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.

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**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].

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**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).

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**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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