

# NeuroImaging Interest Group

14 November 2017



ROYAL  
HOLLOWAY  
UNIVERSITY  
OF LONDON

CUBIC

Scientific Computing

Data Management

Training & Support

Future developments



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# CUBIC – Standard sequences



- Starting points
- Updated as kindly shared by the MRC-CBSU, Cambridge
- Available under „CUBIC“ protocol group
- [http://www.cubic.rhul.ac.uk/wiki/doku.php?id=mri:acquisition\\_sequences](http://www.cubic.rhul.ac.uk/wiki/doku.php?id=mri:acquisition_sequences)

# CUBIC – Standard sequences



- Structural:
  - MPRAGE
  - TSE and TSE FLAIR (for incidental findings)

# CUBIC – Standard sequences



- fMRI:
  - Standard (2 s, 3 mm iso)
  - High resolution (>1.5 mm in-plane)
  - Faster (>1 s)
  - Larger FOV (205 mm)
  - Multi-Band<sup>1</sup> (>~0.5 s, >1.5mm in-plane)
- Fieldmaps: !!! same geometry (FOV, resolution, angle) !!!

# CUBIC – Standard sequences



- Whole-brain Multi-Band fMRI

	3 mm iso	2 mm iso	1.5 mm in-plane
2 s	✓	✓	✓
1 s	✓	✓ (32 slices)	✓ (28 slices)
~0.5 s	✓	✓ (16 slices)	✓ (14 slices)

- Why
  - Faster acquisition: higher power, more precise sampling of the noise
  - Higher resolution: lower PVE, smaller susceptibility effect, MVPA

# CUBIC – Standard sequences

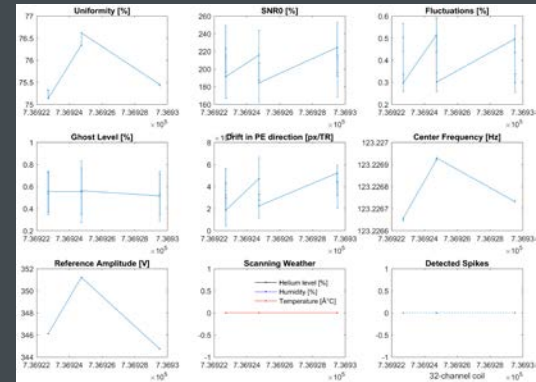
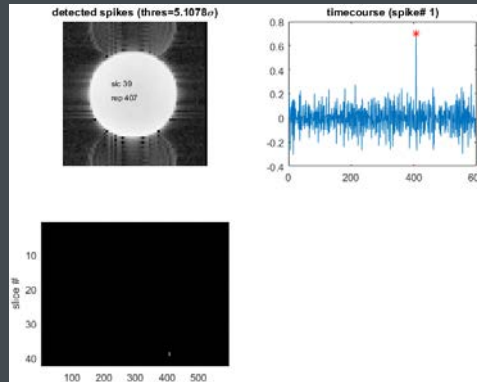
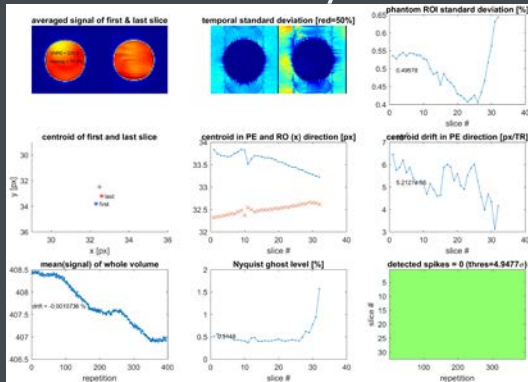


- Diffusion
  - Standard (64 directions, 2 mm iso, ~10 min)
  - DKI (2 b-vals, 30 directions, 2 mm iso, ~15 min)
    - quantifying the non-Gaussianity (microstructural heterogeneity)
    - assess WM regions with complex fiber arrangement
    - tractography, biomarker studies (e.g. AD, PD, tumours, stroke)
  - topup (two acquisitions: AP-PA)

