1. Consider permissions: <https://www.linux.com/learn/how-manage-file-and-folder-permissions-linux>
2. Put Biobank pipeline and Python installation files in Linux folder not a shared Virtualbox folder
3. If using VirtualBox: <http://jessezhuang.github.io/article/virtualbox-tips/>
   1. Run PC as administrator
   2. Open cmd, “cd C:\Program Files\Oracle\VirtualBox”. Then “VBoxManage.exe setextradata Linux VBoxInternal2/SharedFoldersEnableSymlinksCreate/Data 1”
   3. Then run Virtual box as admin too
4. Install git: “sudo apt-get install git”
5. Other essentials:
   1. apt-get install libssl-dev
   2. sudo apt-get install make build-essential libssl-dev zlib1g-dev libbz2-dev libsqlite3-dev
6. Install Python 3.5.1:
   1. “cd /home/cab79/UK\_biobank\_pipeline\_v\_1/bb\_python/python\_installation”
   2. “sudo -H bash install\_bb\_python3.5.1.sh”
   3. If there are errors:
      1. run the file with “dos2unix” first
      2. “sudo apt install gcc-multilib” first
7. ~~Install Python toolboxes: “sudo pip3 install <toolbox>”~~
   1. ~~numpy==1.11.1~~
   2. ~~nibabel==2.1.0~~
   3. ~~pydicom==0.9.9~~
   4. ~~scipy==0.18.0~~
   5. ~~pandas==0.18.1~~
   6. ~~scikit-learn==0.17.1~~
   7. ~~ipython==5.1.0~~
   8. ~~matplotlib==1.5.2~~
   9. ~~nose==1.3.7~~
   10. ~~sphinx==1.4.6~~
8. Install FSL: <https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FslInstallation/Linux>
   1. Go to FSL folder and run “sudo chmod +x etc/fslconf/fsl.sh”
   2. Run also the FEEDS check: <https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FEEDS>
9. Install R: <https://www.datacamp.com/community/tutorials/installing-R-windows-mac-ubuntu>
10. Install FIX and associated R packages: <https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FIX/UserGuide>
    1. Prior to R packages:
       1. sudo apt-get install libxml2-dev
       2. sudo apt-get install libcurl4-openssl-dev
       3. sudo apt-get install libcurl4-gnutls-dev
       4. sudo apt-get install curl
    2. Also:
       1. liblapack-dev
       2. liblapack3
       3. ibopenblas-base
       4. libopenblas-dev
    3. Go into “R”:
       1. install.packages("devtools")
       2. Dependencies:
          1. install.packages("mvtnorm")
          2. install.packages("strucchange")
          3. install.packages("coin")
          4. install.packages("zoo")
          5. install.packages("sandwich")
       3. packageurl <- "<https://launchpad.net/ubuntu/+archive/primary/+sourcefiles/r-cran-kernlab/0.9-24-1/r-cran-kernlab_0.9-24.orig.tar.gz>"
       4. install.packages(packageurl, repos=NULL, type="source")
       5. packageurl <- "https://cran.r-project.org/src/contrib/ROCR\_1.0-7.tar.gz"
       6. install.packages(packageurl, repos=NULL, type="source")
       7. packageurl <- "https://cran.r-project.org/src/contrib/class\_7.3-14.tar.gz"
       8. install.packages(packageurl, repos=NULL, type="source")
       9. packageurl <- "https://cran.r-project.org/src/contrib/Archive/party/party\_1.0-25.tar.gz"
       10. install.packages(packageurl, repos=NULL, type="source")
       11. packageurl <- "https://cran.r-project.org/src/contrib/Archive/e1071/e1071\_1.6-7.tar.gz"
       12. install.packages(packageurl, repos=NULL, type="source")
       13. packageurl <- "https://cran.r-project.org/src/contrib/Archive/randomForest/randomForest\_4.6-12.tar.gz"
       14. install.packages(packageurl, repos=NULL, type="source")
11. Update settings.sh within FIX folder.
12. Install Freesufer: [https://surfer.nmr.mgh.harvard.edu/fswiki/DownloadAndInstall#Installation](https://surfer.nmr.mgh.harvard.edu/fswiki/DownloadAndInstall" \l "Installation)
13. Install Matlab (with statistics, and signal processing, toolboxes)
    1. create symbolic link: <https://uk.mathworks.com/matlabcentral/answers/96149-what-are-symbolic-links-and-why-does-the-matlab-installer-ask-if-i-want-to-create-them>
14. Install FSL NETS and dependencies: [https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FSLNets#Installing\_FSLNets](https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FSLNets" \l "Installing_FSLNets)
15. update paths in bb\_netsmats in functional pipeline folder
16. Install AMICO and dependencies within bb\_ext\_tools folder: <https://github.com/daducci/AMICO>
17. ~~Install: “sudo chmod +x /media/sf\_Data/Matlab/UK\_biobank\_pipeline\_v\_1/bb\_python/python\_installation/install\_bb\_python2.7.12.sh”~~
18. Convert DICOM to NIFTI:
    1. General form: “dcm2niix -b y -z y -f %p\_coil%a\_echo%e\_%2s -o <OUTPUT\_DIR> <DICOM\_DIR>”
    2. E.g. “/home/cab79/UK\_biobank\_pipeline\_v\_1/dcm2niix\_25-Nov-2018\_lnx/dcm2niix -b y -z y -f %p\_coil%a\_echo%e\_%2s -o /home/cab79/Data/MNP\_test1/ /media/sf\_Data/MNP/mri/raw/pilots/MNP\_test1/14180000/”
19. Init\_vars
    1. Update init\_vars file with the correct directory paths
    2. “dos2unix /home/cab79/UK\_biobank\_pipeline\_v\_1/init\_vars”
    3. “source home/cab79/UK\_biobank\_pipeline\_v\_1/init\_vars”
20. Change directory to where the subject folder is: “cd /media/sf\_Data/MNP/mri/raw/pilots/”
21. Run pipeline script;
    1. e.g. “ /home/cab79/UK\_biobank\_pipeline\_v\_1/bb\_pipeline\_tools/bb\_pipeline.py MNP\_test1”
22. Current error:

File "/media/sf\_Data/Matlab/UK\_biobank\_pipeline\_v\_1/bb\_pipeline\_tools/bb\_pipeline.py", line 31, in <module>

from bb\_file\_manager import bb\_file\_manager

File "/media/sf\_Data/Matlab/UK\_biobank\_pipeline\_v\_1/bb\_pipeline\_tools/bb\_file\_manager.py", line 31, in <module>

import bb\_general\_tools.bb\_path as bb\_path

ImportError: No module named 'bb\_general\_tools'

Code changes:

- In bb\_pipeline\_struct.py, set jobPREPAREFIELDMAP="0";

- removed nii.gz from bb\_GDC and bb\_GDC\_halfvoxel

- gradientwarp package: coeffs.py:

line 65: added 'as82': 0.25

line 74/75 and 185: coef\_array\_sz = 20

- bb\_eddy\_wrap – changed from eddy\_cuda to eddy\_openmp (until we buy a CUDA GPU)

- change bb\_prepare\_rfmri: changed line 42 from half-voxel version to just bb\_GDC, because python half-voxel version does not exist. <https://www.jiscmail.ac.uk/cgi-bin/webadmin?A2=UKB-NEUROIMAGING;647b3646.1801>

- removed “.nii.gz” from line 44 to 49 of bb\_prepare\_rfMRI – this was causing FEAT to crash, as the design.fsf file prefers not to have extensions.

- added line to bb\_struct\_init to convert exp notation number to decimal, otherwise doesn’t work with fsl\_maths: printf -v head\_top "%.f" "$head\_top". Also change the interpreter to bash at the top.

Notes:

- turned off struct pipeline as this has completed.

- Need to run dcm2niix before every run of the pipeline

- For DTI eddy, need 8x104x104x72x105 = 654MB of RAM according to FSL website.

TEMP:

On the target computer, append the following to your LD\_LIBRARY\_PATH environment variable:  
  
/usr/local/MATLAB/MATLAB\_Runtime/v95/runtime/glnxa64:/usr/local/MATLAB/MATLAB\_Runtime/v95/bin/glnxa64:/usr/local/MATLAB/MATLAB\_Runtime/v95/sys/os/glnxa64:/usr/local/MATLAB/MATLAB\_Runtime/v95/extern/bin/glnxa64  
  
If MATLAB Runtime is to be used with MATLAB Production Server, you do not need to modify the above environment variable.