



European **Rare Diseases**
Research Alliance

ERDERA

Diagnostic Research Workstream

- An Overview

Holm Graessner, DRW Lead
28.05.2026



Co-funded by
the European Union

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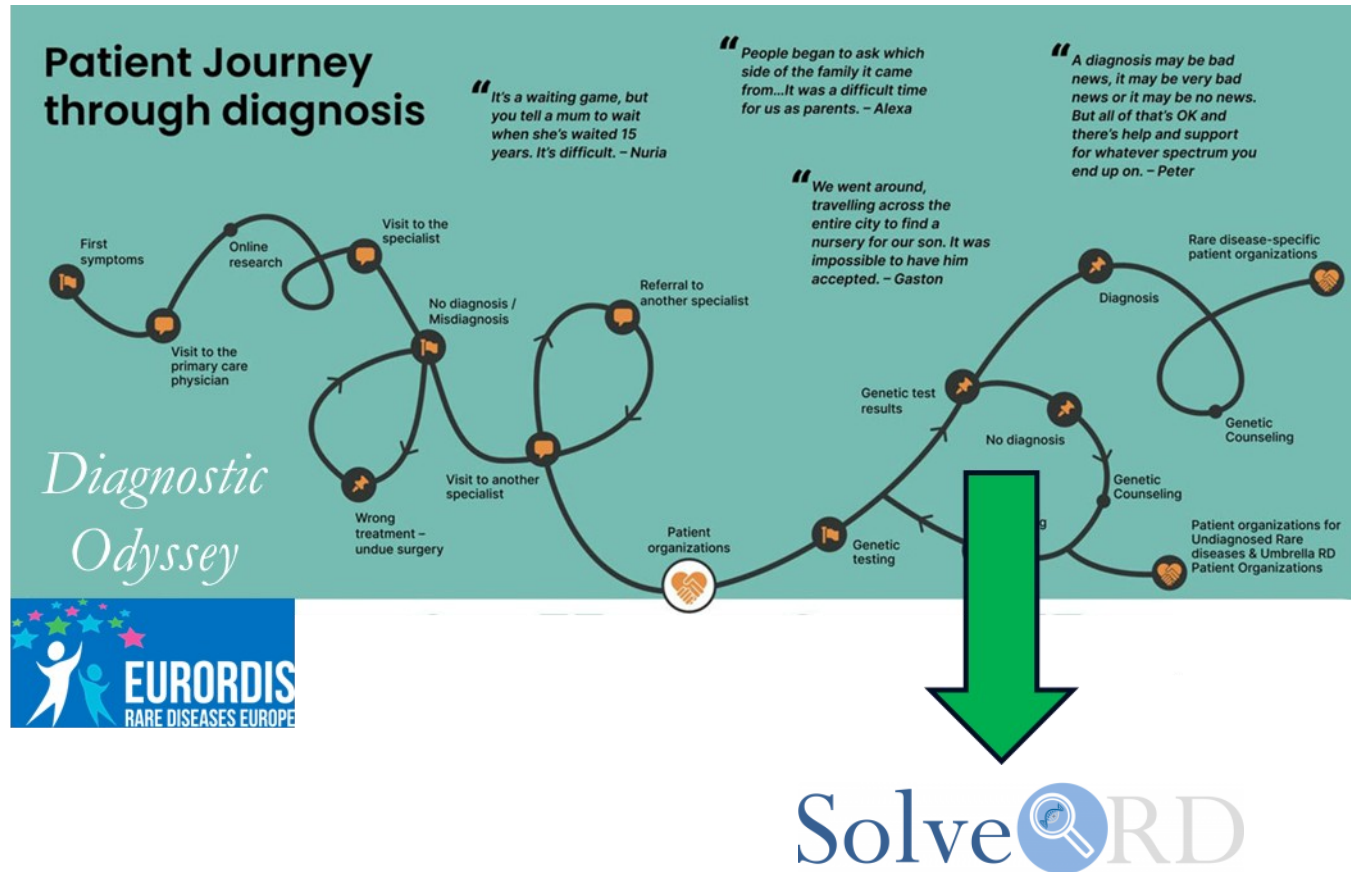
The ERDERA Diagnostic Research Workstream Webinar Series

TODAY

#	Title	Topic	Speakers	Date	Event link
1	The ERDERA Diagnostic Research Workstream – An Overview	General overview of the DRW	Holm Graessner	28 May 2026	View event
2	Data sharing, data management & ethics	DSFA, ethics, data submission, data flow, RD3	Kornelia Ellwanger, Leslie Matalonga	September 2026	Link coming soon
3	The data reanalysis approach of the Diagnostic Research Workstream	Tiered approach, DITF-DATF structure, Solvathon concept	Lisenka Vissers	October 2026	Link coming soon
4	Long-read sequencing and Optical Genome Mapping	WP8 long-read sequencing and OGM	Bart van der Sanden, Alexander Hoischen, Stephan Ossowski / Tobias Haack (tbc)	December 2026	Link coming soon
5	Results of the systematic reanalysis	Results of data reanalysis Tier 1	Sergi Beltran, Gemma Bullich, Lisenka Vissers	February 2027	Link coming soon
6	First results from our innovative reanalysis approach	Results of data reanalysis Tier 2	Sergi Beltran, Lisenka Vissers (tbc)	April 2027 (tbc)	Link coming soon
7	Scaling-up: from distributed to federated reanalysis	Distributed vs. federated approach	Sergi Beltran, Morris Swertz, Julien Thevenon (tbc)	May 2027	Link coming soon
8	Reanalysis of RNAseq data	RNAseq reanalysis results	Vicente Yépez	June 2027	Link coming soon

From Solve-RD to ERDERA's Diagnostic Research Workstream

Pathway to Solve-RD research



- Patients with suspected genetic RD and without a molecularly proven genetic diagnosis
- Patients for whom exome sequencing has been done
- Informed patient consent

SolveORD

Solving the Unsolved Rare Diseases



Neurological Diseases
(ERN-RND)

EURO-NMD

Building bridges and breaking barriers
in rare neuromuscular diseases



ERN-ITHACA focuses on rare
congenital malformation syndromes
and intellectual disability



GENTURIS

rare genetic tumour risk syndromes

SpäinUDP



EpiCARE

European Reference Network for rare
and complex epilepsies

rita

The European Reference Network that
aims at improving the care of patients
with Rare Immunological Disorders



Solve-RD Reanalysis

Goals:

- EU partners **share data** after extensive local expert analyses have proven unsuccessful
- Provide a diagnosis to as many undiagnosed patients as possible

**~22,500 datasets
(~13,000 families)**

UNSOLVED CASES*

Definition: Rare disease cases with an inconclusive exome/genome

Number: 19,000 unsolved exomes/genomes

Main activities: Perform standardised collation and re-analysis

**in collaboration with all ERNs, Undiagnosed Disease Initiatives and further associated partners*

1

SPECIFIC ERN COHORTS

Definition: Disease group specific cohorts from four core ERNs (exome available)

Number: a) 2,000 WGS for more complete (non-)coding sequence & CNV/SVs etc.;

b) 500 long-read WGS;

c) >2,000 cases novel omics approaches

Main activities: Conduct „beyond the exome“ approaches

2

ULTRA RARE RARE DISEASES

Definition: Phenotypically most special/remarkable patients with a rare disease without an exome

Number: 1,200 exomes (300 per core ERN)

Main activities: Carry out phenotype jamborees and exome analysis

3

4 THE UNSOLVABLES

Definition: Highly recognisable clinically defined diseases / syndromes for which no disease gene was identified yet despite WES/WGS and considerable research invested

