Troubleshooting - Dcm2bids + fmriprep

This document contains a list of errors that Yadnesh and Nabarun encountered, as they've tried to run dcm2bids + fmriprep, and details of how these errors can be resolved.

The link to the **editable Google document** is as follows, **where you can also add screenshots of the errors you are unable to resolve:**
https://docs.google.com/document/d/1zIh36UCvBMf9gVQkUlQjI143619CPe5xgopphvWzb2Q/edit?usp=sharing

```
yadnesh@DTI: ~/BIDS

File  Edit  View  Search  Terminal  Help
       * BIDS dataset path: /data.
       * Participant list: ['01'].
       * Run identifier: 20200723-072252_b66ab6ec-aae9-4205-b56a-7b40628d7e24.

Process Process-2:
Traceback (most recent call last):
  File "/usr/local/miniconda/lib/python3.7/multiprocessing/process.py", line 297
, in _bootstrap
    self.run()
  File "/usr/local/miniconda/lib/python3.7/multiprocessing/process.py", line 99,
 in run
    self._target(*self._args, **self._kwargs)
  File "/usr/local/miniconda/lib/python3.7/site-packages/fmriprep/cli/run.py", l
ine 610, in build_workflow
    work_dir=str(work_dir),
  File "/usr/local/miniconda/lib/python3.7/site-packages/fmriprep/workflows/base
.py", line 259, in init_fmriprep_wf
    use_syn=use_syn,
  File "/usr/local/miniconda/lib/python3.7/site-packages/fmriprep/workflows/base
.py", line 478, in init_single_subject_wf
    "All workflows require T1w images.".format(subject_id))
Exception: No T1w images found for participant 01. All workflows require T1w ima
ges.
fMRIPrep: Please report errors to https://github.com/poldracklab/fmriprep/issues
```

[a][b]
Getting this error mostly because there is only one folder in the '003_S_6258' folder - 'Axial_rsfMRI__Eyes_Open_' (whereas 3 were expected according to the doc file). And so

after running dcm2bids only the 'func' folder was created inside the 'sub-01' folder. The 'anat' folder with the T1w.nii.gz file was not created.

```
  File "/usr/local/miniconda/lib/python3.7/site-packages/traits/trait_handlers.py", line 2305, in <listc
omp>
    value = [ validate( object, name, val ) for val in value ]
  File "/usr/local/miniconda/lib/python3.7/site-packages/nipype/interfaces/base/traits_extension.py", li
ne 112, in validate
    self.info_text, value))
traits.trait_errors.TraitError: The trait 'in_files' of an IntraModalMergeInputSpec instance is an exist
ing file name, but the path  '/data/sub-01/fmap/sub-01_magnitude1.nii.gz' does not exist.

During handling of the above exception, another exception occurred:

Traceback (most recent call last):
  File "/usr/local/miniconda/bin/fmriprep", line 10, in <module>
    sys.exit(main())
  File "/usr/local/miniconda/lib/python3.7/site-packages/fmriprep/cli/run.py", line 416, in main
    subject_list, output_dir, work_dir, run_uuid, packagename='fmriprep')
  File "/usr/local/miniconda/lib/python3.7/site-packages/niworkflows/reports/core.py", line 420, in gene
rate_reports
    for subject_label in subject_list
  File "/usr/local/miniconda/lib/python3.7/site-packages/niworkflows/reports/core.py", line 420, in <lis
tcomp>
    for subject_label in subject_list
  File "/usr/local/miniconda/lib/python3.7/site-packages/niworkflows/reports/core.py", line 407, in run_
reports
    subject_id=subject_label, packagename=packagename)
  File "/usr/local/miniconda/lib/python3.7/site-packages/niworkflows/reports/core.py", line 256, in __in
it__
    self._load_config(Path(config))
  File "/usr/local/miniconda/lib/python3.7/site-packages/niworkflows/reports/core.py", line 274, in _loa
d_config
    self.index(settings['sections'])
  File "/usr/local/miniconda/lib/python3.7/site-packages/niworkflows/reports/core.py", line 283, in inde
x
    self.layout = BIDSLayout(self.root, config='figures', validate=False)
  File "/usr/local/miniconda/lib/python3.7/site-packages/bids/layout/layout.py", line 146, in __init__
    raise ValueError("BIDS root does not exist: %s" % root)
ValueError: BIDS root does not exist: /tmp/work/reportlets/fmriprep/sub-01
Sentry is attempting to send 3 pending error messages
Waiting up to 2 seconds
Press Ctrl-C to quit
fMRIPrep: Please report errors to https://github.com/poldracklab/fmriprep/issues
```

I got access and downloaded the ADNI files. The generated fmap folder has only a phase diff file. How to get the other 2?[c]

☐ Select All   Add To Collection   CSV Down

Select	View	Description
☐	VIEW	t1_fl2d_sag
☐	VIEW	Accelerated Sagittal MPRAGE
☐	VIEW	Axial 3D PASL (Eyes Open)
☐	VIEW	Perfusion_Weighted
☐	VIEW	Axial T2 STAR
☐	VIEW	Field Mapping
☐	VIEW	Field Mapping
☐	VIEW	Sagittal 3D FLAIR
☐	VIEW	HighResHippocampus
☐	VIEW	3 Plane Localizer
☐	VIEW	3 Plane Localizer
☐	VIEW	3 Plane Localizer
☐	VIEW	Field Mapping

