PLEASE NOTE THIS DOCUMENT HAS BEEN FROZEN AND YOU SHOULD VISIT https://bids-specification.readthedocs.io/en/bep-009/04-modality-specific-files/09-positron-emission-tomography.html AND THE CORRESPONDING PULL REQUEST https://github.com/bids-standard/bids-specification/pull/633 INSTEAD

BIDS positron emission tomography extension open for public commentary

We are happy to announce that the Positron emission tomography BIDS extension is finally nearing its completion. Hence, we are seeking final community feedback for the PET BIDS standard. We are looking for feedback on GitHub and specifically to the BIDSPET extension proposal: https://github.com/bids-standard/bids-specification/pull/633

We have also developed an extension for the validator https://github.com/bids-standard/bids-validator/pull/1088 and added PET examples into BIDS examples https://github.com/bids-standard/bids-examples/tree/bep009_pet which can be viewed on GitHub.

We are looking forward to hear from all of you,

Melanie

BIDS Extension Proposal 9 (BEP009): Positron Emission Tomography (PET)

version 0.0.1 (working copy)

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Progress/contribution statement

We are currently in a finalizing state of this BEP, mainly finishing the standard and developing the PET BIDS validator before we can proceed with a pull request to the main BIDS. You can download examples of PET BIDS datasets consisting of full 4D TACs, blood data, and MRI data (please see below). Please provide suggestions for improving/changing the standard in this Google Doc or reach out to mganz@nru.dk on how you can contribute.

This document contains a draft for the PET-BIDS data structure. It is a community effort to define standards in data / metadata storage for the field of Positron Emission Tomography. This is a working document in draft stage and any comments are welcome.

This specification is an extension of BIDS, and general principles are shared. The specification should work for many different settings and facilitate the integration with other imaging methods.

To see the original BIDS specification, see this link. This document inherits all components of the original specification (e.g. how to store imaging data, events, stimuli and behavioral data), and should be seen as an extension of it, not a

replacement.

Example datasets:

1) Example 1
This dataset consists of a single dynamic PET measurement of a pig using [11C]CIMBI-36 to measure serotonin 2A availability. There are arterial measurements available for this tracer.
Link: https://www.dropbox.com/sh/m4ulnszi537uovz/AABCmZDLjTVRpJayvA529R8La?dl=0

2) Example 2
This dataset consists of a single dynamic PET measurement of a human brain using [11C]DASB to measure serotonin transporter availability. An anatomical T1-weighted MRI is also available. There are no arterial measurements available for this tracer.
Link: https://www.dropbox.com/sh/nwkskaagh16h2x7/AACoxy-Pnmi3uSIsay34akq3a?dl=0

1 Table of Contents

2 Detailed file description

As specified above, this extension is relevant for PET imaging and its associated data, such as blood data. In addition, the extension is in accordance with the guidelines for reporting and sharing brain PET data (Knudsen et al. 2020, [1]). If you want to share structural magnetic resonance (MR) images with your PET data, please distribute them according to the original BIDS specification (https://bids-specification.readthedocs.io/en/stable). Please pay specific attention to the format the MR images are in, such as if they have been unwarped in order to correct for gradient non-linearities. There is a specific field in the MRI BIDS (https://bids-specification.readthedocs.io/en/stable/04-modality-specific-files/01-magnetic-resonance-imaging-data.html) called “NonlinearGradientCorrection” which indicates this. The reason for this is that the MRI needs to be corrected for nonlinear gradients in order to fit the accompanying PET scans for co-registration [1, 2]. In general, SI units must be used (we refer to https://bids-specification.readthedocs.io/en/stable/99-appendices/05-units.html) and we recommend to use the CMIXF style formatting for SI units e.g. "kBq/mL" rather than "kilobecquerel per ml". An overview of a common PET experiment (with blood data) can be seen in Figure 1, defined on a single time scale relative to a predefined “time zero” (which should be defined either to be scan start or injection time; please note an exception to this definition is possible if a pharmacological within-scan challenge is performed).

