

Our Future Health

Trusted Research Environment

Demonstration Instructions

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1 Summary

As part of the procurement evaluation, Our Future Health shall conduct an exercise to enable Suppliers to demonstrate the capabilities of their platform. The purpose of this demonstration is to evaluate the functionality, usability and current capabilities of the Supplier's platform in completing test scenarios to ensure that Our Future Health has confidence in the ability of the Supplier to deliver within the timescale. The demonstration shall cover main Trusted Research Environment (TRE) features including:

- User interface
- Separation of the workspace
- Cohort browser
- Analytic tools
- Import and export
- User management

To assist Suppliers in providing such a demonstration, a synthetic dataset shall be used to conduct pre-defined test scenarios. Suppliers shall ingest the dataset described below onto their demonstration TRE and configure it for use as would be provided in their proposal to meet requirements set out in TRE Requirements.

2 Demonstration

Suppliers will have an opportunity to provide a live demonstration of the TRE platform which will be evaluated. Each demonstration session will be undertaken as a Microsoft Teams video conference with support for screen sharing, which will be recorded for internal use only.

The demonstrations shall last at most 2.5 hours and will only cover the test scenarios laid out below. There shall be at least 15 minutes allotted to allow any questions from Our Future Health purely in order to clarify bidder's responses to the TRE evaluation questions; as a result, evaluators' scores will either remain unchanged or will be reduced. Scores will not be increased as a result of clarification questions.

We would expect that no more than 4 representatives from each Supplier will need to take part in the demonstration, and no preliminary presentation is required.

Demonstrations will be scored using the evaluation scoring system.

Although in the final Our Future Health deployment the TRE supplier will work with the selected public cloud infrastructure supplier, for the purposes of this demonstration any cloud supplier can be selected.

3 Description of synthetic datasets

We expect to conduct the evaluation of the test scenarios using a synthetic dataset developed by Our Future Health. Our Future Health will make available all the relevant datasets so that they are uploaded onto the platform prior to demonstration. The same datasets will be provided to all Suppliers to ensure consistency.

Our Future Health will provide datasets for 1000 synthetic participants. Each participant will have three types of health datasets generated:

- Questionnaire data

- Hospital Episode Statistics Admitted Patient Care or HES APC
- Genetic data

Phenotypic datasets will have an accompanying data dictionary. It is worth noting that although the variables will closely model the real dataset, the distribution of the data will most likely not.

Lastly all datasets are linked by a 'participant identifier' or PID.

The expected total size of the synthetic dataset is ~100 MB.

3.1 Questionnaire data

This dataset is generated from the actual questions and options available to our participants during our pilot studies. There are five sections:

- About you and your household
- Work and education
- Lifestyle
- Family health history
- Health history

There are a maximum of 205 questions. This dataset will also include demographic data: age and sex.

3.2 Hospital Episode Statistics Admitted Patient Care

HES APC will be amongst the first linked participant datasets that will be available to researchers. Our synthetic dataset includes:

- HES APC admissions and diagnosis
- HES APC procedures

Excluding the header, there are 1000 rows – each representing a single participant. The two former datasets will be combined into a single dataset. Lastly all three HES APC data sets will be accompanied by a data dictionary that also contains a breakdown of the coding and values found within each field.

3.3 Genetic data

The genetic dataset to be used in the POC evaluation will be based on the existing, publicly available 1000 Genome phase 3 genotype data. Our Future Health will provide a subset consisting of 1000 samples from the project and rename the VCF files with PIDs.

4 Evaluation scenario

This section will describe some examples of workflows that are commonly conducted on the TRE and will be expected on Our Future Health's platform. These workflows will be performed on the platforms to provide verification of requirements listed in Our Future Health Lot 2 Procurement Requirements (see details in brackets relating to each scenario).

While there is a requirement for an airlock (please refer to Section 2.6 in Our Future Health Lot 2 Procurement Requirements), Suppliers are not expected to use or demonstrate an air lock for the purposes of this evaluation. The evaluation requires only the ability to import and export data to the TRE, the airlock process will not be evaluated.

4.1 User interface (up to 20 mins)

This example covers the log-in and set up of a new user to the TRE platform.

- 4.1.1 Demonstrate how a new Registered Researcher creates an account and logs-in to the TRE (Our Future Health Lot 2 Requirements 2.1.3).
- 4.1.2 Demonstrate access controls and security measures described in the technical requirements (Our Future Health Lot 2 Requirements 2.1.3), bearing in mind that for this evaluation no integration with Our Future Health systems will be included.
- 4.1.3 Demonstrate how the new Registered Researcher, who is the lead researcher on an Approved Study, configures their workspace, highlighting admin controls available to the lead researcher (Our Future Health Lot 2 Requirements 2.2).
- 4.1.4 Demonstrate how Registered Researchers may collaborate within their workspace (Our Future Health Lot 2 Requirements 2.2).
 - i. For the purposes of the demonstration please populate the workspace with at least 2 associated researcher accounts
- 4.1.5 Demonstrate how a researcher can see an overview of the data available to the researcher in their workspace (Our Future Health Lot 2 Requirements 2.2).
- 4.1.6 Demonstrate features of the platform that highlight best practices in user-centred design and usability (Our Future Health Lot 2 Requirements 2.1.1 - 2.1.2).

