XNAT Workshop

Instructor: Jay Hennessy

camh Enterprise Project Management Office

Welcome to the Online XNAT Workshop!

What you'll lean:

1) What XNAT is and how to use it for your project.

2) What the Neuroinformatics Platform is and how XNAT fits into it.

3) What our standard practices for using XNAT at CAMH

4) How to navigate XNAT

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Who should take this course?

- This is a mandatory course for XNAT user accounts to be approved at CAMH.

- Intended audience: people who are at least somewhat familiar with neuroimaging but have never used XNAT.

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Quizzes

- In order to satisfy the completion criteria, an aggregate score of >80% must be achieved.

- The course can be taken at your own speed and successful completion will be evaluated after all quizzes are submitted.

- Links to the REDCap quizzes will be provided on the workshop wiki and in the following videos.

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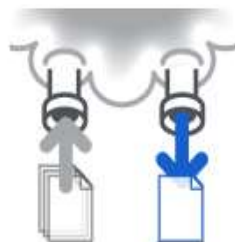# Neuroinformatics Platform System Overview

eXtensible Neuroimaging Toolkit Archive

XNAT

Version:1.7.5.6

https://xnat.camh.ca

Pipeline Processing: Use the power of high-performance computing on your data.

Modular Extensibility: Expand the capabilities of your XNAT to meet your needs.

Developer Community: Benefit from an active and engaged set of XNAT power users.

Full DICOM Integration and Anonymization: Get image data in, and keep PHI out.

Secure Access & Permission Control: You decide who does what with your data.
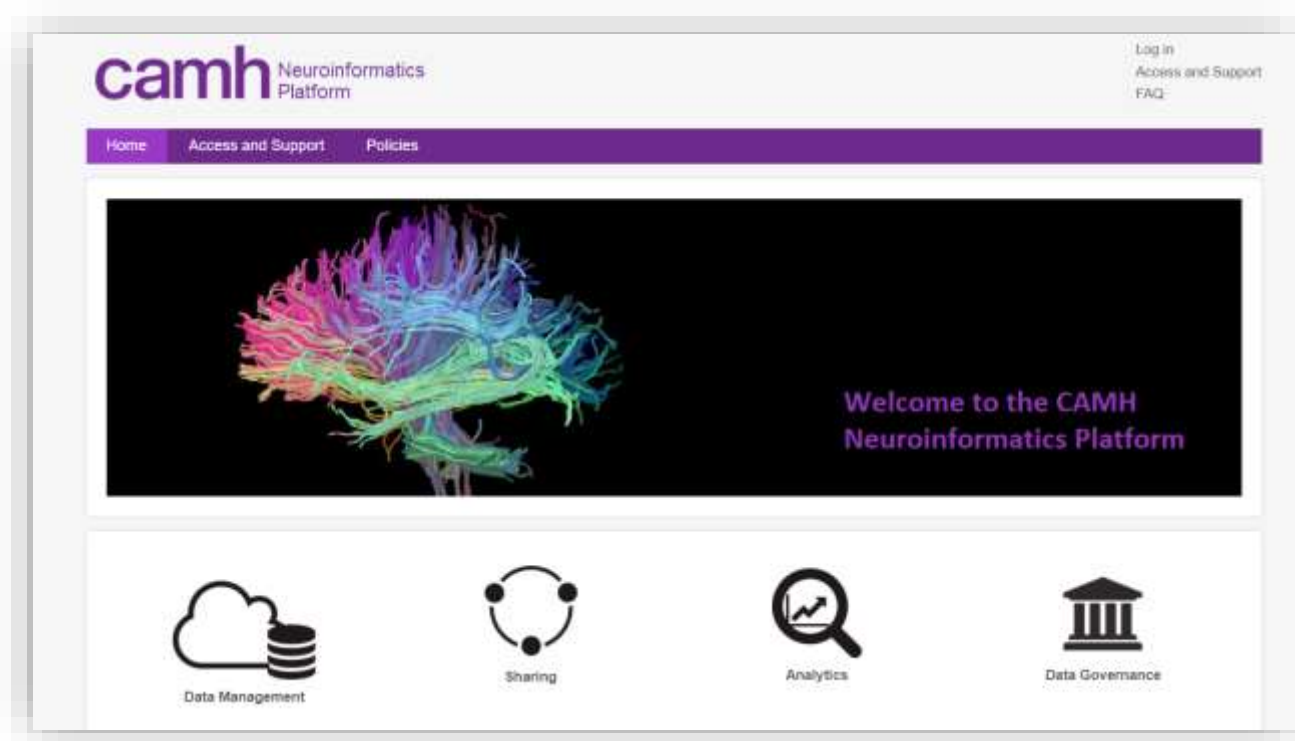
Integrated Search & Reporting: Report on your image and clinical data together.

