

User Manual

version 1.0

Table of Contents:

| | |
|--------------------------------------|----|
| Introduction..... | 3 |
| Installation..... | 4 |
| GUI Usage | 5 |
| XML Output..... | 7 |
| <statistic> Element | 7 |
| <simpleStatisticList_t> Element..... | 7 |
| <activation_t> Element..... | 7 |
| <provenance> Element | 8 |
| <activationParams> Element | 8 |
| <thresh> Element..... | 9 |
| <label> Element..... | 9 |
| <clusters> Element | 9 |
| <voxel> Element..... | 10 |
| Statistics Sub-Schema..... | 10 |
| Sample Output XML File | 12 |

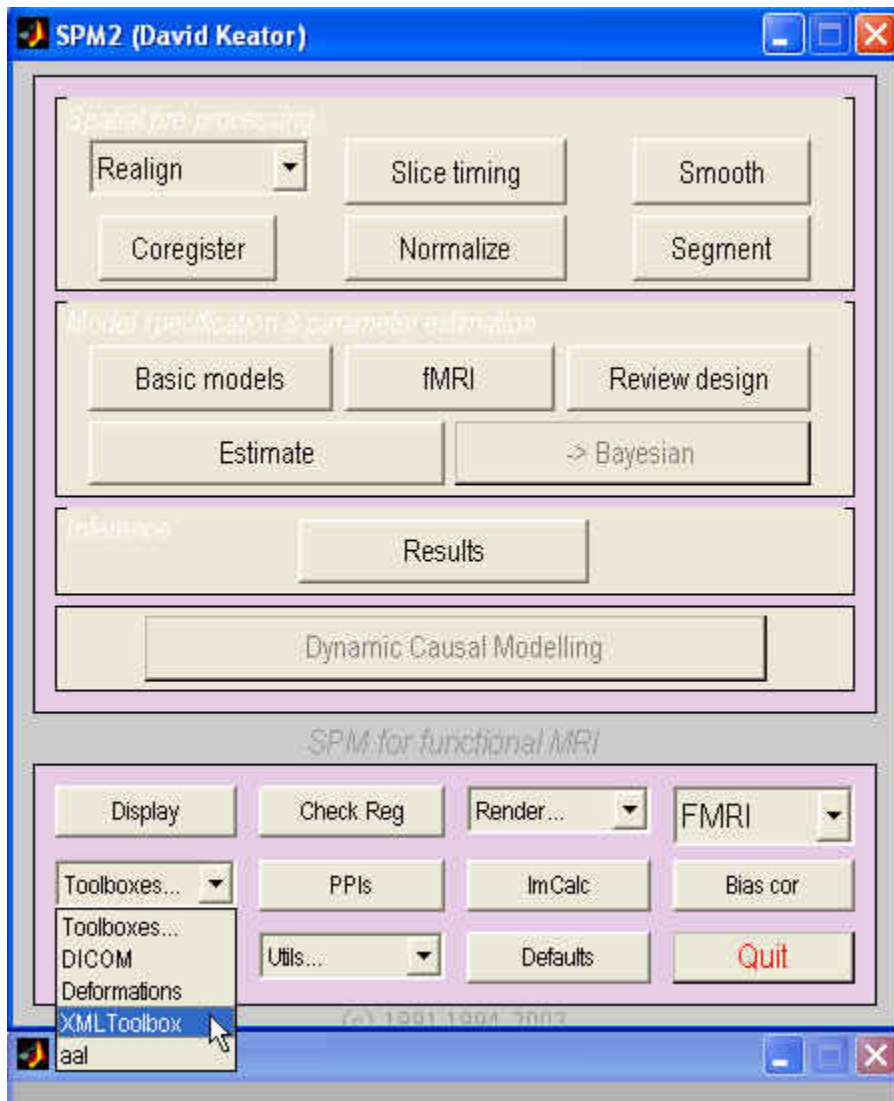
Introduction

This toolbox for Statistical Parametric Mapping (SPM) software (<http://www.fil.ion.ucl.ac.uk/spm/>) was created to capture the results from activation maps using XML. The toolbox supports both SPM99 and SPM2 statistical structures and has been tested on SUN, LINUX, and Microsoft Windows operating systems. The toolbox has been used to capture PET and fMRI analysis results and the associated analysis model specifications. Support for anatomical labeling is provided via the Talairach Daemon (<http://ric.uthscsa.edu/projects/talairachdaemon.html>) and Automated Anatomical Labeling (<http://www.cyceron.fr/freeware/>) toolkits. MNI space to Talairach space corrections are supported via Matthew Brett's mni2tal scripts (<http://www.mrc-cbu.cam.ac.uk/Imaging/Common/mnispace.shtml>). Additional atlas support will be added as those atlases become available and can be integrated into the SPM/matlab environment.

