Using Neuro-Imaging Laboratory Resources to Store, Preprocess, and Analyze fMRI Data

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Introduction

What's the purpose/goal of all this?

The goal is to make available to fMRI researchers in the Psychology Department the computing and data storage resources of the Neuro-Imaging Laboratory (NIL, http://www.nil.wustl.edu). Using these resources will hopefully better integrate the neuroimaging researchers in the Psychology Department with medical school neuroimaging researchers and avoid duplication of efforts with regard to software development, software maintenance, and hardware maintenance.

What is the Neuro-Imaging Laboratory?

The Neuro-Imaging Laboratory is part of the Mallinckrodt Institute of Radiology at the Washington University School of Medicine. Within the Mallinckrodt Institute of Radiology, the Radiological Sciences Division is the division tasked with the development of basic sciences associated with radiology. The Radiological Sciences Division is divided into multiple laboratories each devoted to a different basic radiological science. The Neuro-Imaging Laboratory is one of those laboratories.

How is the Neuro-Imaging Laboratory subdivided?

The Neuro-Imaging Laboratory is itself further divided into sub-groups.

Neuroinformatics Research Group

One such group is the Neuroinformatics Research Group (NRG). The NRG is focused on the integration, mining, and sharing of data across the neurosciences. Neuroinformatics is the application of *information science* to *neuroscience*. Information science is concerned with the analysis, collection, manipulation, storage, retrieval, and dissemination of information. So, roughly speaking, the neuroinformatics group is all about providing resources and techniques for better using computers (software and hardware) for storage, sharing, and analysis of neuroimaging data.

The NRG hosts a data archive for managing and sharing study data collected by the Washington University neuroimaging community. This archive is called the Central Neuro-Imaging Data Archive (CNDA).

Computer Support Group

Another subdivision of the Neuro-Imaging Laboratory is the Computer Support Group (CSG). The CSG is the computer systems administration group within NIL. As its name implies, the CSG provides computer support to the other groups within NIL. The CSG folks are the ones you would turn to in order to get new accounts created, get access to the computers that control the scanners, get access to NIL computer systems in general, get access to NIL computer systems from you home, etc.

In particular, they are responsible for:

- Maintaining and granting access to the Virtual Private Network (VPN) to which you will need to get access in order to use any NIL computer systems
- Maintaining and granting access to the PCs in the scanner rooms (other than the computers that directly control the scanners)
- System administration of NIL Un*x systems, including granting Un*x accounts.[1]

RIIS

The RIIS group is responsible for maintaining and granting access to the computers that actually control the scanners. The RIIS is independent from the CSG. The scanner control computers are maintained separately so that appropriate billing can be done for any hours used on the scanners.

What WUSM resources are we planning to use?

- We will use the Central Neuro-Imaging Data Archive (CNDA) for storage and long-term archiving of “raw” fMRI scanning data. In this context, “raw” refers to data that is retrieved directly from the MRI scanners and has not been through any preprocessing other than that which might have been done by the scanner.
- We will use the CNDA’s pipeline mechanism for performing standardized preprocessing of fMRI data. In particular standardized BOLD preprocessing.
- We will use computers maintained by the Computer Support Group (CSG), which is part of the NIL, to carry out a significant amount of the analysis (after preprocessing) of fMRI data. You will not be limited to using only these NIL maintained computers. You can download the preprocessed data to other computers, including your own desktop system[2], for analysis. This will be useful if the analysis software that you want to use is not available on the NIL/CSG maintained machines. However, the NIL maintained machines should have the most up-to-date and maintained versions of software like FIDL available.[3]
- We will use NIL/CSG maintained disk space for storage of data during analysis. This space is referred to as the Bluearc space.

[1] Un*x systems include systems operating the Linux and SunOS/Solaris operating systems. UNIX is an officially trademarked term owned by The Open Group. “Un*x" is often used to indicate all operating systems similar to UNIX without violating any trademarks.

[2] In this case, and for the rest of this document, the term “desktop computer” or “desktop system” is not intended to be limited to a desktop computer to the exclusion of laptops, notebooks, or netbooks.

[3] Currently (June 2011), the NIL maintained computers we have been assigned to use are

- petsun23 – running Solaris 10 (specifically SunOS 5.10)
- petsun24 – running Solaris 10 (specifically SunOS 5.10)
- linux1 – running Linux kernel 2.6.18 (CentOS distribution release 5.5)

About the CNDA

What does using the CNDA provide for me?

The Central Neuroimaging Data Archive (CNDA) is "a resource for managing study data collected by the Washington University neuroimaging community. It includes a secure database, automated pipelines for processing managed data, and tools for exploring and accessing the data."[4] The primary mechanism for accessing the CNDA is via the CNDA website (https://cnda.wustl.edu).

In addition to providing secure, backed-up, web accessible, sharable archiving of scanning data, the CNDA also makes available standardized pre-processing pipelines. These pre-processing pipelines are analogous to (indeed originally based upon) the pre-processing scripts that were previously used on a number of Un*x based servers in the Psychology Department. Using the CNDA pipelines for preprocessing will help ensure that we will always be using the latest changes and improvements to the standardized fMRI preprocessing.

When the "raw" data has been successfully preprocessed, the resulting files are automatically stored in the CNDA. These "Reconstructions", as they are referred to in the CNDA, are then available for downloading from the CNDA. The downloading can be done via the CNDA's web-based interface or by using command line tools that are available from the CNDA. Using the command line tools allows you to create scripts to download large quantities of data (that may take hours to download) and then run those scripts as "batch" jobs that are left running unattended over several hours or overnight.

How do I get a CNDA account?

To get a CNDA account, use a web browser and visit https://cnda.wustl.edu. Below the User and Password fields and the Login button, is a link labeled "Register". Follow that link to fill out and submit the New User Registration form. Once your account is created you should receive an email from the Neuroinformatics Research Group (NRG) letting you know that your account has been successfully created. The email you receive confirming your account creation should look similar to the following:

```
From: nrgtech@npg.wustl.edu
Date: Thursday, 09 July 2009 14:59
To: tbbrown@wustl.edu
Subject: Welcome to CNDA

Welcome to the CNDA Web Archive!
You can now log on to the CNDA at: https://cnda.wustl.edu
Your username is: tbb
For support, contact the CNDA Management
```

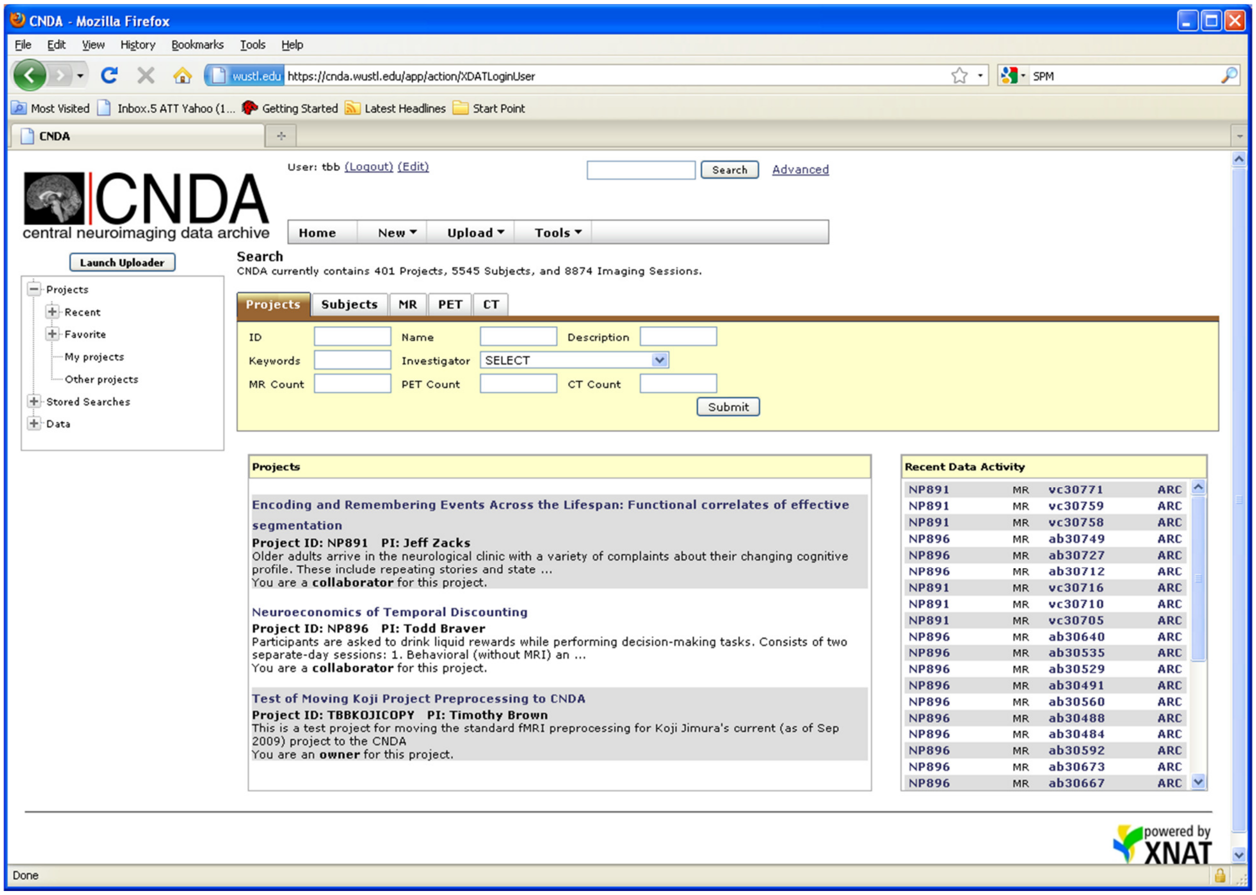
Note that the support contact link is to the email address nrgtech@npg.wustl.edu. That is where you should send email to initiate support requests.

[4] From the CNDA website.

How is data organized within the CNDA?

The primary unit of organization of data within the CNDA is the *Project*. All your scanning data will be associated with a particular CNDA project. Typically you will create a new project for each study you perform.

After logging in to the CNDA, you should be presented with the CNDA Home page for your CNDA account. Your CNDA Home page will look similar to Figure 1. Notice the list of Projects near the bottom of the page. These are the projects for which you have some defined role within the CNDA. Depending on the role you are given in a project (owner, member, or collaborator) and the project accessibility levels defined by the project owner) you may have full access to the project to upload new data, submit pipeline jobs, or even delete project data, or you may only have access to view the project data. Each project has a unique *Project ID*. The project IDs visible in Figure 1 are: NP891, NP896, and TBBKOJICOPY.


CNDA - Mozilla Firefox
File Edit View History Bookmarks Tools Help
wustl.edu https://cnda.wustl.edu/app/action/XDATLoginUser
SPM
Most Visited Inbox.5 ATT Yahoo (1... Getting Started Latest Headlines Start Point
CNDA
User: tbb (Logout) (Edit)
Search Advanced
CNDA
central neuroimaging data archive
Home New Upload Tools
Launch Uploader
Projects
Recent
Favorite
My projects
Other projects
Stored Searches
Data
Projects Subjects MR PET CT
ID Name Description
Keywords Investigator SELECT
MR Count PET Count CT Count
Submit
powered by XNAT
Done

Search
CNDA currently contains 401 Projects, 5545 Subjects, and 8874 Imaging Sessions.

Projects

Encoding and Remembering Events Across the Lifespan: Functional correlates of effective segmentation
Project ID: NP891 PI: Jeff Zacks
Older adults arrive in the neurological clinic with a variety of complaints about their changing cognitive profile. These include repeating stories and state ...
You are a **collaborator** for this project.

Neuroeconomics of Temporal Discounting
Project ID: NP896 PI: Todd Braver
Participants are asked to drink liquid rewards while performing decision-making tasks. Consists of two separate-day sessions: 1. Behavioral (without MRI) an ...
You are a **collaborator** for this project.

Test of Moving Koji Project Preprocessing to CNDA
Project ID: TBBKOJICOPY PI: Timothy Brown
This is a test project for moving the standard fMRI preprocessing for Koji Jimura's current (as of Sep 2009) project to the CNDA
You are an **owner** for this project.

Recent Data Activity

NP891	MR	vc30771	ARC
NP891	MR	vc30759	ARC
NP891	MR	vc30758	ARC
NP896	MR	ab30749	ARC
NP896	MR	ab30727	ARC
NP896	MR	ab30712	ARC
NP891	MR	vc30716	ARC
NP891	MR	vc30710	ARC
NP891	MR	vc30705	ARC
NP896	MR	ab30640	ARC
NP896	MR	ab30535	ARC
NP896	MR	ab30529	ARC
NP896	MR	ab30491	ARC
NP896	MR	ab30560	ARC
NP896	MR	ab30488	ARC
NP896	MR	ab30484	ARC
NP896	MR	ab30592	ARC
NP896	MR	ab30673	ARC
NP896	MR	ab30667	ARC

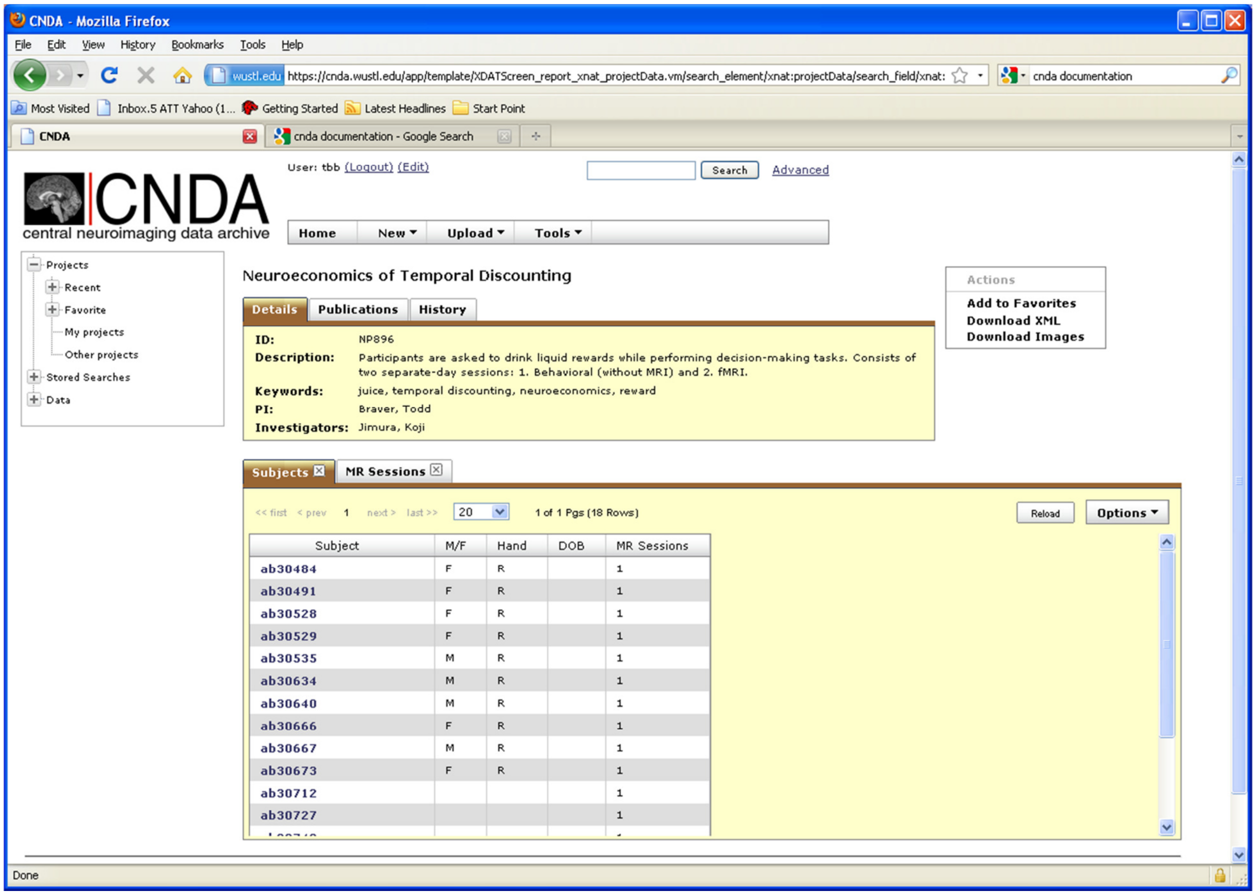
Figure 1: Example CNDA Home page

The next major unit of data organization within the CNDA is the *Subject*. A project can consist of multiple Subjects. Subjects are identified by a *Subject ID*. Data for subjects is further organized into 1 or more *MR Sessions* for the subject. An MR Session is identified by an *MR ID* and consists of a set of scans that came from one scanning session with the Subject.

The Subject ID and the MR ID can at times be the same text. This can possibly lead to some confusion. For example, a subject with the Subject ID of `ab30491` can also have a session with the MR ID of `ab30491`. It is important when interacting with the CNDA to be aware of not only the particular ID that you are specifying in an operation, but also what **type** of ID it is that you are specifying.

Subjects can be shared across multiple Projects. Each subject should initially be associated with only one project. Then the owner of that project can share the subject with other CNDA projects.

If you select a project from the list of projects on your CNDA Home page, you will see the project page for the selected project. The project page will look similar to Figure 2. Notice that the lower portion of the page now has a set of tabs labeled Subjects and MR Sessions. You can select data to work with by Subject ID or by MR Session ID. Selecting the Subjects tab lists all subjects in the project organized by Subject ID; selecting the MR Sessions tab lists all the MR sessions for the project organized by MR ID.



Neuroeconomics of Temporal Discounting

ID: NP896
Description: Participants are asked to drink liquid rewards while performing decision-making tasks. Consists of two separate-day sessions: 1. Behavioral (without MRI) and 2. fMRI.
Keywords: juice, temporal discounting, neuroeconomics, reward
PI: Braver, Todd
Investigators: Jimura, Koji

Subject	M/F	Hand	DOB	MR Sessions
ab30484	F	R		1
ab30491	F	R		1
ab30528	F	R		1
ab30529	F	R		1
ab30535	M	R		1
ab30634	M	R		1
ab30640	M	R		1
ab30666	F	R		1
ab30667	M	R		1
ab30673	F	R		1
ab30712				1
ab30727				1

Figure 2: An Example CNDA Project Page

Getting my data into the CNDA

What is the CNDA Prearchive?

