



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

December 8, 2023

Vetsuisse Faculty



https://padlet.com/ORDVET/open_research_data_vetsuisse



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

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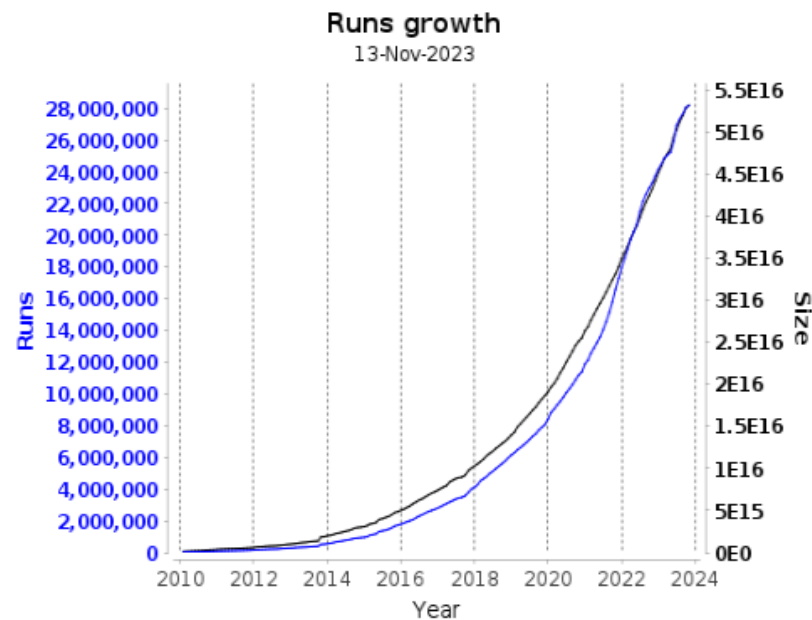
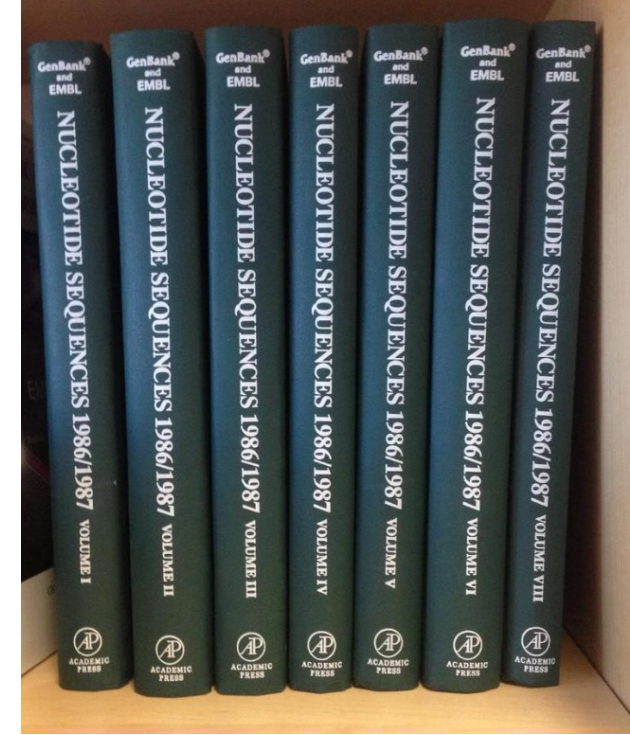
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XX
AC V00179; J00042;
XX
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DT 18-APR-2005 (Rel. 83, Last updated, Version 4)
XX
DE Dog gene encoding insulin.
XX
KW germ line; insulin; signal peptide.
XX
OS Canis sp.
OC Eukaryota; Metazoa; Chordata; 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; 3c32d256fa5e594c99f0540e36ee5b66.
XX
CC Data kindly reviewed (13-JUN-1983) by S.C.M. Kwok
XX
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FT LEINCH"
FT intron 512..775
FT /note="second intron"
FT mRNA 776..1024
FT /note="third exon"
XX
SQ Sequence 1304 BP; 212 A; 459 C; 405 G; 228 T; 0 other;
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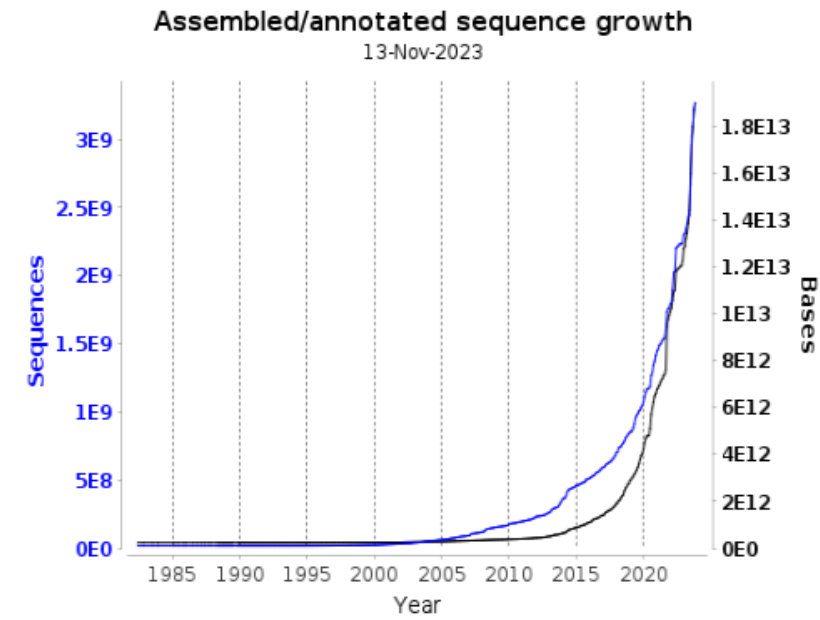
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History

- 1980 EMBL Nucleotide Sequence Data Library
- 1988 Database submission mandatory for publication in Nucl Acids Res
- 2008 European Nucleotide Archive (ENA)



— Runs (28.2 millions) — Size (53.2 petabytes)



— Sequences (3.3 billions) — Bases (19.0 trillions)

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 Responsibilities

- 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 Responsibilities

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 Responsibilities

- 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 Larson³, Jeffrey M. Kidd⁴, Bridgett M. vonHoldt⁵, 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 Frehner¹, Matthias Christen², Iris M. Reichler¹, Vidhya Jagannathan², Marilisa Novacco³, Barbara Riond³, Lauren M. Peters⁴, José Suárez Sánchez-Andrade⁵, Aldona Pieńkowska-Schelling^{2,6}, Claude Schelling⁶, Anja Kipar⁷, 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 Wang³, Heidi G. Parker⁴, Peter Z. Schall⁵, Matteo Bianchi¹, Matthew J. Christnas¹, Katia Bouglouris⁶, Reuben M. Buckley⁴, Christophe Hitté⁶, Anthony K. Nguyen², Chao Wang¹, Vidhya Jagannathan⁷, Julia E. Niskanen⁸, Laurent A. F. Frantz⁹, Meharji Arumilli⁸, Sruthi Hundi⁸, Kerstin Lindblad-Toh^{1,10}, Catarina Ginja¹¹, Kadek Karang Agustina¹², Catherine André⁶, Adam R. Boyko¹³, Brian W. Davis¹⁴, Michaela Drögemüller⁷, Xin-Yao Feng³, Konstantinos Gkagkavouzis¹⁵, Giorgos Iliopoulos¹⁶, Alexander C. Harris⁴, Marjo K. Hytönen⁸, Daniela C. Kalthoff¹⁶, Yan-Hu Liu³, Petros Lymberakis^{17,18,19}, Nikolaos Poulakakis^{17,18,19}, Ana Elisabete Pires¹¹, Fernando Racimo², Fabian Ramos-Almodovar², Peter Savolainen²⁰, Semina Venetsani²¹, Imke Tammen²², Alexandros Triantafyllidis¹⁵, Bridgett vonHoldt²³, Robert K. Wayne²⁴, Greger Larson²⁵, Frank W. Nicholas²², Hannes Lohi⁸, Tosso Leeb⁷, Ya-Ping Zhang³ and Elaine A. Ostrander²¹

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

Andrew Janowczyk
(secretary), HUG

Rainer Grobholz
(vice-president)
Aarau



Inti Zlobec
(president), Bern

Mario
Kreuzfeldt,
Auditor, HUG

SDiPath

What do we do?

Workshops

2019 with B. Williams



seminars

Trailblazers in AI in Medicine

Women in Digital Pathology (September-December, 2023)

September 21, 16:00 CET October 24, 16:00 CET November 14, 16:00 CET December 5, 16:00 CET



Anne Martel University of Toronto, Canada
 Maria Gabrani IBM Research, Switzerland
 Christine Decaestecker Université Libre de Bruxelles, Belgium
 Harshita Sharma Microsoft, UK

Whole slide imaging, self-supervision, breast cancer
 Interdisciplinarity, computational needs, the power of purpose
 Multi-expert annotations, uncertainty, deep learning
 Computational pathology, AI, whole slide images

Industry Fairs (2)

2023 AI fair

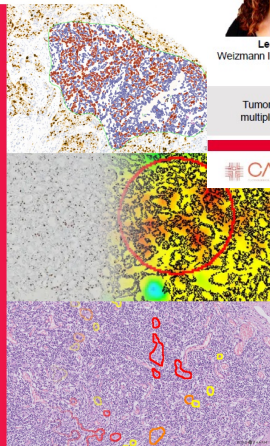


courses

Digital Pathology Course
 1 - 3 December 2021

Key Speakers

Dr. Bernd Bodenmiller
 Prof. Dr. Thomas Fuchs
 Prof. Dr. Rainer Gröbholz
 Prof. Dr. Garry Nolan
 Prof. Dr. Mark Rubin
 Dr. Vanessa Schumacher
 Prof. Dr. Inti Zlobec



Day 1
 Introduction to Digital Pathology
 Key presentation Prof. Dr. Thomas Fuchs
 Basics of Technology
 AI Highlights from the Translational Research Unit

Day 2
 Precision Medicine and Digital Pathology
 Implementation and Workflow
 Digital Pathology in Industry, Clinical Work and Research
 HANDS ON SESSION QuPath

Day 3
 HANDS ON SESSION Visiopharm
 Hans Sigrist Symposium - The Single Cell Revolution and Precision Medicine

COVID CERTIFICATE REQUIRED
 1 ECTS Point

Women in Spatial Omics (January-March, 2024)

January 23, 16:00 CET February 27, 16:00 CET March 11, 8:30 CET

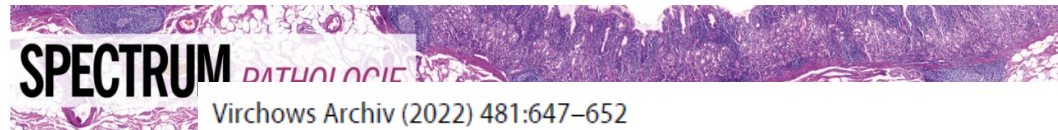


Leeat Keren Weizmann Institute of Science, Israel
 Heba Sailem King's College London, UK
 Mai Chan Lau Bioinformatics Institute/ Singapore Immunology Network Singapore

Tumor immunology, multiplexed imaging, AI
 Explainability, heterogeneity, tumor microenvironment
 Virtual staining, H&E2.0, spatial immunology

SDiPath publications

What do we publish?



