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

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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.

Neuroimaging [3] and genomics[4] databases are dedicated to their own field of research.

Data model
- Described in Python, using reusable modules called “cubes”.
- Modelisation 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, ...

Query all the female subjects of the database, with an age greater than 30
Any S WHERE S is Subject, S age > 30, S gender "female"

Query all the Cmap scans of subjects with an age greater than 25, and that have a score greater than 4.0 for the “algebre” question
Any SA WHERE S is Subject, S age > 25, X is QuestionnaireRun, X concerns S, A is Answer, A questionnaire_run X, A question Q, Q text “algebre”, A value > 4, SA is Scan, SA concerns S, SA type “c map”

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).

Conclusion
- Open source solution to manage brain imaging datasets and associated meta data.
- Powerful querying and reporting tool, customized for emerging imaging-genetics field.

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