

# BioSignalML

## Putting biosignals onto the Semantic Web

David Brooks



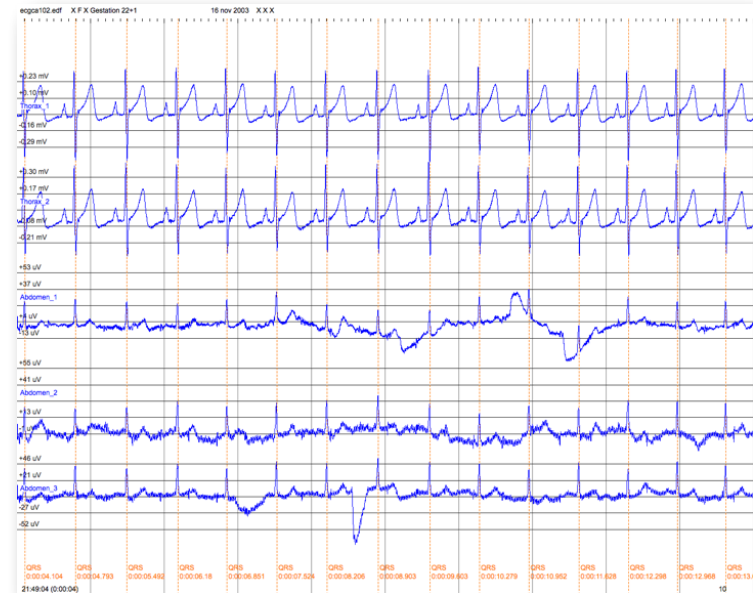
**AUCKLAND  
BIOENGINEERING INSTITUTE**

THE UNIVERSITY OF AUCKLAND  
NEW ZEALAND

Te Whare Wānanga o Tāmaki Makaurau

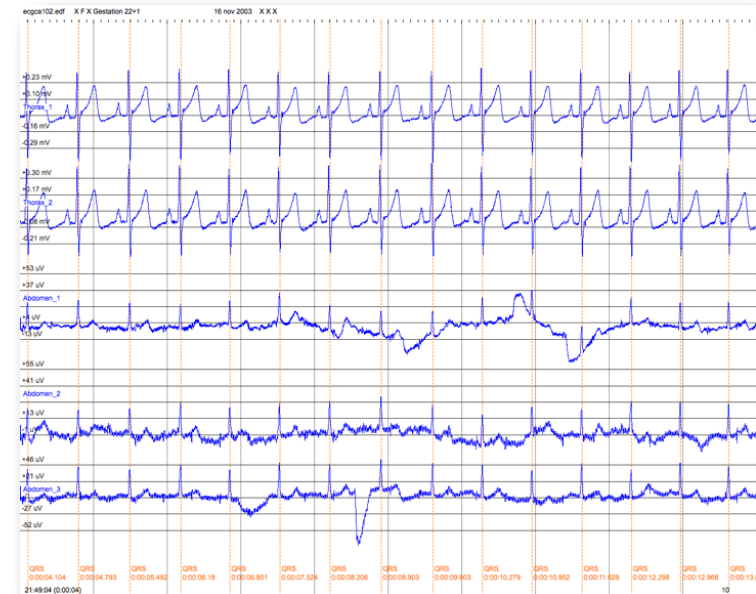
# Background

- Biosignal -- time series data resulting from a biological process.



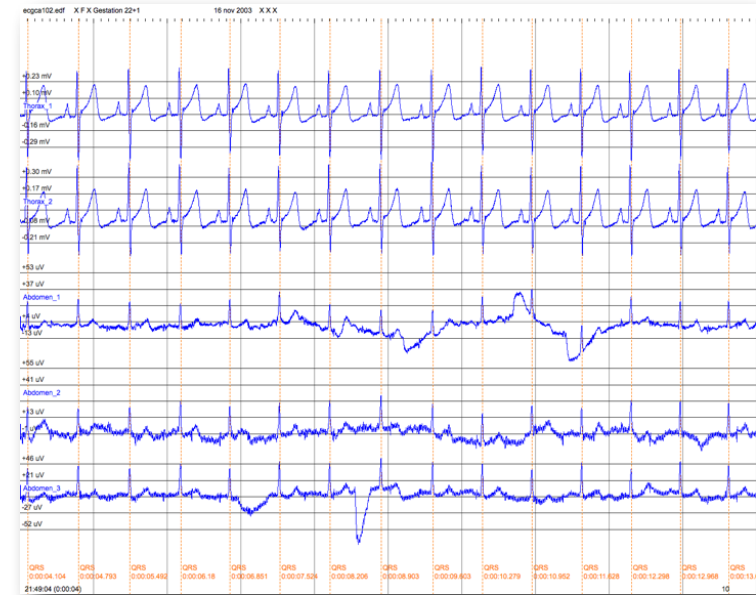
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- Biosignal -- time series data resulting from a biological process.
- Sampled, usually at a regular rate, which is usually much greater than the highest frequency of interest.