The CNDA *prearchive* is a temporary storage location for your image data. Images in the prearchive have not officially been placed into the real archive. In short, the prearchive is a temporary holding area for your image data. This gives you a chance to review the details of images you plan to place in the CNDA before placing the images directly in the archive. It is generally a good idea to place your image data in the prearchive first and then inspect/validate the data before transferring it to the archive proper.

The techniques described below will move image data into the prearchive either directly from the scanner or from another computer. Subsequent sections will cover how to transfer data from the prearchive into the archive

How do I send my data directly from the scanner to the CNDA?

The image browser that is part of the scanner software has a built in option for transferring scanner data to the CNDA prearchive. Open an image browser and click on the folder containing the image data to be transferred. Select Transfer → Send To → CNDA.

When registering a subject (before scanning) you will need to include a line in the "Comments" field of the following form:

Project:NP###, Session:#####, Subject:####

Without this information, when the data is sent to the CNDA prearchive, it will not be associated with your project so that you can see it and import it into the archive proper.

How do I upload data from my desktop computer or the IAC SunOS/Solaris computers to the CNDA?

There are several different ways to upload data to the CNDA. The first is to use what is referred to in the CNDA as "Option 1: Compressed upload". This is likely to be the most efficient uploading mechanism and is described here.

If you have raw image data stored either on your desktop computer or elsewhere that you want to upload to the CNDA using the Compressed upload option, you must first make sure that all image files that you want to upload are available in **uncompressed** DICOM format[5]. Note that if you have already run some analysis or preprocessing software using the images, the software you used may have compressed the DICOM images for you and left only compressed versions behind. It is important to make sure that before you upload the DICOM images, they are first uncompressed.[6]

[5] ECAT format is also supported for PET images.

[6] As the option name "compressed upload" implies, you will ultimately upload a compressed file. However, the "compressed" in the option name refers to compressing the archive file that you will upload. The archive file (a single file containing other files) must be created using uncompressed images and then the archive itself must be compressed before uploading.

Next all the DICOM format image files that you want to upload must be placed in a compressed archive file. One acceptable format for the archive to be uploaded is the ZIP file format which is both a data archive format and a data compression format.[7] Files in this format generally have a `.zip` file extension. Another acceptable format for the archive to be uploaded is the combined tar'd and GNU Zip (gzip) format, which is generally created by using the tar tool (which derives its name from ***ta****pe* ***ar****chive*) to create an archive file with a `.tar` extension and then using gzip to compress the tar file resulting in a file with the multipart extension `.tar.gz`.

Once you have a compressed archive file containing your DICOM format images (`.zip` or `.tar.gz`) , then you can begin the upload process by selecting the Upload → Images menu at the top of your CNDA Home page.

On the CNDA Upload page under "Option 1: Compressed upload" select the project to which the image files should be uploaded. You should see a Project label next to a pull down selection box showing you the Projects to which you may upload images.

For the Destination, select the prearchive. This will give you a chance to review the details of your upload and match the data to the proper subject and session ID before placing the images in the archive proper.

Next, select the Browse button next to the file specification box and select the compressed archive file to be uploaded.

Finally, select the Upload button to start the file upload. You should see a "progress bar" indicating the percent of upload progress. Once the Upload progress has reached 100%, then the Extract/Review progress bar should begin showing the progress of the extracting of files from the uploaded compressed archive. The extract process will look through your compressed archive for DICOM format image files to be placed into the prearchive.

Once the extraction is complete, you should see a message below the progress bars stating, "Your file was successfully uploaded. Click **here** to review and archive your uploaded sessions." Clicking on the **here** link will take you to the CNDA prearchive where you will see any data that you have uploaded to the prearchive sorted by Session ID.

If you need to return to the prearchive (e.g. you forgot to click **here** to visit the prearchive after uploading images, or you needed to logout of the CNDA after uploading and want to return to the prearchive to review your uploaded data at a later time) then you can simply go to your CNDA Home page and choose Upload → Go to prearchive from the menus across the top of the page, and then select the Project to which you have uploaded prearchive data from the dropdown list presented.

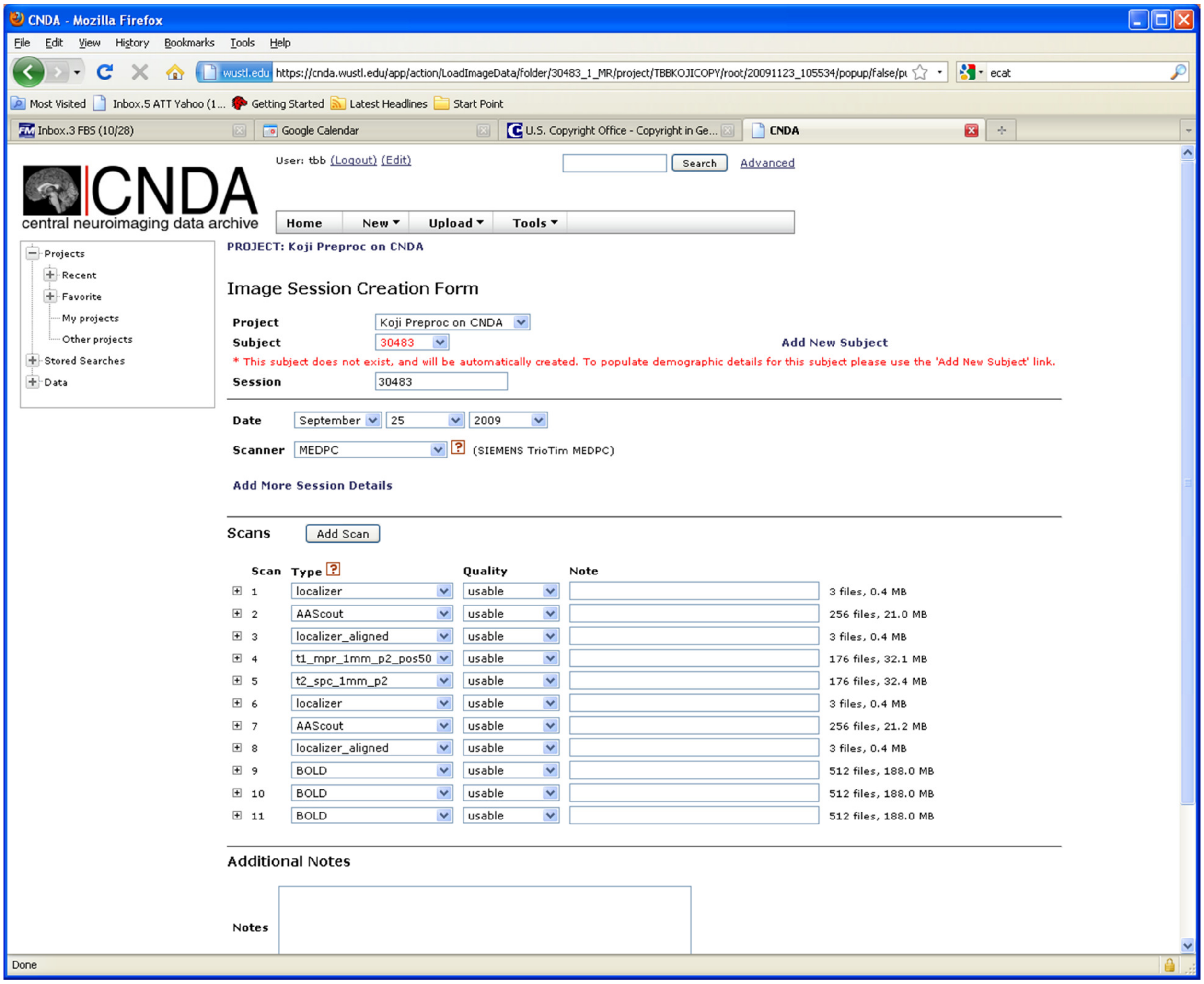
[7] In this context, an archive file is a mechanism for combining a set of files into one file (the archive file) containing the entire set of files. The files placed in the archive file can be accessed and extracted individually or as a group from the archive file. Notice that this type of archiving does not (necessarily) imply that any compression is performed, either on the individual files placed in the archive file or the archive file as a whole. A file in the ZIP file format, both is an archive file and the archive file is compressed.

How do I move my image data from the prearchive into a CNDA project?

If you are not already viewing the prearchive, login to your CNDA account and choose Upload → Go to prearchive. You should then see a list of the sessions that you have uploaded to the prearchive (one row per upload). If you do not see the upload that you are wanting to move into a project, check carefully to see that the correct project is selected in the pull down menu right above the list of uploads.

Once you have found the row for the uploaded data that you wish to move, you can view the uploaded data by clicking on the Session/subject item at the very left of the list of prearchive data. Note that the scissors icon to the immediate right of the Session/subject identifier is "remove icon". Clicking on the scissors will allow you to remove an upload.

When you have selected the Session/subject row for the data you wish to move, you will be presented with an "Image Session Creation Form". See Figure 3 for an example of an Image Session Creation Form.



PROJECT: Koji Preproc on CNDA

Image Session Creation Form

Project	Koji Preproc on CNDA
Subject	30483

* This subject does not exist, and will be automatically created. To populate demographic details for this subject please use the 'Add New Subject' link.

Session	30483
Date	September 25 2009
Scanner	MEDPC (SIEMENS TrioTim MEDPC)

Scans

Scan	Type	Quality	Note	
1	localizer	usable		3 files, 0.4 MB
2	AAScout	usable		256 files, 21.0 MB
3	localizer_aligned	usable		3 files, 0.4 MB
4	t1_mpr_1mm_p2_pos50	usable		176 files, 32.1 MB
5	t2_spc_1mm_p2	usable		176 files, 32.4 MB
6	localizer	usable		3 files, 0.4 MB
7	AAScout	usable		256 files, 21.2 MB
8	localizer_aligned	usable		3 files, 0.4 MB
9	BOLD	usable		512 files, 188.0 MB
10	BOLD	usable		512 files, 188.0 MB
11	BOLD	usable		512 files, 188.0 MB

Additional Notes

Notes

Figure 3: Example Image Session Creation Form page

On this form, you should verify that the information presented about the project, subject, session id, data, scanner, number of scans, scan type, quality, etc. are all correct. As is shown in Figure 3, if the subject does not already exist, it can be automatically created for you. However, you should seriously consider selecting the **Add New Subject** link in order to be able to populate demographic data for the subject including the Subject ID, Birth/Age information, handedness, race, etc.

You should carefully verify the Session ID to be used. If you have a Session ID that is not unique within your project (i.e. matches the ID for an existing session within your project), there should be a message in red stating that your session ID is a duplicate of a session which already exists in the project. If you still proceed to press the Submit button with a duplicate session ID (within a project) you will overwrite the existing session. This is probably **not** what you intend to do.[8]

It is also important to make sure that each scan has the proper scan type listed in the **Type** column. These scan types are used later to specify how the image files are used during preprocessing and to specify which images are to be downloaded using the command line download tools.

Once you have verified and/or updated all the appropriate information for the uploaded data, press the Submit button at the bottom of the page to move the data from the prearchive to the actual CNDA project.

When the data has been successfully moved to the project, you should see an MR Session page that shows the information for the MR Session to which the data has been uploaded. Shortly afterwards you should also receive an email similar to that shown below confirming the successful archiving of the data.

```
From: nrgtech@npg.wustl.edu
Date: Wednesday, 09 Dec 2009 8:50
To: tbbrown@wustl.edu
CC: nrgtech@npg.wustl.edu
Subject: CNDA update: ab30197 Archiving complete

Dear T.Brown,

Ab30197 has been archived without errors.

Details for this session are available at the CNDA website.
```

[8] It would be wise to adopt a convention for assigning session IDs that will help ensure that those IDs are unique within a project. For example, assigning session IDs numerically, e.g. 1, 2, 3, etc. does little to ensure that session IDs are unique within the project. It is easy to mistakenly conceive of such session IDs as only needing to be unique within a subject. So that, for example, a subject with ID `Pilot_1` could have an associated session with ID `1` (the first session for that subject) and another associated session with ID `2` (the second session for that subject). Then it might seem natural to have the subject with ID `Pilot_2` also have an associated session with ID `1`. This would not work as the session ID `1` would not be unique within your project. Only one session with ID `1` should exist within your project. Therefore, a better convention would be to include the subject ID as part of the session ID. In the example given, you would have two unique subject IDs (e.g. `Pilot_1` and `Pilot_2`) and three unique session IDs (e.g. `Pilot_1_Session1`, `Pilot_1_Session2`, and `Pilot_2_Session1`). Appendix B: CCIR Procedure Assessment Form provides an example of how to fill out the Subject ID # and Scan ID# fields of a CCIR Procedure Assessment Form to help ensure that CNDA Session IDs remain unique within your project.

```
CNDA Team.
```

Using CNDA pipelines

What are CNDA pipelines?

CNDA pipelines are a set of standardized processes that can be applied to your scanning data.

The CNDA pipeline that is most likely to be used by Psychology Department fMRI researchers is the pipeline that performs standard BOLD preprocessing. This BOLD preprocessing pipeline is not the only pipeline available. There are also pipelines which:

- create Automated Phantom QA data,
- analyze seed based correlation, and
- build FreeSurfer data

among other things.[9]

How do I associate a CNDA pipeline with a project?

Before a pipeline can be run on a scan session that has been uploaded to the CNDA, the pipeline to be run must first be associated with the project in which the data resides. To do this you first select the project of interest from your CNDA Home page.

When viewing the project page, you will see a set of tabs near the top of the page with headings like: Details, Publications, History, etc. Which tabs you actually see for a project will depend on what rights/permissions you have to that project. If you do not have the necessary permissions to modify the project, you will only see the Details, Publications, and History tabs. If this is the case, and you want to add a pipeline to the project, you will have to ask the project owner to grant you the necessary permissions.

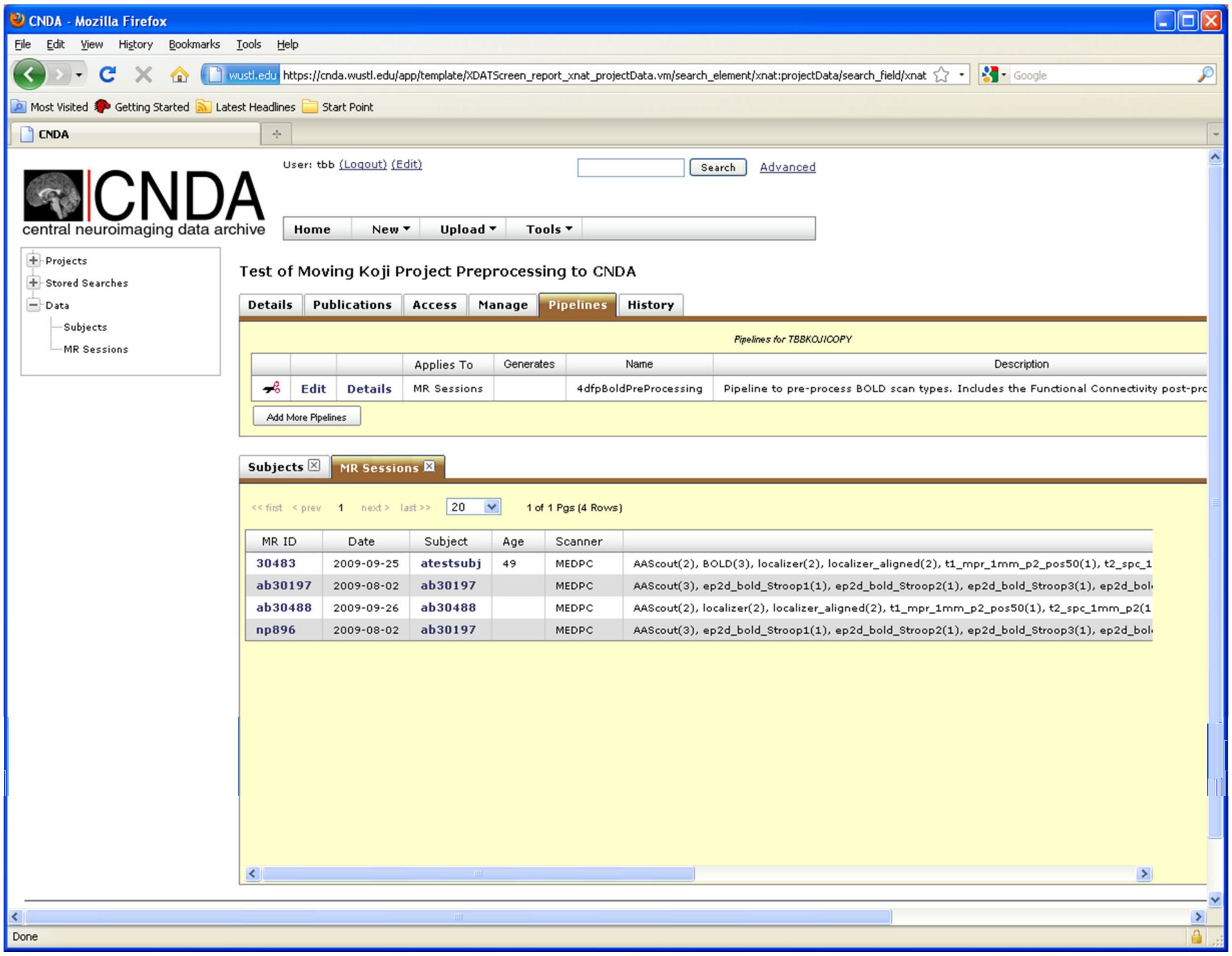
If you do have the appropriate permissions to add a pipeline to the project, you will see a tab labeled “Pipelines”.[10] Select the Pipelines tab to start the process of associating a pipeline with the project. You should then see a display that looks similar to Figure 4.

The top section of the display in Figure 4 should list any pipelines that are already associated with the project.[11] However, there are times when even though some pipelines have already been associated with the project, no pipelines are listed. I’ve found that the following steps can be taken to ensure that all associated pipelines are actually listed. First, select the “Add More Pipelines” button to show a list of possible pipelines to be added. Next, select the “Show Project Pipelines” button under the list of addable pipelines. This returns you to the list of pipelines currently associated with the project and seems to consistently list the correct set of associated pipelines.

[9] It is my understanding that there is a mechanism or process in place by which researchers can request the creation of new pipelines. However, as of this writing, I have not investigated how that is done.

[10] You may also see tabs labeled Access and Manage for the project.

[11] You may have to scroll to the right to view the full pipeline description.