Number: 120 syndromes/ diseases

Main activities: apply all -omics tools to „crack“ the „Unsolvables“

4

Solve-RD Reanalysis

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2

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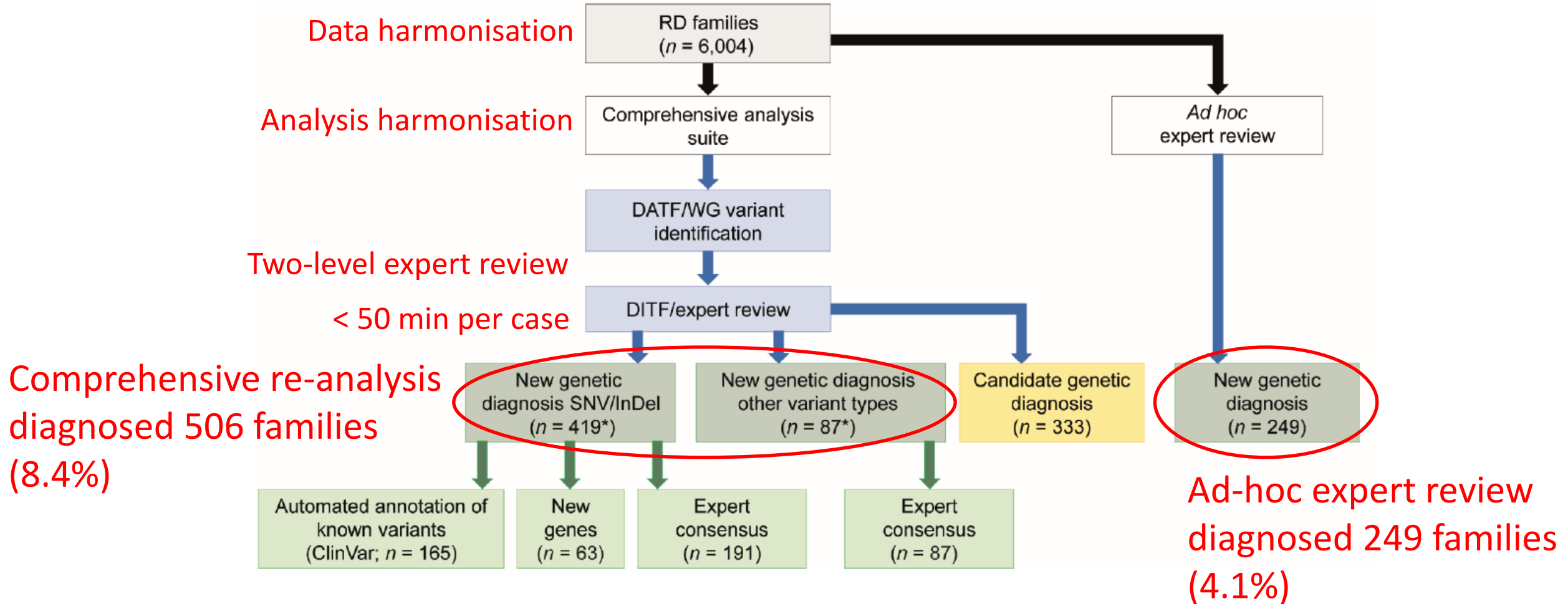
Article | [Open access](#) | Published: 17 January 2025

Genomic reanalysis of a pan-European rare-disease resource yields new diagnoses

[Steven Laurie](#), [Wouter Steyaert](#), [Elke de Boer](#), [Kiran Polavarapu](#), [Nika Schuermans](#), [Anna K. Sommer](#), [German Demidov](#), [Kornelia Ellwanger](#), [Ida Paramonov](#), [Coline Thomas](#), [Stefan Aretz](#), [Jonathan Baets](#), [Elisa Benetti](#), [Gemma Bullich](#), [Patrick F. Chinnery](#), [Jill Clayton-Smith](#), [Enzo Cohen](#), [Daniel Danis](#), [Jean-Madeleine de Sainte Agathe](#), [Anne-Sophie Denommé-Pichon](#), [Jordi Diaz-Manera](#), [Stephanie Efthymiou](#), [Laurence](#)

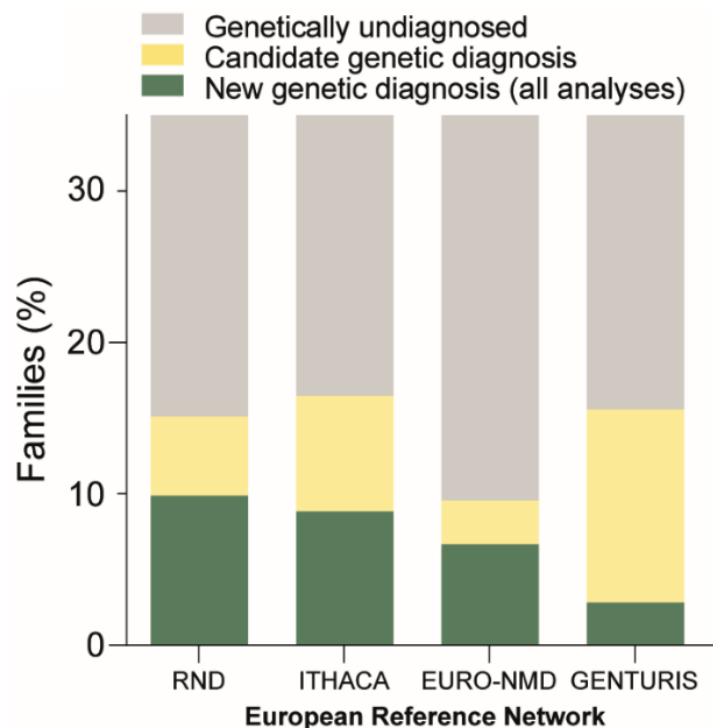
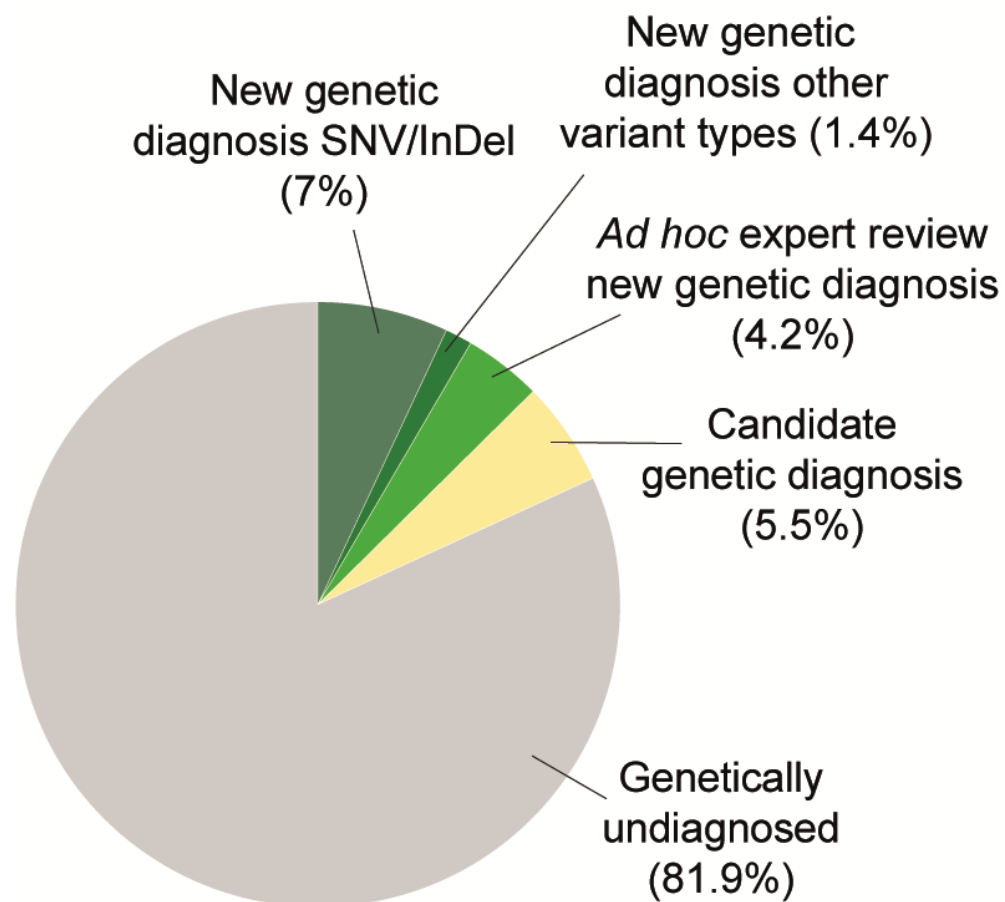