Also below image means the process is completed?[d]

```
200724-06:55:57,722 nipype.workflow INFO:
        [Node] Finished "fmriprep_wf.single_subject_01_wf.func_preproc_task_rest_wf.bold_std_trans_wf.b
old_reference_wf.enhance_and_skullstrip_bold_wf.combine_masks".
200724-06:55:59,463 nipype.workflow INFO:
        [Node] Setting-up "fmriprep_wf.single_subject_01_wf.func_preproc_task_rest_wf.bold_std_trans_wf
.bold_reference_wf.enhance_and_skullstrip_bold_wf.apply_mask" in "/tmp/work/fmriprep_wf/single_subject_0
1_wf/func_preproc_task_rest_wf/bold_std_trans_wf/bold_reference_wf/enhance_and_skullstrip_bold_wf/_key_M
NI152NLin6Asym/apply_mask".
200724-06:55:59,468 nipype.workflow INFO:
        [Node] Running "apply_mask" ("nipype.interfaces.fsl.maths.ApplyMask"), a CommandLine Interface
with command:
fslmaths /tmp/work/fmriprep_wf/single_subject_01_wf/func_preproc_task_rest_wf/bold_std_trans_wf/bold_ref
erence_wf/enhance_and_skullstrip_bold_wf/_key_MNI152NLin6Asym/fixhdr_unifize/uni_xform.nii.gz -mas /tmp/
work/fmriprep_wf/single_subject_01_wf/func_preproc_task_rest_wf/bold_std_trans_wf/bold_reference_wf/enha
nce_and_skullstrip_bold_wf/_key_MNI152NLin6Asym/combine_masks/ref_bold_corrected_brain_mask_maths.nii.gz
 /tmp/work/fmriprep_wf/single_subject_01_wf/func_preproc_task_rest_wf/bold_std_trans_wf/bold_reference_w
f/enhance_and_skullstrip_bold_wf/_key_MNI152NLin6Asym/apply_mask/uni_xform_masked.nii.gz
200724-06:55:59,765 nipype.workflow INFO:
        [Node] Finished "fmriprep_wf.single_subject_01_wf.func_preproc_task_rest_wf.bold_std_trans_wf.b
old_reference_wf.enhance_and_skullstrip_bold_wf.apply_mask".
Error in atexit._run_exitfuncs:
Traceback (most recent call last):
  File "/usr/local/miniconda/lib/python3.7/concurrent/futures/process.py", line 101, in _python_exit
    thread_wakeup.wakeup()
  File "/usr/local/miniconda/lib/python3.7/concurrent/futures/process.py", line 89, in wakeup
    self._writer.send_bytes(b"")
  File "/usr/local/miniconda/lib/python3.7/multiprocessing/connection.py", line 183, in send_bytes
    self._check_closed()
  File "/usr/local/miniconda/lib/python3.7/multiprocessing/connection.py", line 136, in _check_closed
    raise OSError("handle is closed")
OSError: handle is closed
Sentry is attempting to send 0 pending error messages
Waiting up to 2 seconds
Press Ctrl-C to quit
```

config.json file for RADC subject:
After running the dcm2bids_helper command the following files are created in the helper folder.

002_20140508_t1_mpr_ns_sag_pat2_iso_0.json
002_20140508_t1_mpr_ns_sag_pat2_iso_0.nii.gz

```
003_20140508_t1_mpr_ns_sag_pat2_iso_0.json
003_20140508_t1_mpr_ns_sag_pat2_iso_0.nii.gz
004_20140508_DIFF_DTI_45_directions_0.bval
004_20140508_DIFF_DTI_45_directions_0.bvec
004_20140508_DIFF_DTI_45_directions_0.json
004_20140508_DIFF_DTI_45_directions_0.nii.gz
005_20140508_DIFF_DTI_45_directions_0.json
005_20140508_DIFF_DTI_45_directions_0.nii.gz
006_20140508_DIFF_DTI_45_directions_0.bval
006_20140508_DIFF_DTI_45_directions_0.bvec
006_20140508_DIFF_DTI_45_directions_0.json
006_20140508_DIFF_DTI_45_directions_0.nii.gz
007_20140508_DIFF_DTI_45_directions_0.json
007_20140508_DIFF_DTI_45_directions_0.nii.gz
008_20140508_DIFF_DTI_45_directions_0.json
008_20140508_DIFF_DTI_45_directions_0.nii.gz
010_20140508_gre_field_mapping_0_e1.json
010_20140508_gre_field_mapping_0_e1.nii.gz
010_20140508_gre_field_mapping_0_e2.json
010_20140508_gre_field_mapping_0_e2.nii.gz
011_20140508_gre_field_mapping_0_e2_ph.json
011_20140508_gre_field_mapping_0_e2_ph.nii.gz
012_20140508_T2_mapping_0_e1.json
012_20140508_T2_mapping_0_e1.nii.gz
012_20140508_T2_mapping_0_e2.json
012_20140508_T2_mapping_0_e2.nii.gz
012_20140508_T2_mapping_0_e3.json
012_20140508_T2_mapping_0_e3.nii.gz
012_20140508_T2_mapping_0_e4.json
012_20140508_T2_mapping_0_e4.nii.gz
012_20140508_T2_mapping_0_e5.json
012_20140508_T2_mapping_0_e5.nii.gz
013_20140508_FLAIR_Axial_TE_150_0.json
013_20140508_FLAIR_Axial_TE_150_0.nii.gz
014_20140508_FLAIR_Axial_TE_150_0.json
014_20140508_FLAIR_Axial_TE_150_0.nii.gz
015_20140508_t2_fl3d_tra_No_SWI_0.json
015_20140508_t2_fl3d_tra_No_SWI_0.nii.gz
016_20140508_t2_fl3d_tra_No_SWI_0_ph.json
016_20140508_t2_fl3d_tra_No_SWI_0_ph.nii.gz
017_20140508_ep2d_fid_basic_bold_0.json
017_20140508_ep2d_fid_basic_bold_0.nii.gz
```

