Introduction

Welcome to the CHEAR Data Submission and Review Portal!

https://cheardatacenter.mssm.edu/

This User Manual outlines the Major Functions and Processes supported by the CHEAR Data Submission and Review Portal, and how to use them.

This manual is intended for use by Primary Investigators (i.e., “PI”s) and their Co-Investigators. These users will be accessing the portal to upload their study results data, generate CHEAR Participant IDs (PIDs) and Specimen IDs (SIDs), map CHEAR SIDs to PIDs, retrieving lab result data, and other related activities.
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1.0 Getting Access to the Data Submission and Review Portal

As a PI or Co-Investigator, you will be granted access to the Data Submission and Review Portal for a specific project, after that project has successfully moved through the complete Project Application and Review process.

- The Application and Review process is managed through a separate application “MyCHEAR” https://mychear.cheapprogram.org/
- Once your project application has reached the appropriate status in MyCHEAR, you will receive an email, containing a temporary password and a link to the CHEAR Data Submission and Review Portal.
- Upon logging in to the Data Submission and Review Portal for the first time (see the “logging on” section below), you will be prompted to change your password. You will now have access to your Project in the portal.

Note: If you already have access to the Data Submission and Review Portal for previous projects, you will receive an automated email each time an additional project reaches the appropriate status in MyCHEAR, informing you that you can now access that project in the Data Submission and Review Portal.

1.1 System Requirements

The CHEAR Data Submission and Review Portal is an internet based system. To access it, you will need a computer that has:

- A connection to the internet
- A web browser. Note: Internet Explorer (v. 11 or higher) or Google Chrome (v. 50 or higher) is recommended. (Firefox is not recommended).

1.2 Logging on

Access the CHEAR Data Submission and Review Portal Home Page at the following URL.

https://cheardatacenter.mssm.edu/

The Home page displays Summary Info for Subjects and Samples already in the system, as well as a map of participating PI's institutions. The map and Subject, Sample distributions will change when the underlying data change.

- Enter your Email Address and Password, and click the Log In button.
- If this is your first time logging on, please see the “Getting Access” Section above.
2.0 Retrieving CHEAR PIDs and Loading your Data Files

2.1 Accessing Your Projects

Once you have logged in, you can click on the “My Projects” link on the blue Navigation Bar at the top of the screen, which will show a list of the projects that you are assigned to as a PI or Co-Investigator (see Figure below).
• The list can be sorted by Project ID, Title, or Status, by clicking on the column headers.

• The information displayed within the columns has been gathered from your project application submitted via the “MyChear” portal, and the total numbers of subjects and specimens were updated by the Lab Hub and the Data Center.

• Clicking on the Project Title will navigate you to the Project Detail screen.

2.2 Project Details

The “View Project” page lists the high-level project information that was provided on your project application in the “MyCHEAR portal” and the total numbers of subjects and specimens were updated by the Lab Hub and the Data Center.

At the bottom of the page, the set of Analysis for this project as specified within the “MyCHEAR portal” are listed.
The project level details will list the Number of Subjects and Specimens out of the total assigned to the project already allocated. If none have been generated yet, they will be listed as 0 (see circled section in Figure above).

The Page contains several buttons, which will be described in detail below. Stepping through the actions available via the buttons will allow you to perform all the steps necessary for retrieving your CHEAR PIDs, mapping your original subject or specimen IDs, and uploading any project-related data and documents you may have.

2.3 **Step 1: Generate CHEAR PIDs**

The “View Project” page contains a button called “Generate CHEAR Participant IDs” (see figure below).

This button will allow you to generate and retrieve part or all the total number of CHEAR PIDs that have been assigned to you.

- Clicking the button navigates you to a separate “Generate PID page”

![Figure 4 – Generate CHEAR Participant IDs button](image)

![Figure 5 – Generate CHEAR Participant IDs screen](image)
• Enter the Number of CHEAR PIDs that you would like to generate and retrieve, and click the “Generate IDs” button.
  
