Data flow diagram for XNAT

1. Researchers generate a unique ID for subjects, or retrieve existing ones.
2. Researchers enter properly-formed session ID and subject UID.
3. Subjects are scanned.
4. Data is pushed from scanner host to sigma manually, by researchers.
5. Data is automatically copied to XNAT and to the cluster.
6. Researchers/RAs double-check data on sigma and data on cluster/XNAT.
7. Researchers log into XNAT and create new subjects or assign scans to existing subjects.
8. Analysis begins either via XNAT pipeline or by legacy processes, using dicom store at /mindhive/DICOMS.

Pypelines:
Researchers create processing recipes - "pypelines" - and can drop new scan sessions onto a pypeline.