My guess is that for the the SidecarFilename regex for anat should be *_t1_mpr_ns_sag_*
[e]

You can see that there are two T1 images available here for the same subject. However, to run fmriprep to correct for 1 BOLD scan we need only 1 T1 image. In such a case, we generally pick the T1 image of the larger file size (as it will likely be of higher quality).

Thus, in your dcm2bids_helper generated files, see which T1 is bigger. Once you identify that, choose an identifier that is unique to that specific T1 file. Like *003**t1* - there's no other file which has this combination.

and for fmap magnitude1 it should be *010**e1* for magnitude2 *010**e2*, for phasediff *_ph*. Is this correct?

This should work

But I'm not sure of the SidecarFilename for func, is it the _basic_bold_ one or the _FLAIR_Axial_?

It is the basic bold one. I will attach images below of what each modality looks like, so that you can confirm which file name corresponds to which modality yourself.

 Also after that will the EchoTime1 remain 0.00492 for the RADC subject as well?

Although this is likely the case, as RADC also uses a SIEMENS scanner, it is always a good idea to confirm this. EchoTime1 corresponds to the Echo Time of the first magnitude image.

Thus open up the .json file corresponding to it - 10_20140508_gre_field_mapping_0_e1.json - and see what the EchoTime parameter's value there is. This is the value you want to feed as EchoTime1 in the phase diff json.

What Each Modality looks like:

Use a tool called fslview to open up any .nii.gz files and look at the images. For this, all you have to do is open up a terminal, type fslview and press enter. A window will open up, where you can navigate to the file you want to view and open it up.