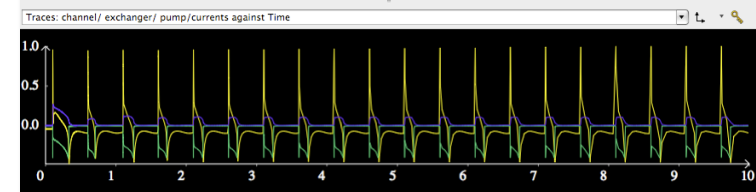
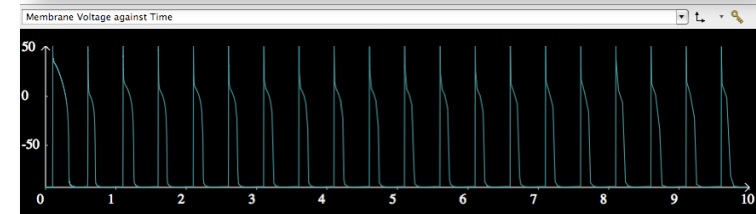
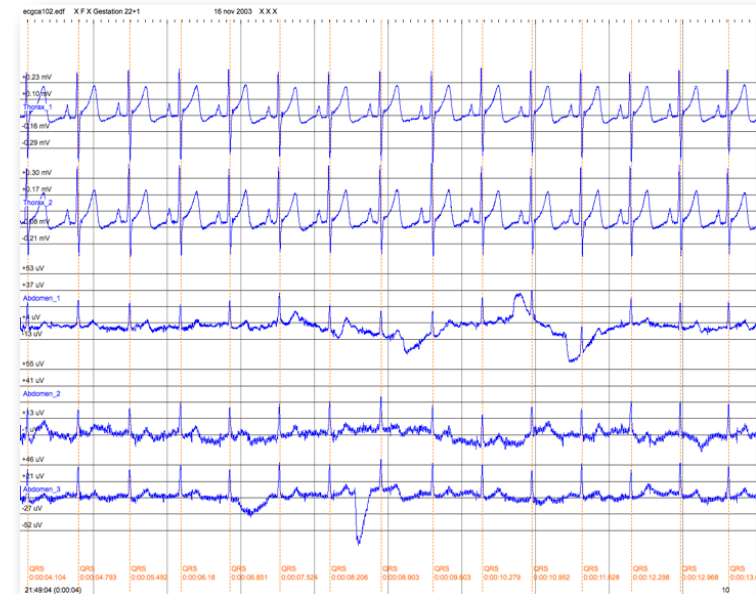
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- Electrical, pressure, concentration, ...
- Simulation time series data.



# Background

- A lot of file formats:
  - manufacturer; research; regulatory; ...



BDF	24 bit version of EDF
EDF	European Data Format
EDF+	European Data Format plus
FDAXML	FDA standard for ECG
GDF	General Data Format (an EDF derivative)
MFER	Medical waveform Format Encoding Rules (ISO)
SCP	Standard Communication Protocol for ECG (CEN)
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- Metadata content tends to be domain specific.



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# Difficulties

- Polysomnography:
  - *“Currently, digital data from most PSG systems can only be viewed if one utilizes the system with which it was collected.”*<sup>[1]</sup>
  - *“Unfortunately, not much has happened since ... no consensus for data sharing has taken root.”*<sup>[2]</sup>

[1] D. Rapoport, I. Ayappa, R. Norman, and S. Herman, “NPSG data interchange-dealing with the Tower of Babel.” *Sleep*, vol. 29, no. 5, p. 599, 2006.

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  - Units:  $\mu\text{V}$ ,  $\text{uV}$ ,  $\text{V} \times 10^{-6}$  ??

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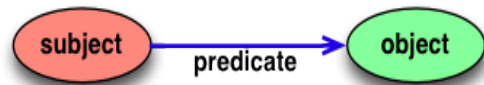


# Semantic Web

- Web content that is meaningful to computers.
  - Knowledge representation, ontologies, reasoning, intelligent agents, ...