SPECTRUM Pathologie | Patho 01|20



Going

28. Oktober 2019

The process of a slide is carried out through components of the diagnostic

The field of digital pathology workflow needed to unlock the fundamental components of the implementation of management systems information technology

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

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

BRIEF REPORT

Towards a national strategy for digital pathology in Switzerland

Andrew Janowczyk^{1,2} · Daniel Baumhoer³ · Stefan Dirnhofer³ · Rainer Grobholz^{4,5} · Anja Kipar⁶ · Laurence de Leval⁷ · Doron Merkler^{8,9} · Olivier Michielin^{1,10,11} · Holger Moch^{12,13} · Aurel Perren¹⁴ · Sven Rottenberg^{15,16} · Laura Rubbia-Brandt^{8,9} · Mark A. Rubin^{16,17} · Christine Sempoux⁷ · Markus Tolnay³ · Inti Zlobec¹⁴ · Viktor Hendrik Koelzer^{4,12} · the Swiss Digital Pathology Consortiumium (SDiPath)



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

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

Status and future development of digital pathology in Switzerland

Zlobec ,⁴ on behalf of the Swiss Digital Pathology Consortiumium (SDiPath)

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

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

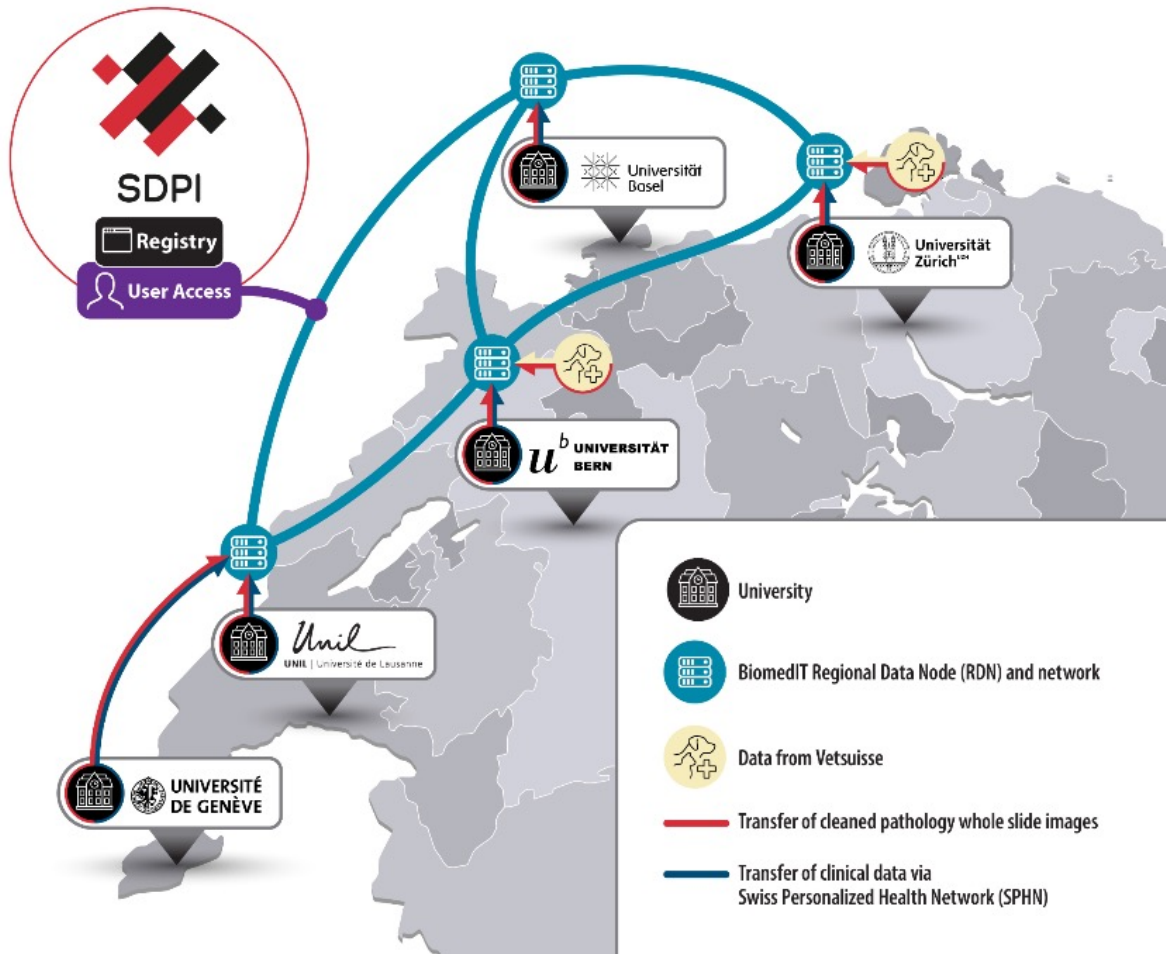
SDPI

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:

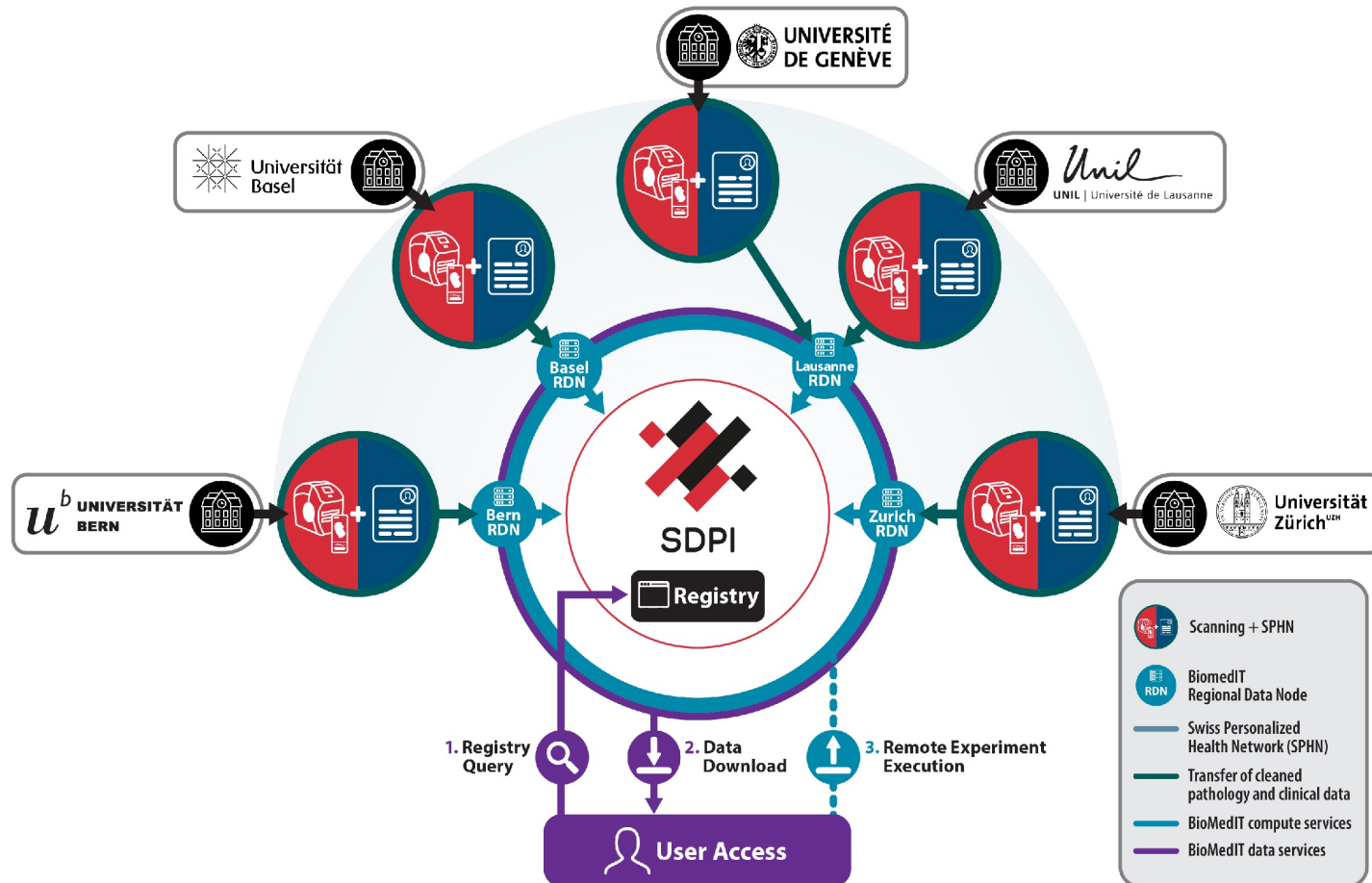
- Prof. V. Kölzer (UZH, lead), Prof. I. Zlobec (UniBe), Prof. A. Janowczyk (UniL/UniGe) on behalf of the Swiss Consortium of Digital Pathology

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”.



