

# How to convert dicom to BIDS for RESSTORE

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**USAGE:** This document describes how to convert dicom files to the BIDS format for the study RESSTORE.

## PREREQUISITES:




- verify that you use python3 or else replace all the commands with python3 by python
- install dcm2niix
- download the library dcm2bids and the two files 'add\_data.py' and 'config.json'

## DISCLAIMERS:

- The terms visit and session refer to the same thing and should have the same numbers.
  - The following instructions allow you to start from scratch. To update the database when a new patient or visit is added you just have to do the STEP 4.
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**STEP 0:** To verify that the `config.json` files match with the description of your DICOM files and modify them if necessary, you need to:

**STEP 1:** Create a working directory containing a combination of Python and shell commands, including 'add\_data.py' script and 'config.json' file and a folder BIDS\_sourcedata which will contain all the dicom files. The directory should look as described below:

	BIDS_sourcedata	3 éléments
	add_data.py	4,0 ko
	config.json	4,8 ko





**STEP 2:** Organize your BIDS\_sourcedata folder as described below. Customize the directory structure so that each subject has a folder named "subject-XXX" containing subfolders for each visit entitled "visit-XX", and ensure **NO** `.par` or `.rec` files are included (if there is one, delete the parrec directory).

**Important:** name the directories as shown.

- Create folders for each subject (`subject-XXX`).
- Inside each subject folder, create subfolders for each visit (`visit-XX`).

```
BIDS_sourcedata/  
├─ subject-001/  
│   ├─ visit-02/  
│   │   └─ DICOM files for patient 001 for visit 02  
│   └─ visit-05/  
│       └─ DICOM files for patient 001 for visit 05  
├─ subject-002/  
│   └─ visit-02/  
│       └─ DICOM files for patient 002 for visit 02  
│   └─ visit-05/  
│       └─ DICOM files for patient 002 for visit 05
```

For example:











Nom	▼	Taille
 subject-001		2 éléments
 subject-002		2 éléments
Nom	▼	Taille
 visit-02		13 éléments
 visit-05		5 éléments

**STEP 3:** Create an output directory and organize it by using the following script:

```
mkdir OUTPUT_DIR
```

```
dcm2bids_scaffold -o OUTPUT_DIR
```

The OUTPUT\_DIR should look like this:

Nom	▼	Taille
 code		0 élément
 derivatives		0 élément
 sourcedata		0 élément
 tmp_dcm2bids		1 élément
 CHANGES		85 octets
 dataset_description.json		261 octets
 participants.json		543 octets
 participants.tsv		90 octets
 README		5,6 ko
 .bidsignore		13 octets

**STEP 4:** Run the code with the following script:

```
python3 add_data.py -s /path/to/BIDS_sourcedata/ -o /path/to/OUTPUT_DIR -c  
/path/to/config.json
```

This step is a bit long. It's important to check the pairing at the end. If the output message indicates 'no pairing' for a useful file you should verify your config.json file. For instance:

```
INFO | SIDECAR PAIRING
INFO | sub-002_ses-05_T1w <- 201_visit-05_3D_T1_MPRAGE_160503_20240506172711
INFO | No Pairing <- 202_visit-05_Cor_20240506172711
```

The dicom file corresponding to the T1 for the subject 002, visit 05 has successfully been converted to BIDS format. However, the "visit-05\_Cor" has not. If it's not a useful file, ignore the message. If it is, try the additional step.

**ADDITIONAL STEP IF SOMETHING DOESN'T WORK :** You probably need to edit the config.json file. To do so you can do a first conversion of your problematic dicom with this command:

```
mkdir JSON_DIR
```

```
dcm2niix -o /path/to/JSON_DIR
/path/to/the/folder/of/one/specific/visit/for/one/specific/subject
```

Be careful this command only deals with one patient at each time. Once this step is done, the JSON\_DIR looks like this:

Volume de 500 GB / data / resstore_1b / BIDS_M1 / JSON_DIR	
Nom	Taille
01-001-V2_3D_FLAIR_Reco0.5_20231106180026_301.json	2,1 ko
01-001-V2_3D_FLAIR_Reco0.5_20231106180026_301.nii	201,3 Mo
01-001-V2_3D_pCASL_FOV_FH125_20231106180026_901_real.json	2,0 ko
01-001-V2_3D_pCASL_FOV_FH125_20231106180026_901_real.nii	205,2 ko
01-001-V2_3D_T1_MPRAGE_160503_20231106180026_201.json	2,0 ko
01-001-V2_3D_T1_MPRAGE_160503_20231106180026_201.nii	25,2 Mo
01-001-V2_Angio_s3DI_MC_20231106180026_801.json	2,1 ko
01-001-V2_Angio_s3DI_MC_20231106180026_801.nii	32,0 Mo
01-001-V2_Body-3.75mm_MPM-T1-PDw_20231106180026_1301_e6.json	2,0 ko
01-001-V2_Body-3.75mm_MPM-T1-PDw_20231106180026_1301_e6.nii	2,9 Mo
01-001-V2_Body-3.75mm_MPM-T1-PDw_20231106180026_1301_e6a.json	2,0 ko
01-001-V2_Body-3.75mm_MPM-T1-PDw_20231106180026_1301_e6a.nii	2,9 Mo
01-001-V2_DTI-6dir_APA_MB2_20231106180026_501.bval	32 octets
01-001-V2_DTI-6dir_APA_MB2_20231106180026_501.bvec	170 octets
01-001-V2_DTI-6dir_APA_MB2_20231106180026_501.json	2,0 ko
01-001-V2_DTI-6dir_APA_MB2_20231106180026_501.nii	18,4 Mo
01-001-V2_DTI-6dir_APP_MB2_20231106180026_401.bval	32 octets
01-001-V2_DTI-6dir_APP_MB2_20231106180026_401.bvec	168 octets

