IMPORT – JSON STRUCTURES

# Json 1 returned when zip is uploaded :

Once the file is uploaded, dicom data is extracted under *patients,* and if the generated subject identifier is found (in Shanoir db) a list of subjects is returned.

{

"fromDicomZip": true,

"fromShanoirUploader": false,

"fromPacs": false,

"patients": [{

"patientID": "10.03.04-19:02:35-STD-1.3.12.2.1107.5.2.36.40296",

"patientName": "DIR OL",

"patientBirthDate": "19870401",

"patientSex": "M",

"subject": {

"id": 1,

"name": "Doe"

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"studies": [{

"studyInstanceUID": "1.3.12.2.1107.5.2.36.40296.30000010030206191446800000091",

"studyDate": "20100304",

"studyDescription": "RECHERCHE^WIP NEURO",

"series": [{

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"seriesInstanceUID": "1.3.12.2.1107.5.2.36.40296.2010030419031359358071443.0.0.0",

"modality": "MR",

"protocolName": "localizer",

"seriesDescription": "localizer",

"seriesDate": "20100304",

"seriesNumber": "1",

"numberOfSeriesRelatedInstances": null,

"sopClassUID": "1.2.840.10008.5.1.4.1.1.4",

"isSpectroscopy": false,

"isMultiFrame": "false",

"equipment": {

"manufacturer": "SIEMENS",

"manufacturerModelName": "Verio",

"deviceSerialNumber": "40296"

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"isCompressed": false,

"nonImages": [],

"nonImagesNumber": "0",

"images": [{

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"seriesDescription": "tse\_vfl\_WIP607",

"seriesDate": "20100304",

"seriesNumber": "2",

"numberOfSeriesRelatedInstances": null,

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"path": "/tmp/7213521692999950655/SERIES/1.3.12.2.1107.5.2.36.40296.2010030419392596271473402.0.0.0/dataset0/IM000075",

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"path": "/tmp/7213521692999950655/SERIES/1.3.12.2.1107.5.2.36.40296.2010030419392596271473402.0.0.0/dataset0/IM000057",

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"path": "/tmp/7213521692999950655/SERIES/1.3.12.2.1107.5.2.36.40296.2010030419392596271473402.0.0.0/dataset0/IM000056",

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"echoNumber": "1"

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"path": "/tmp/7213521692999950655/SERIES/1.3.12.2.1107.5.2.36.40296.2010030419392596271473402.0.0.0/dataset0/IM000020",

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"echoNumbers": {

"echoNumber": "1"

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"imageOrientationPatient": {

"imageOrientationPatient": "-0.9998157117037"

}

}

],

"imagesNumber": "160"

}

]

}]

}]

}

# Json 2 for study/sc/centers/investigator :

Query rest service with Equipment info as parameter in order to set compatible flag for each study / study cards.

(the query result is also based on the user permissions in order to limit study list)

[{

"id": 1,

"name": "Study1",

"compatible": true,

"centers": [{

"id": 1,

"name": "Center 1",

"investigatorList": [{

"id": 1,

"name": "Investigator 1"

},

{

"id": 1,

"name": "Investigator 2"

}

]

},

{

"id": 2,

"name": "Center 2",

"investigatorList": [{

"id": 3,

"name": "Investigator 3"

},

{

"id": 4,

"name": "Investigator 4"

}

]

}

],

"studycards": [{

"id": 1,

"name": "StudyCard1",

"compatible": true,

"center": {

"id": 1,

"name": "Center 1",

"investigatorList": [{

"id": 1,

"name": "Investigator 1"

},

{

"id": 1,

"name": "Investigator 2"

}

]

}

},

{

"id": 2,

"name": "StudyCard2",

"compatible": false,

"center": {

"id": 2,

"name": "Center 2",

"investigatorList": [{

"id": 3,

"name": "Investigator 3"

},

{

"id": 4,

"name": "Investigator 4"

}

]

}

}

]

},

{

"id": 2,

"name": "Study2",

"compatible": false,

"centers": [{

"id": 1,

"name": "Center 1",

"investigatorList": [{

"id": 1,

"name": "Investigator 1"

},

{

"id": 1,

"name": "Investigator 2"

}

]

}]

}

]

## Comportement IHM

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Json 2 | Find y as compatible study card (in study A) | Find y,z as compatible study card (in study A) | Find y as compatible study card in study A  Find x as compatible study card in study B | Find y,z as compatible study card in study A  Find x as compatible study card in study B | Find something but nothing compatible | Find ∅ |
| IHM | select A as study  select y as study card | Select A as study  Offer choice to use for study card (y, z in study card list) | Offer choice to user for study.  , autoselect sc | Manual input for both | Manual input for both  Notify user of non compatible SC | Should not happen since the import button should be disabled  Note : same happen if user not allowed to import data |

# Json 3 for subject + rel subject study

Query Shanoir for all subject + rel subject study (if any) available

[{

"id": 1,

"identifier": "FFAADE12354355",

"name": "common name 1",

"subjectStudyList": {

"subjectId": 1,

"studyId": 1,

"physicallyInvolved": true,

"subjectType": "HEALTHY\_VOLUNTEER",

"subjectStudyIdentifier": "toto"

}

}, {

"id": 2,

"identifier": "FFAADE1235435",

"name": "common name 2",

"subjectStudyList": {

"subjectId": 2,

"studyId": 1,

"physicallyInvolved": true,

"subjectType": "HEALTHY\_VOLUNTEER",

"subjectStudyIdentifier": "titi"

}

}]

## Comportement IHM

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Json 1  *subject* | Find y | Find y | ~~Find y,z~~ | ~~Find y,z~~ | ~~Find y,z~~ | Find ∅ |
| Json 3 | Find [X]  y ∉ [X] | Find [X]  y ∈ [X] | ~~Find [X]~~  ~~y ∈ [X]~~  ~~z ∉ [X]~~ | ~~Find [X]~~  ~~y,z ∈ [X]~~ | ~~Find [X]~~  ~~y,z ∉ [X]~~ | Find [X] |
| IHM neurinfo | Create subject  OR  add y to [X] list (preselected by default)  OR  Selection of subject (change preselection) | Create subject  OR  add y to [X] list (preselected by default)  OR  Selection of subject (change preselection) | ~~select y~~  ~~Put z as second choice in list with warning z ∉ [X]~~  ~~+ add [X] - y to list~~ | ~~select y~~  ~~Put z as second choice in list~~  ~~add [X] - y - z to list~~ | ~~select y~~  ~~Add warning : y ∉ [X]~~  ~~Put z as second choice in list with warning z ∉ [X]~~  ~~+ add [X] to list~~ | No preselection  Create subject  OR  Selection of subject |
| IHM ofsep | TBD |  |  |  |  |  |

# Changes in the table are justified because we can have an anonymized patient with the same name and birth date in the zip file for different real patients.

# Json 4 for examinations

Select examination based on selected study and subject

[{

"id": 1,

"comment": "exam 1",

"date": 145645721 (TBD)

},

{

"id": 2,

"comment": "exam 2",

"date": 145645723 (TBD)

}

]

# Json for dataset type selection

# Json for dataset processing

# Json for spectroscopy dataset selection

# Json sent to import MS once user has filled all mandatory fields and clicked on process import button.