see below) for publication;
2. require, as a condition of funding, free and unrestricted data release from community resource projects to appropriate central and searchable public databases, and vigorously ensure that this occurs;
3. encourage more investigators to serve the community through involvement in such projects. In particular, the agencies should ensure that investigators engaged in generation of such datasets have sufficient support for curation, maintenance and distribution of the data to the community, as well as resources to perform initial analyses using the resources that they have generated;
4. ensure that a centralized view of existing community resource projects is available as an information source for the community;
5. support central databases that will house and distribute the data in a way that prevents fragmentation of the data.

Tripartite Reponsibilities

B. **Resource producers.** Community resources are often expensive efforts. For this and other reasons, they are frequently established and supported as unique facilities. The scientists who organize and operate community resources are, accordingly, in a uniquely responsible position. The community is dependent on the success of their efforts and they often face relatively little direct competition. Resource producers should:

1. when feasible, publish a Project Description. The purpose of the Project Description, which will be a new type of scientific publication, is to inform the scientific community about the resource project and to provide a citation to reference the source of the data. The Project Description should be written at the beginning of the project and describes the plans for and scope of the production and analyses that the data producer intends to undertake. It will often include a timeline for production goals and data release.
2. produce data of consistently high quality;
3. make the data generated by the resource immediately and freely available without restriction;
4. recognize that even if the resource is occasionally used in ways that violate normal standards of scientific etiquette, this is a necessary risk set against the considerable benefits of immediate data release.

Tripartite Reponsibilities

C. **Resource Users.** Community resource data sets benefit the users enormously, giving them the opportunity to analyse the data without the need to generate it first. The data sets are, in general, much larger, richer and of higher quality than individual laboratories could normally generate. In contributing to what ideally is a symbiotic and synergistic situation, resource users should:

1. appropriately cite the source of the data analysed and acknowledge the resource producers. The early publication of a Project Description, as suggested above, would provide users with an appropriate reference to cite before the data are formally published;
2. recognize that the resource producers have a legitimate interest in publishing prominent peer-reviewed reports describing and analyzing the resource that they have produced (and that neither the Project Descriptions nor data deposits in databases are the equivalent of such publications);
3. respect the producer's legitimate interests as set out, e.g. in a Project Description, while being free to use the data in any creative way. There should be no restrictions on the use of the data, but the best interests of the community are served when all act responsibly to promote the highest standards of respect for the scientific contribution of others. In some cases, this might best be done by discussion or coordination with the resource producers;
4. assist journals and funding agencies to play their proper roles in ensuring, through the peer review system, that the system works fairly for all constituents.

Join!
Mitmachen!

Vetsuisse-Verhaltenskodex: Unser Wertesystem

Is it better? Ist es besser?

Is it worth it? Ist es das wert?

Is it fair? Ist es fair?

The Dog10K Project

Project description

Dog10K: the International Consortium of Canine Genome Sequencing

Guo-Dong Wang[1,2], Greger Larson[3], Jeffrey M. Kidd[4], Bridgett M. vonHoldt[5], Elaine A. Ostrander[6,*] and Ya-Ping Zhang[1,2,*]

Dogs (*Canis lupus familiaris*) were the first species to enter into a domestic relationship with people [1] and are a source of fascination all over the world, not only due to their history of domestication and dispersal along with human beings [2], but also because of their diverse phenotypes and behaviors, driven by both artificial and natural selection [3]. Dogs and humans have often been subjected to similar selection pressures [4], and these shared evolutionary trajectories have led to the emergence of the same common disorders including heart disease, neurologic disorders, diabetes and cancer [5].

The worldwide canine genetics genomics communities recently formed the International Consortium of Canine Genome Sequencing, also called the Dog10K Consortium (http://www.dog10kgenomes.org), to address major 10th International Conference on Canine and Feline Genetics and Genomics (Fig. 1b) with 15 participants representing 13 institutions.

The primary goals of this collaborative endeavor are to generate WGSs of 10 000 canine/canids within 5 years, refine the existing reference genome from a Boxer, create new reference genomes from additional canids and apply the data to a myriad of scientific questions. The resulting catalog will contain comprehensive high-density genomic data, including single nucleotide variants (SNVs), structural variants (SVs), which include copy number variations (CNVs), and

Natl Sci Rev (2019) 6: 611-613

Publication by Resource User

RESEARCH ARTICLE

Autosomal recessive hyposegmentation of granulocytes in Australian Shepherd Dogs indicates a role for *LMBR1L* in myeloid leukocytes

Bianca Lourdes Frehner[1☯], Matthias Christen[2☯], Iris M. Reichler[1], Vidhya Jagannathan[2], Marilisa Novacco[3], Barbara Riond[3], Laureen M. Peters[4], José Suárez Sánchez-Andrade[5], Aldona Pieńkowska-Schelling[2,6], Claude Schelling[6], Anja Kipar[7], Tosso Leeb[2‡*], Orsolya Balogh[1,8‡]

PLoS Genet (2023) 19: e1010805

Publication by Resource Producer

Meadows *et al. Genome Biology* (2023) 24:187
https://doi.org/10.1186/s13059-023-03023-7

Genome Biology

RESEARCH Open Access

Genome sequencing of 2000 canids by the Dog10K consortium advances the understanding of demography, genome function and architecture

Jennifer R. S. Meadows[1*†], Jeffrey M. Kidd[2*†], Guo-Dong Wang[3], Heidi G. Parker[4], Peter Z. Schall[2], Matteo Bianchi[1], Matthew J. Christmas[1], Katia Bougiouri[5], Reuben M. Buckley[4], Christophe Hitte[6], Anthony K. Nguyen[2], Chao Wang[1], Vidhya Jagannathan[7], Julia E. Niskanen[8], Laurent A. F. Frantz[9], Meharji Arumilli[8], Sruthi Hundi[8], Kerstin Lindblad-Toh[1,10], Catarina Ginja[11], Kadek Karang Agustina[12], Catherine André[6], Adam R. Boyko[13], Brian W. Davis[14], Michaela Drögemüller[7], Xin-Yao Feng[3], Konstantinos Gkagkavouzis[15], Giorgos Iliopoulos[16], Alexander C. Harris[4], Marjo K. Hytönen[8], Daniela C. Kalthoff[16], Yan-Hu Liu[3], Petros Lymberakis[17,18,19], Nikolaos Poulakakis[17,18,19], Ana Elisabete Pires[11], Fernando Racimo[5], Fabian Ramos-Almodovar[2], Peter Savolainen[20], Semina Venetsani[21], Imke Tammen[22], Alexandros Triantafyllidis[15], Bridgett vonHoldt[23], Robert K. Wayne[24], Greger Larson[25], Frank W. Nicholas[22], Hannes Lohi[8], Tosso Leeb[7], Ya-Ping Zhang[31] and Elaine A. Ostrander[4*†]

Genome Biol (2023) 24: 187

Acknowledgments

The authors would like to thank all dog owners and breeders for donating samples and information. The Australian Shepherd Club Switzerland is acknowledged for promoting the study and continued support throughout the project. Katharina Windbichler contributed to the pathological investigations of the stillborn puppies. We also wish to thank the Next Generation Sequencing Platform of the University of Bern for performing whole-genome sequencing experiments and the Interfaculty Bioinformatics Unit for providing high performance computing infrastructure. We acknowledge the DBVDC consortium, the Dog10K genomes project and all researchers who deposited dog or wolf whole genome sequencing data into public databases.

Swiss Digital Pathology Initiative

Inti Zlobec

Institute of Pathology, University of Bern

Head of Digital Pathology

The Swiss Digital Pathology Initiative (SDPI)

Prof. Inti Zlobec, on behalf of the Swiss Digital Pathology Consortium

Institute of Tissue Medicine and Pathology, University of Bern

ORDVET

08.12.2023

Agenda

- Short introduction Swiss Digital Pathology Consortium (SDiPath; www.sdipath.ch)
- Swiss Digital Pathology Initiative

SDiPath

Who are we?

- Founded 2018,
- WG SGPath,
- >170 members
- Benefit from each other's experiences in dig path /AI
- Pathologists, computer scientists, IT, technicians, biobankers, researchers

SDiPath

What do we do?

seminars

courses

Workshops

Industry Fairs (2)

SDiPath publications

What do we publish?

SPECTRUM PATHOLOGIE

Virchows Archiv (2022) 481:647–652
https://doi.org/10.1007/s00428-022-03345-0

« SPECTRUM Pathologie | Patho 01|20

Going

28. Oktober 2019

The proces
of a slide s
carry out th
componen
diagnostic

The field of pat
digital workflov
digital patholog
needed to unlo
remain fundam
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implementatior
management s
information tec
amounts of data typically generated in routine practices. In this short article, practical first-hand experiences are discussed to aid readers towards a smoother implementation of their own DP workflows.

Scanners and practical issues

BRIEF REPORT

Check for updates

Towards a national strategy for digital pathology in Switzerland

Andrew Janowczyk[1,2] · Daniel Baumhoer[3] · Stefan Dirnhofer[3] · Rainer Grobholz[4,5] · Anja Kipar[6] · Laurence de Leval[7] · Doron Merkler[8,9] · Olivier Michielin[1,10,11] · Holger Moch[12,13] · Aurel Perren[14] · Sven Rottenberg[15,16] · Laura Rubbia-Brandt[8,9] · Mark A. Rubin[16,17] · Christine Sempoux[7] · Markus Tolnay[3] · Inti Zlobec[14] · Viktor Hendrik Koelzer[4,12] · the Swiss Digital Pathology Consortium (SDiPath)

Author: Prof. Dr. Andrew Janowczyk
Precision Oncology Center, Department of Oncology, Lausanne University Hospital and Lausanne University, Switzerland

Koelzer VH, *et al. J Clin Pathol* 2022;**75**:687–689. doi:10.1136/jclinpath-2021-207768

Original research

Current opinion, status and future development of digital pathology in Switzerland

Julia Unternaehrer,[1] Rainer Grobholz,[2] Andrew Janowczyk,[3] Inti Zlobec ,[1] on behalf

J Clin Pathol. 2020 Jun;73(6):341-346. doi: 10.1136/jclinpath-2019-206155. Epub 2019 Dec 19.

Original research

us and future
Switzerland in

iec ,[4]
gy Consortium (SDiPath)

Swiss Digital Pathology Initiative (SDPI)

A national network for digital pathology

- DP represents a major technological advance for precision medicine
- Large, structured datasets are essential for competitive biomedical research and technology development
- National programs are crucial for the development, testing and validation of data-driven research tools and translation to clinical care
- Existing national programs in the UK, Germany, Sweden and the Netherlands are highly successful (research, education, IP, start-ups). Switzerland is losing ground

UK: Pathology Image Data Lake for Analytics Knowledge & Education (PathLAKE)
Germany: EcosysteM for Pathology Diagnostics with AI Assistance (EMPAIA)
Sweden: Linköping Digital Pathology Network
Netherlands: Pathology Image Exchange (PIE)
H2020 bigpicture:

Dutch national platform for sharing digital Pathology images

SDPI

Strategic importance

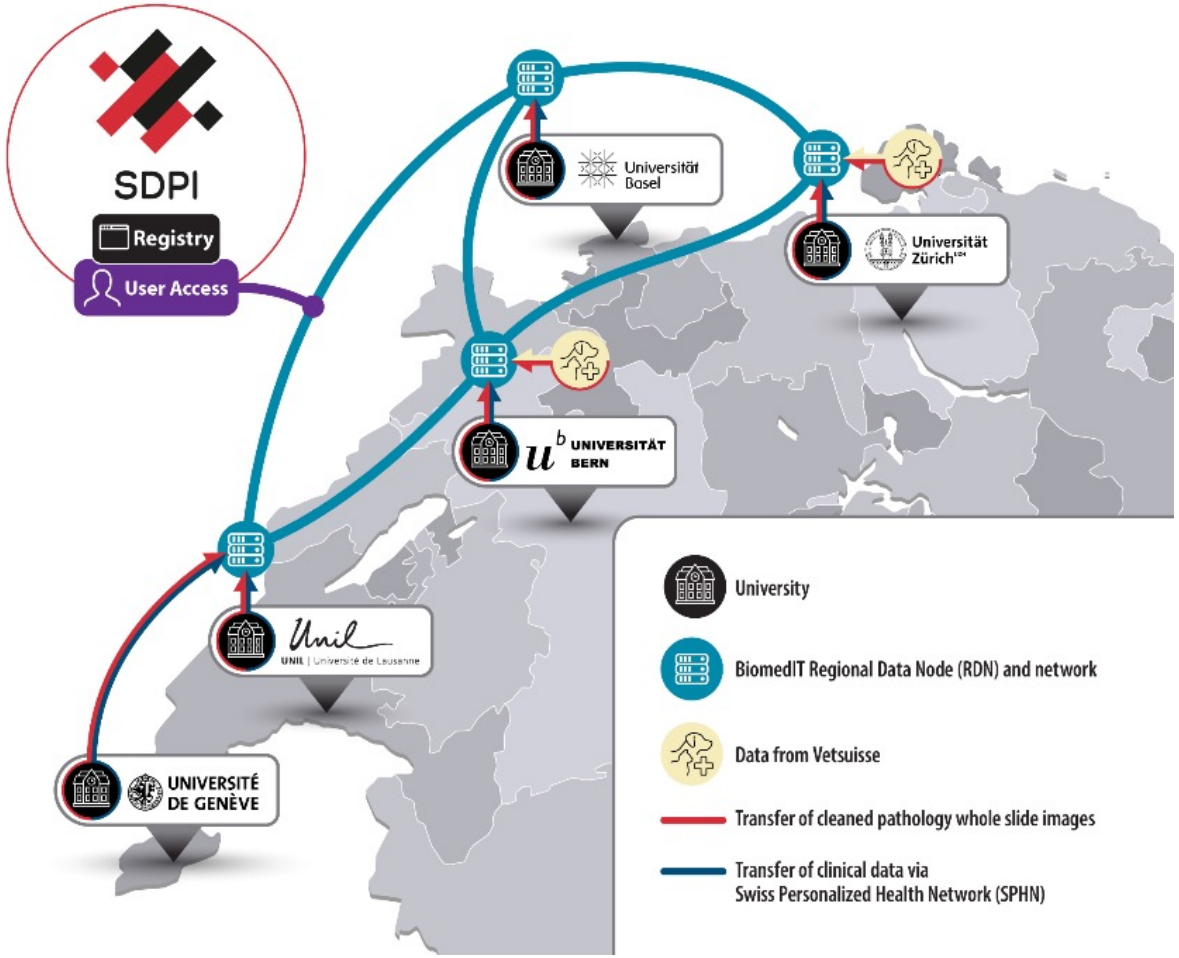
- To develop a **unified national DP network** bringing together the Swiss Personalized Health Network (SPHN) with Swiss university hospitals and subsequent inclusion of cantonal and private institutions

- SDPI is highly coherent with the **digitalization strategy** across Swiss University Centers and synergizes with investments for clinical data harmonization and enrichment

- SDPI directly addresses the needs of the national support initiative “Personalised Medicine” by providing unprecedented access to well-curated clinico-pathological datasets for biomedical research and technology development

Who does it involve?

