https://wustl.box.com/v/OHBM2019EtzelQC

Dataset QC

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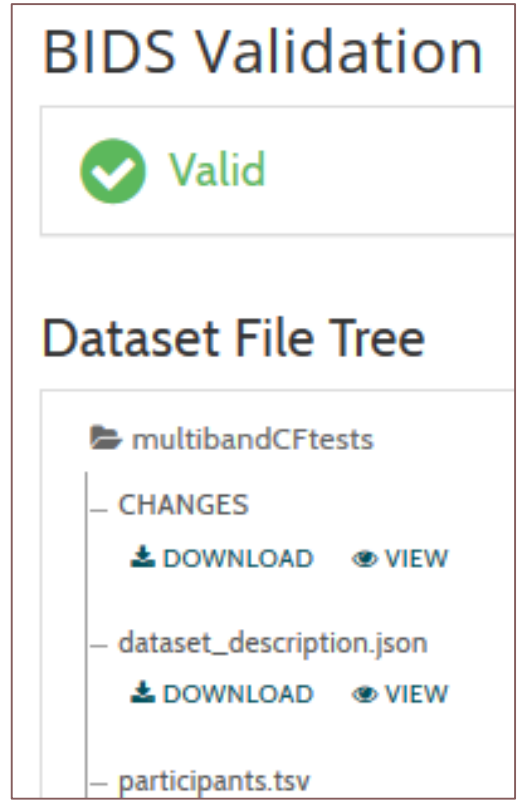
The goal of Dataset QC is verify that a dataset's contents match its description.

In the narrow sense, this is a defined problem: are the expected files and structure present?

Organized files are necessary (BIDS is good!) but not sufficient: a valid dataset can still be unusable. … contaminated by artifact, incorrect participant instructions, etc., etc.

Dataset QC is not only a chore to be done at the end of a project, but **procedures** to be **woven into all stages**: data acquisition, processing, and analysis.

> … this talk is organized into acquisition, processing, and analysis stages, but the concepts and suggestions are not that discrete.



Why are Dataset QC procedures needed?

So that your dataset is **usable**, both by you now and by people (including you) in the future.

To maximize chances that analyses produce **accurate** results: very nice (but false) blobs can come from errors.

To prepare for **submitting** the dataset to a repository (e.g., NDAR, openneuro.org).

What can Dataset QC look like in practice?

I'll start with how I ran an experiment back in 2007, which will probably still sound very familiar.

Two people were involved in data collection; we used scripts for key screening questions and instructions.

I put the files for each participant in separate directories, checking by eye that the naming was consistent.

I did preprocessing in SPM with a combination of clicking through menus and batch jobs, documented with Word notes and screenshots.

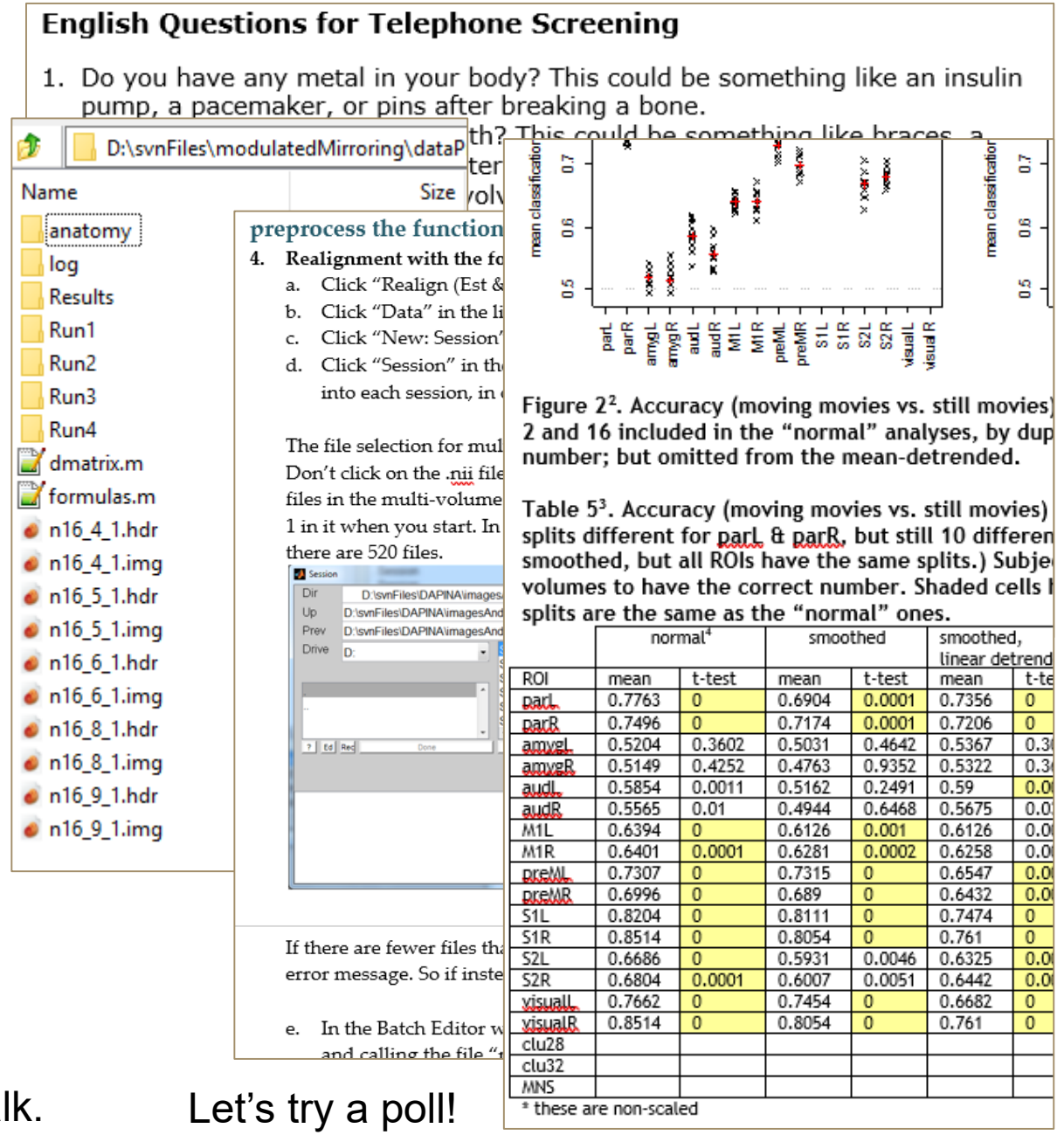
I later summarized analyses and results in Word, copy-pasting images and tables from SPM and R output.

Is this "manual" procedure horrible?

No. I **could** find the files and results after 12 years. With only 16 participants (!) and two people running the experiment, I think we did keep everything consistent and as described.

Is this "manual" procedure perfect?

No. I'll point out flaws and better solutions in the rest of this talk.



Let's try a poll!

LIVE POLL SLIDE IS NEXT - WEBSITE: gmp3.cnf.io

Live Content Slide

When playing as a slideshow, this slide will display live content

Poll: How many participants are in a typical neuroimaging dataset you work with now?

A fundamental problem with manual workflows: they don't scale up.

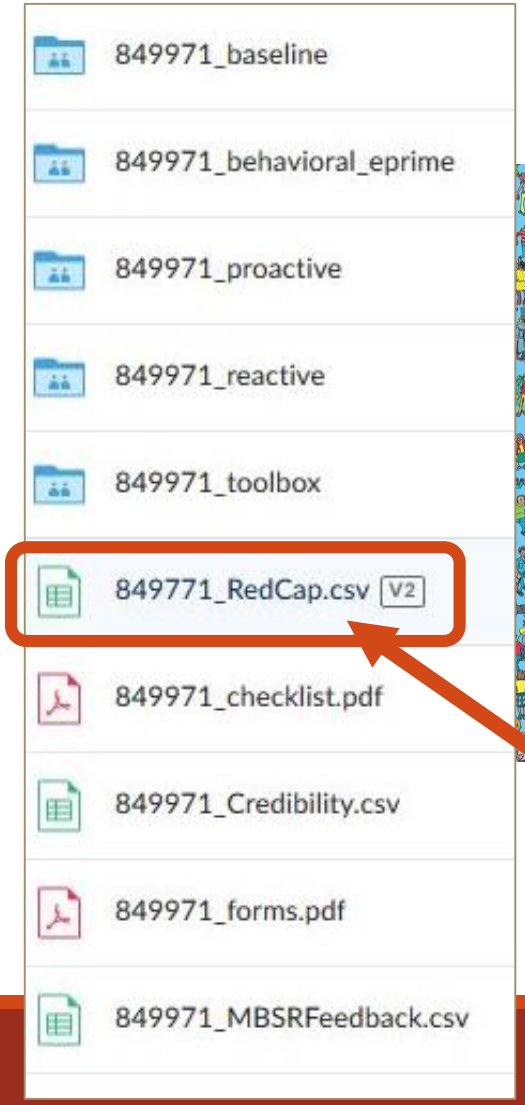
In the DMCC project we have around 90 subjects (so far), each of whom have at least 3 scanning sessions; 8 task and 2 resting state runs per session.

https://pages.wustl.edu/dualmechanisms

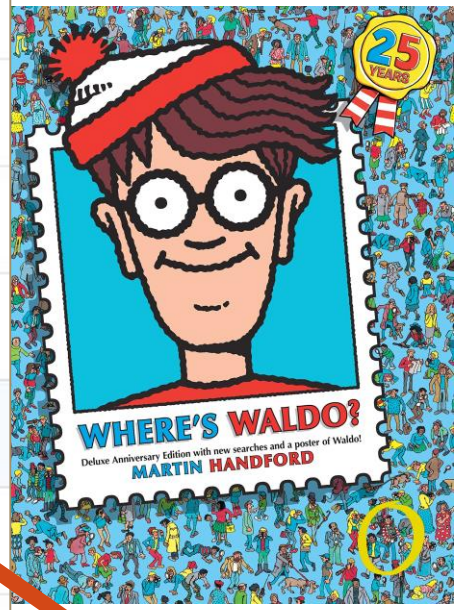
And the DMCC is not an extraordinarily large project: 1200 participants in the Young Adult HCP, 500,000 in the UK Biobank.

