

# Using & Creating Software & Toolboxes for Research: Cases from Neuroimaging Data Analyses

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COMPUTER ENGINEERING,

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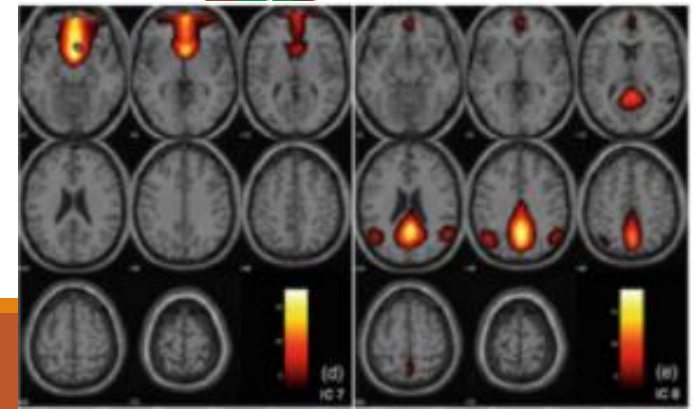
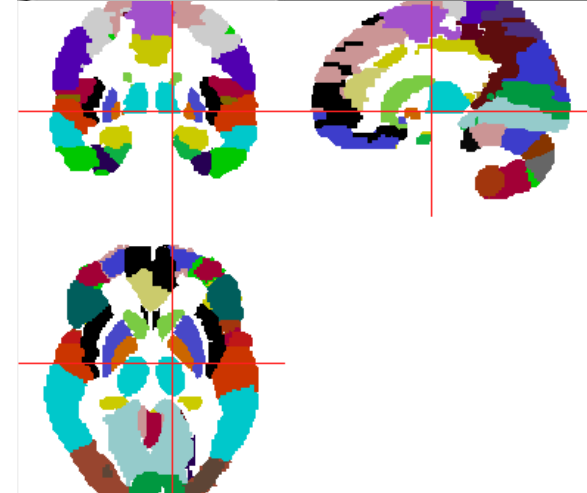
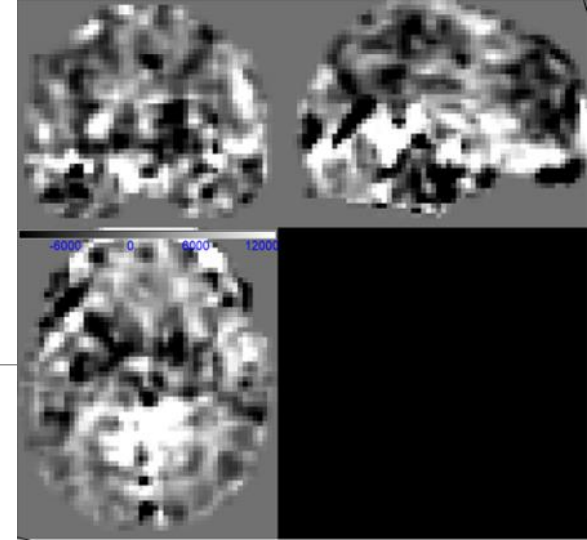




# Neuroimaging Research Data is complex/sophisticated...

- ❑ Multidimensional: 3D or 4D (and also include surely 2D and 1D)
- ❑ Saved in special formats: DICOM, ANALYZE, NIFTI, ...
- ❑ Large in size, and also:
- ❑ Accompanied with lots of other data (behavioral, genetic, other imaging modalities, ...)
- ❑ Overall, neuroimaging research data has large number of pieces/files that need to be stored neatly (with easy to reach/query database hierarchy)
- ❑ Sophisticated analysis pipeline(s) (sequence of methods) used

