



IberGrid 07, Santiago de Compostela, May 15th 2007

Multi-voxel non-linear fMRI analysis: a Grid computing approach

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Outline



- Background concepts on fMRI
- Why a non-parametric approach
- Grid-enabled solution concept
- Experiments and early results

IEETA at a glance

- IEETA is one of the 17 Research Units at Universidade de Aveiro (~12,500 students)
- Selected keywords
 - ▶ information systems, computer systems, electronics, telematics, signal processing,...
- Healthcare informatics is one of the main areas
 - ▶ medical images, biosignals, telemedicine, multimodal brain studies, neuroinformatics, etc.



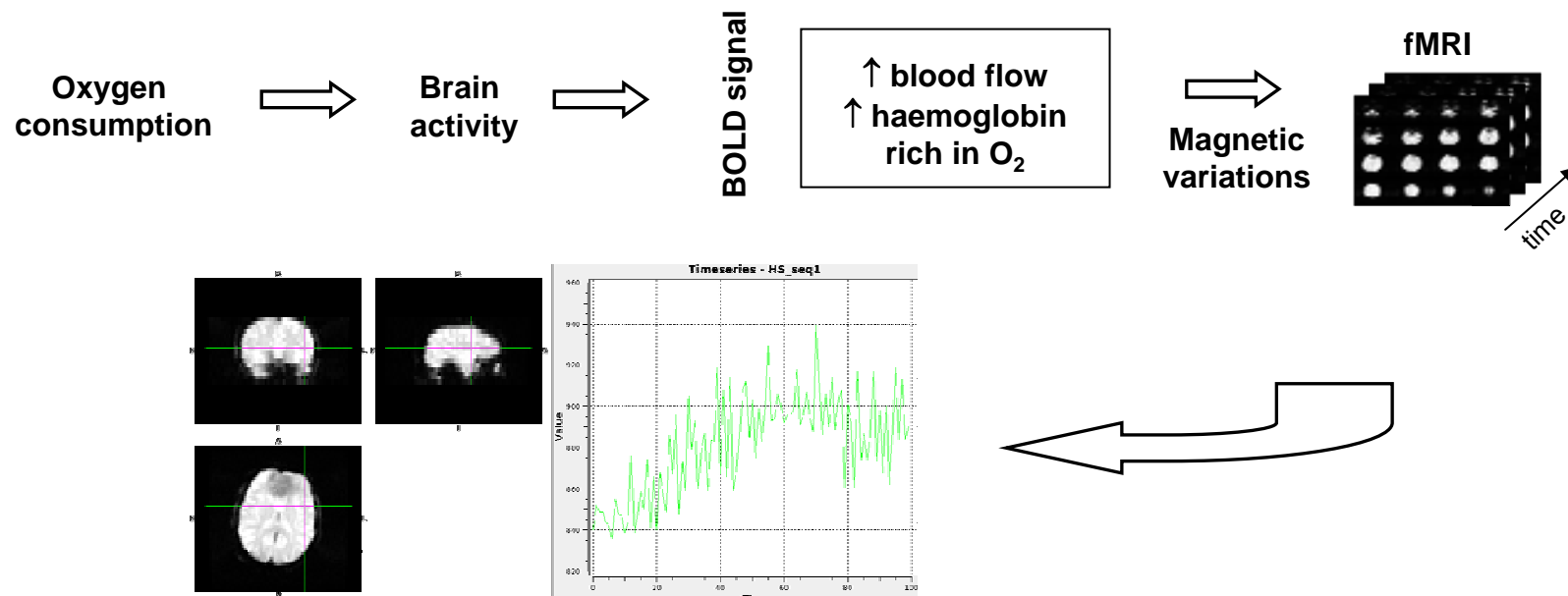
IEETA/R. Andrade | IberGrid'07, San



Functional MRI imaging



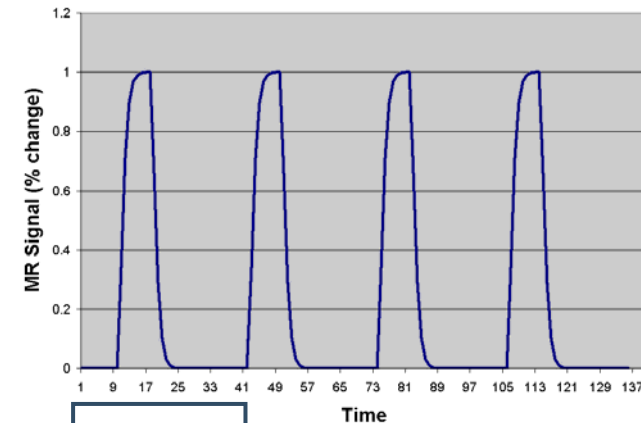
- fMRI allow us to study brain function
- Generates a great quantity of images
 - ▶ e.g. 1 volume every 3s during 5 minutes