5 University hospitals, 2 Vet faculties, with rollout potential



Coordination team:

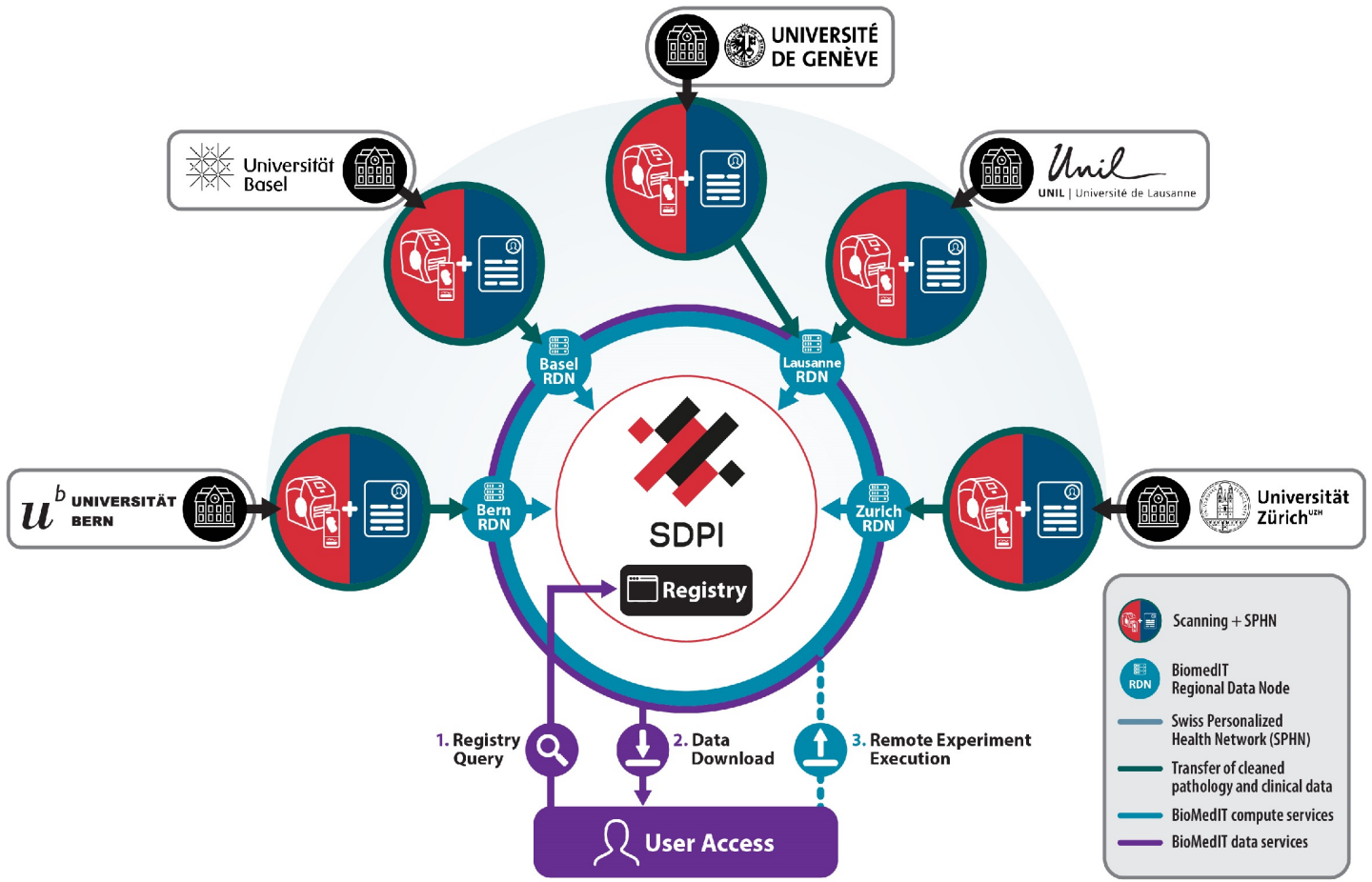
- Prof. V. Kölzer (UZH, lead), Prof. I. Zlobec (UniBe), Prof. A. Janowczyk (UniL/UniGe) on behalf of the Swiss Consortium of Digital Pathology

Investigators:

- UZH (Medical Faculty & Vetsuisse) – Profs. Moch, Kölzer, Kipar, Grobholz
- UniBas (Medical Faculty) – Profs. Tolnay, Baumhoer, Dirnhofer
- UniBe (Medical Faculty & Vetsuisse) – Profs. Perren, Zlobec, Rubin, Rottenberg
- UniL (Medical Faculty) – Profs. De Leval, Sempoux
- UniGe (Medical Faculty) – Profs. Rubbia Brandt, Merkler, Janowczyk
- SPHN/SPO – Profs. Michielin, Rubin

What is planned?

Commitment to Findable, Accessible, Interoperable, Reusable (FAIR) data usage



- **SDPI registry**: Single-access point for researchers across Switzerland to view, process, and download the SDPI data in a distributed manner.
- **Formation of one data hub** for all five Swiss Universities enabling the formation of internationally competitive research cohorts.
- **Planned expansion / offer to join** for cantonal and private institutions

→ **Any Swiss affiliated researcher** will have access to the entirety of the SDPI to engage in their own self-directed algorithm and biomarker studies/research

Swiss Roadmap for Research Infrastructure

2025-2028

- The Swiss Roadmap for Research Infrastructures is used to register newly planned or major upgrades of research infrastructures with national importance with the State Secretariat for Education, Research and Innovation (SERI).

"This project is of utmost importance for future translational projects"

Budget: "The level of investment seems appropriate and is comparable to other similar initiatives, such as the UK's PathLAKE with respect to the size of the population in Switzerland".

Koelzer, Virchows Arch, 2022


WE DID IT!
makeameme.org

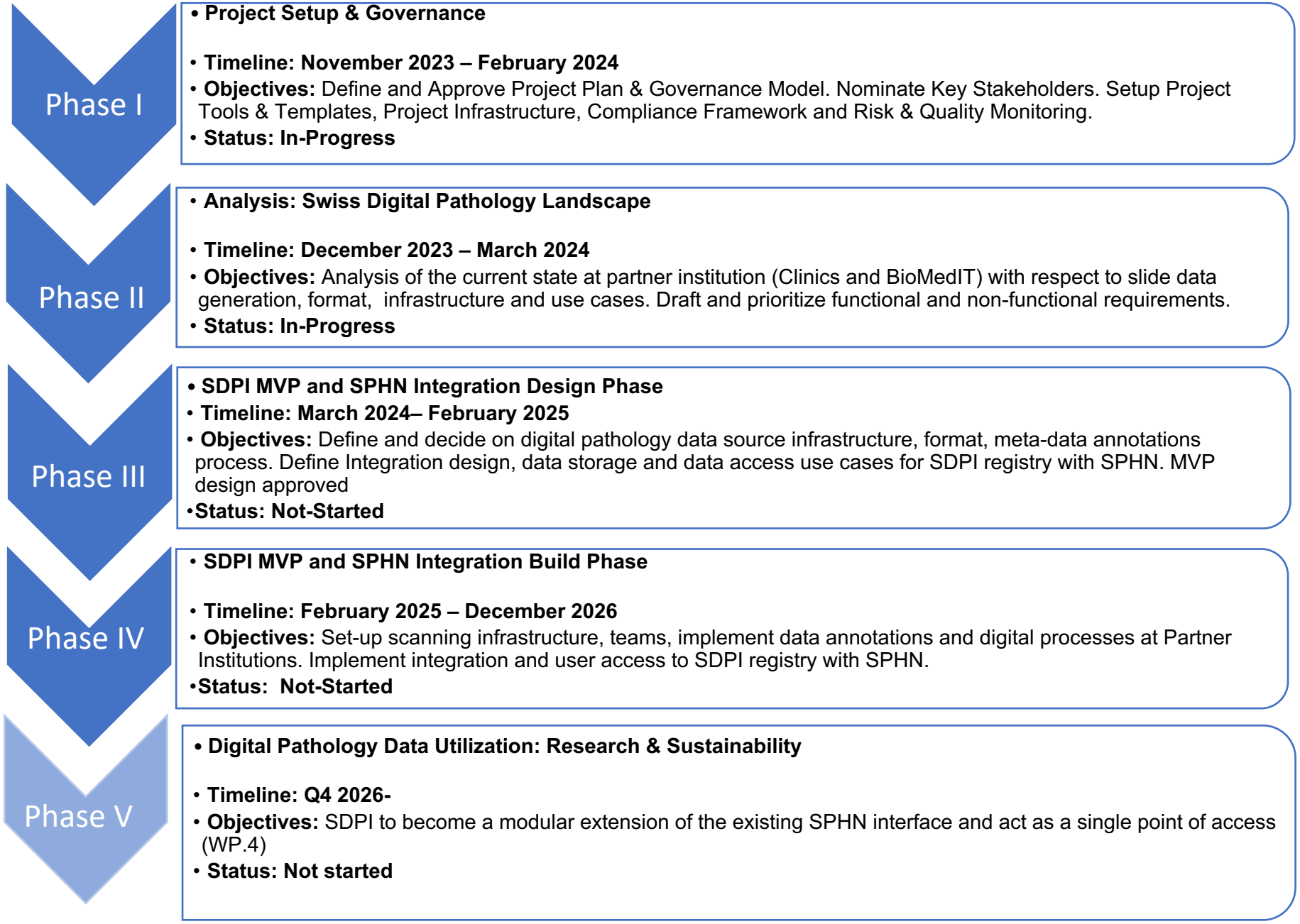
What's next?

Pre-project phase (2023-2024)

Additional funds from the University of Zurich (lead of SDPI) for:

- project management
- consultancy fees

Courtesy of Mitja Jahr, Project Manager, SDPI



Conclusion

- Digitisation at different levels throughout the country
- SDPI will support the digital transition at the University Hospitals and beyond
- SDPI aims together with SPHN to enhance Swiss research, development of AI tools, and the advancement of personalized medicine approaches by making available standardized pathology, clinical data, and corresponding images of tissues from patients across Switzerland

Thank you for your attention

Questions ?

https://www.digitalpathologybern.com/

ORDVET survey - results (part 2)

Elena Dhein

Institute of Veterinary Pathology, Vetsuisse Faculty, University of Zurich

Postdoctoral researcher

Survey: Status quo at the Vetsuisse Faculty

- Online survey (1st July 2023 – 15th September 2023)
- Distributed among the employees at the Vetsuisse Faculty
- Up to 19 questions
- 212 participants (167 total answers, 45 partial answers)
- 2 parts:
  1. Open Research Data (general)
  2. Data standardization/vocabularies

Status quo at the Vetsuisse Faculty

Do you standardize the (meta)data when it is generated and/or stored? If yes, how do you achieve this? (absolute numbers)

Data standardization	Generating data	Storing data	Not used
Official, standardized data format (e.g. sequence data, image data)	58	69	85
Own system for standardization of metadata (e.g. drop-down list for animal breeds)	31	40	141
Own system for standardization of data (e.g. drop-down list for diagnoses)	27	32	153
Official classification system (e.g. SNOMED-CT, ICD-11, Vet-ICD-O-canine-1)	13	10	189
Official coding system (e.g. SNOMED-CT, ICD-11, Vet-ICD-O-canine-1)	8	13	191

Status quo at the Vetsuisse Faculty

Do you think systems for standardizing (meta)data are useful in everyday life? (%)

	Yes	No	N/A
Yes, if intuitive to use.	**48**	31	21
Yes, even if there is a little extra effort required.	27	**52**	21
No, I think it is too complicated.	8	**71**	21

Status quo at the Vetsuisse Faculty

Thank you! ☺

Survey questions and structure available in the padlet:
https://padlet.com/ORDVET/open_research_data_vetsuisse

Introduction: Vetsuisse Biobanking Information Management System

Franco Guscetti

Institute of Veterinary Pathology, Vetsuisse Faculty, University of Zurich

Contents

- IT structure
- Data structure
- Special features
- Contractual conditions & costs

Vision: The Vetsuisse Biobanking Information System (Vetsuisse BIMS) is a professional software offering cutting-edge biobanking functions. It is accessible to any unit at the Vetsuisse Faculty both in Bern and Zurich wishing to participate in order to manage biological samples and to allow and facilitate their sharing.