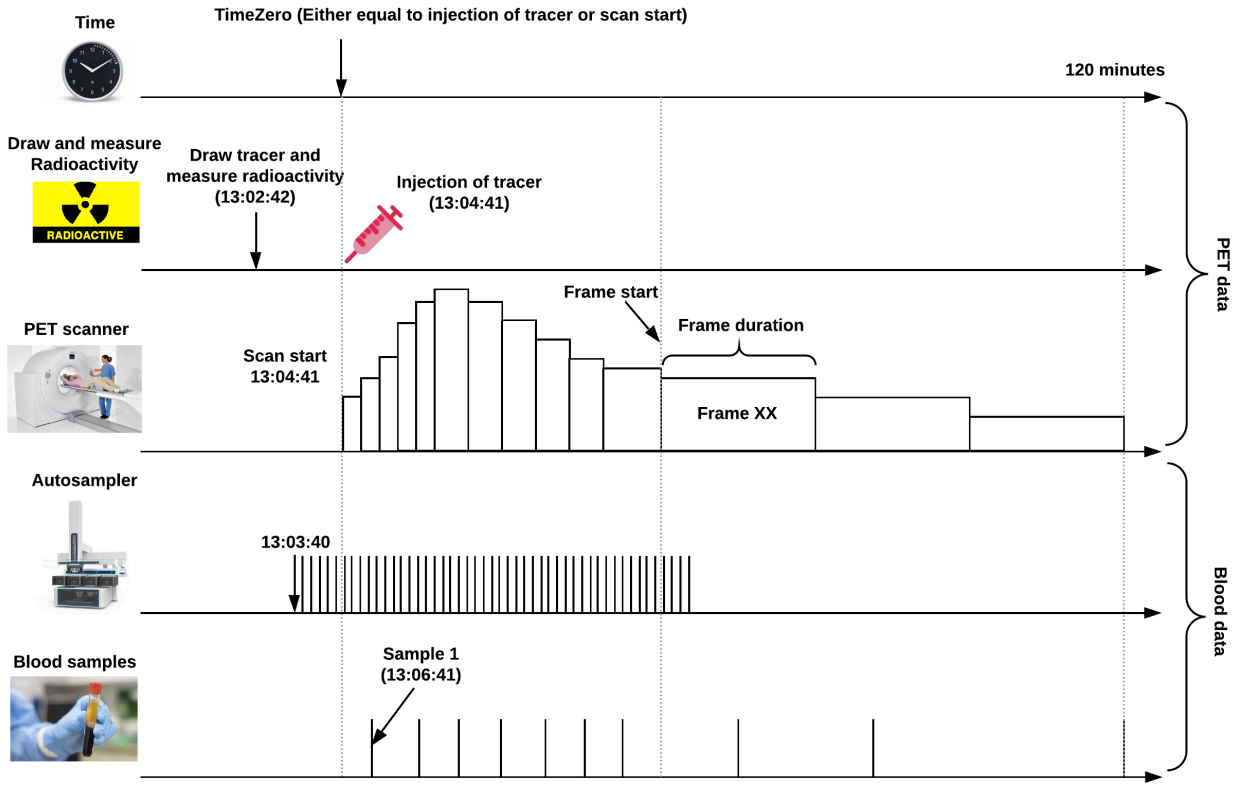

Figure 1: Overview of a common PET experiment, including blood measurements, and defined on a common time scale. Note, “time zero”can either be defined as time of injection or scan start, and all the PET and blood data should be decay-corrected to this time point. Furthermore, although in this example tracer injection coincides with scan start, this is not always the case and hence we allow for the flexibility of specifying either time of injection or scan start as “time zero”.

2.1 PET Imaging data

Template:

```
sub-<participant_label>/
      [ses-<session_label>/]
      pet/
            sub-<participant_label>[_ses-<session_label>][_task-<task_label>]
      [_acq-<label>][_rec-<label>][_run-<index>]_pet.nii[.gz]

            sub-<participant_label>[_ses-<session_label>][_task-<task_label>]
      [_acq-<label>][_rec-<label>][_run-<index>]_pet.json
```

PET data belongs in the `/pet` folder. PET imaging data will be stored in 4D (or 3D if only one volume was acquired) NifTI files with `_pet` suffix. Volumes should be stored in chronological order (the order they were acquired in).

