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Radboud University Medical Center, Nijmegen

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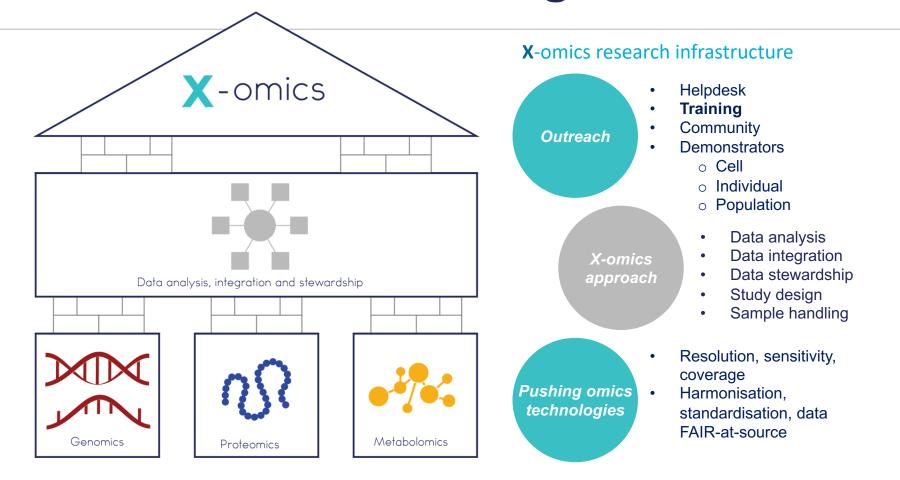
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(X-omics project
management team)



Strategies to overcome your challenges in multi-omics data integration





18th June - Data standards and multi-omics data integration

22nd June - Linked data in practice

25th June - Showcases of multi-omics data integration

30th June - Pitch your own multi-omics project

Visit and register: https://www.x-omics.nl/training-outreach/see-all-events



Strategies to overcome your challenges in multi-omics data integration



Expertise

X-omics-nl

Genomics

Proteomics

Metabolomics

Data analysis, integration and stewardship

Other

Workshop Series

Strategies to overcome your challenges in multi-omics data integration

Thursday 18th June 2020

Data standards and multi-omics data integration



Data standards and multi-omics data integration

- 10.00 Opening and intro by Anna Niehues, Radboud UMC
- **10.05** Keynote by Juan Antonio Vizcaino, EMBL-EBI
- 11.00 FAIR genomes showcase by Joeri van der Velde, umcu Groningen
- 11.15 EGA data standard showcase by Jasmin Böhmer, umcu utrecht
- 11.30 Interactive Quiz
- **11.45** Q&A



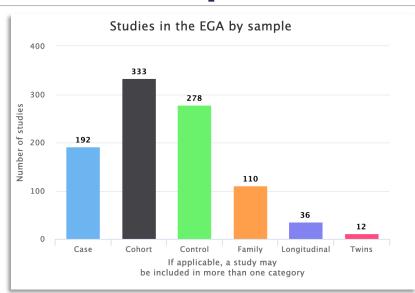


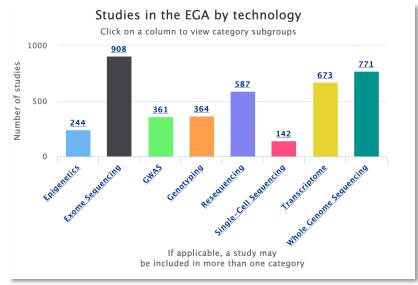
EGA Data Standard

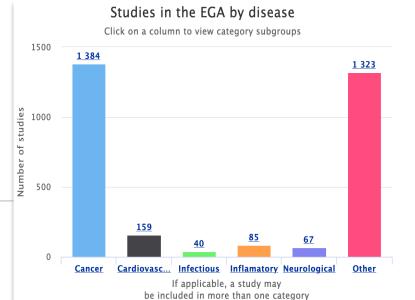
- EGA intro
- Submitting and Requesting to/from the EGA
- Data Use Ontology (DUO)



The European Genome Phenome Archive











EGA and Data Access Committee









Data Access Requirements
Informed Consent
Data Transfer Agreement – DTA
EU GDPR Contract









DAC example



Services we support

TRAINING Training we provide

DATA CONTACT V Data Stewardship Get in touch!

DATA ACCESS COMMITTEE

Welcome to the website of the Data Access Committee of the Division of Biomedical Genetics UMC Utrecht for the European Genome-Phenome Archive - EGA.