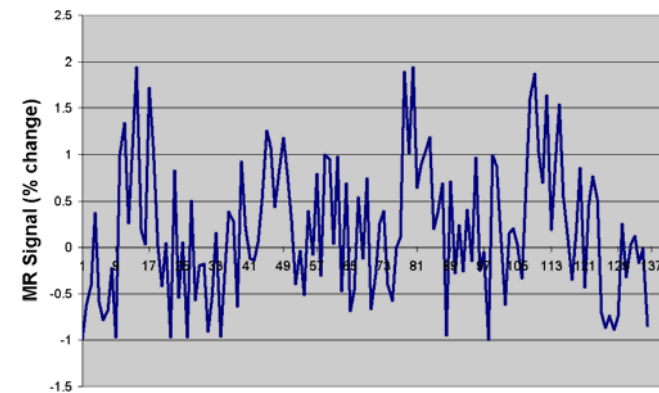
fMRI analysis: parametric vs non-parametric



- Parametric analysis
 - ▶ based on accepted assumptions
- Non-parametric analysis
 - ▶ hypothesis depend on relating spatial areas with relevant occurring events
- Non-parametric analysis advantages
 - ▶ No model is assumed
 - ▶ Find voxels that have similar “behaviour” along time – pair wise analysis
 - ▶ Nonlinear approach, namely association measures to identify “similar” voxels



Model



Time-serie

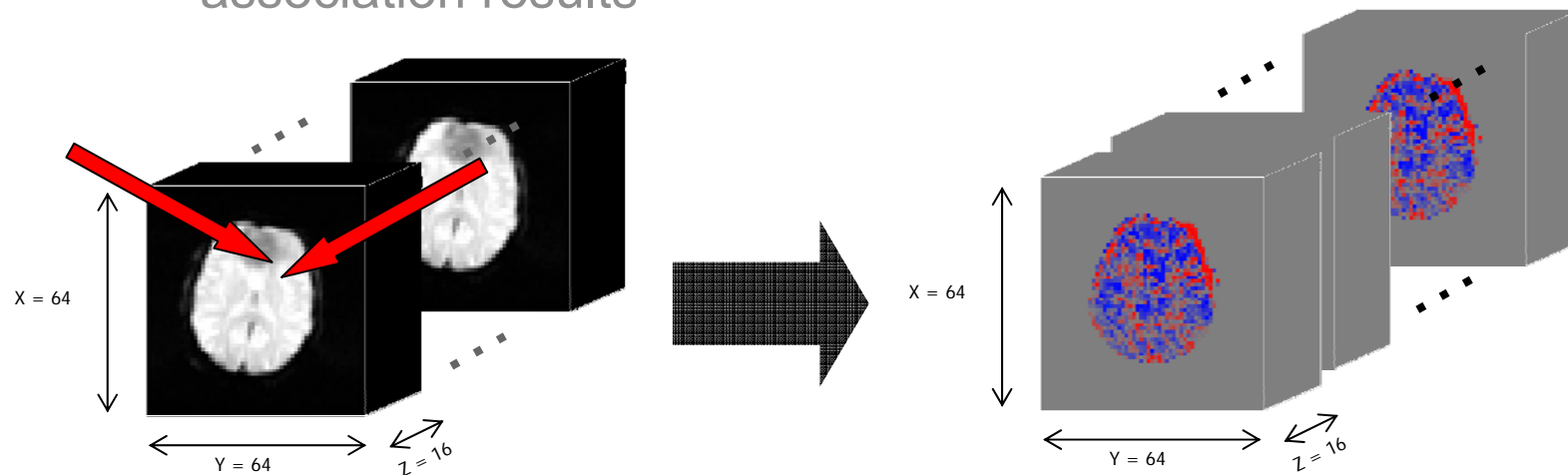
Source of images: Jody Culham's [fMRI for newbies](#) web site

fMRI analysis: voxel pair wise analysis



- One voxel association analysis with all the others
 - ▶ $64 \times 64 \times 16$ (voxels in a fMRI volume) possible associations
 - ▶ The result is one volume with $64 \times 64 \times 16$ association results
- With all the voxels
 - ▶ $(64 \times 64 \times 16) \times (64 \times 64 \times 16)$ possible associations
 - ▶ The result are $64 \times 64 \times 16$ volumes, each with $64 \times 64 \times 16$ association results