… I won't be clicking through 100,000 files to confirm they're present and have sensible contents.

But even if I wanted to try, I'd probably make **mistakes**.



Find the subject ID with a typo!



ID is 84**97**71
instead of 84**99**71

Manual workflows are not robust to human nature.

For example, we humans aren't great at visual search.

… that's a small error, but could cause large problems:

- if the transposed ID matches another ID we could use the wrong file
- the file will appear missing when the dataset is submitted to a repository … etc.

File checking after data collection is **necessary, but not sufficient.**

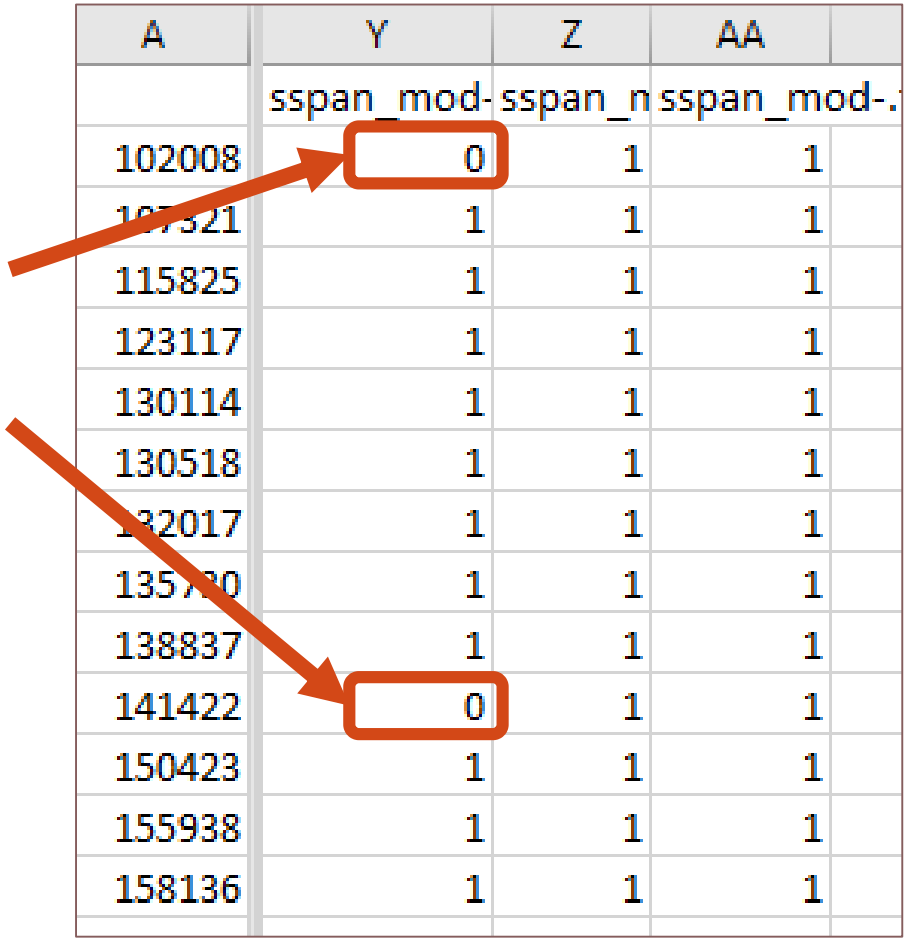
We can of course automate that type of file checking: **use a script** to search the directory structures and report which files are present.

> This questionnaire is missing because the RA forgot to bring a copy … should we invite the participant back?
>
> There's a file in this person's directory named `s_span` but not `sspan`; should I consider that just a typo and change its name?

etc., etc. … it's so much better to collect the needed data properly than try to fix errors afterwards.

Inconsistencies will multiply with the scale and complexity of the project.

We're all human; mistakes and surprises will happen. The goal is not to eliminate all errors, but to **minimize** their likelihood and severity.



A	Y	Z	AA
	sspan_mod-	sspan_n	sspan_mod-.
102008	0	1	1
107321	1	1	1
115825	1	1	1
123117	1	1	1
130114	1	1	1
130518	1	1	1
132017	1	1	1
135730	1	1	1
138837	1	1	1
141422	0	1	1
150423	1	1	1
155938	1	1	1
158136	1	1	1

How? Checklists and SOPs.

Checklists?

Yes, I mean to follow and physically mark a checklist for every single participant.

if you (or your RAs) need convincing, consider:

My husband was a Jumpmaster. He had to know all the parachute and harness parts, how to tell if each was in working order, safety procedures, etc. He took courses and passed tests proving he knew all the details.

sensible: you don't want just anyone telling you it's ok to jump out of a plane.

But even after being fully qualified, he didn't rely on his memory or invent his own system for checking jumpers: he used a standard checklist. Pilots had checklists, too.

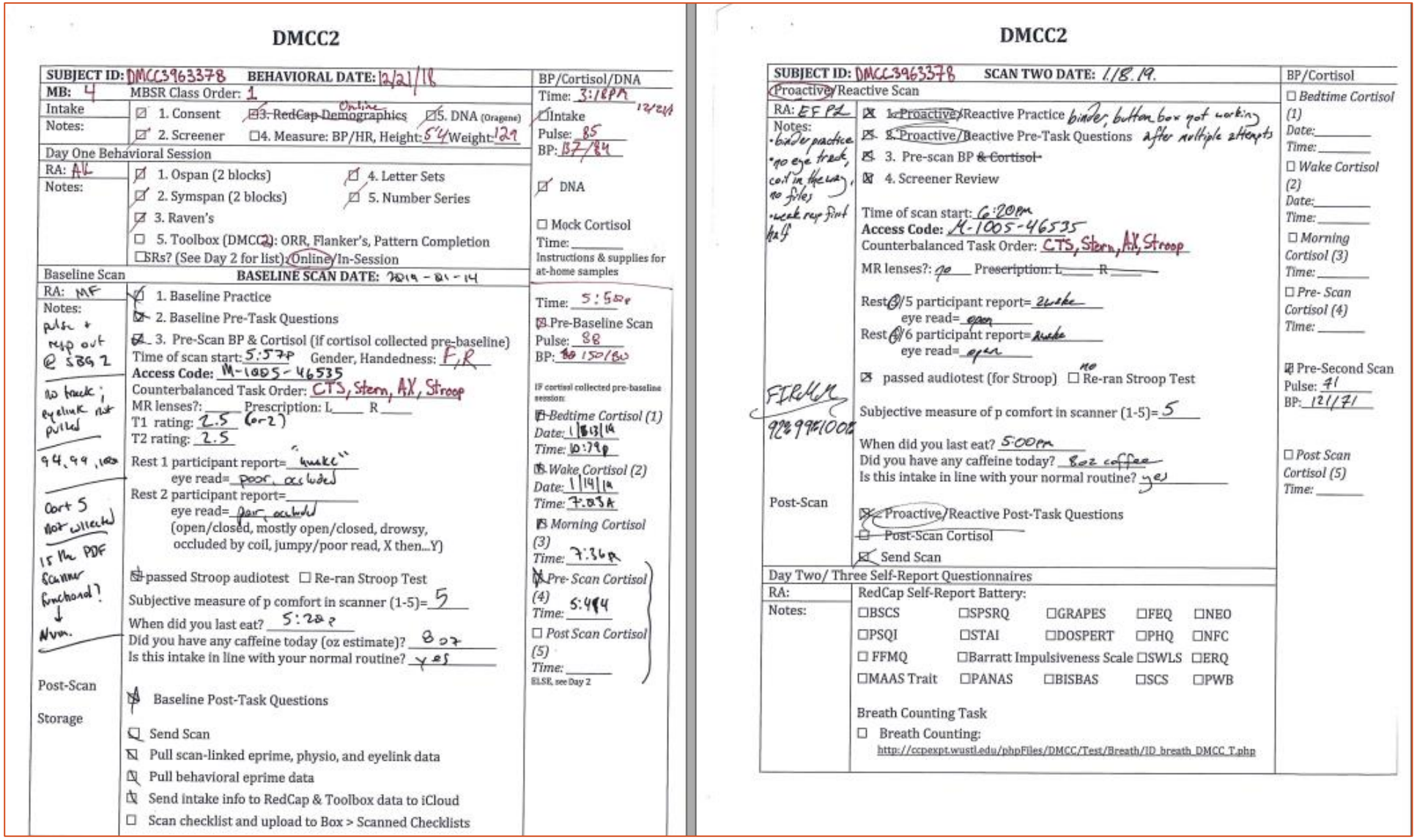
Why? Pilot and Jumpmasters are smart, educated, and experienced; can't we just trust them to do things right?