# CUBIC – QA (fMRI)



- Sequence
  - Standard BOLD EPI (2 s, 3 mm iso)
  - With and without GRAPPA (factor = 2)
  - 400 volumes per series
- Real-time analysis on StimPC based on CBSU code

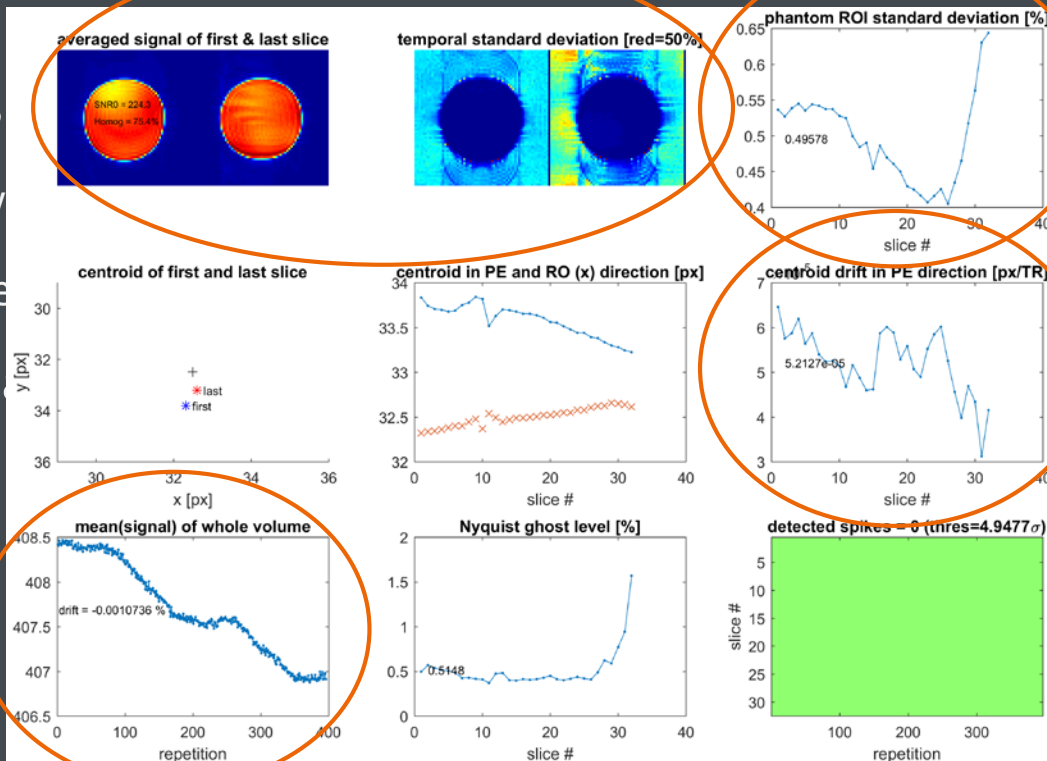




# CUBIC – QA (fMRI)



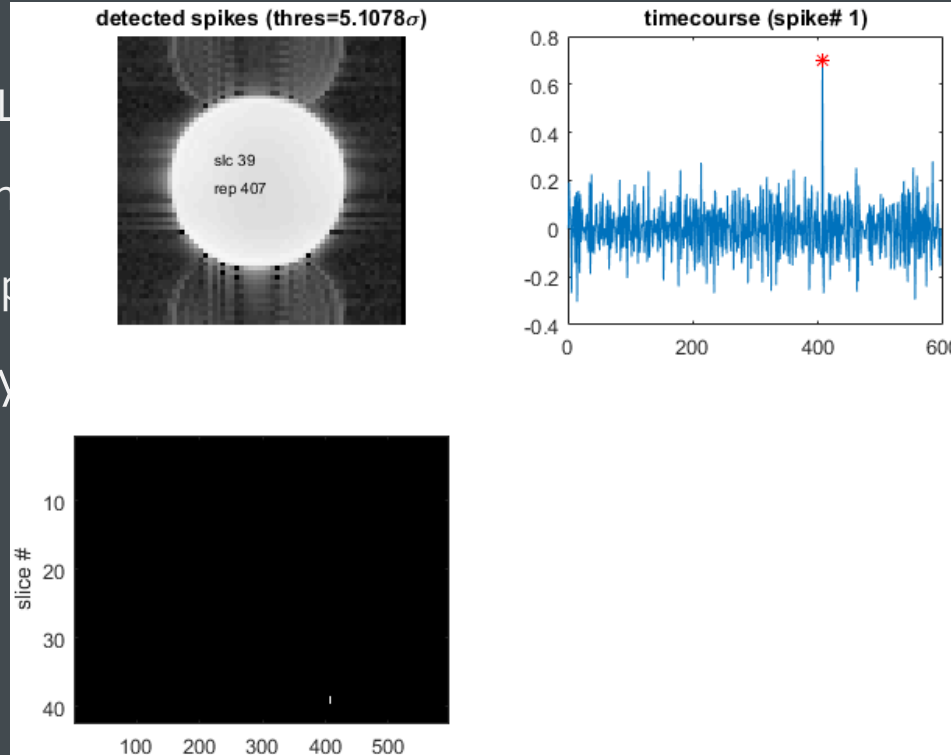
- Sequence
  - Standard B
  - With and w
  - 400 volume
- Real-time an