Installation

1. To install the toolbox just download the TAR or ZIP file.
2. Uncompress it in your SPM_ROOT/toolbox directory.
3. Restart SPM
4. Now you should see "XML_Toolbox" as a selection in the "Toolboxes" drop down menu within SPM's user interface (Figure 1).
5. To use anatomical labeling support you must install either AAL or Talarach (Point2TD) Daemon tools:
 - a. <http://ric.uthscsa.edu/projects/talairachdaemon.htm>
 - b. <http://www.cyceron.fr/freeware/>
 - c. <http://www.mrc-cbu.cam.ac.uk/Imaging/Common/mnispace.shtml>

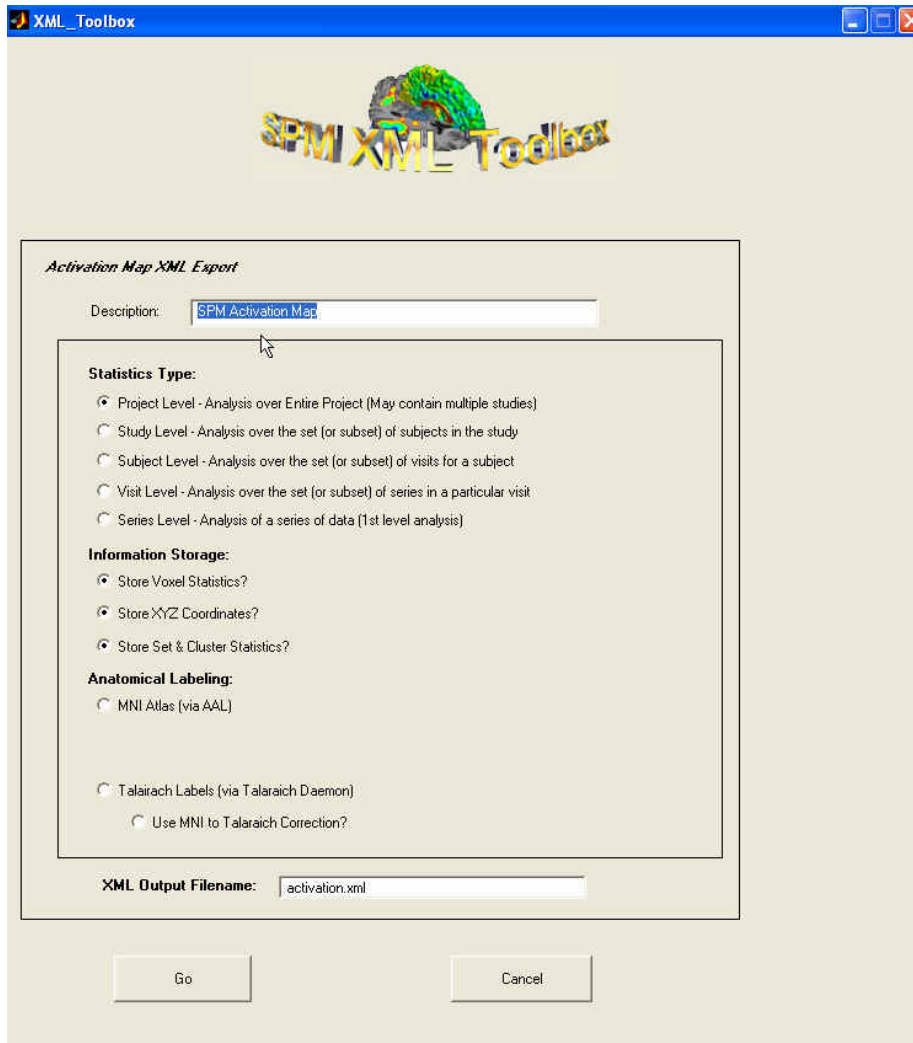
Figure 1:



GUI Usage

The XML toolbox allows the user to specify a variety of output options. The *description* field is a free form text box allowing customized annotation for the statistical output (Figure 2). The information in the description field is directly mapped to the description tags in the XML output file `<description>SPM Activation Map</description>`.