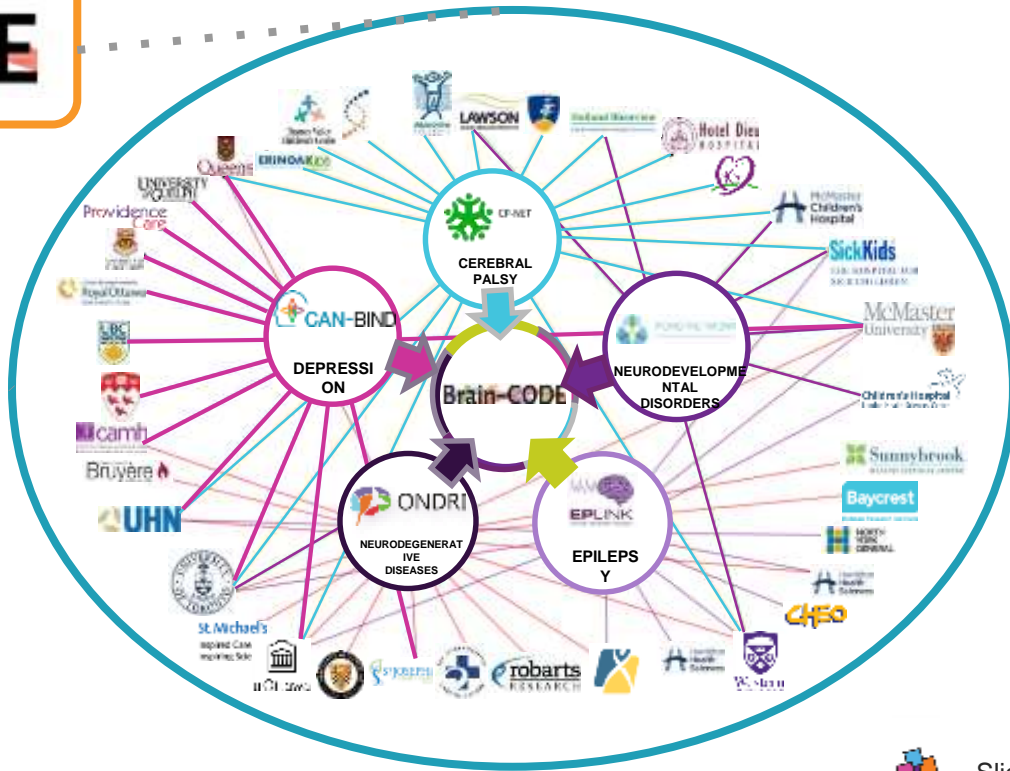camh

NeuroInformatics Platform

https://neuroinformatics.camh.ca/
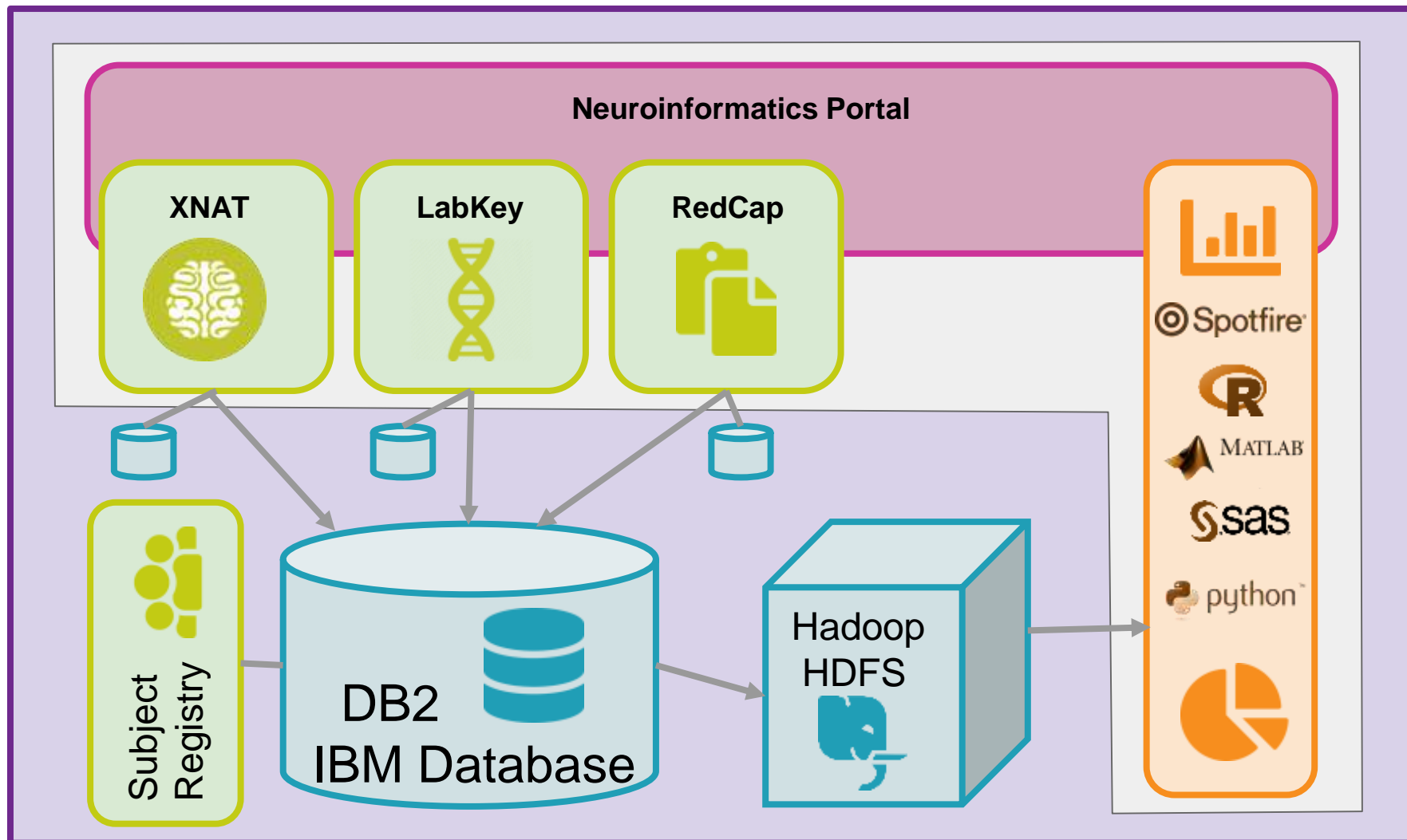
NeuroInformatics Platform