Well, no. **Expert humans are still human**; we all miss things. Strictly following well-designed checklists is a practical way to increase the chances that critical steps are completed every time.

I think checklists are more accepted for parachutists and pilots because the consequences of failure are so obvious and immediate, but they're serious for us, too:

… an unusable dataset is a tremendous waste of time and money.

There’s no perfect or all-purpose checklist. Start with what you think are the key steps and critical information for your experiment, then **update as needed**. (something missed with a participant? add it to the checklist!)



DMCC2

SUBJECT ID: DMCC3963378 BEHAVIORAL DATE: 12/21/18

MB: 4 MBSR Class Order: 1

Intake
Notes:
☑ 1. Consent ☑ 3. RedCap Demographics (Online) ☑ 5. DNA (Oragene)
☑ 2. Screener ☐ 4. Measure: BP/HR, Height: 5'4 Weight: 129

Day One Behavioral Session
RA: AL
Notes:
☑ 1. Ospan (2 blocks) ☑ 4. Letter Sets
☑ 2. Symspan (2 blocks) ☑ 5. Number Series
☑ 3. Raven’s
☐ 5. Toolbox (DMCC2): ORR, Flanker’s, Pattern Completion
☐ SRs? (See Day 2 for list): Online/In-Session

Baseline Scan BASELINE SCAN DATE: 2019-01-14
RA: MF
Notes: pulse + resp out @ 58g 2
no track; eyelink not pulled
94, 99, 100
Cort 5 not collected
Is the PDF scanner functional? ↓ Nvm.
☑ 1. Baseline Practice
☒ 2. Baseline Pre-Task Questions
☑ 3. Pre-Scan BP & Cortisol (if cortisol collected pre-baseline)
Time of scan start: 5:57p Gender, Handedness: F, R
Access Code: M-1005-46535
Counterbalanced Task Order: CTS, Stern, AX, Stroop
MR lenses?: ____ Prescription: L____ R____
T1 rating: 2.5 (or 2)
T2 rating: 2.5
Rest 1 participant report= “wake”
eye read= poor, occluded
Rest 2 participant report=____
eye read= poor, occluded
(open/closed, mostly open/closed, drowsy, occluded by coil, jumpy/poor read, X then...Y)
☑ passed Stroop audiotest ☐ Re-ran Stroop Test
Subjective measure of p comfort in scanner (1-5)= 5
When did you last eat? 5:28?
Did you have any caffeine today (oz estimate)? 8 oz
Is this intake in line with your normal routine? yes

Post-Scan
☒ Baseline Post-Task Questions

Storage
☐ Send Scan
☒ Pull scan-linked eprime, physio, and eyelink data
☒ Pull behavioral eprime data
☒ Send intake info to RedCap & Toolbox data to iCloud
☐ Scan checklist and upload to Box > Scanned Checklists

BP/Cortisol/DNA
Time: 3:18PM 12/21
☑ Intake
Pulse: 85
BP: 137/84
☑ DNA
☐ Mock Cortisol
Time: ____
Instructions & supplies for at-home samples
Time: 5:50p
☒ Pre-Baseline Scan
Pulse: 88
BP: 130/80
IF cortisol collected pre-baseline session:
☒ Bedtime Cortisol (1)
Date: 1/13/19
Time: 10:19p
☒ Wake Cortisol (2)
Date: 1/14/19
Time: 7:03A
☒ Morning Cortisol (3)
Time: 7:36A
☒ Pre-Scan Cortisol (4)
Time: 5:44
☐ Post Scan Cortisol (5)
Time: ____
ELSE, see Day 2

DMCC2

SUBJECT ID: DMCC3963378 SCAN TWO DATE: 1.18.19.
(Proactive)/Reactive Scan
RA: EF PZ
Notes:
• binder practice
• no eye track, coil in the way, no files
• weak resp first half
☒ 1. ~~Proactive~~/Reactive Practice binder, button box not working
☒ 2. ~~Proactive~~/Reactive Pre-Task Questions after multiple attempts
☒ 3. Pre-scan BP ~~& Cortisol~~
☒ 4. Screener Review

Time of scan start: 6:20pm
Access Code: A-1005-46535
Counterbalanced Task Order: CTS, Stern, AX, Stroop
MR lenses?: no Prescription: L____ R____
Rest 5/5 participant report= awake
eye read= open
Rest 6/6 participant report= awake
eye read= open
☒ passed audiotest (for Stroop) ☐ Re-ran Stroop Test (no)
FIRMM
92 99 100
Subjective measure of p comfort in scanner (1-5)= 5
When did you last eat? 5:00pm
Did you have any caffeine today? 8oz coffee
Is this intake in line with your normal routine? yes

Post-Scan
☒ ~~Proactive~~/Reactive Post-Task Questions
☐ ~~Post-Scan Cortisol~~
☒ Send Scan

Day Two/ Three Self-Report Questionnaires
RA:
Notes:
RedCap Self-Report Battery:
☐BSCS ☐SPSRQ ☐GRAPES ☐FEQ ☐NEO
☐PSQI ☐STAI ☐DOSPERT ☐PHQ ☐NFC
☐ FFMQ ☐Barratt Impulsiveness Scale ☐SWLS ☐ERQ
☐MAAS Trait ☐PANAS ☐BISBAS ☐SCS ☐PWB

Breath Counting Task
☐ Breath Counting:
http://ccpexpt.wustl.edu/phpFiles/DMCC/Test/Breath/ID_breath_DMCC_T.php

BP/Cortisol
☐ Bedtime Cortisol (1)
Date:____
Time:____
☐ Wake Cortisol (2)
Date:____
Time:____
☐ Morning Cortisol (3)
Time:____
☐ Pre- Scan Cortisol (4)
Time:____
☒ Pre-Second Scan
Pulse: 71
BP: 121/71
☐ Post Scan Cortisol (5)
Time:____

It can work well to print a copy of the checklist for each participant; scan and archive afterwards.

Aim is for everyone to know that checklists are not optional; a sign of **project importance**, not lack of trust.

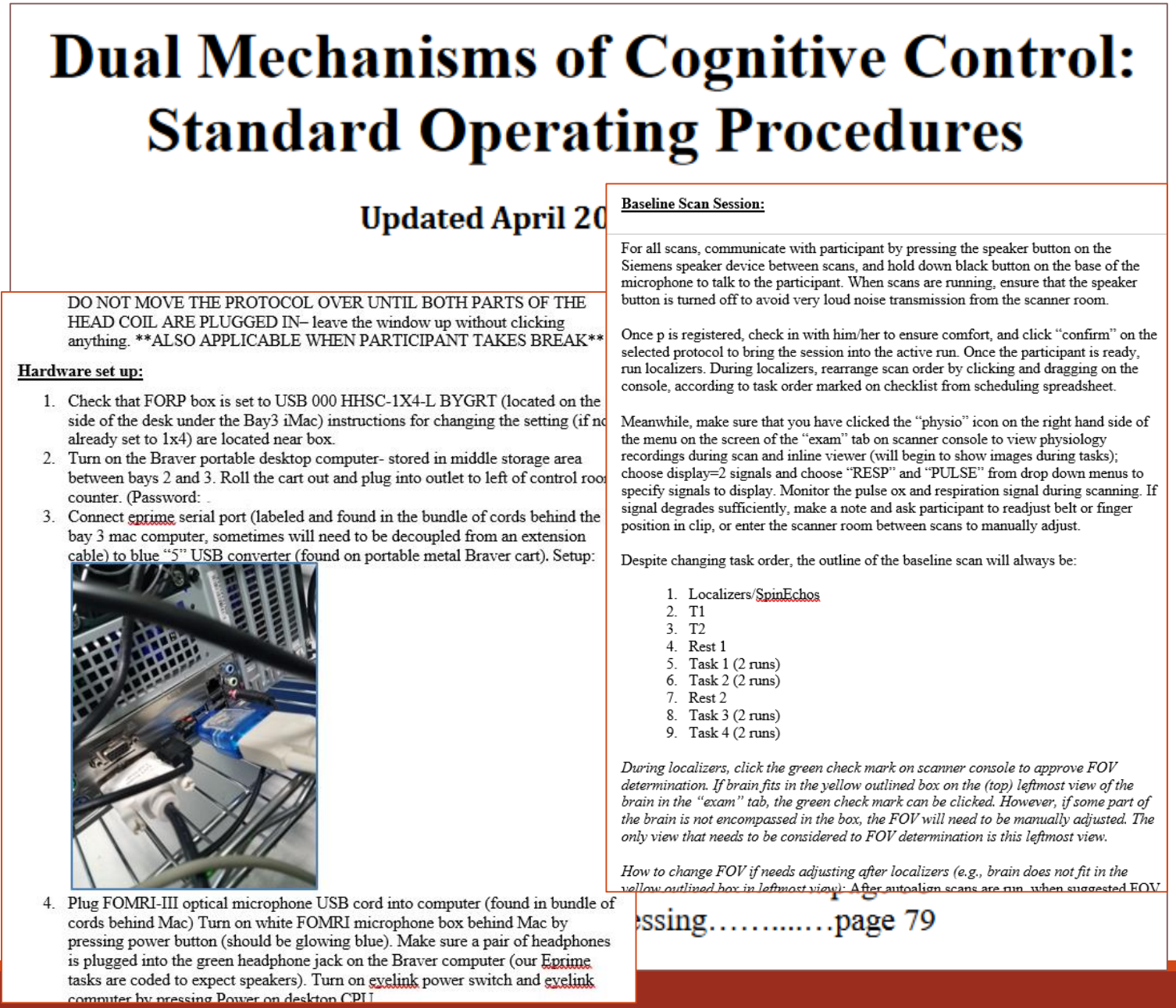
Beyond Checklists: SOPs ("Standard Operating Procedures")

SOPs explain **how** to do the steps listed on the checklists: recruitment, running the experiment, data storage, generating reports, etc.