DiData

https://swissdidata.com/

Currently affiliated biobanks (biocollections):

Vet-Path-ZH, Institute of Veterinary Pathology, University of Zurich

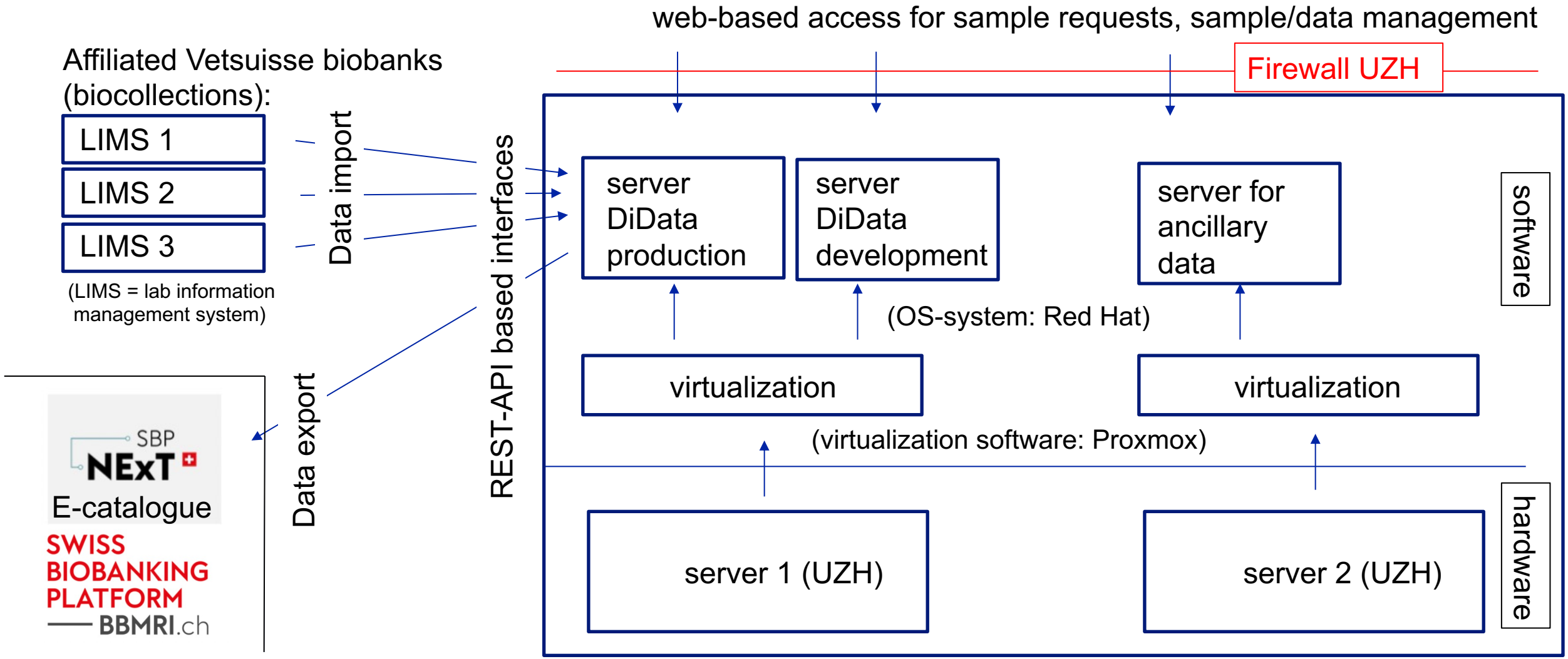
Vet-Lab-ZH, Veterinär-medizinisches Labor, University of Zurich

Vet-Gen-BE, Institute of Genetics, University of Bern

Vet-Path-BE, Institute of Animal Pathology, University of Bern

Vet-Neuro-BE, Division of Neurological Sciences, University of Bern

Vetsuisse BIMS – IT structure



Vetsuisse BIMS – Data structure production system

Open partition

project SMD (shared minimal dataset)

access: all Vetsuisse researchers, read-only, upon request of a User name

To search for and ordering of samples

- breed
- age
- sex
- other non-personal sample-related data

Vetsuisse BIMS – Data structure production system

Open partition

project SMD (shared minimal dataset)

access: all Vetsuisse researchers, read-only, upon request of a User name

To search for and ordering of samples

- breed
- age
- sex
- other non-personal sample-related data

Restricted-access partitions of affiliated biobanks

access: affiliated biobanks have exclusive read & write rights for the own project

Data and sample management

project Vet-Gen-BE

- breed
- age
- sex
- other n non-personal sample-related data

personal data, e.g.:
- owner's name
- (chip-nr.)

Further collection-specific data
- attribute x1
- attribute x2
- attribute x3

access: only Vet-Gen-User

various roles (technician, researcher…)

Vetsuisse BIMS – Data structure production system

Open partition

project SMD (shared minimal dataset)

access: all Vetsuisse researchers, read-only, upon request of a User name

To search for and ordering of samples

- breed
- age
- sex
- other non-sensitive sample-related data

Restricted-access partitions of affiliated biobanks

access: affiliated biobanks have exclusive read & write rights for the own project

Data and sample management

project Vet-Gen-BE

- breed
- age
- sex
- other non-personal sample-related data
- personal data, e.g.:
  - owner's name
  - (chip-nr.)
- Further collection-specific data
  - attribute x1
  - attribute x2
  - attribute x3

access: only Vet-Gen-User

various roles (technician, researcher…)

project Vet-Path-ZH

- breed
- age
- sex
- other non-personal sample-related data
- personal data, e.g.:
  - owner's name
  - (chip-nr.)
- Further collection-specific data
  - attribute x1
  - attribute x2
  - attribute x3

Vetsuisse BIMS – Data structure production system

Open partition

project SMD (shared minimal dataset)

access: all Vetsuisse researchers, read-only, upon request of a User name

To search for and ordering of samples

- breed
- age
- sex
- other non-personal sample-related data

Restricted-access partitions of affiliated biobanks

access: affiliated biobanks have exclusive read & write rights for the own project

Data and sample management

project Vet-Gen-BE

- breed
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- Further collection-specific data
  - attribute x1
  - attribute x2
  - attribute x3

access: only Vet-Gen-User

various roles (technician, researcher…)

project Vet-Path-ZH

- breed
- age
- sex
- other non-personal sample-related data
- personal data, e.g.:
  - owner's name
  - (chip-nr.)
- Further collection-specific data
  - attribute x1
  - attribute x2
  - attribute x3

Restricted-access partition

project DC (duplicate check)

access: semi-automated system, superadministrator has read & write rights

Duplicate check = identification of samples from the same animal

- breed
- age
- sex
- personal data, e.g.:
  - owner's name
  - owner's address
  - (chip-nr.)
  - (medical record nr.)
  - (animal's name)

Vetsuisse BIMS – Data structure of the production system - Summary

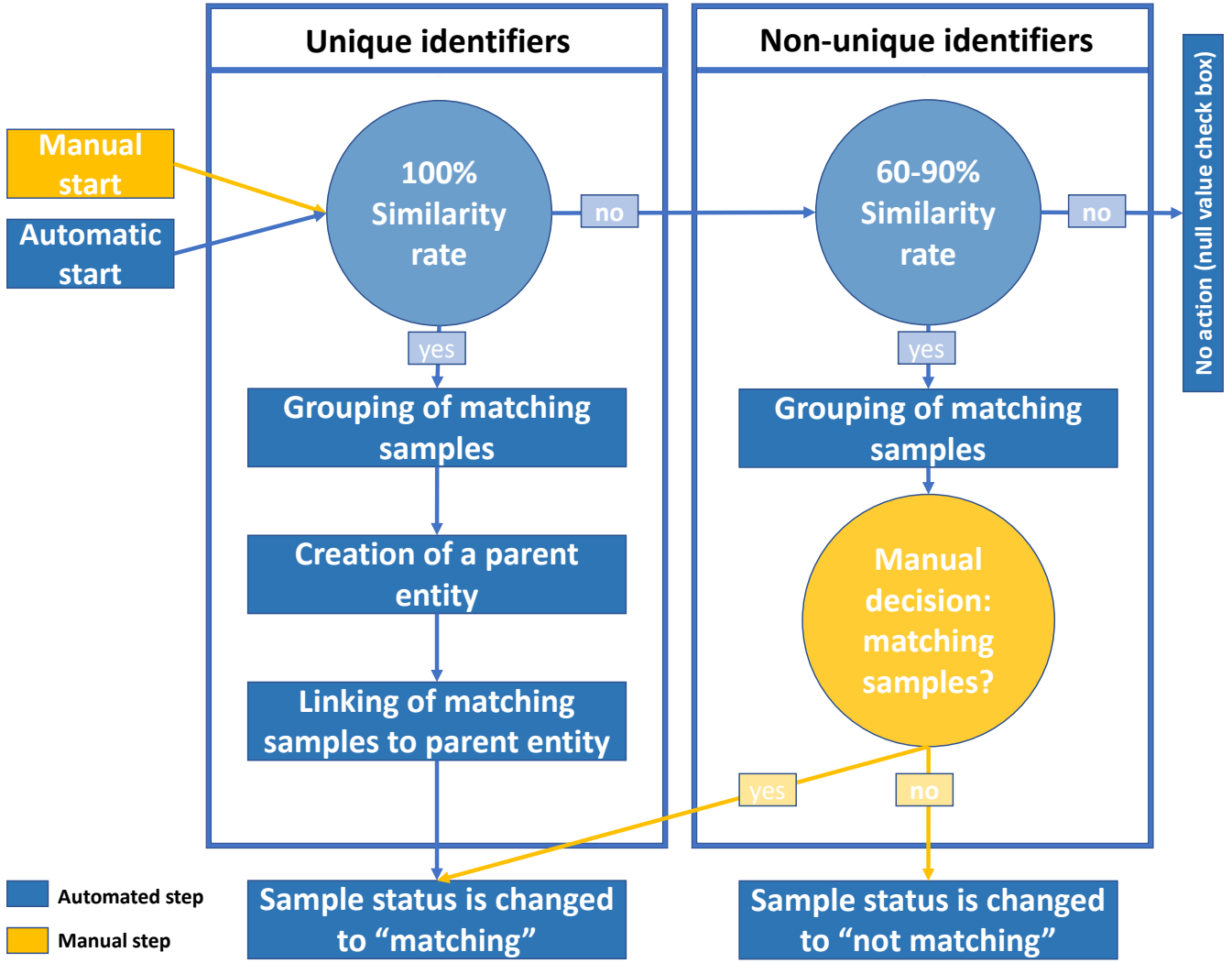
- Each partner biocollection manages probes and data in an own project.
- The own project contains non-sensitive, sensitive and further own data.
- The partner own projects can only be accessed by members of the own unit.
- The SMD project contains non-sensitive, sample-related data. The samples shown are cleared by the project owners.
- The SMD contents are exported to the NExT SBP catalogue.
- The project Duplicate Check has the scope to identify samples of the same animal within and across collections. Only a superadministrator has access to this semi-automated process.

Vetsuisse BIMS - Special features: Synonyms

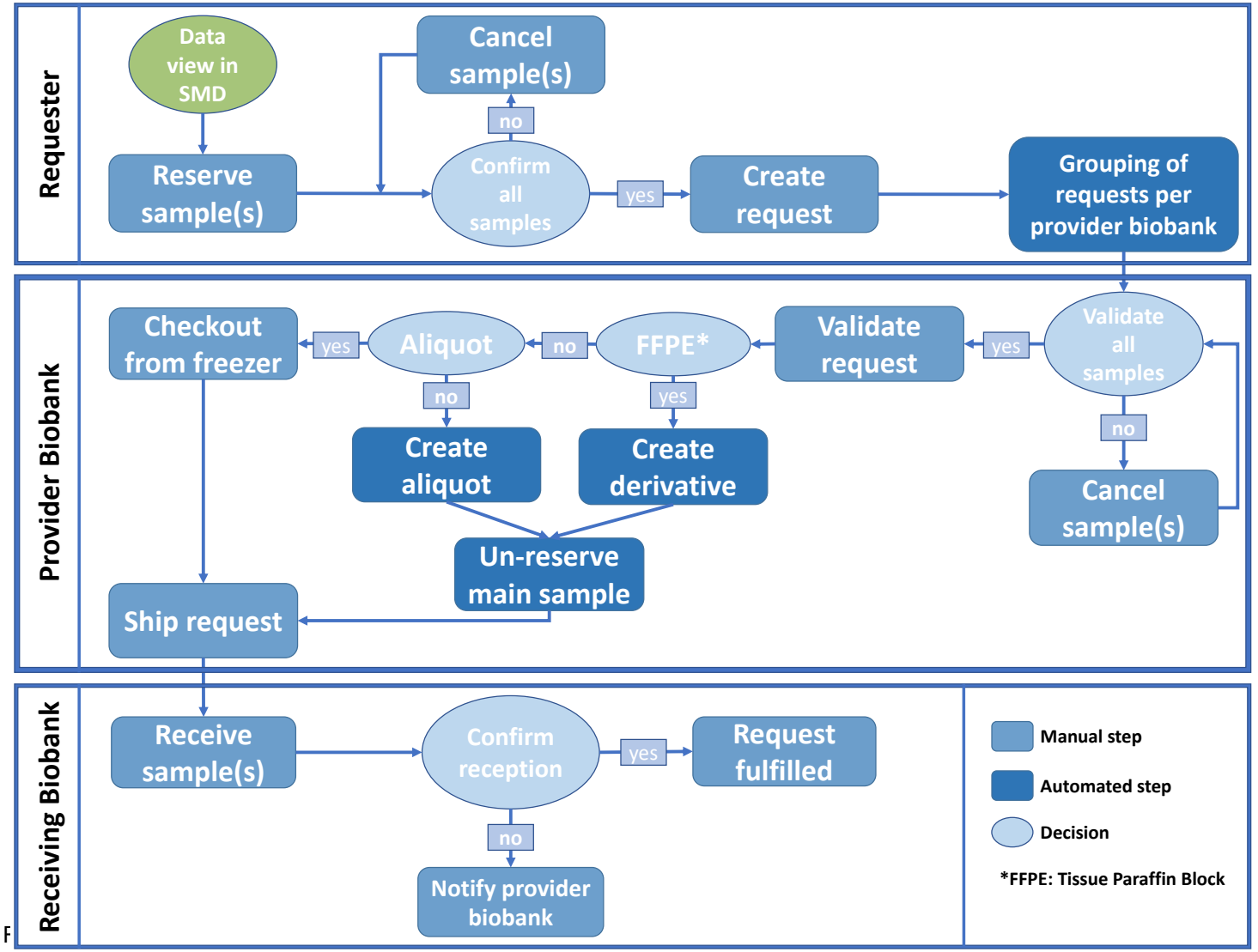
Export | Import | + Create | Refresh | Search entities