  **Note:** you can enter part or all of the total number of PIDs you had specified for your project.
  
  If you enter more than the total number, however, you will receive an alert message.

• The following page will appear with a downloadable set of CHEAR PIDs.

  ![Figure 6 – Generated Participant IDs file](image)

• The CHEAR PID file will open in Excel and will contain two columns as shown by the following figure, one containing the set of CHEAR PIDs and another blank column that can be used to map your original subject IDs to CHEAR PIDs, and save on your computer for reference, if desired.

  ![Figure 7 – PIDs, once downloaded](image)

• **Note:** The CHEAR PIDs are also always available for download from the “View Project” page (see Figure below)
2.4 **Step 2a: (Optional) Map Original Subject ID’s to CHEAR PIDs**

The “View Project” page contains a button called “Map Original Subject IDs” (see figure below). This button allows you to enter and map your original subject ID’s (that you may have used to identify your subjects up to this point), to your CHEAR PIDs.

**NOTE:** A Single CHEAR PID must represent a single unique individual subject within your study. Each CHEAR PID can only be mapped to a single original subject ID.
• Clicking the “Map Original Subject IDs” button navigates you to a separate “Map Original Subject IDs” page (see figure below)

```
Figure 9 – Map Original Subject IDs button – on the View Project page

Figure 10 – Map Original Subject IDs page
```
There are two methods for mapping Original Subject IDs to CHEAR PIDs:
  - One by One, or
  - In Bulk (copy and paste all at once)

To map "One by One", begin entering the desired CHEAR PID in the Upper Left Hand field (the field will "auto-complete" by searching your CHEAR PIDs, as you type)

Then enter the Original subject ID and click “Assign”
The resulting Mapping will appear at the bottom of the screen (and can be deleted if necessary via the “remove link”)

Map Original Subject IDs

To map by the “In Bulk (copy and paste all at once)” method, enter a Tab-Delimited set of CHEAR PID – to Original Subject ID rows in the Lower right Text Area.

NOTE: These values may be copied and pasted directly from an excel spreadsheet

For example,

Copy the desired pairs from your local spreadsheet

Paste them into the lower right text area, and click the “Assign” button.
The resulting mapping of multiple pairs will now appear at the bottom of the screen, and can be deleted if necessary via the “remove link”.

NOTE: Once the PIDs have been mapped to original subject ID’s (by either method), the mapped values will always be accessible to download from the View Project screen, within the CHEAR Participant ID’s file (mentioned above).
2.5 Step 2b: (Optional) Map Original Specimen IDs to Subjects

The “View Project” page contains a button called “Map Original Specimen IDs” (see figure below).

This button allows you to enter and map your original specimen ID’s (that you may have used to identify your specimens up to this point), to your subjects. You can map specimens to subjects either by linking to “CHEAR PID” or to “Original Subject ID” (if you have already provided Original Subject IDs, see previous section).

**NOTE:** While a subject can have more than one original specimen ID, the same specimen ID cannot be mapped to more than one subject.

- Clicking the “Map Original Specimen IDs” button navigates you to a separate “Map Original Specimen IDs” page (see figure below)

- The screen provides a Choice of which Subject Identifier to map Original Specimen IDs to:
  - Original Subject ID (if these had previously been entered)
Once the CHOICE of subject identifier to be used for mapping is selected, the screen presents two methods for mapping Original Specimen ID’s to subjects:

- One by One, or
- In Bulk (copy and paste all at once)

To map “One by One”, begin entering the desired CHEAR PID / Original Subject ID (depending on your initial choice) in the Upper Left Hand field (the field will “auto-complete” as you type)
• Then enter the **original specimen ID** and click “Assign”

**Map Original Specimen IDs**

CHeAR Project ID: 200-2017  
CHeAR Project Status: Approved

Please select one of the following mapping options

- Mapping of Original Subject ID’s to Original Specimen ID’s
- Mapping CHeAR PID to Original Specimen ID’s

