

## Reviewer Report

**Title: The genetics-BIDS extension:Easing the search for genetic data associated with human brain imaging**

**Version: Original Submission    Date: 8/22/2020**

**Reviewer name: Jean-Baptiste Poline**

### Reviewer Comments to Author:

# The genetics-BIDS extension: Easing the search for genetic data associated with human brain imaging

## General recommendation

This reviewer finds the work very commendable and thinks that the development of standards is one of the key area to work on to improve the efficiency and solidity of research.

## General remarks

The abstract contains words like "ontologies" and "databases" but the work is about lexicons and disk / filename organization. The abstract should be rewritten to better describe the work.

Github repo: while the BIDS overarching project link is given, it takes a while to find where the specific sub field standard is described. It seems that the specific subfield standard is described in page 72 and 73 of the current BIDS specification, but pointing directly to a web page and a git repository containing the documentation would help the reader.

Links to related projects and organization: This short paper does not reference or place the work in the context of standardization organizations in genetic and neuroscience.

Links to datasets available into the format: The standard is probably instantiated in at least one dataset, and hopefully in several datasets. It would be important for the reader to be able to see explore these datasets.

Relation to linked data principles. Since this work attempt to ease linking brain and genetic/genomic data, it would be useful to see how the json file could be turned into a json-ld file (associating a context and pointing to specific definitions for the terms).

## Specific remarks or questions:

- The "URL pointing to the genetic data" : does this mean that "wget URL" will download all data ?
- In which circumstances the link of the genetic participant and the brain imaging data could be sensitive and if it is, how can this be handled ?
- It is unclear which values are permitted in the for the "GeneticLevel" or "SampleOrigin" or "TissueOrigin"
- If AnalyticApproach is of particular importance, why is it not a required field ?
- While the keys of the json descriptors are specified,
- While this is not specific to this work, it would be interesting to see how a json schema could be built for the validation of the specification.

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