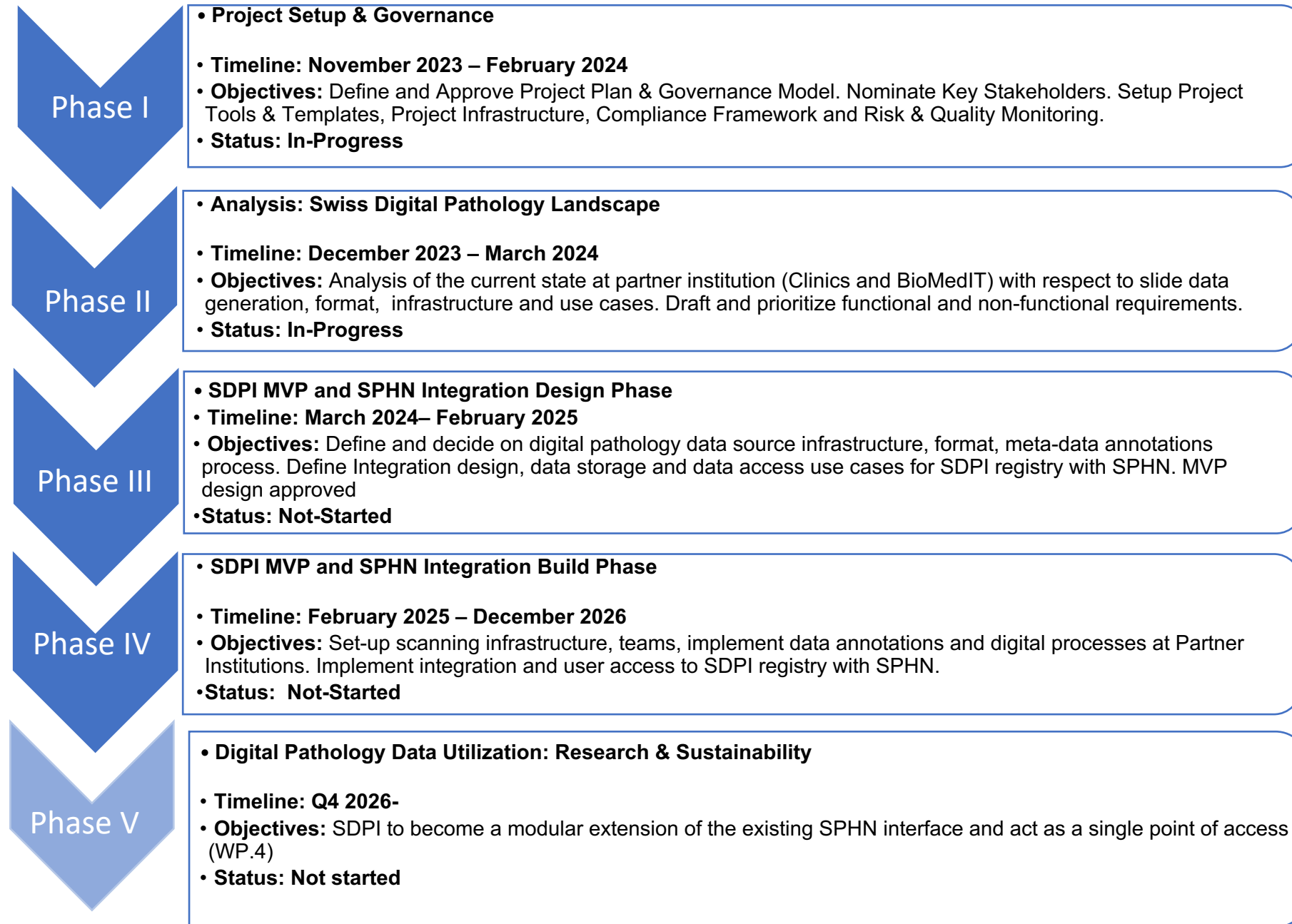
What's next?

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 Guscelli

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.

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



<https://swissdidata.com/>

Vetsuisse BIMS – IT structure

web-based access for sample requests, sample/data management

Affiliated Vetsuisse biobanks
(biocollections):

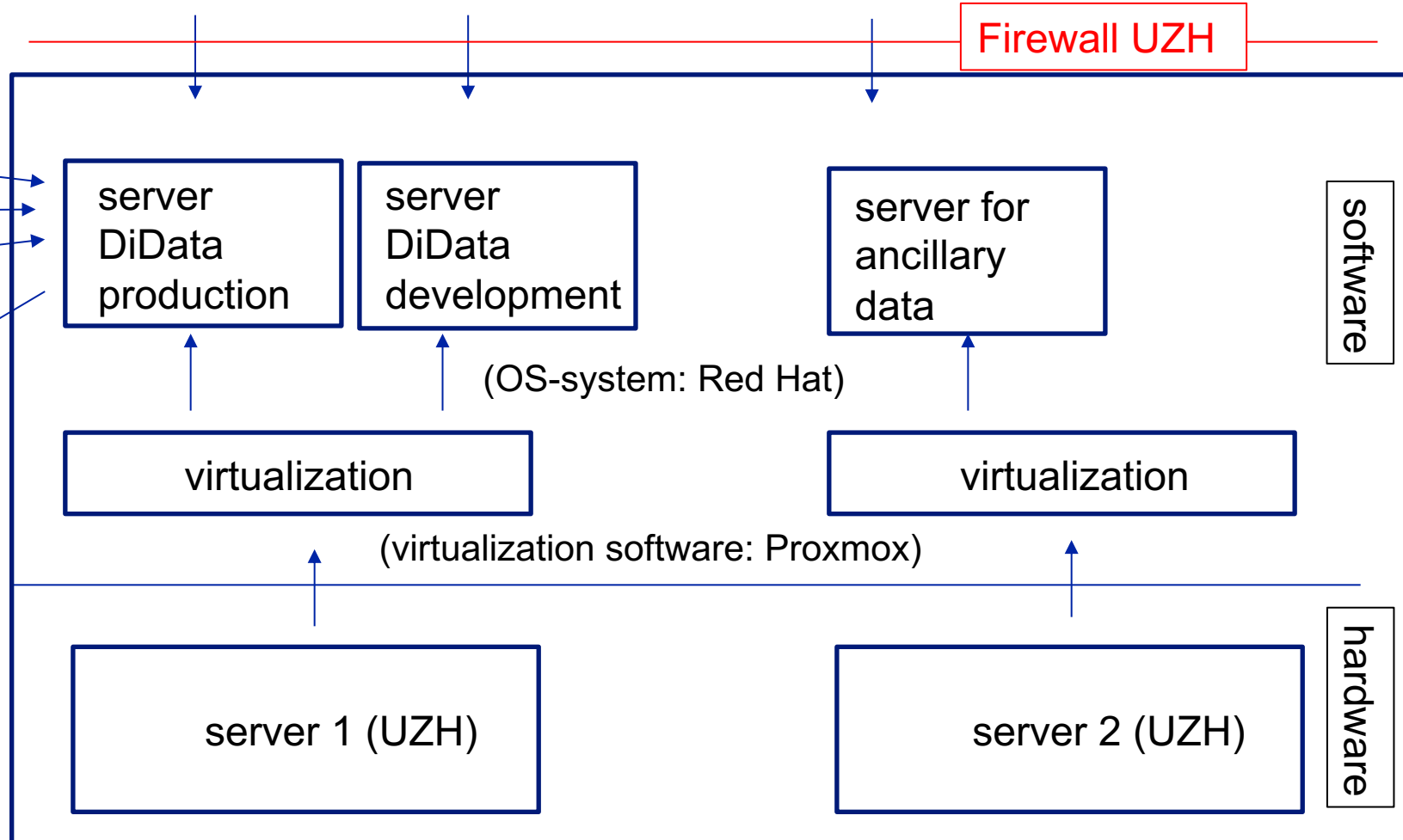
- LIMS 1
- LIMS 2
- LIMS 3

(LIMS = lab information management system)

Data import

Data export

REST-API based interfaces



(SBP quality label needed)



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



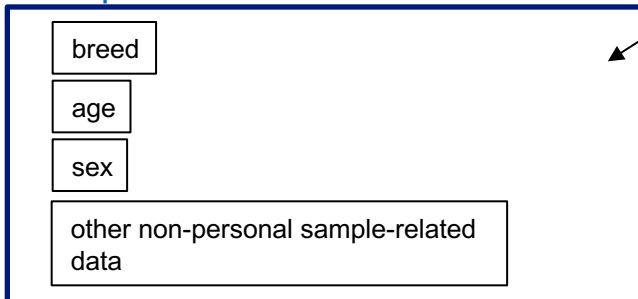


Open partition

project SMD (shared minimal dataset)

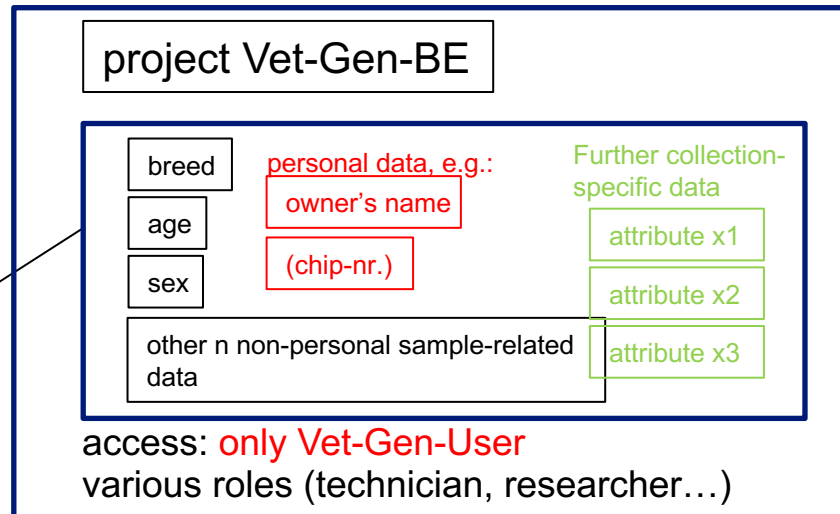
access: all Vetsuisse researchers, read-only, upon request of a User name