SOP detail should increase with the number of people and time involved in data collection.

But every neuroimaging dataset has key procedures and settings – **if an experiment is important enough to be run, it should have an SOP**.

… I think every dataset release should include its SOP.



Dual Mechanisms of Cognitive Control: Standard Operating Procedures

Updated April 20

DO NOT MOVE THE PROTOCOL OVER UNTIL BOTH PARTS OF THE HEAD COIL ARE PLUGGED IN– leave the window up without clicking anything. **ALSO APPLICABLE WHEN PARTICIPANT TAKES BREAK**

Hardware set up:

1. Check that FORP box is set to USB 000 HHSC-1X4-L BYGRT (located on the side of the desk under the Bay3 iMac) instructions for changing the setting (if nc already set to 1x4) are located near box.
2. Turn on the Braver portable desktop computer- stored in middle storage area between bays 2 and 3. Roll the cart out and plug into outlet to left of control roo counter. (Password: .
3. Connect eprime serial port (labeled and found in the bundle of cords behind the bay 3 mac computer, sometimes will need to be decoupled from an extension cable) to blue "5" USB converter (found on portable metal Braver cart). Setup:

4. Plug FOMRI-III optical microphone USB cord into computer (found in bundle of cords behind Mac) Turn on white FOMRI microphone box behind Mac by pressing power button (should be glowing blue). Make sure a pair of headphones is plugged into the green headphone jack on the Braver computer (our Eprime tasks are coded to expect speakers). Turn on eyelink power switch and eyelink computer by pressing Power on desktop CPU

Baseline Scan Session:

For all scans, communicate with participant by pressing the speaker button on the Siemens speaker device between scans, and hold down black button on the base of the microphone to talk to the participant. When scans are running, ensure that the speaker button is turned off to avoid very loud noise transmission from the scanner room.

Once p is registered, check in with him/her to ensure comfort, and click "confirm" on the selected protocol to bring the session into the active run. Once the participant is ready, run localizers. During localizers, rearrange scan order by clicking and dragging on the console, according to task order marked on checklist from scheduling spreadsheet.

Meanwhile, make sure that you have clicked the "physio" icon on the right hand side of the menu on the screen of the "exam" tab on scanner console to view physiology recordings during scan and inline viewer (will begin to show images during tasks); choose display=2 signals and choose "RESP" and "PULSE" from drop down menus to specify signals to display. Monitor the pulse ox and respiration signal during scanning. If signal degrades sufficiently, make a note and ask participant to readjust belt or finger position in clip, or enter the scanner room between scans to manually adjust.

Despite changing task order, the outline of the baseline scan will always be:

1. Localizers/SpinEchos
2. T1
3. T2
4. Rest 1
5. Task 1 (2 runs)
6. Task 2 (2 runs)
7. Rest 2
8. Task 3 (2 runs)
9. Task 4 (2 runs)

During localizers, click the green check mark on scanner console to approve FOV determination. If brain fits in the yellow outlined box on the (top) leftmost view of the brain in the "exam" tab, the green check mark can be clicked. However, if some part of the brain is not encompassed in the box, the FOV will need to be manually adjusted. The only view that needs to be considered to FOV determination is this leftmost view.

How to change FOV if needs adjusting after localizers (e.g., brain does not fit in the yellow outlined box in leftmost view): After autoalign scans are run, when suggested FOV

…ssing……..…page 79

Practical QC Strategy: Don’t click if you can script

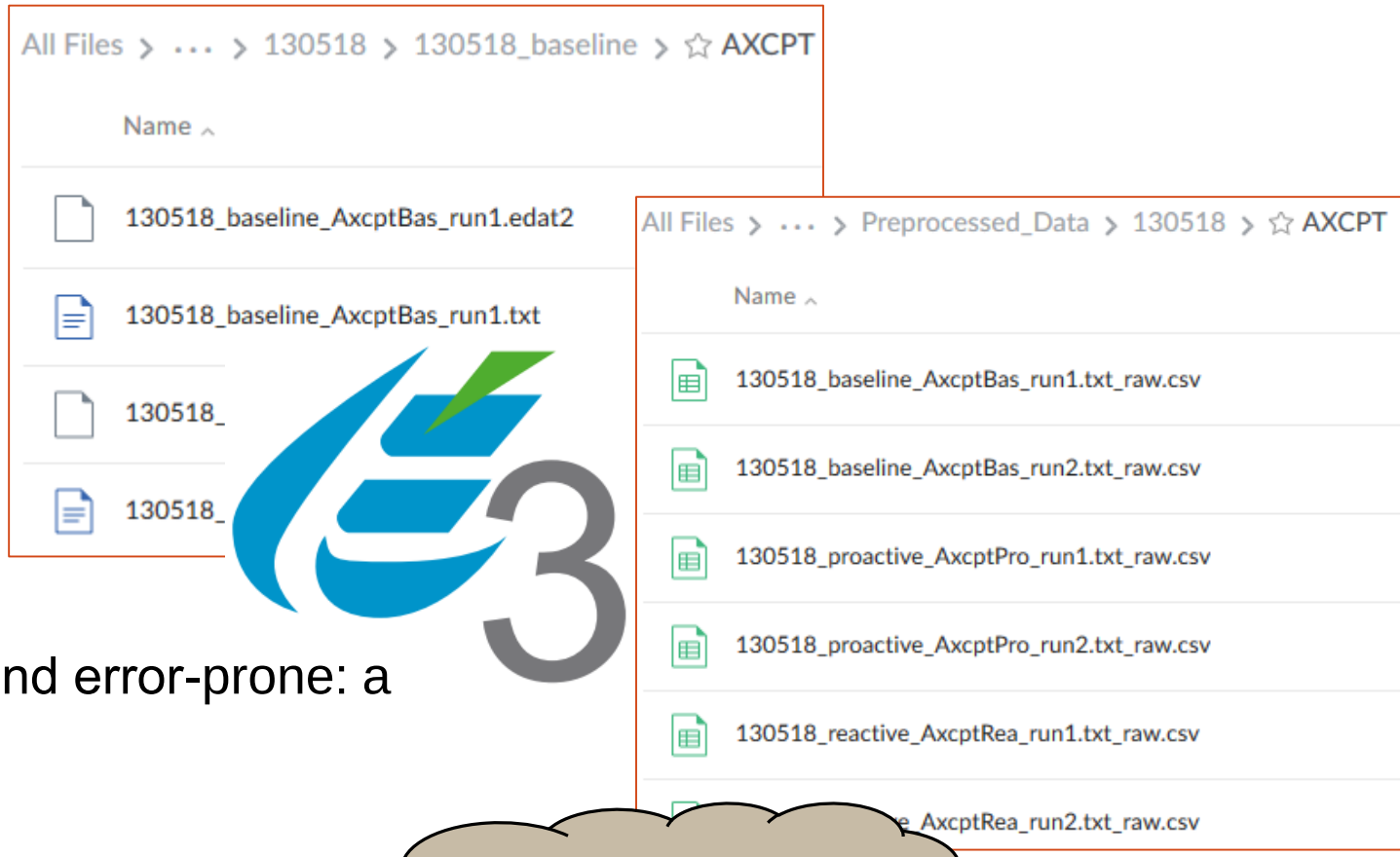
A bit of scripting can make a big difference is how quickly errors are caught (and reducing how many are created).

Concrete example: converting eprime files to text.

1: click through box to the “raw” directory for the person, select, then download the files.

2: open each in eprime, click the menu conversion option, and save locally with the new name.

3: click through box to the person’s “preprocessed” directory and drag the converted files to upload.



This works … but is incredibly tedious, slow, and error-prone: a perfect candidate for scripting.

did I name the converted file correctly?

did I drag it into the correct directory?

should I do it again to be sure?

