DATA CONTRIBUTION GUIDE
PRIMatE Data Exchange (PRIME-DE)

Outlined below are the steps that need to be completed to successfully contribute data to PRIME. The primary goal of the data preparation process is to provide the minimum organization necessary for the INDI team to successfully handle your contribution. A member of the INDI team will be available to help with and troubleshoot any difficulties that arise in the process, to provide support and to ensure the process goes smoothly.

Share that brain!

The INDI Team

1. **Data Requirements**
    a. At a minimum, we require one T1-weighted anatomical scan per subject. It is preferred to also have at least one functional MRI or diffusion MRI dataset per subject as well (when available, please include field maps). We will gladly accept any additional data you are willing to contribute (e.g., T2 or ASL scans, phenotypic information).
    b. NIFTI is the default data format for INDI due to the decreased risk of unintended information being present in the header when handling human data. If you'd prefer to make your contribution in DICOM, our team can handle the necessary conversions.

3. **Data Organization**

The preferred directory structure and naming convention is as follows (though any organization is acceptable, as the INDI team ensures standardization prior to release):

0000001/session_1/anat_1/anat.nii.gz
0000001/session_2/anat_1/anat.nii.gz
0000001/session_1/rest_1/rest.nii.gz
0000001/session_1/rest_2/rest.nii.gz
0000001/session_1/rest_3/rest.nii.gz
0000001/session_2/rest_1/rest.nii.gz
0000001/session_2/rest_2/rest.nii.gz
0000001/session_2/rest_3/rest.nii.gz
0000001/session_2/dti_1/rest.nii.gz
0000001/session_2/dti_2/rest.nii.gz
0000001/session_2/dti_3/rest.nii.gz
etc.

Note: In the event of multiple sessions, it is important that you maintain session order by numbering them chronologically.

4. **Data Reorientation**
   To ensure uniformity across datasets provided by INDI, we provide all datasets in RPI orientation. We can accept data in any orientation, though if possible, please reorient all scans to RPI and ensure the header information of the images is set accordingly. Finally, check that the left/right orientation is in accordance with your original data. *Following receipt and review of the images received from your site, the INDI team will send you axial images from five randomly selected datasets from your site to verify left-right orientation.*

5. **Data Phenotyping**
   We require age, sex, and species information for all contributed datasets. We gladly accept any additional phenotypic information you would like to share (e.g., rearing variables, hand preference, exposures/interventions). Organize your data in a .csv or Excel workbook spreadsheet.

6. **Data Uploading**
   Let us know when your data are ready. We will have you carry out three simple steps:
   i. TAR file generation.
   usage: tar -zcvf <tar-archive-name.tar.gz> <source-folder-name>
   note: for large collections, we recommend tarring the data into archives of size 2-3GB.

   ii. TAR file encryption.
   usage: EncryptForUpload.sh <input file> <password>)
   note: each site will be provided its own password and sent EncryptForUpload.sh

   iii. TAR file upload. We will then send you login information for the upload portal on NITRC. At that time, you will be given an encryption simple *sftp* call is required to upload your data. **Please note that we will double-check the data before they are publicly released.**

7. **Webpage Contents**
   To optimally share your data, we will put together a **webpage** dedicated to your data sample. For this we require:
   - A name for your data sample
   - A logo for your site (.png is the preferred file format)
   - A list of the names and titles of the PI and all senior personnel affiliated with your data sample
   - Acknowledgements - you can be as generous as you would like with this list
   - A list of grants that you want acknowledged
   - A list of any publications using the data you are contributing
   - Any behavioral information about the resting state scan.

- Were the subjects awake or anesthetized? If awake, what was the scan state (e.g., rest, movie viewing, task performance)? If anesthetized, what was the protocol used (e.g., agents, dosing, timing)?
- Scan Parameters

  A PDF of each scan's sequence protocol (e.g., anatomical, resting state, DTI…) obtained from the scanner console.

8. **Data Downloading**

   We will send you the completed webpage before making it public. After you have approved it, the page will be made public and people can start downloading your data. You will then achieve ultimate happiness and will be remembered as a great, sharing scientist.