To search for and ordering of samples



Restricted-access partitions of affiliated biobanks

access: **affiliated biobanks have exclusive read & write rights for the own project**
Data and sample management



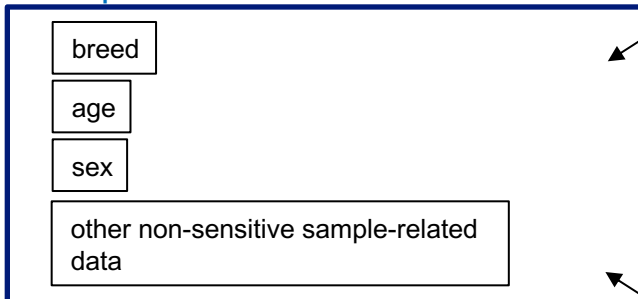


Open partition

project SMD (shared minimal dataset)

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

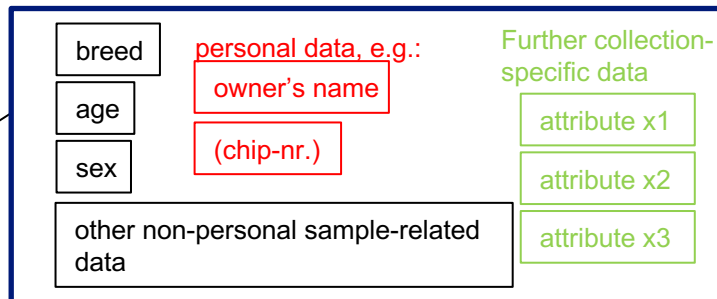
To search for and ordering of samples



Restricted-access partitions of affiliated biobanks

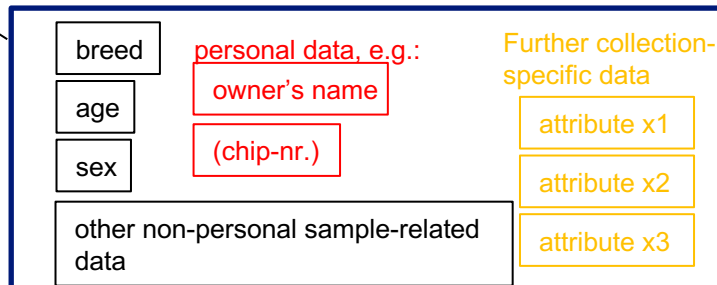
access: **affiliated biobanks have exclusive read & write rights for the own project**
Data and sample management

project Vet-Gen-BE



access: **only Vet-Gen-User**
various roles (technician, researcher...)

project Vet-Path-ZH



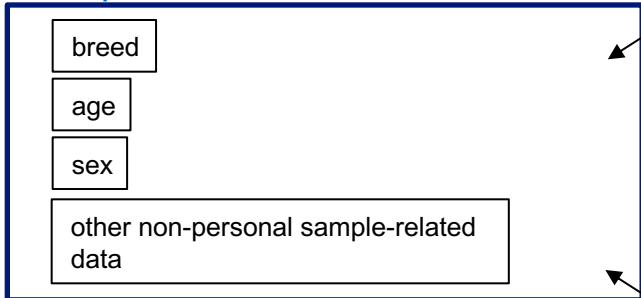


Open partition

project SMD (shared minimal dataset)

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

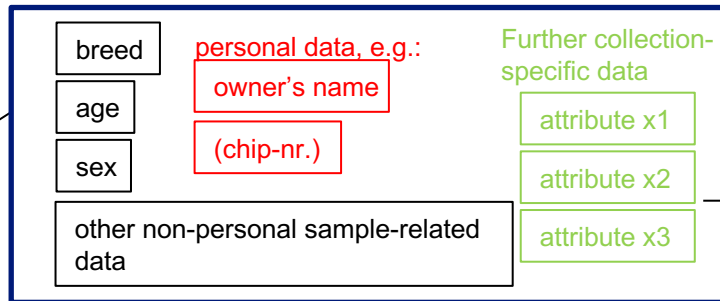
To search for and ordering of samples



Restricted-access partitions of affiliated biobanks

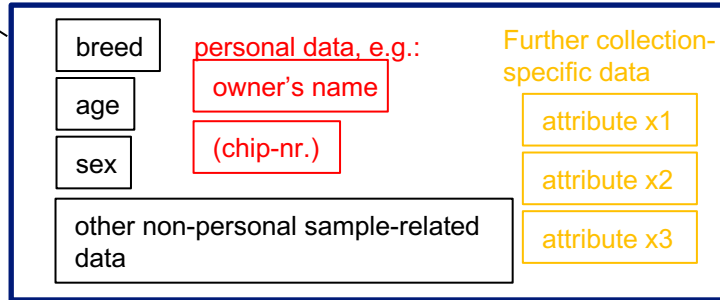
access: **affiliated biobanks have exclusive read & write rights for the own project**
Data and sample management

project Vet-Gen-BE



access: **only Vet-Gen-User**
various roles (technician, researcher...)

project Vet-Path-ZH

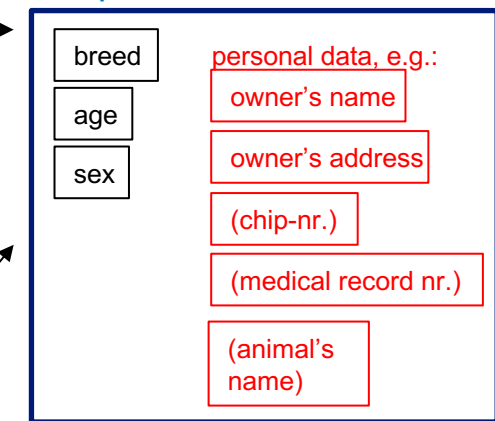


Restricted-access partition

project DC (duplicate check)