(0)	Breed value	Breed name - calculated	Owner Land	Land owner calculated
	Chodenländerhund	Chodenland Dog/ Chodský pes (364)	Schweiz	Switzerland (CH)
	Chodský pes	Chodenland Dog/ Chodský pes (364)	Italien	Italy EU (IT)
	Nova Scotia Duck Tolling	Nova Scotia Duck Tolling Retriever (312)	Deutschland	Germany EU (DE)
	Böhmischer Schäferhund	Chodenland Dog/ Chodský pes (364)	CH	Switzerland (CH)
	Mops	Pug (253)	IT	Italy EU (IT)
	Schweizer Schäferhund	Berger Blanc Suisse (347)	Frankreich	France EU (FR)

Vetsuisse BIMS - Special features: «Duplicate check»



Vetsuisse BIMS - Special features: Requests management



Vetsuisse BIMS – Contractual conditions & costs

- All costs of the current configuration are covered until march 31st 2027.
- The price of 950 CHF (w/o VAT) per licence and year (entailing a 20% discount on listed prices) is guaranteed for the following 5-year period as well.
- Access to all upgrades is guaranteed.
- If number of licences reaches 25 (up to 50): a flat-rate 25’000 CHF (w/o VAT) per year applies.
- In case Vetsuisse terminates the contract: BIMS can be used only in read-only mode.
- If a partner biocollection wishes to abandon the BIMS: the totality of the data can be exported as Excel files.

Any questions or comments?

The financial support from the SNSF (Project Biolink 31BL30_189698) is kindly acknowledged.

Biobanking Information Management System User Interface

Elena Dhein

Institute of Veterinary Pathology, Vetsuisse Faculty, University of Zurich

Postdoctoral researcher

Universität Zürich[UZH]

UNIVERSITÄT BERN

Biobanking Information Management System for the Vetsuisse Faculty

ACCREDITED BY EAEVE/FVE

Universität Bern | Universität Zürich
vetsuisse-fakultät

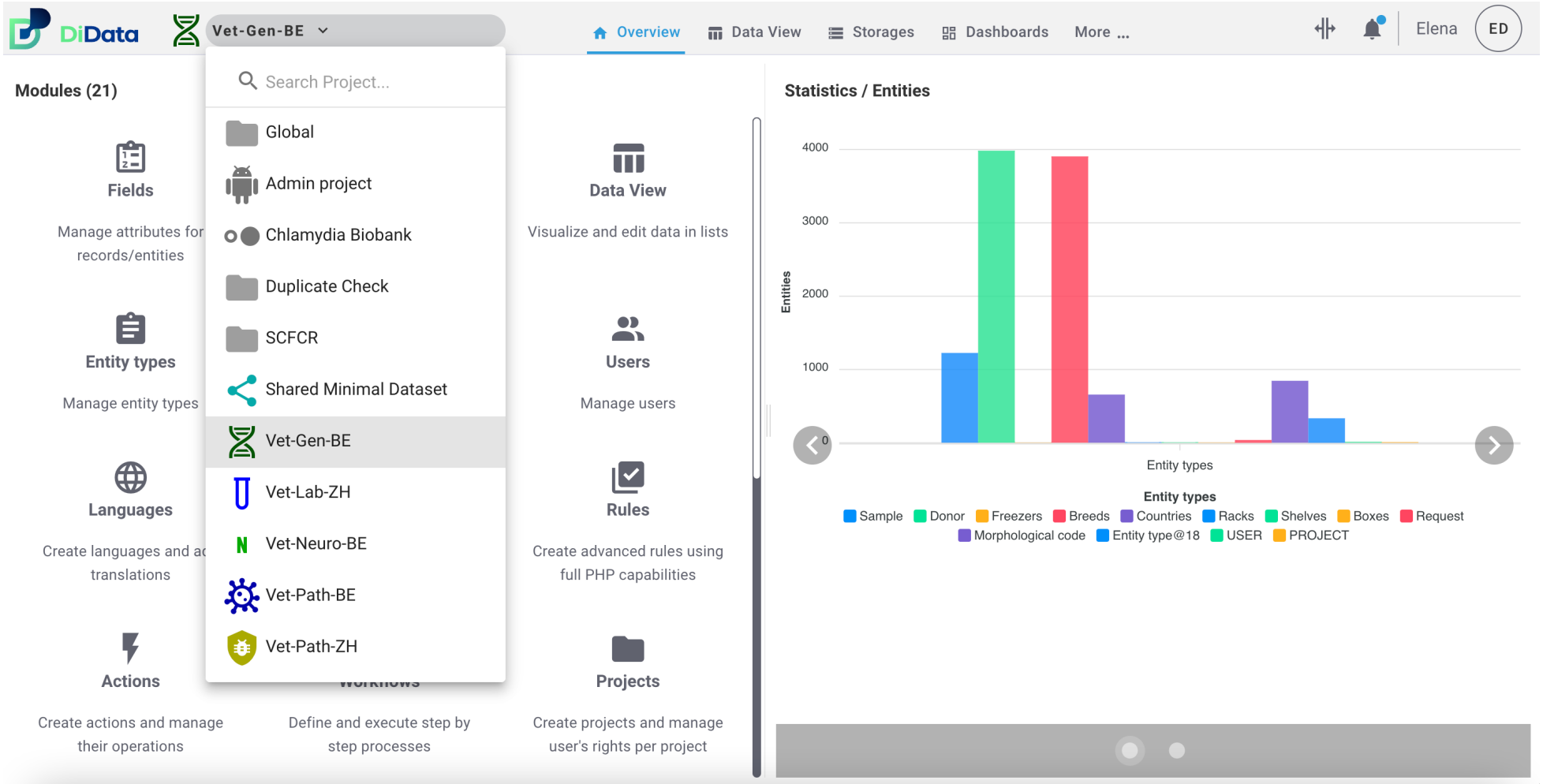
Outline

1. General user interface
2. Features:
   - Storages
   - Workflows
   - Data standardization (vocabulary and codes)
   - Samples from same donor
3. Sample request:
   - How to search for samples
   - How to request samples
   - Processing of requested samples
4. Summary