CNDA - Mozilla Firefox
File Edit View History Bookmarks Tools Help
wustl.edu https://cnda.wustl.edu/app/template/XDATScreen_report_xnat_projectData.vm/search_element/xnat:projectData/search_field/xnat
Google
Most Visited Getting Started Latest Headlines Start Point
CNDA
CNDA
central neuroimaging data archive
User: tbb (Logout) (Edit)
Search Advanced
Home New ▾ Upload ▾ Tools ▾
Projects
Stored Searches
Data
Subjects
MR Sessions
Details Publications Access Manage Pipelines History
Add More Pipelines
Subjects ☒ MR Sessions ☒
<< first < prev 1 next > last >> 20
Done

Test of Moving Koji Project Preprocessing to CNDA

Pipelines for TBBKOJICOPY

			Applies To	Generates	Name	Description
	Edit	Details	MR Sessions		4dfpBoldPreProcessing	Pipeline to pre-process BOLD scan types. Includes the Functional Connectivity post-prc

1 of 1 Pgs (4 Rows)

MR ID	Date	Subject	Age	Scanner	
30483	2009-09-25	atestsubj	49	MEDPC	AAScout(2), BOLD(3), localizer(2), localizer_aligned(2), t1_mpr_1mm_p2_pos50(1), t2_spc_1
ab30197	2009-08-02	ab30197		MEDPC	AAScout(3), ep2d_bold_Stroop1(1), ep2d_bold_Stroop2(1), ep2d_bold_Stroop3(1), ep2d_bol
ab30488	2009-09-26	ab30488		MEDPC	AAScout(2), localizer(2), localizer_aligned(2), t1_mpr_1mm_p2_pos50(1), t2_spc_1mm_p2(1
np896	2009-08-02	ab30197		MEDPC	AAScout(3), ep2d_bold_Stroop1(1), ep2d_bold_Stroop2(1), ep2d_bold_Stroop3(1), ep2d_bol

Figure 4: Example project pipeline display

Once you've seen the list of already associated pipelines and verified that the one you want to use is not already associated with the project. You can select the "Add More Pipelines" button.

Now the list of pipelines should include only those pipelines that are not already associated with the project. For this example, we will add the standard BOLD preprocessing pipeline. The pipeline's name is listed as "GenericBoldPreprocessing.xml" and the description reads:

> Pipeline to pre-process BOLD scan types. Includes the Functional Connectivity post-processing.

Further description of this preprocessing pipeline can be viewed by clicking on the "More Info" link to the right of the pipeline description.

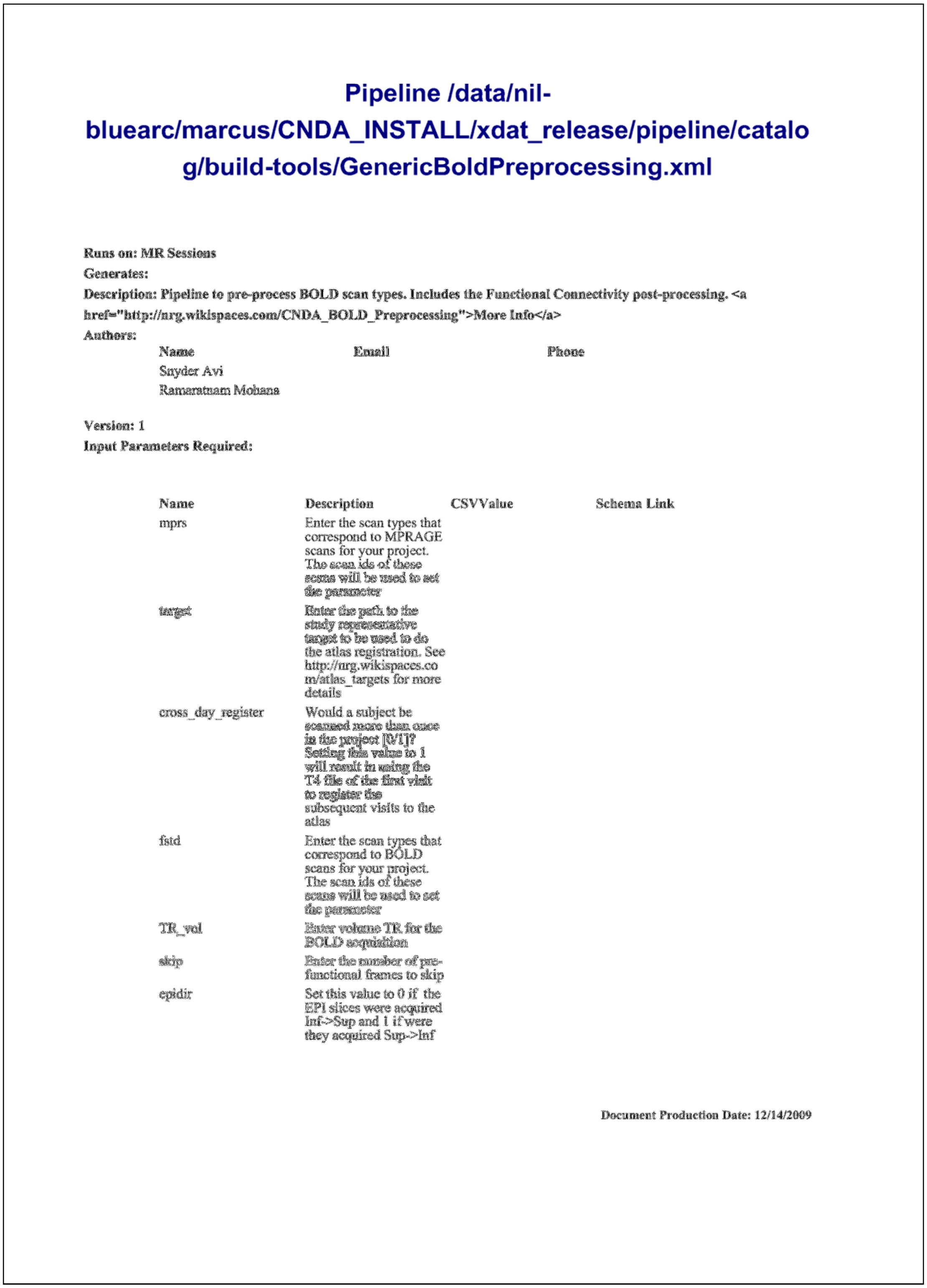
To the left end of each row in the list of available pipelines are links labeled "Add" and "Details". It is a good idea to select the Details link to the left of the pipeline you are planning to add. This will take you to a page that describes the input parameters required to run the preprocessing pipeline. You will probably want to print out that "details" page to have available as a reference before actually adding the pipeline to the project.

The details pages for the Generic Bold Preprocessing pipeline are shown in Figure 5, Figure 6, and Figure 7.

In the processing details document, after the pipeline authors, there is a description of the "Input Parameters Required" for the current version of the pipeline. If you have previously been using C-shell scripts that were originally created by Avi Snyder and then modified on a case-by-case basis for preprocessing your BOLD images, then you should find the set of input parameters listed for the preprocessing pipeline very similar to the set of variables for which you set values at the beginning of the preprocessing C-shell scripts.

In fact, there is often a correspondence between the variables in the C-shell scripts and the pipeline input parameters. However, the values for the pipeline input parameters should not always be set to the same value that you would use for the corresponding script variables.

For example, the `mprs` pipeline input parameter corresponds to the `mprs` C-shell script variable. However, when setting the value for the C-shell script variable, you specify the scan number within the scanning session (e.g. 4) that corresponds to the MPRAGE scans for your project. When specifying the value for the pipeline input parameter, you need to specify the *scan type*. The *scan type* for each set of scans is listed on the session page for each session. An example session page is shown in Figure 8.



Pipeline /data/nil-bluearc/marcus/CNDA_INSTALL/xdat_release/pipeline/catalog/build-tools/GenericBoldPreprocessing.xml

Runs on: MR Sessions

Generates:

Description: Pipeline to pre-process BOLD scan types. Includes the Functional Connectivity post-processing. <a href="http://nrg.wikispaces.com/CNDA_BOLD_Preprocessing">More Info</a>

Authors:

Name	Email	Phone
Snyder Avi		
Ramaratnam Mohana		

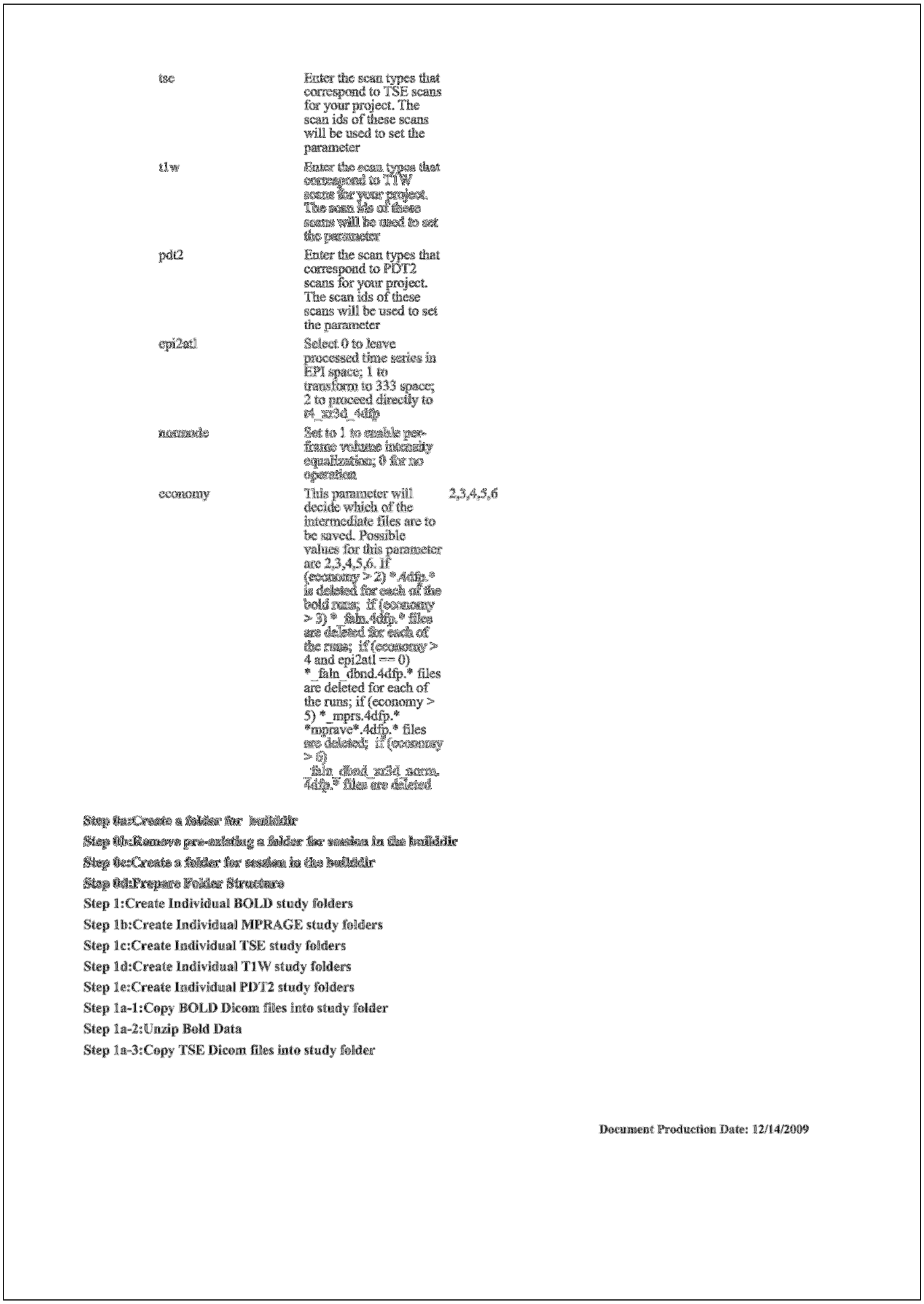
Version: 1

Input Parameters Required:

Name	Description	CSVValue	Schema Link
mprs	Enter the scan types that correspond to MPRAGE scans for your project. The scan ids of these scans will be used to set the parameter		
target	Enter the path to the study representative target to be used to do the atlas registration. See http://nrg.wikispaces.com/atlas_targets for more details		
cross_day_register	Would a subject be scanned more than once in the project [0/1]? Setting this value to 1 will result in using the T4 file of the first visit to register the subsequent visits to the atlas		
fstd	Enter the scan types that correspond to BOLD scans for your project. The scan ids of these scans will be used to set the parameter		
TR_vol	Enter volume TR for the BOLD acquisition		
skip	Enter the number of pre-functional frames to skip		
epidir	Set this value to 0 if the EPI slices were acquired Inf->Sup and 1 if were they acquired Sup->Inf		

Document Production Date: 12/14/2009

Figure 5: Page 1 of Generic BOLD Preprocessing Details



tse	Enter the scan types that correspond to TSE scans for your project. The scan ids of these scans will be used to set the parameter	
t1w	Enter the scan types that correspond to T1W scans for your project. The scan ids of these scans will be used to set the parameter	
pdt2	Enter the scan types that correspond to PDT2 scans for your project. The scan ids of these scans will be used to set the parameter	
epi2atl	Select 0 to leave processed time series in EPI space; 1 to transform to 333 space; 2 to proceed directly to t4_xr3d_4dfp	
normode	Set to 1 to enable per-frame volume intensity equalization; 0 for no operation	
economy	This parameter will decide which of the intermediate files are to be saved. Possible values for this parameter are 2,3,4,5,6. If (economy > 2) *.4dfp.* is deleted for each of the bold runs; if (economy > 3) *_faln.4dfp.* files are deleted for each of the runs; if (economy > 4 and epi2atl == 0) *_faln_dbnd.4dfp.* files are deleted for each of the runs; if (economy > 5) *_mprs.4dfp.* *mprave*.4dfp.* files are deleted; if (economy > 6) _faln_dbnd_xr3d_norm.4dfp.* files are deleted	2,3,4,5,6

Step 0a:Create a folder for buildir

Step 0b:Remove pre-existing a folder for session in the buildir

Step 0c:Create a folder for session in the buildir

Step 0d:Prepare Folder Structure

Step 1:Create Individual BOLD study folders

Step 1b:Create Individual MPRAGE study folders

Step 1c:Create Individual TSE study folders

Step 1d:Create Individual T1W study folders

Step 1e:Create Individual PDT2 study folders

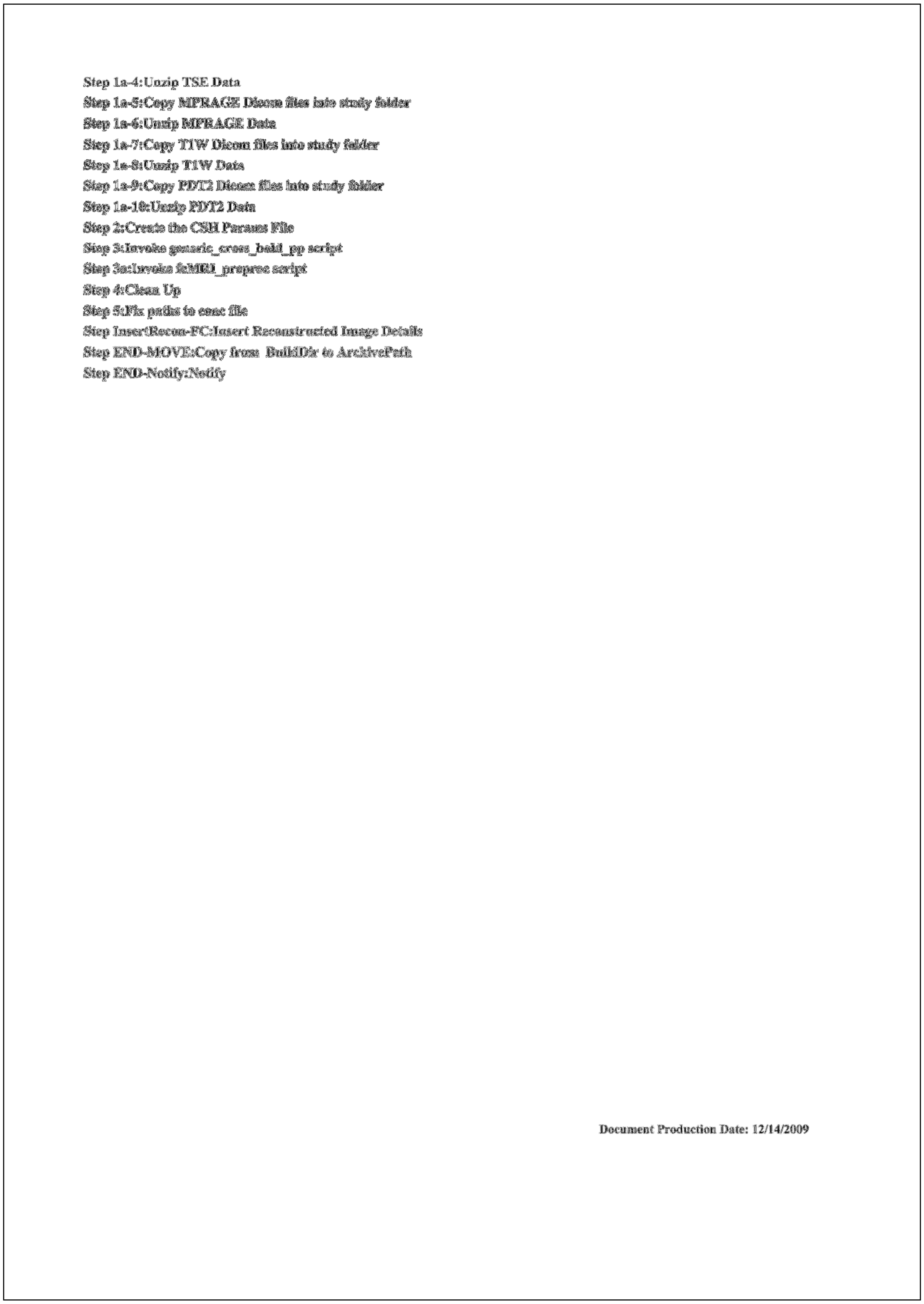
Step 1a-1:Copy BOLD Dicom files into study folder