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

Duplicate check = identification of samples from the same animal



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

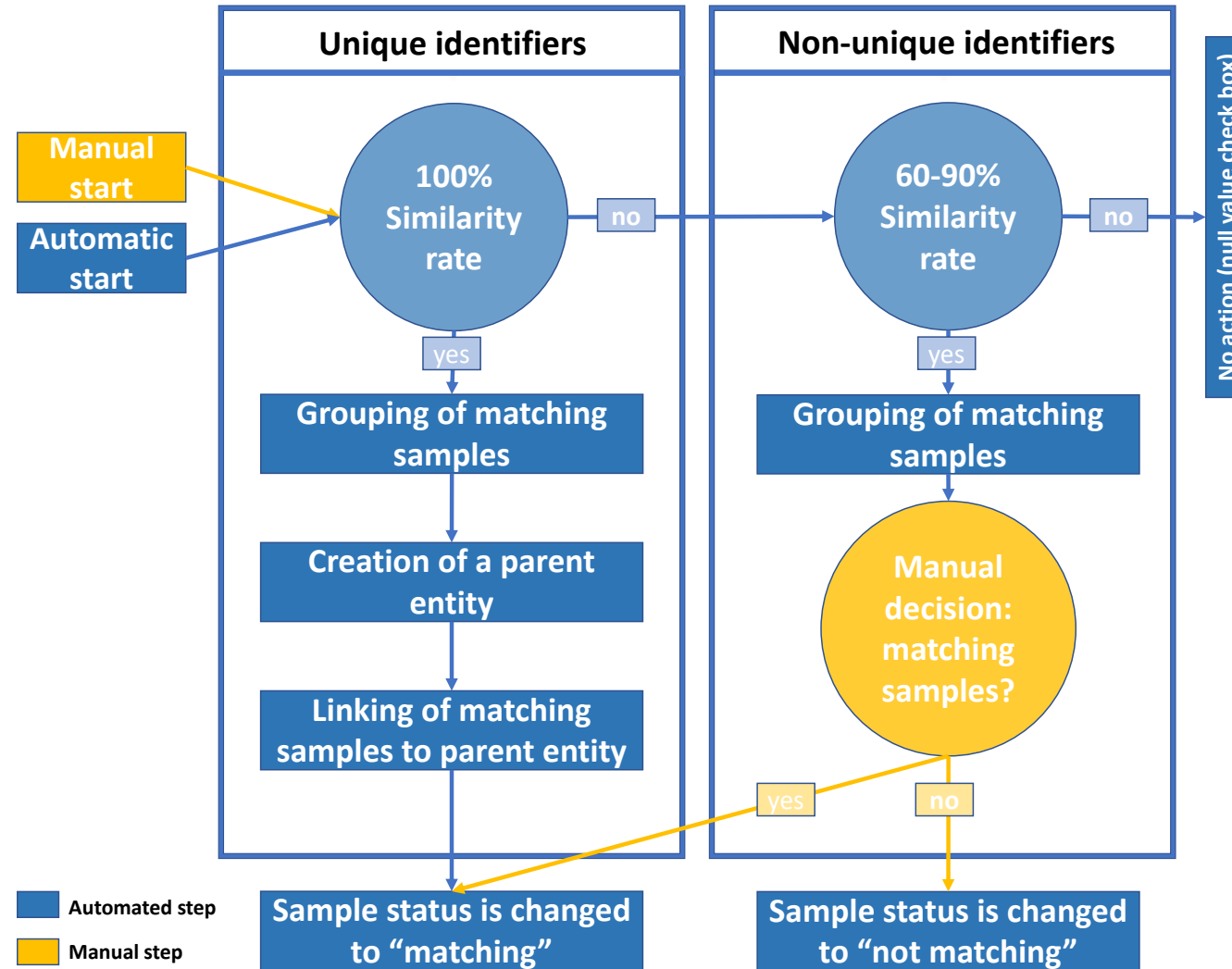


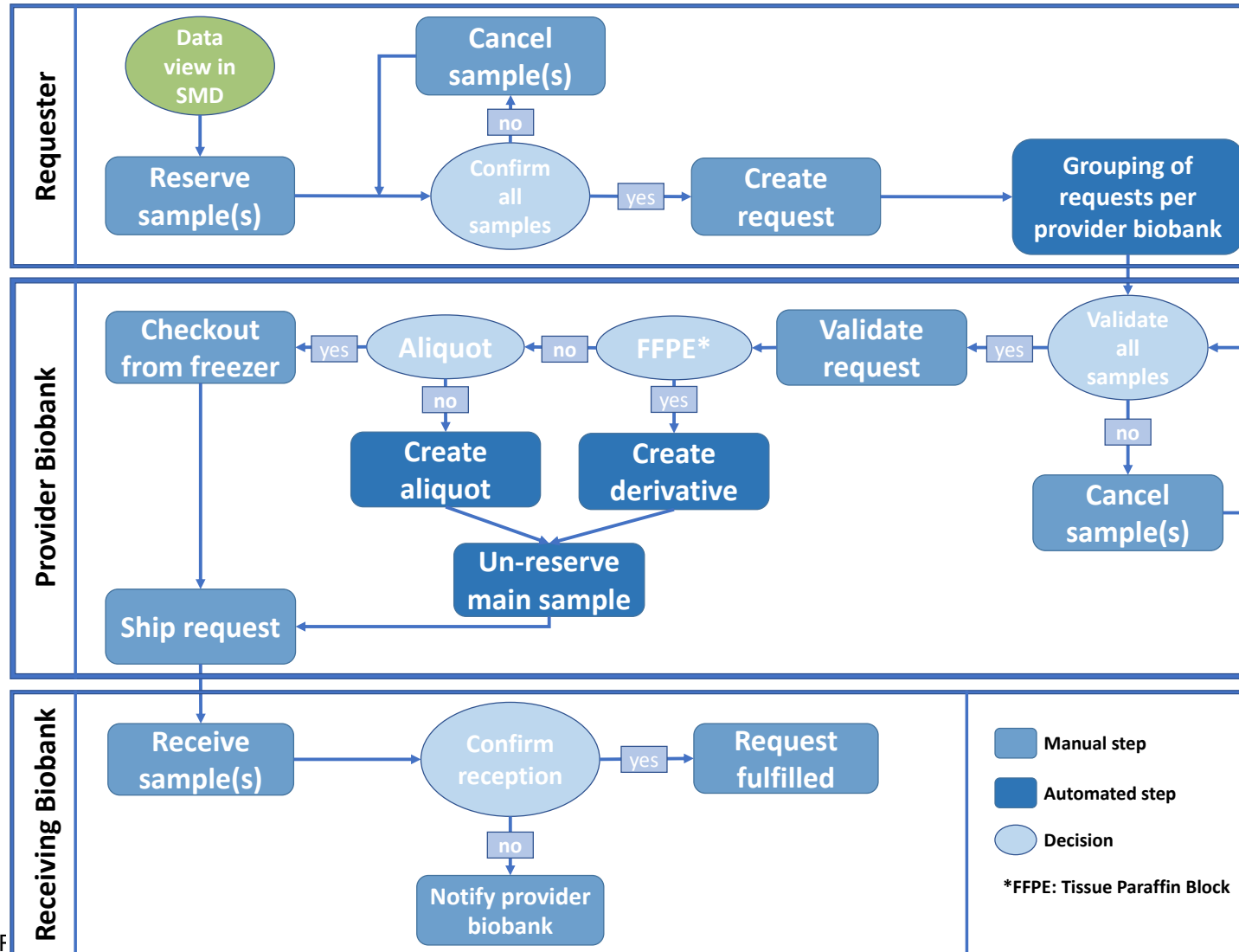
Search entities



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

Vetsuisse BIMS - Special features: «Duplicate check»





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?



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Biobanking Information Management System User Interface

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Postdoctoral researcher



Biobanking Information Management System for the Vetsuisse Faculty

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

The screenshot shows the DiData user interface for the 'Vet-Gen-BE' project. A dropdown menu is open, listing various projects including Global, Admin project, Chlamydia Biobank, Duplicate Check, SCFCR, Shared Minimal Dataset, Vet-Gen-BE (highlighted), Vet-Lab-ZH, Vet-Neuro-BE, Vet-Path-BE, and Vet-Path-ZH. The main interface features a sidebar with modules like Fields, Entity types, Languages, and Actions. The central area displays 'Data View', 'Users', 'Rules', and 'Projects' options. On the right, a 'Statistics / Entities' bar chart shows the count of entities for various types: Sample (~1200), Donor (4000), Breeds (~3800), Countries (~600), Racks (~300), Morphological code (~800), Entity type@18 (~200), and PROJECT (~100).

1. User interface – Data view

Data View Vet-Gen-BE total

Search entities

Created at ↓	Donor Pedigree Name	Donor Call Name	Donor_Kennel	Donor Registration Number	Donor Chip-Nr/ Eartag-Nr	Donor Date of Birth	Do
05-12-2023 14:04:28	Kigali	Kigali	Bernh_Example	XXXXXXX	12345678910111200	15-04-2020	2
05-12-2023 14:04:27	Icar	Icar	Bernh_Example	XXXXXXX	12345678910111200	20-10-2018	1
05-12-2023 14:04:27	Irex	Irex	Bernh_Example	XXXXXXX	12345678910111200	20-10-2018	1
05-12-2023 14:04:27	Isky	Isky	Bernh_Example	XXXXXXX	12345678910111200	20-10-2018	11
05-12-2023 14:04:27	Indy	Indy	Bernh_Example	XXXXXXX	12345678910111200	20-10-2018	1
05-12-2023 14:04:27	Inka	Inka	Bernh_Example	XXXXXXX	12345678910111200	20-10-2018	3
05-12-2023 14:04:27	Isola	Isola	Bernh_Example	XXXXXXX	12345678910111200	20-10-2018	2
05-12-2023 14:04:27	Illy	Illy	Bernh_Example	XXXXXXX	12345678910111200	20-10-2018	2
05-12-2023 14:04:27	Arco	Arco	Bernh_Example	XXXXXXX	12345678910111200	11-02-2013	1
05-12-2023 14:04:27	Aaron	Aaron	Bernh_Example	XXXXXXX	12345678910111200	11-02-2013	3
05-12-2023 14:04:27	Artus	Artus	Bernh_Example	XXXXXXX	12345678910111200	11-02-2013	3
05-12-2023 14:04:27	Jomiko	Jomiko	Bernh_Example	XXXXXXX	12345678910111200	25-05-2019	0
05-12-2023 14:04:27	Jessy	Jessy	Bernh_Example	XXXXXXX	12345678910111200	25-05-2019	0
05-12-2023 14:04:27	Jaron	Jaron	Bernh_Example	XXXXXXX	12345678910111200	25-05-2019	0
05-12-2023 14:04:27	Kalani-Remy	Kalani-Remy	Bernh_Example	XXXXXXX	12345678910111200	15-04-2020	6
05-12-2023 14:04:27	Kenzo	Kenzo	Bernh_Example	XXXXXXX	12345678910111200	15-04-2020	3
05-12-2023 14:04:27	Knutt-Karlo	Knutt-Karlo	Bernh_Example	XXXXXXX	12345678910111200	15-04-2020	2
05-12-2023 14:04:27	Kaiwa	Kaiwa	Bernh_Example	XXXXXXX	12345678910111200	15-04-2020	6

Rows per page 50 0 - 50 to 1226 1 >

1. User interface – Users

User:

i Elena

Credentials

User type

DiData user

Authentication driver

Username

Elena

Password

User role

administrator

Password Confirmation

User language

Show global project

Use two-factor authentication (2FA)

Personal Information

First Name

Elena

Change password on next login

Last Name

Dhein

✕ CLOSE

Roles/Permissions:

Permission	Public role	administrator	Project user	Super Administrator	importbot
Access to sensitive fields	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input checked="" type="checkbox"/> Yes
Manage all projects	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No
Create field	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No
Edit field	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No
Delete field	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No
Batch import of fields	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No
Batch export of fields	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No	<input type="checkbox"/> No	<input type="checkbox"/> No
Edit field dynamic tooltip	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No
Create entity type	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No
Edit entity type	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No
Delete entity type	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No
Manage entity type order	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No
Configure study entitytype manager	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No
Create entity	<input checked="" type="checkbox"/> Yes	<input checked="" type="checkbox"/> Yes	<input checked="" type="checkbox"/> Yes	<input checked="" type="checkbox"/> Yes	<input checked="" type="checkbox"/> Yes
Batch import of Entities	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input checked="" type="checkbox"/> Yes	<input checked="" type="checkbox"/> Yes	<input checked="" type="checkbox"/> Yes
Export entities	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input checked="" type="checkbox"/> Yes	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No
Edit entity	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input checked="" type="checkbox"/> Yes	<input checked="" type="checkbox"/> Yes	<input checked="" type="checkbox"/> Yes
Delete entity	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input checked="" type="checkbox"/> Yes	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No
Manage genealogy settings	<input type="checkbox"/> No	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No	<input type="checkbox"/> No	<input type="checkbox"/> No