The files generated by dcm2bids_helper can be viewed using this tool.
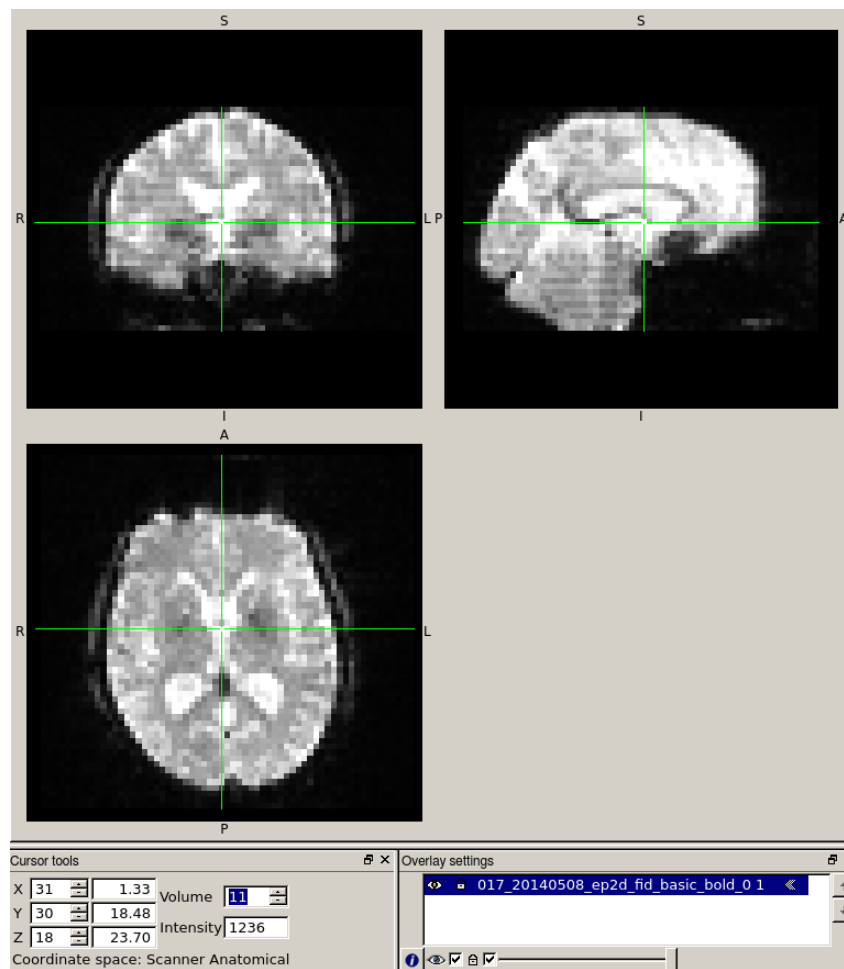
This is what a **BOLD (functional) image** looks like. You can also see that a BOLD image has **multiple volumes (**as the volumes parameter on the cursor tools tab is active)
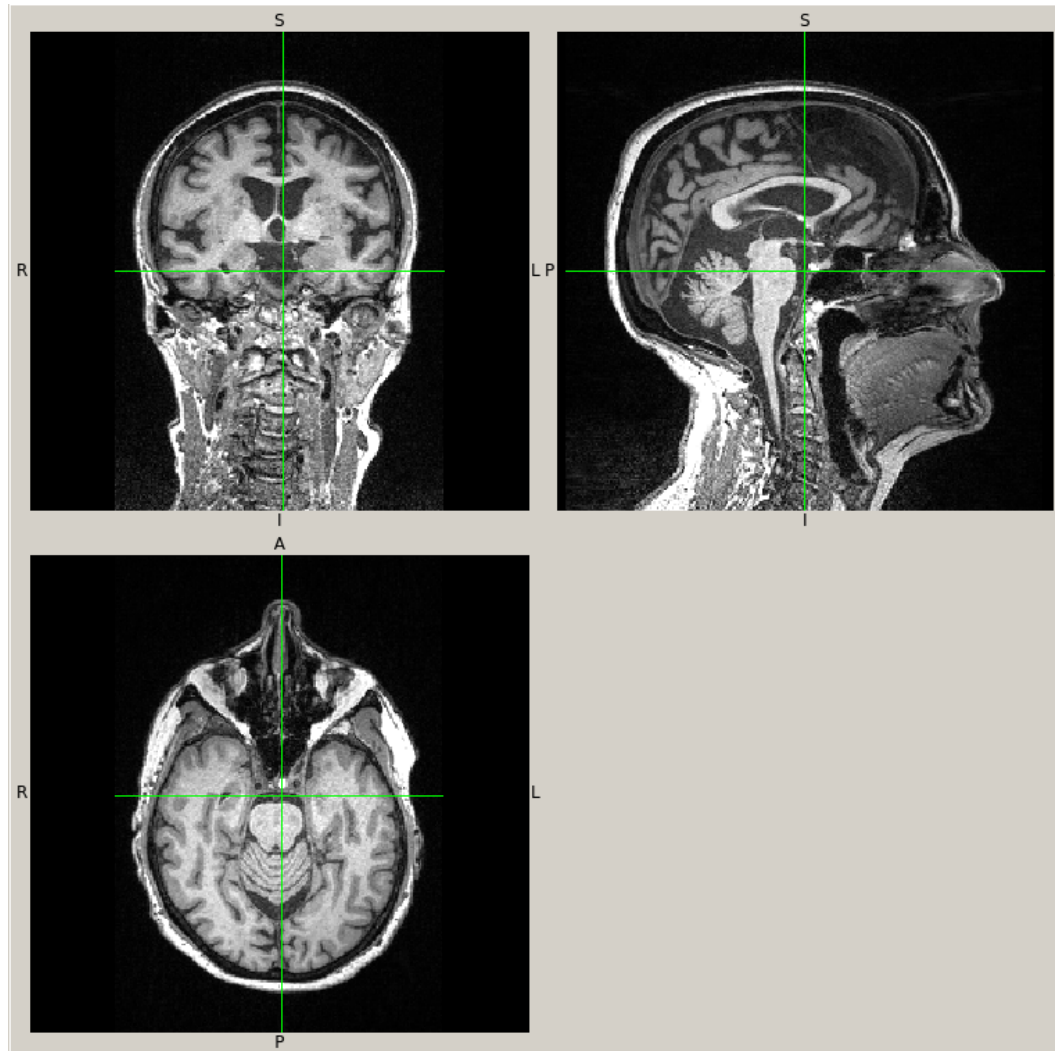
This is a **T1 image (anatomical image).** You can see that the spatial resolution is a lot higher, the distinction between Grey matter, white matter and CSF is a lot more marked.