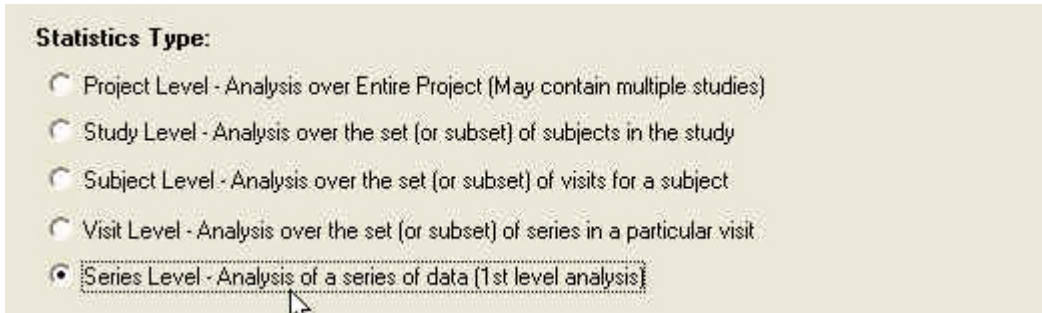
Figure 2:



The *Statistics Type* selections in the GUI allow the results to be classified into project, study, subject, visit, or series level statistics (Figure 3). By classifying the results under a specific level, additional meta-data can be stored with the statistical results. For instance, one may want to store the statistical activations of a project level analysis across multiple subjects with the description of the protocols used in that project. Support for this type of extended meta-data is provided in the XCEDE XML schema, a detailed discussion of

which can be found at:
(<http://www.nbirn.net/Resources/Users/Applications/xcede/index.htm>).

Figure 3:



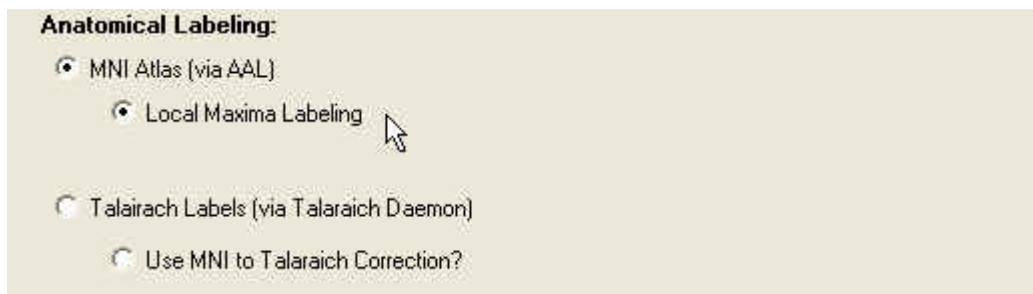
The *Information Storage* selections in the GUI allow the user to specify which statistics are output from SPM. All cluster and set statistics are stored in the <clusters> tags where each cluster is described by an <events> list. All voxel level statistics are stored below <voxel> element in <location> tags.

Figure 4:



The *Anatomical Labeling* selections allow the user to specify the “Local Maxima Labeling” routine from the AAL toolbox or the Talairach Labeling routines from the UTHSCA daemon with MNI to Talairach corrections (Figure 5). Each anatomical label will be documented with the atlas name. Brodman area and laterality designations are parsed from the anatomical toolbox outputs and stored in the XML file.

Figure 5:



XML Output

The XML output file corresponds to the XML-based Clinical Experiment Data Exchange Schema (XCEDE). A description of the tags specific to this toolbox are listed below as well as the schema.

<statistic> Element

This element is allowed as a child of the root element in XML files at any level. It stores statistical information that is generated from the data described in this XML file. This is implemented as a bare-bones statistics type which more specialized statistics elements can derive from. The base statistic element has the following children:

- <sourceData>:
- <process>:
- <provenanceID>:
- <description>:
- <annotation>:

Additional elements are allowed by more specialized statistics types, described below.