Step 1a-2:Unzip Bold Data

Step 1a-3:Copy TSE Dicom files into study folder

Document Production Date: 12/14/2009

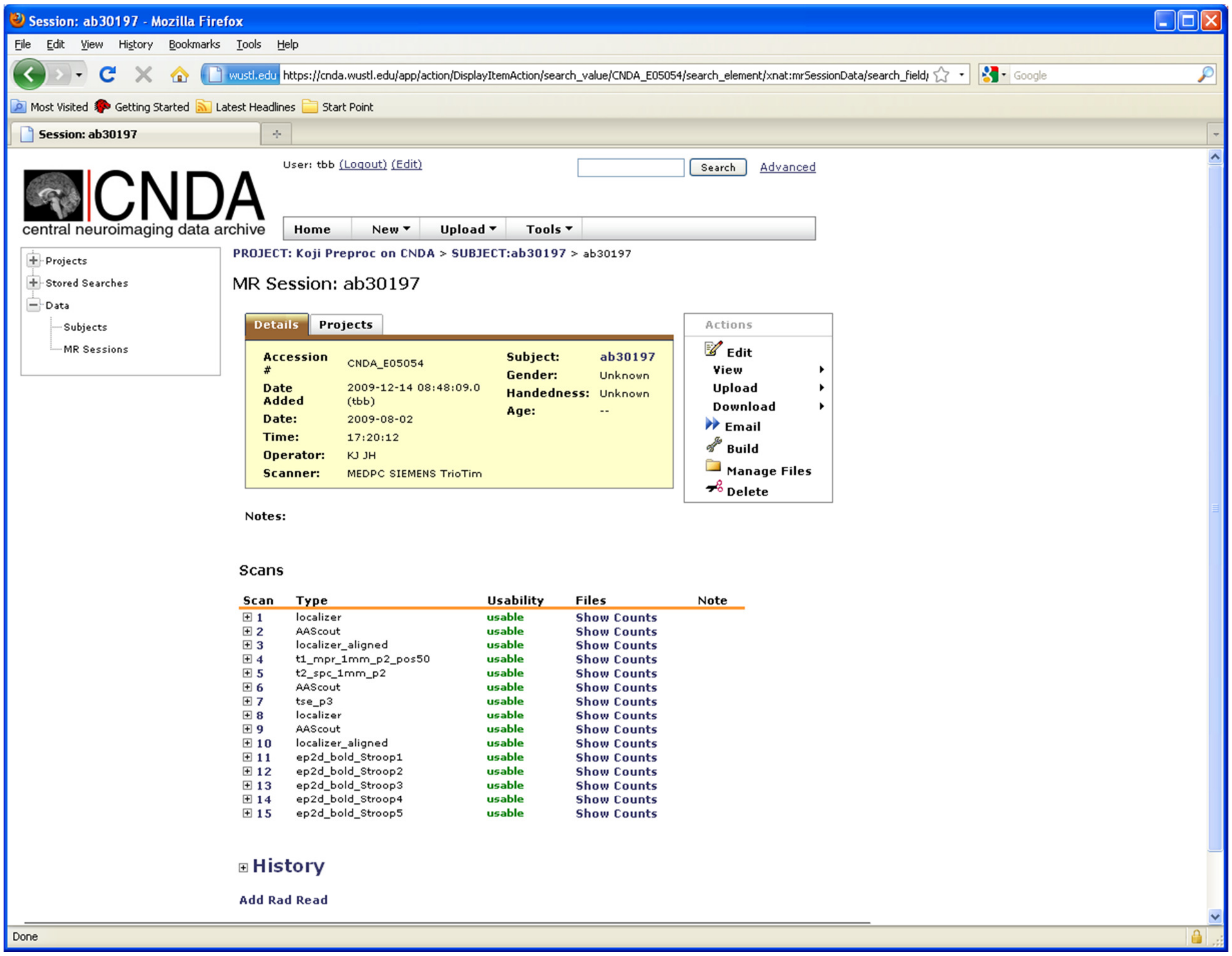
Figure 6: Page 2 of Generic BOLD Preprocessing Details



Step 1a-4:Unzip TSE Data
Step 1a-5:Copy MPRAGE Dicom files into study folder
Step 1a-6:Unzip MPRAGE Data
Step 1a-7:Copy T1W Dicom files into study folder
Step 1a-8:Unzip T1W Data
Step 1a-9:Copy PDT2 Dicom files into study folder
Step 1a-10:Unzip PDT2 Data
Step 2:Create the CSH Params File
Step 3:Invoke generic_cross_bold_pp script
Step 3a:Invoke fcMRI_preproc script
Step 4:Clean Up
Step 5:Fix paths to conc file
Step InsertRecon-FC:Insert Reconstructed Image Details
Step END-MOVE:Copy from BuildDir to ArchivePath
Step END-Notify:Notify

Document Production Date: 12/14/2009

Figure 7: Page 3 of Generic BOLD Preprocessing Details


Session: ab30197 - Mozilla Firefox
File Edit View History Bookmarks Tools Help
wustl.edu https://cnda.wustl.edu/app/action/DisplayItemAction/search_value/CNDA_E05054/search_element/xnat:mrSessionData/search_field
Google
Most Visited Getting Started Latest Headlines Start Point
Session: ab30197
CNDA
central neuroimaging data archive
User: tbb (Logout) (Edit)
Search
Advanced
Home New Upload Tools
Projects
Stored Searches
Data
Subjects
MR Sessions
Details
Projects
Actions
Edit
View
Upload
Download
Email
Build
Manage Files
Delete
Done

PROJECT: Koji Preproc on CNDA > SUBJECT:ab30197 > ab30197

MR Session: ab30197

Accession #	CNDA_E05054	Subject:	ab30197
Date Added	2009-12-14 08:48:09.0 (tbb)	Gender:	Unknown
Date:	2009-08-02	Handedness:	Unknown
Time:	17:20:12	Age:	--
Operator:	KJ JH		
Scanner:	MEDPC SIEMENS TrioTim		

Notes:

Scans

Scan	Type	Usability	Files	Note
⊞ 1	localizer	usable	Show Counts	
⊞ 2	AAScout	usable	Show Counts	
⊞ 3	localizer_aligned	usable	Show Counts	
⊞ 4	t1_mpr_1mm_p2_pos50	usable	Show Counts	
⊞ 5	t2_spc_1mm_p2	usable	Show Counts	
⊞ 6	AAScout	usable	Show Counts	
⊞ 7	tse_p3	usable	Show Counts	
⊞ 8	localizer	usable	Show Counts	
⊞ 9	AAScout	usable	Show Counts	
⊞ 10	localizer_aligned	usable	Show Counts	
⊞ 11	ep2d_bold_Stroop1	usable	Show Counts	
⊞ 12	ep2d_bold_Stroop2	usable	Show Counts	
⊞ 13	ep2d_bold_Stroop3	usable	Show Counts	
⊞ 14	ep2d_bold_Stroop4	usable	Show Counts	
⊞ 15	ep2d_bold_Stroop5	usable	Show Counts	

⊞ History

Add Rad Read

Figure 8: Session Page for session ab30197

Note that the "Scans" section of the page shows a table with headers Scan, Type, Usability, Files, and Note. It is the value listed under the Type header that needs to be specified for the `mprs` pipeline input parameter.

So for the example shown in Figure 8, if you would have specified scan set `4` for `mprs` in the shell script, you will need to specify `t1_mpr_1mm_p2_pos50` for the `mprs` pipeline input parameter.

Sometimes the value that you would set for a script variable and the value for a pipeline input parameter are identical. For example, the script variable `economy` and the pipeline input parameter `economy` both take numeric values (from 0 to 6) that have the same meanings.

So, when specifying values for the pipeline input parameters using a C-shell script as an example, be careful to note whether you should specify the parameter in the same manner for the CNDA pipeline as it was specified in the C-shell script.

Two of the pipeline input parameters for the Generic BOLD Preprocessing script warrant further discussion here. The first is the `target` input parameter. The details page for the pipeline states that for the `target` input parameter you should, "Enter the path to the study representative target to be used to do the atlas registration." It also directs you to the web page http://nrg.wikispaces.com/atlas_targets for more details. The specified web page tells you a file system path name to use to specify a particular target. For example, to specify target `711-2C` you are told to specify the path `/data/petsun43/data1/atlas` as the value for the `target` input parameter.

This turns out to be incorrect. Instead, the value to be specified for the `target` input parameter is much more straightforward. You should simply specify the target name. So to use atlas target `711-2C`, you should specify `711-2C` for this parameter. The web page at http://nrg.wikispaces.com/atlas_targets is still useful as a listing of the atlas targets that are available.

The other input parameter that needs discussion here is the `t1w` input parameter. It is unclear to me as of this writing what the `t1w` input parameter actually specifies. The name and description on the details page seem to indicate that the user should specify the scan types for T1-weighted scans. However, I haven't found an example C-shell script that actually uses a corresponding `t1w` variable, and the MPRAGE scans that are specified by the `mprs` input parameter seem to be the T1-weighted scans for the session. My experience to date has been that you can leave the `t1w` input parameter blank.

It is also worth noting that there is a difference in how you specify multiple values for a pipeline input parameter compared to how multiple values are specified for a variable in a C-shell preprocessing script. In the C-shell script, multiple values for a single variable were separated by spaces. For example, you might specify the BOLD scans for a session in the C-shell script by setting the values for the fstd variable as follows:

```
set fstd =  ( 11  12  13  14  15  )
```

For the input parameters specified for a CNDA pipeline, multiple values are to be separated with commas. So the values for the fstd input parameter, which are specified by scan type instead of scan number, might be listed like:

```
ep2d_bold_Stroop1, ep2d_bold_Stroop2, ep2d_bold_Stroop3,
ep2d_bold_Stroop4, ep2d_bold_Stroop5
```

You should be aware that when you associate a pipeline with a project, you are not causing the pipeline to automatically execute for each subject in the project. Also, the input parameters that you specify when associating a pipeline with a project are project-wide default values for the parameters. These default values can be checked and changed when you actually request that a pipeline be run for a particular scan session.

To go ahead and associate a pipeline with a project:

- Have the details page for the pipeline available to use as a reference
- Press the "Add" button to the left of the pipeline you want to associated with the project
- Fill in the input parameters page, and
- Press the Submit button.

How do I use a CNDA pipeline for preprocessing a set of data?

Once you have a particular pipeline associated with a project, you can invoke that pipeline on an MR session. To invoke the pipeline, you will need to first go to the MR Session page for the session to be processed using the pipeline. See Figure 8 above for an example MR Session page.

In the "Actions" box near the top of the page to the right of the "Details" and "Projects" tabs there is an action labeled "Build" with a icon of a wrench next to it. This is where you initiate a run of a preprocessing script. On the page for the MR session for which you want to run a pipeline, select the "Build" action.

A browser window will pop up asking you to select the pipeline to launch for the MR session. Select the appropriate pipeline and press the "Submit" button. (If the appropriate pipeline is not available for selection, see the "How do I associate a CNDA pipeline with a project?" section above.)

Once you have pressed the "Submit" button, you will be presented with a page asking you to set/verify the input parameters for this run of the pipeline. This is where you can verify/change the input parameters from the default values that were specified when the pipeline was associated with the project.

When the pipeline processing is complete, an email will be sent to the email address associated with your CNDA account. If you want to specify other email addresses to receive notification, list them in the box provided at the bottom of the page.

When the pipeline parameters have been specified to your satisfaction, press the "Run processing" button at the bottom of the page. You should then receive a notice that the "build process was successfully launched."

If the pipeline fails, you will receive an email with a subject line similar to:

```
CNDA update: Processing failed for MR Session ID
```

If the pipeline succeeds, you will receive an email with a subject line similar to:

```
CNDA update: Session MR Session ID processed
```

Who do I contact to get help with the CNDA?

The proper email address for getting support for the CNDA is:

cnda-help@npg.wustl.edu

That email address should always get your question to a CNDA support person.

As of this writing, the support for CNDA is handled by Genevieve Gurney. Her contact information is:

Name: Genevieve Gurney
Email: gurneyj@wustl.edu

Using NIL maintained resources for analysis outside of the CNDA

What is a NIL Un*x account and how do I get one?

In order to analyze data using Washington University standard tools for fMRI analysis (e.g. FIDL) and other Un*x based software, we will make use of computer systems maintained by the Computer Support Group (CSG) within the Neuro-Imaging Laboratory (NIL). To access these systems, you will need to have a NIL Un*x account. A NIL Un*x account gives you login/shell level access to NIL/CSG maintained Un*x systems.

A NIL Un*x account is not the same as an RIIS account which is necessary for you to use the scanners. Even though your NIL Un*x account may have the same username as your RIIS account and may, if you choose, have the same password as your RIIS account, the two accounts are separate entities. You may have one without having the other.

To get a NIL Un*x account, visit the NIL homepage at http://www.nil.wustl.edu. In the menu of links to the left of the page, you should see a link labeled “Documents and Forms”. When you select the “Documents and Forms” link, you will be presented with a list of forms from which to choose. One of those forms/links should be the “New User Request Form”. Selecting that link will allow you to download or open a Microsoft Word™ format document titled “MIR Client Computer Access Request Form”.

Fill out this form to request a NIL Un*x account. When filling out the form:

- Be sure that on page 3 you fill in “Section C” and check the box requesting a “UNIX login (Sun or Linux)” and the box requesting “VPN Access”.
- In the line labeled “Other” in “Section C”, please note the user group(s) to which you would like your account to belong (e.g. ccp, staff, shimony, etc.) If you do not know what groups you should be in, please ask your lab director.
- Also on the “Other” line, please include an indication of what command line shell you would like to have as your default login shell (e.g. csh, tcsh, bsh, bash, ksh, etc.) If you do not know which shell to request, tcsh is a reasonable default choice. Users transferring their work from the IAC Solaris systems will likely be most comfortable with the tcsh shell. If you have some other shell preference, feel free to make your choice known on this line.
- Also on page 3, you will need to get the approval signature of a Lab or Section Chief.

FAX the form to the MIR Executive Director’s office at the phone number given at the top of the form.

How do I set up the VPN connection to access NIL maintained computer systems?

In order to connect to the NIL machines to process your data, you will not only need a NIL Un*x account, you will also need to become part of a Virtual Private Network (VPN). A VPN connection becomes a new network connection (apart from your standard internet connection) that uses the same hardware as your standard internet connection.

To setup this VPN connection, you will need to install VPN client software on the computer you will be using to connect to the VPN. To get the VPN client software, take the following steps:

1. Make sure your system is not currently running a VPN client. If you have not previously installed or run VPN client software, it is not likely that you will be running a VPN client. If you have previously installed and used a VPN client, then you should make sure to close down your current VPN client software before trying to install the VPN client software described below.
2. Make sure your system is connected to the internet.
3. Use your internet browser to visit: https://mirvpn.wustl.edu/nil

   The page you arrive at should display "CISCO SSL VPN Service" in the upper left and have a login dialog in the middle prompting you to entry your username and password.
4. Enter you NIL VPN username and password.

   Note that the username and password to be used here are **not** your NIL Un*x username and password, but your NIL VPN username and password. When you requested a NIL Un*x account, you should have also indicated that you needed NIL VPN access and thus been supplied with a NIL VPN username and password.
5. A Java applet will be launched that will "analyze your system" (check your hardware, operating system, etc.) to determine what software needs to be installed on your system. It will then download and install the appropriate VPN client software. You may have to click "yes" or "OK" to approve the installation of the software.
6. After the software is downloaded and installed, it should automatically start the VPN Client software (Cisco AnyConnect VPN Client). However, the connection that it automatically establishes is to a VPN called `mirvpn.wustl.edu`. This is not the VPN to which you want to be connected. To fix this, start the VPN client software (from your Start menu in Windows or from the Finder in Mac OS X). You should see a window titled "Cisco AnyConnect VPN Client" and containing three tabs labeled Connection, Statistics, and About. Select the Connection tab, and ***press the Disconnect button to disconnect from the*** **`mirvpn.wustl.edu`** ***VPN***.
7. Next, modify the contents of the "Connect to:" box changing the specification from `mirvpn.wustl.edu` to `mirvpn.wustl.edu/nil`, and then press the Select button at the bottom of the window.
8. You'll be prompted for your Username and Password. (Again, this is your NIL VPN username and password being requested, and your Username will probably already be correctly filled in.) Verify your Username, enter your Password, and press the Connect button.
9. When the Cisco AnyConnect VPN Client window goes away, you should be successfully connected to the VPN. Verify this by either using `ssh` to connect to one of the NIL machines or using your VNC client software to attach to an existing VNC Server session.
10. To disconnect from the VPN, start the VPN client software as is described in step 6 above. Then choose the Connection tab, and select Disconnect.

11. To reconnect to the VPN later, start the VPN client. Notice that on the Connection tab now the "Connect to:" field is already prepopulated with the correct VPN specification (`mirvpn.wustl.edu/nil`) and your Username should already be correctly prepopulated. Simply enter your NIL VPN password and press the Connect button.

12. You should then be able to access NIL systems and resources.

Special Note 1:

The VPN client software installed using the above process has some advantages over the client software that was recommended in previous versions of this document. First, the previous client software had some difficulty working correctly under some of the most recent versions of Mac OS X. The previous client software also had difficulties at times working when the desktop system using the software was attached to the network via a wired (not wireless) connection in the Psychology Building. This version of the VPN client software is purported to no longer have these problems.

Special Note 2:

Similarly, when using previously provided VPN client software, you could not access local network resources like printers when attached to the VPN. This should not be the case with the VPN client software installed using the process described above.

Special Note 3:

If, when you try to attach to the NIL VPN using the VPN client installed with the above steps, you find yourself completely cut off from network access while the VPN client is running, then you are probably not properly registered in the Active Directory group which allows you to access the NIL VPN using this client software.

If this happens to you, shut down the NIL VPN client software and send an email to NIL systems support at nil-systems@npg.wustl.edu describing the situation. They should be able to get you registered in the appropriate Active Directory group to allow you NIL VPN access via this client software.

How do I change my VPN password?

The VPN username assigned to you when you were granted VPN access is intended to remain your VPN username for as long as you have reason to have VPN access. The VPN password assigned to you when you were granted VPN access is intended to be temporary. You should change that password. However, it is not obvious how to do so. The following are the necessary steps for changing your VPN password.

1. Visit the following link: https://nilmail07.wustl.edu/IISADMPWD/aexp2b.asp

2. You will be shown a form to fill in with the following fields:

   Domain:
   Account:
   Old password:
   New password:
   Confirm new password:

3. To change your password, fill in the form and press the OK button.
4. The Domain field should be filled in with `neuroimage.wustl.edu`

What NIL maintained CPUs should I use?