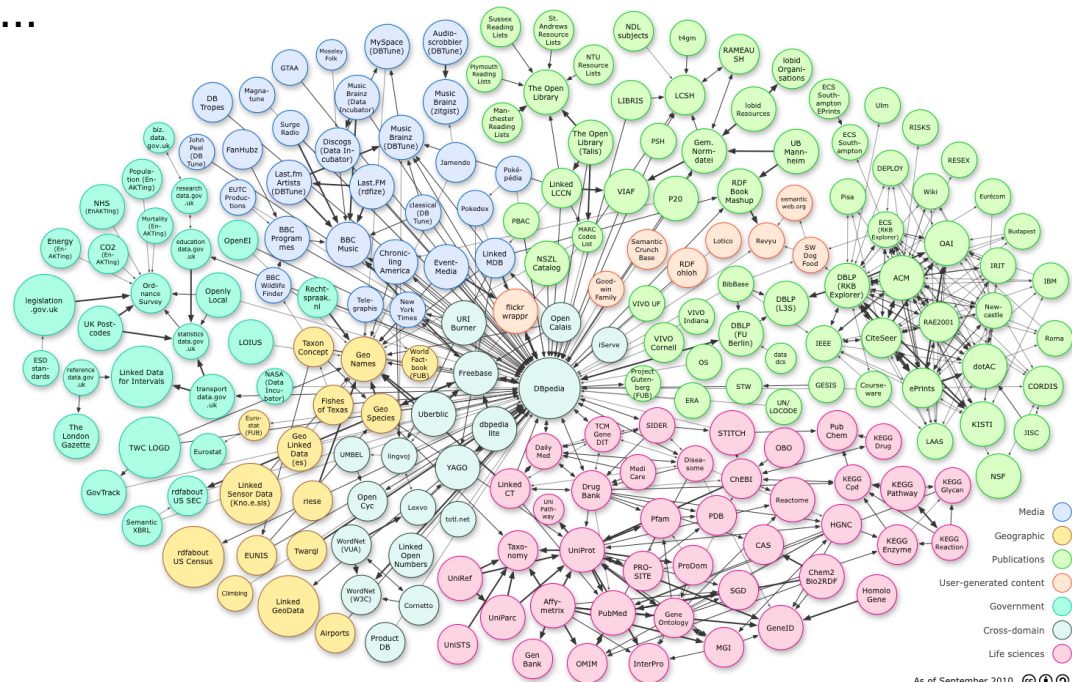
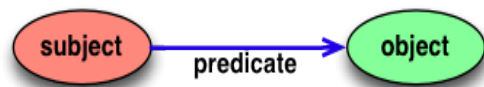
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- <http://www.w3.org/standards/semanticweb/>
  - Resource Description Framework (RDF)
  - RDFS, OWL, SPARQL, ...



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- Linking Open Data



Linking Open Data cloud diagram, by Richard Cyganiak and Anja Jentzsch. <http://lod-cloud.net/>





# **BioSignalML**

- Abstract common elements of storage formats.



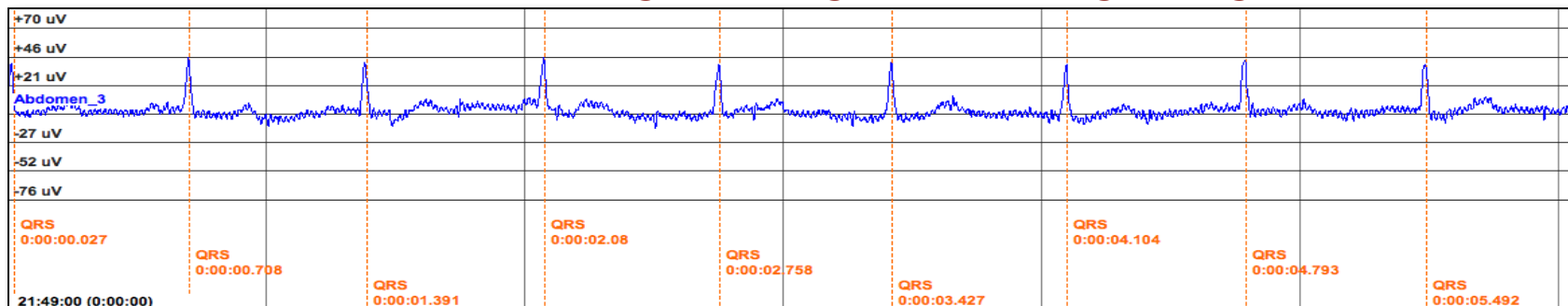
# BioSignalML

- Abstract common elements of storage formats.
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  - Objects have web identifiers.
  - Ontologies define terms, properties, relationships.

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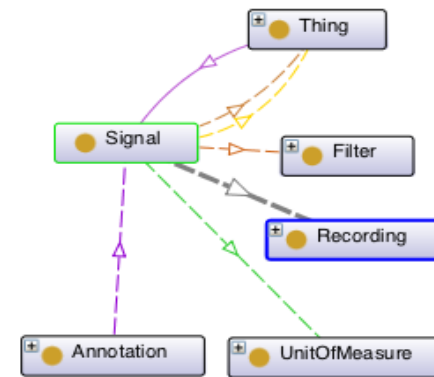
- Abstract common elements of storage formats.
- Use Semantic Web standards/technologies.
  - Objects have web identifiers.
  - Ontologies define terms, properties, relationships.
- Time series data is in native format; everything else is available as RDF metadata.

<http://repository.biosignal.org/recording3/signal/4>



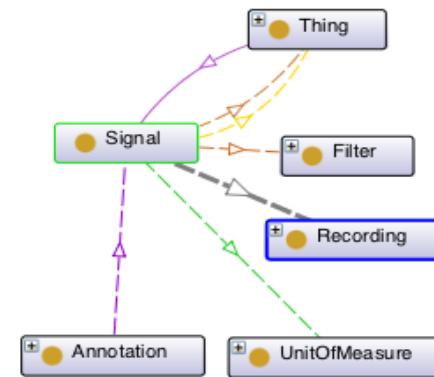
# BioSignalML as RDF

- Core concepts:
  - Recordings
  - Signals
  - Events and Annotations.