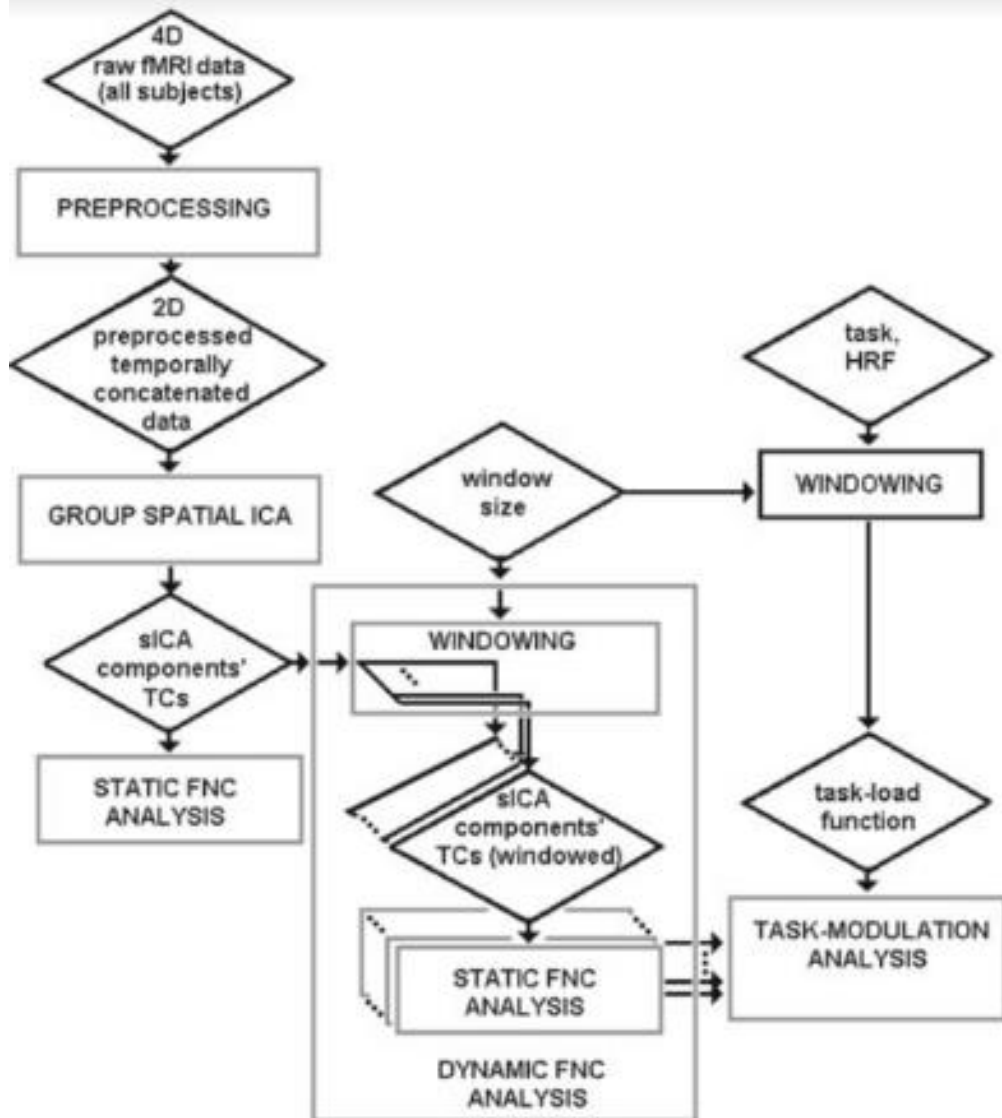
and the pipelines are not fixed, constantly evolving/ being updated over time as new techniques are developed!



# Analyses produce more and more (intermediate) data

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- ❑ There are many processing & analyses steps:
- ❑ data cleanup, QC/inspection, pre-processing, noise-removal, filtering, slice-time correction, motion correction / co-registration, warping to a common template, reslicing, plus various high-level statistics, and then higher-level meta analyses, group analyses, etc,...
- ❑ There are various methods for each step (constantly scan recent methods papers)
- ❑ There are various tools which can do one or some of these steps (and each may be requiring different file formats!!!)
  - so, data conversion tools/software may be needed (compatibility)
- ❑ As a result:
  - for each GB of original/raw data → 100s of GBs of intermediate data may be generated!