4.2 Epidemiology scenario (up to 45 mins)

This example covers a common epidemiology scenario to carry out an exploratory analysis of diabetes-associated phenotypes, using a cohort browser and interactive notebook to generate and export results. Our Future Health will provide example code in Python to support the below analysis in an interactive notebook.

- 4.2.1 Demonstrate how a researcher uses a graphical interactive method to define and save a cohort by applying multiple inclusion and exclusion criteria and inspect output data counts and distribution (Our Future Health Lot 2 Requirements 2.3).
 - i. Define phenotypic variables for diabetic dataset using cohort browser;
 - ii. Select variable(s) from questionnaire dataset for analysis – Diabetic status in questionnaire (question q-019f4cea-245c-43f4-b0f5-bcb00b1fc8b2, answer Diabetes (value 6));
 - iii. Select variable(s) from HES dataset for analysis - HES APC Admissions and diagnosis dataset, select fields: diag1_icd10 to diag20_icd10; ICD10 code = E10.0;
 - iv. Join the questionnaire and HES datasets;
 - v. Save this cohort definition to the local workspace for use in subsequent analyses.
- 4.2.2 Demonstrate how a researcher can access datasets via an interactive notebook, import tools and packages, run complex queries and analysis, and generate graphs and tables (Our Future Health Lot 2 Requirements 2.4).
 - i. Load the filtered dataset into the interactive notebook and run analysis;
 - ii. Import relevant packages from a library;

- iii. Execute the correlation/regression analysis (as per sample code);
- iv. Convert the statistical output to a data table where appropriate;
- v. Save the output of the results in local workspace as a plain text, comma-separated values (csv) or spreadsheet file;
- vi. Generate graphs using the relevant libraries.

4.2.3 Demonstrate how a researcher may export the code, graphs and summary level data tables (from above step 4.2.3) to share with other researchers for review (Our Future Health Lot 2 Requirements 2.6.2).

4.3 Genetic scenario (up to 60 mins)

This example covers a common genetic analysis scenario to conduct a genome wide association analysis on participants with diabetes phenotypes (defined above in step 4.2.1), using a cohort browser, analytical tools, workflows, interactive notebooks, CLI, import and export. Our Future Health will provide example bash code to support the below analysis.

- 4.3.1 Demonstrate how a researcher may use a graphical interactive method to define and save a cohort by filtering genetic data for regions of interest (e.g., specific SNPs, genomic regions) (Our Future Health Lot 2 Requirements 2.4.4).
- 4.3.2 Demonstrate how a researcher can search and access a repository of tools and workflows and select specific versions (Our Future Health Lot 2 Requirements 2.4.4).
- 4.3.3 Demonstrate how a researcher can build and share a custom workflow in the platform - performed via a web-based interface, notebook or CLI (Our Future Health Lot 2 Requirements 2.4.6). We would be pleased to see multiple methods available.
 - i. Conduct basic quality control on the genetic data (e.g., minor allele frequency, relatedness, duplicates, Hardy-Weinberg equilibrium);
 - ii. Perform principal component analysis and save the output;
- 4.3.4 Demonstrate how a researcher can run genome wide association study (GWAS) and downstream analysis via a web-based interface, notebook or CLI (Our Future Health Lot 2 Requirements 2.4.4.1).
 - i. Import script/code for genome wide association analysis on cohort (defined above in step 4.2.1).

- 4.3.5 Demonstrate how a researcher can create, import and modify a workflow management system (e.g., Nextflow, WDL, Snakemake) to handle large data processing pipelines (Our Future Health Lot 2 Requirements 2.4.8).
- 4.3.6 Demonstrate how a researcher can assign computing resources (e.g. compute cores and RAM) to perform tasks (Our Future Health Lot 2 Requirements 2.5).
- 4.3.7 Demonstrate how a researcher collaborates and shares knowledge with other researchers on the platform (Our Future Health Lot 2 Requirements 2.4.7).

4.4 Activity logging (up to 10 mins)

- 4.4.1 Demonstrate how a researcher can monitor jobs that are running, as well as a log of previously run jobs (with status) via both web-based UI and CLI (Our Future Health Lot 2 Requirements 2.4.9).
- 4.4.2 At the end of the demonstration, display any logs or audit trails of the activity recorded during the user sessions that would be available to Our Future Health.