<simpleStatisticList_t> Element

This type adds support for a list of simple values. To use the following additional element, the <statistics> element must include `xsi:type="fbx:simpleStatisticList_t"` as one of its attributes, where `xsi` is the XML Schema Instance namespace.

The following element is added to the base statistic element:

- <item> This element encapsulates a single value, and may appear more than once. This element has the following attributes:
 - name
 - type: One of float, boolean, varchar, integer.

<activation_t> Element

The activation element is a general storage location for categorizing threshold and anatomically labeled functional imaging statistical maps. The element provides a versatile set of storage locations to describe the process of statistical analysis, data provenance, statistical map thresholding, and anatomical labeling.

- <sourceData>: This element is a text field for describing the source data used to produce the data contained in this statistics element. For example the tag might contain the contrast name when the statistical map is created using a general linear model to analyze the data or might contain an actual image file name of beta values or other statistic calculated on the data.

- <process>: This element is a text field for describing the processing steps or parameters set during the statistical analysis. There is not always a perfect correspondence between the data provenance command arguments and the process elements here.
- <description>: Free text field used for notes or titles of the statistical map.
- <annotation>: The annotation element can be repeated any number of times to document who and when the file was updated. This tag in combination with the provenance tag should provide a fairly complete history of the data which follows.
 - <text>: The text field of the annotation tag can be used to document the program name used to generate the statistical map.
 - <annotator>: The annotator is the user-name of the person who updated the XML file at the timestamp.
 - <timeStamp>: Date and time of this annotation.

<provenance> Element

The <provenance> element describes a pipeline that was used to generate data described in this file. This element may appear more than once. A full discussion of the <provenance> elements can be found in the XCEDE schema documentation.

<activationParams> Element

The activationParams tag elements are used to describe the thresholding, number of voxels, clusters, degrees of freedom, smoothness, and related parameters of a statistical parametric map.

- <expVoxPerCluster>: Given a number of clusters in the thresholded statistical map, this tag documents the expected number of voxels per cluster by chance.
- <expNumClusters>: This tag documents the expected number of clusters in the parametric map by chance.
- <df>: This tag documents the degrees of freedom in the analysis.
- <fwhmSmoothness>: This tag documents the smoothness estimates of the analysis.
- <fwhmUnits> This attribute to the fwhmSmoothness tag describes the units used to cite the FWHM smoothness estimate. Common attributes are cubic mm, voxels, etc.
- <searchVol>:
 - <fwhmUnits> This attribute to the searchVol tag describes the units used to cite the search volume of the parametric map. Common attributes are cubic mm, voxels, etc.
 - <voxelSize>: The sizes of voxel elements (3D) or pixel elements (2D) in the parametric map.
 - <voxelUnits> This attribute to the voxel-Size tag describes the units used to cite the voxel size.

<thresh> Element

The thresh element is used as a general description of thresholding, describing the type of thresholding, the value, and the p-values both corrected and uncorrected for multiple comparisons.

- <threshType>: The type of thresholding, for example, Z-score or T-score.
 - <value>: The actual value of the threshold.
 - <pUncorrected>: The uncorrected probability value (p-value).
 - <pCorrected>: The corrected p-value.
 - The correctionType attribute for the corrected p-value can be used to document the correction methods.

<label> Element

The label element is used to describe an anatomical or other atlas labeling of the data. The label element is contained within the cluster element and the voxel element to precisely label each significant cluster or voxel. More than one label element is allowed for each voxel or cluster, supporting many such anatomical labelings of a single activation.

- <atlas>: The atlas attribute describes the atlas used to provide the values for this label.
 - <value>: The anatomical label from the atlas.
 - <brodman>: The brodman area if the atlas provides this information.
 - <lateralization>: The left-right lateralization of the activation if the atlas provides this information.

<clusters> Element

The clusters element is made up of multiple extents elements. Each extents element describes a significant cluster in the thresholded activation map.

- <extents> The extents element is used to describe significant clusters in the activation map. The extents element can contain any number of label elements to provide anatomical labels for the cluster.
 - <locationFoci> The locationFoci attribute describes where in this extent the x,y, and z coordinates are cited from and hence where any anatomical labeling of this cluster are categorized from.
 - <units> The units attribute describes the units used to cite the x,y, and z coordinates of this cluster.
 - <X>
 - <Y>
 - <Z>
 - <size> The size of the cluster in voxel elements as indicated in the voxelSize element in the activation params element source graph drawing software.
 - <pUncorrected> The uncorrected p-value of the cluster.