Analyses  
produce more  
and more  
(intermediate)  
data

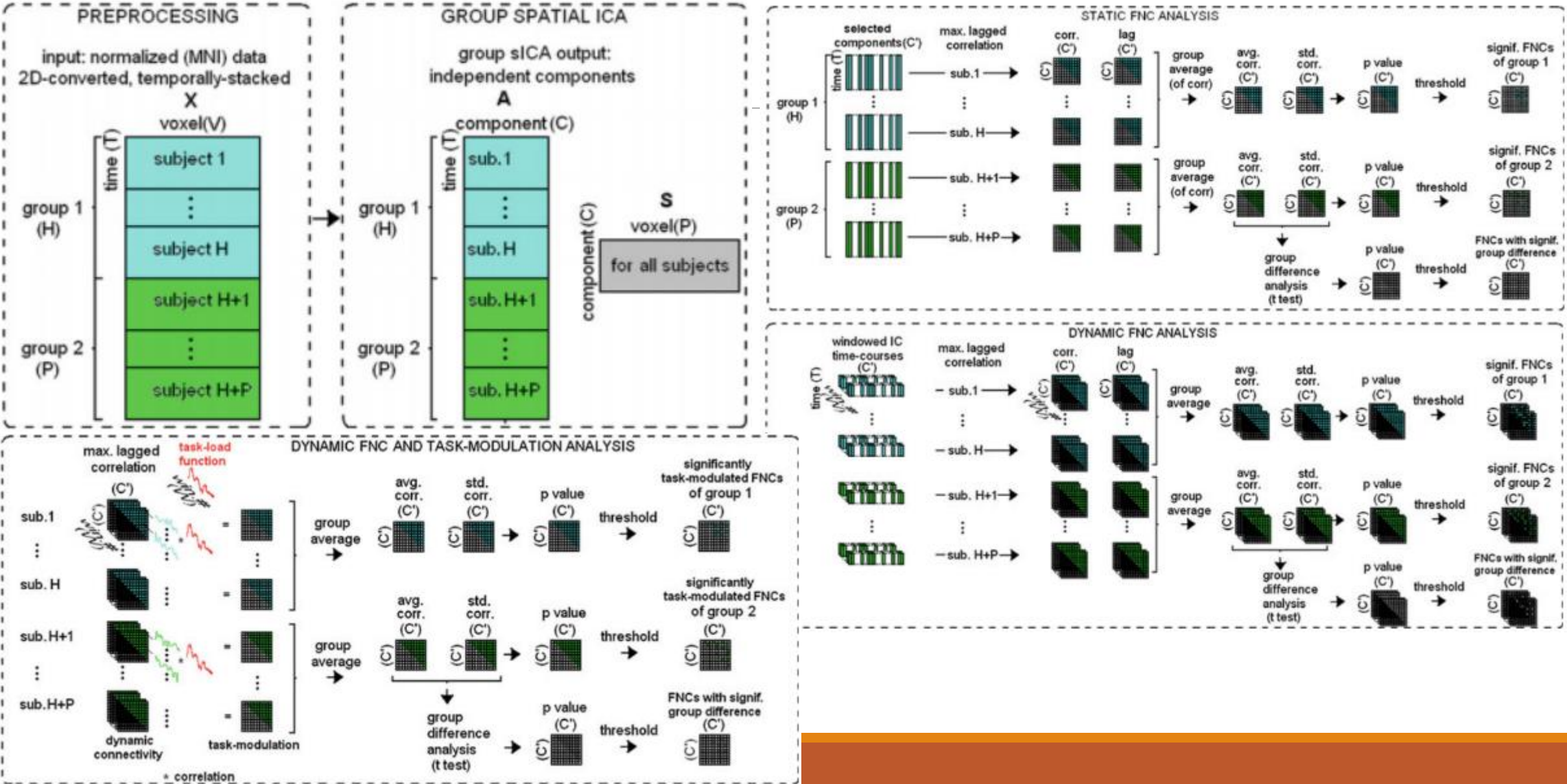
Magn Reson Mater Phy (2010) 23:351–366  
DOI 10.1007/s10334-010-0197-8

#### RESEARCH ARTICLE

## A method for evaluating dynamic functional network connectivity and task-modulation: application to schizophrenia

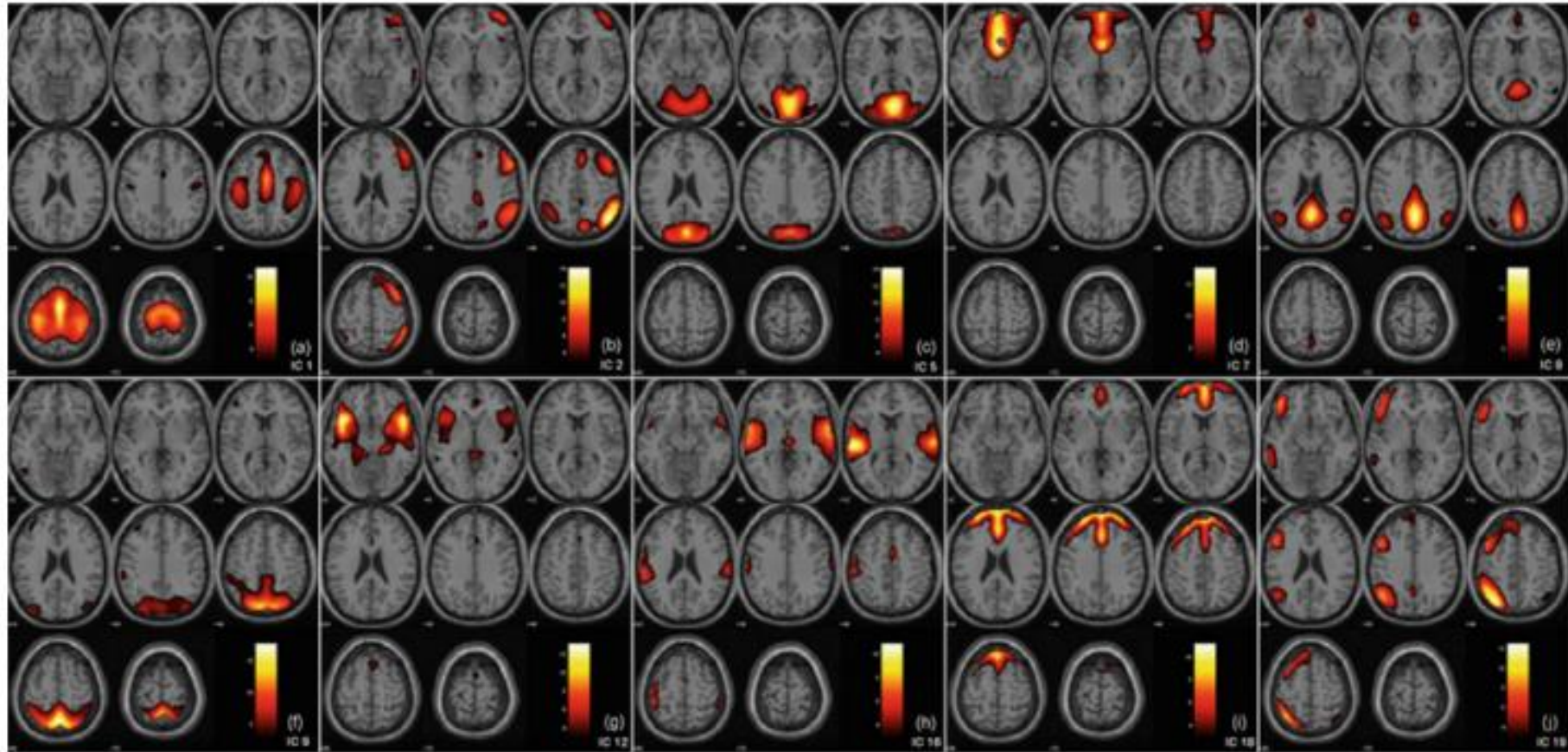
Ünal Sakoğlu · Godfrey D. Pearlson · Kent A. Kiehl ·  
Y. Michelle Wang · Andrew M. Michael ·  
Vince D. Calhoun