Here you can find the instructions on how to request access to the data-sets on EGA that are administrated by this Data Access Committee - DAC.

Both, the data access request and data submission process include the completion of a certain set of forms. On the right side you can find the forms as empty templates.

You would like to get access:

- Familiarise yourself with the Access Request forms.
- Fill in the Data Access Request Form.
- · Send this form and your CV to our DAC email-address.
- Please submit one access request per data-set.
- If you apply from outside of the European Union please show the DTA and Data Protection Adequacy Clause to your legal department.

The access request process:

- · You submit a data access request to us.
- We review your application and provide you with an initial evaluation of your application.
- . Within 60 working days the DAC will congregate and come to a final
- We inform you about the DAC decision based on your application documents.
- If affirmative, we send you the pre-filled DTA to you with the request approval email.
- Once we have received the signed DTA (and EU clause where applicable) from you back, we iniated the signature with our management team.
- As soon as you have received the final signed DTA back from us, we inform the EGA support desk to enable the access to the data-sets that you have applied for.

DAC FORMS FOR ACCESS REQUESTS

Data Access Request Form

Apply for the access to a data-set with this form. One acces request per data-

Data Transfer Agreement

The UMC Utrecht DTA template is our leading form for this type of contract.

Data Protection Adequacy

If you are an applicant outside of the European Union, you have to complete this data protection clause to ensure you comply to GDPR regulations.

DAC FORMS FOR SUBMISSIONS

Data Access

> Requirements

Define the permissions and limitations of the reuse of your published data.

Informed Consent

> Report about the informed consent you have applied for this data and how the participant have decided upon it.

EGA submission statement

Supply EGA with this submission statement to publish your data via our

DAC

Division of Biomedical Genetics UMC Utrecht

Dac ID	Contact Person	Email	Access Information
EGAC00001000432	DAC DBG	dacdbg [at] umcutrecht [dot] nl	http://ubec.nl/data-access-committee/

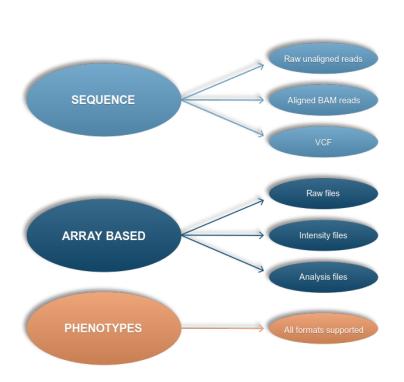
This DAC controls 35 datasets:

Dataset ID ^	Description Y	Technology ~	Samples ~
EGAD00001001900	DNA sequencing reads of human adult stem cell cultures from liver, colon and small intestine. Including biopsy or blood samples of the donors.	HiSeq X Ten,Illumina HiSeq 2500,NextSeq 500	61
EGAD00001002242	This dataset contains RNA-seq and Hi-C data files of induced pluripotent stem (iPS) cells and iPS cell-derived neural progenitors (NPCs) derived from a germline chromothripsis patient and both parents. iPS cells of the patient (cell lines 14 and 15), the father (lines 23 (with two replicates) and 32) and mother (line 30) were differentiated to NPCs and RNA was collected on day 0, day 7 and day 10 of differentiation. In addition, Hi-C data for two iPS cell-derived NPC lines from the patient (14 and 15) and two lines from the father (23 and 32) was generated.	AB 5500xl Genetic Analyzer,Illumina HiSeq 2500,NextSeq 500	22
EGAD00001002719	This dataset contains whole-genome sequencing data files from colon organoid cultures, which were mutated using CRISPR-Cas9 for specific genes (APC, KRAS, TP53 and SMAD4) to generate in vitro transformed cancer cells. After introducing each mutation, the resulting cultures were subjected to whole-genome sequencing. In addition, some cultures were xenotransplanted in recipient mice. The resulting primary tumors and corresponding metastases were subjected to whole-genome sequencing.	HiSeq X Ten	30
EGAD00001003291	This dataset represents RNA-sequencing data from 278 primary colon cancers obtained from fresh-frozen tumor sections. RNA-sequencing was performed using TruSeq library preparation and samples were sequenced on Illumina NextSeq and HiSeq. The data are available as Illumina NextSeq and HiSeq fastq files (_R1.fastq and _R2.fastq for each tumor sample, 556 files in total).	Illumina HiSeq 2500,NextSeq 500	278