Practical QC Strategy: Don't click if you can script

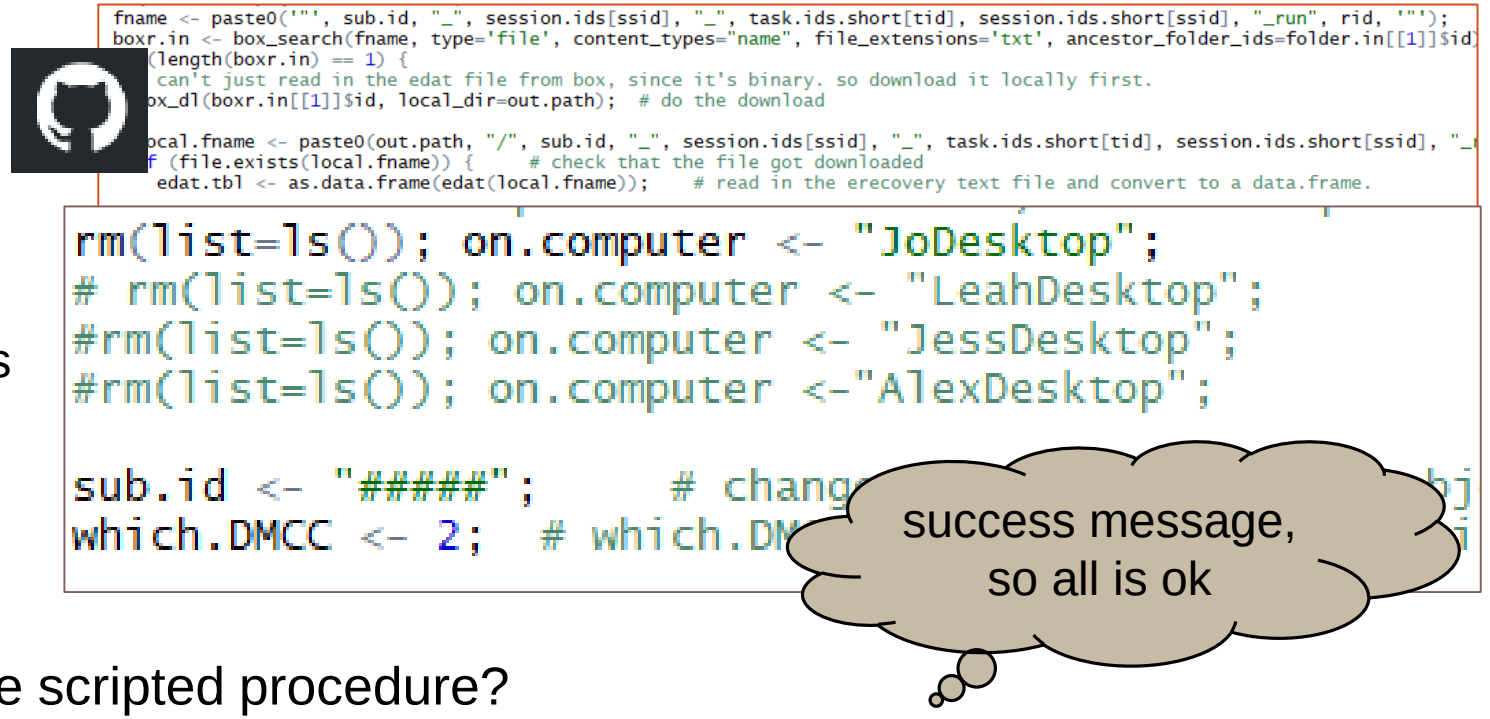
This R script replaces all of that clicking!

eprime conversion steps using the script:

1: navigate to the template script file in git; make a local copy if needed.

2: open the script in R and set the three variables at the top of the template (`on.computer`, `sub.ID`, `which.DMCC`) for the current person.

3: run the script, watching for error messages.



Why am I more confident of success with the scripted procedure?

Because it was **designed to fail** if something is **not exactly correct** (and updated whenever a problem or oversight is found).

> For example: the input file name and box source directory is specified in this template code, so a typo will be immediately caught (file missing?). Important file contents can also be tested (e.g., is the start time plausible?).

Like the checklists and SOPs, these standard template scripts are part of the dataset; saved (and later potentially released) to increase reproducibility.

Practical QC Strategy: Pull out what's most important or diagnostic for you

Even the best automatically-generated summary won't be used if it's too long or difficult to navigate.

… fMRIPrep reports for a single DMCC participant are > 50 pages; impossible to quickly survey across runs or people.

… XNAT BIRN QA reports have useful summaries, but clicking through every run is tedious.

Yes, this is whiny, but **practicality** and **human nature** matter. I can't efficiently or accurately compare across thousands of QC report pages.

Alternative: make summary files (using knitr or another **dynamic report generation** tool) for what you think are the most important or diagnostic metrics for the particular experiment; consult the full reports as needed.