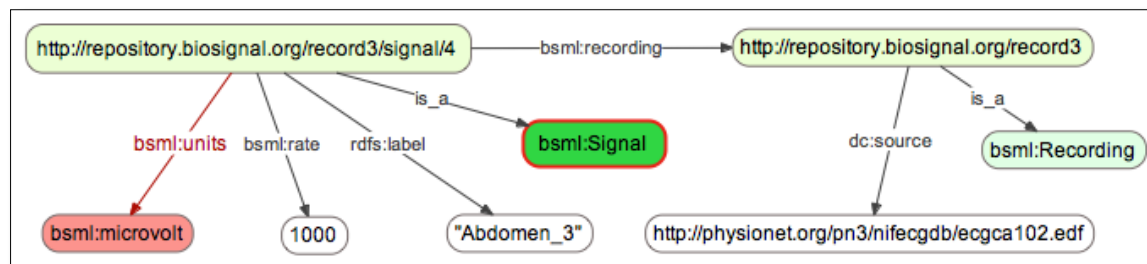


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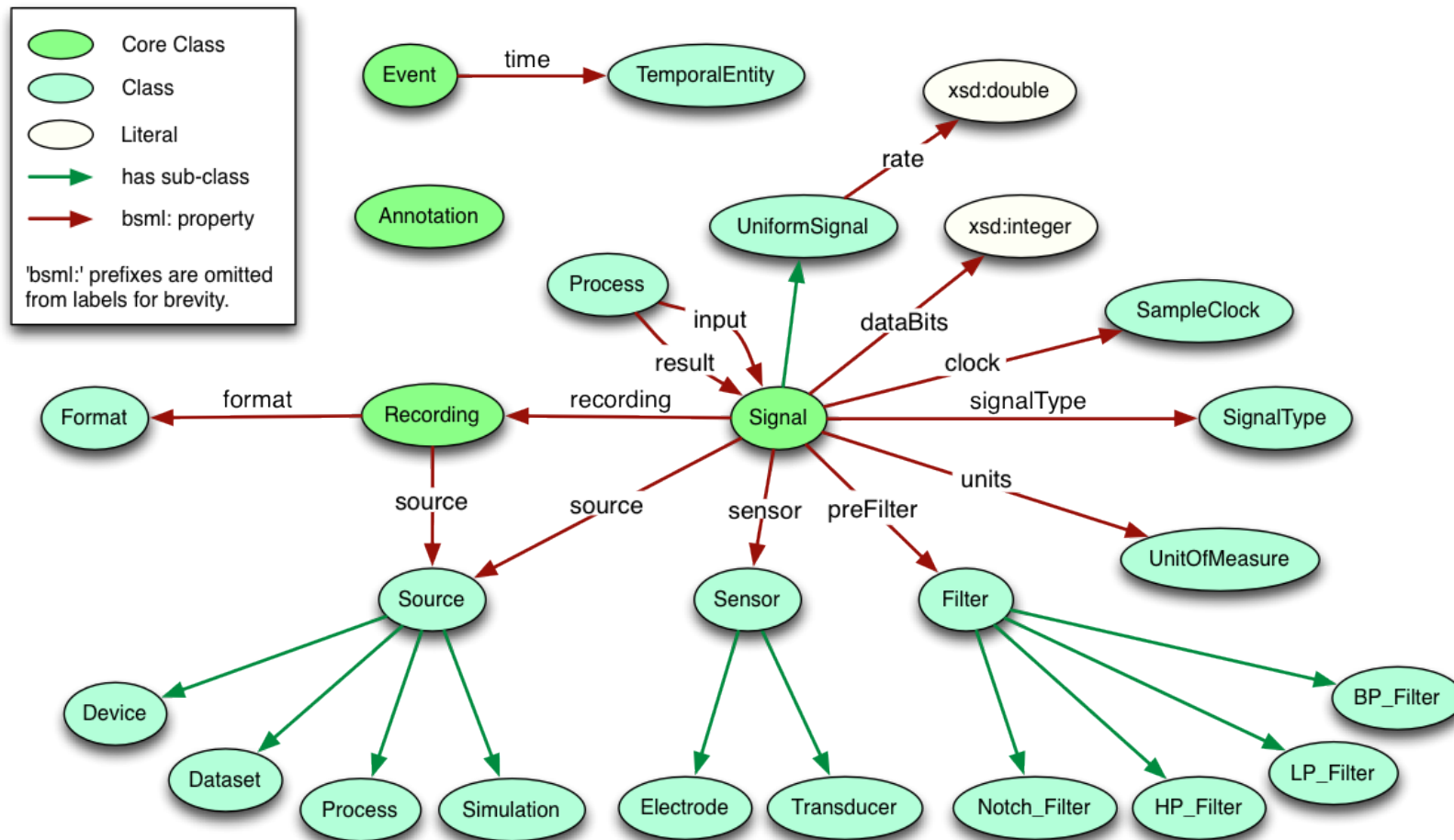


- RDF graph:




# BioSignalML as an ontology

- Classes, terms, properties, relationships:



# BioSignalML as an ontology

- Classes, terms, properties, relationships:



The screenshot shows a web browser window titled "BioSignalML: An ontology for working with biosignals". The address bar displays the URL "http://www.biosignalml.org/ontologies/2011/04/biosignalml#Signal". The main content area displays the details for the class "bsml:Signal".