Re-analysis: yield





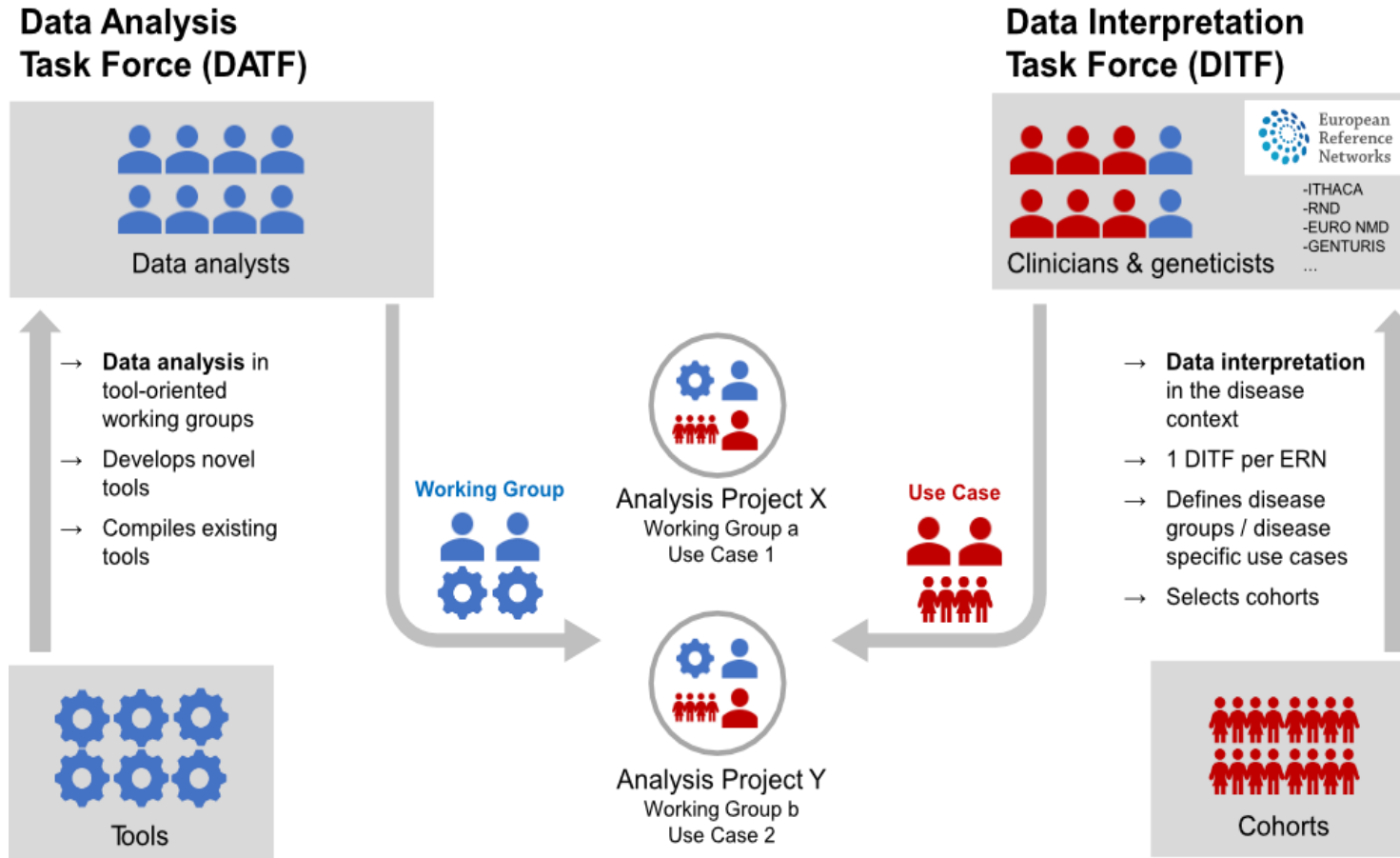
Re-analysis: yield per ERN



Total families with new diagnosis:

- Systematic re-analysis: 506
- *Ad hoc*: 249
- Candidates: 333

Joint Expert Reanalysis

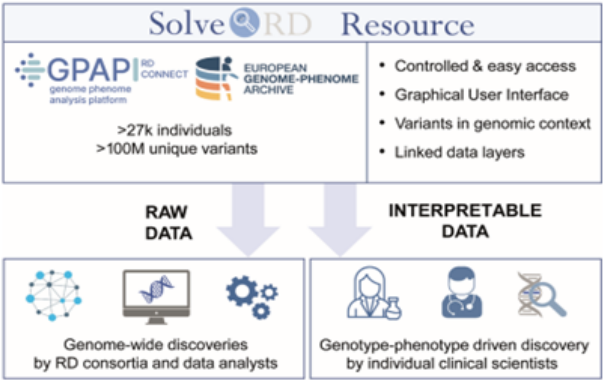


Zurek et al, 2021

From Solve-RD to ERDERA

Use case: systematic diagnostic research re-analysis

2018 - 2024



> 15% diagnoses



WES, WGS	Omics type	WES, WGS, RNAsequ, Epigenetic
Short read	Technology	Short & long read
6 ERNs	Diseases	> 15 ERNs
23.000	Numbers	> 100.000
Selected EU countries	Geographic outreach	EU + incl. underrepr.
distributed	Analysis type	Distributed and federated