Multiple sessions (visits) are encoded by adding an extra layer of directories and file names in the form of `ses-<label>`. Session labels can consist only of alphanumeric characters [a-zA-Z0-9] and should be consistent across subjects. If numbers are used in session labels we recommend using zero padding (for example ses-01, ses-11 instead of ses-1, ses-11). This makes results of alphabetical sorting more intuitive. The extra session layer (at least one /ses-<label> subfolder) should be added for all subjects if at least one subject in the dataset has more than one session. Skipping the session layer for only some subjects in the dataset is not allowed. If a /ses-<label> subfolder is included as part of the directory hierarchy, then the same ses-<label> tag must also be included as part of the file names themselves. In general, we assume that a new session wrt PET starts with either a new injection (probably most common case) or with the subject being taken out of the scanner (same injection, but subject leaves the scanner and returns). However, for example, if a subject has to leave the scanner room and then be re-positioned on the scanner bed e.g. to use the bathroom, the set of PET acquisitions will still be considered as a session and match sessions acquired in other subjects. Similarly, in situations where different data types are obtained over several visits (for example FDG PET on one day followed by amyloid PET a couple days after) those can be grouped in one session. Please see the difference with the `run-<label>` below.

Wrt the `task-<label>`, data is arranged in a similar way as task-based and resting state BOLD fMRI data. In case of studies using combined PET/fMRI, subject-specific tasks may be carried

out during the acquisition within the same session. Therefore, it is possible to specify task-<label> in accordance with the fMRI data. For more information please see https://bids-specification.readthedocs.io/en/stable/04-modality-specific-files/01-magnetic-resonance-imaging-data.html#task-including-resting-state-imaging-data.

In case of studies with multiple acquisitions per subject using different tracers, the `acq-<label>` must be used to distinguish between different tracers. Please keep in mind that the label used is arbitrary and each file requires a separate JSON sidecar with details of the tracer used (see below). Examples are e.g. acq-18FFDG for fludeoxyglucose, acq-11CPIB for Pittsburgh compound B, etc.

The reconstruction key (`rec-<label>`) has four reserved values: `acdyn`, for reconstructions with attenuation correction of dynamic data; `acstat`, for reconstructions with attenuation correction of static data; `nacdyn`, for reconstructions without attenuation correction of dynamic data; and `nacstat`, for reconstructions without attenuation correction of static data. Further details regarding reconstruction are in the _pet.json file. In case of multiple reconstructions of the data with the same type, we allow for using a number after the <label> in order to distinguish, e.g. `rec-acdyn1` and `rec-acdyn2`.

The `run` entity is used if one scan type/contrast is repeated multiple times within the same scan session/visit. If several scans of the same modality are acquired they MUST be indexed with a key-value pair: _run-1, _run-2, _run-3 etc. (only integers are allowed as run labels). When there is only one scan of a given type the run key MAY be omitted. An example of this would be two consecutive scans performed within the same session, e.g. two short FDG scans right after each other. It is our assumption that the `run-<label>` is used in PET for the cases where the subject does not leave the scanner. Otherwise, we refer to the `ses-<label>` definition.

In addition to the imaging data a `_pet.json` sidecar file needs to be provided. The included metadata are divided into sections described below.

2.1.1 The "Info" section

This section is mandatory and contains general information about the imaging experiment. Some of the fields are marked optional (MAY), e.g. anaesthesia; for those fields a BIDS PET validator will not throw an error even if they are not present. Note, although bodyweight is a recommended information in (Knudsen et al. 2020, JCBFM [1]), this consists of meta information at the participant level and should hence be part of the `participants.tsv` or `session.tsv` file in case of multiple measurements.