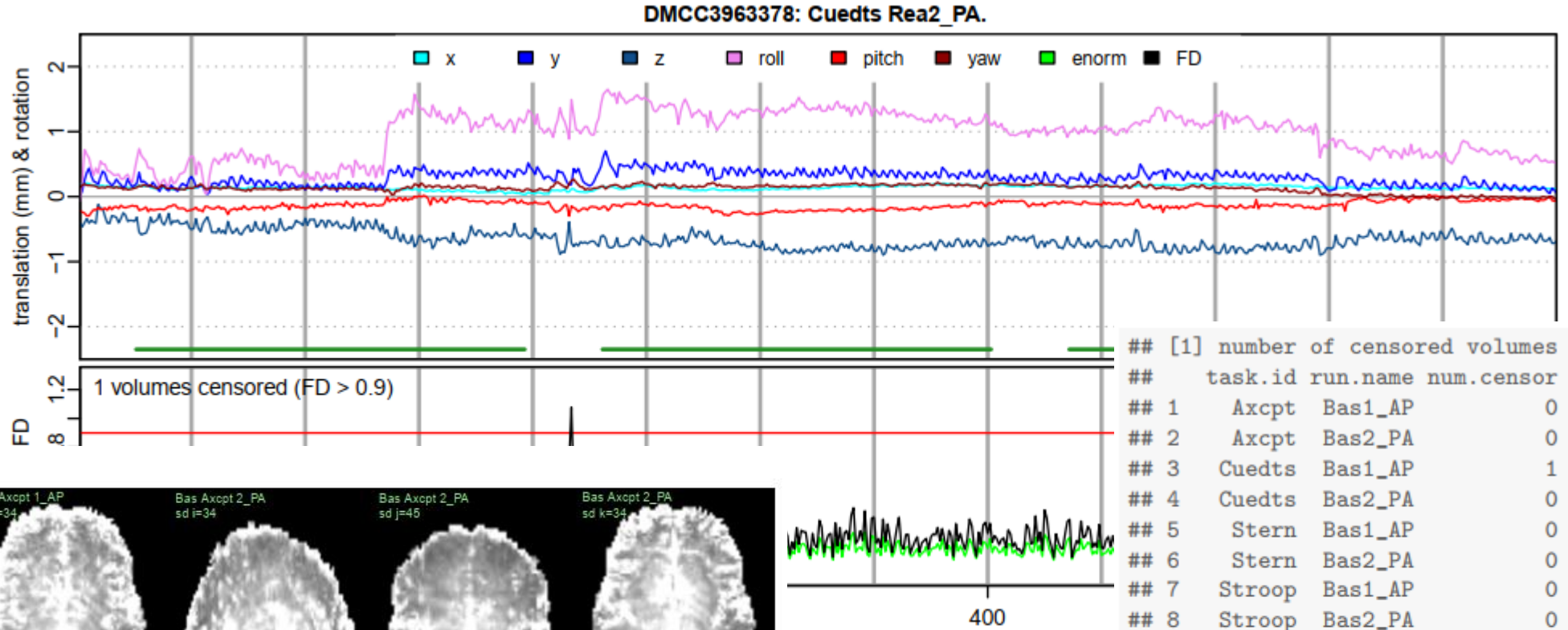
a few concrete examples

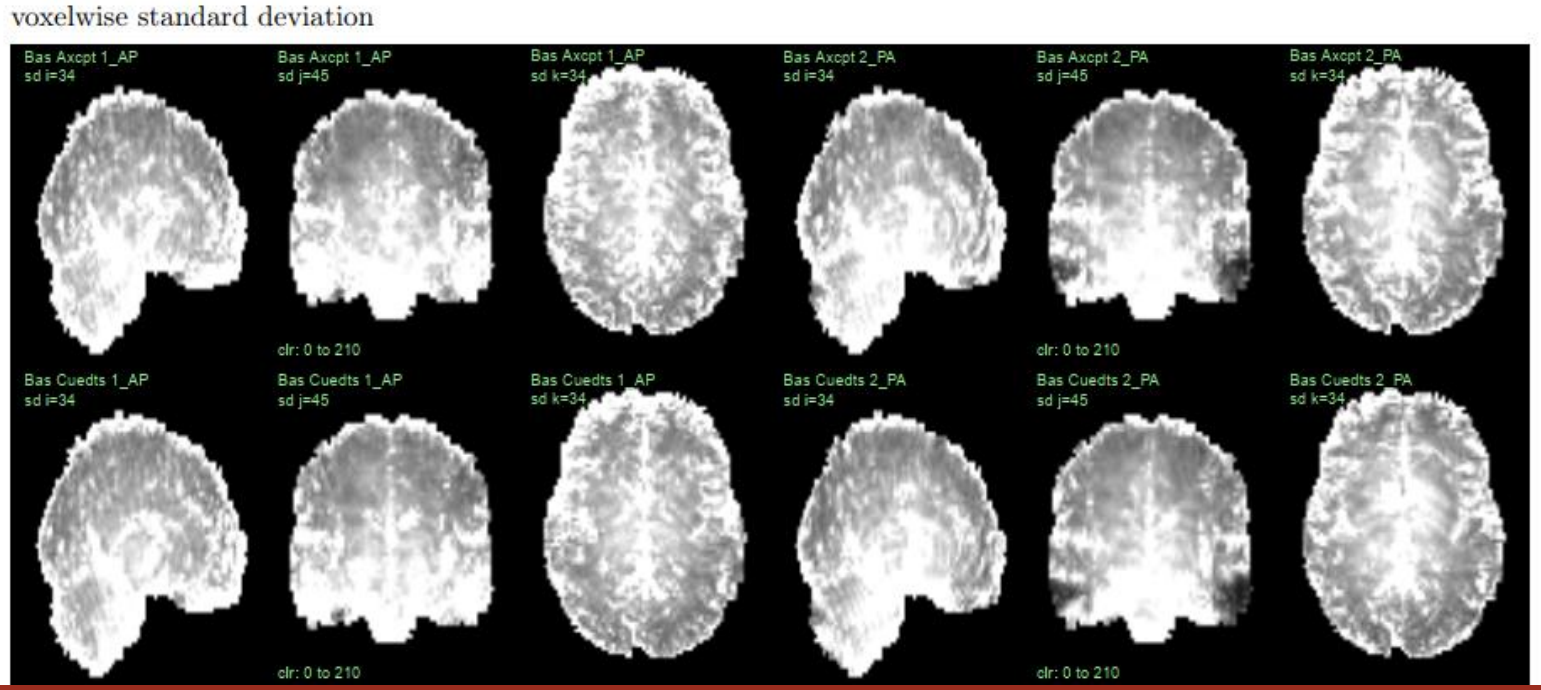
Practical QC Strategy: Pull out what's most important or diagnostic for you

example #1: SUBID_fMRI_movementSummary.pdf (https://wustl.box.com/v/OHBM2019EtzelQC GLM templates)

movement regressor & FD plots for each run, showing censored frames in relation to our task blocks.

3-slice views of mean, SD, and tSNR volumes for each run.



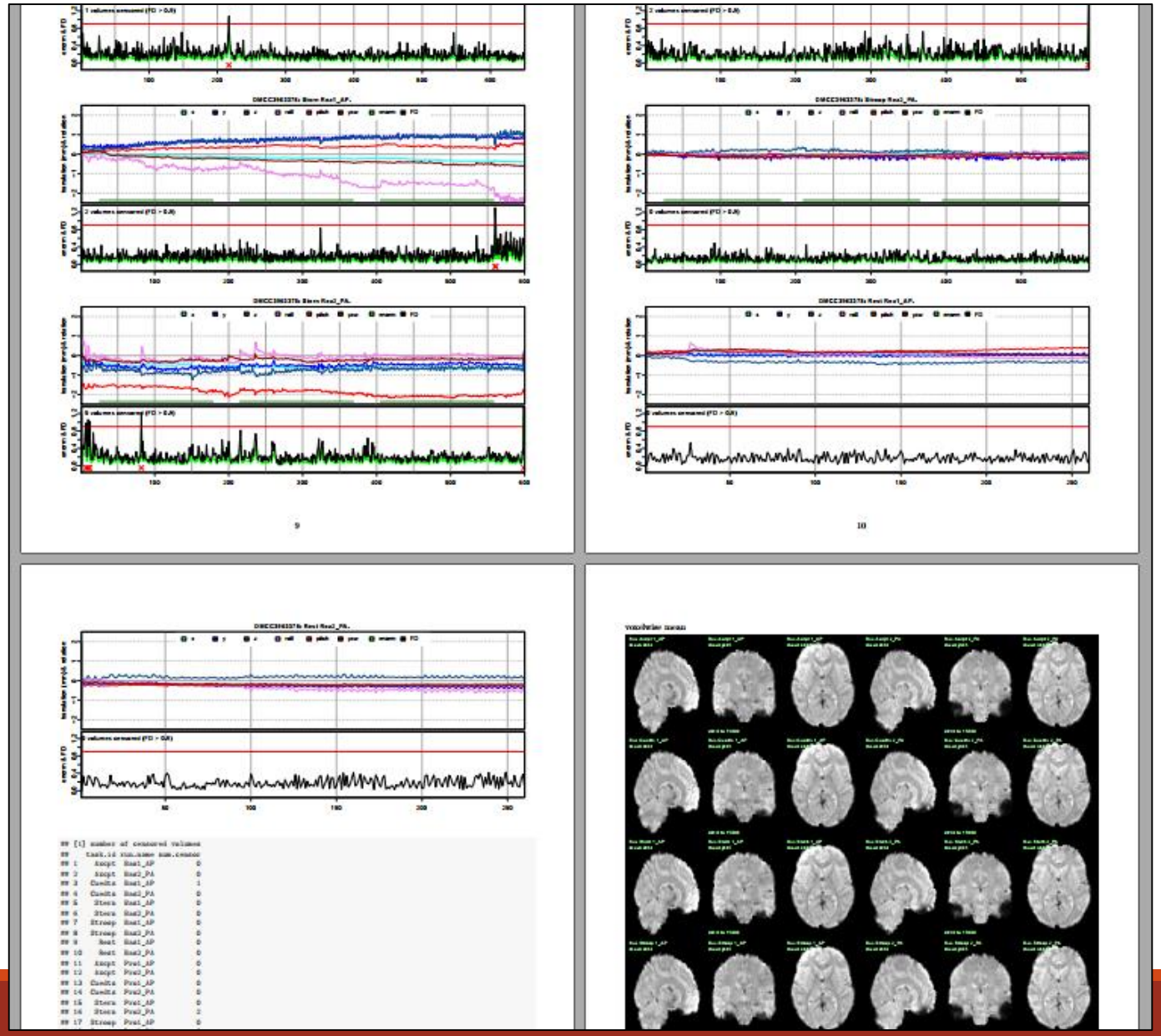



```
## [1] number of censored volumes
##    task.id run.name num.censor
## 1    Axcpt  Bas1_AP          0
## 2    Axcpt  Bas2_PA          0
## 3   Cuedts  Bas1_AP          1
## 4   Cuedts  Bas2_PA          0
## 5    Stern  Bas1_AP          0
## 6    Stern  Bas2_PA          0
## 7   Stroop  Bas1_AP          0
## 8   Stroop  Bas2_PA          0
## 9     Rest  Bas1_AP          0
## 10    Rest  Bas2_PA          0
## 11   Axcpt  Pro1_AP          0
## 12   Axcpt  Pro2_PA          0
##      iedts  Pro1_AP          0
##      iedts  Pro2_PA          0
##      Stern  Pro1_AP          0
##      Stern  Pro2_PA          2
##      troop  Pro1_AP          0
## 18  Stroop  Pro2_PA          0
## 19    Rest  Pro1_AP          0
## 20    Rest  Pro2_PA          0
```

Table listing total numbers of censored frames.

Practical QC Strategy: Pull out what's most important or diagnostic for you

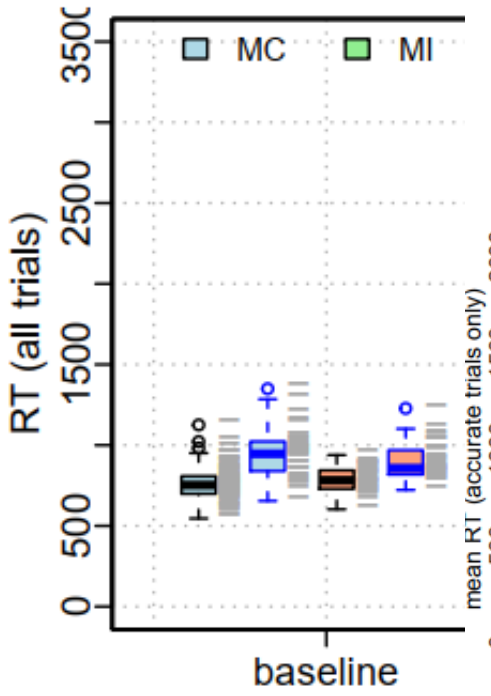
example #1: SUBID_fMRI_movementSummary.pdf (https://wustl.box.com/v/OHBM2019EtzelQC GLM templates)



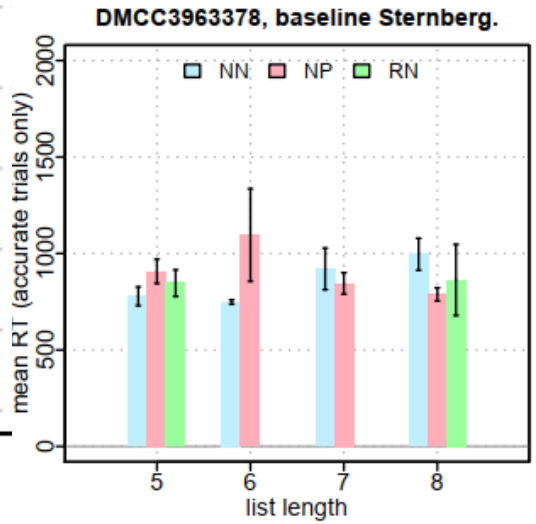
The plots for each task and run are collected into a single, more interpretable report.