2024 - 2031

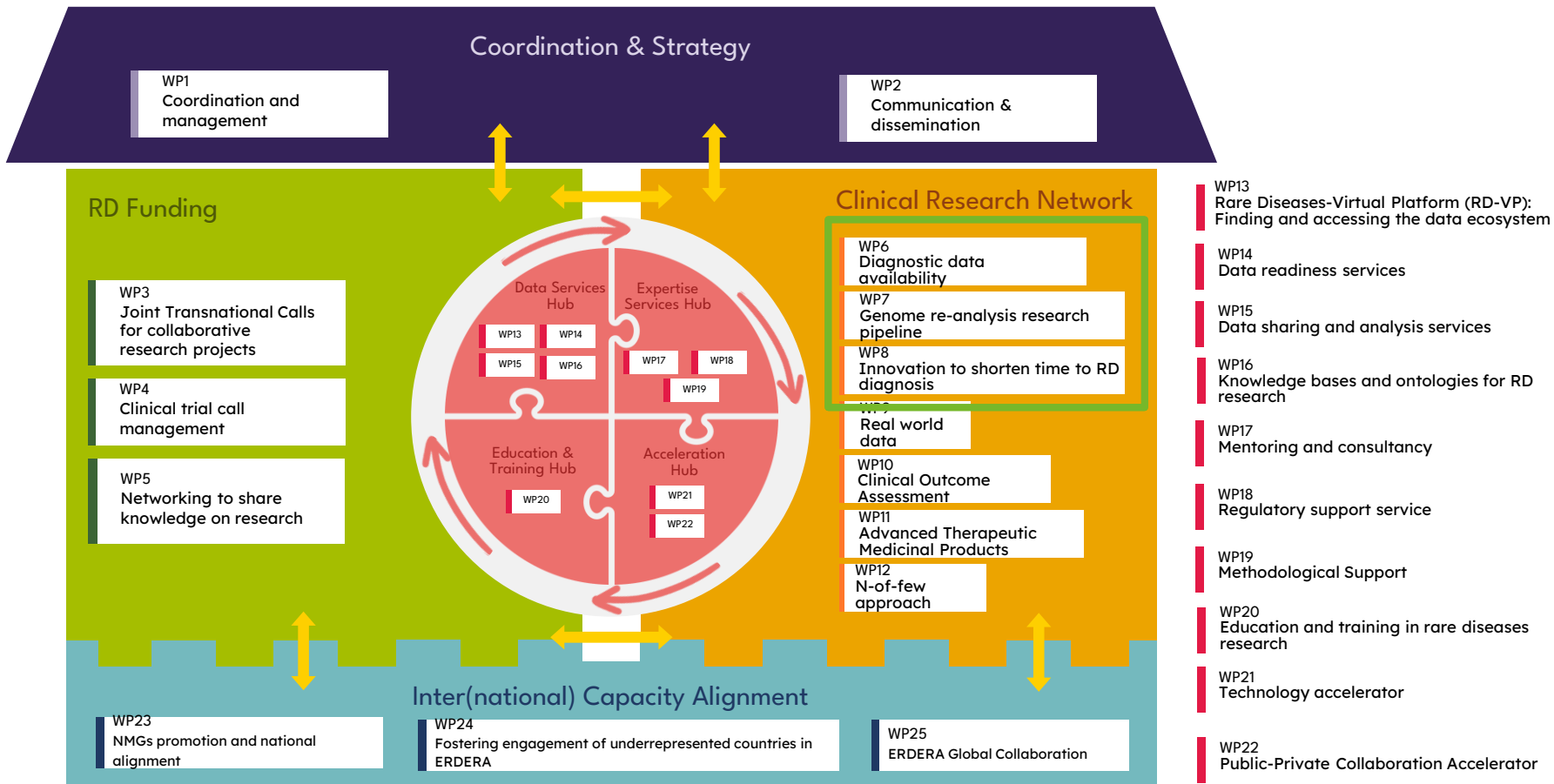


> ? % diagnoses

Diagnostic Research Workstream

ERDERA
European Rare Diseases
Research Alliance

Diagnostic Research Workstream of ERDERA

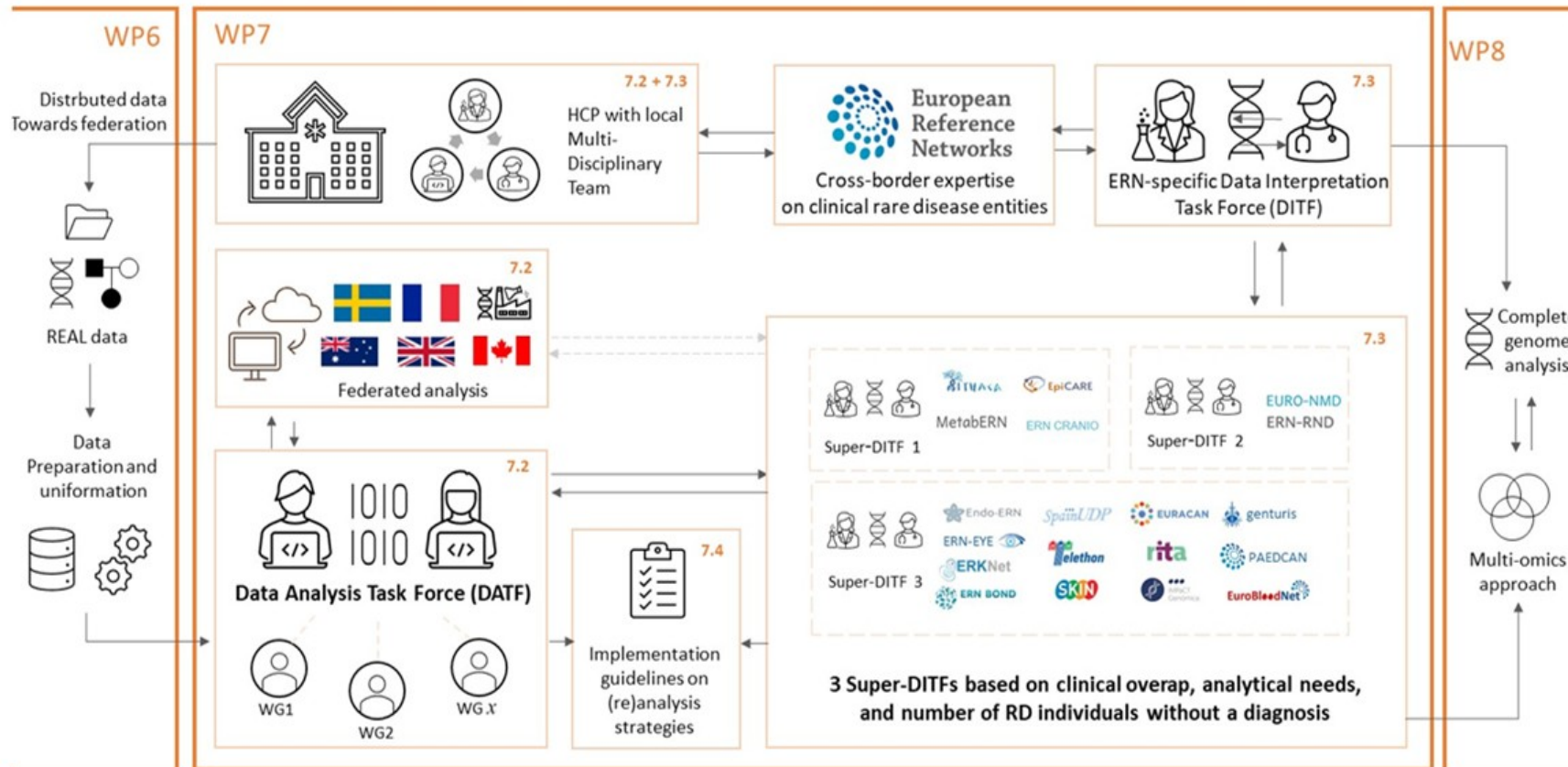


DRW Work Packages

Data Availability

Genome Re-Analysis Research Pipeline

Innovation to shorten time to RD diagnosis



WP6

Data Availability

WP6 Objectives and Governance

1. Expand diagnostic data availability and collation effort
2. Implement data standardization and quality criteria for other omics data besides WES and WGS
3. Operationalise results return workflow and facilitate collaborative variant interpretation

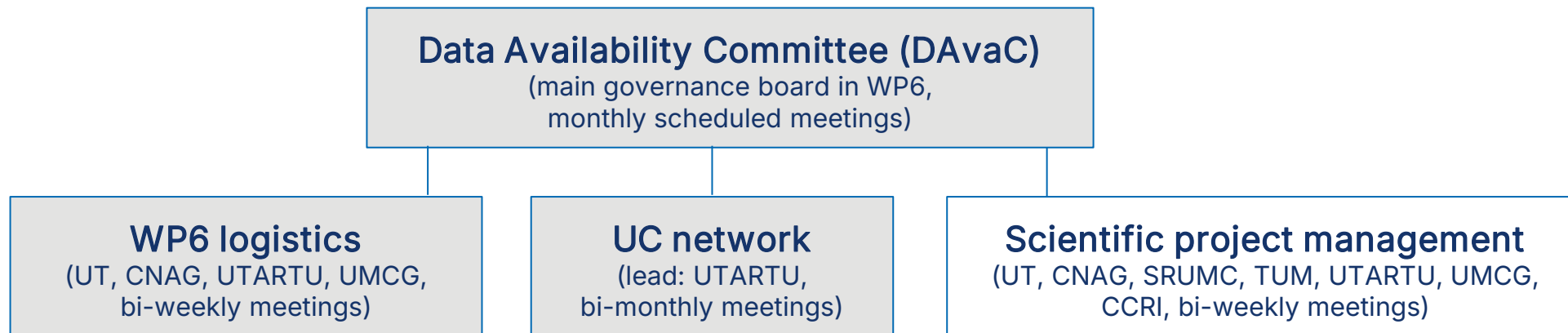
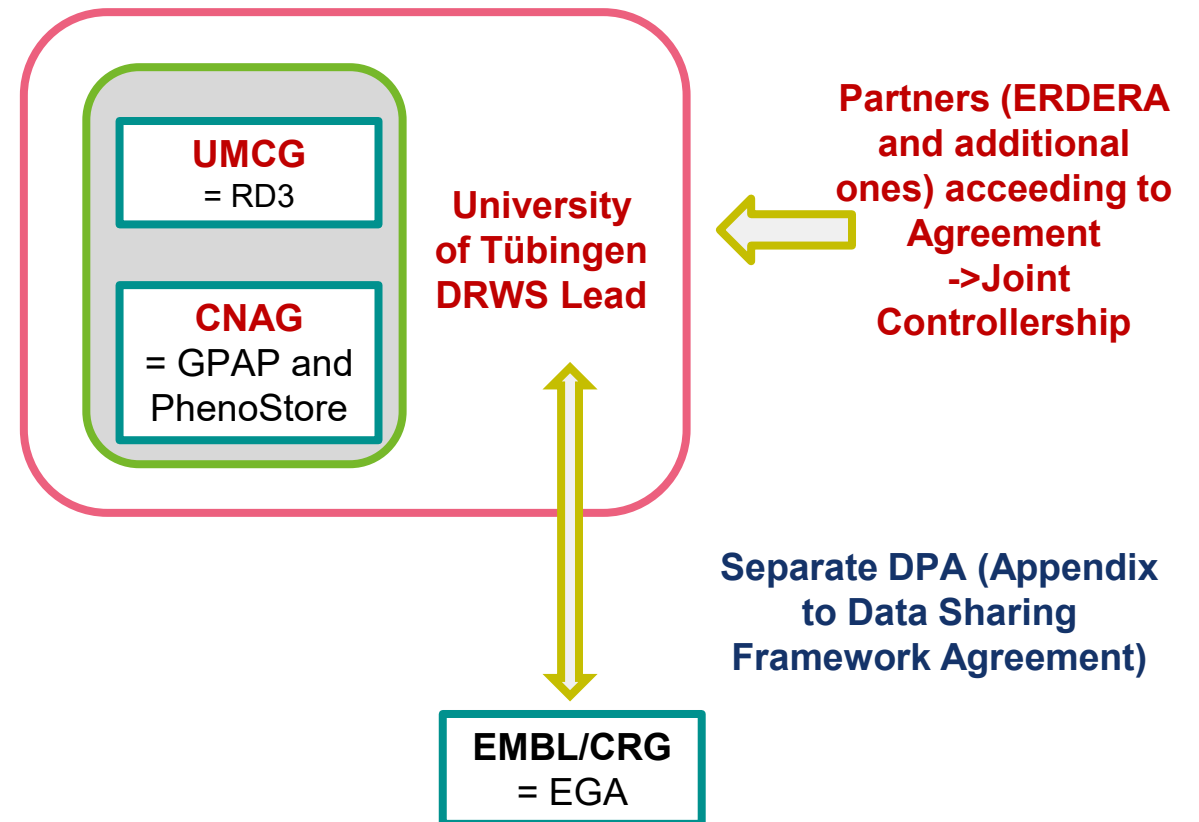