**Figure 21 – Map Original Specimen IDs to PIDs page (one by one) – enter Original Specimen ID**

• The resulting Mapping will appear at the bottom of the screen (and can be deleted if necessary via the “remove link”)

**Map Original Specimen IDs**

CHeAR Project ID: 200-2017  
CHeAR Project Status: Approved

Please select one of the following mapping options

- Mapping of Original Subject ID’s to Original Specimen ID’s
- Mapping CHeAR PID to Original Specimen ID’s

**Figure 22 – Mapped Original Specimen IDs, Original Subject IDs and PIDs**
To map by the “**Bulk (copy and paste all at once)**” method, enter a Tab-Delimited set of CHEAR-PID to Original Specimen ID pairs, or Original Subject ID to Original Specimen ID pairs in the Lower right Text Area. (corresponding to your initial mapping choice selection)

**NOTE:** These values may be copied and pasted directly from an excel spreadsheet

For example,

- Copy the desired pairs from your local spreadsheet

<table>
<thead>
<tr>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
</tr>
</thead>
<tbody>
<tr>
<td>CHEAR PID</td>
<td>Original Subject ID</td>
<td>Original Specimen ID</td>
<td></td>
</tr>
<tr>
<td>656135</td>
<td>ori_sub_1</td>
<td>ori_spe_1</td>
<td></td>
</tr>
<tr>
<td></td>
<td>ori_sub_2</td>
<td>ori_spe_2</td>
<td></td>
</tr>
</tbody>
</table>

*Figure 23 – Researcher’s CHEAR PID - Original Subject ID – Original Specimen ID mapping file*

- Paste them into the lower right text area, and click the “Assign” button.

**Map Original Specimen IDs**

<table>
<thead>
<tr>
<th>CHEAR Project ID:</th>
<th>200-2017</th>
</tr>
</thead>
<tbody>
<tr>
<td>CHEAR Project Status:</td>
<td>Approved</td>
</tr>
</tbody>
</table>

Please select one of the following mapping options

- Mapping of Original Subject ID’s to Original Specimen ID’s
- Mapping CHEAR PID to Original Specimen ID’s

Type in a Original Subject ID

Type in a Original Specimen ID

OR

<table>
<thead>
<tr>
<th>Example</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
</tr>
<tr>
<td>---</td>
</tr>
<tr>
<td>PH/67</td>
</tr>
<tr>
<td>TV/03</td>
</tr>
<tr>
<td>UAEA8</td>
</tr>
</tbody>
</table>

*Figure 24 – Map Original Specimen IDs to Original Subject IDs (in bulk)*

- The resulting mapping of **multiple pairs** will now appear at the bottom of the screen, (and can be deleted if necessary via the “remove link”). Note that a single subject can be mapped to multiple Original Specimen IDs.
• **NOTE:** Once the Original Specimen IDs have been mapped (by either method), the mapped values will always be accessible to download from the View Project screen, within the Original_Specimen_ID_mapping file.

![Table showing mapped Original Specimen IDs, Original Subject IDs, and CHEAR PIDs](image)

### Figure 25 – Mapped Original Specimen IDs, Original Subject IDs and PIDs

#### 2.6 Step 3: Upload Study Results Data

The “View Project” page contains a button called “Upload Data” (see figure below). This button allows you to upload any project-related data that you have collected for your project (e.g., epidemiological data, questionnaire answers, demographics, etc.). You may also upload any additional supporting documents related to your project.
View Project

CHEAR Project ID: 200-2017  CHEAR Project Status: Approved
Project Title: Production Placeholder
Significance: Placeholder Placeholder
Specific Aims: Placeholder Placeholder
Subject Number: Assigned 2 of 10  Sample Number: Assigned 0 of 20
Date Accepted to CHEAR: 02/01/2017
Principal Investigator: PI-tester Sinai, Xin Zheng
Contributing:

Step 1: Generate CHEAR Participant IDs (2 allocated already)
Step 2 (optional): Map Original Subject IDs  Map Original Specimen IDs
Step 3: Upload Data
Step 4, Update Status: Ready for Stats Core Review

Figure 27 – Upload Data button – on the View Project page

- Clicking the “Upload Data” button navigates you to a separate “Upload Project Data” page (see figure below)

![Figure 28 – Upload Project Data Screen](image)

- The Category menu contains 3 categories of documents that you may upload (see figure below)
• At least one “Data Dictionary / Codebook “ must be uploaded per project, since Project Result data files will need to be linked to it (see below).