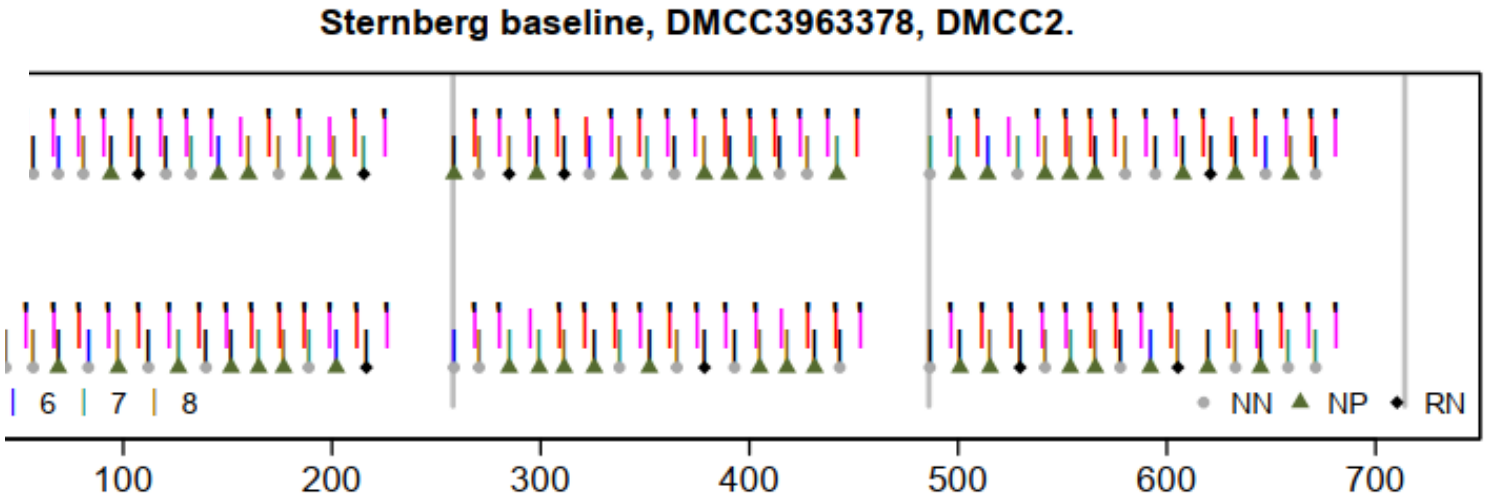
Practical QC Strategy: Pull out what's most important or diagnostic for you

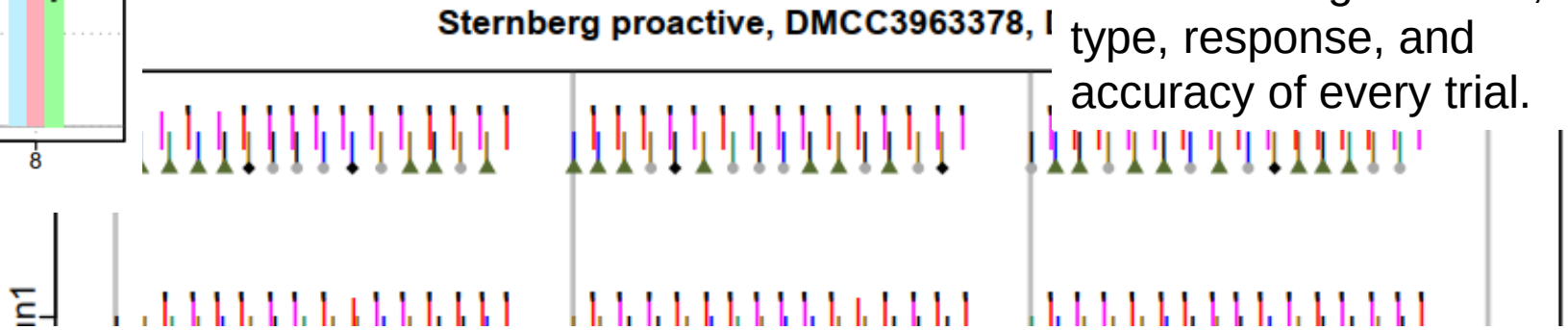
example #2: SUBID_fMRI_behavioralSummary.pdf (at https://github.com/ccplabwustl/dualmechanisms)



Key single-subject performance statistics in graphs and tables.







Plots showing the time, type, response, and accuracy of every trial.

Checks that the expected number and types of trials were presented in each task.

```
## [1] "Found an error in the AX-CPT trial counting or stimulus matching? FALSE"
```

```
## [1] "was there an error with the NN, NP, or RN trial words? FALSE"
```

Practical QC Strategy: Dynamic Report Generation

Those were dynamic reports: pdfs compiled from knitr code templates.

(I really like R and knitr, and will be giving a “lightning talk” on them in the open science room Tuesday – ask me for more!)

Dynamic report generation is not restricted to R, LaTeX, or pdfs: other language options exist for the code (e.g., python), text (e.g., markdown), and the output (e.g., html).

https://yihui.name/knitr/

What is “dynamic report generation”?

A bit like Jupyter notebooks (mixed code and text in a single source file), but compiled to produce a static document.

LaTeX descriptions and headers

NIfTI images read in an R code loop, plotted with a function (code at mvpa.blogspot.com, knitr tag)

123117_GLMs_Buttons_brains˙censored.rnw

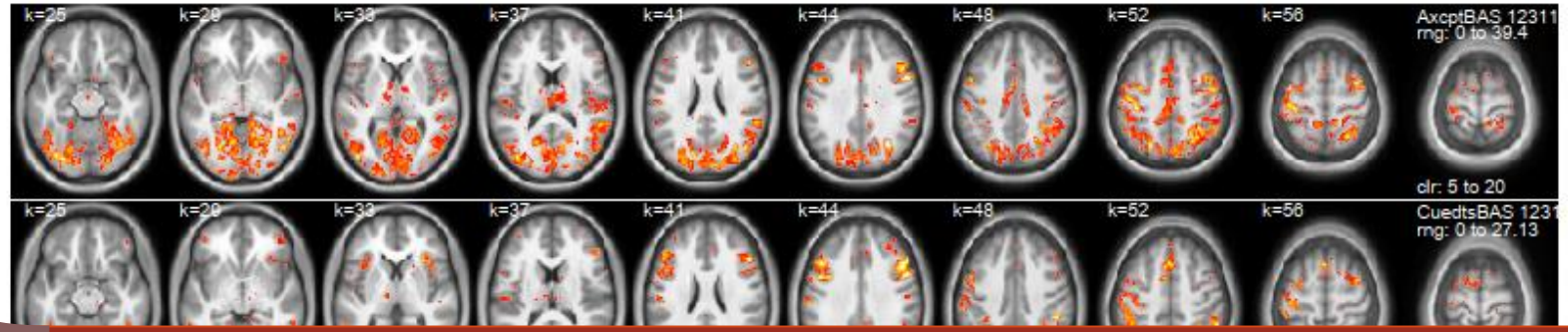
compiled July 27, 2018

set 2aFix: with blockONandOFF, polort A, BLOCK (convolved block); durations fixed.

123117, DMCC Phase 2, who was scanned at MB4. Buttons GLM results, for the AX-CPT, CuedTS, and Sternberg tasks. All are REML, not ICA-FIX, 2 TRs for each TENT knot for MB4, 3 TRs for MB8 knots. TENTs are mean coefficients. In each task the contrast was button1 - button2 == B1_B2; only the button and block-related regressors were in the model.

Buttons GLMs: button1_Fstats

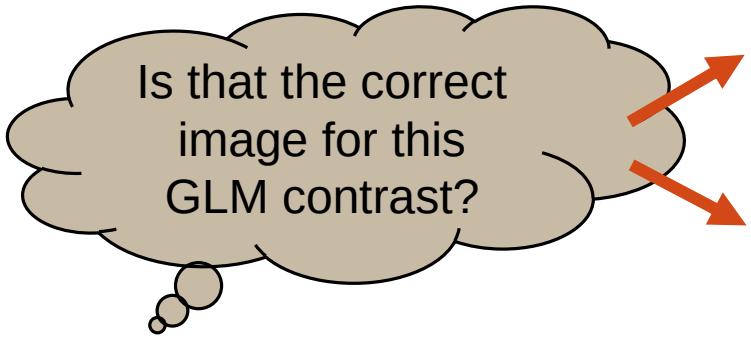
```
## [1] "123117 BAS: Buttons GLM button1_Fstat"
```



Practical QC Strategy: Dynamic Report Generation

In that 2007 study I summarized results for my collaborators by copy-pasting images and tables into Word.

Dynamic (knitr) documents serve the same purpose, but have major advantages for reproducibility: the source of images, tables, and figures can be checked, and much more efficiently updated.



look in the corresponding `.rnw` code block and check if the correct contrast image path and thresholds were sent to the plotting function.

look in the Word document (or other notes) for a description of which image file corresponds to the contrast; open the statistic image as an overlay (e.g., in afni); apply the statistical threshold and slicing; compare to plotted image.