# CUBIC – QA (fMRI)



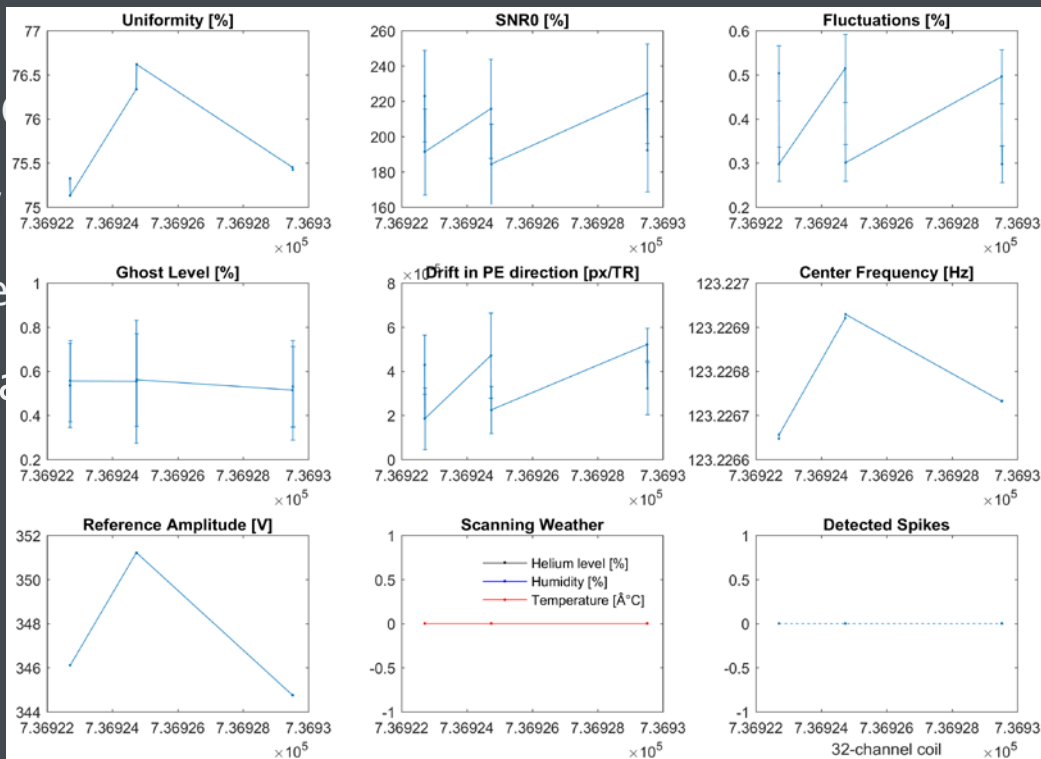
- Sequence
  - Standard BOLD
  - With and without
  - 400 volumes per
- Real-time analysis



# CUBIC – QA (fMRI)



- Sequence
  - Standard BOLD
  - With and without
  - 400 volumes
- Real-time analysis