Figure: WP6 governance structure

Expand diagnostic data availability and collation effort

- Implemented **Data Sharing Framework Agreement** as a core enabler for secure and compliant transnational data sharing



Expand diagnostic data availability and collation effort

- Implemented **Data Sharing Framework Agreement** as a core enabler for secure and compliant transnational data sharing
- >44 centres have joined the **joint controllership**, including all key data-contributing centres active in the first two project years; partner accession remains ongoing (incl. Non-ERDERA partners)
- Implemented option to **access data** for partners under the agreement based on study proposals. Access is carefully governed to ensure data protection and **full compliance with the Data Sharing Framework**

Diagnostic Research Programme - Joint Controller



Figure: Institutions and countries that have signed the Data Sharing Framework Agreement as of 03/2026

Data Standardization & quality criteria

- ❖ Data standards for WES, WGS and RNAseq based submission and re-analysis (developed and adopted and approved by the Data Availability Committee (DAvaC))
- ❖ Adoption of data standards for LR-WGS and OGM submission in progress
- ❖ Established results return workflow and collaborative variant interpretation

ERDERA - datasets inclusion criteria

version v2.0 (04. December 2025)

Preamble:

The ERDERA Diagnostic Research Workstream is dedicated to advancing the understanding and diagnosis of rare diseases (RD). The workstream serves as a centralised platform for the collection and distribution of phenotypic and -omics data from individuals with rare diseases, enabling collaborative, distributed analyses aimed at resolving diagnostically challenging cases. Partners involved in the ERDERA Diagnostic Research Workstream are not only responsible for contributing data, but must also play an active role in the interpretation of results and update patient information in case of changes in the clinical phenotype or proband resolution.

ERDERA will collate datasets from **undiagnosed patients (and relatives)** submitted by ERNs, UDPs and national diagnostic centers. These datasets must include Pheno-clinical and pedigree information linked with their corresponding genomic datasets and (optionally) other omics data such as transcriptomics, epigenomics, proteomics, and metabolomics.

This document provides detailed information on the types of pheno-clinical information and (gen)omics data accepted by ERDERA for the distributed approach. Our data standards align with international initiatives such as GA4GH¹, the 1+MG framework and GDI², and will be used as a starting point for defining the federated approach common standards in ERDERA:

1. [Pheno-Clinical and Pedigree information](#)
2. [Genomics data](#)
3. [Other Omics](#)
4. [Annexes](#)

Glossary:

Pheno-clinical data: comprehensive information that includes both phenotypic (observable characteristics and traits) and clinical (medical history, symptoms, and diagnostic results) details of a patient, used to aid in the diagnosis and management of medical conditions.

Proband: The individual in a family who is first identified as having a particular genetic disorder or trait and who brings the family to medical attention for genetic study and testing.

Pedigree information: a diagram that represents the familial relationships and transmission of the disorder of the proband across multiple generations.

(Re)analysis / (re)evaluation: process of reviewing and interpreting previously collected genomic data of a proband with the goal of identifying new genetic variants, reassessing previously identified variants, or incorporating updated knowledge and methodologies.

Undiagnosed patient: An individual suspected of having a rare genetic disease, whose molecular cause remains unidentified despite having completed the national and/or local diagnostic pathway.

¹ <https://www.ga4gh.org/>

² <https://gdi.onemilliongenomes.eu/>

Expand diagnostic data availability and collation effort

- Data sharing of > 10,000 WES/WGS in year 1;
Additional >29,000 WES/WGS/omics submissions for ERDERA Year 2 in progress
- Successful deposition of the first Year 1 datasets at the **EGA**, establishing the basis for controlled sharing of raw genomic data among joint controllers
- Expanding Network of Underrepresented Countries (Ucs) in the Diagnostic Research Programme. Regular webinars to address specific needs: Ethics/GDPR, sample processing, and AI-driven diagnosis