NeuroInformatics Platform

NeuroInformatics Platform

RedCap

REDCap
Research Electronic Data Capture

- **Demographics / Clinical Data**

- Fully deployed at CAMH

- Flexible and intuitive

- Implement **Common Data Elements**

- Standardized Demographics & Assessments

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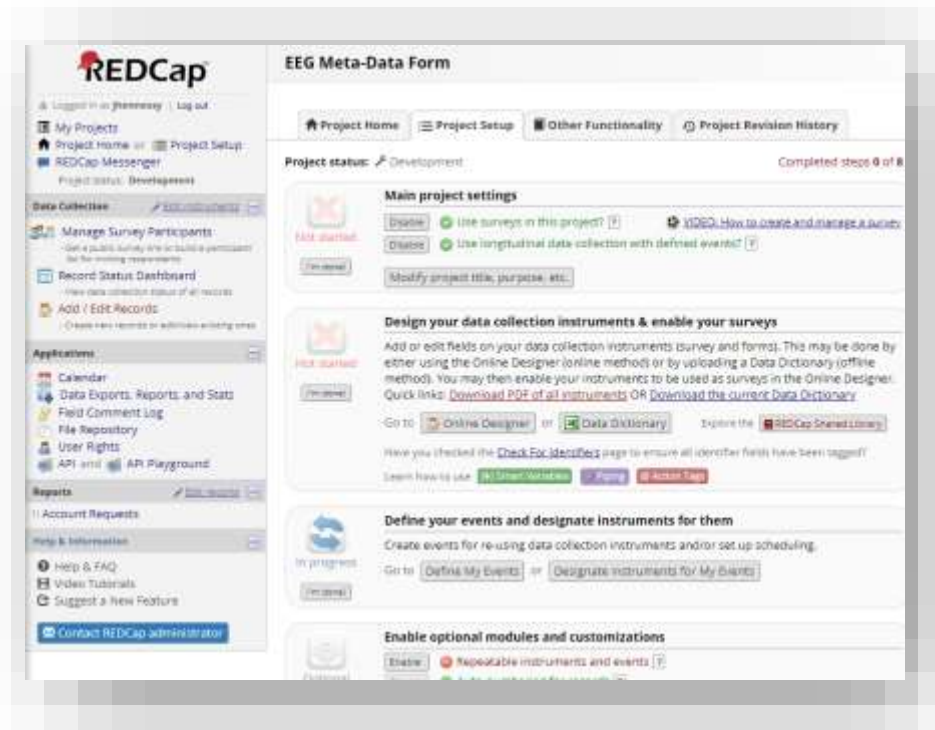
NeuroInformatics Platform

LabKey

- **Molecular**: 'Omics, Tissues

- Highly flexible database for molecular data:

    - Genetics

    - Epigenetics

    - Proteomics

    - Tissue samples

- Enable sample management and collaboration

LabKey®

Get More from Your Data Through Integration

Achieve Consistency of Process and Repeatability of