Data name:	Data description:	Data status:	Data type(s):	Example values:
Manufacturer	Scanner manufacturer	MUST	string	"Siemens"
ManufacturersModelName	PET scanner model name	MUST	string	
Anaesthesia	Details of anaesthesia used, if any.	MAY	string	

InstitutionName	The name of the institution in charge of the equipment that produced the composite instances. Corresponds to DICOM Tag 0008, 0080 *InstitutionName*.	RECOMMENDED	string	
InstitutionAddress	The address of the institution in charge of the equipment that produced the composite instances. Corresponds to DICOM Tag 0008, 0081 *InstitutionAddress*.	RECOMMENDED		
InstitutionalDepartmentName	The department in the institution in charge of the equipment that produced the composite instances. Corresponds to DICOM Tag 0008, 1040 *Institutional Department Name*.	RECOMMENDED		
BodyPart	Name of the organ / body region scanned.	RECOMMENDED	string	"brain", "neck", "torso","cardiac","gut", "hip","leg","knee","foot", "hand","arm","lung"
Unit	Unit of the image file; please see BIDS main spec section 6. SI unit for radioactivity (Becquerel) should be used.	MUST	string	“Bq/ml”
TracerName	Name of the tracer compound used	MUST	string	"CIMBI-36", "raclopride"
TracerRadLex	ID of the tracer compound from the RadLex Ontology.	RECOMMENDED	string	
TracerSNOMED	ID of the tracer compound from the SNOMED Ontology (subclass of Radioactive isotope).	RECOMMENDED	string	
TracerRadionuclide	Radioisotope labelling tracer.	MUST	string	"C11", "O15", "F18", "N13"
TracerMolecularWeight	Accurate molecular weight of the tracer used.	RECOMMENDED	number	
TracerMolecularWeightUnit	Unit of the molecular weights measurement.	RECOMMENDED	string	“g/mol”
PharmaceuticalName	Name of pharmaceutical coadministered with tracer.	MAY	string	
PharmaceuticalDoseAmount	Dose amount of pharmaceutical coadministered with tracer.	MAY	number / string	
PharmaceuticalDoseUnit	Unit format relating to pharmaceutical dose.	RECOMMENDED	string	"mg", "mg/kg", "ug", “ug/kg”

PharmaceuticalDose Regimen	Details of the pharmaceutical dose regimen. Either adequate description or short-code relating to regimen documented elsewhere.	RECOMMENDED	string	"single IV bolus", "single oral bolus", "IV infusion"
PharmaceuticalDose Time	Time of administration of pharmaceutical dose, relative to time zero (please see below). For an infusion, this should be a vector with two elements specifying the start and end of the infusion period. For more complex dose regimens, the regimen description should be complete enough to enable unambiguous interpretation of the DoseTime vector. Unit format of the specified pharmaceutical dose time should be seconds.	RECOMMENDED	number / array	

2.1.2 The "Radiochem" section

This section is mandatory and contains information regarding the radioactive material used in the experiment.

Data name:	Data description:	Data status:	Data type(s):	Example values:
InjectedRadioactivity	Total amount of radioactivity injected into subject. Corresponds to DICOM Tag (0018,1074) *Radionuclide Total Dose*.	MUST	number	
InjectedRadioactivityUnit	Unit format of the specified injected radioactivity.	MUST	string	"MBq"
InjectedMass	Total mass of radiolabeled compound injected into subject. This can be derived as the ratio of the InjectedRadioactivity and MolarRadioactivity. *Note this is not required since not available for an FDG acquisition.	MUST	number	
InjectedMassUnit	Unit format of the mass of compound injected. *Note this is not required since not available for an FDG acquisition.	MUST	string	"µg","µmol"
InjectedMassPerWeight	Injected mass per kilogram bodyweight.	RECOMMENDED	number	