# Analyses produce more and more (intermediate) data





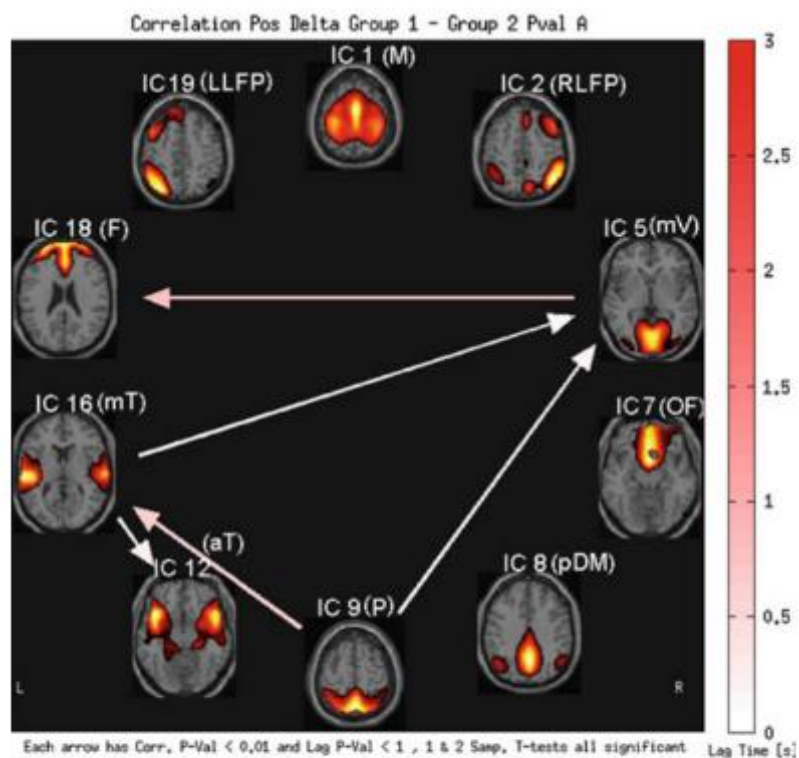
# Analyses produce more and more (intermediate) data