• Additionally “Supporting Documents for Project” allows any type of file to be uploaded.

• The page allows you to search your own local directory for a file to upload, and attach a short description

• Once the “Upload” button is clicked, the uploaded file will appear in the “Data Uploaded” section of the View Project page (see figure below).
NOTE: CHEAR Data Center personnel also have the ability to upload documents into your project space (this is especially relevant if you are collaborating with them on the content / structure of your data). You can tell who uploaded a file by looking at the “Uploaded By” column.

- Uploading data for the “Project Results Data” requires some additional input.
  - You must indicate the Associated Data Dictionary / Codebook (already uploaded).
  - You may select to indicate whether this data is de-identified.

- Note: This is the category under which any Study Data should be uploaded (epidemiological data, demographics data, etc.)
2.7 Archiving Uploaded Files

Files that you have uploaded may be “archived” (if they are incorrect or outdated, or have been replaced by a newer version).

- To archive a file, click on the “archive” icon, next to the document (see figure above).
  - The system will prompt you for confirmation, and then archive your file.

- To see files that you have already archived, toggle the “File view selection box” to “Archived” (see figure below).
• To see your CURRENT set of files, toggle the selection back to "Active" (see figure below).

![Figure 34 – File View selection box](image)

2.8 Step 4: Submitting your Study Data for Review

Once you have uploaded ALL of your relevant study data, you should set the status of your Project to “Ready for Review by Stats Core”. This will automatically notify Data Center Statistical personnel that your data is ready for initial review.

![Figure 35 – Update Status](image)

• Clicking the “Ready for Stats Core Review” will update the status of your project, and send a notification to Data Center Statistical-Core personnel.
  o **Note:** You will still have full access to your project and files after this step.
Once the “Ready for Stats Core Review” is clicked, the project Status appears as “Awaiting Review.”

The option to update the project status is no longer available.

The project Status will change to “Initial Data Reviewed by Stats Core” when the DC Statistical Core finishes its review and release SIDs to the CHEAR Coordinating Center (CC).
3.0 Mapping CHEAR SIDs to PIDs, and Shipping your Samples

**NOTE:** This section assumes that you have already received the electronic set of SIDs and associated labels from the Coordinating Center.

Once you have received your set of sample labels from the Coordinating Center, which each have a barcoded SID (Specimen ID) encoded upon them, you can map each barcoded Label / SID directly to a corresponding study participant via several methods available in the Data Submission and Review Portal.

3.1 Navigate to the Map CHEAR Specimens to Participants page

- Log on and Navigate to your project.
- Click on the relevant project title that you want to map specimens for.
- Note: You can confirm that your project is ready for SID-to-PID mapping by seeing that the status reads “**Initial Data Reviewed by Stats Core**”

![Figure 37 – Project Status on Project Review page](image)

![Figure 38 – Map CHEAR Specimens to Participants button on Project Review page](image)
3.2 Map Specimens to Participants

- Click on the “Map CHEAR Specimens to Participants” button. You will be navigated to the “Map CHEAR Specimen IDs page (see next section).
  - Note: this button will only be available once the status of your project has been marked as “Initial Data Reviewed by Stats Core”

**Map CHEAR Specimen IDs**

![Map CHEAR Specimen IDs](image)

- The “Map CHEAR Specimen IDs page” provides several OPTIONS for how to map each CHEAR SID.
  - Map to CHEAR PID
  - Map to Original Subject ID (if these were previously uploaded. See preceding sections)
  - Map to Original Specimen ID (if these were previously uploaded. See preceding sections)
  - Note: The system will only let you map a CHEAR SID to one of the above three options at a time.
However, if you have selected to map to a CHEAR PID / Original Subject ID, AND that ID already has Original Specimen IDs mapped to it, the system will force you to further select a specific Original Specimen ID to map the CHEAR SID to.