# CUBIC – Real-time fMRI



## Siemens Standard

- File-based
  - File-management ,overhead'
  - Via HOST
- Implementation
  - Drive mapping + ideacmdtool
  - FileIO

## Direct

- TCP/IP-based
  - No ,overhead'
  - Directly from IRS
- Implementation
  - Configuration Scrip (Win32 Shell)
  - MATLAB interface (using tcp/udp/ip Toolbox)
    - TCPIPClass.m
    - ImageTCPIPClass.m

# CUBIC – StimPC



- Not backed up
- Not connected to the internet, no real-time antivirus scan
  - Performance
  - Security risk → Scan any USB drive before (and after) plugging!
- NI Card for scanner synch pulse
  - ScannerSynchClass: MATLAB interface  
<https://github.com/RHULPsychology/mrisync>
- 'Clone' in the Elaine Funnell lab

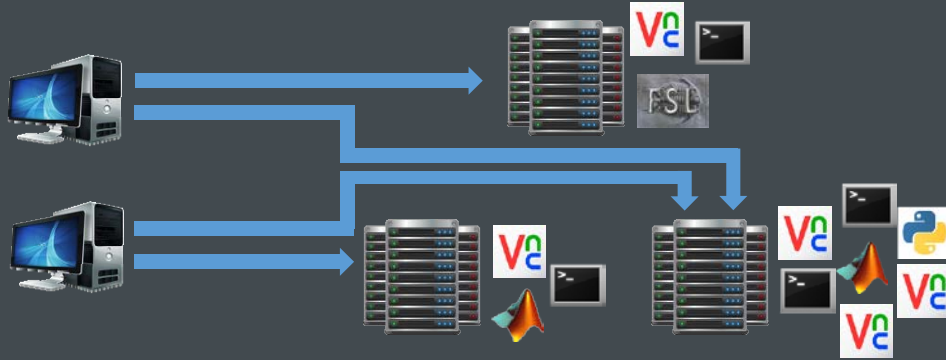
# Scientific Computing - GitHub



- Departmental account <https://github.com/RHULPsychology>:
  - Collection of scripts/tools for experiments and analysis
  - Open, collaboration, back-up, version control
  
- Contribute
  - Contribute to repository
  - Fork (your) repository
  - Create repository

# Scientific Computing – Cluster

- Old cluster – non-scheduled system:

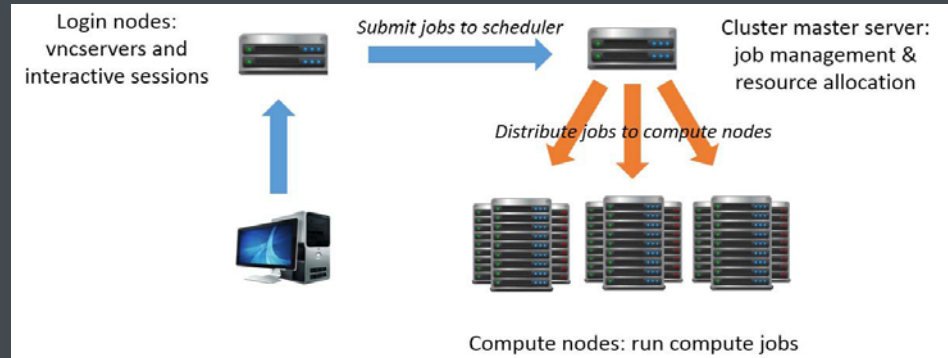


- No distinction between login and compute nodes
  - → run both interactive sessions and large compute jobs on the same machines
- No management of jobs → e.g. machines can run out of memory

# Scientific Computing – Cluster



- New cluster (scheduled system)