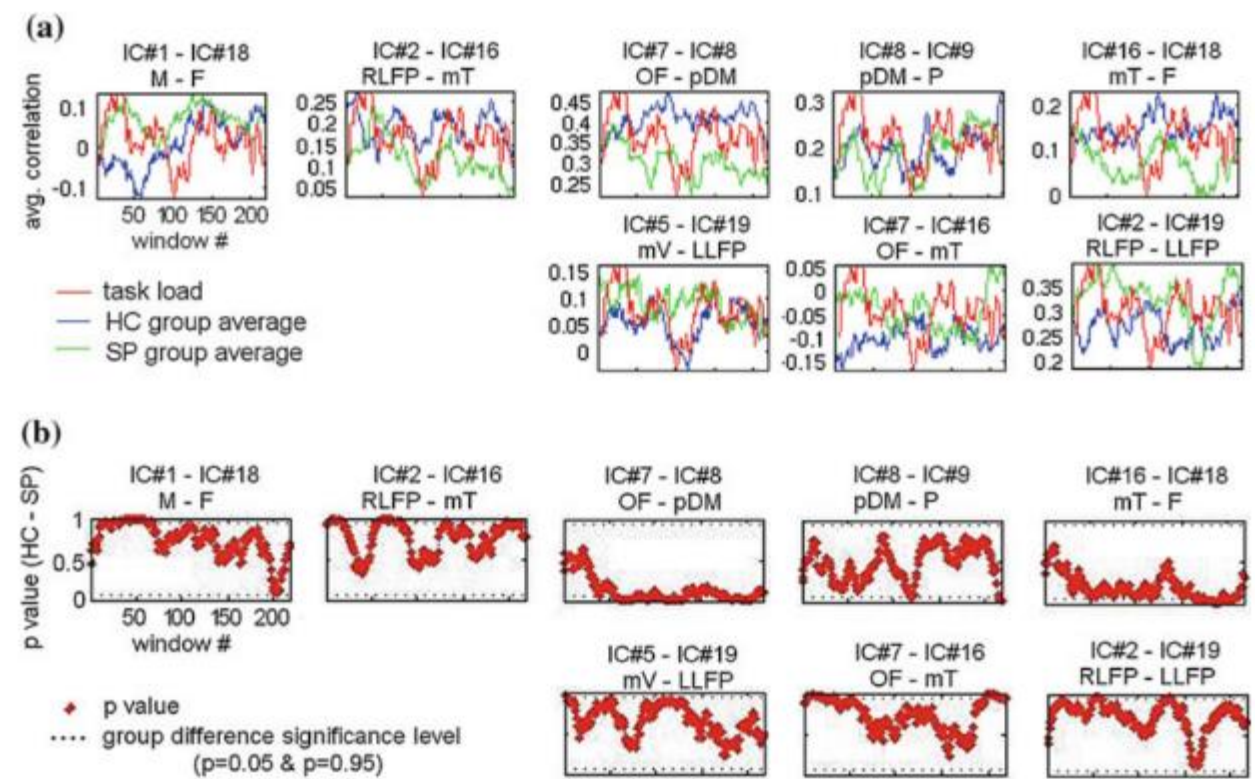
**Fig. 9** Ten selected spatial ICA components (networks). **a** IC#1: motor network (M), **b** IC#2: right lateral fronto-parietal network (RLFP), **c** IC#5: medial visual network (mV), **d** IC#7: orbito-frontal network (OF), **e** IC#8: posterior default mode network (pDM), **f** IC#9: parietal

network (P), **g** IC#12: anterior temporal network (aT), **h** IC#16: medial temporal network (mT), **i** IC#18: frontal network (F), and **j** IC#19: left lateral fronto-parietal network (LLFP)

# Analyses produce more and more (intermediate) data



**Fig. 10** HC-SP static FNC analysis results. Connections with significant group difference are shown ( $P < 0.01$ ). The lag differences are ignored (lag difference  $P < 1$ ). Bootstrap results with 20 subjects per group, 1,000 randomized trials, resulted in 100% occurrence (of the significant group difference of the same connections)



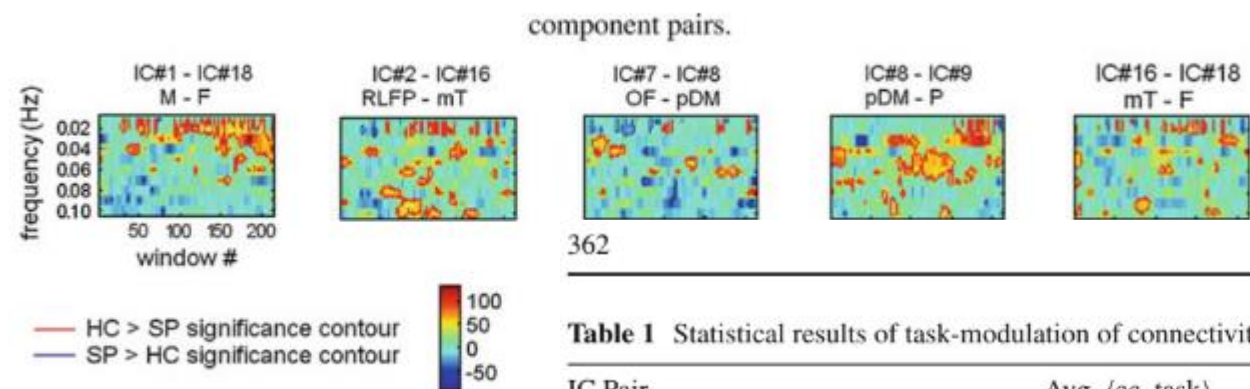
**Fig. 11** Dynamic FNC analysis results. **a** Temporal evolution of average correlation coefficient for the two groups (blue: HC group average, green: SP group average), for selected pairs. Temporal evolution of task-

load (red) is also presented for comparison. **b** Corresponding dynamic  $P$ -values of group significance of the dynamic correlation for these pairs