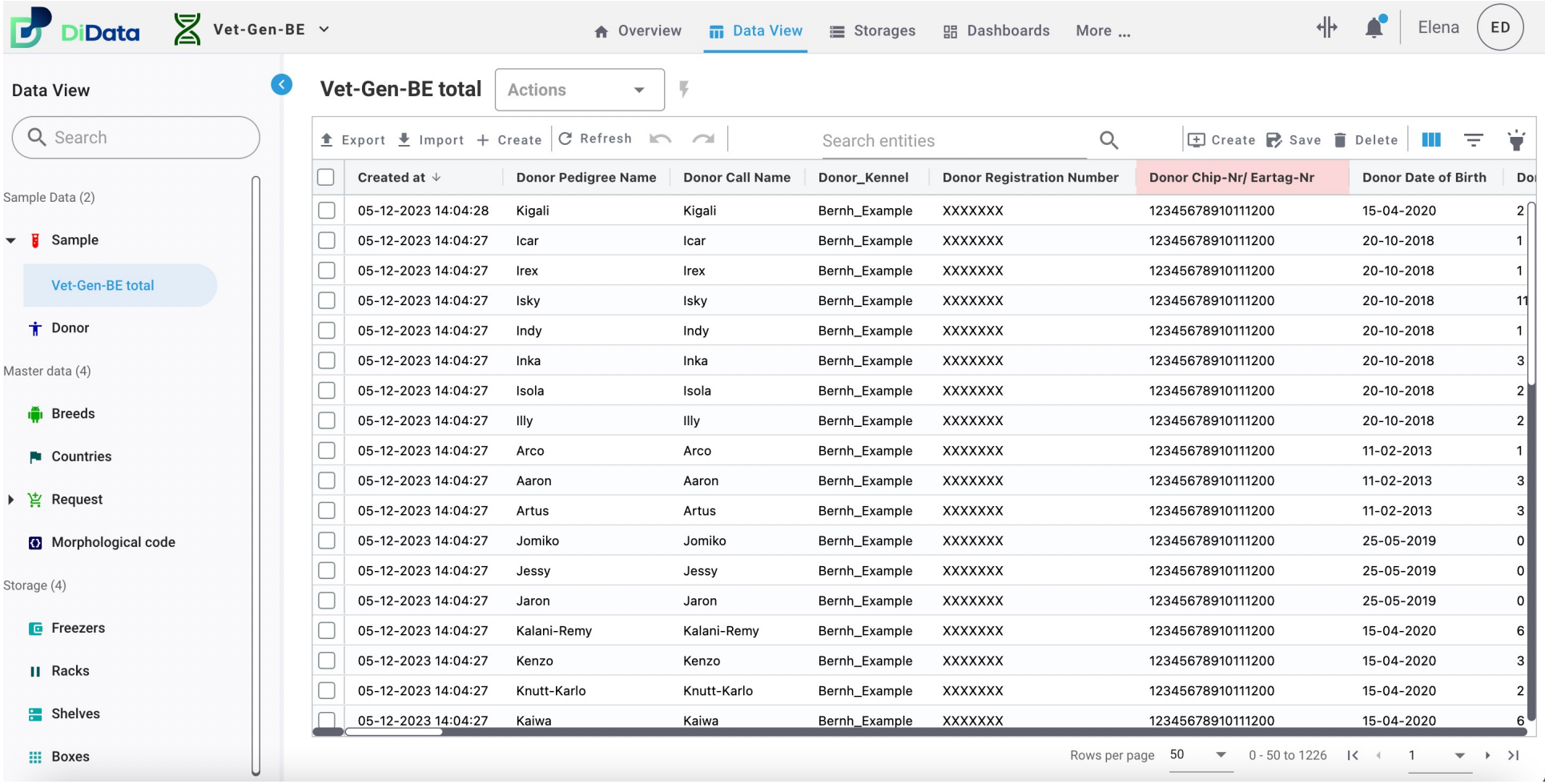
Vetsuisse researcher

Biobank members

1. User interface – Projects

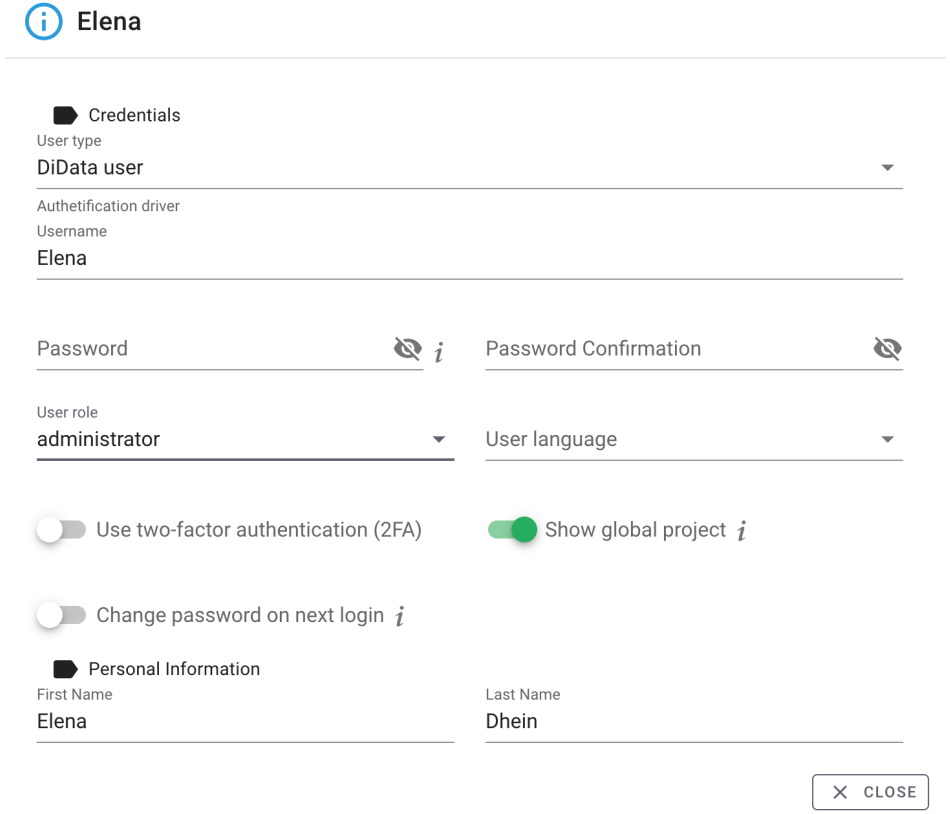


1. User interface – Data view



1. User interface – Users

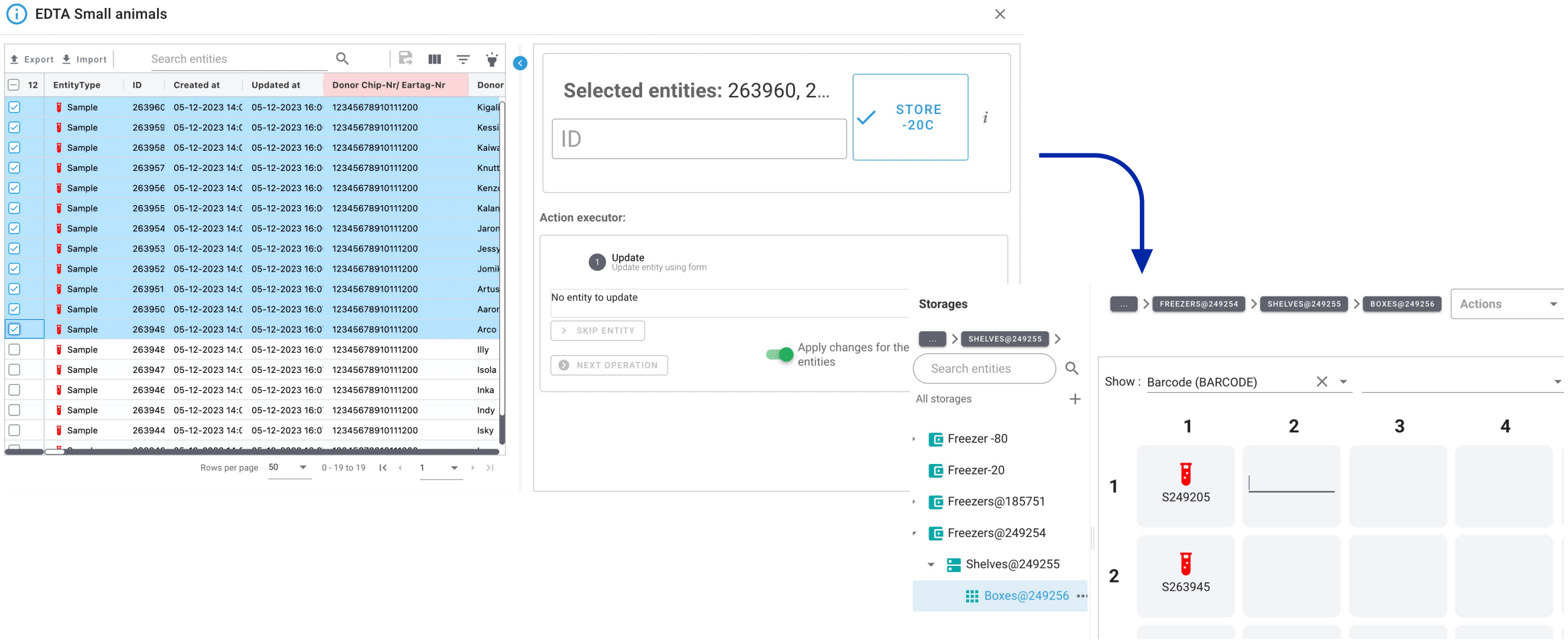
User:



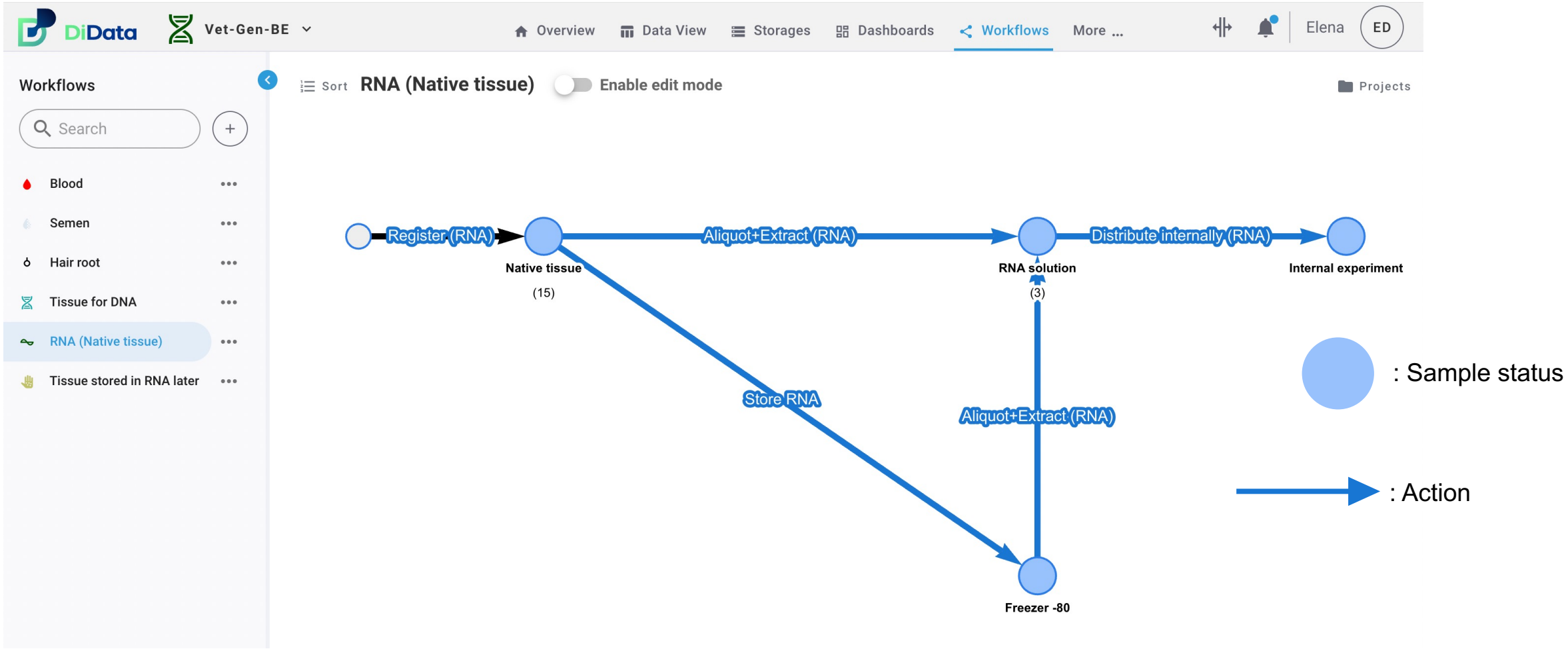
Roles/Permissions:

Permission	Public role	administrator	Project user	Super Administrator	importbot
Access to sensitive fields	No	Yes	No	Yes	Yes
Manage all projects	No	Yes	No	Yes	No
Create field	No	Yes	No	Yes	No
Edit field	No	Yes	No	Yes	No
Delete field	No	Yes	No	Yes	No
Batch import of fields	No	Yes	No	Yes	No
Batch export of fields	No	Yes	No	No	No
Edit field dynamic tooltip	No	Yes	No	Yes	No
Create entity type	No	Yes	No	Yes	No
Edit entity type	No	Yes	No	Yes	No
Delete entity type	No	Yes	No	Yes	No
Manage entity type order	No	Yes	No	Yes	No
Configure study entitytype manager	No	Yes	No	Yes	No
Create entity	Yes	Yes	Yes	Yes	Yes
Batch import of Entities	No	Yes	Yes	Yes	Yes
Export entities	No	Yes	Yes	Yes	No
Edit entity	No	Yes	Yes	Yes	Yes
Delete entity	No	Yes	Yes	Yes	No

