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Brainomics - A management system for exploring and merging heterogeneous brain mapping data

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Introduction
- Number of large datasets for brain mapping have been released [1, 2].
- Neuroimaging datasets more routinely include clinical data or genetics data.
- Exploitation requires:
  ➔ An efficient organization to integrate all the measures
  ➔ An easy access to the relevant information.

Data model
- Described in Python, using reusable modules called “cubes”.
- Modelling of Scans, Questionnaires, Genomics results, Behavioral results, Subjects and Studies information.
- Data model optimized for large volumes (> 2000 subjects).
- Tested with several publicly available datasets [1, 2].

Query using RQL
- Similar to the W3C’s SPARQL [6].
- Supports the basic operations (selection, insertion, etc.).
- Subquerying, ordering, counting, ...

Views
- Each query result can be seen using different views.
- HTML pages, ZIP files, spreadsheets, XCEDE XML, ...
- May include processing (stat. maps computed on the fly).

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References
[2] fcon_1000.projects.nitrc.org/indi/abide/

Data management framework, 10 years of industrial uses (e.g. [5]).
- Well established core technologies: SQL, Python, HTML5, Javascript.
- Licensed under LGPL since 2008.
- Used in production environments since 2005.
- Fine-grained security system coupled to the data model definition.
- Migration mechanisms controls model version / ensures data integrity.

CubicWeb
- http://www.cubicweb.org/
- Open source solution to manage brain imaging datasets and associated meta data.
- Powerful querying and reporting tool, customized for emerging imaging-genetics field.

Conclusion