We have been asked to use the following systems for our fMRI analysis.

- `petsun23.neuroimage.wustl.edu`
- `petsun24.neuroimage.wustl.edu`
- `linux1.neuroimage.wustl.edu`

How do I access NIL systems?

Once you have your VPN client up and running and have established a VPN connection to the `neuroimage.wustl.edu` domain, you should be able to get simple shell-level access to the NIL systems by using client software like `telnet` or `ssh`. After establishing a connection using `telnet` or `ssh`, use your Un*x account name and password to login.

Just as you changed your temporary VPN password, you will most likely also want to change your assigned Un*x account password. Use the `passwd` command to change your Un*x password.

How do I setup my shell startup files to handle both Linux and Sun OS/Solaris Systems?

Some of the environment variables and settings that are appropriate for your account when you login to a Linux-based system are not appropriate when you login to a Solaris-based system and vice versa. In fact, some of the commands that you would like to run upon logging in to a Solaris system can handicap you greatly if they are run upon logging in to a Linux system.

However, your home directory will be the same regardless of whether you login to a NIL managed Linux system or a NIL managed Solaris system. Therefore, the same files from your home directory will be used to setup your environment (set environment variables, set aliases for commands, set default file protections for files you create while logged in, etc.)

This presents a minor problem in creating account setup files that will perform different setup actions based upon the operating system of the computer on which you are working. To help alleviate this problem, a set of template account setup files for C-Shell users have been created. These template setup files check to see what operating system is currently being used and then execute other setup files that are appropriate for that operating system.

The template account setup files are in the directory:

```
/home/usr/wupsy/login_templates.
```

The files currently in that directory are:

- `.cshrc`
- `.login`

- `.hp.cshrc`
- `.hp.login`
- `.linux.cshrc`
- `.linux.login`
- `.sgi.cshrc`
- `.sgi.login`
- `.sol.cshrc`
- `.sol.login`
- `.sun.cshrc`
- `.sun.login`

The two basic startup configuration files for the C-Shell[12] are `.cshrc` and `.login`. Both of these files are used by the C-Shell (the tool which presents you with a command line prompt, interprets your commands, and attempts to carry out your commands by executing programs and scripts) to setup your environment.[13] The `.cshrc` file is executed *before* the `.login` file and is executed every time the system creates a new environment for you (e.g. every time you start a new command-line terminal.) The `.login` file is executed after the `.cshrc` file, but is only executed once for each time the user logs in to the system.

The distinction between when `.cshrc` and `.login` are executed can be confusing if you don't already understand how and when a Un*x system decides to "create a new environment" for you. Rather than trying to describe the details of that mechanism, it is usually sufficient to follow the guidelines below when deciding what environment setup commands should go in your `.cshrc` file and what environment setup commands should go in your `.login` file.

- Commands that set environment variables (e.g. `setenv` commands) should go in the `.login` file. The most common exception to this is setting the path (list of directories) in which you want the system to look for the implementations of commands that you enter.
- Commands that produce "output" to a terminal screen that you want to be should go in the `.login` file.
- Commands that create aliases (abbreviations) for other commands (e.g. `alias rm 'rm -i'` which forces the "remove" command to prompt you and wait for confirmation before actually removing a file) should be placed in the `.cshrc` file.

The template `.cshrc` and `.login` files do nothing more than determine what operating system is currently in use and then execute the commands in a corresponding platform-specific `.cshrc` or `.login` file. For example, if you are starting a new C-shell on a Linux-based system, the template `.cshrc` file will do nothing more than to execute the `.linux.cshrc` file. Similarly,

[12] The most common login shell/environment for Psychology Department users of NIL managed Un*x systems.

[13] Setting up your environment includes such things as determining where the shell will look for the executable programs that correspond to commands that you enter, determining what aliases (abbreviations) for commands will be recognized, setting environment variables which determine how other programs will behave.

when logging in to a Solaris-based system, the `.cshrc` file will do nothing more than to execute the `.sol.cshrc` file.

Steps to take for new users

If you are a relatively new user of NIL managed Un*x systems, then I suggest you simply copy all of the template shell startup files into your home directory. This can be done with the following commands:

```
$ cd ~
$ mv .login .login.orig
$ mv .cshrc .cshrc.orig
$ mv .sol.login .sol.login.orig
$ mv .sol.cshrc .sol.cshrc.orig
$ cp /home/usr/wupsy/login_templates/.* .
```

(Do not worry about the warning messages you get indicating that `/home/usr/wupsy/login_templates/.` and `/home/usr/wupsy/login_templates/..` are directories.)

Steps to take for not so new users

If you have been using NIL managed Solaris systems (cnindsXX, petsunXX, etc.) for a while and have made changes to the existing shell startup files, then I suggest taking the following steps:

Login to a NIL managed Solaris based system (such as petsun23 or petsun24) and replace your existing `.cshrc` and `.login` files using the following commands:

```
$ mv ~/.login ~/.login.preLinux
$ cp /home/usr/wupsy/login_templates/.linux.login ~/.linux.login
$ cp /home/usr/wupsy/login_templates/.login ~/.login
$ mv ~/.cshrc ~/.cshrc.preLinux
$ cp /home/usr/wupsy/login_templates/.linux.cshrc ~/.linux.cshrc
$ cp /home/usr/wupsy/login_templates/.cshrc ~/.cshrc
```

If you have previously made modifications to your `.sol.cshrc` file, you **may** want to edit the `.linux.cshrc` file just copied into your home directory to add command aliases, paths to commands, and other changes similar to those you may have mad to the `.sol.cshrc` file. However, before you do any editing of the `.linux.cshrc` file, please take the following into account:

First, the existing template version of the `.linux.cshrc` file already takes care of the following items. You do not need to change the `.linux.cshrc` file to account for these things:

1. It places your current directory (referred to as “.”) in your path. So you can execute scripts that are in your current directory by just typing the script’s file name.
2. It looks for a `bin` directory in your home directory. If such a directory exists, it places that directory in your path. This allows you to place your own personal scripts into your own `~/bin` directory and execute them from the command line prompt by simply typing the script’s file name.

3. It sets the `noclobber` variable to try to prevent file redirection operations from accidentally overwriting existing files.
4. It turns on file name completion and autolisting so that you can get a list of the files that match the partial name you've typed so far by pressing the tab key.
5. It sets up an alias for the `rm` command to prompt you before deleting files.
6. It sets up an alias for the `cp` command to try to prevent accidental overwriting of files by copying.
7. It sets up an alias for the `mv` command to try to prevent accidental overwriting of files by moving/renaming.
8. It sets a umask value that tries to ensure that other users in the same user group can access files that you have created.

Again, all these things are already done in the template `.linux.cshrc` file. So you should not need to make any changes to your copy of that file to get those "features".

Second, **simply copying your existing `.sol.cshrc` file to a new file named `.linux.cshrc` in order to try to get all your changes made for the Solaris environment to happen for a Linux environment is a <u>bad idea</u>.**

Some commands that many users already have in their `.sol.cshrc` file will cause corruption of your `PATH` environment variable when you log in to a Linux system. This corruption will cause you to lose access to even simple commands like `ls` and `cd`.

If you find that you need to alter your path for use on a Linux-based system, simply edit your `.linux.cshrc` file and add commands like:

```
set path = ($path /usr/local/bin)
```

to add `/usr/local/bin` (for example) to your path.

However, before adding a directory to your path, please first check to see if it is already on your path. Some of the directories that you had to add to your path for a Solaris-based system are already added to your path by the system-wide login files for Linux. For example, `/usr/local/bin` should already be on your path. So adding it yourself as is shown above should not be necessary.

To see a space separted list of the directories that are already on your path when logged in to a Linux-based system, enter the following command:

```
$ echo $path
```

How do I use VNC to access NIL Systems?

You probably will not be able to run all the analysis software that you would like using a simple `telnet` or `ssh` connection to the NIL systems. Instead, you will likely want to establish a Virtual Network Computing (VNC) connection from your desktop computer to the NIL systems. Establishing a VNC connection involves:

1. Selecting VNC Client software for your desktop system and installing that software.

2. Starting a VNC Server on one of the NIL systems.
3. Connecting your VNC Client software with the VNC Server that you have started on the NIL systems.

What VNC Client software should I use on my desktop?

There are many choices for VNC Client software for your desktop computer. For Microsoft Windows™ systems, I've had pretty good luck with UltraVNC (http://www.unvc.com/). For Macs, Chicken of the VNC seems to be the default local choice. For Linux, "almost all Linux distributions include an updated/customized version of the RealVNC free edition. For example, in Debian and its derivatives, the RealVNC server and client appear under the packages named vnc4server and xvnc4viewer, respectively."[14]

How do I start a VNC Server on NIL systems?

To start a VNC Server to interact with your local VNC client software, you will need to use `ssh` or `telnet` to start a terminal session with the NIL machine with which you want to interact. Remember that to make such a connection to a NIL machine you will need to first establish a VPN connection to the NIL network.

Once you've successfully connected to one of those machines, then you will need to issue a command to start a VNC Server.

Issue a command similar to the following in order to start a VNC Server for the first time.

```
% vncserver -depth 24 -nolisten local -geometry 1250x800
```

Note that you will want to change the `1250x800` in the command to something that is appropriate for the width and height (width x height) for the display of the system from which you will be connecting to this VNC Server.[15]

The first time you issue this command, you will be prompted to enter a password to be used to access the VNC Server that you are creating. You will need to enter this password whenever you connect to this server using your VNC client.

If you successfully start a VNC Server process for the first time, the response you will receive from the system will include a line that identifies the new "desktop". The line will look similar to:

```
New 'petsun23:2 (tbbrown)' desktop is petsun23:2
```

At the time you start your first VNC Server process, you should also see messages indicating that a new default startup script has been created for you, that applications in that default startup script are being started, and that a log file for the session is being maintained. E.g.:

```
Creating default startup script /home/usr/tbbrown/.vnc/xstartup
Staring applications specified in /home/usr/tbbrown/.vnc/xstartup
```

[14] From http://en.wikipedia.org/wiki/RealVNC. Retrieved 03 Jan 2010.

[15] See http://www.realvnc.com/products/free/4.1/man/vncserver.html for a description of the `-geometry` and `-depth` command line switches. As an alternative to the `-depth` option `-cc 3` can be used. However, The –cc 3 option is intended for use with "old" X applications. The –depth option seems to be the better choice.

```
   Log file is /home/usr/tbbrown/.vnc/petsun23:2.log
```

The machine name reported (petsun23 in the above example), the username (tbbrown in the above example), and the session number (shown as :2 in the above example) will all be specific to the machine you are using, your username, and the VNC Server *session number* assigned by the vncserver command in your case.

Also note that if the server is created correctly, there will now be a .vnc subdirectory in your home directory. If you change directory (cd) down into the .vnc subdirectory, you will see files named petsun23:2.log, petsun23:2.pid, passwd, and xstartup.

The item of particular interest to you for using the VNC Server that you've just started is the number after the colon (:) in the .pid file. This is the VNC Server *session number* and is needed in order to connect to or shut down the VNC Server. In the example above, the session number is 2.

What should be in my xstartup file?

To make your VNC session more useful, I suggest that after the first time you start a VNC Server, you immediately shutdown the server and modify the xstartup file in your ~/.vnc directory.

Stop the VNC server using a command like the one shown in the "How do I kill/stop my VNC Server?" section below.

Replace the file ~/.vnc/xstartup in your home .vnc directory by issuing the following commands:

```
   % cd ~/.vnc
   % mv xstartup xstartup.original
   % cp /home/usr/wupsy/vnc_templates/xstartup ~/.vnc/xstartup
```

Once you have made this change to the xstartup file, you should start a new VNC Server process. Then you can exit from the telnet or ssh connection. The VNC Server will be left running even after you log out.

How do I find my VNC Server session number if I forget it?

If you want to connect to a VNC Server session but have forgotten the session number (which is needed to connect), then you can find the session number by:

1. Logging into the machine on which the VNC Server session is running.
2. Change to the ~/.vnc directory: cd ~/.vnc
3. List the contents of the directory: ls
4. Look for a file with a name that begins with the machine name (e.g. petsun23) and ends with the extension .pid. For example, petsun23:2.pid.
5. The number after the colon and before the .pid extension is your VNC Server session number.

How do I connect to the VNC Server that I've started?

To connect to the VNC Server you have created, first make sure you have established a VPN connection to the `neuroimage.wustl.edu` network. Next, start your VNC client software. Use the VNC client software to "connect" to the VNC Server session. The server session will be specified by giving the node name (machine name) of the machine to which you want to connect (e.g. `petsun23.neuroimage.wustl.edu`), followed by a colon (`:`), followed by the result of adding 5900 to your VNC Server session number.

In the above example, we would specify the server session to which to connect as:

```
petsun23.neuroimage.wustl.edu:5902
```

The exact mechanism used to connect your VNC Client to the VNC Server will depend upon what VNC Client software you are running. You will most likely need to specify your VNC Server password (established the first time you started a VNC Server on the NIL systems) in order to connect.

Once you have successfully established a connection between your VNC client and the VNC Server, you are likely to have at least a single terminal window on the desktop provided by the window manager.

If there is no terminal window, you are using the template `xstartup` file as is suggested above, and you are connecting to a Solaris system, you can start a terminal window by "right clicking" on your desktop, selecting Tools, and then selecting Terminal. You can then start X-terminals from the command line window of an existing terminal by entering:

```
% xterm &
```

If there is no terminal window, you are using the template `xstartup` file as is suggested above, and you are connecting to a Linux system, you can start a terminal window by selecting the Applications menu in the upper left hand corner of your screen and proceeding through menus and submenus as follows:

Applications → Accessories → Terminal

How do I run FIDL on the NIL maintained machines?

FIDL can be invoked on the NIL maintained systems by simply issuing the fidl command at the shell command prompt in any terminal window, similar to:

```
% fidl &
```

How do I run background jobs using the Sun Grid Engine?

Long running "background" jobs can be run on an NRG maintained computing cluster. Shell scripts that are generated by FIDL that are expected to run for a relatively long time would be good candidates for consideration to be run on this Sun Grid Engine cluster.

See http://nrg.wikispaces.com/SGE_QSubWiki for instructions on how to use the cluster.

How do I kill/stop my VNC Server?

To kill/stop your VNC Server, you will need to know the server session number (in the above examples that session number is `2`) and the machine on which the server session is running (e.g. `petsun23`). Log in to the machine using `ssh` or `telnet` and issue a command like the following:

```
% vncserver -kill :2
```

Replace the `2` in the above command with your server session number.

How can I make sure I receive important notifications about using NIL Systems?

An email mailing list (NIL USERS IN PSYCH) has been created to which users of NIL managed systems in the Psychology Department should subscribe. If you use any computing resources (servers like linux1, petsunXX; BlueArc disk space; etc) managed by the Computer Support Group (CSG) of the Neuro-Imaging Laboratories (NIL), and are using those resources because of your affiliation with the Washington University Department of Psychology, then you should subscribe to this list.

The list is intended to be used to send out notifications that are important to all such users (e.g. availability of new server machines, availability and installation locations for new software packages, warnings about system outages, etc.)

To subscribe to this list, send an email message to LISTSERV@ARTSCI.WUSTL.EDU containing a single line similar to the following:

```
subscribe nilusersinpsych@artsci.wustl.edu <your full name>
```

Things to note:

1. `<your full name>` should be replaced with at least your first and last name. If you give just one name, like “Tim”, your subscription request will be automatically rejected by the LISTSERV.
2. Do not include the angle brackets (less than and greater than signs) in your single line of the email. That is, your subscription line should look something like:

    ```
    subscribe nilusersinpsych@artsci.wustl.edu Tim Brown
    ```

    Not like:

    ```
    subscribe nilusersinpsych@artsci.wustl.edu <Tim Brown>
    ```

3. Send the subscription request email to LISTSERV@ARTSCI.WUSTL.EDU, not to nilusersinpsych@artsci.wustl.edu.

    You cannot send anything to nilusersinpsych@artsci.wsutl.edu until you are a member of the list.

4. *After* you have submitted a subscription request *and* your membership has been approved, you can then send messages to the list by sending email to: nilusersinpsych@artsci.wustl.edu.

5. In order to try to avoid having spam emails sent through this list, only members of the list can send email to the list, and membership has to be granted through a quick review process.

Getting data out of the CNDA for further analysis

Where should I store my data for access by NIL maintained computer systems?

In order to use FIDL or other software to analyze your data on the NIL systems, you will need to download the data from the CNDA to some file system accessible from the NIL systems. Often you will not want to download all of the data from the original scanning session. Instead, you may select to download just a few of the files created during the original scanning session and most (or all) of the files generated by the BOLD preprocessing pipeline.

Of course, you could choose to download the data directly to your desktop computer or any lab specific computer on which you want to perform analysis. However, for the most efficient access from the NIL systems, the data downloaded needs to be stored in a place that is easily and efficiently accessible by those systems. We (the Psychology Department) have space available under the `/data/nil-external` directory.

There are two subdirectories under `/data/nil-external` that are specifically for use by laboratories in the Psychology Department. They are `/data/nil-external/psych` and `/data/nil-external/psychf`. In these directories there should be lab specific subdirectories for storage of your data (e.g. `CCP`, `DCL`, and `HRL`). The directory structure to use within the lab specific directories is to be decided by your lab directors. Contact your lab director to determine how to organize your data within the lab specific directories.