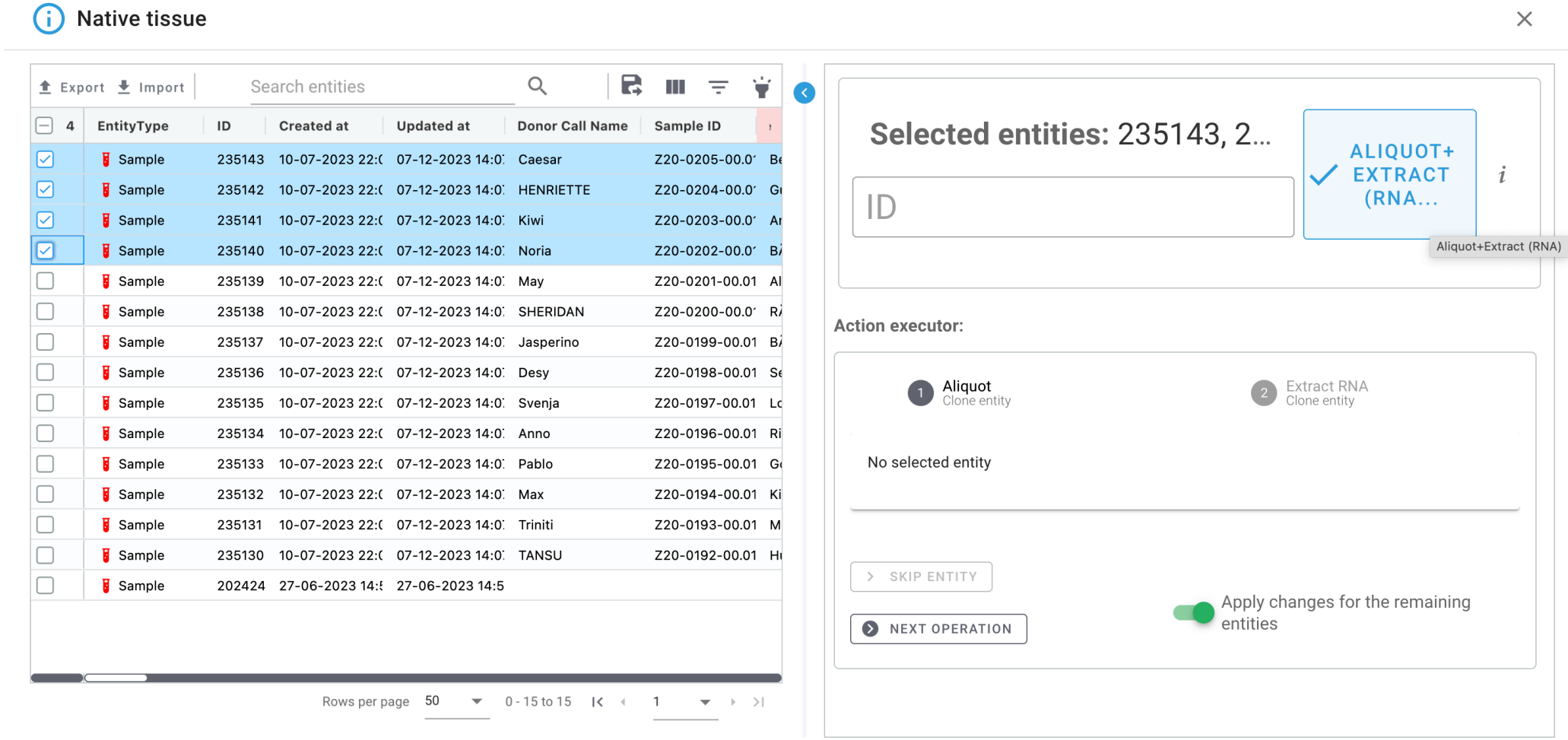
2. Features – Storages



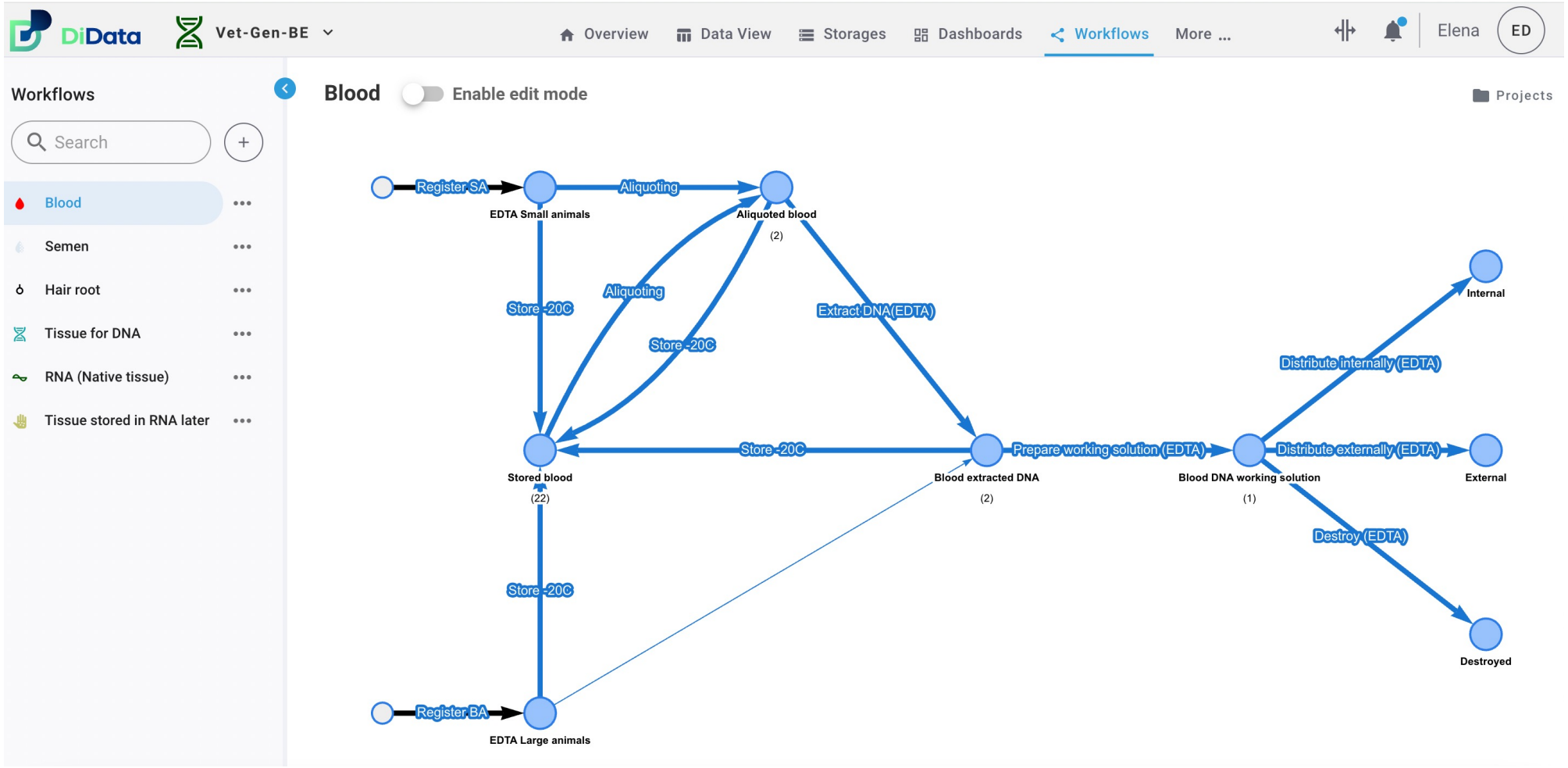
2. Features – Workflows



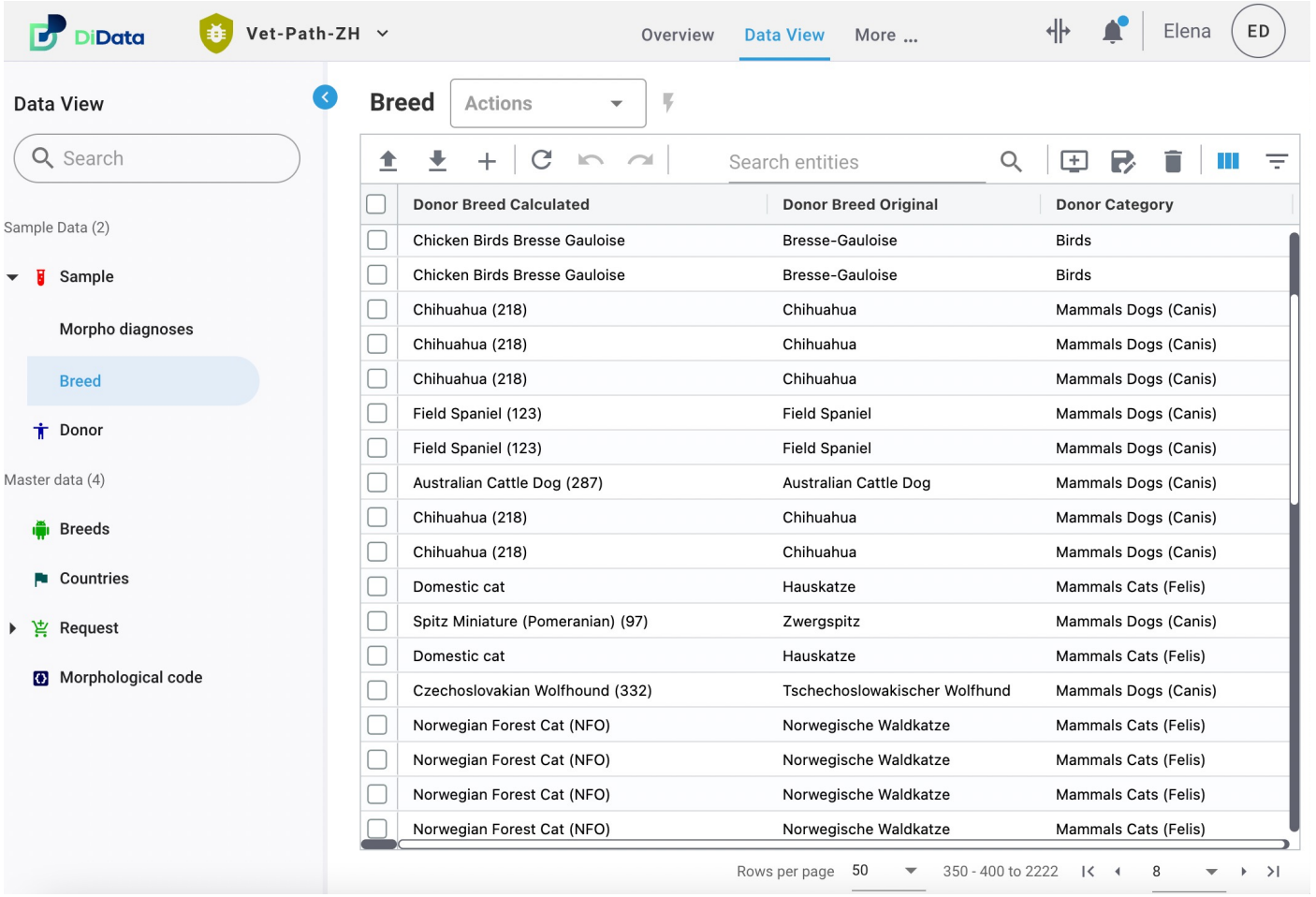
2. Features – Workflows (Action)



2. Features – Workflows



2. Features – Data standardization (Breeds)



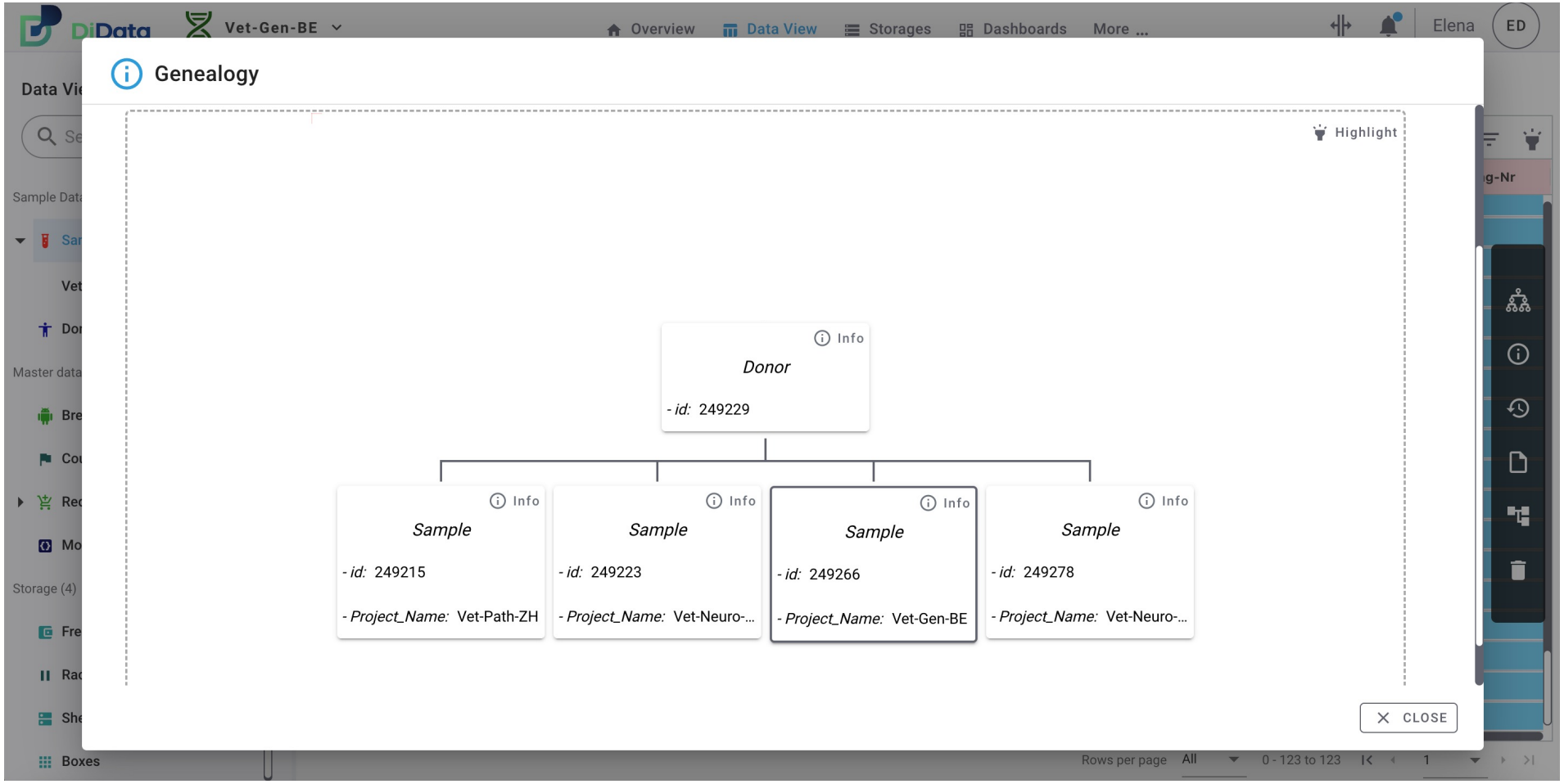
2. Features – Data standardization (Morphologies)

Sample Actions

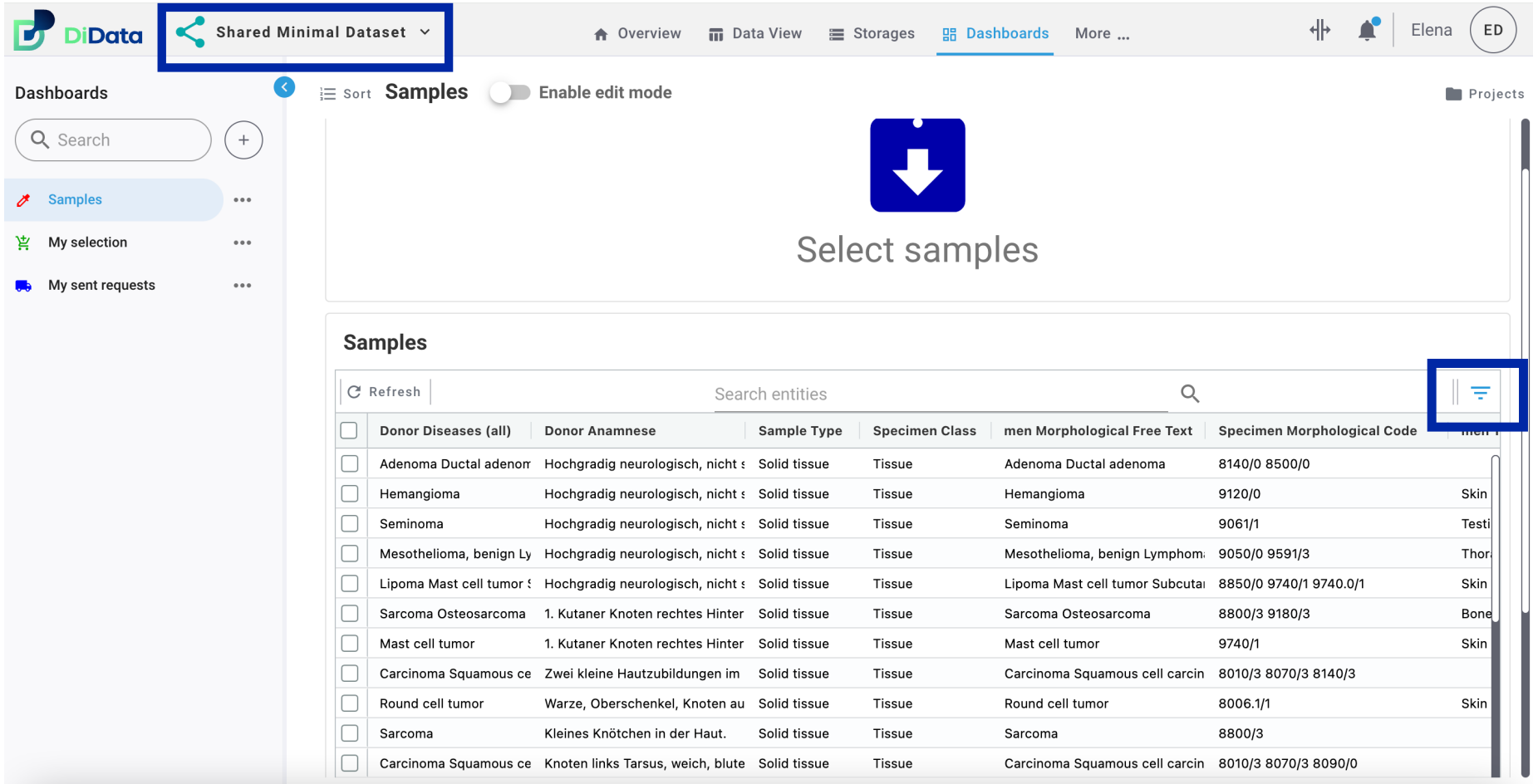
Export Import Create Refresh Search entities Custom View Save Columns