Without considering delay





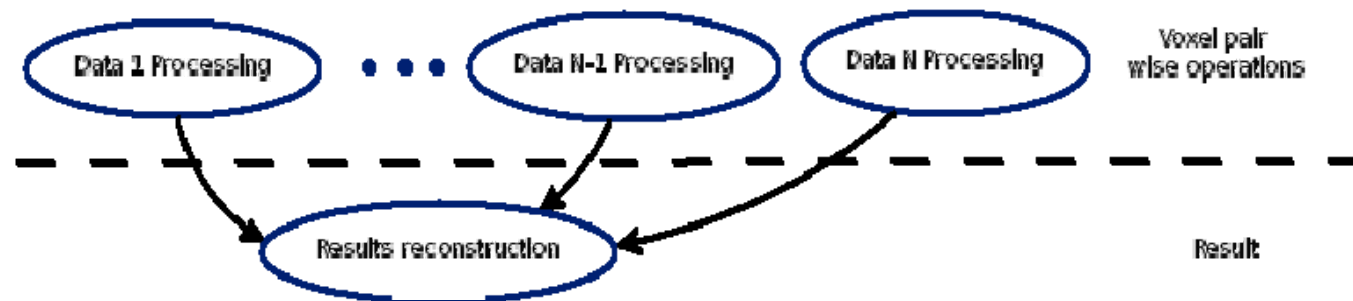
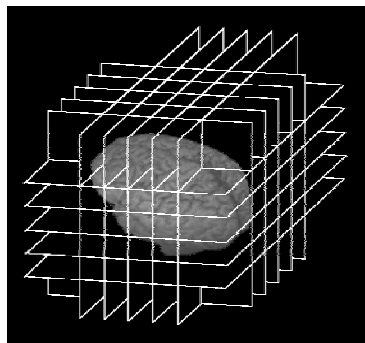
- New opportunities for brain imaging research
 - ▶ Large-scale, distributed data management
 - ▶ Complex analysis (processing)
 - ▶ Workflows (e.g.: pre-processing, analysis and integration, post-processing)
- fMRI voxel pair wise analysis
 - ▶ processing time is limitative (about 5h30 in a normal workstation for a single voxel)
- Previous work in association analysis of biosignals using non linear methods¹

¹ J. P. Cunha and P. G. de Oliveira. A new and fast nonlinear method for association analysis of biosignals. IEEE Trans. Biomed. Eng., 47(6):757–63, 2000.