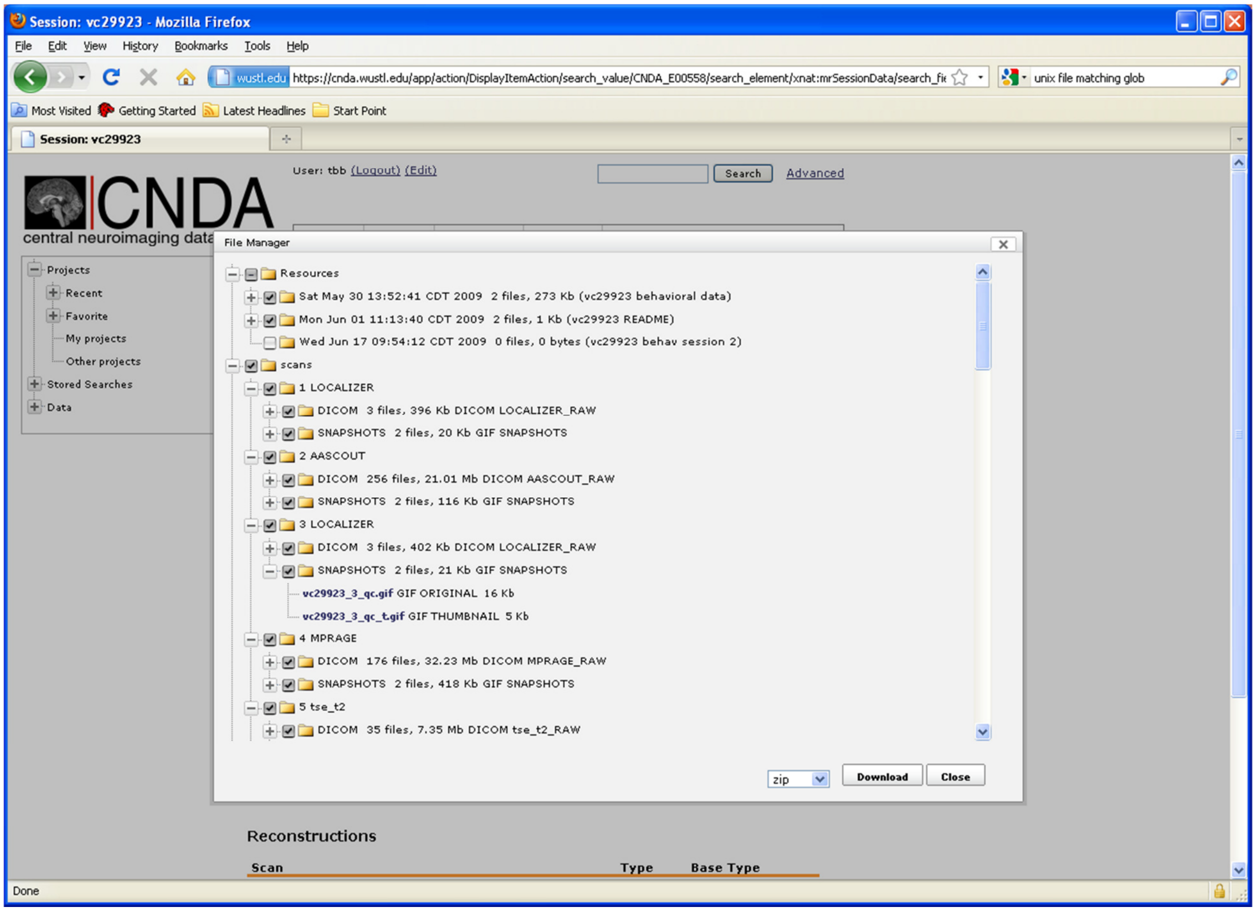
How do I retrieve/download data from the CNDA using the standard CNDA Web interface?

There is more than one way to download files for a session using the standard CNDA Web interface. One of the more flexible ways is to select the project of interest from your CNDA homepage, select the session of interest from the project page, and then select "Manage Files" in the Actions box at the upper right hand side of the session page.

Selecting the "Manage Files" action will cause a "File Manager" window to pop-up in front of your session page. The File Manager window looks like a traditional file folder navigation tree with + and – characters to the far left of folder (i.e. directory) names and a specialized check box just to the right of the + or – character. See Figure 9 for an example.

The + or – character indicates whether the view you are seeing of the file is "closed" or "open". The + means you are seeing only the folder name and not the contents of the folder, the – means you are seeing the folder and an indented list of its contents below the folder name. Clicking on the + or – toggles the view that you see.

The specialized check box to the right of the + or – indicates the selection status for the folder, with a check mark on a grey background indicating that the entire folder and all its subfolders and files have been selected, a minus sign on a grey background indicating that some but not all of the content of the folder have been selected, and an empty box with a white background indicating that none of the content of the folder has been selected. You change the selection status by clicking on the check box for a folder or subfolder.



https://cnda.wustl.edu/app/action/DisplayItemAction/search_value/CNDA_E00558/search_element/xnat:mrSessionData/search_fi

```
☑ Resources
  ☑ Sat May 30 13:52:41 CDT 2009  2 files, 273 Kb (vc29923 behavioral data)
  ☑ Mon Jun 01 11:13:40 CDT 2009  2 files, 1 Kb (vc29923 README)
  □ Wed Jun 17 09:54:12 CDT 2009  0 files, 0 bytes (vc29923 behav session 2)
☑ scans
  ☑ 1 LOCALIZER
    ☑ DICOM  3 files, 396 Kb DICOM LOCALIZER_RAW
    ☑ SNAPSHOTS  2 files, 20 Kb GIF SNAPSHOTS
  ☑ 2 AASCOUT
    ☑ DICOM  256 files, 21.01 Mb DICOM AASCOUT_RAW
    ☑ SNAPSHOTS  2 files, 116 Kb GIF SNAPSHOTS
  ☑ 3 LOCALIZER
    ☑ DICOM  3 files, 402 Kb DICOM LOCALIZER_RAW
    ☑ SNAPSHOTS  2 files, 21 Kb GIF SNAPSHOTS
        vc29923_3_qc.gif GIF ORIGINAL  16 Kb
        vc29923_3_qc_t.gif GIF THUMBNAIL  5 Kb
  ☑ 4 MPRAGE
    ☑ DICOM  176 files, 32.23 Mb DICOM MPRAGE_RAW
    ☑ SNAPSHOTS  2 files, 418 Kb GIF SNAPSHOTS
  ☑ 5 tse_t2
    ☑ DICOM  35 files, 7.35 Mb DICOM tse_t2_RAW
```

Figure 9: CNDA File Manager

Once you have selected the folders that you want to download, you can select the format for the resulting downloaded file in the pull down menu near the lower right hand corner of the File Manager (options are zip and tar.gz). Then selecting the Download button will download the contents of the selected folders.

How do I retrieve/download data from the CNDA using URI specifications from a browser?

Since downloading files using the standard Web interface from the CNDA can be tedious and cannot easily be scripted for submittal as a long running "batch" job, the Neuroinformatics Research Group (NRG, the maintainers of the CNDA) have made available a mechanism for listing and retrieving data stored in the CNDA using a Representational State Transfer (REST) software architecture. While the details of the REST software architectural style are well beyond the scope of this document, the effect for users wanting to list or retrieve the files stored in the CNDA is significant.

This software architecture makes viewing and downloading listings of files, individual files, and groups of files straightforward once you understand the "file system"-like hierarchy that the REST interface makes available and you understand how to build a Universal Resource Identifier (URI) that identifies the file(s) and what you would like to retrieve.

The easiest way to understand the "file system" and construction of URI's is to examine the results of creating URI's and entering them into the address field of a web browser. For these examples, we'll start out looking at listings and data from the project titled "Encoding and Remembering Events Across the Lifespan: Functional correlates of effective segmentation". This project has a CNDA Project ID of NP891.

First example URI

The first example URI we will use is:[16]

```
https://cnda.wustl.edu/REST/projects/NP891/experiments/vc29901/DIR?format=html
```

This URI can be broken down as follows:

`https:`	Indicates that we will be using HyperText Transfer Protocol in secure mode for requesting and receiving results
`cnda.wustl.edu`	Is the name of the host to which we are making a request
`REST`	This is the beginning of the file-system-like path name indicating what we want to retrieve from the server (`cnda.wustl.edu`). The use of `REST` indicates that we are making a request that involves the REST software mechanism.
`projects`	The path continues with an indication that we are looking for information (a listing or file) that is organized by project ids.
`NP891`	This is the project id
`experiments`	The path continues with an indication that we are looking for information (a listing or file) that is organized by experiments. In this context the term "experiment" corresponds to an MR session.
`vc29901`	The MR Session ID
`DIR`	Allows access directly to the session directory in the archive.
`?format=html`	Indicates that we would like the results provided back to us in HTML format (a web browser compatible markup language)

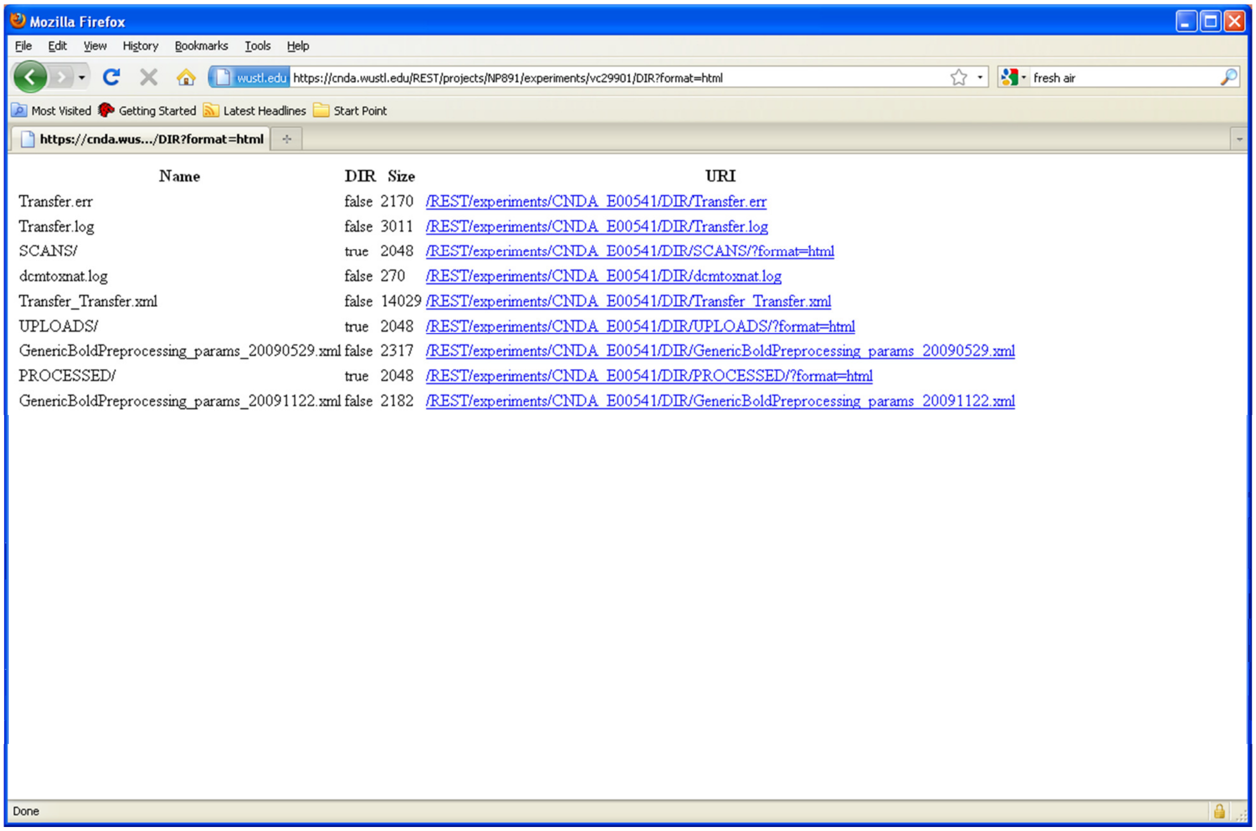
Let's consider the result of entering the above URI into the address bar of a web browser.

[16] In order to use the URI specified and see the results shown, your CNDA account must have access to the NP891 project. Many readers will not have such access to the NP891 project. If this is the case, you will need to select a project to which your CNDA account does have access and substitute that project ID for NP891 in the examples. Similarly, you will need to choose a valid MR Session ID that is part of your chosen project and substitute that session ID for vc29901 in the examples.

The first thing to note is that if we are not already logged in to the CNDA using the browser, we will be prompted for a username and password in order to get access to the CNDA data specified by the URI. Use your normal CNDA username and password.

After successfully validating our username and password, we get a listing of the contents of the "directory" specified by our path. That is a listing of the contents of the `vc29901` session within project `NP891`.

The results are provided back to the requesting client software, in this case the web browser. The browser will use those results to present something similar to Figure 10.



Name	DIR	Size	URI
Transfer.err	false	2170	/REST/experiments/CNDA_E00541/DIR/Transfer.err
Transfer.log	false	3011	/REST/experiments/CNDA_E00541/DIR/Transfer.log
SCANS/	true	2048	/REST/experiments/CNDA_E00541/DIR/SCANS/?format=html
dcmtoxnat.log	false	270	/REST/experiments/CNDA_E00541/DIR/dcmtoxnat.log
Transfer_Transfer.xml	false	14029	/REST/experiments/CNDA_E00541/DIR/Transfer_Transfer.xml
UPLOADS/	true	2048	/REST/experiments/CNDA_E00541/DIR/UPLOADS/?format=html
GenericBoldPreprocessing_params_20090529.xml	false	2317	/REST/experiments/CNDA_E00541/DIR/GenericBoldPreprocessing_params_20090529.xml
PROCESSED/	true	2048	/REST/experiments/CNDA_E00541/DIR/PROCESSED/?format=html
GenericBoldPreprocessing_params_20091122.xml	false	2182	/REST/experiments/CNDA_E00541/DIR/GenericBoldPreprocessing_params_20091122.xml

Figure 10: More user-friendly presentation of first URI results

What we have effectively retrieved is similar to what we would get when issuing an `ls` command from a Un*x shell prompt.

These are the files and subdirectories that are at the path:

```
/REST/projects/NP891/experiments/vc29901
```

on the `cnda.wustl.edu` server.

Of the contents shown in Figure 10, several items are files:

- `Transfer.err`
- `Transfer.log`
- `dcmtoxnat.log`

- `Transfer_Transfer.xml`
- `GenericBoldPreprocessing_Params20090529.xml`
- `GenericBoldPreprocessing_Params20091122.xml`

Several are "subdirectories":

- `SCANS/`
- `UPLOADS/`
- `PROCESSED/`

Notice that, just as is often true of the Un*x `ls` command, the names that end with slashes / represent subdirectories.

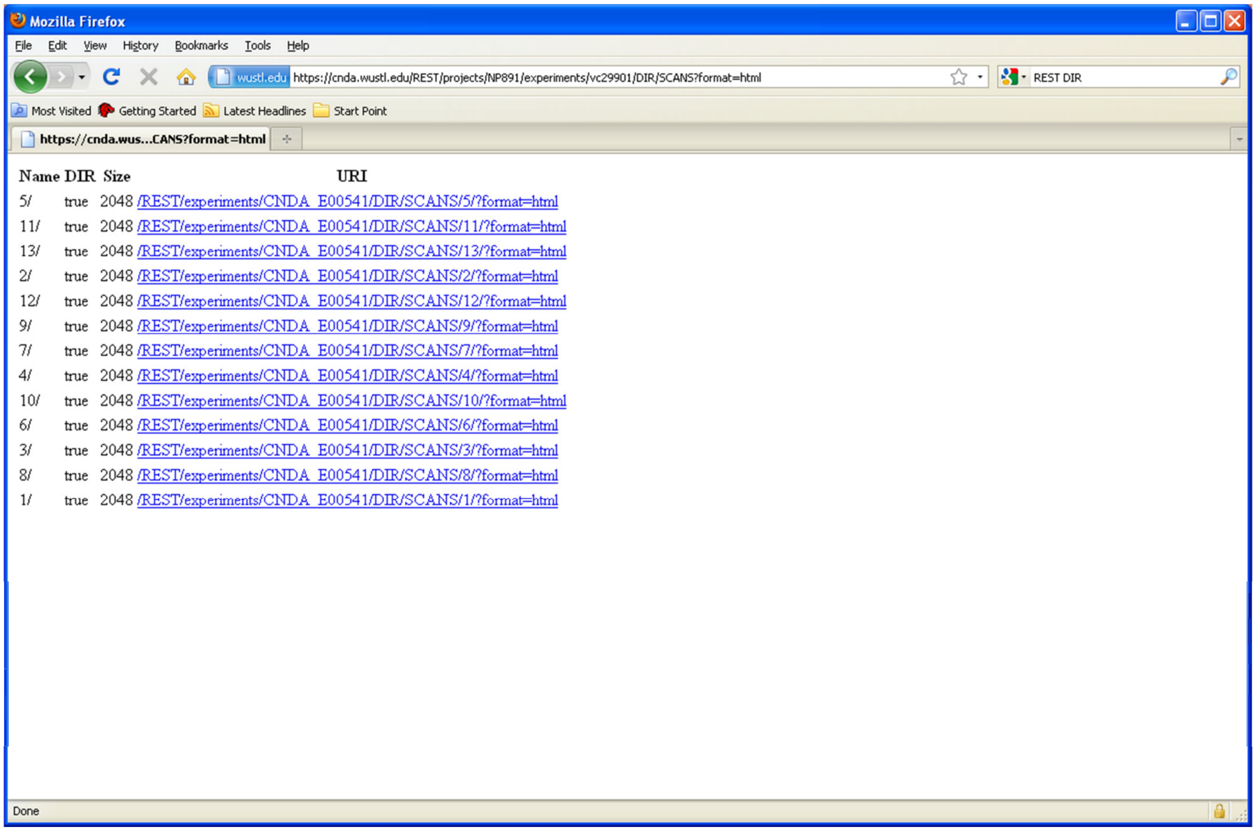
Moving down through the directory structure

Suppose I wanted to list the contents of the SCANS subdirectory. How would I construct a URI to to use to get those results? It seems natural that you would add `SCANS` into the URI to end up with a URI like:

```
https://cnda.wustl.edu/REST/projects/NP891/experiments/vc29901/DIR/SCANS?format=html
```

Notice that the `?format=html` clause is always placed at the end.

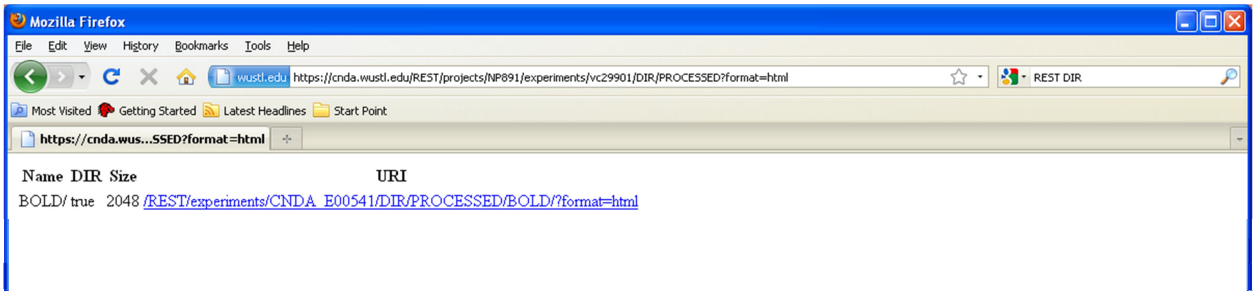
Figure 11 shows the result of entering that URI into a browser. Indeed, this is the set of subdirectories of the SCANS directory.