# Analyses produce more and more (intermediate) data

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**Table 1** Statistical results of task-modulation of connectivity

IC Pair	Avg. (cc, task)		HC–SP ( <i>T</i> -test)	Bootstrap results ( <i>N</i> <sub>1</sub> = <i>N</i> <sub>2</sub> = 20, Repetition = 1,000)
	HC	SP	<i>P</i> -value	<i>P</i> < 0.05 (%)
IC#1 (M) & IC#18 (F)	0.0604	0.1221	0.0107 (SP > HC)*	69.4
IC#2 (RLFP) & IC#16 (mT)	0.1069	0.0562	0.0223 (HC > SP)*	54.6
IC#2 (RLFP) & IC#19 (LLFP)	0.0974	0.0960	0.4815 (HC > SP)	
IC#5 (mV) & IC#19 (LLFP)	0.1173	0.0786	0.0655 (HC > SP)	
IC#7 (OF) & IC#8 (pDM)	0.0528	0.0951	0.0128 (SP > HC)*	63.5
IC#7 (OF) & IC#16 (mT)	0.0868	0.0564	0.0566 (HC > SP)	
IC#8 (pDM) & IC#9 (P)	0.0456	0.0970	0.0133 (SP > HC)*	69.1
IC#16 (mT) & IC#18 (F)	0.0708	0.0376	0.0195 (HC > SP)*	55.0

*R*<sup>2</sup> value of regression of dynamic average correlation coefficients with the task load function for all component pairs, for the two groups and *P* value of the group difference. The component pairs marked with “\*” show significant group difference, hence show significant group difference (*P* < 0.05) in specified task modulation of the functional connectivity between the specified component pair. None of them are significant when the Bonferroni correction is applied (*P* < 0.002). When a false discovery rate of *P* < 0.05 was applied, the cut-off value in the original *P* values was 0.0223. Bootstrapping results, in terms of percentage of the subgroups that provide *P* < 0.05 are also provided. Subgroups consisted of 20 subjects randomly chosen out of 28 subjects per each group and 1,000 random repetitions

\* Statistically significant (*P* < 0.05)

# So, lots of scripting, coding, batch processing

most of the time in different coding environments, and even with different OS & HW

```
pv2nifti_mouse.sh - Notepad
File Edit Format View Help
#!/bin/bash
programe='basename $0'
cwd=$PWD

if [ $OSTYPE == 'solaris' ]
then
MYGAWK=/app/abt/nosw/bin/gawk
MYGREP=/usr/bin/grep
RM=/bin/rm
else
MYGAWK=/bin/gawk
MYGREP=/bin/grep
RM=/bin/rm
fi

# Subroutines
#####
usage ()
{
echo "USAGE: $programe input <y/n>"
echo " * for input use 'subject' (to convert all image sets) or '2dseq' (to convert just one)"
echo " * output filenames are automatically generated in the base directory like directory.subject.rev"
echo " use and y to automatically overwrite existing files and n to automatically skip existing files (
}

getpar ()
{
${MYGREP} $2 $1 | awk -F= '{print $2}'
}

Ln 690, Col 3
```

e.g. shell scripting  
in Unix/Linux for  
preprocessing...

```
US_ICATCextract.m - Notepad
File Edit Format View Help
cd('C:\UHCL\DODProjectGopi\DFNCofGWN\ResearchWork\DataAtEmory\DOD_GWI\...
Unal_old_MNIdata\Group_ICA\Anals_July25_dtAROMA_niC44\GWS2_NCVC_FNC_regressionresults\...
Anals_Oct17_dtAROMA_CtrlsAndGWS2\gica_cmd_scaling_components_files')

clear all
myfilenames=ls
myfilenames2=myfilenames(3:55,:);

%Extract ICA TCs for each i subject
for i=1:size(myfilenames2,1),
    mydata=spm_read_vols(spm_vol(myfilenames2(i,:)));
    mydataICATC_all53subj(:,i)=mydata;
end

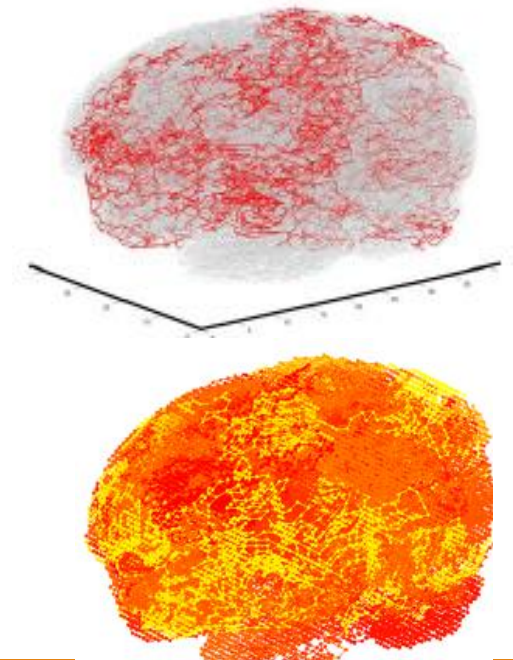
%Static FC
for i=1:53,
    subjData=mydataICATC_all53subj(:,i);
    mycc=corrcoef(subjData), %
    mycc_all53subj(:,i)=mycc;
end

%Dynamic FC
for i=1:53,
    subjData=mydataICATC_all53subj(:,i);
    for k
        compute k dynamic mycc matrices for each i
        mycc_all53subj_dynamic(:,k,i)=kth mycc matrix;
    end
end

Ln 1, Col 1
```