Conduct Holistic Analysis of Complete Data

Provide Transparency for Funders and Collaborators

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NeuroInformatics Platform

- **Central repository** for research subjects

- Single **unique ID** for all participants

- Incorporates **standard naming convention (**study, site and lab)

- **Accepts and Encrypts OHIP Numbers**

  - Identify subjects across studies

    - Reduce Risk

    - Map longitudinally

- Assists in linking data across systems

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NeuroInformatics Platform
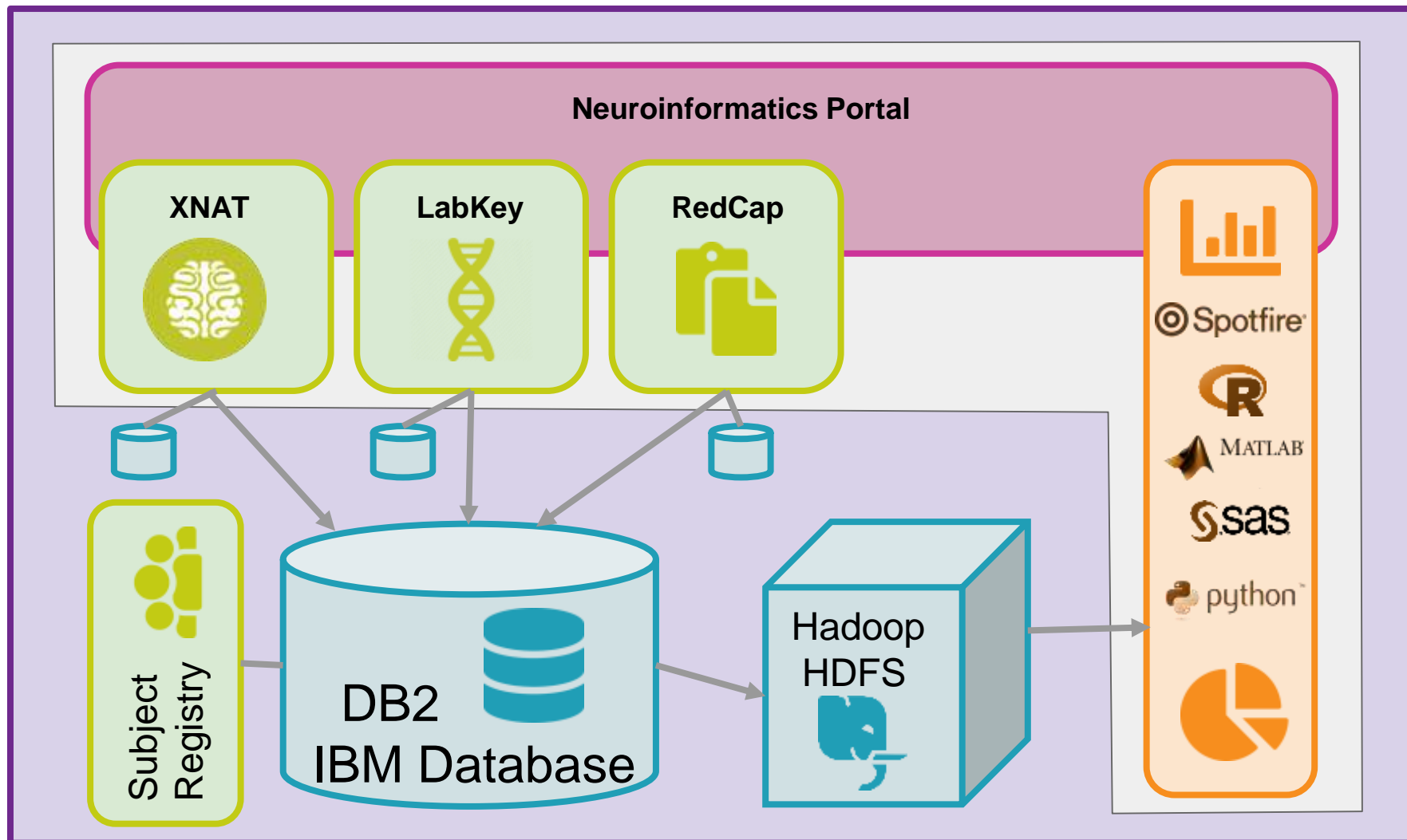
Getting Started with the Neuroinformatics Platform