- <pCorrected> The corrected p-value of the cluster.

<voxel> Element

The voxel element is used to describe significant voxels in the activation map. The sub-elements could be all significant voxels or some subset of activated voxels. For instance in some systems only the activated voxels that are greater than some distance apart are cited.

- <location> The voxel element is made up of any number of location elements which describe the actual coordinates and any anatomical labels of the significant voxels. The labeling scheme works just as with the extents elements and can be anatomical labels from any number of atlases.
 - <X>
 - <Y>
 - <Z>
 - <thresh>

Statistics Sub-Schema

Below is a copy of the relevant sections of the XCEDE schema:

```
<xsd:group name="statistic_g">
  <xsd:sequence>
    <xsd:element name="sourceData" type="xsd:string" minOccurs="0" maxOccurs="unbounded"/>
    <xsd:element name="process" type="xsd:string" maxOccurs="unbounded"/>
    <xsd:element name="provenanceID" type="xsd:string" minOccurs="0"/>
    <xsd:element name="description" type="xsd:string"/>
    <xsd:element name="annotation" type="fbx:annotation_t" minOccurs="0" maxOccurs="unbounded"/>
  </xsd:sequence>
</xsd:group>
<xsd:complexType name="pCorrected_t">
  <xsd:simpleContent>
    <xsd:extension base="xsd:float">
      <xsd:attribute name="correctionType" type="xsd:string"/>
    </xsd:extension>
  </xsd:simpleContent>
</xsd:complexType>
<xsd:complexType name="thresh_t">
  <xsd:sequence>
    <xsd:element name="value" type="xsd:float"/>
    <xsd:element name="pUncorrected" type="xsd:float"/>
    <xsd:element name="pCorrected" type="fbx:pCorrected_t" maxOccurs="unbounded"/>
  </xsd:sequence>
  <xsd:attribute name="threshType" type="xsd:string" use="required"/>
</xsd:complexType>
<xsd:complexType name="extent_t">
  <xsd:complexContent>
    <xsd:extension base="fbx:location_t">
      <xsd:sequence>
        <xsd:element name="size" type="xsd:float"/>
      </xsd:sequence>
    </xsd:extension>
  </xsd:complexContent>
</xsd:complexType>
```

```

        <xsd:element name="pUncorrected" type="xsd:float" minOccurs="0"/>
        <xsd:element name="pCorrected" type="fbx:pCorrected_t" minOccurs="0"
maxOccurs="unbounded"/>
    </xsd:sequence>
    <xsd:attribute name="locationFoci" type="xsd:string" use="required"/>
</xsd:extension>
</xsd:complexContent>
</xsd:complexType>
<xsd:complexType name="setLevel_t">
    <xsd:sequence>
        <xsd:element name="numClusters" type="xsd:float"/>
        <xsd:element name="p" type="xsd:float"/>
        <xsd:element name="extents" type="fbx:extent_t" maxOccurs="unbounded"/>
    </xsd:sequence>
</xsd:complexType>
<xsd:complexType name="voxelLevel_t">
    <xsd:sequence>
        <xsd:element name="location" type="fbx:location_t" maxOccurs="unbounded"/>
    </xsd:sequence>
</xsd:complexType>
<xsd:complexType name="location_t">
    <xsd:sequence>
        <xsd:element name="label" type="fbx:label_t" minOccurs="0" maxOccurs="unbounded"/>
        <xsd:element name="X" type="xsd:float"/>
        <xsd:element name="Y" type="xsd:float"/>
        <xsd:element name="Z" type="xsd:float"/>
        <xsd:element name="thresh" type="fbx:thresh_t" minOccurs="0" maxOccurs="unbounded"/>
    </xsd:sequence>
    <xsd:attribute name="units" type="xsd:string" use="required"/>
</xsd:complexType>
<xsd:complexType name="label_t">
    <xsd:sequence>
        <xsd:element name="value" type="xsd:string" maxOccurs="unbounded"/>
        <xsd:element name="brodman" type="xsd:string" minOccurs="0"/>
        <xsd:element name="lateralization">
            <xsd:simpleType>
                <xsd:restriction base="xsd:string">
                    <xsd:enumeration value="left"/>
                    <xsd:enumeration value="right"/>
                    <xsd:enumeration value="bilateral"/>
                </xsd:restriction>
            </xsd:simpleType>
        </xsd:element>
    </xsd:sequence>
    <xsd:attribute name="atlas" type="xsd:string" use="required"/>
</xsd:complexType>
<xsd:complexType name="fwhm_t">
    <xsd:annotation>
        <xsd:documentation xml:lang="en"> Smoothness FWHM of the parametric map. Units are in mm,
voxels, etc.</xsd:documentation>
    </xsd:annotation>
    <xsd:sequence>
        <xsd:element name="fwhm" type="xsd:float" maxOccurs="unbounded"/>
    </xsd:sequence>
    <xsd:attribute name="fwhmUnits" type="xsd:string" use="required"/>
</xsd:complexType>
<xsd:complexType name="searchVol_t">
    <xsd:annotation>
        <xsd:documentation xml:lang="en"> Volume searched in the parametric map. Units are in mm, voxels,
resels, etc.</xsd:documentation>
    </xsd:annotation>
    <xsd:sequence>
        <xsd:element name="S" type="xsd:float"/>
    </xsd:sequence>
    <xsd:attribute name="searchUnits" type="xsd:string" use="required"/>
</xsd:complexType>