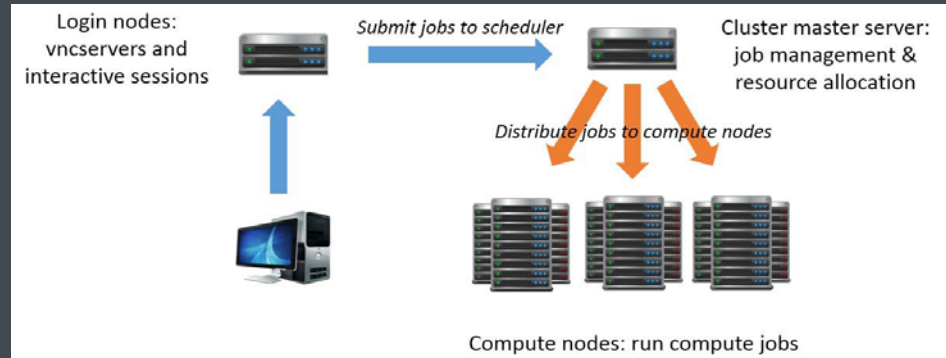
- Distinction between login and compute nodes
  - Login and run interactive sessions on a login node
  - Run large compute jobs on compute nodes
- Scheduling system manages allocation of resources to compute jobs



# Scientific Computing – Cluster



- New cluster (scheduled system)



- Resource management
  - Dedicated resources for jobs → running jobs do not compete for the same resources
  - Resources are fully utilized, but not overloaded
- [http://www.cubic.rhul.ac.uk/wiki/doku.php?id=cluster:cluster\\_root](http://www.cubic.rhul.ac.uk/wiki/doku.php?id=cluster:cluster_root)



# Scientific Computing – Software



- Central repository at `/usr/local/apps/psycapps`<sup>1</sup>:  
[http://www.cubic.rhul.ac.uk/wiki/doku.php?id=cluster:cluster\\_architecture#software](http://www.cubic.rhul.ac.uk/wiki/doku.php?id=cluster:cluster_architecture#software)
  - SPM, FSL, Freesurfer
  - R 3.4
  - python via (mini)conda<sub>3</sub> with python 2.7 and 3.6
    - `source /usr/local/apps/psycapps/config/conda_bash [options]`
      - `<pyenv>`      *python environment: py27 for python 2.7, py36 for python 3.6 (default)*
      - `quit`          *quit python environment*
      - `help`          *display this help*
  - automatic analysis

# Scientific Computing – Software

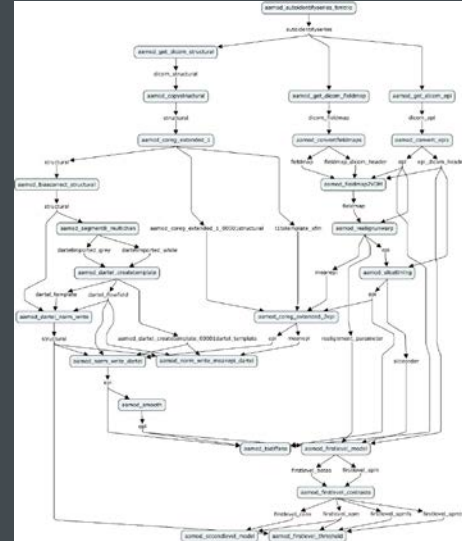
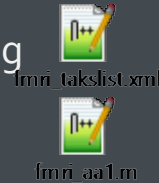


- automatic analysis <https://github.com/RHULPsychology/automaticanalysis>
  - A pipeline system for neuroimaging written in Matlab
    - MRI: structural, fMRI, DTI/DKI (also with topup), MTI, MPM
    - MEG/EEG
  - Implements most SPM 12, as well as some FSL and Freesurfer functions
  - Toolboxes (GITF, BrainWavelet, VBQ)
  - State-of-art solutions from contributors and external scientists
  - Developed and tested/used: MRC-CBSU, WUST, UWO, RHUL, TCD, UEA

# Scientific Computing – Software



- automatic analysis <https://github.com/RHULPsychology/automaticanalysis>
  - High-level based on standardised recipes → Transparent, replicable
    - Tasklist: processing steps
    - User Master Script: customise processing
  - Examples for quick start
  - Tracks processes → Restartable
  - Notifies via e-mail
  - Parallel processing (subjects, sessions, steps)<sup>1</sup>



# Scientific Computing – Software



- automatic analysis <https://github.com/RHULPsychology/automaticanalysis>

- Within-subject summary



- Between-subject summaries

- Motion correction



- Spatial Normalisation



- First-level activations





# Data Management – Department



- Cluster
  - Local<sup>1</sup>
  - Backed up daily (12.10am), 30 days retention
  
- Solutions
  - MRIRAw      5 TB, read-only, raw data
  - MRIWork     1 TB / PI, read/write, working data with internal share
  - MRIArchive 1 TB / PI, read/write, completed data with internal share