2. Features – Storages

EDTA Small animals

Export	Import	Search entities	ID	Created at	Updated at	Donor Chip-Nr/ Eartag-Nr	Donor
<input checked="" type="checkbox"/>	Sample	263960	05-12-2023 14:00	05-12-2023 16:00	12345678910111200	Kigali	
<input checked="" type="checkbox"/>	Sample	263959	05-12-2023 14:00	05-12-2023 16:00	12345678910111200	Kessi	
<input checked="" type="checkbox"/>	Sample	263958	05-12-2023 14:00	05-12-2023 16:00	12345678910111200	Kaiwa	
<input checked="" type="checkbox"/>	Sample	263957	05-12-2023 14:00	05-12-2023 16:00	12345678910111200	Knut	
<input checked="" type="checkbox"/>	Sample	263956	05-12-2023 14:00	05-12-2023 16:00	12345678910111200	Kenzi	
<input checked="" type="checkbox"/>	Sample	263955	05-12-2023 14:00	05-12-2023 16:00	12345678910111200	Kalan	
<input checked="" type="checkbox"/>	Sample	263954	05-12-2023 14:00	05-12-2023 16:00	12345678910111200	Jaron	
<input checked="" type="checkbox"/>	Sample	263953	05-12-2023 14:00	05-12-2023 16:00	12345678910111200	Jessy	
<input checked="" type="checkbox"/>	Sample	263952	05-12-2023 14:00	05-12-2023 16:00	12345678910111200	Jomik	
<input checked="" type="checkbox"/>	Sample	263951	05-12-2023 14:00	05-12-2023 16:00	12345678910111200	Artus	
<input checked="" type="checkbox"/>	Sample	263950	05-12-2023 14:00	05-12-2023 16:00	12345678910111200	Aaror	
<input checked="" type="checkbox"/>	Sample	263949	05-12-2023 14:00	05-12-2023 16:00	12345678910111200	Arco	
<input type="checkbox"/>	Sample	263948	05-12-2023 14:00	05-12-2023 16:00	12345678910111200	Illy	
<input type="checkbox"/>	Sample	263947	05-12-2023 14:00	05-12-2023 16:00	12345678910111200	Isola	
<input type="checkbox"/>	Sample	263946	05-12-2023 14:00	05-12-2023 16:00	12345678910111200	Inka	
<input type="checkbox"/>	Sample	263945	05-12-2023 14:00	05-12-2023 16:00	12345678910111200	Indy	
<input type="checkbox"/>	Sample	263944	05-12-2023 14:00	05-12-2023 16:00	12345678910111200	Isky	

Selected entities: 263960, 2...

ID

STORE -20C

Action executor:

1 Update
Update entity using form

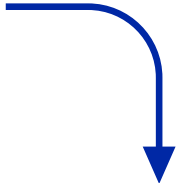
No entity to update

Apply changes for the entities

Storages

All storages

- Freezer -80
- Freezer-20
- Freezers@185751
- Freezers@249254
- Shelves@249255
- Boxes@249256**



... > FREEZERS@249254 > SHELVES@249255 > BOXES@249256

Actions

Show: Barcode (BARCODE)

	1	2	3	4
1				
2				

2. Features – Workflows

DiData Vet-Gen-BE

Overview Data View Storages Dashboards **Workflows** More ...

Elena ED

Workflows

Sort RNA (Native tissue) Enable edit mode

Projects

Search +

- Blood
- Semen
- Hair root
- Tissue for DNA
- RNA (Native tissue)**
- Tissue stored in RNA later

```

    graph LR
      Start(( )) -- Register (RNA) --> NT((Native tissue  
(15)))
      NT -- Aliquot+Extract (RNA) --> RS((RNA solution  
(3)))
      NT -- Store RNA --> F80((Freezer -80))
      F80 -- Aliquot+Extract (RNA) --> RS
      RS -- Distribute internally (RNA) --> IE((Internal experiment))
  
```

● : Sample status

➔ : Action

2. Features – Workflows (Action)

i Native tissue

Export Import Search entities

4	EntityType	ID	Created at	Updated at	Donor Call Name	Sample ID
<input checked="" type="checkbox"/>	Sample	235143	10-07-2023 22:00	07-12-2023 14:00	Caesar	Z20-0205-00.0'
<input checked="" type="checkbox"/>	Sample	235142	10-07-2023 22:00	07-12-2023 14:00	HENRIETTE	Z20-0204-00.0'
<input checked="" type="checkbox"/>	Sample	235141	10-07-2023 22:00	07-12-2023 14:00	Kiwi	Z20-0203-00.0'
<input checked="" type="checkbox"/>	Sample	235140	10-07-2023 22:00	07-12-2023 14:00	Noria	Z20-0202-00.0'
<input type="checkbox"/>	Sample	235139	10-07-2023 22:00	07-12-2023 14:00	May	Z20-0201-00.01
<input type="checkbox"/>	Sample	235138	10-07-2023 22:00	07-12-2023 14:00	SHERIDAN	Z20-0200-00.0'
<input type="checkbox"/>	Sample	235137	10-07-2023 22:00	07-12-2023 14:00	Jasperino	Z20-0199-00.01
<input type="checkbox"/>	Sample	235136	10-07-2023 22:00	07-12-2023 14:00	Desy	Z20-0198-00.01
<input type="checkbox"/>	Sample	235135	10-07-2023 22:00	07-12-2023 14:00	Svenja	Z20-0197-00.01
<input type="checkbox"/>	Sample	235134	10-07-2023 22:00	07-12-2023 14:00	Anno	Z20-0196-00.01
<input type="checkbox"/>	Sample	235133	10-07-2023 22:00	07-12-2023 14:00	Pablo	Z20-0195-00.01
<input type="checkbox"/>	Sample	235132	10-07-2023 22:00	07-12-2023 14:00	Max	Z20-0194-00.01
<input type="checkbox"/>	Sample	235131	10-07-2023 22:00	07-12-2023 14:00	Triniti	Z20-0193-00.01
<input type="checkbox"/>	Sample	235130	10-07-2023 22:00	07-12-2023 14:00	TANSU	Z20-0192-00.01
<input type="checkbox"/>	Sample	202424	27-06-2023 14:00	27-06-2023 14:00		

Rows per page 50 0 - 15 to 15 1

Selected entities: 235143, 2...

ALIQUOT+ EXTRACT (RNA...)

ID

Action executor:

- 1 Aliquot Clone entity
- 2 Extract RNA Clone entity

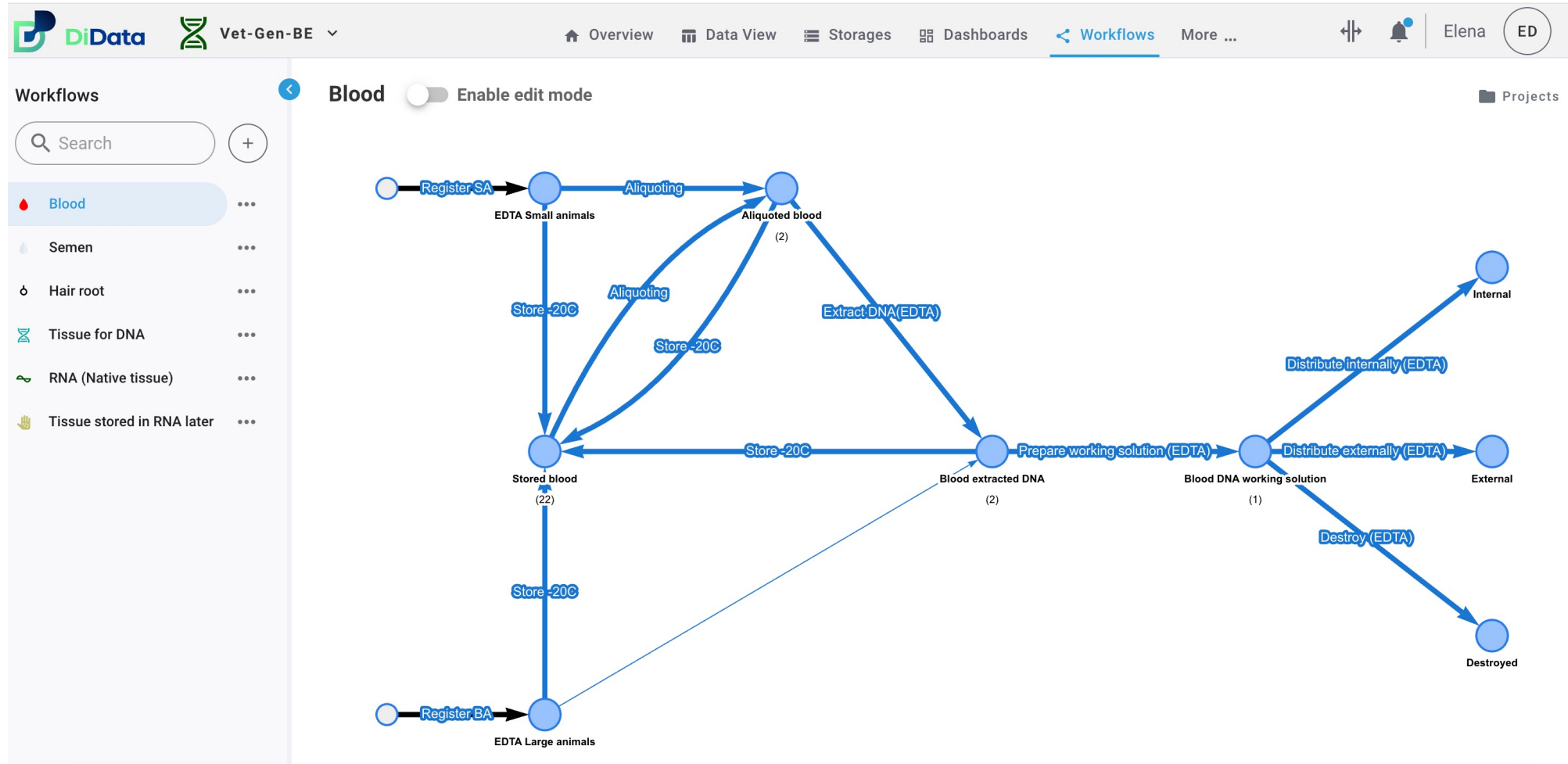
No selected entity

> SKIP ENTITY

> NEXT OPERATION

Apply changes for the remaining entities

2. Features – Workflows



2. Features – Data standardization (Breeds)

The screenshot shows the 'Data View' interface for 'Breed' in the 'Vet-Path-ZH' system. The table displays the following data:

Donor Breed Calculated	Donor Breed Original	Donor Category
Chicken Birds Bresse Gauloise	Bresse-Gauloise	Birds
Chicken Birds Bresse Gauloise	Bresse-Gauloise	Birds
Chihuahua (218)	Chihuahua	Mammals Dogs (Canis)
Chihuahua (218)	Chihuahua	Mammals Dogs (Canis)
Chihuahua (218)	Chihuahua	Mammals Dogs (Canis)
Field Spaniel (123)	Field Spaniel	Mammals Dogs (Canis)
Field Spaniel (123)	Field Spaniel	Mammals Dogs (Canis)
Australian Cattle Dog (287)	Australian Cattle Dog	Mammals Dogs (Canis)
Chihuahua (218)	Chihuahua	Mammals Dogs (Canis)
Chihuahua (218)	Chihuahua	Mammals Dogs (Canis)
Domestic cat	Hauskatze	Mammals Cats (Felis)
Spitz Miniature (Pomeranian) (97)	Zwergspitz	Mammals Dogs (Canis)
Domestic cat	Hauskatze	Mammals Cats (Felis)
Czechoslovakian Wolfhound (332)	Tschechoslowakischer Wolfhund	Mammals Dogs (Canis)
Norwegian Forest Cat (NFO)	Norwegische Waldkatze	Mammals Cats (Felis)
Norwegian Forest Cat (NFO)	Norwegische Waldkatze	Mammals Cats (Felis)
Norwegian Forest Cat (NFO)	Norwegische Waldkatze	Mammals Cats (Felis)
Norwegian Forest Cat (NFO)	Norwegische Waldkatze	Mammals Cats (Felis)

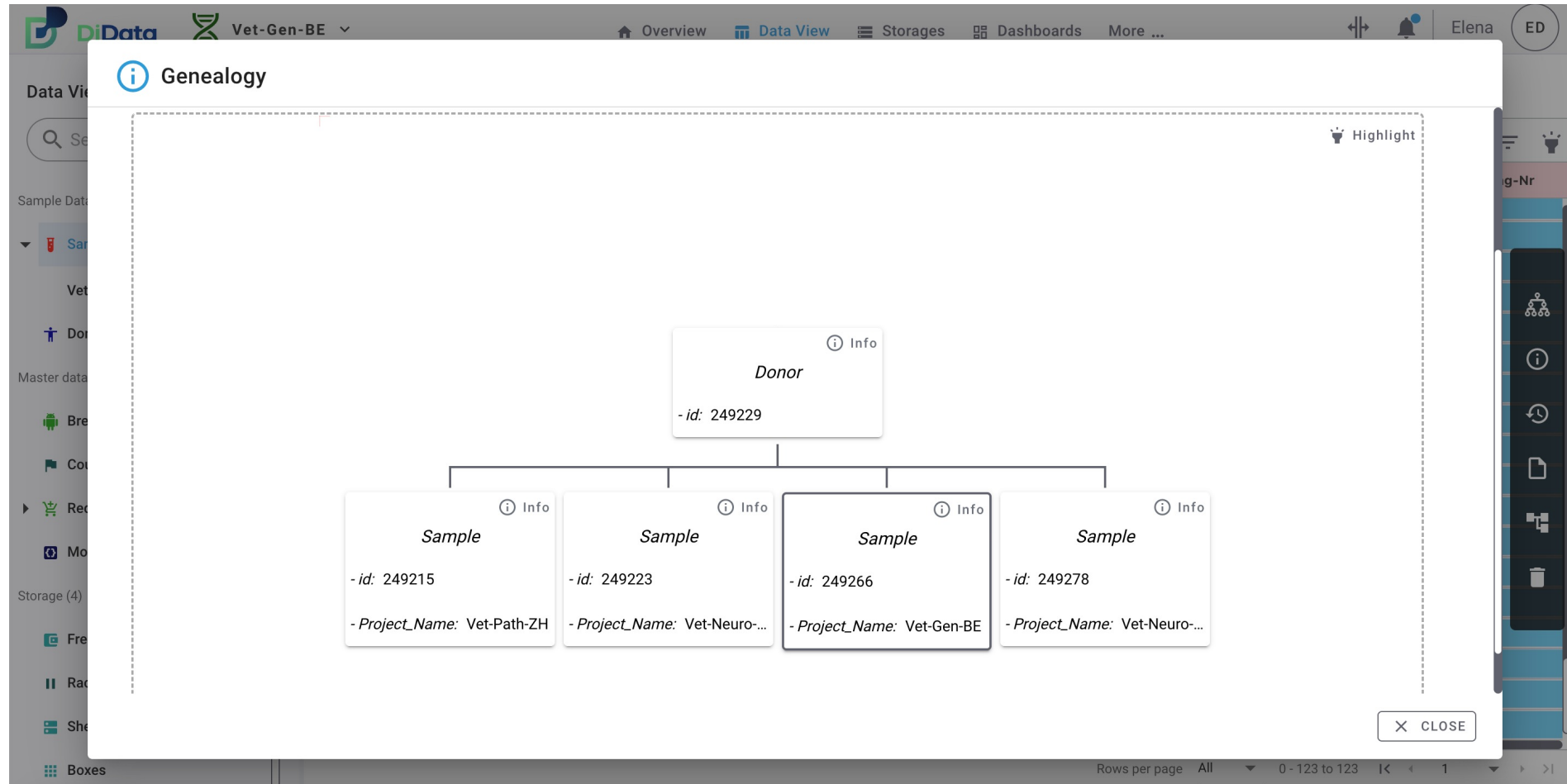
2. Features – Data standardization (Morphologies)

Sample Actions ⚡

Export Import Create Refresh Search entities Custom View Save Columns

<input type="checkbox"/>	Specimen Morphological All Text	Specimen Morphological Free Text	Specimen Morphological Code
<input type="checkbox"/>	Adenoma, vollständig exziiert Kommentar: Es handelt sich um eine benigne, von Schweissdrüsen ausgehende	Adenoma	8140/0
<input type="checkbox"/>	- Spleen: Focal hemangioma, NOS - Right ovary: Multiple follicular cysts- Left ovary: No histological change is	Hemangioma	9120/0
<input type="checkbox"/>	Interstitial cell tumour and intratubular Seminoma, NOS Comment: Testicular neoplasias of the dog have a lov	Seminoma	9061/1
<input type="checkbox"/>	Rectum: The tissue specimen consists of highly edematous submucosa, which is covered by stratified, non-ker	Carcinoma Leydig cell tumor Seminoma	8010/3 8650/1 9061/1
<input type="checkbox"/>	lymphoma Spleen - non-diagnostic Immunocytochemistry can be attempted if further differentiation is requir	Mesothelioma, benign Lymphoma	9050/0 9591/3
<input type="checkbox"/>	- 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
<input type="checkbox"/>	Peritoneum All tissue specimens have similar histological features, and are comprised of a core of fibrovascular	Sarcoma Osteosarcoma	8800/3 9180/3
<input type="checkbox"/>	in the center of the latter tissue sample there is a non-encapsulated, well-demarcated mass in the dermis. The i	Mast cell tumor	9740/1
<input type="checkbox"/>	Tumour lesion from the nasal cavity, carcinoma Comment: The histological examination revealed a neoplastic	Carcinoma	8010/3
<input type="checkbox"/>	Round cell tumor , possibly histiocytoma in regression with spindle cells proliferation Comment: A cutaneous i	Round cell tumor	8006.1/1
<input type="checkbox"/>	The subcutis and deep dermis are infiltrated and replaced by a multinodular mass composed of plump to elong	Sarcoma	8800/3
<input type="checkbox"/>	- Skin tumor: Cutaneous basilar epithelial neoplasm (previously known as basal cell tumor) with mild cellular ne	Basal cell tumor	8090/0
<input type="checkbox"/>	All three biopsies display a multifocal-coalescing severe infiltrate of histiocytes (mainly macrophages, few supe	Canine cutaneous histiocytoma	9751.1/0
<input type="checkbox"/>	Carcinoma with moderate mixed-cell inflammation with prevalence of neutrophils	Carcinoma	8010/3
<input type="checkbox"/>	Sarcoma - The macroscopically described neoplasm is relatively well demarcated, unencapsulated, invasively g	Sarcoma	8800/3
<input type="checkbox"/>	The dermis is focally expanded by a cell-dense, wedge-shaped proliferation of intermediate size round cells grc	Canine cutaneous histiocytoma	9751.1/0
<input type="checkbox"/>	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
<input type="checkbox"/>	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

The screenshot shows the DiData interface. At the top, there is a navigation bar with 'Overview', 'Data View', 'Storages', 'Dashboards', and 'More ...'. A 'Shared Minimal Dataset' dropdown is highlighted with a blue box. Below the navigation bar, there is a 'Dashboards' sidebar with a search bar and three items: 'Samples', 'My selection', and 'My sent requests'. The main content area features a large blue arrow icon and the text 'Select samples'. Below this is a table titled 'Samples' with a 'Refresh' button and a search bar. The table has columns for 'Donor Diseases (all)', 'Donor Anamnese', 'Sample Type', 'Specimen Class', 'men Morphological Free Text', and 'Specimen Morphological Code'. A blue box highlights the table's header area.