```

```

<xsd:complexType name="vox_t">
  <xsd:annotation>
    <xsd:documentation xml:lang="en"> Voxel size. Units are in mm, cm, etc.</xsd:documentation>
  </xsd:annotation>
  <xsd:sequence>
    <xsd:element name="vox" type="xsd:float" maxOccurs="unbounded"/>
  </xsd:sequence>
  <xsd:attribute name="voxelUnits" type="xsd:string" use="required"/>
</xsd:complexType>
<xsd:complexType name="activationParams_t">
  <xsd:sequence>
    <xsd:element name="thresh" type="fbx:thresh_t" maxOccurs="2"/>
    <xsd:element name="expVoxPerCluster" type="xsd:float"/>
    <xsd:element name="expNumClusters" type="xsd:float"/>
    <xsd:element name="df" type="xsd:float" maxOccurs="unbounded"/>
    <xsd:element name="fwhmSmoothness" type="fbx:fwhm_t" maxOccurs="unbounded"/>
    <xsd:element name="searchVol" type="fbx:searchVol_t" maxOccurs="unbounded"/>
    <xsd:element name="voxelSize" type="fbx:vox_t" maxOccurs="unbounded"/>
  </xsd:sequence>
</xsd:complexType>
<xsd:complexType name="activation_t">
  <xsd:complexContent>
    <xsd:extension base="fbx:statistic_t">
      <xsd:sequence>
        <xsd:element name="activationParams" type="fbx:activationParams_t" minOccurs="0"/>
        <xsd:element name="clusters" type="fbx:setLevel_t"/>
        <xsd:element name="voxel" type="fbx:voxelLevel_t"/>
      </xsd:sequence>
    </xsd:extension>
  </xsd:complexContent>
</xsd:complexType>
<xsd:complexType name="simpleStatisticList_t">
  <xsd:complexContent>
    <xsd:extension base="fbx:statistic_t">
      <xsd:sequence>
        <xsd:element name="item" type="fbx:compactValue_t" maxOccurs="unbounded"/>
      </xsd:sequence>
    </xsd:extension>
  </xsd:complexContent>
</xsd:complexType>

```

Sample Output XML File

```

<?xml version="1.0" encoding="utf-8"?>
<projectlevel xmlns="http://www.nbirn.net/Resources/Users/Applications/xcede/index.htm"
xmlns:xlink="http://www.w3.org/1999/xlink" xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance"
xsi:schemaLocation="http://www.nbirn.net/Resources/Users/Applications/xcede/index.htm xcedeschema.xsd">
  <!--XML SPM Activation Output File.-->
  <provenance id="SPM2_2005-02-02T16:27:31">
    <processStep>
      <programName>XML SPM Statistics Toolbox (fBIRN.m)</programName>
      <programArgument>ProjectLevel,SPM Activation
Map,activation.xml,1,1,1,0,1,1,0,0</programArgument>
      <version>1.0</version>
      <timeStamp>83-80-77T50:2005:022-16-27T31:</timeStamp>
      <user>dbkeator</user>
      <machine>tcsh: No entry for terminal type "MATLAB Command Window"
tcsh: using dumb terminal settings.
i686 athlon
    </machine>
      <platform>tcsh: No entry for terminal type "MATLAB Command Window"

```

tcsh: using dumb terminal settings.