Coding in MATLAB,  
in Windows for  
analyses  
(have written  
hundreds of  
functions/subroutine  
s/modules and tens  
of thousands of lines  
of code... )

Visualization using  
MATLAB, or another  
language (ImageJ, MRICro,  
MRICron, AFNI, FSL etc.)

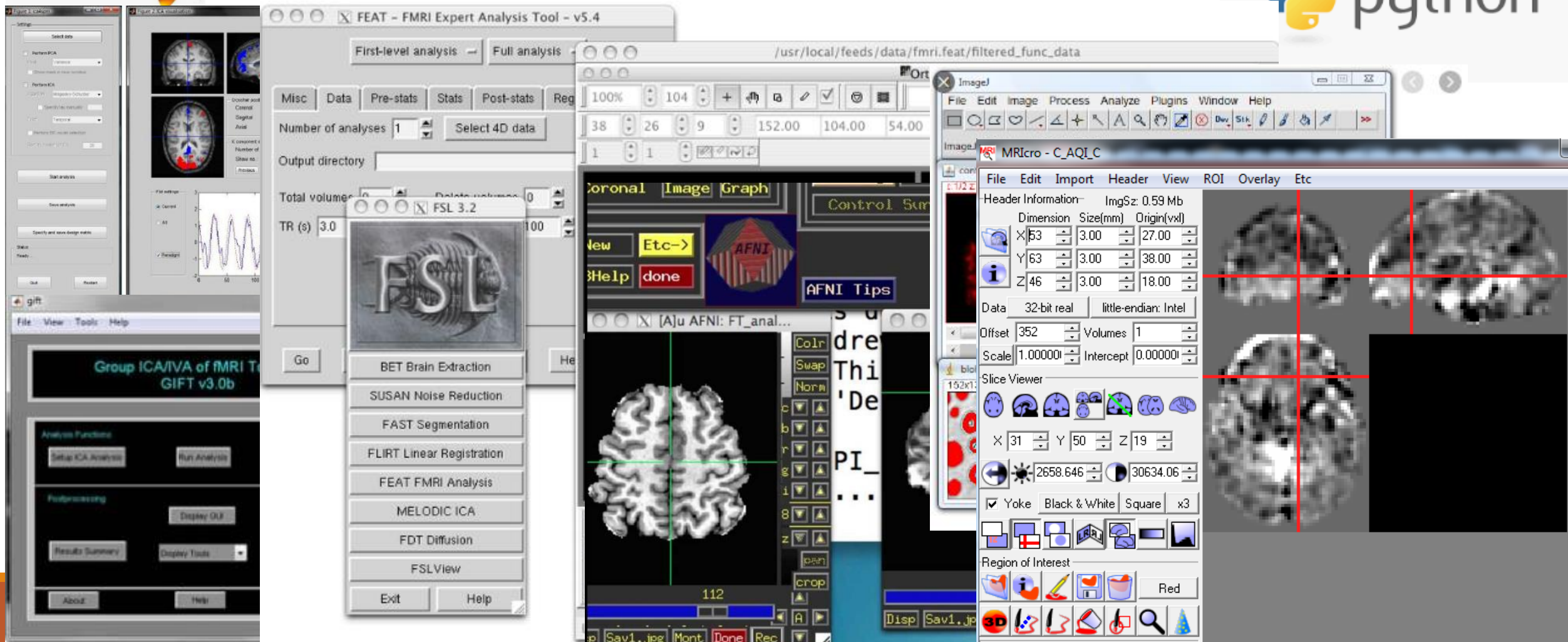




# So, lots of scripting, coding, batch processing and using existing resources/software (versions, constantly evolving!)

Matlab

python™



Researchers are not necessarily efficient coders/programmers  
So if there are resources (time or \$\$) we try to develop easy to use “toolboxes”  
This is needed for continuity, transparency, replicate-ability, ...