InjectedMassPerWeightUnit	Unit format of the injected mass per kilogram bodyweight.	RECOMMENDED	string	"µg/kg"
SpecificRadioactivity	Specific activity of compound injected. *Note this is not required since not available for an FDG acquisition.	MUST	number	
SpecificRadioactivityUnit	Unit format of specified specific radioactivity.*Note this is not required since not available for an FDG acquisition.	MUST	string	"Bq/g"
SpecificRadioactivityMeasTime	Time to which specific radioactivity measurement above applies in the default unit "hh:mm:ss".	RECOMMENDED	string	
MolarActivity	Molar activity of compound injected. Corresponds to DICOM Tag (0018,1077) *Radiopharmaceutical Specific Activity*.	RECOMMENDED	number	
MolarActivityUnit	Unit of the specified molar radioactivity.	RECOMMENDED	string	"Bq/mol"
MolarActivityMeasTime	Time to which molar radioactivity measurement above applies in the default unit "hh:mm:ss".	RECOMMENDED	string	
ModeOfAdministration	Mode of administration of the injection.	MUST	string	“bolus”, “infusion”, “bolus-infusion”
InfusionSpeed	If given, infusion speed.	RECOMMENDED	number	
InfusionSpeedUnit	Unit of infusion speed.	RECOMMENDED	string	“ml/s”
InjectedVolume	Injected volume of the radiotracer.	RECOMMENDED	number	
InjectedVolumeUnit	Unit of the injected volume of the radiotracer.	RECOMMENDED	string	“ml”
Purity	Purity of the radiolabeled compound.	RECOMMENDED	number	
PurityUnit	Unit of the radiochemical purity.	RECOMMENDED	string	"percent", "fraction"

2.1.3 The "Time" section

This section is mandatory and contains timing information about the imaging experiment.

Data name:	Data description:	Data status:	Data type(s):	Example values:
ScanDate	Date of scan in the default unit “yyyy:mm:dd”.	RECOMMENDED	string	time string
TimeZero	Time zero to which all scan and/or blood measurements have been	MUST	string	time string

	adjusted to, in the unit “hh:mm:ss”. This should be equal to InjectionStart or ScanStart.			
ScanStart	Time of start of scan wrt TimeZero in the default unit seconds.	MUST	number	
InjectionStart	Time of start of injection wrt TimeZero in the default unit seconds. This corresponds to DICOM Tag (0018,1042) converted to seconds relative to timezero.	MUST	number	
InjectionEnd	Time of end of injection wrt TimeZero in the default unit seconds.	RECOMMENDED	number	
FrameTimesStart	Start times for all frames relative to TimeZero in default unit seconds.	MUST	array of numbers	
FrameDuration	Time duration of each frame in default unit seconds. This corresponds to DICOM Tag (0018,1242) converted to seconds.	MUST	array of numbers	

2.1.4 The "Recon" section

This optional section includes information about the image reconstruction. All reconstruction specific parameters that are not specified, but one wants to include, should go into the ReconMethodParameterValues field.

Data name:	Data description:	Data status:	Data type(s):	Example values:
AcquisitionMode	Type of acquisition of the PET data.	MUST	string	”list mode”, ...
ImageDecayCorrected	Boolean flag specifying whether the image data have been decay-corrected.	MUST	Boolean	true, false
ImageDecayCorrectionTime	Point in time from which the decay correction was applied wrt TimeZero in the default unit seconds.	MUST	number	
ReconMethodName	Reconstruction method or algorithm.	MUST	string	"3d-op-osem", ...
ReconMethodParameterLabels	Names of reconstruction parameters.	MUST	array of strings	["subsets", "iterations", ...]
ReconMethodParameterUnit	unit of reconstruction parameters.	MUST	array of strings	["none", "none", ...]
ReconMethodParameterValues	Values of reconstruction parameters.	MUST	arrays of numbers	[21, 3, ...]

ReconMethodImplementationVersion	Identification for the software used, such as name and version.	RECOMMENDED	string	
ReconFilterType	Type of post-recon smoothing.	MUST	array of strings	["none"],["Shepp",” Z filter”], ...
ReconFilterSize	Kernel size of post-recon filter (FWHM).	MUST	array of numbers	
AttenuationCorrection	Short description of the attenuation correction method used.	MUST	string	
AttenuationCorrectionMethodReference	Reference paper for the attenuation correction method used.	RECOMMENDED	string	
ScaleFactor	Scale factor for each frame	RECOMMENDED	array of numbers	
ScatterFraction	Scatter fraction for each frame	RECOMMENDED	array of numbers	
DecayCorrectionFactor	Decay correction factor for each frame	RECOMMENDED	array of numbers	
PromptRate	Prompt rate for each frame	RECOMMENDED	array of numbers	
RandomRate	Random rate for each frame	RECOMMENDED	array of numbers	
SinglesRate	Singles rate for each frame	RECOMMENDED	array of numbers	