Specimen Morphological All Text	Specimen Morphological Free Text	Specimen Morphological Code
Adenoma, vollständig exzidiert Kommentar: Es handelt sich um eine benigne, von Schweissdrüsen ausgehende	Adenoma	8140/0
- Spleen: Focal hemangioma, NOS - Right ovary: Multiple follicular cysts¶- Left ovary: No histological change is	Hemangioma	9120/0
Interstitial cell tumour and intratubular Seminoma, NOS ¶¶Comment: Testicular neoplasias of the dog have a lov	Seminoma	9061/1
Rectum: The tissue specimen consists of highly edematous submucosa, which is covered by stratified, non-kera	Carcinoma Leydig cell tumor Seminoma	8010/3 8650/1 9061/1
lymphoma Spleen - non-diagnostic¶¶Immunocytochemistry can be attempted if further differentiation is require	Mesothelioma, benign Lymphoma	9050/0 9591/3
- Right leg: subcutaneous mast cell tumor, MItotic rate: 3 per 10 high power fields, complete excision¶- Thorax	Lipoma Mast cell tumor Subcutaneous m	8850/0 9740/1 9740.0/1
Peritoneum All tissue specimens have similar histological features, and are comprised of a core of fibrovascular	Sarcoma Osteosarcoma	8800/3 9180/3
in the center of the latter tissue sample there is a non-encapsulated, well-demarcated mass in the dermis. The	Mast cell tumor	9740/1
Tumour lesion from the nasal cavity, carcinoma ¶¶Comment.¶The histological examination revealed a neoplastic	Carcinoma	8010/3
Round cell tumor , possibly histiocytoma in regression with spindle cells proliferation¶¶Comment: A cutaneous l	Round cell tumor	8006.1/1
The subcutis and deep dermis are infiltrated and replaced by a multinodular mass composed of plump to elonga	Sarcoma	8800/3
- Skin tumor: Cutaneous basilar epithelial neoplasm (previously known as basal cell tumor) with mild cellular ne	Basal cell tumor	8090/0
All three biopsies display a multifocal-coalescing severe infiltrate of histiocytes (mainly macrophages, few supe	Canine cutaneous histiocytoma	9751.1/0
Carcinoma with moderate mixed-cell inflammation with prevalence of neutrophils	Carcinoma	8010/3
Sarcoma - The macroscopically described neoplasm is relatively well demarcated, unencapsulated, invasively g	Sarcoma	8800/3
The dermis is focally expanded by a cell-dense, wedge-shaped proliferation of intermediate size round cells grc	Canine cutaneous histiocytoma	9751.1/0
B-cell lymphoma ¶¶Comment: The neoplastic population was observed in multiple lymph nodes, histology and i	Lymphoma B-cell lymphoma	9591/3 9591.1/3
Lung: Neoplastic cells infiltrating replace the lung. There is no encapsulation. The neoplastic cells form a solid r	Neoplasm, metastatic Carcinoma	8000/6 8010/3

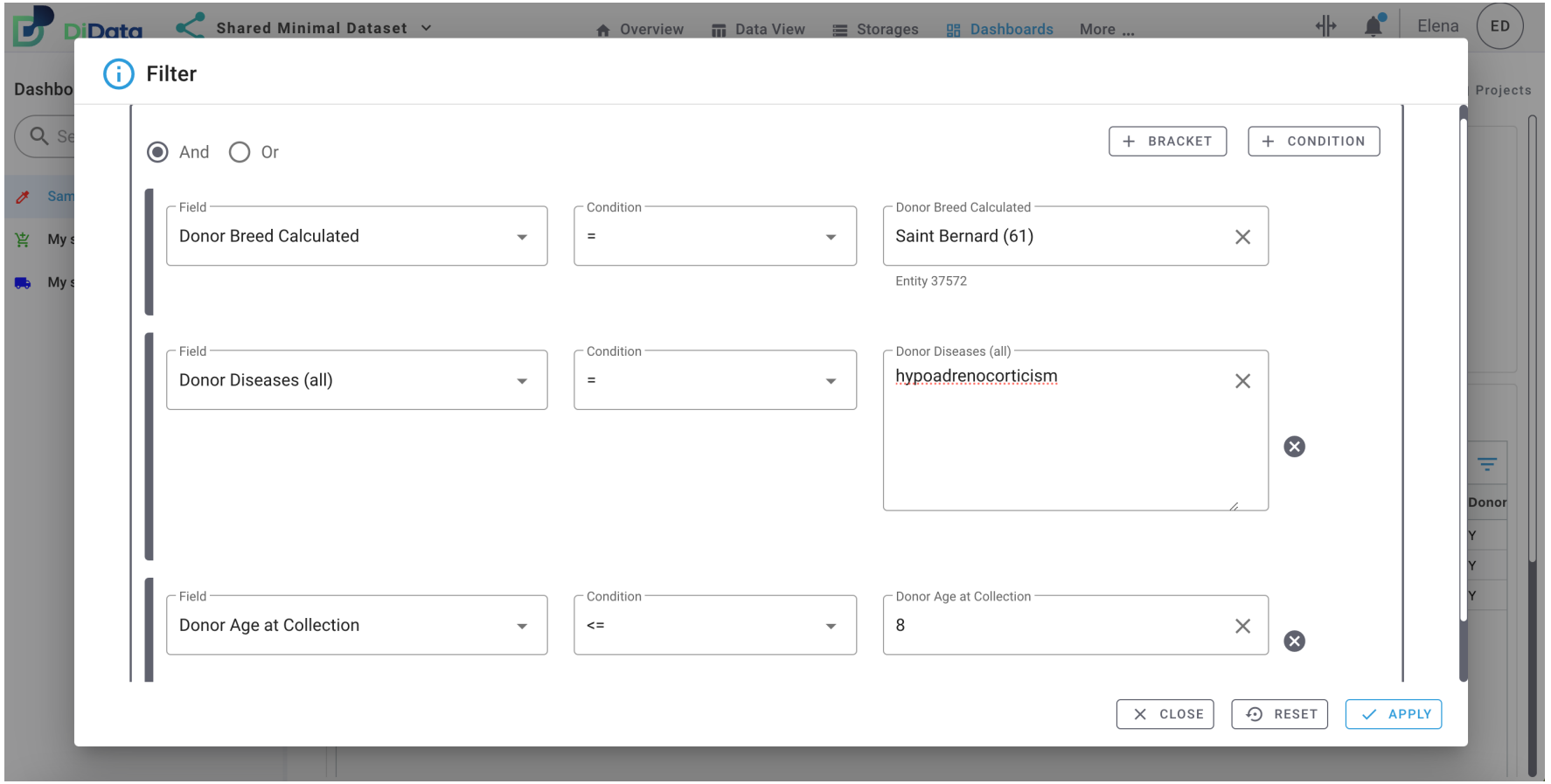
2. Features – Samples from the same donor



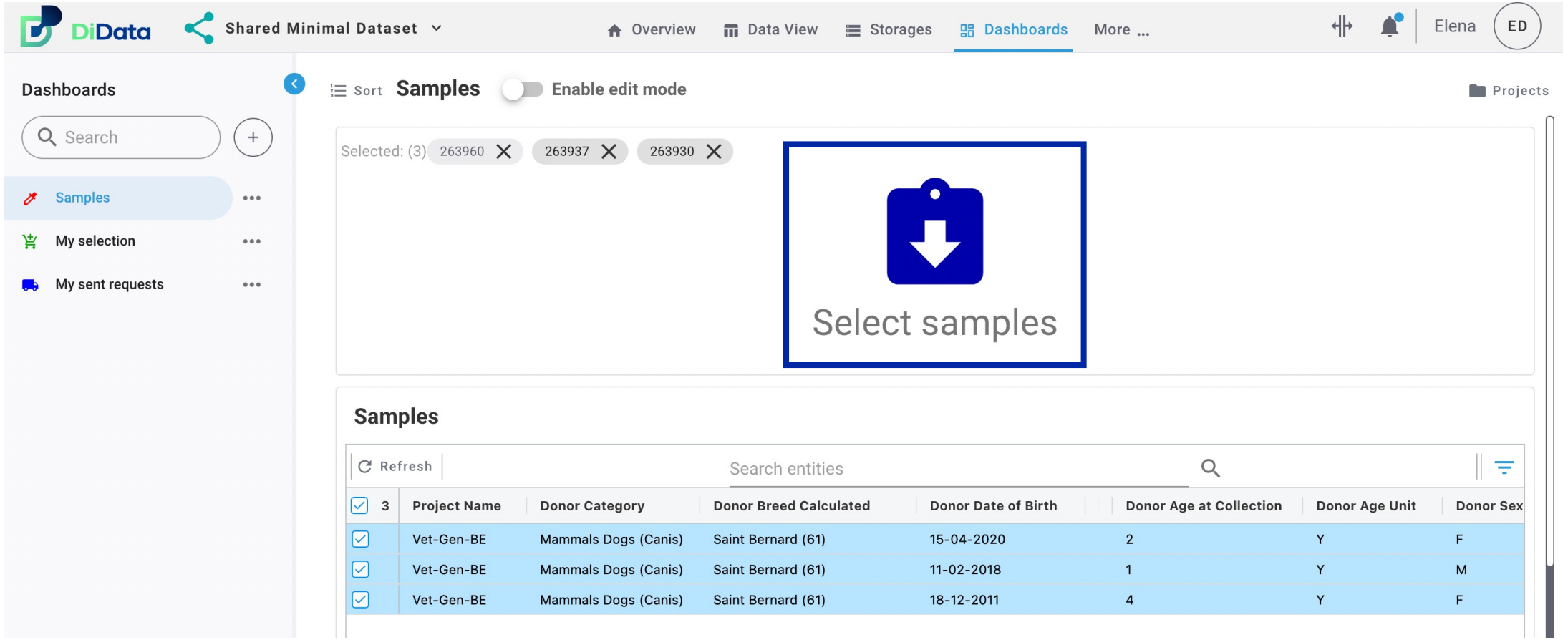
3. Sample requests – How to search samples



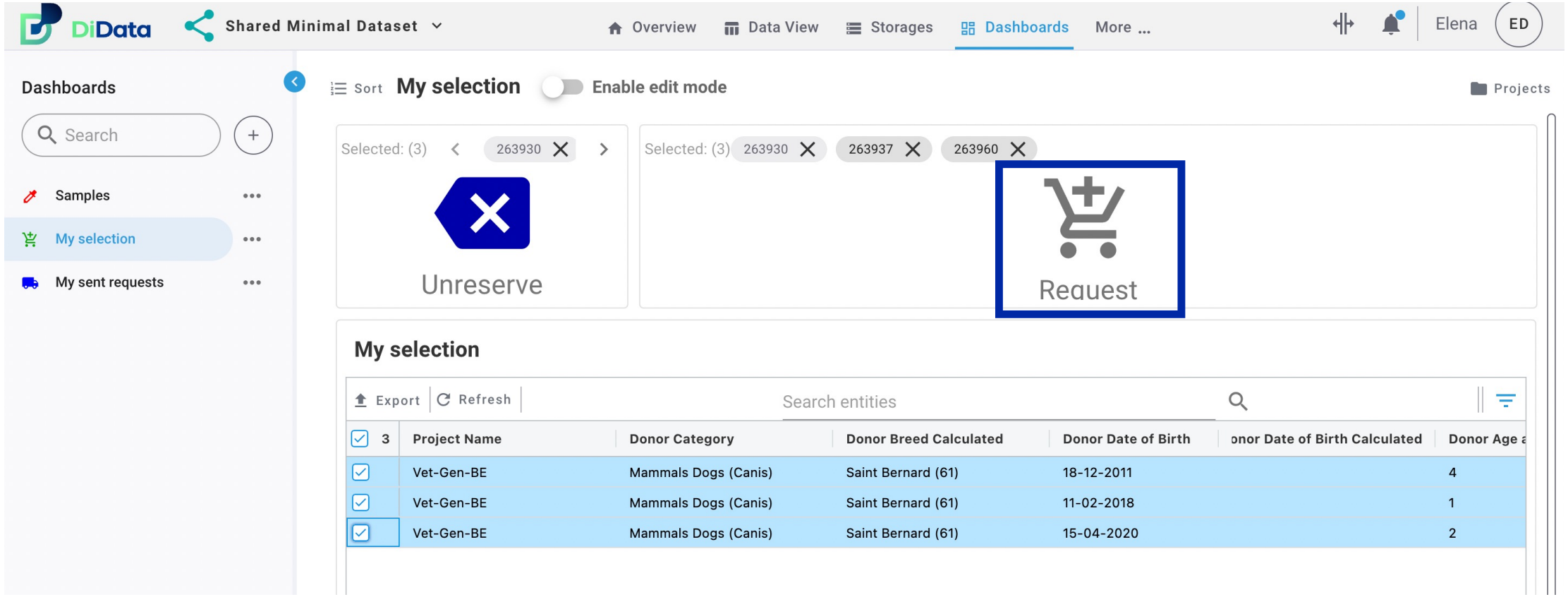
3. Sample requests – How to search samples (Filter)