**Class: bsml:Signal**

URI: <http://www.biosignalml.org/ontologies/2011/04/biosignalml#Signal>

A sequence of periodic measurements of some quantity, ordered by some sampling dimension, normally time. A Signal is part of some Recording.

**Properties include:** [units](#) [signalType](#) [sensor](#) [clock](#) [minValue](#) [maxValue](#) [maxFrequency](#) [preFilter](#) [minFrequency](#) [recording](#)

**Has sub class:** [UniformSignal](#)

**OWL Class**

[\[#\]](#) [\[back to top\]](#)

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**Class: bsml:SignalType**

URI: <http://www.biosignalml.org/ontologies/2011/04/biosignalml#SignalType>

The class or type of signal (e.g. EEG, ECG).

**Used with:** [signalType](#)

**OWL Class**

[\[#\]](#) [\[back to top\]](#)

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**Class: bsml:Simulation**

URI: <http://www.biosignalml.org/ontologies/2011/04/biosignalml#Simulation>

A computer simulation or modelling process that created the Signal or Recording.

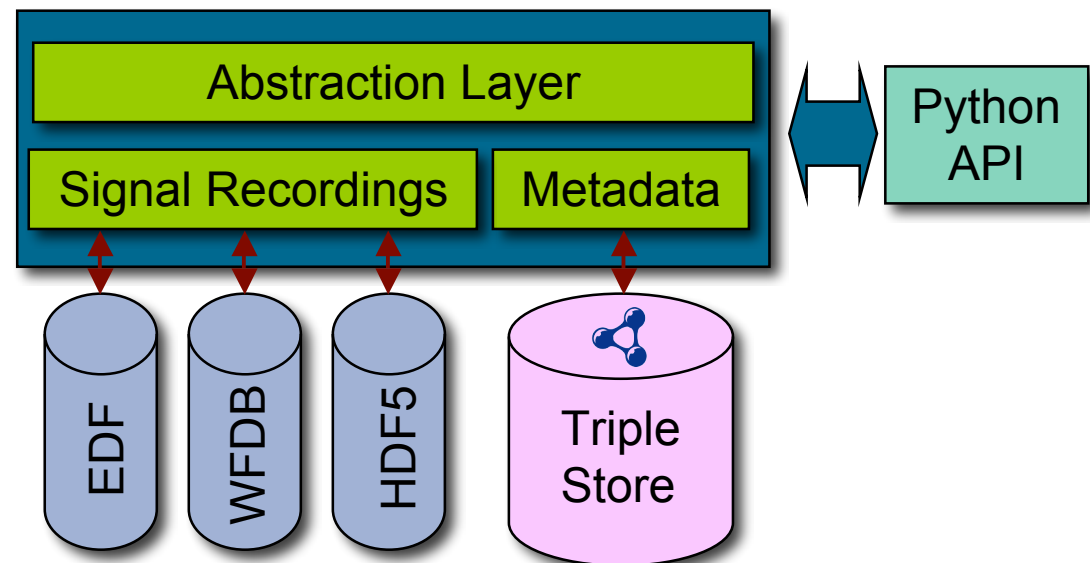
**Sub class of:** [Source](#)

**OWL Class**

[\[#\]](#) [\[back to top\]](#)