2.1.5 The "Blood" section

In order to simplify a distinction between PET data acquired with and without blood measurements, we have added a specific section detailing blood measurements in the `*_pet.json`. If blood data is available, meaning some of the “Avail” below with a given prefix are true, the following fields with the given prefix are required and at the same time we require the presence of a `*_blood.tsv` with a corresponding `*_blood.json` detailing the column content. If true, please see the section 2.2 Blood data.

Data name:	Data description:	Data status:	Data type(s):	Example values:
PlasmaAvail	Boolean that specifies if plasma measurements are available. If this is false, all of the plasma fields should be excluded	MUST	boolean	true, false
PlasmaFreeFraction	Measured free fraction in plasma, i.e. concentration of free compound in plasma	RECOMMENDED	number	

	divided by total concentration of compound in plasma.			
PlasmaFreeFractionMethod	Method used to estimate free fraction.	RECOMMENDED	string	
MetaboliteAvail	Boolean that specifies if metabolite measurements are available. If this is false, all of the metabolite fields should be excluded.	MUST	boolean	true, false
MetaboliteMethod	Method used to measure metabolites	MUST	string	“HPLC”, “Fraction Collector”, “SPE”
MetaboliteRecoveryCorrectionApplied	Metabolite recovery correction from the HPLC, for tracers where it changes with time postinjection. If “true” please include recovery fractions from the HPLC as a column in the table with blood data (section 2.2)	MUST	boolean	true, false
ContinuousBloodAvail	Boolean that specifies if continuous blood measurements are available. If this is false, all of the continuous blood fields should be excluded.	MUST	boolean	true, false
ContinuousBloodWithdrawalRate	The rate at which the blood was withdrawn from the subject. The unit of the specified withdrawal rate should be in ml/s.	RECOMMENDED	number	
ContinuousBloodTubingType	Description of the type of tubing used, ideally including the material and (internal) diameter.	RECOMMENDED	string	
ContinuousBloodTubingLength	The length of the blood tubing, from the subject to the detector in the default unit centimeter.	RECOMMENDED	number	
ContinuousBloodDispersionConstant	External dispersion time constant resulting from tubing in default unit seconds.	RECOMMENDED	number	
ContinuousBloodDispersionCorrected	Boolean flag specifying whether the continuous blood data have been dispersion-corrected.	MUST	boolean	true, false
DiscreteBloodAvail	Boolean that specifies if discrete blood measurements are available. If this is false, all of the discrete blood fields should be excluded.	MUST	boolean	true, false

DiscreteBloodHaematocrit	Measured haematocrit, i.e. the volume of erythrocytes divided by the volume of whole blood.	RECOMMENDED	number	
DiscreteBloodDensity	Measured blood density. Unit of blood density should be in g/ml.	RECOMMENDED	number	