3. Sample requests – How to search samples (Selection)

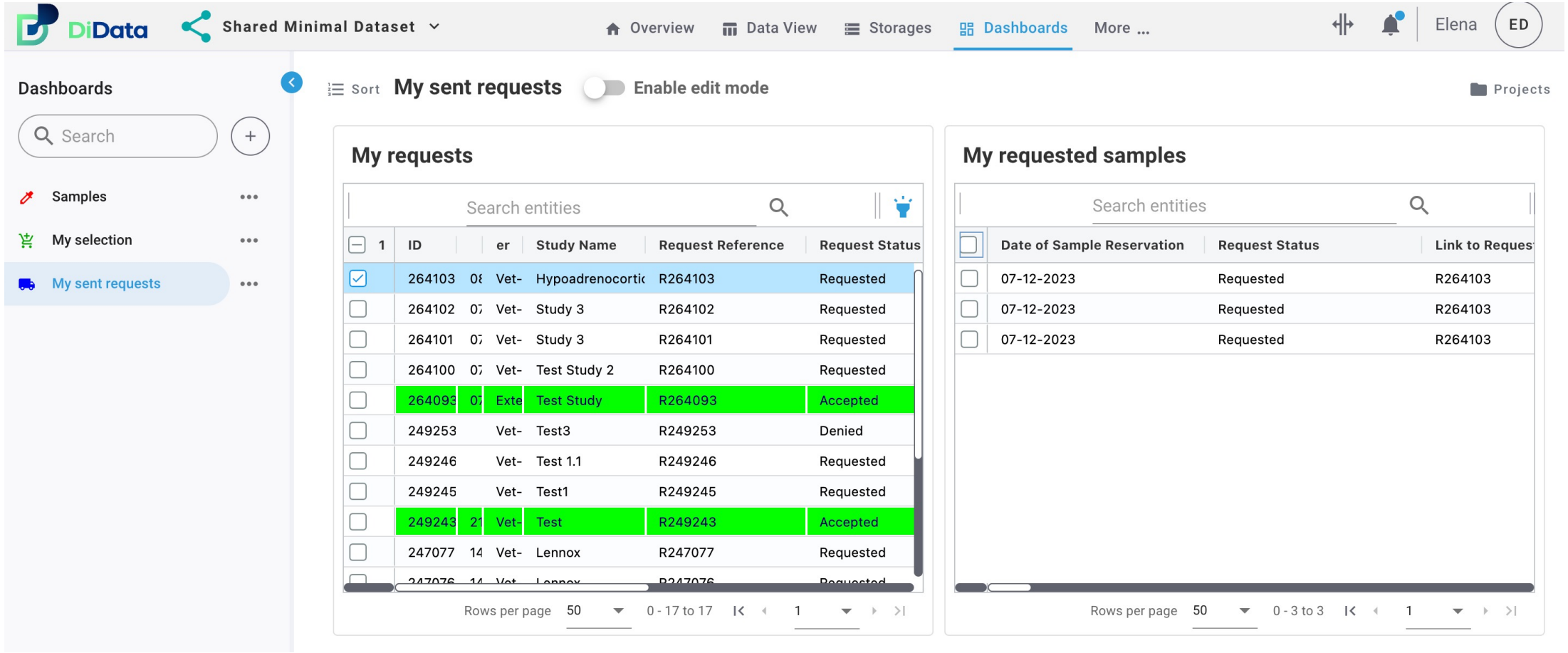


3. Sample requests – How to request samples (Selection)

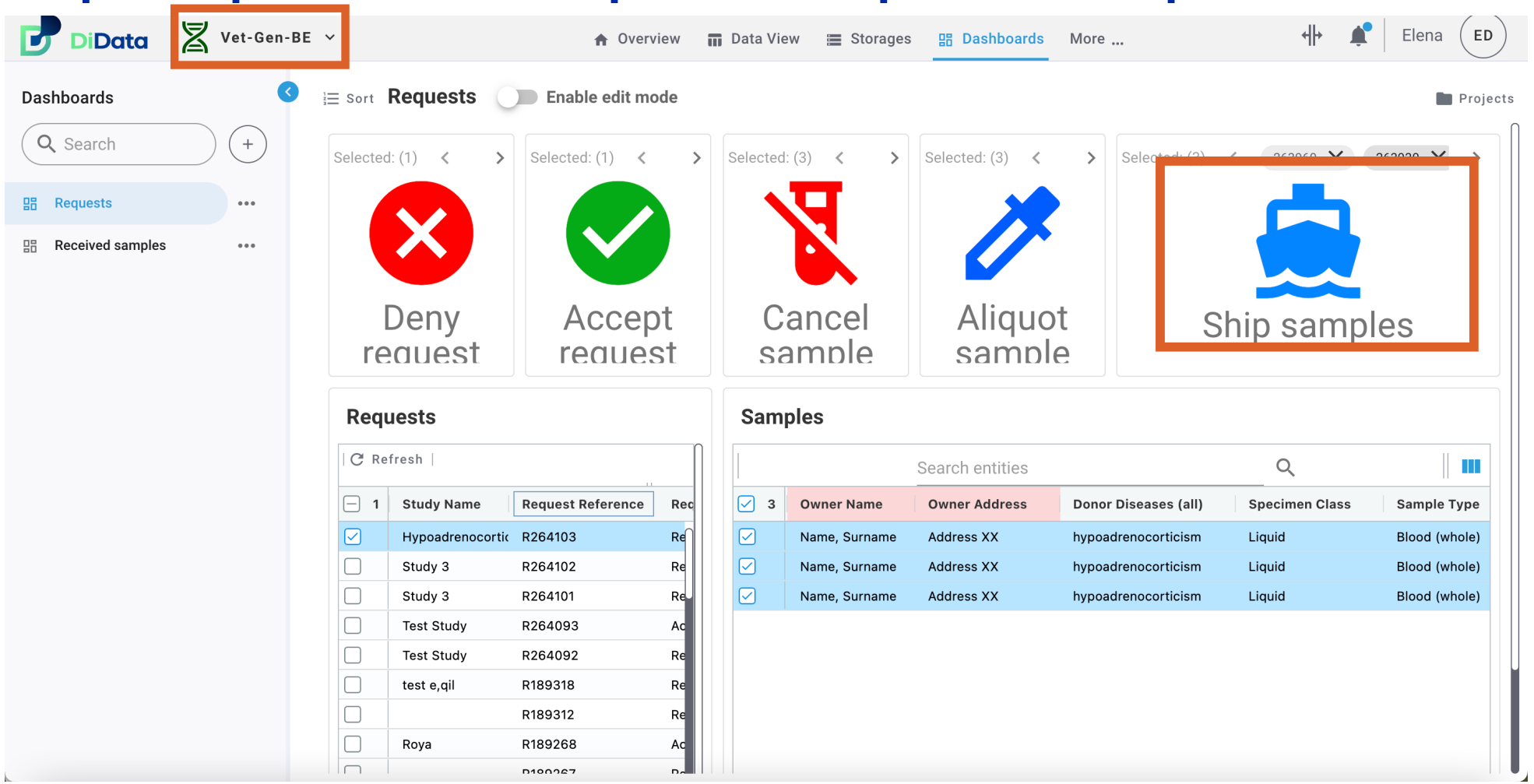


3. Sample requests – How to request samples (Request form)

3. Sample requests – How to request samples (Request sent)

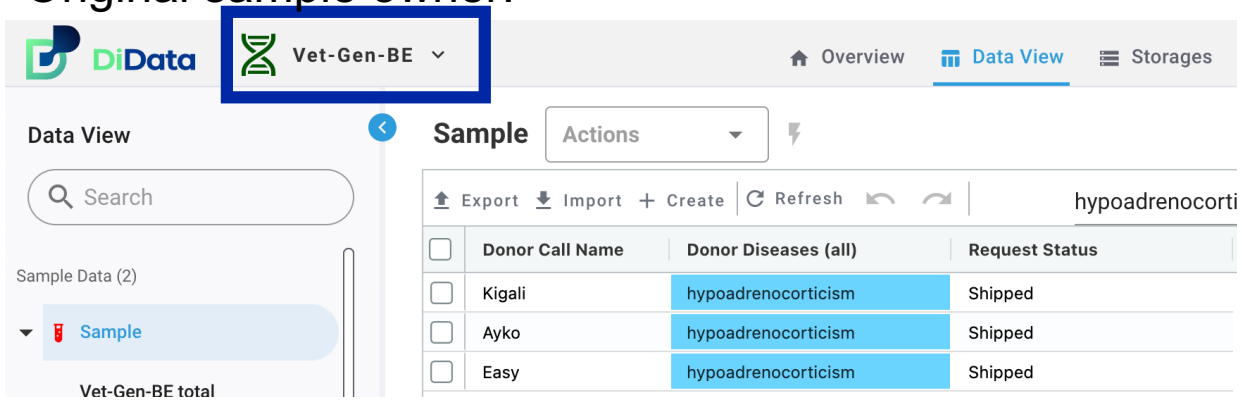


3. Sample requests – How to process requested samples

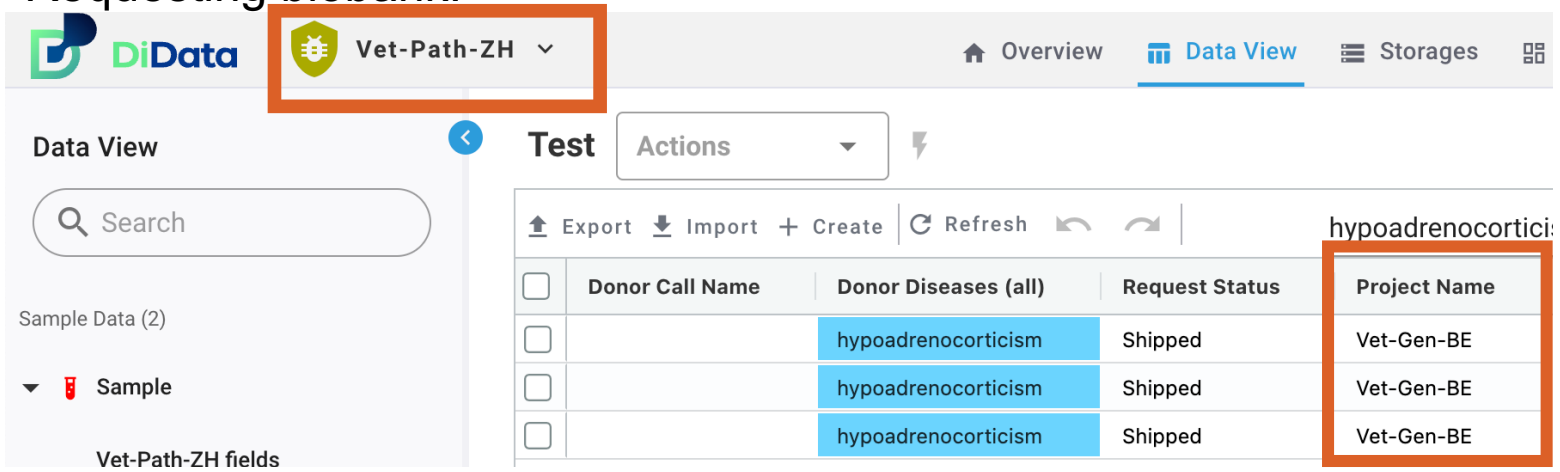


3. Sample requests – How to process requested samples

Original sample owner:



Requesting biobank:



4. Summary

- Work in progress
- Flexible solution
- Open for new members → Reach out to Franco Guscetti (franco.guscetti@vetpath.uzh.ch)

Thank you! ☺

Open Research Data in Veterinary Medicine: What's next?

Do you want your biobank to become part of the Biobanking Information Management System?

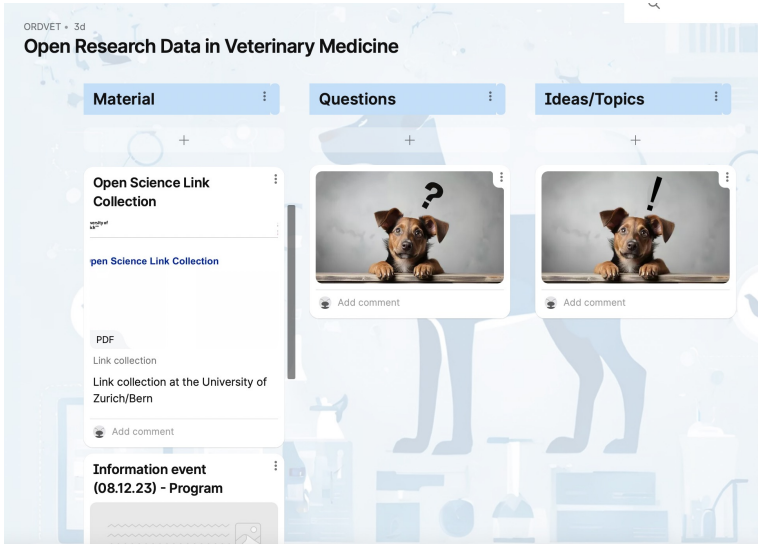
Reach out to: Franco Guscetti (franco.guscetti@vetpath.uzh.ch)

General questions, remarks, ideas (open science, controlled vocabularies):

Reach out to: Elena Dhein (elena.dhein@uzh.ch)

Collection of material, questions, ideas, and topics:
https://padlet.com/ORDVET/open_research_data_vetsuisse

ORDVET website is coming soon…



Questions and Answers

Universität Zürich[UZH]

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Thank you!

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