Linux

</platform>

<platformVersion>tcsh: No entry for terminal type "MATLAB Command Window"

tcsh: using dumb terminal settings.

2.4.20-30.9smp

</platformVersion>

</processStep>

</provenance>

<statistic xsi:type="activation_t">

<sourceData>SPM Activation Map</sourceData>

<sourceData>spmT_0011.img</sourceData>

<process>hrf (with time derivative)</process>

<process>2</process>

<process>3 3 </process>

<process>3.00 {s}</process>

<process>Cutoff: 120 {s}</process>

<process>i.i.d</process>

<process>mean voxel value</process>

<process>session specific</process>

<process>None</process>

<description>SPM Activation Map</description>

<annotation>

<text>SPM2</text>

<annotator/>

<timeStamp>2005-02-02T16:27:31</timeStamp>

</annotation>

<activationParams>

<thresh threshType="height threshold T">

<value>3.81</value>

<pUncorrected>0.000</pUncorrected>

<pCorrected>0.932</pCorrected>

</thresh>

<thresh threshType="extent threshold (voxels)">

<value>0</value>

<pUncorrected>1.000</pUncorrected>

<pCorrected>0.932</pCorrected>

</thresh>

<expVoxPerCluster>8.001</expVoxPerCluster>

<expNumClusters>2.69</expNumClusters>

<df>1.0</df>

<df>268.0</df>

<fwhmSmoothness fwhmUnits="mm">

<fwhm>10.2</fwhm>

<fwhm>9.9</fwhm>

<fwhm>10.1</fwhm>

</fwhmSmoothness>

<fwhmSmoothness fwhmUnits="voxels">

<fwhm>5.1</fwhm>

<fwhm>4.9</fwhm>

<fwhm>5.1</fwhm>

</fwhmSmoothness>

<searchVol searchUnits="mm^3">

<S>1825784</S>

</searchVol>

<searchVol searchUnits="voxels">

<S>228223</S>

</searchVol>

<searchVol searchUnits="resels">

<S>1672.7</S>

</searchVol>

<voxelSize voxelUnits="mm">

<vox>2.0</vox>

<vox>2.0</vox>

<vox>2.0</vox>

</voxelSize>

```

</activationParams>
<clusters>
  <numClusters>22</numClusters>
  <p>0.000</p>
  <extents locationFoci="maxima" units="mm">
    <label atlas="MNI Atlas via Automated Anatomical Labeling (Copyright 2002 Groupe d'Imagerie
Fonctionnelle Reference NeuroImage 15, 273-289, (2002))">
      <value>Rolandic_Oper_R</value>
      <lateralization>right</lateralization>
    </label>
    <X>-54</X>
    <Y>-4</Y>
    <Z>18</Z>
    <size>126</size>
    <pUncorrected>0.001</pUncorrected>
    <pCorrected>0.001</pCorrected>
  </extents>
  <extents locationFoci="maxima" units="mm">
    <label atlas="MNI Atlas via Automated Anatomical Labeling (Copyright 2002 Groupe d'Imagerie
Fonctionnelle Reference NeuroImage 15, 273-289, (2002))">
      <value>Temporal_Mid_L</value>
      <lateralization>left</lateralization>
    </label>
    <X>56</X>
    <Y>-72</Y>
    <Z>12</Z>
    <size>33</size>
    <pUncorrected>0.045</pUncorrected>
    <pCorrected>0.113</pCorrected>
  </extents>
  <extents locationFoci="maxima" units="mm">
    <label atlas="MNI Atlas via Automated Anatomical Labeling (Copyright 2002 Groupe d'Imagerie
Fonctionnelle Reference NeuroImage 15, 273-289, (2002))">
      <value>Occipital_Sup_L</value>
      <lateralization>left</lateralization>
    </label>
    <X>16</X>
    <Y>-92</Y>
    <Z>36</Z>
    <size>47</size>
    <pUncorrected>0.020</pUncorrected>
    <pCorrected>0.051</pCorrected>
  </extents>
  <extents locationFoci="maxima" units="mm">
    <label atlas="MNI Atlas via Automated Anatomical Labeling (Copyright 2002 Groupe d'Imagerie
Fonctionnelle Reference NeuroImage 15, 273-289, (2002))">
      <value>Parietal_Sup_L</value>
      <lateralization>left</lateralization>
    </label>
    <X>22</X>
    <Y>-50</Y>
    <Z>70</Z>
    <size>26</size>
    <pUncorrected>0.070</pUncorrected>
    <pCorrected>0.173</pCorrected>
  </extents>
  <extents locationFoci="maxima" units="mm">
    <label atlas="MNI Atlas via Automated Anatomical Labeling (Copyright 2002 Groupe d'Imagerie
Fonctionnelle Reference NeuroImage 15, 273-289, (2002))">
      <value>Cerebelum_6_R</value>
      <lateralization>right</lateralization>
    </label>
    <X>-34</X>
    <Y>-38</Y>
    <Z>-38</Z>
    <size>41</size>