What You'll Learn

- Project On-Boarding Steps
  - How to create a new user account
  - How to create a new project

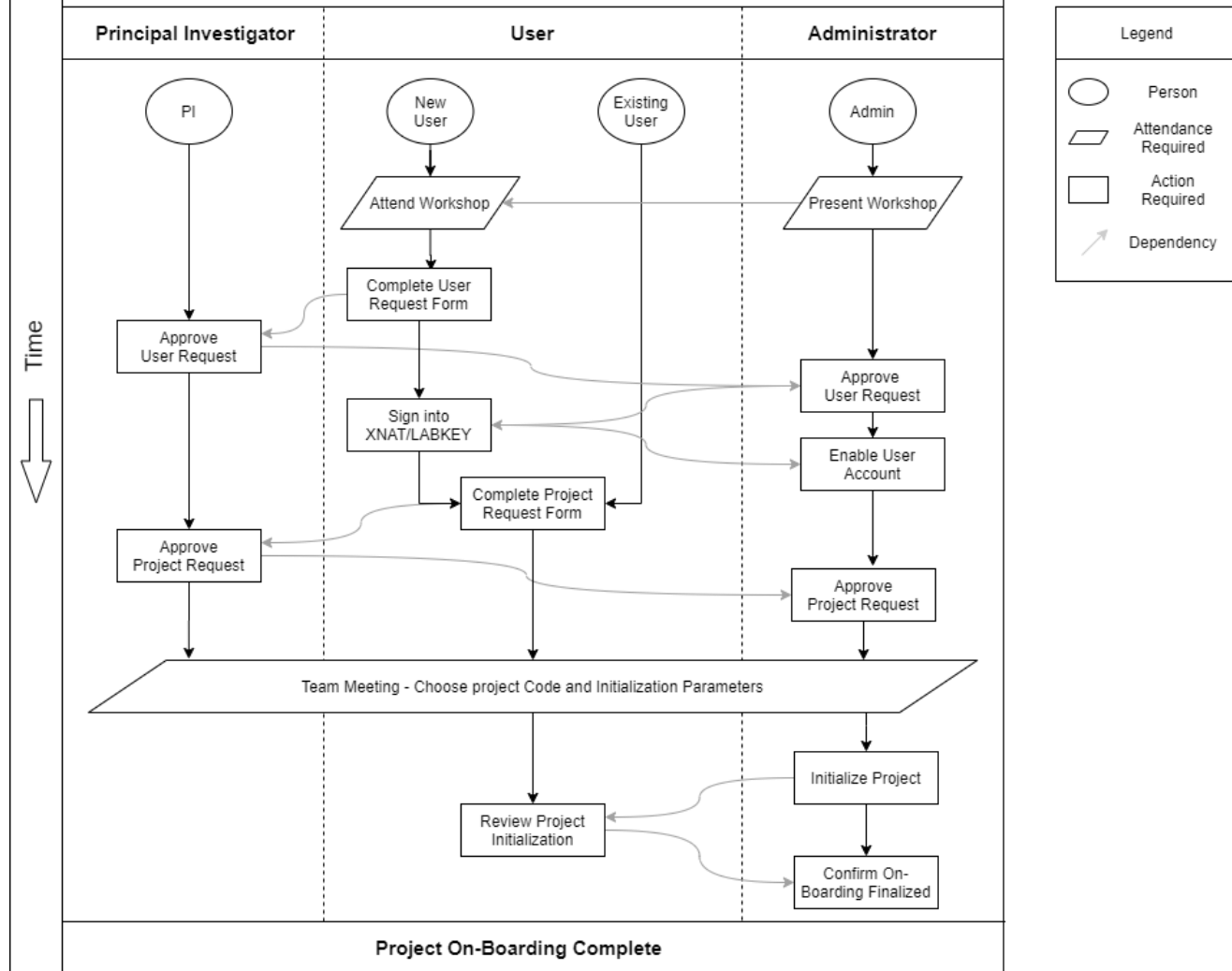- XNAT Roles and Permissions

- Neuroinformatics Naming Convention

Project On-Boarding

- Create a User account

- Create a project

- Share your project requirements

- Enjoy the Platform

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Neuroinformatics Platform Project On-Boarding Action Workflow

Time

| Principal Investigator | User | Administrator |

PI — New User — Existing User — Admin

Attend Workshop ← Present Workshop

Complete User Request Form

Approve User Request

Sign into XNAT/LABKEY

Approve User Request

Enable User Account

Complete Project Request Form

Approve Project Request

Approve Project Request

Team Meeting - Choose project Code and Initialization Parameters

Initialize Project

Review Project Initialization

Confirm On-Boarding Finalized

Project On-Boarding Complete

Legend

- Person
- Attendance Required
- Action Required
- Dependency

User Resources

1. Workshop Signup: http://ishare/sites/researchit/training/Pages/Workshops-Registration.aspx

2. User Account Request Form: https://neuroinformatics.camh.ca/access-support

3. Project Request Form: https://neuroinformatics.camh.ca/access-support

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Create a User Accout

- Navigate to Neuroinformatics Platform User Request Form
    - https://edc.camhx.ca/redcap/surveys/?s=8C74RY7MR8
    - Or navigate from neuroinformatics.camh.ca

- Complete the User Request Form
    - Wait for PI/admin approval

- Log into XNAT with CAMH username and password