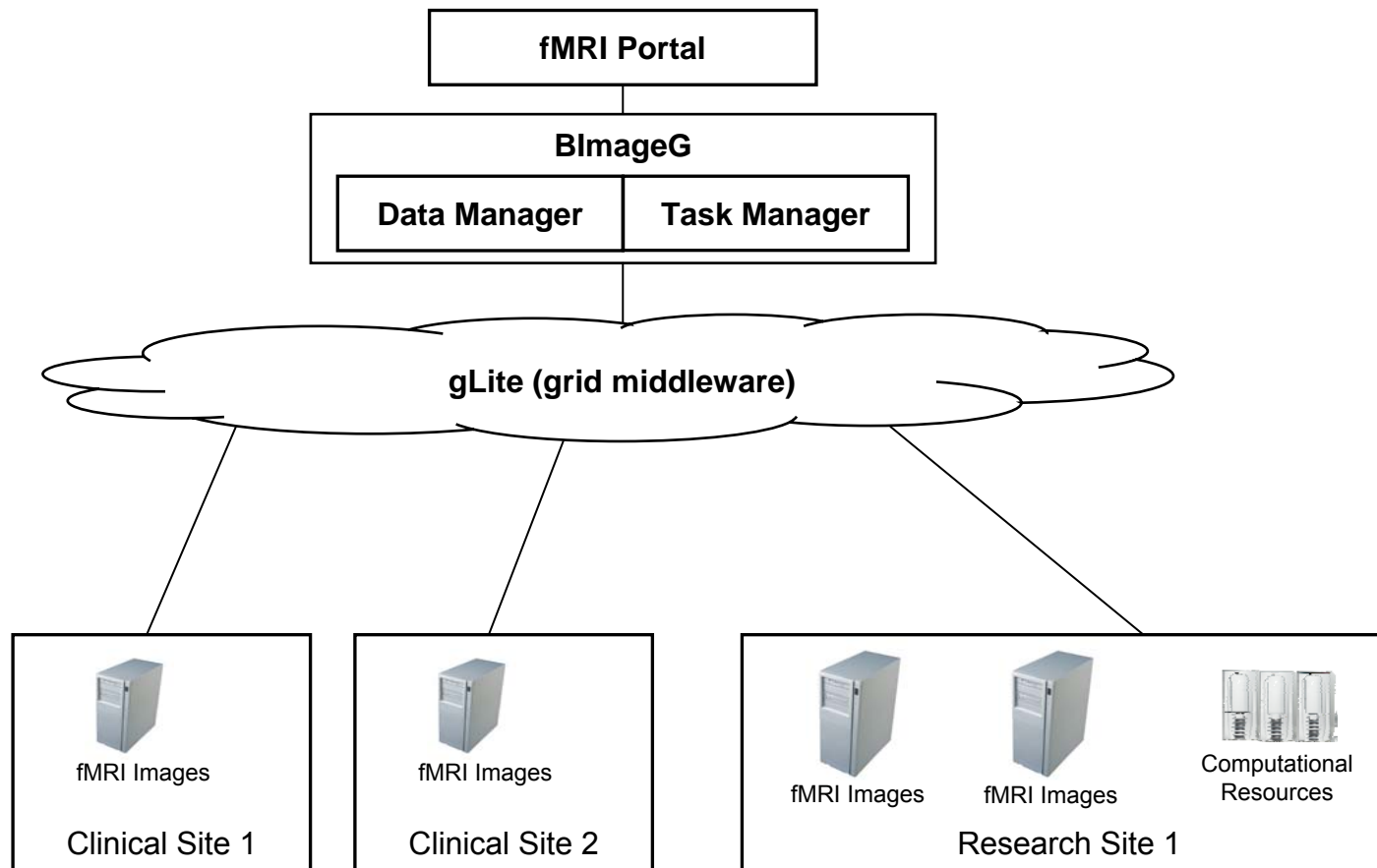
Solution concept



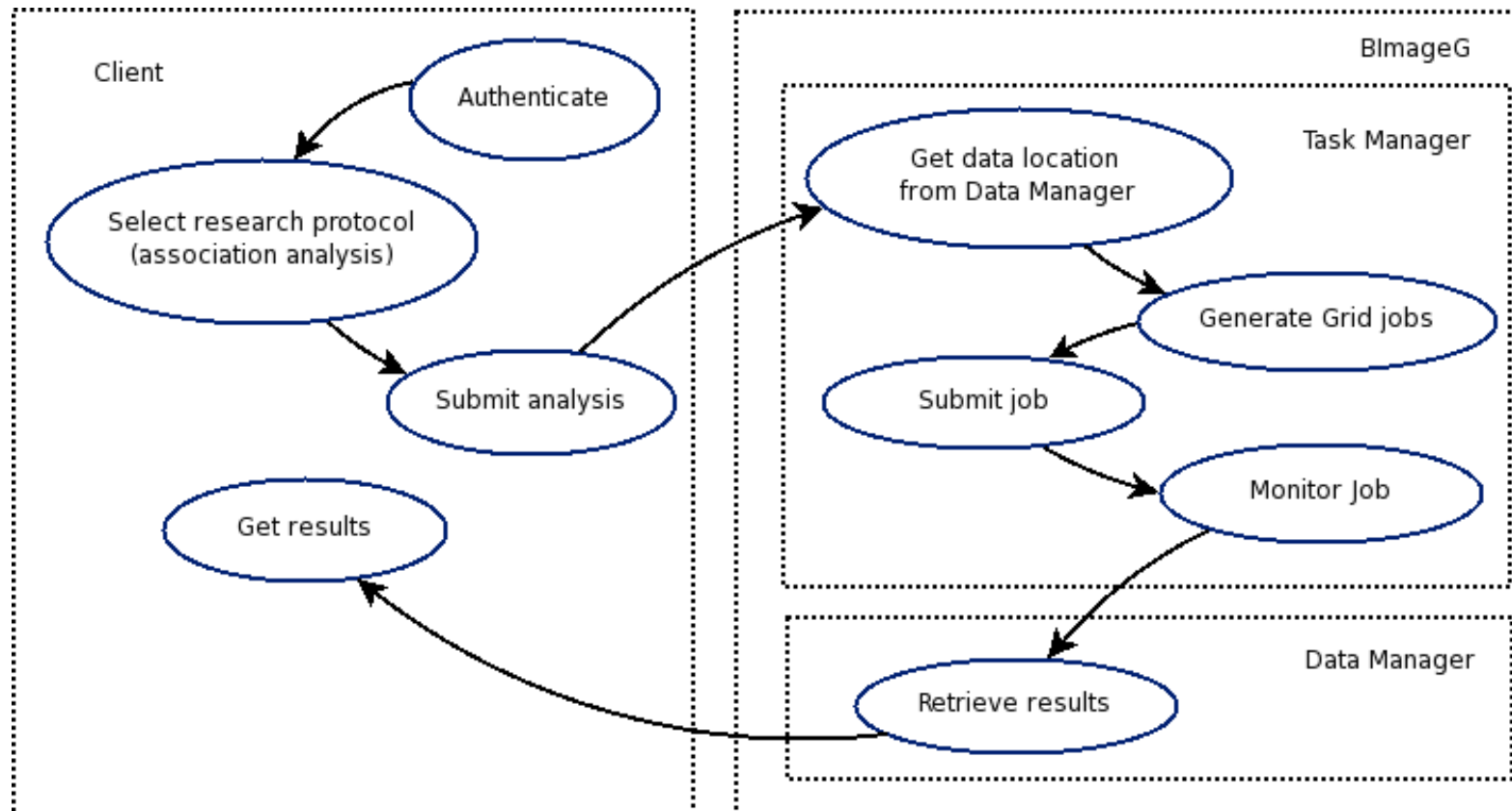
- Natural parallelization of the analysis
 - ▶ Pair wise analysis allows the creation of N independent jobs
- Grid “pluses”
 - ▶ Natural scalability: can evolve this approach
 - ▶ Access to high throughput computation
 - ▶ Access control/authorization provisions (medical data!)
- Approach: a framework to interact with the Grid services and allow a researcher to run fMRI analysis through a simple interface



Architecture



Job Submission workflow

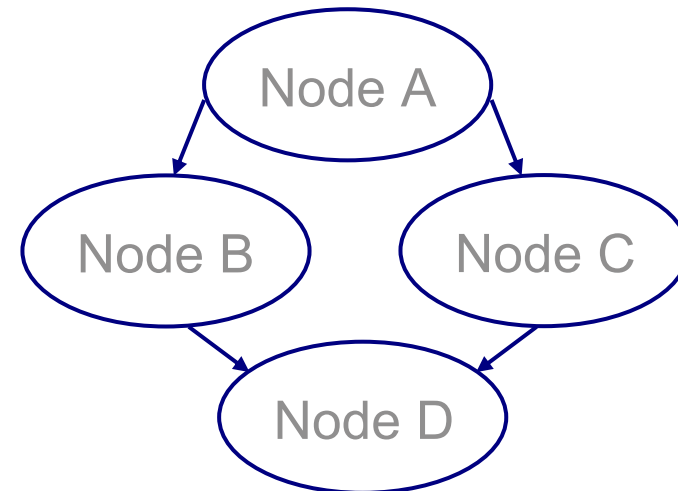


BImageG Implementation



- Integration in the Pre-Production testbed of EGEE
 - ▶ IEETA-PPS: 2 Worker Nodes, 1 Computing Element, 1 User interface, 1 Storage Element and 1 MON
 - ▶ Implemented in virtual hosts using Xen
- Task Manager uses gLite APIs and CLIs to submit and monitor jobs.
- Currently using WMPProxy for job submission
- Job parallelization accomplish by Direct Acyclic Graph (DAG) jobs.
- The Data Manager is being developed

Direct Acyclic Graph



Early Results



- User portal
 - ▶ allows a user to run association analysis, monitor the state of his tasks and manage them.
 - ▶ Each analysis interface is defined in a XML file.