Mozilla Firefox
File Edit View History Bookmarks Tools Help
wustl.edu https://cnda.wustl.edu/REST/projects/NP891/experiments/vc29901/DIR/SCANS?format=html
REST DIR
Most Visited Getting Started Latest Headlines Start Point
https://cnda.wus...CANS?format=html
Done

Name	DIR	Size	URI
5/	true	2048	/REST/experiments/CNDA_E00541/DIR/SCANS/5/?format=html
11/	true	2048	/REST/experiments/CNDA_E00541/DIR/SCANS/11/?format=html
13/	true	2048	/REST/experiments/CNDA_E00541/DIR/SCANS/13/?format=html
2/	true	2048	/REST/experiments/CNDA_E00541/DIR/SCANS/2/?format=html
12/	true	2048	/REST/experiments/CNDA_E00541/DIR/SCANS/12/?format=html
9/	true	2048	/REST/experiments/CNDA_E00541/DIR/SCANS/9/?format=html
7/	true	2048	/REST/experiments/CNDA_E00541/DIR/SCANS/7/?format=html
4/	true	2048	/REST/experiments/CNDA_E00541/DIR/SCANS/4/?format=html
10/	true	2048	/REST/experiments/CNDA_E00541/DIR/SCANS/10/?format=html
6/	true	2048	/REST/experiments/CNDA_E00541/DIR/SCANS/6/?format=html
3/	true	2048	/REST/experiments/CNDA_E00541/DIR/SCANS/3/?format=html
8/	true	2048	/REST/experiments/CNDA_E00541/DIR/SCANS/8/?format=html
1/	true	2048	/REST/experiments/CNDA_E00541/DIR/SCANS/1/?format=html

Figure 11: Listing of contents of SCANS subdirectory

You can use a similar technique to get list the contents of the PROCESSED subdirectory which itself just contains a subdirectory named BOLD (see Figure 12).


Mozilla Firefox
File Edit View History Bookmarks Tools Help
wustl.edu
REST DIR
Most Visited Getting Started Latest Headlines Start Point

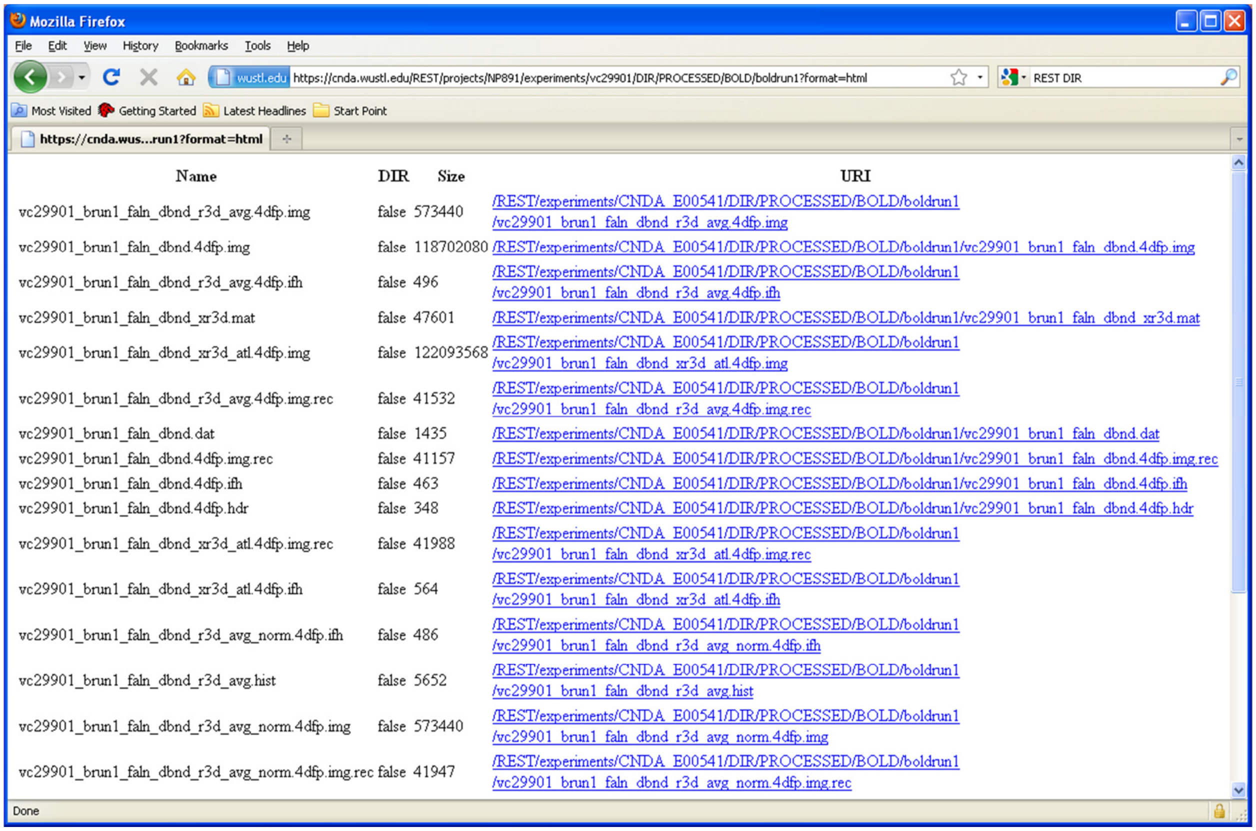
https://cnda.wustl.edu/REST/projects/NP891/experiments/vc29901/DIR/PROCESSED?format=html

https://cnda.wus...SSED?format=html

Name	DIR	Size	URI
BOLD/	true	2048	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/?format=html

Figure 12: Contents of PROCESSED subdirectory

We can continue working our way down through the directory structure to the `PROCESSED/BOLD/boldrun1` subdirectory to get something like Figure 13.


Mozilla Firefox
File Edit View History Bookmarks Tools Help
wustl.edu
REST DIR
Most Visited Getting Started Latest Headlines Start Point
Done

https://cnda.wustl.edu/REST/projects/NP891/experiments/vc29901/DIR/PROCESSED/BOLD/boldrun1?format=html

https://cnda.wus...run1?format=html

Name	DIR	Size	URI
vc29901_brun1_faln_dbnd_r3d_avg.4dfp.img	false	573440	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1 /vc29901_brun1_faln_dbnd_r3d_avg.4dfp.img
vc29901_brun1_faln_dbnd.4dfp.img	false	118702080	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1/vc29901_brun1_faln_dbnd.4dfp.img
vc29901_brun1_faln_dbnd_r3d_avg.4dfp.ifh	false	496	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1 /vc29901_brun1_faln_dbnd_r3d_avg.4dfp.ifh
vc29901_brun1_faln_dbnd_xr3d.mat	false	47601	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1/vc29901_brun1_faln_dbnd_xr3d.mat
vc29901_brun1_faln_dbnd_xr3d_atl.4dfp.img	false	122093568	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1 /vc29901_brun1_faln_dbnd_xr3d_atl.4dfp.img
vc29901_brun1_faln_dbnd_r3d_avg.4dfp.img.rec	false	41532	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1 /vc29901_brun1_faln_dbnd_r3d_avg.4dfp.img.rec
vc29901_brun1_faln_dbnd.dat	false	1435	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1/vc29901_brun1_faln_dbnd.dat
vc29901_brun1_faln_dbnd.4dfp.img.rec	false	41157	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1/vc29901_brun1_faln_dbnd.4dfp.img.rec
vc29901_brun1_faln_dbnd.4dfp.ifh	false	463	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1/vc29901_brun1_faln_dbnd.4dfp.ifh
vc29901_brun1_faln_dbnd.4dfp.hdr	false	348	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1/vc29901_brun1_faln_dbnd.4dfp.hdr
vc29901_brun1_faln_dbnd_xr3d_atl.4dfp.img.rec	false	41988	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1 /vc29901_brun1_faln_dbnd_xr3d_atl.4dfp.img.rec
vc29901_brun1_faln_dbnd_xr3d_atl.4dfp.ifh	false	564	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1 /vc29901_brun1_faln_dbnd_xr3d_atl.4dfp.ifh
vc29901_brun1_faln_dbnd_r3d_avg_norm.4dfp.ifh	false	486	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1 /vc29901_brun1_faln_dbnd_r3d_avg_norm.4dfp.ifh
vc29901_brun1_faln_dbnd_r3d_avg.hist	false	5652	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1 /vc29901_brun1_faln_dbnd_r3d_avg.hist
vc29901_brun1_faln_dbnd_r3d_avg_norm.4dfp.img	false	573440	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1 /vc29901_brun1_faln_dbnd_r3d_avg_norm.4dfp.img
vc29901_brun1_faln_dbnd_r3d_avg_norm.4dfp.img.rec	false	41947	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1 /vc29901_brun1_faln_dbnd_r3d_avg_norm.4dfp.img.rec

Figure 13: The boldrun1 directory

Actually downloading some files

While it's useful to be able to navigate around the directory structure like this, the real goal here is to be able to download some of the files to a local machine (e.g. your desktop machine or the NIL systems) for further processing. Once you've found a URI that lists the files that you want, all you have to do to download the files is change the `format` argument that we've added to the end of the URI.

Let's use `format=zip` instead of `format=html` to access the contents of the boldrun1 directory that is shown in Figure 13. So now our URI is:

```
https://cnda.wustl.edu/REST/projects/NP891/experiments/vc29901/DIR/PROCESSED/BOLD/bold
run1?format=zip
```

Using this URI will result in a ZIP format file being downloaded through your browser to wherever you specify to save the ZIP file. The ZIP file will contain the files that we saw listed in Figure 13.

Creating a shorter form of the URI using the accession number

As you listed the contents of directories in your browser using URIs, you may have noticed that one of the columns in each listing is titled URI. If the item in the column is a file, the URI column shows a URI that will cause that file to be downloaded. If the item in the column is a subdirectory, the URI in that column will get you a listing of the contents of that directory. In either case, these URIs are supplied as a link that you can click on to either cause a file to be downloaded or to list the contents of a subdirectory.

You also may have noticed that the URIs specified in that column look slightly different than the ones we've been using above to get to the various subdirectories. That is because the URI supplied for that column use a slightly different navigation technique to get to the appropriate files and directories.

Each session that is uploaded to the CNDA is assigned a unique identifier. That unique identifier is called the session's *accession number*. If you know the MR session's accession number, you can use that information to create shorter URIs to access parts of the session.

In the example shown above, the MR Session `vc29901` in project `NP891` was assigned accession number `CNDA_E00541`. Using this information, you can replace the portion of the path specified in the URI that reads:

```
/projects/<project id>/experiments/<session id>
```

with:

```
/experiments/<accession number>
```

Thus:

```
https://cnda.wustl.edu/REST/projects/NP891/experiments/vc29901/
DIR?format=html
```

can be shortened to:

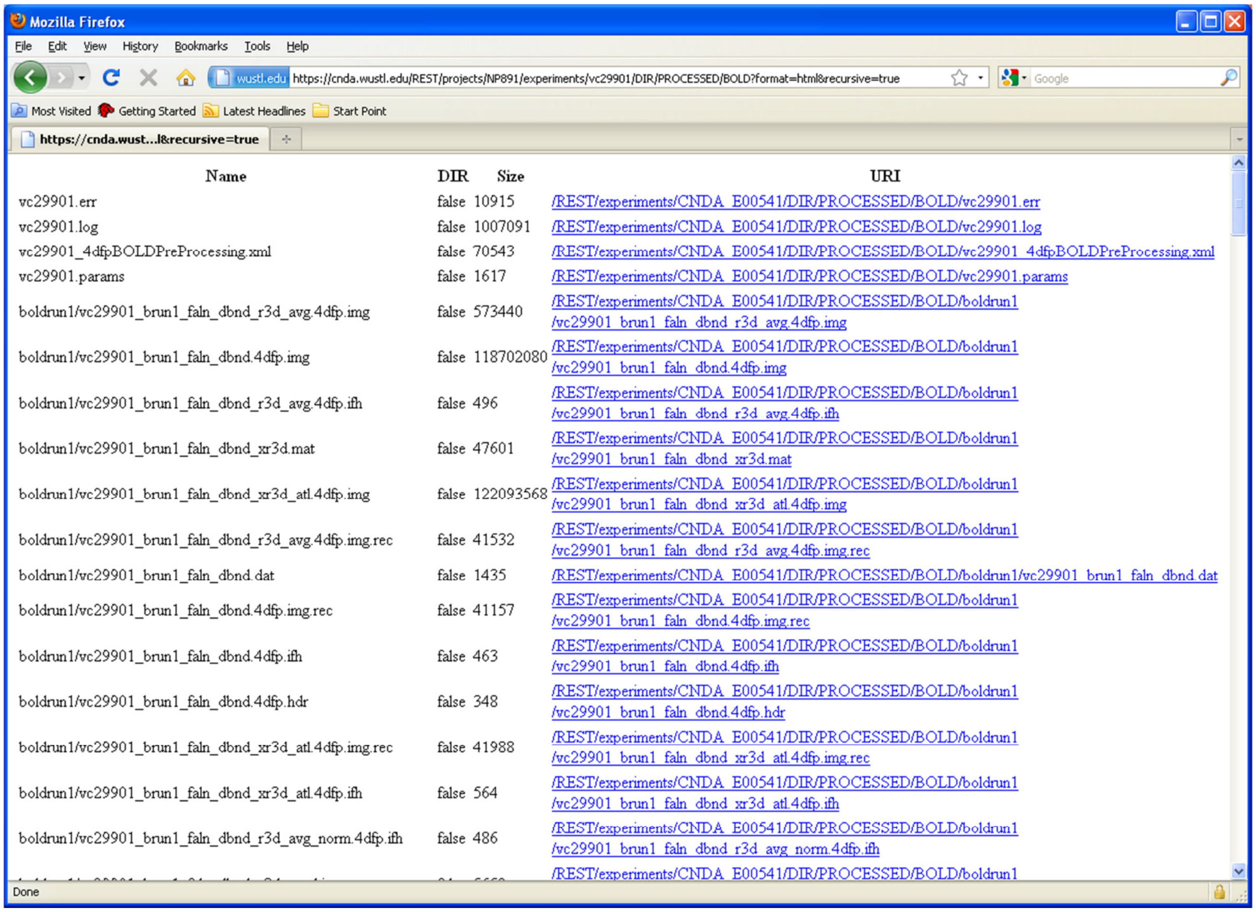
```
https://cnda.wustl.edu/REST/experiments/CNDA_E00541/DIR?format=html
```

You and others on your team probably will know the Project ID and the MR Session ID for the data you want to access. You are less likely to know (at least initially) the accession number that has been assigned to your MR session data. So your URIs will probably be easier to read and understand if you use the longer form, which includes the Project ID and the MR Session ID. But you need to at least understand how the shorter form URIs are created.

Using recursion to see or retrieve more data

Earlier we saw how to create a URI to list (and then to retrieve) data in the `PROCESSED/BOLD/boldrun1` subdirectory for or selected example session. Of course, it would be tedious if we had to construct a separate URI to list or retrieve each of the `boldrun1`, `boldrun2`, `boldrun3`, `boldrun4`, and `boldrun5` subdirectories.

Instead of creating separate URIs for each of the `boldrunN` subdirectories, we can simply add another "argument" to the end of the URI. Let's add the text "`&recursive=true`" to the end of the URI. Part of the result of using this URI is shown in Figure 14.


Mozilla Firefox
File Edit View History Bookmarks Tools Help
wustl.edu
Google
Most Visited Getting Started Latest Headlines Start Point
https://cnda.wust...l&recursive=true
Done

https://cnda.wustl.edu/REST/projects/NP891/experiments/vc29901/DIR/PROCESSED/BOLD?format=html&recursive=true

Name	DIR	Size	URI
vc29901.err	false	10915	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/vc29901.err
vc29901.log	false	1007091	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/vc29901.log
vc29901_4dfpBOLDPreProcessing.xml	false	70543	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/vc29901_4dfpBOLDPreProcessing.xml
vc29901.params	false	1617	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/vc29901.params
boldrun1/vc29901_brun1_faln_dbnd_r3d_avg.4dfp.img	false	573440	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1/vc29901_brun1_faln_dbnd_r3d_avg.4dfp.img
boldrun1/vc29901_brun1_faln_dbnd.4dfp.img	false	118702080	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1/vc29901_brun1_faln_dbnd.4dfp.img
boldrun1/vc29901_brun1_faln_dbnd_r3d_avg.4dfp.ifh	false	496	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1/vc29901_brun1_faln_dbnd_r3d_avg.4dfp.ifh
boldrun1/vc29901_brun1_faln_dbnd_xr3d.mat	false	47601	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1/vc29901_brun1_faln_dbnd_xr3d.mat
boldrun1/vc29901_brun1_faln_dbnd_xr3d_atl.4dfp.img	false	122093568	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1/vc29901_brun1_faln_dbnd_xr3d_atl.4dfp.img
boldrun1/vc29901_brun1_faln_dbnd_r3d_avg.4dfp.img.rec	false	41532	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1/vc29901_brun1_faln_dbnd_r3d_avg.4dfp.img.rec
boldrun1/vc29901_brun1_faln_dbnd.dat	false	1435	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1/vc29901_brun1_faln_dbnd.dat
boldrun1/vc29901_brun1_faln_dbnd.4dfp.img.rec	false	41157	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1/vc29901_brun1_faln_dbnd.4dfp.img.rec
boldrun1/vc29901_brun1_faln_dbnd.4dfp.ifh	false	463	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1/vc29901_brun1_faln_dbnd.4dfp.ifh
boldrun1/vc29901_brun1_faln_dbnd.4dfp.hdr	false	348	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1/vc29901_brun1_faln_dbnd.4dfp.hdr
boldrun1/vc29901_brun1_faln_dbnd_xr3d_atl.4dfp.img.rec	false	41988	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1/vc29901_brun1_faln_dbnd_xr3d_atl.4dfp.img.rec
boldrun1/vc29901_brun1_faln_dbnd_xr3d_atl.4dfp.ifh	false	564	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1/vc29901_brun1_faln_dbnd_xr3d_atl.4dfp.ifh
boldrun1/vc29901_brun1_faln_dbnd_r3d_avg_norm.4dfp.ifh	false	486	/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1/vc29901_brun1_faln_dbnd_r3d_avg_norm.4dfp.ifh
			/REST/experiments/CNDA_E00541/DIR/PROCESSED/BOLD/boldrun1

Figure 14: Adding recursion to a URI

Notice that the immediate contents of the `BOLD` directory are included **and** the contents of each subdirectory of the `BOLD` directory are also included. If any subdirectory of the BOLD directory had further subdirectories, then the contents of those sub-subdirectories would also be included and so on down the directory structure. Of course, to download all of these files, we would simply need to change the `format=html` argument to `format=zip` in the URI.