    - xnat.camh.ca

NOTE: This one form allows you to sign up for a Labkey, Spotfire and Subject Registry accounts too.

XNAT: Roles & Permissions

Role / Activity	Project Owners (Admin)	Project Members (PIs,Researchers,Students)	Project Collaborators (Visitors)
Create data	X	X	
Read/Download Data	X	X	X
Update Data	X	X	
Delete Data	X		

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Create an XNAT Project

- Navigate to Neuroinformatics Platform Project Request Form

  - https://edc.camhx.ca/redcap/surveys/?s=K9RMLPFRRF

  - Or navigate from neuroinformatics.camh.ca

- Complete the Project Request Form

  - Wait for PI/admin approval

- Log into XNAT with CAMH username and password

NOTE: This one form allows you to sign up for a Labkey, Spotfire and Subject Registry Projects too.

Sharing data between XNAT projects

- **Shared Data (Read-Only) -** Data which is shared into a project cannot be modified by the users in that project. Modification can only be performed by members of the data's primary project.

- Data shared from Project A into Project B is not *copied* into Project B. It is the same data element, so any changes to the data in Project A are reflected in Project B

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Neruroinformatics Platform Naming Convention

- Standardization is very important across large studies and institutions.

- Data is linked in the database by matching proper project/subject/experiment codes.

- It's crucial for equipment operators and RA's to follow proper naming.

- For MRI/PET/DICOM:
  - PatientName DICOM header should be filled out using the experiment naming convention.