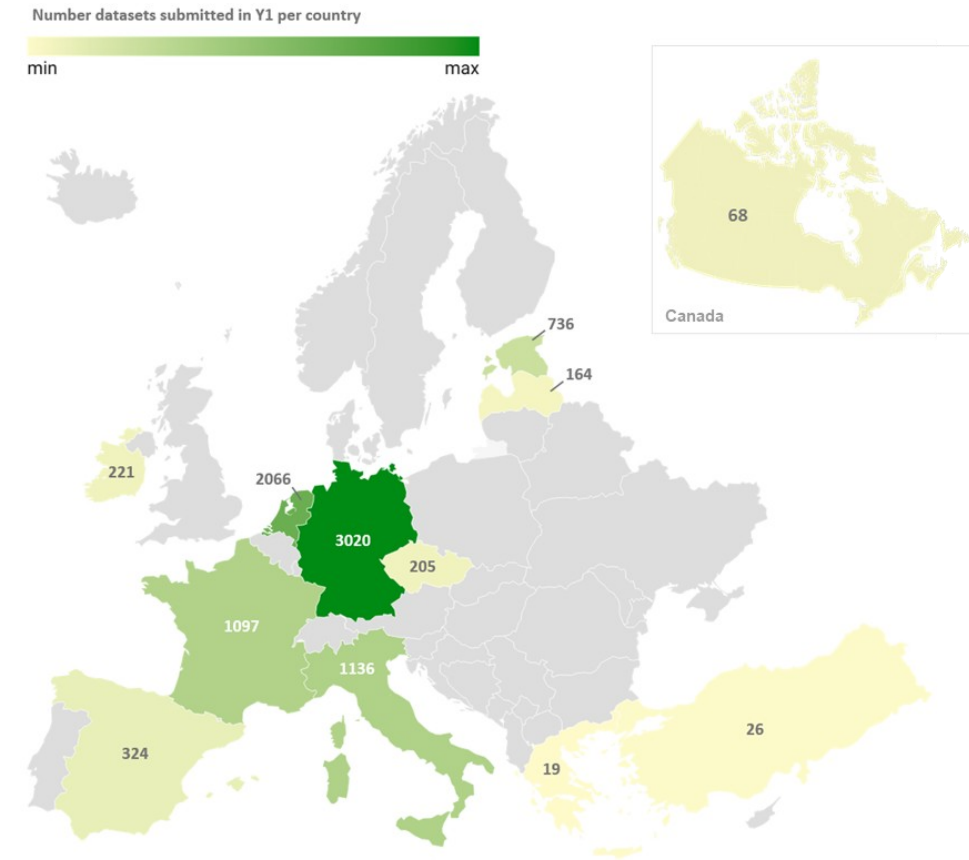


Figure: WES/WGS dataset submission numbers per country in year 1

Created with Datawrapper

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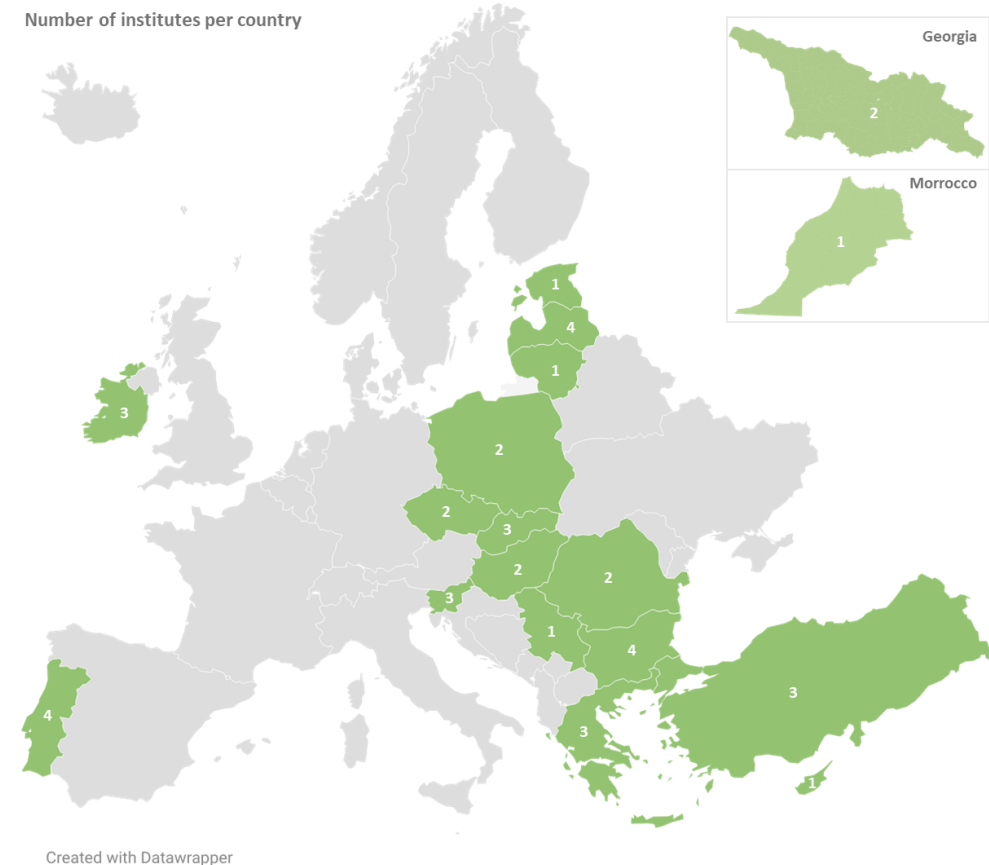


Figure: WP6 network of Underrepresented Countries (UCs) as of 10/2025

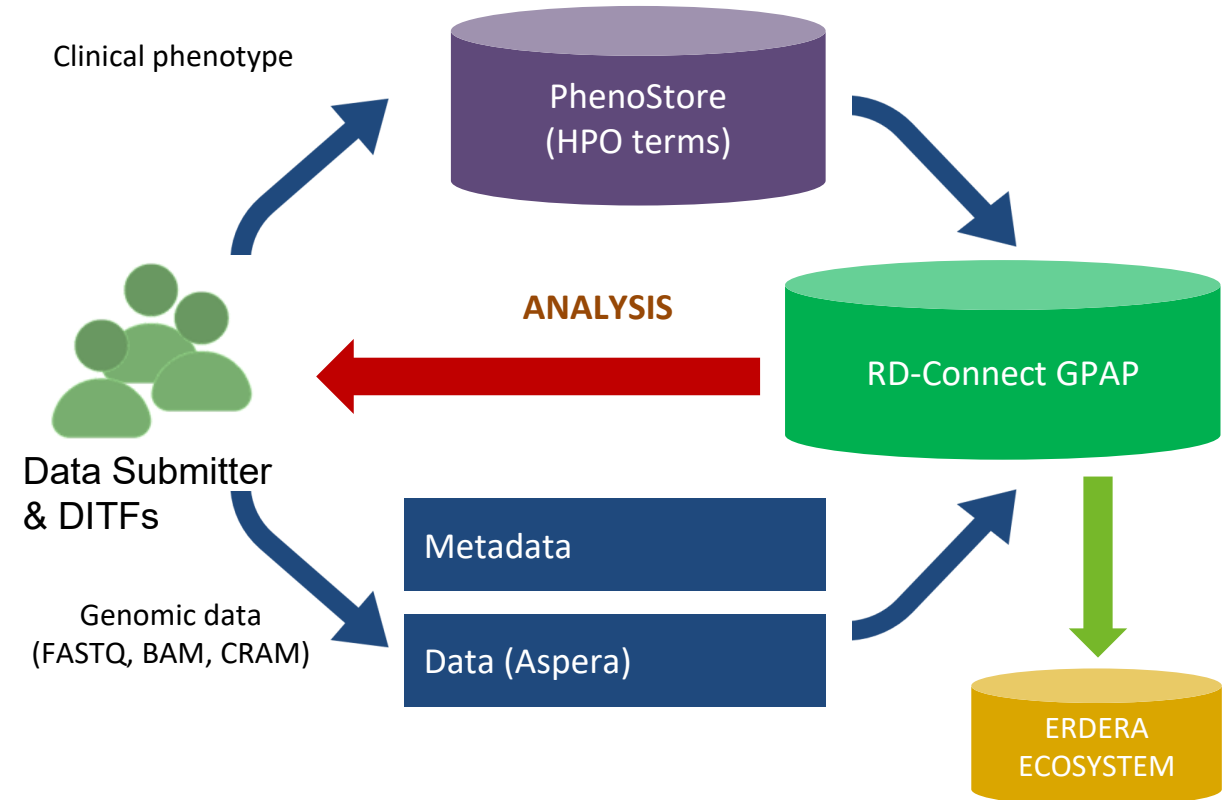
Current Submission Workflow

distributed approach

WES/WGS (for re-analysis)

1. Pheno-clinical information will be collated through GPAP-PhenoStore using standards and ontologies.
2. Genomic information from srWES and srWGS:
 - metadata will be collated in GPAP
 - Files submitted through Aspera

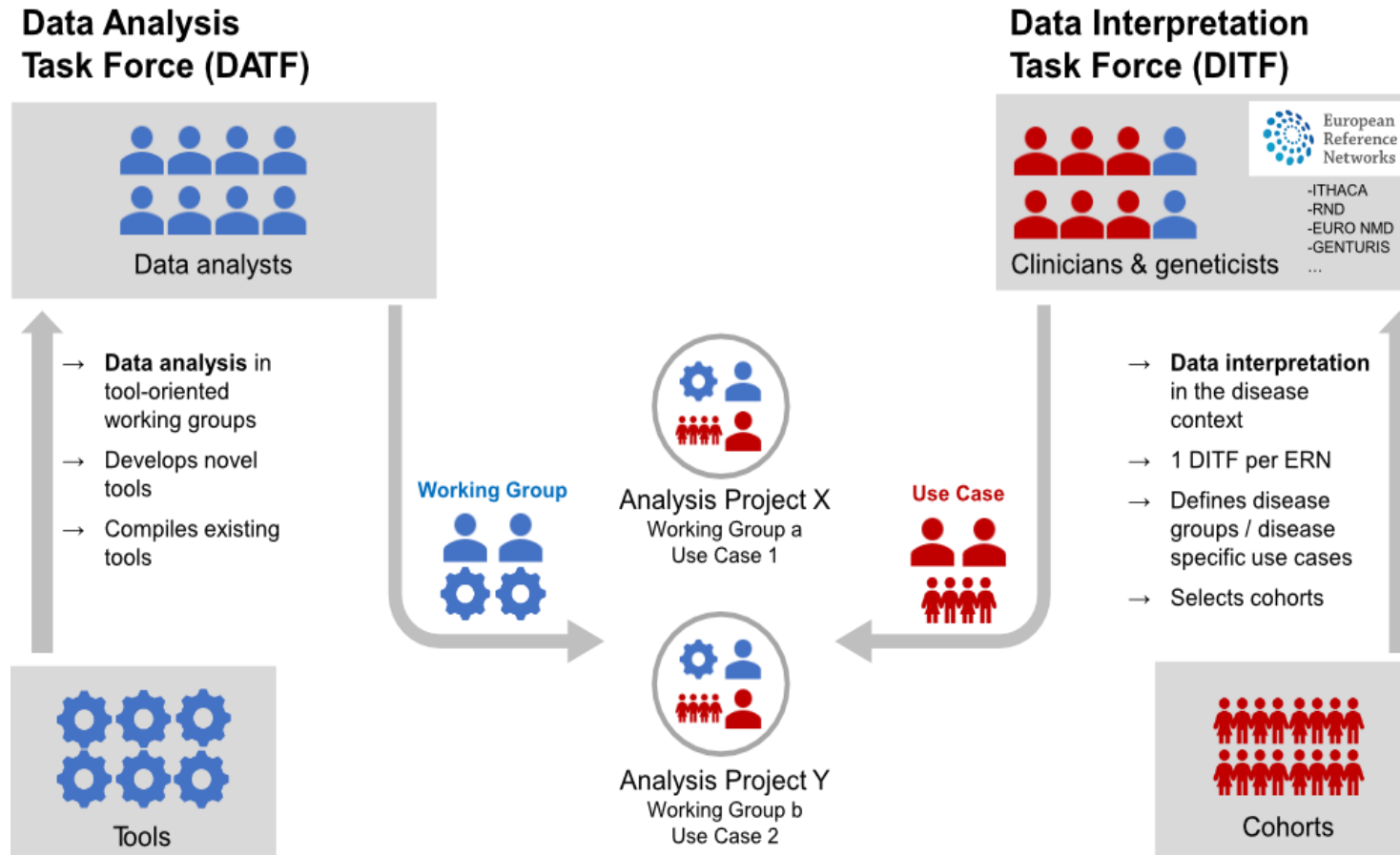
Processes for submission of RNAseq and LR-WGS data are currently in progress