Note that the order of the arguments is not relevant. The `recursive=true` could come before the `format=zip` in the URI. The important thing to understand is that the question mark (`?`) in the URI signals the beginning of the arguments and the ampersand (`&`) separates multiple arguments.

So that reversing the order of the arguments in the URI used in Figure 14 would result in the end of that URI reading:

```
BOLD?recursive=true&format=html
```

We could list the entire contents of the PROCESSED directory and all of its subdirectories by using a URI like:

```
https://cnda.wustl.edu/REST/projects/NP891/experiments/vc29901/
DIR/PROCESSED?format=html&recursive=true
```

Of course, we could then retrieve the entire contents of the PROCESSED directory and all of its subdirectories by changing format=html to format=zip. At the time of this writing, this results in a 1.55GB zip compressed file being downloaded.

Expanding upon this, we could download the entire set of data for the MR Session vc29901 within project NP891 with the following URI.

```
https://cnda.wustl.edu/REST/projects/NP891/experiments/vc29901/
DIR?format=zip&recursive=true
```

At the time of this writing, this results in a 1.72GB zip compressed file being downloaded.

Using wildcards to see or retrieve more data

The SCANS subdirectory for the vc29901 session itself has subdirectories that are numbered 1 through 13 for each of the various scans that made up the session. Each of these numbered subdirectories has subdirectories of its own named DICOM and SNAPSHOTS.

Suppose we wanted to get a list of (or retrieve) all the files in the DICOM subdirectories for all of the 13 scans, and we did not want the contents of the SNAPSHOTS subdirectories included. We could do this using "wildcard" characters. A URI like:

```
https://cnda.wustl.edu/REST/projects/NP891/experiments/vc29901/
DIR/SCANS/*/DICOM?format=html
```

would give us a listing of those DICOM files.

Of course, changing the format to zip instead of html would download a zip file containing those files.

Some additional notes

There are a couple other things that are worth knowing about accessing the CNDA data files using URIs. First, sometimes you will get a page that says something to the effect of, "Specified request didn't match any stored files" or "The server has not found anything matching the request URI". These are most likely to be the result of an incorrectly composed URI (project id incorrect, session id misspelled, etc.)

However, you will sometimes get a similar response when you have typed the URI correctly. This is generally attributable to your CNDA account not having access to the session you have specified. You may need to contact the owner of the project in question and make sure that your account has access to the project in order to access the files using these URIs.

A second thing to note is that if you mistype the name of the format that you want, say you accidentally type format=ziip instead of format=zip, then the results will be formatted as if you had not specified any format at all. Thus, the results will be an XML file and will be handled by your browser the way it handles XML files.

The last thing to note, at least for now, is that the above example using wildcards is just a “scratch the surface” introduction. You should feel free to experiment and try placing wildcard characters at other places in the URI to see what happens. If you are familiar with filename wildcard characters used within Un*x shells, then you might want to try some of those wildcard characters too.

How do I retrieve/download data from the CNDA using command line tools?

The previous section contains examples to help understand the construction of URIs to list or retrieve files from the CNDA. But entering those URIs into a browser’s address bar doesn’t allow you to put downloads of files from the CNDA into script files and run them as “background” or `cron` jobs. To do that we need a command line tool that can issue requests to a web server (URIs) and save the result of those requests.

One such tool is cURL (http://curl.haxx.se). cURL is open source and binary installation packages are available for a large variety of operating systems (Windows, DOS, HP-UX, various flavors of Linux, Solaris, and Mac OS X among them). cURL has been installed on the NIL systems for our use.

cURL has a lot of features, and we do not plan to cover them all (or anywhere close to all of them) in this short section. For more information about using cURL, you should refer to the cURL manual (http://curl.haxx.se/docs/manual.html).

As in the previous section, we’ll learn by viewing some simple examples. We’ll start by using the first URI that we used in the previous section

```
https://cnda.wustl.edu/REST/projects/NP891/experiments/vc29901/DIR
```

We’ll issue the command

```
% curl https://cnda.wustl.edu/REST/projects/NP891/experiments/vc29901/DIR
```

at the shell command prompt.

The first problem you’ll note is that since you are issuing an `https` request, cURL will want to verify a Secure Socket Layer (SSL) certificate. For now, we’ll bypass that issue by adding the –k option to the command line.

```
% curl -k https://cnda.wustl.edu/REST/projects/NP891/experiments/vc29901/DIR
```

This command gives us output that looks like:

```
<html>
<head>
   <title>Status page</title>
</head>
<body>
<h3>The request requires user authentication</h3><p>You can get technical
details <a href="http://www.w3.org/Protocols/rfc2616/rfc26
0.4.2">here</a>.<br>
```

```
Please continue your visit at our <a href="/">home page</a>.
</p>
</body>
</html>
```

Figure 15: First cURL ouput

Two things to note about this output are:

1. It is indicating that you need to have “user authentication” (a specified username and password) to access the data of interest.
2. The output was sent right back to the console (the standard output location).

We’ll first deal with the user authentication issue, then see how to send the results elsewhere.

The easiest way to specify a username when using cURL is to use the –u command line option.

```
% curl -k -u tbb https://cnda.wustl.edu/REST/projects/NP891/experiments/vc29901/DIR
```

This works, but causes cURL to prompt us for the appropriate password. The results are again sent to the standard output location (our shell window), but they are now in XML format.

The prompting for a password will have to be removed if we’re going to use this in a background shell script. We can fix that by using `-u <username>:<password>`. We can change to HTML output by adding the same `?format=html` that we used in the previous section.

```
% curl -k -u tbb:password
https://cnda.wustl.edu/REST/projects/NP891/experiments/vc29901/DIR?format=html
```

If you redirect the output from the standard output location to a file (the technique that usually works is to add `> <filename>` to the end of the command line) and then open up the file in a browser, you’ll see that we now have used a command line to download a file that corresponds to Figure 10.

Now you can begin to see how cURL commands can be embedded in scripts to download the data that you need from the CNDA. Let’s skip ahead to where (in the previous section) we built a URI to download the entire contents of the `PROCESSED` directory and all of its subdirectories. That URI was

```
https://cnda.wustl.edu/REST/projects/NP891/experiments/vc29901/
DIR/PROCESSED?format=zip&recursive=true
```

If we use that URI in a cURL command with `-k` and `-u <username>:<password>`, we will have created a command line that will download a zip file containing all the specified files. In some command line shells, the ampersand before the recursive=true part of the command will cause problems. These can usually be fixed by putting double quotes (`“”`) around the entire URI.

Don’t forget to redirect the output from this command to a file. If you don’t redirect the output, the entire multi-gigabyte zip file will be sent to your terminal/console/standard output.

You might notice that cURL displays a “progress meter” indicating the amount of transferred data, transfer speeds, estimated time left, etc. To turn off this display add the `-s` option to the command line.

A better way to specify an output file.

If you redirect the output from a cURL command using the standard redirect operator (a greater than sign, `>`, added to the end of the command line followed by the name of the file to which to send the output) then there is a limit on the size of the output file that can be created. That limit is roughly 2GB. So if you issue a cURL command like:

```
% curl -k -u tbb:password myuri > myfile.zip
```

where *`password`* is replaced with your CNDA password, and *`myuri`* is replaced with the URI specifying what you want to download, then if the resulting `myfile.zip` file should be larger than 2GB, then the download will fail with an error message indicating, “Failed writing body”.

To avoid this problem, you should specify the output file for your cURL command using the `-o` command line option. This would change the above command to:

```
% curl -k -u tbb:password -o myfile.zip myuri
```

IMPORTANT NOTE: Unzipping large files

The standard unzip command that is available at `/usr/bin/unzip` on Solaris machines and is likely to be the command used when you just enter:

```
% unzip myfile.zip
```

from those machines, does not support “large” zip files. In this case, “large” is defined as being greater than 2GB. It is very likely that many of the zip files that you download from the CNDA will exceed this size limit. Therefore, a version of the unzip command has been installed on the Solaris machines that does support large files. The unzip command with large file support has been installed at `/usr/local/bin/unzip`. So you should use a command like:

```
% /usr/local/bin/unzip myfile.zip
```

to unzip large files downloaded from the CNDA when using Solaris.

Removing your username and password from the cURL command line

It is not really a good idea to put your CNDA username and password in cURL command lines. It is probably even less of a good idea to embed your CNDA username and password in scripts that you’ve written to use cURL to download sets of files.

One way to avoid this is to use the `-n` command line option on the `curl` command. This option causes cURL to look in the user’s home directory for a file named `.netrc` (`_netrc` on Windows) for the user’s login name and password.

Lines in your `.netrc` file take the form:

```
machine <host-name> login <user-name> password <password>
```

where you substitute the machine name for *`<host-name>`*, your username for *`<user-name>`*, and your password for *`<password>`*.

You should protect your `.netrc` file so that only you can read or write it. Use the following command to properly protect your `.netrc` file.

```
% chmod u+rw-x,go-rwx .netrc
```

Once you've created the `.netrc` file, you can leave the `-u` option out of your curl command lines and replace it with `-n`.

An alternative to cURL: wget

Another command line tool that can be used to download files with specified URIs is the `wget` tool. A command of the following form should download the appropriate zip file from the CNDA:

```
% wget --http-user your_CNDA_username
       --http-passwd your_CNDA_password
       -O desired_name_for_zip_file
       "https://cnda.wustl.edu/REST/projects/..."
```

Note that this command should be issued all on one line as opposed to being broken across lines as the example shows. Also note that the –O option is a hyphen and an uppercase letter O. The lowercase letter o means something entirely different and should not be used. The numeral zero, 0, does not work either.

If you have created a `.netrc` file as described in the previous section, you will not need to specify your username or password on the command line. `wget` will automatically look in your `.netrc` file for that information. So then your `wget` command will look something like the following:

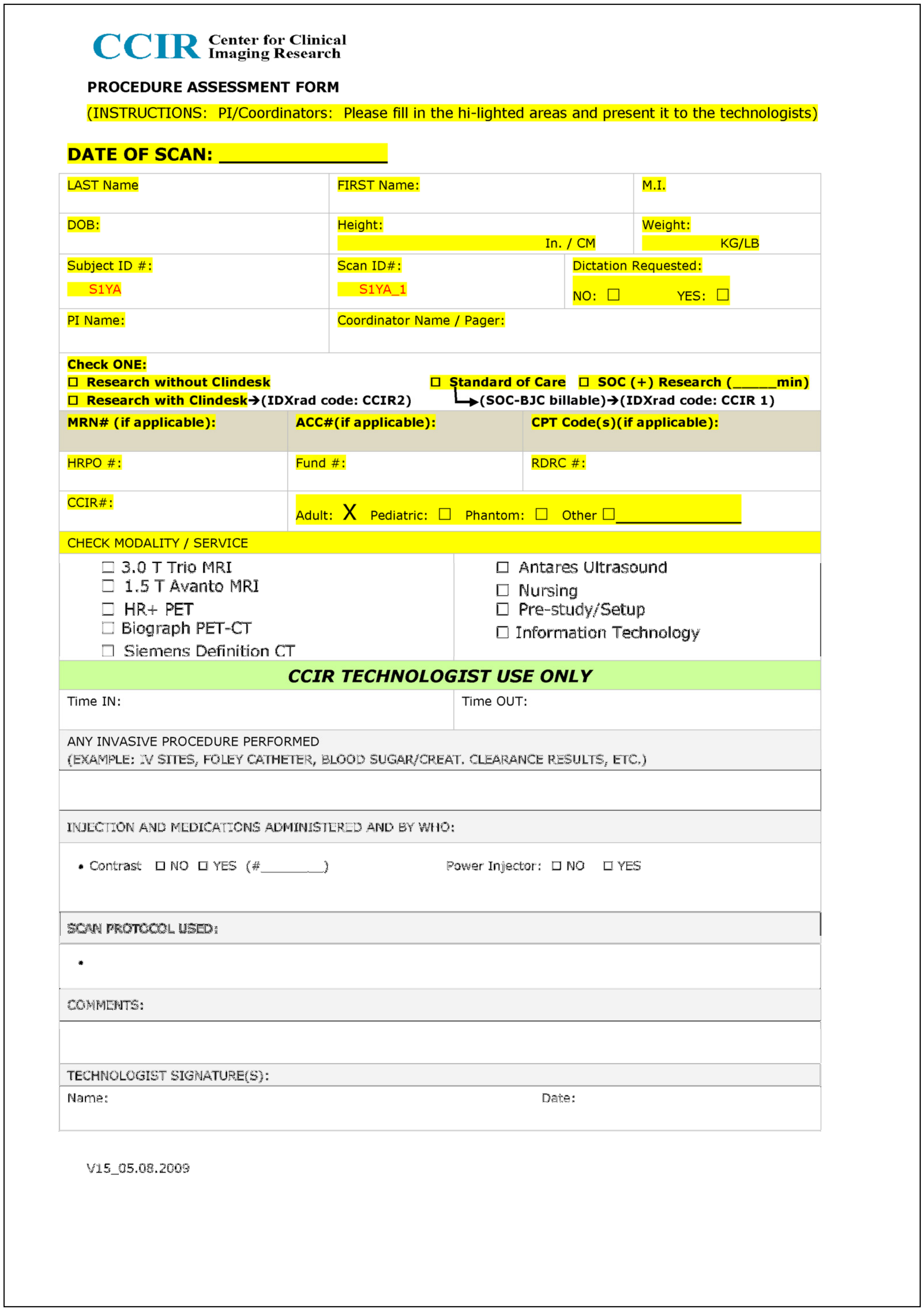
```
% wget -O desired_name_for_zip_file "https://cnda.wustl.edu/REST/..."
```

Appendix A: Document Revision History

Date	Description
08 Jun 2011	• Modified discussion of getting and installing VPN client software to refer to using the newer CISCO SSL VPN Service client software available at https://mirvpn.wustl.edu/nil. See the section *How do I set up the VPN connection to access NIL maintained computer systems?* Removed instructions for previously recommended VPN client software. • Removed references to cnindsXX machines and referred users to petsun23, petsun24, and linux1 instead. See the section *What NIL maintained CPUs should I use?* • Added section on creating login/startup files to allow login to both Linux and Sun OS/Solaris. See the section *How do I setup my shell startup files to handle both Linux and Sun OS/Solaris* Systems? • Added instructions for subscribing to NIL Users in Psych email mailing list. See the section *How can I make sure I receive important notifications about using NIL Systems?*
19 May 2010	• Crossed out text indicating that users should use the built-in VPN client software in Snow Leopard. (Did not delete because the built-in VPN client software in Snow Leopard is actually the officially supported VPN client software. But there seems to be something unique to the configuration of the Psychology Building wired network that is causing a problem.) Added text indicating that Snow Leopard users should (for now) behave as if they were using the previous version of the OS (Leopard).
05 May 2010	• Added footnote emphasizing session ID uniqueness within a project • Added footnote indicating that using the example URIs requires the user's CNDA account to have access to the specified project. • Added Example CCIR Procedure Assessment Form Appendix to illustrate one way to keep session IDs unique within a project.
26 Apr 2010	• Added instructions on using sed to modify xstartup file.
12 Apr 2010	• Added note about unzipping large zip files using the version of the unzip command which has been compiled to have large file support.
07 Apr 2010	• Added explanation of using the `-o` option to the `curl` command for

	downloading files greater than 2GB. • Added better description of using `wget` as an alternative to `curl` • Added information about properly protecting a user's `.netrc` file
26 Mar 2010	• Removed incorrect phone number for CNDA support contact. • Added Document Revision History Section

Appendix B: CCIR Procedure Assessment Form



CCIR Center for Clinical Imaging Research

PROCEDURE ASSESSMENT FORM

(INSTRUCTIONS: PI/Coordinators: Please fill in the hi-lighted areas and present it to the technologists)

DATE OF SCAN: ________________

LAST Name	FIRST Name:	M.I.
DOB:	Height: In. / CM	Weight: KG/LB
Subject ID #: S1YA	Scan ID#: S1YA_1	Dictation Requested: NO: □ YES: □
PI Name:	Coordinator Name / Pager:	

Check ONE:
□ Research without Clindesk **□ Standard of Care** **□ SOC (+) Research (_____min)**
□ Research with Clindesk→(IDXrad code: CCIR2) **→(SOC-BJC billable)→(IDXrad code: CCIR 1)**

MRN# (if applicable):	**ACC#(if applicable):**	**CPT Code(s)(if applicable):**
HRPO #:	Fund #:	RDRC #:
CCIR#:	Adult: X Pediatric: □ Phantom: □ Other □______________	

CHECK MODALITY / SERVICE

☐ 3.0 T Trio MRI
☐ 1.5 T Avanto MRI
☐ HR+ PET
☐ Biograph PET-CT
☐ Siemens Definition CT

☐ Antares Ultrasound
☐ Nursing
☐ Pre-study/Setup
☐ Information Technology

CCIR TECHNOLOGIST USE ONLY

Time IN: Time OUT:

ANY INVASIVE PROCEDURE PERFORMED
(EXAMPLE: IV SITES, FOLEY CATHETER, BLOOD SUGAR/CREAT. CLEARANCE RESULTS, ETC.)

INJECTION AND MEDICATIONS ADMINISTERED AND BY WHO:

- Contrast □ NO □ YES (#________) Power Injector: □ NO □ YES

SCAN PROTOCOL USED:

-

COMMENTS:

TECHNOLOGIST SIGNATURE(S):

Name: Date:

V15_05.08.2009

Note the filled in Subject ID # and Scan ID # (in red). Notice that the Scan ID #, which corresponds to the CNDA MRI Session ID, starts with the Subject ID #. This will help ensure unique CNDA MRI Session IDs within your project.