```

```

    <pUncorrected>0.027</pUncorrected>
    <pCorrected>0.071</pCorrected>
  </extents>
  <extents locationFoci="maxima" units="mm">
    <label atlas="MNI Atlas via Automated Anatomical Labeling (Copyright 2002 Groupe d'Imagerie
Fonctionnelle Reference NeuroImage 15, 273-289, (2002))">
      <value>Precentral_R</value>
      <lateralization>right</lateralization>
    </label>
    <X>-58</X>
    <Y>8</Y>
    <Z>26</Z>
    <size>26</size>
    <pUncorrected>0.070</pUncorrected>
    <pCorrected>0.173</pCorrected>
  </extents>
  <extents locationFoci="maxima" units="mm">
    <label atlas="MNI Atlas via Automated Anatomical Labeling (Copyright 2002 Groupe d'Imagerie
Fonctionnelle Reference NeuroImage 15, 273-289, (2002))">
      <value>Paracentral_Lobule_L</value>
      <lateralization>left</lateralization>
    </label>
    <X>16</X>
    <Y>-22</Y>
    <Z>72</Z>
    <size>28</size>
    <pUncorrected>0.062</pUncorrected>
    <pCorrected>0.153</pCorrected>
  </extents>
  <extents locationFoci="maxima" units="mm">
    <label atlas="MNI Atlas via Automated Anatomical Labeling (Copyright 2002 Groupe d'Imagerie
Fonctionnelle Reference NeuroImage 15, 273-289, (2002))">
      <value>Cerebellum_Crus1_L</value>
      <lateralization>left</lateralization>
    </label>
    <X>34</X>
    <Y>-94</Y>
    <Z>-24</Z>
    <size>10</size>
    <pUncorrected>0.246</pUncorrected>
    <pCorrected>0.484</pCorrected>
  </extents>
  <extents locationFoci="maxima" units="mm">
    <label atlas="MNI Atlas via Automated Anatomical Labeling (Copyright 2002 Groupe d'Imagerie
Fonctionnelle Reference NeuroImage 15, 273-289, (2002))">
      <value>Caudate_L</value>
      <lateralization>left</lateralization>
    </label>
    <X>4</X>
    <Y>6</Y>
    <Z>-6</Z>
    <size>10</size>
    <pUncorrected>0.246</pUncorrected>
    <pCorrected>0.484</pCorrected>
  </extents>
  <extents locationFoci="maxima" units="mm">
    <label atlas="MNI Atlas via Automated Anatomical Labeling (Copyright 2002 Groupe d'Imagerie
Fonctionnelle Reference NeuroImage 15, 273-289, (2002))">
      <value>Occipital_Sup_R</value>
      <lateralization>right</lateralization>
    </label>
    <X>-28</X>
    <Y>-90</Y>
    <Z>38</Z>
    <size>9</size>
    <pUncorrected>0.270</pUncorrected>

```

```

    <pCorrected>0.517</pCorrected>
  </extents>
  <extents locationFoci="maxima" units="mm">
    <label atlas="MNI Atlas via Automated Anatomical Labeling (Copyright 2002 Groupe d'Imagerie
Fonctionnelle Reference NeuroImage 15, 273-289, (2002))">
      <value>Frontal_Mid_L</value>
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