WP7

Genome Re-Analysis Research Pipeline

Joint Expert Reanalysis – DATF and DITFs

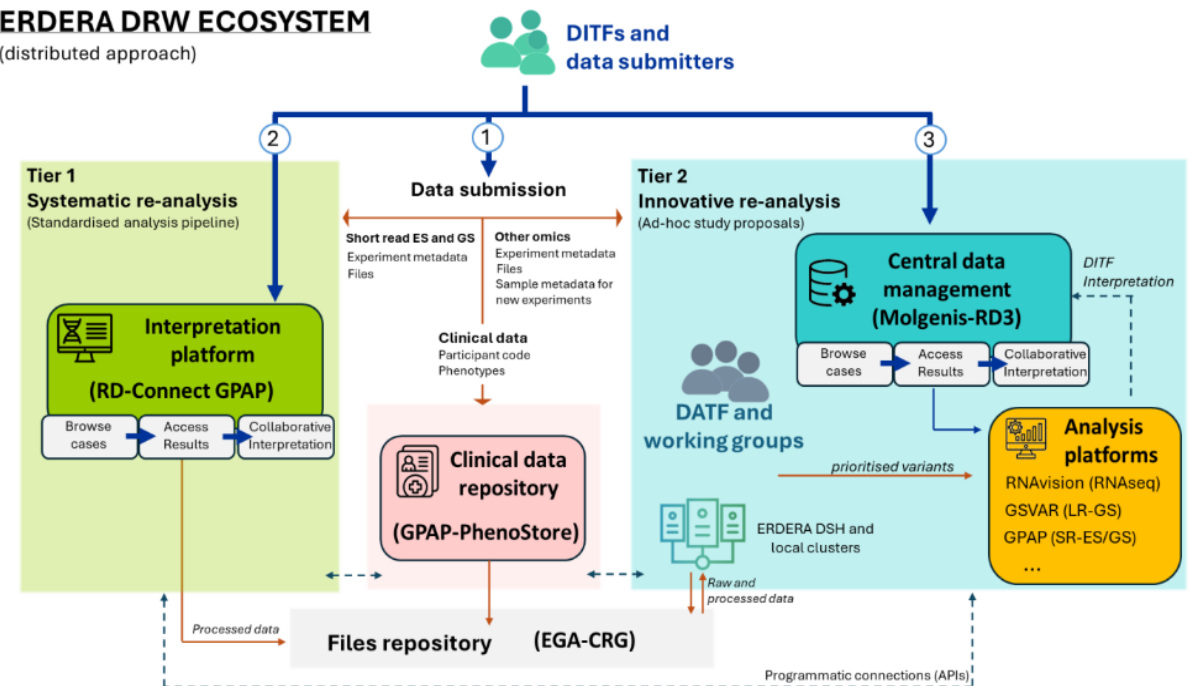


Reanalysis Workflow (for unsolved exome and genome datasets)

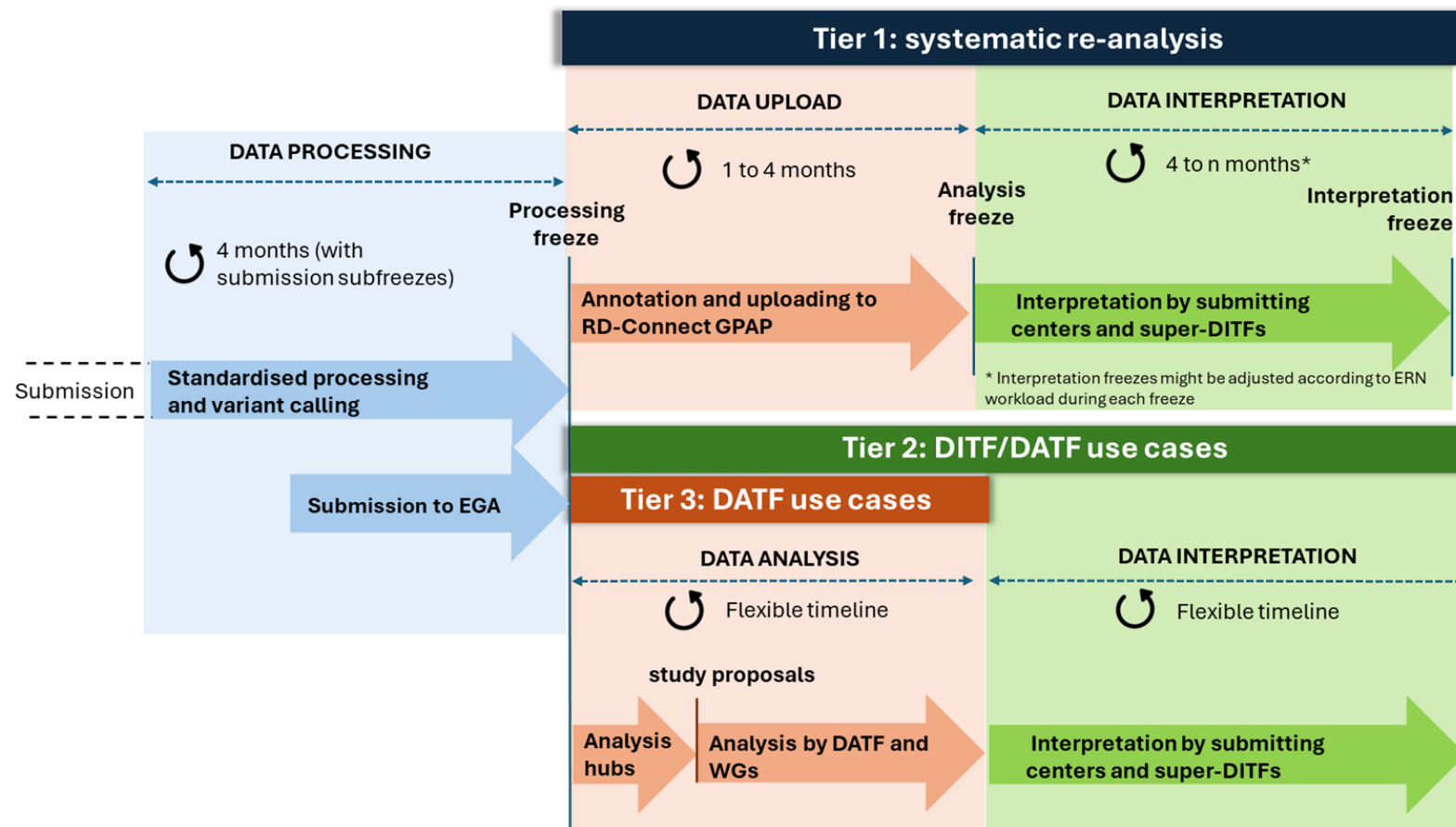
- **Submission** of data of diagnostically unsolved patients
- Central **re-annotation and re-analysis** for WES/WGS pipeline via CNAG (DRAGEN v4.4.6)
- **Additional analysis tailored to variant type** in analysis hubs – DATF Working Groups
- **Case based interpretation** by submitting centres in GPAP
- **Group based interpretation** led by ERN led/informed DITF
- **Availability of result data** via EGA (CRG)
- **Flagship publication** of results via ERDERA
- **DITF specific publications** via DITFs and DATF WG