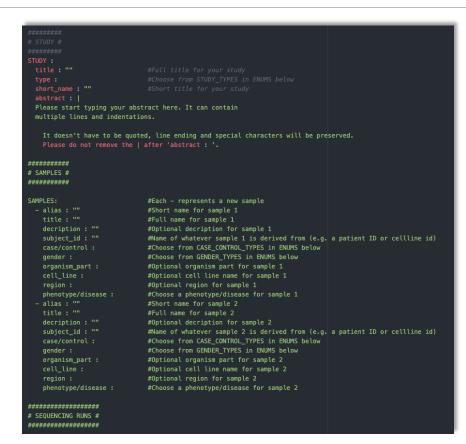




Submitting to EGA



Accepted Data Types by EGA



Requested Metadata by EGA

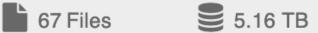




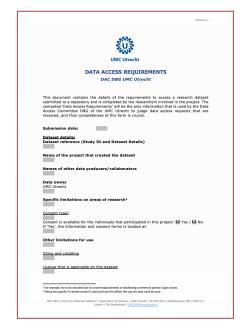
Submitting to EGA via the DAC













European Genome-phenome Archive c/o European Bioinformatics Institute Wellcome Trust Genome Campus Hinxton This document refers to the submission account, ega-box-521, which will be used to submit data and metadata to the European Genome phenome Archive (EGA) for the purpose of controlled access for individuals approved by a Data Access Committee (DAC). data and metadata to the EGA for archiving and distribution as part of your submission We can confirm that this submission is consistent with the informed consent of the participants of the study or has been granted ethical approval and is in accordance with the applicable laws and regulations. We understand that should any information referenced in this document be subject to change, an updated Submission statements document should be provided to the EGA. Sincerely, TITLE FULL NAME PI, Principal Investigator TILE FULL NAME PI, Principal Inve-

Access Requirements Informed Consent

EGA Submission Statement

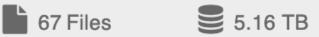




Requesting Access from EGA via the DAC



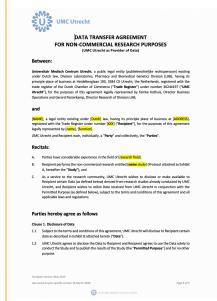








Access Request and Application



Data Transfer Agreement



EC GDPR Clause outside of EU

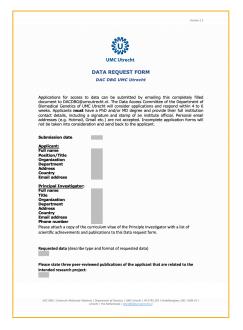




Assessing data access applications

ACCESS REQUEST:

Affiliation Collaboration Research Question

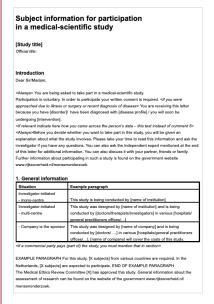




ACCESS RESTRICTIONS:

Re-use consent Further research limitations Other restrictions









Standardising data use conditions

Data Use Categories and Requirements (Consent Codes)



	Consent (Codes	
Name	Abbreviation	Description	
Primary Categories (I ^{ry})		<u> </u>	
no restrictions	NRES	No restrictions on data use.	
general research use and clinical care	GRU(CC)	For health/medical/biomedical purposes and other biological research, including the study of population origins or ancestry.	
health/medical/biomedical research and clinical care	HMB(CC)	Use of the data is limited to health/medical/biomedical purposes, does not include the study of population origins or ancestry.	
disease-specific research and clinical care	DS-[XX](CC)	Use of the data must be related to [disease].	
population origins/ancestry research	POA	Use of the data is limited to the study of population origins or ancestry.	
Secondary Categories (IIry) (can be	one or more extra cond	litions, in addition to Iry category)	
other research-specific restrictions	RS-[XX]	Use of the data is limited to studies of [research type] (e.g., pediatric research).	
research use only	RUO	Use of data is limited to research purposes (e.g., does not include its use in clinical care).	
no "general methods" research	NMDS	Use of the data includes methods development research (e.g., development of software or algorithms ONLY within the bounds of other data use limitations	
genetic studies only	GSO	Use of the data is limited to genetic studies only (i.e. no research using only the phenotype data).	
Requirements			
not-for-profit use only	NPU	Use of the data is limited to not-for-profit organizations.	
publication required	PUB	Requestor agrees to make results of studies using the data available to the larger scientific community.	
collaboration required	COL-[XX]	Requestor must agree to collaboration with the primary study investigator(s).	
return data to database/resource	RTN	Requestor must return derived/enriched data to the database/resource.	
ethics approval required	IRB	Requestor must provide documentation of local IRB/REC approval.	
geographical restrictions	GS-[XX]	Use of the data is limited to within [geographic region].	
publication moratorium/embargo	MOR-[XX]	Requestor agrees not to publish results of studies until [date].	
time limits on use	TS-[XX]	Use of data is approved for [x months].	
user-specific restrictions	US	Use of data is limited to use by approved users.	
project-specific restrictions	PS	Use of data is limited to use within an approved project.	
institution-specific restrictions	IS	Use of data is limited to use within an approved institution.	