Cursor tools   ◻ ✕

X 63 ⇅   0.05   Volume 0 ⇅

Y 64 ⇅   16.92   Intensity 733

Z 32 ⇅   25.15

Coordinate space: Scanner Anatomical

Overlay settings   ◻

👁 ▪ 010_06131380_00_gre_field_mapping_0_e1 1 «
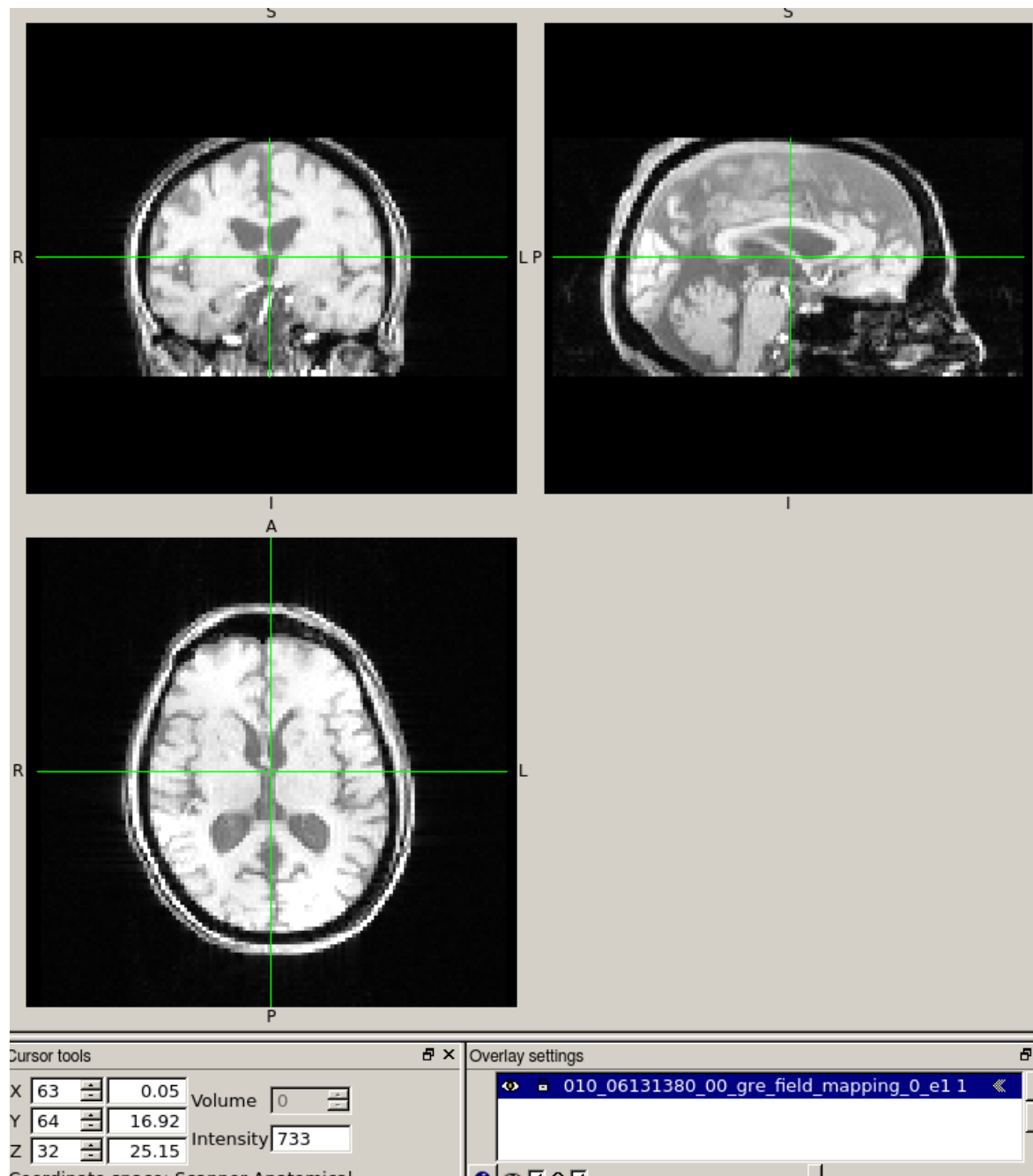
This is a **GRE fieldmap magnitude image**. Both magnitude images will look similar. **Each magnitude image (e1 and e2) contains only one volume**, hence the volume parameter is greyed out
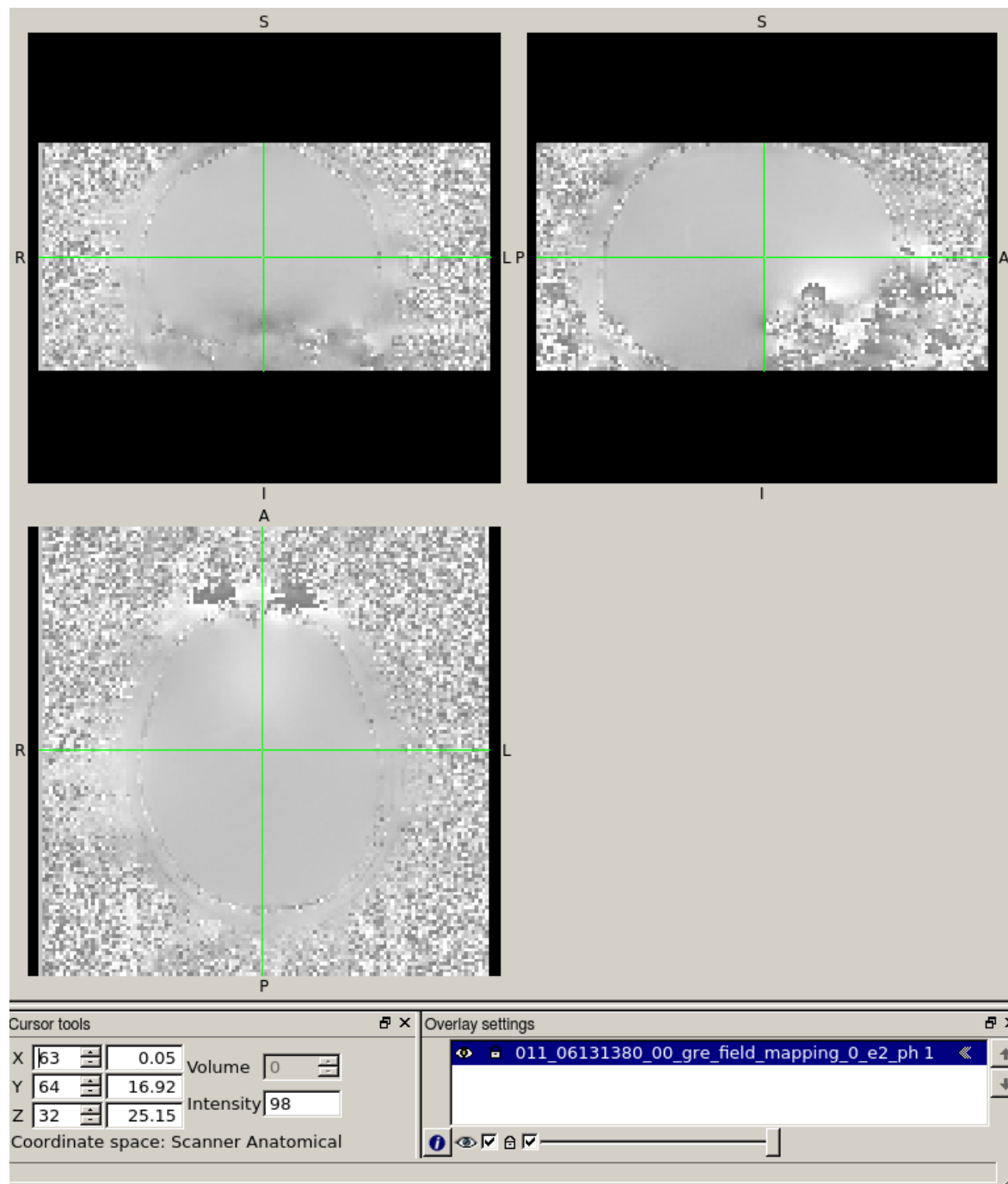
The **phase difference field map image (e2_ph)** looks like this. Again, there's only 1 volume.