- For EEG:
  - EEG files should be saved with the experiment naming convention

- Naming Convention guide can be found here:
  - http://neurowiki.camh.ca/mediawiki/index.php/XNATNamingConvention

Why bother with Neuroinformatics Platform?

- Why can't I keep going the way I'm going with excel sheets, it works and I know how to do it?
  - FAIR data principles
  - BIG DATA
  - Interoperability between institutions
  - Reproducibility crisis in science (esp. neuroscience)
  - Provenance tracking
  - Project tracking
  - Cross domain analysis

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Working with XNAT

What You'll Learn

- XNAT Data Model

- Navigating the XNAT UI

- Archive vs. Pre-Archive

XNAT Data Model
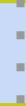
XNAT

- Navigating XNAT

- Archive vs. Pre-archive

- Viewing Images

- Modifying/Editing elements

- Deleting Data

https://xnat.camh.ca/xnat

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MR/PET Data

What You'll Learn

- Uploading MR/PET Data

- Anonymization

- Downloading Data

Uploading MR data: Automated

- The most common upload method is to configure automated MR data uploads from the MRI Unit at CAMH directly to XNAT.

- To setup automated upload:
    - Email xnat@camh.ca and ask to setup automated MR uploads
    - Supply your CAMH MR FTP server login credentials given to you by the MRI Unit
    - Ensure the MRI Unit fills out the patient name DICOM header with our experiment naming convention (ex. ABC01_CMH_342523_01_SE01_MR)

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Uploading MR data: Manual

- Compressed Image Uploader

- Desktop Client
  - **https://download.xnat.org/desktop-client/**

- XNAT API
  - curl
  - Python: xnatpy or pyxnat

- (DICOM inbox)

https://xnat.camh.ca/xnat

Anonymization

- No default anonymization set

- Send email to xnat@camh.ca to request anonymization
    - Anonymizes automatically on upload
    - Easy to scrub dicom headers
    - More time needed to deface images

Downloading MR Data

- UI download
  - File Manager

- Desktop Client download

- API download

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EEG Data

What You'll Learn

- Uploading EEG Data

- Downloading Data

Uploading EEG data: Automated

- The most common upload method is to configure automated EEG data uploads from storage at CAMH directly to XNAT.

- To setup automated upload:
    - Email xnat@camh.ca and ask to setup automated EEG uploads
    - Supply the root project folder path and the name of the raw data folder that will be used for each scan.
    - Provide access for XNAT admin to access the root project folder (and subfolders).
    - Each data file must follow the experiment naming convention with an added trial code to the end.
        - Ex. ABC01_CMH_00001_01_SE01_EEG_rest.cnt
        - Here the trial code is "rest". This will be the scan label used in XNAT.

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Uploading EEG data: Manual

- Cannot use Compressed Image Uploader or Desktop Client as they require DICOM data.

- Use File Manager

- XNAT API
  - curl
  - Python: xnatpy or pyxnat

https://xnat.camh.ca/xnat

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Downloading EEG Data

- UI download
  - File Manager

- API download
  - Curl
  - Xnatpy
  - pyxnat

QC and Processing Pipelines

What You'll Learn

- QC pipelines available to you and how to use them

- Data pre-processing pipelines available to you and how to use them

- Upcoming pipeline developments

Pipelines Available

	MR	EEG
Quality Control	• Naming Convention Check • Manual QC • fMRI fBIRN QC • Protocol Check	• Naming Convention Check • Protocol Check
Pre-process Pipeline	• Dicom to NIFTI Conversion	• Basic pre-processing (filter, normalize, etc)
Analysis	• Coming Soon	• Coming Soon

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QC: Name Convention Check

- Summary: Checks all Projects, Subjects, and Experiments to ensure they adhere to proper naming convention. Runs automatically, every night on all data.

- Input: All Projects, Subjects, Experiments on XNAT

- Output: A hidden file that logs all successful experiments. And, an email if any projects/subjects/experiments fail the check.

QC: fBIRN (fMRI)

- Summary: The Function Biomedical Informatics Research Network (FBIRN) created an fMRI QA/QC pipeline meant for large multi-site neuroimaging projects to track scanner metrics longitudinally. Runs automatically on all fMRI data on XNAT at upload.

- Input: fMRI data on XNAT

- Output: A summary html file is sent to XNAT and will email you upon completion.