# BioSignalML implementation

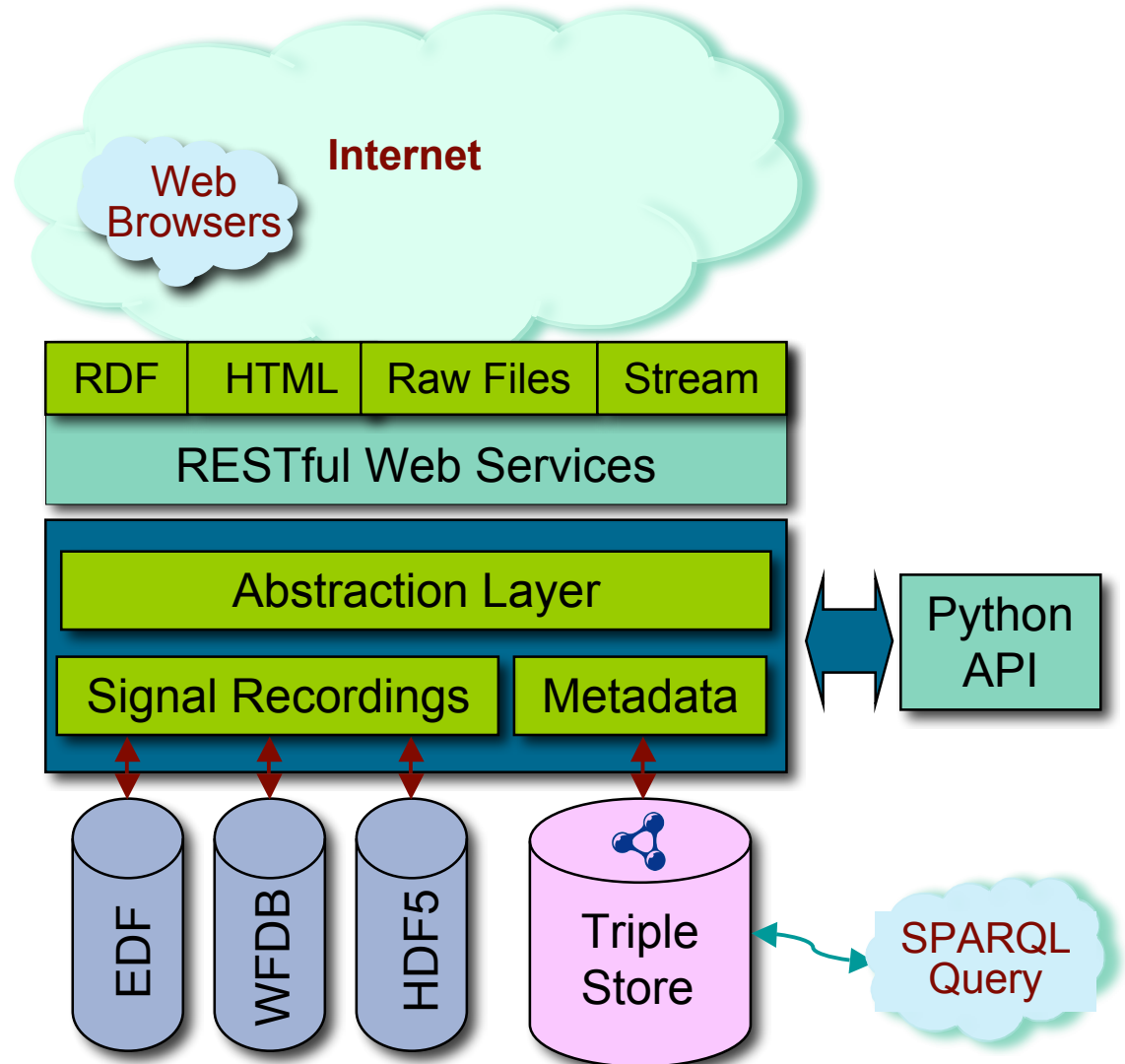
- Biosignal repository:





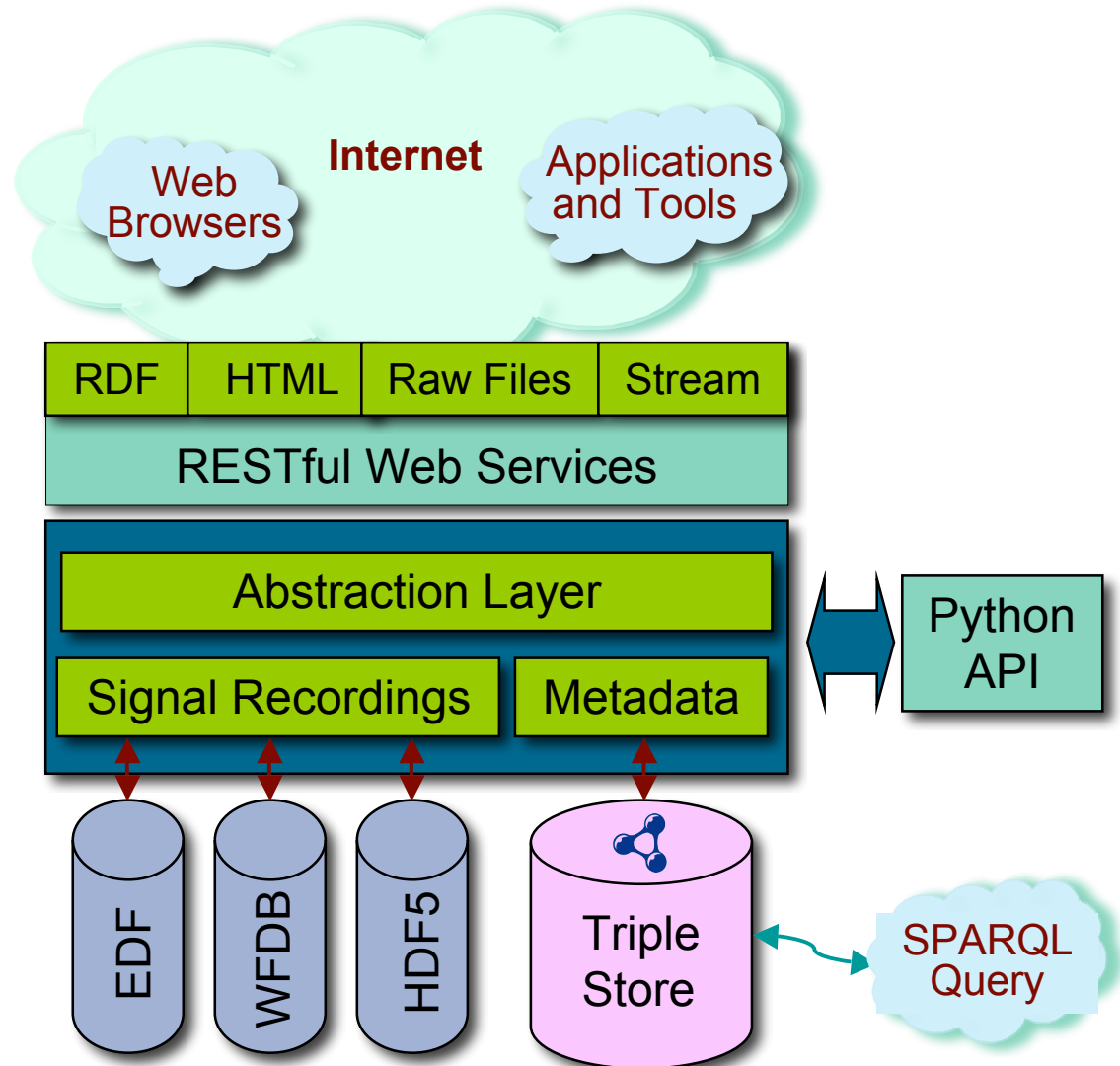
# BioSignalML implementation

- Biosignal repository:
- Web based with HTTP endpoints:
  - File import/export
  - RDF metadata
  - Data streamed via web-sockets.



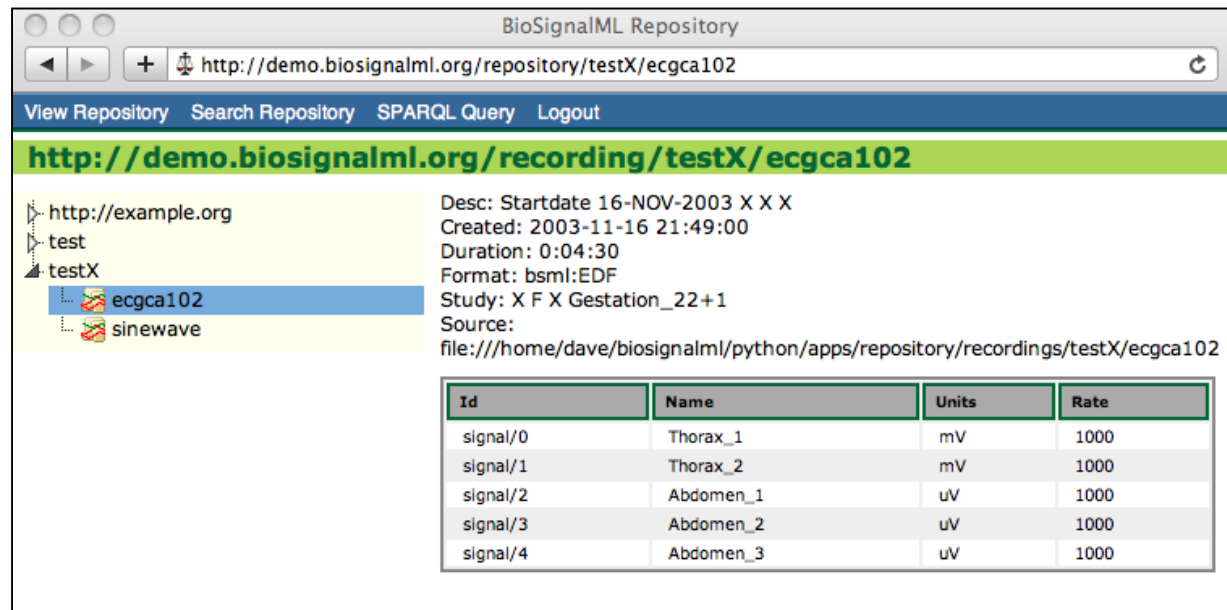
# BioSignalML implementation

- Biosignal repository:
- Web based with HTTP endpoints:
  - File import/export
  - RDF metadata
  - Data streamed via web-sockets.
- C client (plus Python, Javascript, ...)



# BioSignalML clients

- Web browser:



View Repository Search Repository SPARQL Query Logout

<http://demo.biosignalml.org/repository/testX/ecgca102>

http://example.org  
test  
testX  
ecgca102  
sinewave

Desc: Startdate 16-NOV-2003 X X X  
Created: 2003-11-16 21:49:00  
Duration: 0:04:30  
Format: bsm1:EDF  
Study: X F X Gestation\_22+1  
Source:  
file:///home/dave/biosignalml/python/apps/repository/recordings/testX/ecgca102

Id	Name	Units	Rate
signal/0	Thorax_1	mV	1000
signal/1	Thorax_2	mV	1000
signal/2	Abdomen_1	uV	1000
signal/3	Abdomen_2	uV	1000
signal/4	Abdomen_3	uV	1000

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signal/4	Abdomen_3	uV	1000

- RDF browser:

URI ▶ <http://devel.biosignalml.org/recording/physiobank/nifecgdb/ecgca102/signal/4>

Filter HP:0.01Hz LP:100Hz NF:50Hz  
Max Frequency 500.0  
Max Value 500.0  
Min Value -500.0  
Recording ▶ ● ecgca102  
Sample Rate 1000.0  
Transducer AgAgCl electrodes  
Units uV  
Type ▶ ● Signal  
▶ ● document  
▶ ● data document  
Label Abdomen\_3