- Select the PID / Original Subject ID / Original Specimen ID that you are mapping a particular CHEAR SID to.
- You can then SCAN the full CHEAR SID directly from the Label into “CHEAR SID” textbox (Red square in Figure 38)
  - Note: you can also type it in, if you prefer
- Complete the “Required Fields” information (the system will alert if you do not fill out these fields)
- Complete the “Optional Fields” information, if you prefer
- Click the “Assign” Button

**Special Feature:** If there are multiple Samples that will require having the same / similar information entered in each of the Required / Optional fields, you can click on the “**Keep Values in Fields for Next Assignment**” checkbox (see screenshot below). This option will keep the values entered in the Required / Optional fields present for each CHEAR SID assignment. When this option is not selected, the fields are cleared after each assignment.

![Box-Position:][1]

![Keep Values in Fields for Next Assignment][2]

**Figure 39 – Keep Values in Fields for Next Assignment flag**
### 3.3 Review the mapping

![Optional Fields](image)

The bottom of the screen displays the SID to PID mappings that you have completed.

- **Please NOTE:** currently the screen only displays some of the mapped information (although all of the information that you have entered is stored in the background in the database. In an upcoming released upgrade for this screen, all data entered will be displayed here).

- If any of the mappings as entered are incorrect, they can be deleted by clicking on the associated “Remove” icon on the right-hand side.

- Once the mappings have been reviewed, clicking the **Done** button, which will navigate you back to the Project View.

---

**Figure 40 – Specimen ID – Participant ID mapping**

<table>
<thead>
<tr>
<th>Participant ID</th>
<th>Specimen ID</th>
<th>Lab Hub</th>
<th>Sample Group ID</th>
<th>Sample Collection Date</th>
<th>Sample Matrix</th>
<th>Sample Collection Method</th>
<th>Sample Container Type</th>
<th>Remove</th>
</tr>
</thead>
<tbody>
<tr>
<td>1567362</td>
<td>SWP03</td>
<td>T2 - Michigan</td>
<td></td>
<td>WB</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2144921</td>
<td>NW06</td>
<td>T2 - Michigan</td>
<td></td>
<td>WB</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>6801380</td>
<td>LSV06</td>
<td>T2 - Michigan</td>
<td></td>
<td>WB</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

---

3.4 Retrieve your Shipping Manifest

View Project

CHEAR Project ID: 200-06
Project Title: User Guide Demo 1
Significance: In health services research, it is often necessary to adjust for confounding due to comorbidity, the presence of one or more additional disorders co-occurring with a primary disorder. One popular method of comorbidity adjustment is the Elixhauser comorbidity system, [1] a set of 30 comorbidity indicators.
Specific Aims: The Elixhauser comorbidity system was developed and is most often used in administrative datasets. Two examples of such datasets are the Nationwide Inpatient Sample (NIS) and the State Inpatient Database (SID), which are both maintained by the Healthcare Cost and Utilization Project (HCUP, see http://hcup-us.ahrq.gov). HCUP provides software for converting International Classification of Diseases, 9th Revision, Clinical Modification (ICD-9-CM) diagnosis codes to Elixhauser comorbidity indicators (see http://hcup-us.ahrq.gov/tools/software/comorbidity/comorbidity.jsp). van Walraven and colleagues [2] developed a summary score for the Elixhauser comorbidities by modeling in-hospital mortality with inpatient admission data. The summary score is a weighted combination of the 30 Elixhauser comorbidities, where a larger comorbidity weight indicates a stronger association between the comorbidity and in-hospital mortality.
Subject Number: Assigned 10 of 20
Date Accepted to CHEAR: 08/01/2016
Principal Investigator: Alex Zhimirsksy; PI-tester Sinai;
Contributing: Co-PI-Tester Sinai;

