## HANDS ON WORKSHOPS

### TRACK 1: Using DNAnexus Apollo for Exploring and Analyzing Clinical and Multi-Omics Data

DNAnexus Apollo offers researchers and bioinformaticians an environment to store and query population-scale sets of integrated clinical, phenotypic, multi-omic, and ad hoc structured data. Researchers can bring their data to the Apollo Platform, run DNAnexus apps, and ingest the data into databases.

Learn how to explore these data using the DNAnexus Apollo Cohort Browser, a visual interface that allows point-and-click data exploration and cohort creation, or through a Spark cluster-enabled JupyterLab environment, allowing ad hoc exploration and analysis using Python or R.  During this workshop, you will:

- Launch a Cohort Browser and visually explore a large dataset containing phenotypic and genotypic information.
- Apply filtering criteria, select, and save cohorts.
- Perform a GWAS analysis using selected, case-control cohorts.
- Explore and analyze clinical and multi-omics data using a JupyterLab notebook with Python.

### Prerequisites

To get the most out of this workshop, you'll need a few things:

1. **DNAnexus account** - During the workshop we will build and run various tools on the DNAnexus Platform.
2. **Access to the workshop projects** - Example input and reference files are on the DNAnexus Platform. You can use the files to run and debug your tools and we will share with you the project ahead of time.
3. **Basic skills of programming in Python** - This isn't strictly necessary, but would help in understanding how can one perform an advanced analysis using the DNAnexus Apollo system.

### TRACK 2: Developing Portable Pipelines: Using WDL and Docker to Develop Locally and Scale to the Cloud

Curious about best practices of app(let) building on the DNAnexus Platform and how to optimize for the cloud? Want to instead use existing tools maintained and built by third party groups? Learn how to do *both* on the DNAnexus Platform.  Our centralized and flexible environment provides scientists the ability to build apps, create workflows, monitor jobs, and debug tools, all in a highly efficient manner.

In this workshop we will highlight best platform practices along with identifying practices to avoid. We will also learn how to use public Docker containers as part of an app and show you how to run WDL workflows both locally and on DNAnexus.  Finally, we will provide templates and code snippets useful for daily work. By the end of the workshop, you will have built a portable pipeline that can be executed—efficiently and securely—on DNAnexus.

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3. **Basic experience with DNAnexus** - This isn't strictly necessary, however to save time we will skip over several of the basic functionality on DNAnexus in order to focus on building applets.
4. **Install software:** To participate in the hands-on portion of the workshop, please have Java 1.8+ installed on your computer and download the [Cromwell](#) and [dxWDL](#) JAR files.