Error jsonencode:

```
                                    yadnesh@DTI: ~/RADC_Bids

File  Edit  View  Search  Terminal  Help
Warning: Directory permission denied:
/media/varsha/B6DC3C44DC3BFD65/eeglab14_0_0b/functions/miscfunc
Warning: Directory permission denied:
/media/varsha/B6DC3C44DC3BFD65/eeglab14_0_0b/functions/timefreqfunc
Warning: Directory permission denied:
/media/varsha/B6DC3C44DC3BFD65/eeglab14_0_0b/functions/statistics
Warning: Directory permission denied:
/media/varsha/B6DC3C44DC3BFD65/eeglab14_0_0b/functions/popfunc
Warning: Directory permission denied:
/media/varsha/B6DC3C44DC3BFD65/eeglab14_0_0b/functions/studyfunc
Warning: Directory permission denied:
/media/varsha/B6DC3C44DC3BFD65/eeglab14_0_0b/functions/guifunc
Warning: Directory permission denied:
/media/varsha/B6DC3C44DC3BFD65/eeglab14_0_0b/functions/sigprocfunc
Warning: Directory permission denied:
/media/varsha/B6DC3C44DC3BFD65/eeglab14_0_0b/functions
Warning: Directory permission denied:
/media/varsha/B6DC3C44DC3BFD65/eeglab14_0_0b/functions/adminfunc

To get started, type one of these: helpwin, helpdesk, or demo.
For product information, visit www.mathworks.com.


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1
Example in:
/home/yadnesh/RADC_Bids/BIDS/BIDS_Subject1/tmp_dcm2bids/helper
Undefined function or variable 'jsonencode'.

Error in Automate (line 112)
    config_json = jsonencode(config);

Error in run (line 96)
evalin('caller', [script ';']);

>>
```

I am getting this error: Undefined function or variable 'jsonencode'.
It maybe because there are several warnings when I run the script saying Directory
permission denied.
I ran the Automate.m script using the following command
matlab -nodisplay -nosplash -nodesktop -r
"run('/home/yadnesh/RADC_Bids/Automate.m');exit;"