1 Start 2 Select Job 3 Monitoring

| Task | State | Task Nodes | | | | | Options |
|------------------|-------|------------|-------|-----------|---------|------|--------------------------------------|
| | | Total | Ready | Scheduled | Running | Done | |
| Cortex_RF_483907 | Idle | 1 | 0 | 0 | 0 | 0 | <input type="button" value="Start"/> |

1 Start 2 Select Job 3 Monitoring

Task Name:

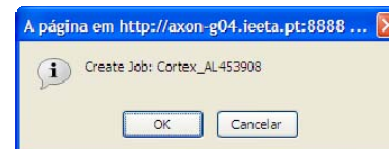
Select Process:

InputData:

Cube Vertice: x: y: z:

Edge of Cube:

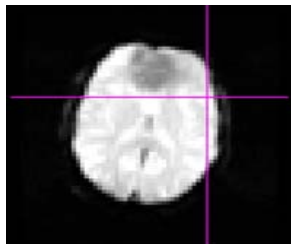
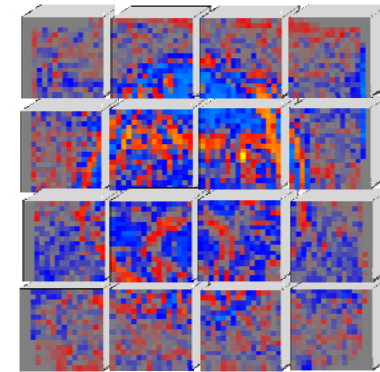
Reference Voxel: x: y: z:



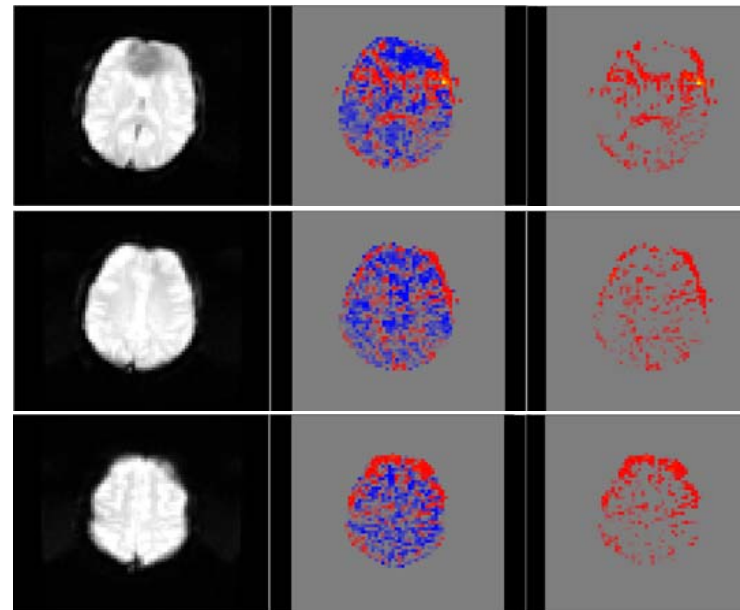
Early Results



- Pair-wise association results
 - ▶ Computing time reduced from 5h30 to approximately 47m



Slice #8 Voxel 45,39



Slice #8

Slice #10

Slice #12

Future work



- User authentication
- Improve data management
 - ▶ Continue the development of the DataManager
 - ▶ Test integration with Medical Data Manager Services
 - Anonymization issues
 - Integration with DICOM servers
- Extend the pair-wise analysis (all brain)
- Migrate to EGEE Production

Summary



- Non-parametric analysis time can be substantially reduced using Grid resources
- Pair-wise analysis is ideal to Grid computing because it can be easily parallelised
- Towards a virtual lab



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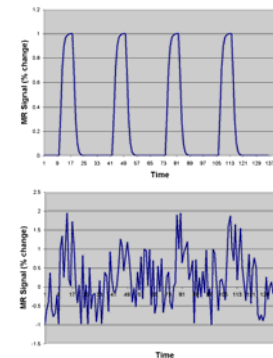
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- The fMRI analysis can be parametric or non parametric
 - ▶ Parametric analysis
 - A model is assumed for a signal associated to a given event/brain function
 - Which are the voxels that “correlate” with this model
 - Statistics are used to see how well the voxels fit the model → associate brain areas
 - ▶ Non parametric analysis
 - No model is assumed
 - Find voxels that have similar “behaviour” along time – pair wise analysis
 - Nonlinear approach, namely association measures to identify “similar” voxels



Source of images: Jody Culham's [fMRI FOR NEWBIES](#) web site