# BioSignalML clients

- Python code:

```
import biosignalml
import biosignalml.units as units

repo = biosignalml.Repository('http://demo.biosignalml.org')
rec = repo.new_recording('http://example.org/recording/test')
sig = rec.new_signal(id='a1', units=units.millivolt)
for data in datasource:
    sig.append(data)
rec.close()

sig = repo.get_signal('http://example.org/recording/test/signal/a1')
print sig.uri, sig.label, sig.units

start = 0.0
end = 10.0
duration = 1.0
while start < end:
    interval = sig.recording.interval(start, duration)
    for data in sig.read(interval):
        print data # SignalSegment
    start += duration
```

# BioSignalML clients

- CellML modelling:

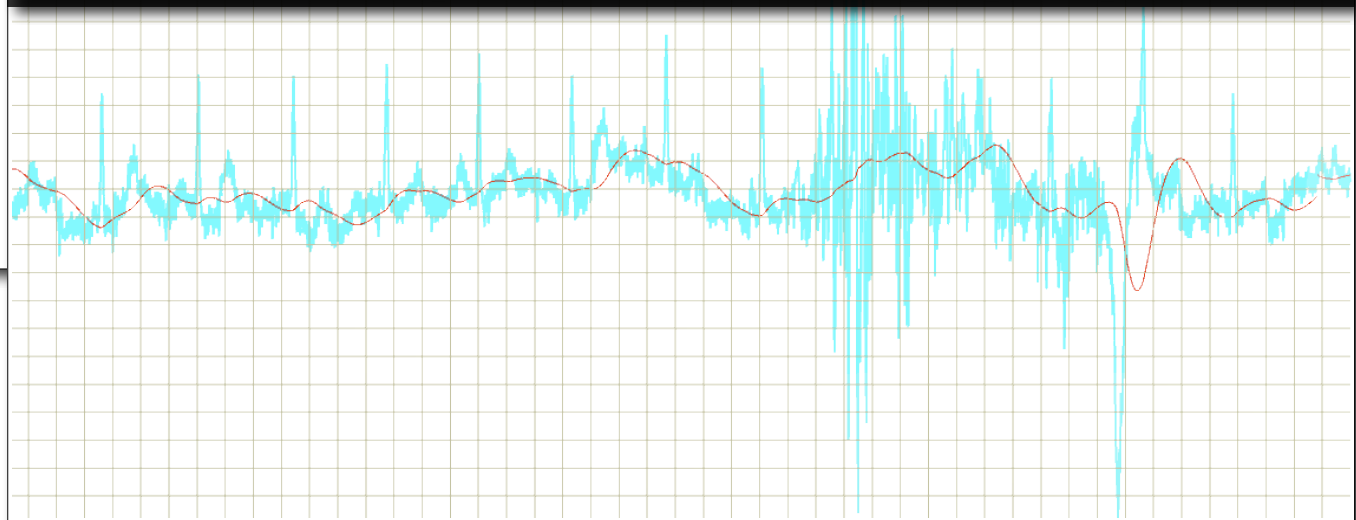
```
<model name="bwfilter" cmeta:id="bwfilter" xmlns="http://www.cellml.org/cellml"
  <component name="filter">
    <variable cmeta:id="time" name="t" units="second"/>
    <variable cmeta:id="input" name="v_i" units="volt" initial_value="0"/>
    <variable cmeta:id="output" name="v_o" units="volt"/>
    <variable name="R" units="ohm" initial_value="1"/>
    <variable name="C" units="farad" initial_value="1.333333"/>
    <variable name="L1" units="henry" initial_value="1.5"/>
    <variable name="L2" units="henry" initial_value="0.5"/>
    <variable name="v_c" units="volt" initial_value="0"/>
    <variable name="i_1" units="ampere" initial_value="0"/>
    <variable name="i_2" units="ampere" initial_value="0"/>
    <math xmlns="http://www.w3.org/1998/Math/MathML">
      <apply>
        <eq/>
        <ci>v_o</ci>
        <apply>
          <times/>
          <ci>i_2</ci>
          <ci>R</ci>
        </apply>
      </apply>
      <apply>
        <eq/>
        <apply>
          <diff/>
          <bvar>
            <ci>t</ci>
          </bvar>
          <ci>i_2</ci>
        </apply>
        <apply>
          <divide/>
          <apply>
            <minus/>
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        </apply>
      </math>
    </component>
  </model>
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        </apply>
      </math>
    </component>
  </model>
```

```
$ ./bwfilter http://devel.biosignalml.org/recording/physiobank/nifecgdb/ecgca102/signal/3
```





# Ongoing work

- Interfacing with simulation tools (OpenCOR, SED/ML)
  - real world applications.
- Adding a Semantic Web layer to PhysioBank.
- Integrate Units of Measurement Expressions:
  - <http://www.sbpax.org/uome/index.html>
  - Ontology to derive units from other units.
  - An extensible way to automate units validation and conversion.





**Thank you**