I also tried with sudo but then I'm getting

```
File  Edit  View  Search  Terminal  Help

Warning: Name is nonexistent or not a directory: /media/varsha/B6DC3C44DC3BFD65/eeglab14_0_0b
Warning: Name is nonexistent or not a directory: /media/varsha/B6DC3C44DC3BFD65/eeglab14_0_0b/plugins/firfilt1.6.2
Warning: Name is nonexistent or not a directory: /media/varsha/B6DC3C44DC3BFD65/eeglab14_0_0b/plugins/dipfit2.3
Warning: Name is nonexistent or not a directory: /media/varsha/B6DC3C44DC3BFD65/eeglab14_0_0b/plugins
Warning: Name is nonexistent or not a directory: /media/varsha/B6DC3C44DC3BFD65/eeglab14_0_0b/functions/javachatfunc
Warning: Name is nonexistent or not a directory: /media/varsha/B6DC3C44DC3BFD65/eeglab14_0_0b/functions/resources
Warning: Name is nonexistent or not a directory: /media/varsha/B6DC3C44DC3BFD65/eeglab14_0_0b/functions/miscfunc
Warning: Name is nonexistent or not a directory: /media/varsha/B6DC3C44DC3BFD65/eeglab14_0_0b/functions/timefreqfunc
Warning: Name is nonexistent or not a directory: /media/varsha/B6DC3C44DC3BFD65/eeglab14_0_0b/functions/statistics
Warning: Name is nonexistent or not a directory: /media/varsha/B6DC3C44DC3BFD65/eeglab14_0_0b/functions/popfunc
Warning: Name is nonexistent or not a directory: /media/varsha/B6DC3C44DC3BFD65/eeglab14_0_0b/functions/studyfunc
Warning: Name is nonexistent or not a directory: /media/varsha/B6DC3C44DC3BFD65/eeglab14_0_0b/functions/guifunc
Warning: Name is nonexistent or not a directory: /media/varsha/B6DC3C44DC3BFD65/eeglab14_0_0b/functions/sigprocfunc
Warning: Name is nonexistent or not a directory: /media/varsha/B6DC3C44DC3BFD65/eeglab14_0_0b/functions
Warning: Name is nonexistent or not a directory: /media/varsha/B6DC3C44DC3BFD65/eeglab14_0_0b/functions/adminfunc


To get started, type one of these: helpwin, helpdesk, or demo.
For product information, visit www.mathworks.com.


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1
Warning: Directory already exists.
> In Automate (line 29)
  In run (line 96)
Warning: Directory already exists.
> In Automate (line 35)
  In run (line 96)
No handlers could be found for logger "dcm2bids.dcm2niix"
Example in:
/home/yadnesh/RADC_Bids/BIDS/BIDS_Subject1/tmp_dcm2bids/helper
Undefined function or variable 'jsonencode'.

Error in Automate (line 112)
    config_json = jsonencode(config);
```
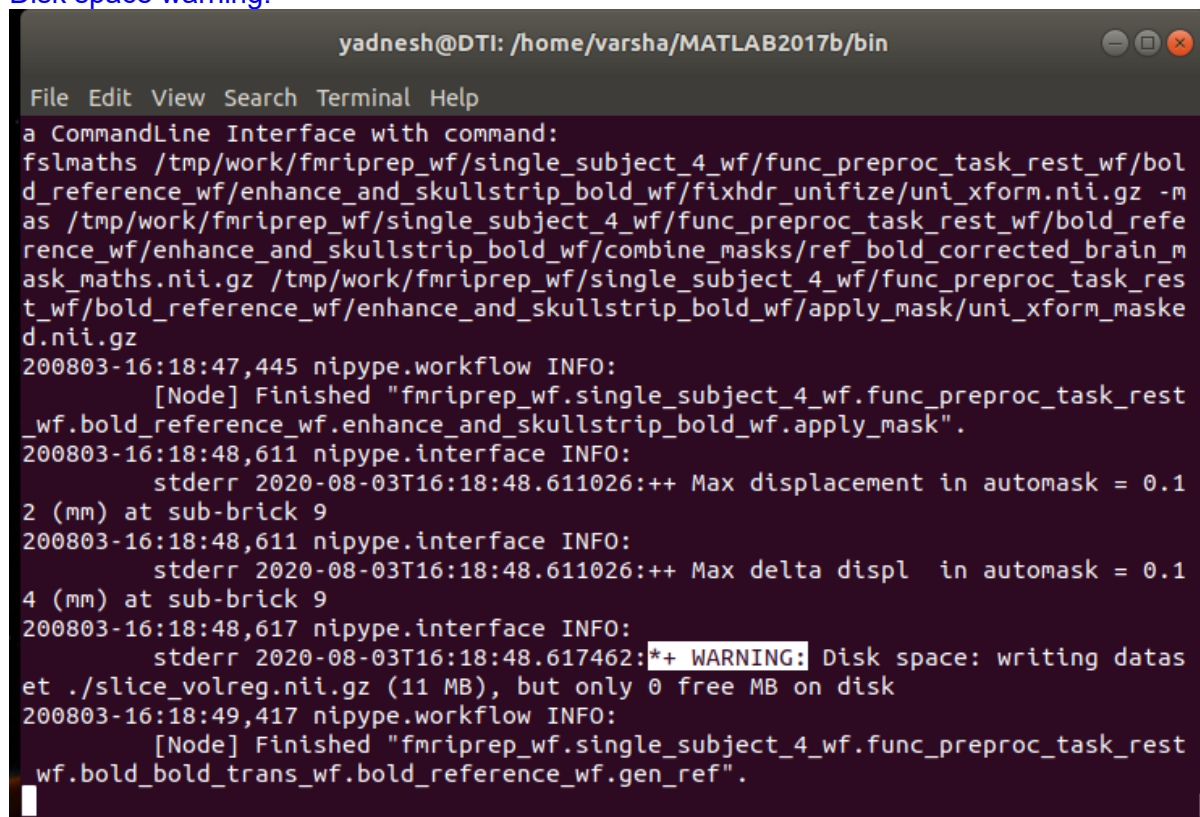
[f]