2.1.6 Example

FILE: _pet.json


```
{
	"Manufacturer": "Siemens",
	"ManufacturersModelName": "High-Resolution Research Tomograph (HRRT, CTI/Siemens)",
	"BodyPart": "Brain",
	"Unit": "Bq/mL",
	"TracerName": "CIMBI-36",
	"TracerRadionuclide": "C11",
	"TracerMolecularWeight": 380.28,
	"TracerMolecularWeightUnit": "g/mol",
	"TracerInjectionType": "bolus",
	"InjectedRadioactivity": 573,
	"InjectedRadioActivityUnit": "MBq",
	"InjectedMass": 0.62,
	"InjectedMassUnit": "ug",
	"SpecificRadioactivity": 929.6,
	"SpecificRadioactivityUnit": "MBq/ug",
	"ModeOfAdministration": "bolus",
	"MolarActivity": 353.51,
	"MolarActivityUnit": "GBq/umol",
	"MolarActivityMeasTime": "13:04:42",
	"TimeZero": "13:04:42",
	"ScanStart": 0,
	"InjectionStart": 0,
	"FrameTimesStart": [0, 10, 20, 30, 40, 50, 60, 80, 100, 120, 140, 160, 180, 240, 300, 360, 420, 480, 540,
660, 780, 900, 1020, 1140, 1260, 1380, 1500, 1800, 2100, 2400, 2700, 3000, 3300, 3600, 3900, 4200, 4500, 4800,
5100, 5400, 5700, 6000, 6300, 6600, 6900],
	“FrameDuration": [10, 10, 10, 10, 10, 10, 20, 20, 20, 20, 20, 20, 60, 60, 60, 60, 60, 60, 120, 120, 120, 120,
120, 120, 120, 120, 300, 300, 300, 300, 300, 300, 300, 300, 300, 300, 300, 300, 300, 300, 300, 300, 300, 300, 300, 300],
	"AcquisitionMode": "list mode",
	"ImageDecayCorrected": "true",
	"ImageDecayCorrectionTime": 0,
	"ReconMethodName": "3D-OSEM-PSF",
	"ReconMethodParameterLabels": ["subsets","iterations"],
	"ReconMethodParameterUnit": ["none","none"],
	"ReconMethodParameterValues": [16,10],
	"ReconFilterType": "none",
	"AttenuationCorrection": "[137Cs]transmission scan-based",
	“PlasmaAvail”: “false”
	“MetaboliteAvail”: “false”
	“ContinuousBloodAvail: “false”
```

“DiscreteBloodAvail: “false”
}

2.2 Blood data

This section includes all data needed to perform blood analysis for PET data. The section may be omitted if blood measurements of radioactivity were not made. It contains the values and information regarding plasma samples, discrete blood samples, continuous blood samples from an autosampler, and metabolite fractions. All these measurements should be defined according to a single time-scale in relation to time zero defined by the PET data (Figure 1). Additionally, if blood and metabolite measurements were made one should always report radioactivity in plasma and corresponding parent fraction measurements, including fractions of radiometabolites. All definitions used below are in accordance with Innis et al. 2007 [3]. All method specific information related to the measurements can be stated in the field “description”.

Template:

```
sub-<participant_label>/
      [ses-<session_label>/]
      pet/
            sub-<participant_label>[_ses-<session_label>][_task-<task_label>]
      [_acq-<label>][_rec-<label>][_run-<index>]_recording-<label>_blood.tsv
            sub-<participant_label>[_ses-<session_label>][_task-<task_label>]
      [_acq-<label>][_rec-<label>][_run-<index>]_recording-<label>_blood.json
```

Blood data belongs in the `/pet` folder along with the corresponding PET data. However, the blood data also follows the inheritance principle (https://bids-specification.readthedocs.io/en/stable/02-common-principles.html#the-inheritance-principle) and may be moved to an upper level folder if it does not change e.g. with multiple reconstructions. The blood data is most often recorded using an autosampler for continuous blood samples, or manually for discrete blood samples. Therefore, the recording key (`recording-<label>`) has two reserved values: `continuous`, for continuous whole blood data measurements (2.2.4); and `discrete`, for discrete blood data, including whole blood (2.2.4), plasma (2.2.2), parent fraction and metabolite fractions (2.2.3). Blood data will be stored in tabular *.tsv files with a `_blood` suffix (https://bids-specification.readthedocs.io/en/stable/02-common-principles.html#tabular-files). The first column in the *.tsv file should be a time column (2.2.1), defined in relation to time zero defined by the _pet.json file. All other information relevant to the blood measurements are recommended, and can be added as an additional column. It is expected that all values are (if relevant) decay corrected to time zero.

2.2.1 Time

Data name:	Data description:	Data type(s):	Data status:	Example values:
ColumnName	time	string	MUST	

Description	Time in relation to time zero defined by the _pet.json	string	MUST	
Units	Unit of time steps	string	MUST	“s”

2.2.2 The "Plasma" section

This section may be omitted if discrete plasma measurements of radioactivity were not made. It contains information regarding discretely sampled plasma data.