# Data Management – College



- Cloud
  - Access to files from web, desktop and mobile devices
  - Working data with external share<sup>1</sup> (even with those who don't use them)
  - Version history and deleted file recovery
  
- Solutions
  - OneDrive for Business      1TB
  - Dropbox Business            unlimited storage

# Data Management – College



- Figshare for Institutions
  - Mediated access (no browsing)
  - Open access with DOI (also confidential and/or embargoed)
    - Discoverable
    - Persistently identifiable
  - Comply with external funding requirements
  - Completed data with open share



# Data Management – Summary



1. Plan: DMPonline <https://dmponline.dcc.ac.uk>
  - Templates for most of the UK, EU and US institutes and funders
  - Guidance from the DCC, as well as from the institutes and the funder
  - Exports to PDF and Microsoft Word
2. Create
  - i. Cluster: raw → working → results → complete
  - ii. Cloud: working → results
3. Preserve (complete): Figshare



- Wiki <http://www.cubic.rhul.ac.uk/wiki/doku.php>
  - Standard sequences  
[http://www.cubic.rhul.ac.uk/wiki/doku.php?id=mri:acquisition\\_sequences](http://www.cubic.rhul.ac.uk/wiki/doku.php?id=mri:acquisition_sequences)
  - Cluster  
[http://www.cubic.rhul.ac.uk/wiki/doku.php?id=cluster:cluster\\_root](http://www.cubic.rhul.ac.uk/wiki/doku.php?id=cluster:cluster_root)
  - Workshop slides
    - Cluster [http://www.cubic.rhul.ac.uk/wiki/doku.php?id=cluster:cluster\\_root](http://www.cubic.rhul.ac.uk/wiki/doku.php?id=cluster:cluster_root)
    - fMRI <http://www.cubic.rhul.ac.uk/wiki/doku.php?id=how-to>



- Workshops (with hands-on)
  - Scientific Computing <https://doodle.com/poll/rtncigei559p6n3b>
    - Introduction to RHUL-Psychology computing system
    - Linux (for FSL and FreeSurfer users): primer, advanced, parallel computing
    - MATLAB: primer, advanced, parallel computing
  - fMRI: part of the RTS



- 'Clinic': Tibor Auer
  - Phone and e-mail: 6594, [Tibor.Auer@rhul.ac.uk](mailto:Tibor.Auer@rhul.ac.uk)
  - Drop-in session: W129, Wednesdays, 12.00 - 13.00 and 15.00 - 16.00
  - Topics
    - Advising, revising, contributing to grants and manuscripts
    - Programming, cluster usage
    - Study and experiment design
    - Acquisition
    - Processing, analysis and interpretation

# Further Developments



- NI Card for button boxes (both Lunitouch and Nata)
  - Unified solution for experiments (+MATLAB interface: ScannerSynchClass)
  - Faster and more reliable than USB
  - More elegant and tidy
  - <£30 (+ in-house engineering)

# Further Developments

- AutoAlign: <https://www.healthcare.siemens.co.uk/magnetic-resonance-imaging/options-and-upgrades/clinical-applications/autoalign-head-ls>
  - Automated positioning and alignment of the slices using anatomical landmarks
  - High cross-participant robustness → maximize FOV overlap across participants
  - Longitudinal studies: ensure spatial correspondence
  - Multiple acquisitions/series: minimize registration required
  - +Partial FOV: essential!
  - <1 min
- ~£4000

# Further Developments



- BIOPAC <https://www.biopac.com/application/magnetic-resonance-imaging-with-biopac-equipment>
  - MR Safe and MR Conditional acquisition of physiological signals
    - ECG, EMG, EOG, EGG
    - Respiration, O<sub>2</sub>, CO<sub>2</sub>, Pulse Oximerty
    - EDA, Temperature, Hand Grip Strength
    - ...
  - Import into SPSS, MATLAB<sup>1</sup>

# Further Developments



- EEG/EMG

- ...