Step 1:
Step 2 (optional):
Step 3:
Step 4, Update Status: (Already updated) Current status: Lab Data Reviewed by Stats Core

Data Uploaded

<table>
<thead>
<tr>
<th>File Name</th>
<th>File Description</th>
<th>Date Uploaded</th>
<th>File</th>
<th>Uploaded By Category</th>
</tr>
</thead>
<tbody>
<tr>
<td>CHEAR_DRMC_User_Manual_v2.pdf</td>
<td>testing for size</td>
<td>02/13/2017</td>
<td></td>
<td>PI-tester Sinai Supporting Documents for Project</td>
</tr>
<tr>
<td>MSDW Pamphlet v3 .pptx</td>
<td>test supporting document</td>
<td>08/25/2016</td>
<td></td>
<td>PI-tester Sinai Supporting Documents for Project</td>
</tr>
</tbody>
</table>

Generated IDs

<table>
<thead>
<tr>
<th>File Name</th>
<th>Date Uploaded</th>
<th>File</th>
<th>Uploaded By</th>
</tr>
</thead>
<tbody>
<tr>
<td>CHEAR_Participant_IDs.xls</td>
<td></td>
<td></td>
<td>System Generated</td>
</tr>
<tr>
<td>Original_Specimen_ID_mapping.xls</td>
<td></td>
<td></td>
<td>System Generated</td>
</tr>
<tr>
<td>Shipping Manifest - Lab Hub T1 - Emory</td>
<td></td>
<td></td>
<td>System Generated</td>
</tr>
</tbody>
</table>

Figure 41 Shipping Manifest file
Once you have mapped PIDs to SIDs, a Shipping Manifest now appears in the Generated IDs section on the specific Analysis view (for which you had mapped the specimens). See circled portion on the screenshot above.

To download the Manifest, click on the “xls” icon.

**Important NOTE:** due to a very recent Microsoft release, there is an error opening the Excel file that may appear. We are working on fixing this. In the meantime the workaround is:

- The file may not open initially, or may look “blank” when opened
- In windows, Right-click on the downloaded excel file, and click “Properties”
- In the General tab of the properties window, click the **Unblock** button (see screenshot below), and then click OK.
Now, try to re-open the excel file. You may be presented with the following alert. Click **Yes**

![Image of Microsoft Excel alert]

The Shipping Manifest will open as a fully editable formatted excel document. Any data that had been entered on the screen shall be present on the Manifest.

![Image of Shipping Manifest Excel file]

**Note:** Any changes made directly on the Excel file will not make their way back into the portal system unless directly entered onto the portal screen.
Note: When saving the Shipping Manifest on your local computer, you should change the File Type to .xls / .xlsx to avoid re-encountering the formatting alerts mentioned above. (See screenshot below).

### 4.0 Retrieving Lab Analysis Data from the portal

**NOTE:** This section assumes that the Lab Hub has completed their sample analysis, and has uploaded their result data to the Data Submission and Review Portal.

#### 4.1 Step One: Navigate to the Relevant “Analysis”
Log on and Navigate to your project.
Click on the Relevant Analysis Name that you want to retrieve Lab Data for. You will be navigated to the Analysis Level view.
4.2 Step Two: Retrieve Analysis Data

- Any data uploaded at the Analysis Level will appear in the “Data Uploaded” section.
  - You will see the file Name, Description, date of upload and Who uploaded the file listed.
  - You can download each file listed by clicking on the “xls” icon.

- **NOTE:** for Metabolomics data (that has separately been posted to the Metabolomics Workbench) – a link ICON will appear, that when clicked will (in a separate browser tab) open the Metabolomics workbench directly for that project. (see screenshot below).
Figure 44– Metabolomics Result link