Data name:	Data description:	Data type(s):	Data status:	Example values:
ColumnName	plasma_radioactivity	string	MUST	
Description	Radioactivity in plasma samples	string	MUST	
Units	Unit of plasma radioactivity		MUST	“kBq/ml”

2.2.3 The "Metabolite" section

This section may be omitted if metabolite measurements were not made. It may contain information regarding metabolite info, such as the following three column examples:

Data name:	Data description:	Data type(s):	Data status:	Example values:
ColumnName	metabolite_parent_fraction	string	MUST	
Description	Parent fraction of the radiotracer (0-1)	string	MUST	
Units	Unit of parent fraction	string	MUST	unitless

Data name:	Data description:	Data type(s):	Data status:	Example values:
ColumnName	metabolite_polar_fraction	string	RECOMMENDED	
Description	Polar metabolite fraction of the radiotracer (0-1)	string	RECOMMENDED	
Units	Unit of polar metabolite fraction	string	RECOMMENDED	unitless

Data name:	Data description:	Data type(s):	Data status:	Example values:
ColumnName	hplc_recovery_fractions	string	RECOMMENDED	
Description	HPLC recovery fractions (the fraction of activity that gets loaded onto the HPLC)	string	RECOMMENDED	
Units	Unit of recovery fractions	string	RECOMMENDED	unitless

2.2.4 The "WholeBlood" section

This section may be omitted if whole blood measurements of radioactivity were not made. It contains information regarding sampled whole blood data.

Data name:	Data description:	Data type(s):	Data status:	Example values:
ColumnName	whole_blood_radioactivity	string	RECOMMENDED	

Description	Radioactivity in whole blood samples	string	RECOMMENDED	
Units	Unit of radioactivity measurements in whole blood samples	string	RECOMMENDED	“kBq/ml”

2.2.6 Example

FILE: recording-discrete_blood.json

```
{
   "time": {
      "Description": "Time in relation to time zero defined by the _pet.json",
      "Units": "s"
   },
   "plasma_radioactivity": {
      "Description": "Radioactivity in plasma samples. Measured using COBRA counter.",
      "Units": "kBq/ml"
   },
   "whole_blood_radioactivity": {
      "Description": "Radioactivity in whole blood samples. Measured using COBRA counter.",
      "Units": "kBq/ml"
   },
   "metabolite_parent_fraction": {
      "Description": "Parent fraction of the radiotracer.",
      "Units": "unitless"
   },
   "metabolite_polar_fraction": {
      "Description": "Polar metabolite fraction of the radiotracer.",
      "Units": "unitless"
   },
   "metabolite_lipophilic_fraction": {
      "Description": "Lipophilic metabolite fraction of the radiotracer.",
      "Units": "unitless"
   }
}
```

FILE: recording-discrete_blood.tsv

time	plasma_radioactivity	whole_blood_radioactivity	metabolite_parent_fraction	metabolite_polar_fraction	metabolite_lipophilic_fraction
0	0	0	1	0	0
145	43.31	33.79	0.5749	0.1336	0.2914
292	48.96	37.42	0.3149	0.2746	0.4105
602	39.84	32.05	0.1469	0.3548	0.4983
1248	37.38	31.52	0.073	0.444	0.483
1785	36.40	28.83	0.078	0.429	0.493
2390	33.13	26.32	0.061	0.453	0.486
3059	30.83	25.22	0.049	0.473	0.478
4196	27.28	21.98	0.036	0.503	0.46
5407	22.70	19.49	0.032	0.523	0.445
7193	19.71	15.70	0.02	0.559	0.422

Figure 2: Caption of the corresponding _blood.tsv file.

3 Appendix I: Useful resources

This website is an extremely useful resource:
http://www.turkupetcentre.net/petanalysis/quantification.html

An extensive resource for background knowledge on kinetic modeling can be found here:
https://nru.dk/index.php/misc/category/3-pet-kinetic-course

4 References

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