The directory already exists warning is because the BIDS directory got formed in an earlier
run and I did not delete it. But still the error is Undefined function or variable 'jsonencode'

Disk space warning:


```
                    yadnesh@DTI: /home/varsha/MATLAB2017b/bin

File  Edit  View  Search  Terminal  Help
a CommandLine Interface with command:
fslmaths /tmp/work/fmriprep_wf/single_subject_4_wf/func_preproc_task_rest_wf/bol
d_reference_wf/enhance_and_skullstrip_bold_wf/fixhdr_unifize/uni_xform.nii.gz -m
as /tmp/work/fmriprep_wf/single_subject_4_wf/func_preproc_task_rest_wf/bold_refe
rence_wf/enhance_and_skullstrip_bold_wf/combine_masks/ref_bold_corrected_brain_m
ask_maths.nii.gz /tmp/work/fmriprep_wf/single_subject_4_wf/func_preproc_task_res
t_wf/bold_reference_wf/enhance_and_skullstrip_bold_wf/apply_mask/uni_xform_maske
d.nii.gz
200803-16:18:47,445 nipype.workflow INFO:
        [Node] Finished "fmriprep_wf.single_subject_4_wf.func_preproc_task_rest
_wf.bold_reference_wf.enhance_and_skullstrip_bold_wf.apply_mask".
200803-16:18:48,611 nipype.interface INFO:
        stderr 2020-08-03T16:18:48.611026:++ Max displacement in automask = 0.1
2 (mm) at sub-brick 9
200803-16:18:48,611 nipype.interface INFO:
        stderr 2020-08-03T16:18:48.611026:++ Max delta displ  in automask = 0.1
4 (mm) at sub-brick 9
200803-16:18:48,617 nipype.interface INFO:
        stderr 2020-08-03T16:18:48.617462:*+ WARNING: Disk space: writing datas
et ./slice_volreg.nii.gz (11 MB), but only 0 free MB on disk
200803-16:18:49,417 nipype.workflow INFO:
        [Node] Finished "fmriprep_wf.single_subject_4_wf.func_preproc_task_rest
_wf.bold_bold_trans_wf.bold_reference_wf.gen_ref".
```

df -h command

```
                          yadnesh@DTI: ~                        ⊖ ▭ ✕

File  Edit  View  Search  Terminal  Help
 * Management:      https://landscape.canonical.com
 * Support:         https://ubuntu.com/advantage


102 packages can be updated.
88 updates are security updates.

Last login: Mon Aug  3 18:24:39 2020 from 10.3.1.44
yadnesh@DTI:~$ ls
BIDS  examples.desktop  RADC_Bids
yadnesh@DTI:~$ df -h
Filesystem      Size  Used Avail Use% Mounted on
udev             16G     0   16G   0% /dev
tmpfs           3.2G  9.9M  3.2G   1% /run
/dev/sda6       326G  309G  646M 100% /
tmpfs            16G  220K   16G   1% /dev/shm
tmpfs           5.0M  4.0K  5.0M   1% /run/lock
tmpfs            16G     0   16G   0% /sys/fs/cgroup
cgmfs           100K     0  100K   0% /run/cgmanager/fs
tmpfs           3.2G   60K  3.2G   1% /run/user/1000
tmpfs           3.2G     0  3.2G   0% /run/user/1009
tmpfs           3.2G     0  3.2G   0% /run/user/1014
tmpfs           3.2G     0  3.2G   0% /run/user/1015
yadnesh@DTI:~$
```

[g][h]
sda is full. But all the output files were created for all 4 subjects.

[a]Hi, the last line in your description is exactly what is causing this fmriprep error. To perform fMRI preprocessing, we require both the functional and structural (T1) scans. From running the command myself, I see that the DICOM folder for the sample subject only contains fMRI data, and does not have T1 data at all. I'll upload a new sample subject which has both modalities present, so you can try it out.
[b]Ok thanks.
[c]Did you try to download data for the same ADNI subject that I had provided as a sample? For some subjects, the magnitude images are just not available. However for this subject (003_S_6258), all 3 files are available. Please check the image I have added below your question (full image and close up) You will find 3 fieldmapping images. Select all of them prior to performing the DICOM download
[d]Yes, this means the process has been completed. Just to confirm, see of the visual quality assessment report (.html) has been generated in the output folder.

Additionally, see if the output folders have the same files shown in the example in the documentation I have provided (instructions for dcm2bids)

[e]Answers provided directly in document

[f]The version of Matlab required for this command is 2017b or higher.

The default version in the parker server is 2015a

please use the following commands in the parker server to open up Matlab 2017b.

cd /home/varsha/MATLAB2017b/bin/

and then type in ./matlab

[g]The disk space is limited, so the only way here is to run the command for a few subject visits at a time, move out the output folders into a different location and move in the new raw data.

I'll talk to SD about using a different server in the meantime

[h]okay