- Information about the QC metrics calculated can be found here.
  - https://onlinelibrary.wiley.com/doi/full/10.1002/jmri.20583

QC: Manual QC (MR)

- Summary: A manual assessment of the quality of uploaded images to determine if an image is usable (i.e. pass or fail). To be completed by project members based on visual artifacts present in your scans. Manual QC should be completed within 48 hours of scans being uploaded.

- Input: MR experiments/scans on XNAT.

- Output: QC summary in the XNAT UI
- A great reference for MR quality control is here:
    - https://bit.ly/2SDMmpN

Pipeline: Dicom to Nifti (MR)

- Summary: Converts raw MRI dicoms to nifti format. Can run automatically upon upload to xnat.

- Input: MR data on XNAT

- Output: Nifti data on XNAT.

- This pipeline uses the popular dcm2niix script from the Rorden Labn.

QC: Protocol Check (MR)

- Summary: Compares your expected scan protocol against a "gold standard" that you have supplied for each MR scan type. Can run automatically on each experiment upload

- Input: Any MR session on XNAT

- Output: A summary is sent to XNAT and will email you upon completion.

- To have protocol QC run on your MR images:
  - Email xnat@camh.ca
  - Fill out the schematron with the expected parameters for each scan (or ask xnat admin for help)

QC: Protocol Check (EEG)

- Summary: Compares your expected EEG protocol against a "gold standard" that you have supplied for each EEG scan. Can run automatically on each experiment on upload.

- Input: EEG data on XNAT, and REDCap parameter questionnaire.

- Output: A summary sent to XNAT and will email you upon completion.

- To have protocol QC run on your EEG experiments:
  - Complete the EEG Project Form here:
    - https://edc.camhx.ca/redcap/surveys/?s=3C4DJWTRHF
    - Make sure to fill out the section titled "Quality Control and Pre-Processing"
  - Once all your parameters are set in the RedCap form, every time EEG data is uploaded to xnat, the protocol check will automatically run.
  - Email xnat@camh.ca for assistance

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Pipeline: Pre-Processing (EEG)

- Summary: Pre-processes your EEG data on upload to XNAT according to parameters specified in REDCap form. Can run automatically on each experiment on upload. Options include:
    - Adding events
    - Epoching Data
    - Baseline correcting
    - Dropping channels
    - Re-sampling data
    - Filtering Data

- Input: EEG data on XNAT, and REDCap parameters for each step.

- Output: A output from each pre-processing step is sent to XNAT along with a provenance summary document.

- To have pre-processing run on your EEG experiments:
    - Complete the EEG Project Form here:
        - https://edc.camhx.ca/redcap/surveys/?s=3C4DJWTRHF
        - Make sure to fill out the section titled "Quality Control and Pre-Processing"
    - Email xnat@camh.ca for assisstance

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Pipeline: Requesting New Pipelines

- If you have developed a image processing/QC/analysis pipeline or know of one that you would like to run automatically on your data, let us know and we can help you set it up.

- Email us at xnat@camh.ca

- There are a few ways to setup a pipeline:
    - Plugins
    - Containers
    - API script

- As we make new pipelines available, we will post them with instructions here.

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Pipeline: Looking Forward

- We are currently in the process of collaborating the TIGR Lab at CAMH.

- We are going to adopt their MR QC procedures and their MR analysis pipelines

- The TIGR Lab pipelines are based on BIDS and therefore it will be very easy to add new BIDS pipelines in the future.

- When this transition is complete, users will be notified and these instructional videos will be updated.

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Spotfire

SPOTFIRE Visualization

- Spotfire is a data visualization tool used by the Neuroinformatics Platform

- It can be accessed through the Neuroinformatics Platform Portal or by going to:

spotfire.camh.ca

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Useful Resources

Useful Resources

- Questions? : **xnat@camh.ca**

- Our XNAT website: **http://xnat.camh.ca**

- The Neuroinformatics Platform Website: **http://neuroinformatics.camh.ca**

- Get help at the Neuroinformatics Platform Wiki: **http://neurowiki.camh.ca**

- Manual QC guide:
  http://cbs.fas.harvard.edu/usr/mcmains/CBS_MRI_Qualitative_Quality_Control_Manual.pdf

- fBIRN paper: https://onlinelibrary.wiley.com/doi/full/10.1002/jmri.20583