ERDERA DRW ECOSYSTEM

(distributed approach)



Reanalysis Workflow (for unsolved exome and genome datasets)



Super-DITF/DITF Structure

Leads Super DITF 1
Lisenka Vissers
Holger Lerche/Christian Boßelmann



Leads Super DITF 2
Ana Topf/ Volker Straub
Bart Dermaut/ Dimitri Hemelsoet



Leads Super DITF 3
Richarda de Voer
Beatriz Martinez Delgado



DATF - WGs

WP7

DATF leads
Stephan Ossowski (UT), Christian Gilissen (SRUMC), Julien Thevenon (INSERM-CAD), and Sergi Beltran (CNAG)

Small DNA Variants WG
Leads: Gemma Bullich (CNAG),
Lennart Johansson (UMCG)

Large DNA Variants WG
Leads: German Demidov (UT)

**Integration and Decision
Support WG**
Leads: Julien Thevenon (INSERM-
CAD), Steven Laurie (CNAG)

**Statistical Testing and
Association Studies WG**
Leads: Christian Gilissen
(SRUMC)

Mt DNA Variants sub-WG
Lead: Ida Paramonov (CNAG)

Mosaic Variants sub-WG
Lead: Jessika Nordin (UU)

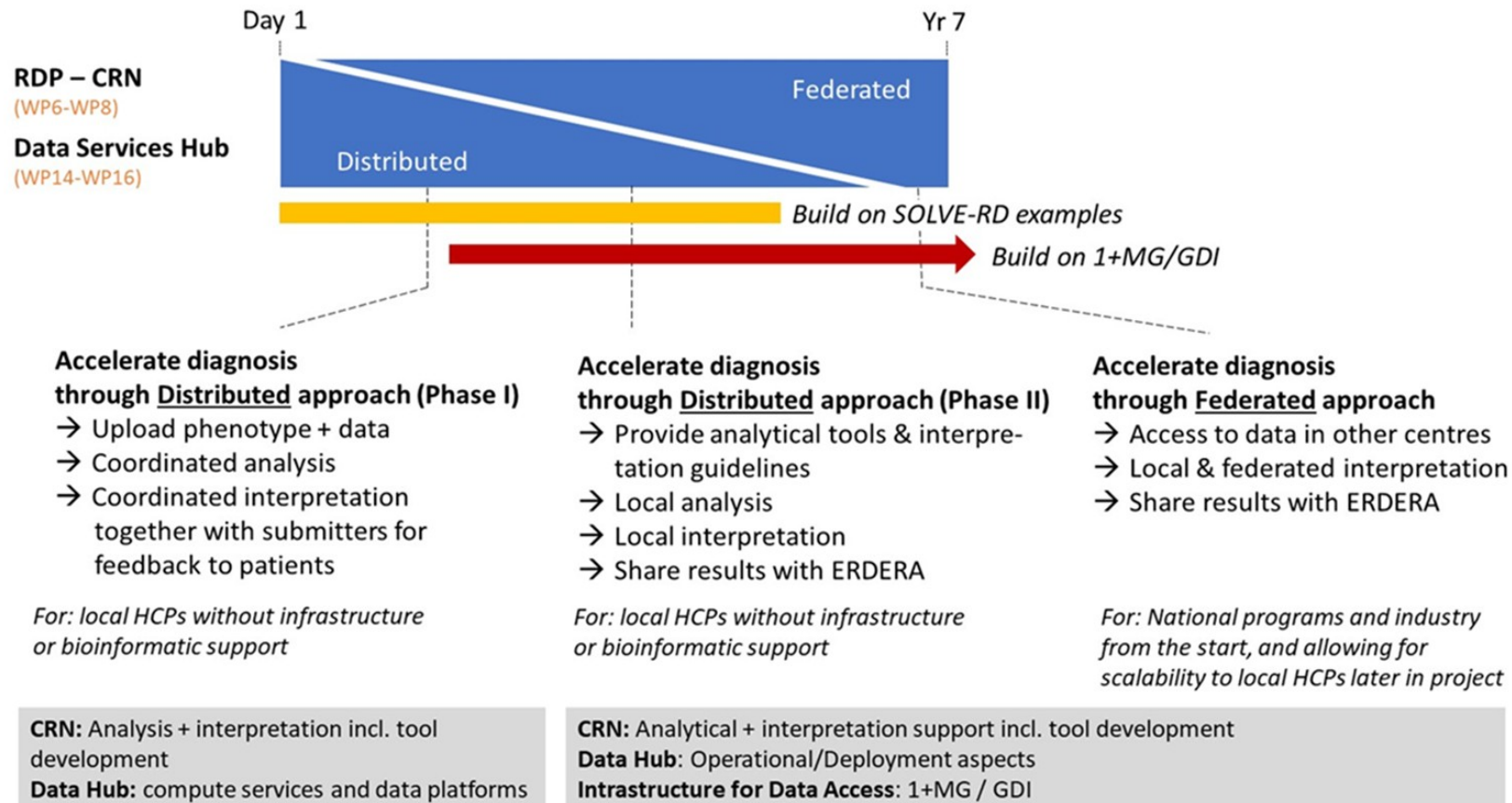
WP8

Long-Read Sequencing WG
Leads: Alexander Hoischen
(SRUMC), Stephan
Ossowski (UT), Tobias
Haack (UT)

**Optical Genome Mapping
WG**
Leads: Alexander Hoischen
(SRUMC), Stephanie
Efthymiou (UCL)

RNAseq WG
Leads: Vicente Yépez
(TUM), Anna Esteve (CNAG)

From distributed to federated reanalysis



WP8

Innovation to shorten time to RD diagnosis

WP8 - Innovations to Shorten Time to Diagnosis

Cutting-edge genomics and integrated multi-omics approaches to accelerate the diagnosis of rare diseases

Key activities

- Conducting novel **IrWGS** and **OGM** and **comprehensive analyses** for challenging rare disease cases from Underrepresented Countries (UC).
- Developing RNAseq- and **integrated multi-omics methods** to improve the analysis and interpretation of genetic variation.
- Facilitating the **adoption of innovative approaches across Europe**, strengthening diagnostic solidarity and capacity.
- Organizing **dedicated training sessions** and **Solvathons** focused on RNAseq, IrWGS and OGM data interpretation and diagnosing undiagnosed cases.

WP8 - Opportunities for centers from Underrepresented Countries (UCs)

Submit biosamples for the generation of novel data for analysis together with experts in the field

Long-read genome sequencing

PacBio

160 samples

Radboudumc, Nijmegen, Netherlands

 **OXFORD
NANOPORE**
Technologies

160 samples

University of Tübingen, Tübingen, Germany

Optical genome mapping

bionano
GENOMICS

200 samples

Radboudumc, Nijmegen, Netherlands

Centers from UCs interested in submitting samples for lrWGS and/or OGM data generation? Complete the [linked template](#) and submit it to [Bart van der Sanden](#) (Radboudumc, the Netherlands) to see if your samples/cases qualify for lrGS/OGM data generation.

Links and contacts

Resources

- [Dataset inclusion criteria](#) (standards, formats and minimum quality criteria for data submission)
- [Data submission toolkit](#) (incl. links to dedicated submission guidelines)
- [Data Sharing Framework Agreement](#)
- [RD-Connect GPAP registration](#)

Questions or comments?

Please contact us!

ERDERA-diagnostic-research@med.uni-tuebingen.de

help@rd-connect.eu

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NEXT



European Rare Diseases
Research Alliance



Thank you!

For further information get in touch with us:

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