First verify that your file has been successfully converted to a JSON format.

Then, Ensure the file aligns with the specifications in the config.json file. This includes:

- SeriesDescription: Confirm that the description matches.
- Name: Verify that the name is correct.
- Suffix: Check that the suffix is appropriate and accurate.

**Important:** For the DWI sequence, make sure to add the phase encoding direction in the JSON config file (with special attention on Philips NMR machines).

- For PA direction the phase encoding is “j”
- For AP direction the phase encoding is “j-”

Ex:

```
{
  "datatype": "dwi",
  "suffix": "dwi",
  "custom_entities": "acq-abcd2_dir-PA",
  "criteria": {
    "SeriesDescription": "DTI 2_2mm"
  },
  "sidecar_changes": {
    "PhaseEnPhasecodingDirection": "j"
  }
},
```

**HOW TO SEE ALL THE JSON FILES :** Create an intermediate JSON directory and run the code with the following script:



















```
mkdir JSON_DIR
```

```
dcm2niix -o dossier_stockage_json_intermediaire chemin_d'accès_fichier_patient
```

**for example:**

```
dcm2niix -o '/Path/toJSON_DIR' '/Path/to/BIDS_M1/01-001-V2'
```

The JSON directory will look like this:

Volume de 500 GB / data / resstore_1b / BIDS_M1 / JSON_DIR		:	Q	
Nom				Taille
 01-001-V2_3D_FLAIR_Reco0.5_20231106180026_301.json				2,1 ko
 01-001-V2_3D_FLAIR_Reco0.5_20231106180026_301.nii				201,3 Mo
 01-001-V2_3D_pCASL_FOV_FH125_20231106180026_901_real.json				2,0 ko
 01-001-V2_3D_pCASL_FOV_FH125_20231106180026_901_real.nii				205,2 ko
 01-001-V2_3D_T1_MPRAGE_160503_20231106180026_201.json				2,0 ko
 01-001-V2_3D_T1_MPRAGE_160503_20231106180026_201.nii				25,2 Mo
 01-001-V2_Angio_s3DI_MC_20231106180026_801.json				2,1 ko
 01-001-V2_Angio_s3DI_MC_20231106180026_801.nii				32,0 Mo
 01-001-V2_Body-3.75mm_MPM-T1-PDw_20231106180026_1301_e6.json				2,0 ko
 01-001-V2_Body-3.75mm_MPM-T1-PDw_20231106180026_1301_e6.nii				2,9 Mo
 01-001-V2_Body-3.75mm_MPM-T1-PDw_20231106180026_1301_e6a.json				2,0 ko
 01-001-V2_Body-3.75mm_MPM-T1-PDw_20231106180026_1301_e6a.nii				2,9 Mo
 01-001-V2_DTI-6dir_APA_MB2_20231106180026_501.bval				32 octets
 01-001-V2_DTI-6dir_APA_MB2_20231106180026_501.bvec				170 octets
 01-001-V2_DTI-6dir_APA_MB2_20231106180026_501.json				2,0 ko
 01-001-V2_DTI-6dir_APA_MB2_20231106180026_501.nii				18,4 Mo
 01-001-V2_DTI-6dir_APP_MB2_20231106180026_401.bval				32 octets
 01-001-V2_DTI-6dir_APP_MB2_20231106180026_401.bvec				168 octets

## STUDIES FOR EACH PATIENT:

With the provided config.json file, for each patient after conversion, the following files will be organized according to BIDS format:

- **‘anat’ for anatomical data**
  - **T1:** This may include 3D T1, sT1w, MPRAGE.
  - **FLAIR:** 3D FLAIR.
- **‘dwi’ for diffusion data and ‘fmap’ for field map data**

**Two Diffusion protocols are used:**

1- Hermes (single shell) with a ‘dwi\_h’ directory including DTI 60dir file and a ‘fmap\_h’ directory including DTI 6dir APA, DTI 6dir APP.

2- **ABCD** (multishell) with a ‘dwi’ directory including DTI 1 and DTI 2 files and a ‘fmap’ directory including DTI Fieldmap A and DTI Fieldmap P. In case a patient had both studies, all the corresponding files will be present.

- **‘func’ for functional data:** This is an optional file located within the func folder, which may include task-related fMRI (e.g. Left Hand or Paretic Hand tasks) or resting-state fMRI.