Not secure | drsakoglu.com/p/dynaconnfdctoolbox.html

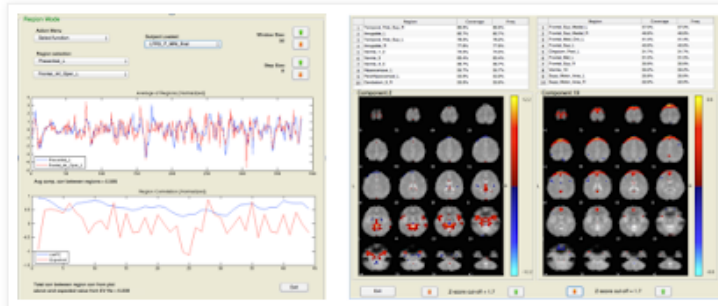
Welcome to Dr. Unal "Zak" Sakoglu's website.

#### Menu

- Home
- Faculty Page
- Publications
- DynaConn
- Photos/Misc

## DynaConn

Dynamic Functional Connectivity (DynaConn) Graphical User Interface (GUI) Toolbox for fMRI.  
With this toolbox, you can do dynamic sliding time-window analyses of fMRI datasets.



It is MATLAB-based, so you need MATLAB. It should work with any version of MATLAB that is installed 2013 or later. It uses some, mostly modified, SPM8 functions. but those are already bundled in it so you do not have to download them.

It also works with C. You can find and download the source code from <https://bitbucket.org/UnalSakoglu/dynaconn> in order to have a

Please contact Dr. Sakoglu (sakoglu[at]uhcl[dot]edu) if you download it and for any question

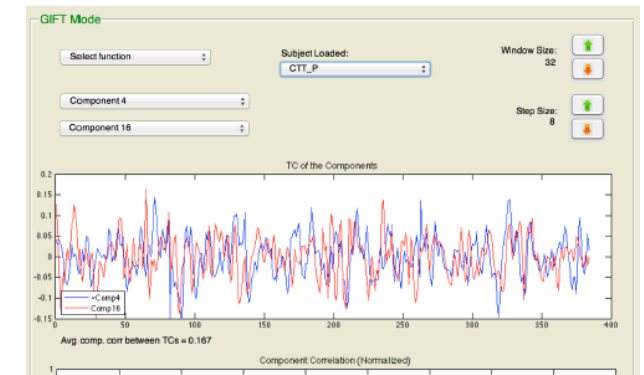
Collaborators: Dr. Mutlu Mete, Associate Professor; and John E. Esquivel, MS Student, TAMU

If you download DynaConn & use it for your analysis, please cite the following work:  
(Visit <https://www.drsakoglu.com/p/publications.html> for links to full text of these publications  
On the DynaConn toolbox:

John Esquivel, Mutlu Mete, Unal Sakoglu, "DynaConn: A Software for Analyzing Brain's Dynamic Functional Connectivity", Midsouth Computational Biology and Bioinformatics Society Conference (MCBIOS), March 2013, Dallas, TX.  
John Esquivel, Mutlu Mete, Unal Sakoglu, "Software for Analyzing Brain's Dynamic Functional Connectivity", Annual Medical Device Symposium, November 2013, Dallas, TX.

## DynaConn Users Guide

Dynamic Function Connectivity Graphical User Interface



YouTube channel page for w00tIt00w (3 subscribers). The page shows the channel name, subscriber count, and a list of uploads. The uploads include:

- Using DynaConn (95 views • 5 years ago)
- DynaConn Setup (84 views • 5 years ago)
- Preprocess with GIFT (59 views • 5 years ago)
- Downloading DynaConn (79 views • 5 years ago)



# Picking the right s/w, and developing (in-house/custom development) if necessary, is important!!!

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- Takes a lot of effort (\$\$ and time)
- Are they well-documented, is support available?
- Hire/invest in/budget for a software developer if you can (\$\$? )  
or ask for help if they have the time (again \$\$? or time??)
- Not much grant \$\$ for that (even NSF?), even if there is, it is tough
- Most of the time we develop & distribute the toolboxes for free  
.... or in some cases it can be commercialized (FSL, etc.)



Fig 1: Brain 3D Voxel representation

# CI/IT personnel:

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- Be flexible with researchers, familiarize with their research

Research s/w needs are varied, and continually evolve and change

- Planning and (prompt) communication is very important!!!

Never start with phrase “Nope, it is not possible...” for a response (never say never)

- In many cases researchers need & ask for high-level system access to be able to do modifications to the s/w (otherwise the red-tape takes just too long to add/install/modify any s/w, toolboxes, etc...), reasonably accommodate them
- Some research groups may have a dedicated IT/CI personnel & infrastructure that they want full/quick access/control of, and if they have the \$\$, they will establish a dedicated IT/CI personnel & infrastructure for better efficiency





# Thank you!!!

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- [sakoglu@uhcl.edu](mailto:sakoglu@uhcl.edu) if you have any further questions and/or comments



Fig 1: Brain 3D Voxel representation