	Donor Diseases (all)	Donor Anamnese	Sample Type	Specimen Class	men Morphological Free Text	Specimen Morphological Code	men
<input type="checkbox"/>	Adenoma Ductal adenorr	Hochgradig neurologisch, nicht s	Solid tissue	Tissue	Adenoma Ductal adenoma	8140/0 8500/0	
<input type="checkbox"/>	Hemangioma	Hochgradig neurologisch, nicht s	Solid tissue	Tissue	Hemangioma	9120/0	Skin
<input type="checkbox"/>	Seminoma	Hochgradig neurologisch, nicht s	Solid tissue	Tissue	Seminoma	9061/1	Testi
<input type="checkbox"/>	Mesothelioma, benign Ly	Hochgradig neurologisch, nicht s	Solid tissue	Tissue	Mesothelioma, benign Lymphom:	9050/0 9591/3	Thor
<input type="checkbox"/>	Lipoma Mast cell tumor s	Hochgradig neurologisch, nicht s	Solid tissue	Tissue	Lipoma Mast cell tumor Subcuta	8850/0 9740/1 9740.0/1	Skin
<input type="checkbox"/>	Sarcoma Osteosarcoma	1. Kutaner Knoten rechtes Hinter	Solid tissue	Tissue	Sarcoma Osteosarcoma	8800/3 9180/3	Bone
<input type="checkbox"/>	Mast cell tumor	1. Kutaner Knoten rechtes Hinter	Solid tissue	Tissue	Mast cell tumor	9740/1	Skin
<input type="checkbox"/>	Carcinoma Squamous ce	Zwei kleine Hautzubildungen im	Solid tissue	Tissue	Carcinoma Squamous cell carcin	8010/3 8070/3 8140/3	
<input type="checkbox"/>	Round cell tumor	Warze, Oberschenkel, Knoten au	Solid tissue	Tissue	Round cell tumor	8006.1/1	Skin
<input type="checkbox"/>	Sarcoma	Kleines Knötchen in der Haut.	Solid tissue	Tissue	Sarcoma	8800/3	
<input type="checkbox"/>	Carcinoma Squamous ce	Knoten links Tarsus, weich, blute	Solid tissue	Tissue	Carcinoma Squamous cell carcin	8010/3 8070/3 8090/0	

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

The screenshot shows the DiData application interface with a 'Filter' dialog box open. The dialog is titled 'Filter' and has radio buttons for 'And' (selected) and 'Or'. It contains three filter rows. The first row has 'Donor Breed Calculated' as the field, '=' as the condition, and 'Saint Bernard (61)' as the value. The second row has 'Donor Diseases (all)' as the field, '=' as the condition, and 'hypoadrenocorticism' as the value. The third row has 'Donor Age at Collection' as the field, '<=' as the condition, and '8' as the value. Buttons for '+ BRACKET', '+ CONDITION', 'X CLOSE', 'RESET', and 'APPLY' are visible.

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

DiData Shared Minimal Dataset

Overview Data View Storages **Dashboards** More ...

Elena ED


Dashboards

Search

Samples My selection My sent requests

Sort Samples Enable edit mode

Selected: (3) 263960 X 263937 X 263930 X



Select samples

Samples

Refresh Search entities

<input checked="" type="checkbox"/>	3	Project Name	Donor Category	Donor Breed Calculated	Donor Date of Birth	Donor Age at Collection	Donor Age Unit	Donor Sex
<input checked="" type="checkbox"/>		Vet-Gen-BE	Mammals Dogs (Canis)	Saint Bernard (61)	15-04-2020	2	Y	F
<input checked="" type="checkbox"/>		Vet-Gen-BE	Mammals Dogs (Canis)	Saint Bernard (61)	11-02-2018	1	Y	M
<input checked="" type="checkbox"/>		Vet-Gen-BE	Mammals Dogs (Canis)	Saint Bernard (61)	18-12-2011	4	Y	F

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

The screenshot shows the DiData interface for a 'Shared Minimal Dataset'. The top navigation bar includes 'Overview', 'Data View', 'Storages', 'Dashboards', and 'More ...'. The user is logged in as 'Elena' with a profile icon 'ED'. The main content area is titled 'My selection' and includes a search bar, a 'Sort' button, and a toggle for 'Enable edit mode'. Below this, there are two buttons: 'Unreserve' (with a blue 'X' icon) and 'Request' (with a shopping cart icon, highlighted with a blue border). A table below shows the selected items:

3	Project Name	Donor Category	Donor Breed Calculated	Donor Date of Birth	Donor Date of Birth Calculated	Donor Age
<input checked="" type="checkbox"/>	Vet-Gen-BE	Mammals Dogs (Canis)	Saint Bernard (61)	18-12-2011		4
<input checked="" type="checkbox"/>	Vet-Gen-BE	Mammals Dogs (Canis)	Saint Bernard (61)	11-02-2018		1
<input checked="" type="checkbox"/>	Vet-Gen-BE	Mammals Dogs (Canis)	Saint Bernard (61)	15-04-2020		2




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

Request ✕

te>

Date of Request

 08-12-2023

Laboratory Requester

Vet-Path-ZH 

Requester

Elena

Study Name

Hypoadrenocorticism

Email

elena.dhein@uzh.ch

Comments

 CREATE REQUEST

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

DiData Shared Minimal Dataset Overview Data View Storages Dashboards More ... Elena ED

Dashboards Search +

- Samples
- My selection
- My sent requests**

Sort **My sent requests** Enable edit mode Projects

My requests

Search entities					
ID	er	Study Name	Request Reference	Request Status	
<input checked="" type="checkbox"/>	264103	08 Vet-	Hypoadrenocortic	R264103	Requested
<input type="checkbox"/>	264102	07 Vet-	Study 3	R264102	Requested
<input type="checkbox"/>	264101	07 Vet-	Study 3	R264101	Requested
<input type="checkbox"/>	264100	07 Vet-	Test Study 2	R264100	Requested
<input type="checkbox"/>	264093	07 Exte	Test Study	R264093	Accepted
<input type="checkbox"/>	249253	Vet-	Test3	R249253	Denied
<input type="checkbox"/>	249246	Vet-	Test 1.1	R249246	Requested
<input type="checkbox"/>	249245	Vet-	Test1	R249245	Requested
<input type="checkbox"/>	249243	27 Vet-	Test	R249243	Accepted
<input type="checkbox"/>	247077	14 Vet-	Lennox	R247077	Requested
<input type="checkbox"/>	247076	14 Vet-	Lennox	R247076	Requested

Rows per page 50 0 - 17 to 17

My requested samples

Search entities			
Date of Sample Reservation	Request Status	Link to Request	
<input type="checkbox"/>	07-12-2023	Requested	R264103
<input type="checkbox"/>	07-12-2023	Requested	R264103
<input type="checkbox"/>	07-12-2023	Requested	R264103

Rows per page 50 0 - 3 to 3

3. Sample requests – How to process requested samples

The screenshot shows the DiData interface for the Vet-Gen-BE project. The top navigation bar includes 'Overview', 'Data View', 'Storages', 'Dashboards', and 'More ...'. The user 'Elena' is logged in. The main area is titled 'Requests' and features a sidebar with 'Requests' and 'Received samples'. A toolbar contains icons for 'Deny request', 'Accept request', 'Cancel sample', 'Aliquot sample', and 'Ship samples'. Below the toolbar are two data tables: 'Requests' and 'Samples'.

Requests Table:

1	Study Name	Request Reference	Rec
<input checked="" type="checkbox"/>	Hypoadrenocortic	R264103	Re
<input type="checkbox"/>	Study 3	R264102	Re
<input type="checkbox"/>	Study 3	R264101	Re
<input type="checkbox"/>	Test Study	R264093	Ac
<input type="checkbox"/>	Test Study	R264092	Re
<input type="checkbox"/>	test e,qil	R189318	Re
<input type="checkbox"/>		R189312	Re
<input type="checkbox"/>	Roya	R189268	Ac
<input type="checkbox"/>		R189267	Re

Samples Table:

3	Owner Name	Owner Address	Donor Diseases (all)	Specimen Class	Sample Type
<input checked="" type="checkbox"/>	Name, Surname	Address XX	hypoadrenocorticism	Liquid	Blood (whole)
<input checked="" type="checkbox"/>	Name, Surname	Address XX	hypoadrenocorticism	Liquid	Blood (whole)
<input checked="" type="checkbox"/>	Name, Surname	Address XX	hypoadrenocorticism	Liquid	Blood (whole)

3. Sample requests – How to process requested samples

Original sample owner:

The screenshot shows the DiData interface for the 'Vet-Gen-BE' project. The 'Sample' section is active, displaying a table with the following data:

Donor Call Name	Donor Diseases (all)	Request Status
<input type="checkbox"/> Kigali	hypoadrenocorticism	Shipped
<input type="checkbox"/> Ayko	hypoadrenocorticism	Shipped
<input type="checkbox"/> Easy	hypoadrenocorticism	Shipped

Requesting biobank:

The screenshot shows the DiData interface for the 'Vet-Path-ZH' project. The 'Test' section is active, displaying a table with the following data:

Donor Call Name	Donor Diseases (all)	Request Status	Project Name
<input type="checkbox"/>	hypoadrenocorticism	Shipped	Vet-Gen-BE
<input type="checkbox"/>	hypoadrenocorticism	Shipped	Vet-Gen-BE
<input type="checkbox"/>	hypoadrenocorticism	Shipped	Vet-Gen-BE



4. Summary

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



Universität
Zürich ^{UZH}

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b
UNIVERSITÄT
BERN

Thank you! 😊

ACCREDITED BY EA/EVE/FVE

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 Guscelli (franco.guscelli@vetpath.uzh.ch)

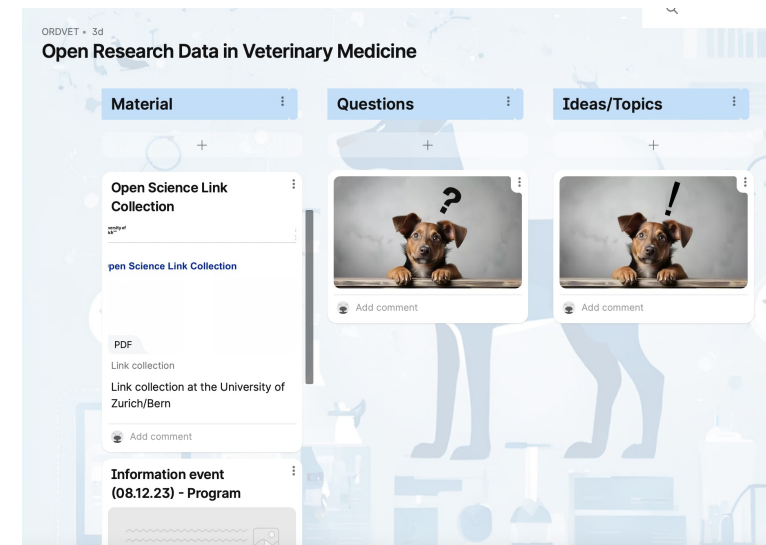
General questions, remarks, ideas (open science, controlled vocabularies):

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



Thank you!