SOM Dyke, et al. Consent Codes: Upholding Standard Data Use Conditions. PLoS Genetics 12(1): e1005772. http://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1005772

Contact: Dr. Stephanie Dyke (stephanie.dyke@mcgill.ca)

Data Use Ontology at EGA

The EGA is committed to its involvement in the work of GA4GH. In an effort to enhance data discoverability & streamline data access, EGA have implemented the use of the Data Use Ontology (DUO), based on consent codes as described in Dyke et al. 2017. The Data Use Ontology codes will be displayed on the live dataset page of your submission to advise any would be requestor on how the data can be used and also to enhance data discoverability as users will be able to search on these codes to find applicable datasets.

Detailed in the table below are the current DUO codes that should be added into the policy section of your submission in **webin** or used in your XML where submitting programmatically. These terms are verified against the current version **here**.

For each policy please select a maximum of one primary code and any number of secondary category codes (if appropriate), which are given in the table below.

Term	Label	Description
Primary Terms		
DUO:0000004	no restriction	This consent code primary category indicates there is no restriction on use.
DUO:0000005	general research use and clinical care	This primary category consent code indicates that use is allowed for health/medical/biomedical purposes and other biological research, including the study of population origins or ancestry.
DUO:0000006	health/medical/biomedical research and clinical care	This primary category consent code indicates that use is allowed for health/medical/biomedical purposes; does not include the study of population origins or ancestry.
DUO:0000007	disease-specific research and clinical care	This primary category consent code indicates that use is allowed provided it is related to the specified disease.
DUO:0000011	population origins or ancestry research	This primary category consent code indicates that use of the data is limited to the study of population origins or ancestry.

https://ega-archive.org/data-use-conditions



Data Use Ontology (DUO) tags on EGA

GWG Dataset

Dataset ID	Technology	Samples
EGAD00010001874	Infinium HD Super Microarray	576

Dataset Description

Patients with T1DM genotyped on Illumina HiScan using Illumina Infinium OmniExpress Exome-8 v1.4 arrays

Data Use Conditions









See further information on Data Use Conditions

Label Y	Code Y	Version ~	Modifier ~
health or medical or biomedical research	DUO:0000006	2019-01-07	
research use only	DUO:0000014	2019-01-07	
ethics approval required	DUO:0000021	2019-01-07	
user specific restriction	DUO:0000026	2019-01-07	





Benefits of DUO tags

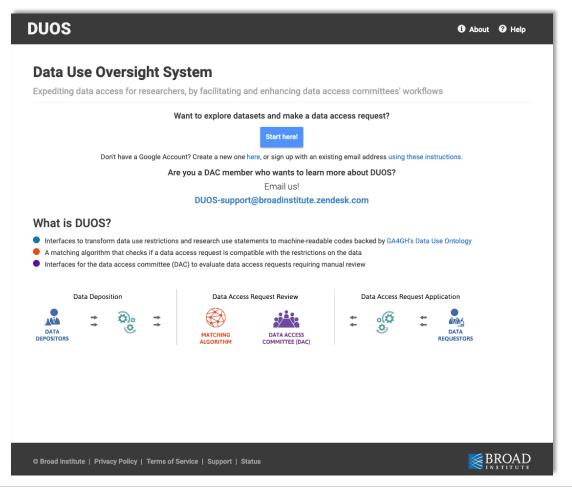
- Standardised and harmonised use conditions
- Better indexing and querying
- Enables future automation
- Enables better interoperability across platforms

 Better informed consent options for study/project participants in the future





The future: Data Use Oversight System (DUOS)







DAC's, DUO-tags, and DUOS in X-Omics?







Summary

- Publishing and archiving data via the EGA requires a DAC
- Informed consent conditions are crucial to enable and define future re-use by others
- Data Use Conditions help standardise
- The future is to enable automatised application reviews
- X-Omics will carefully consider to implement DUO and DUOS standards