The confirmation is much easier (and unambiguous) with the knitr … if **both** the compiled `.pdf` and source `.rnw` files are kept together.

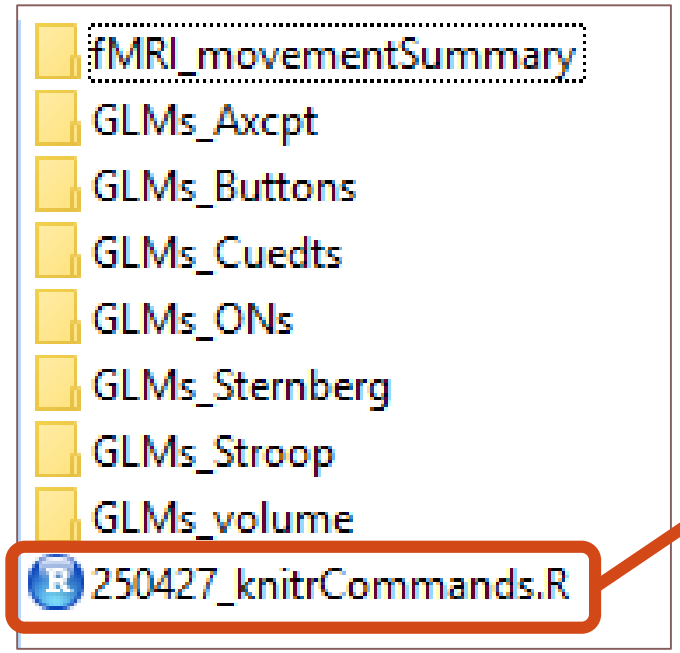
Practical QC Strategy: Automate report generation

It's fine to compile several knitrs "by hand," but not dozens at once: automate with templates.

Templates are normal knitr code, except that key variables are blank.

A "`startHERE`" script copies the templates and fills in their blanks, so to make a set of reports you change then run the `startHERE` script …

```
sub.id <- "###";
MB.lbl <- "###";    #  MB.lb
dir.suffix <- "###";    #
which.DMCC <- 0;    # filler
```



which generates the needed set of directories with ready-to-compile `.rnw` files ...

along with a script, which, when sourced, compiles all the knitrs and moves each resulting `.pdf` and `.rnw` to a single directory for easy checking and archiving.

```
library(knitr);  # for knit2pdf

setwd('/scratch1/AlexaRakusin/250427vol/fMRI_movementSummary/');
knit2pdf('250427_fMRI_movementSummary.rnw');

setwd('/scratch1/AlexaRakusin/250427vol/GLMs_Axcpt/GLMs_Axcpt_brains/');
knit2pdf('250427_Axcpt_brains_censored.rnw');
file.copy(from='/scratch1/AlexaRakusin/250427vol/GLMs_Axcpt/GLMs_Axcpt_b
file.copy(from='/scratch1/AlexaRakusin/250427vol/GLMs_Axcpt/GLMs_Axcpt_b
```

We've found this process to work well: an expert initially writes and then maintains the scripts and templates, but anyone can generate the reports, and they can be altered for new projects.

Practical QC Strategy: Control analyses

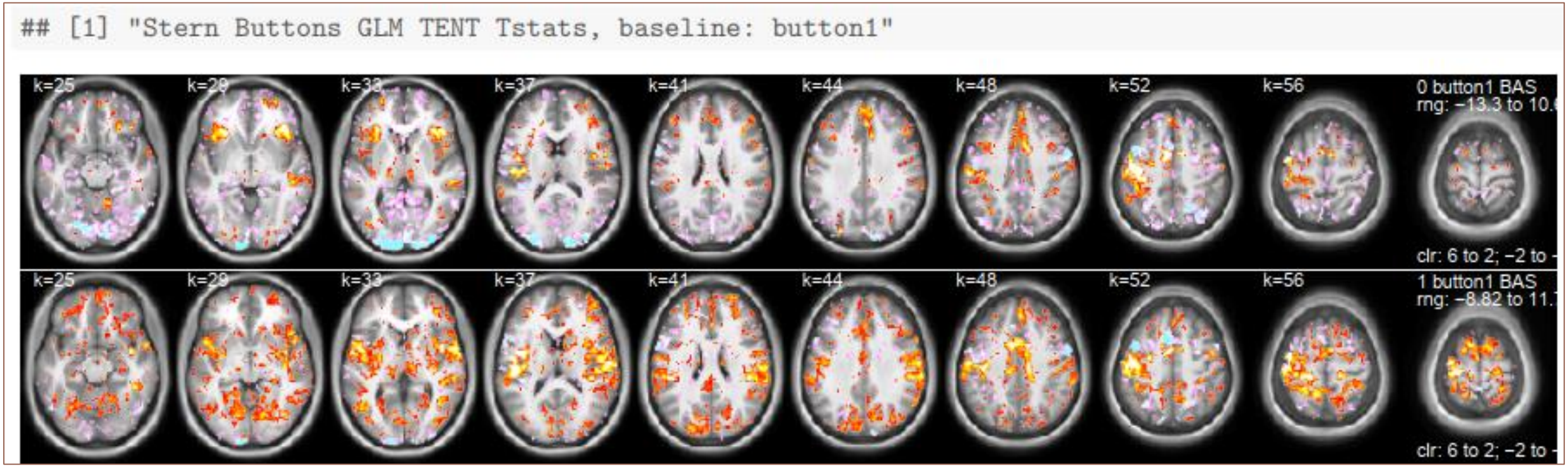
Before running the key analyses, run a **positive control**: is a strong effect that must be present, actually present?

One of my favorites is button-pressing: we know when the person made a motor response, and M1's location.

If a GLM (or whatever) fit to the button presses doesn't find motor activation, something is wrong!

… **should I believe** a cognitive effect that appears if the (presumably) stronger and focal motor effect does not?

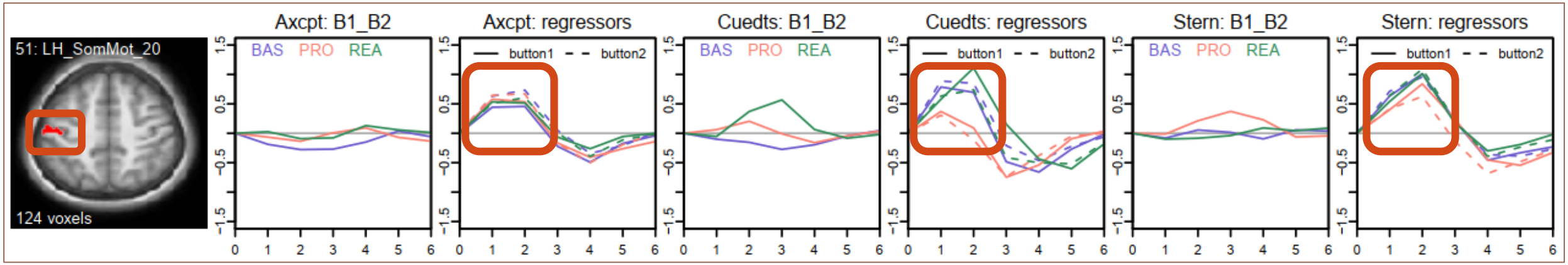
Including controls in the standard (automated) reports make it easy to check any subject or group.



https://wustl.box.com/v/OHBM2019EtzelQC /DMCC3963378_analyses/GLMs_volume/DMCC3963378_Buttons_brains_censored.pdf

Practical QC Strategy: Control analyses

The positive control analyses are a **powerful quality check** of the dataset as a whole, especially when combined with scripts, automation, and dynamic report generation.



TENT coefficient increases in a left motor ROI at the proper time in all tasks and sessions.

For this part of the knitr to be automatically created and have the expected activation:

R read the GLM output files from the expected locations, which means the afni scripts completed properly,

which mean the event onsets were specified correctly, which means the eprime files were processed,

which means the event files are in the expected location, etc. etc. etc.

I could make similar arguments about the fMRI image quality, preprocessing, subject behavior, etc.

https://wustl.box.com/v/OHBM2019EtzelQC /DMCC3963378_analyses/GLMs_volume/DMCC3963378_Buttons_Schaefer_censored.pdf

Some Final Dataset QC Thoughts

I started by stating that the goal of Dataset QC is to “verify that the dataset’s contents match its description”; something that must be true for a dataset to be usable.

Dataset QC is not a chore to be done once at the end of a project, but rather **woven into all its stages**: checklists, SOPs, scripts, dynamic reports, and control analyses are all valuable strategies to increase the chance of a high-quality dataset.

The consequences may not be as severe as for a failed parachute, but they are serious. I’ve been involved in projects in which problems were found late (fraud, missed artifacts, unacceptable movement, etc.), and recovery is slow and difficult, if possible at all.

There is no perfect solution; nothing that will guarantee a flawless dataset for every experiment. Instead, we should aim to create an environment in which problems are **less likely** to occur – and **discovered quickly** when they do – because surprises and errors will happen.

Dataset QC

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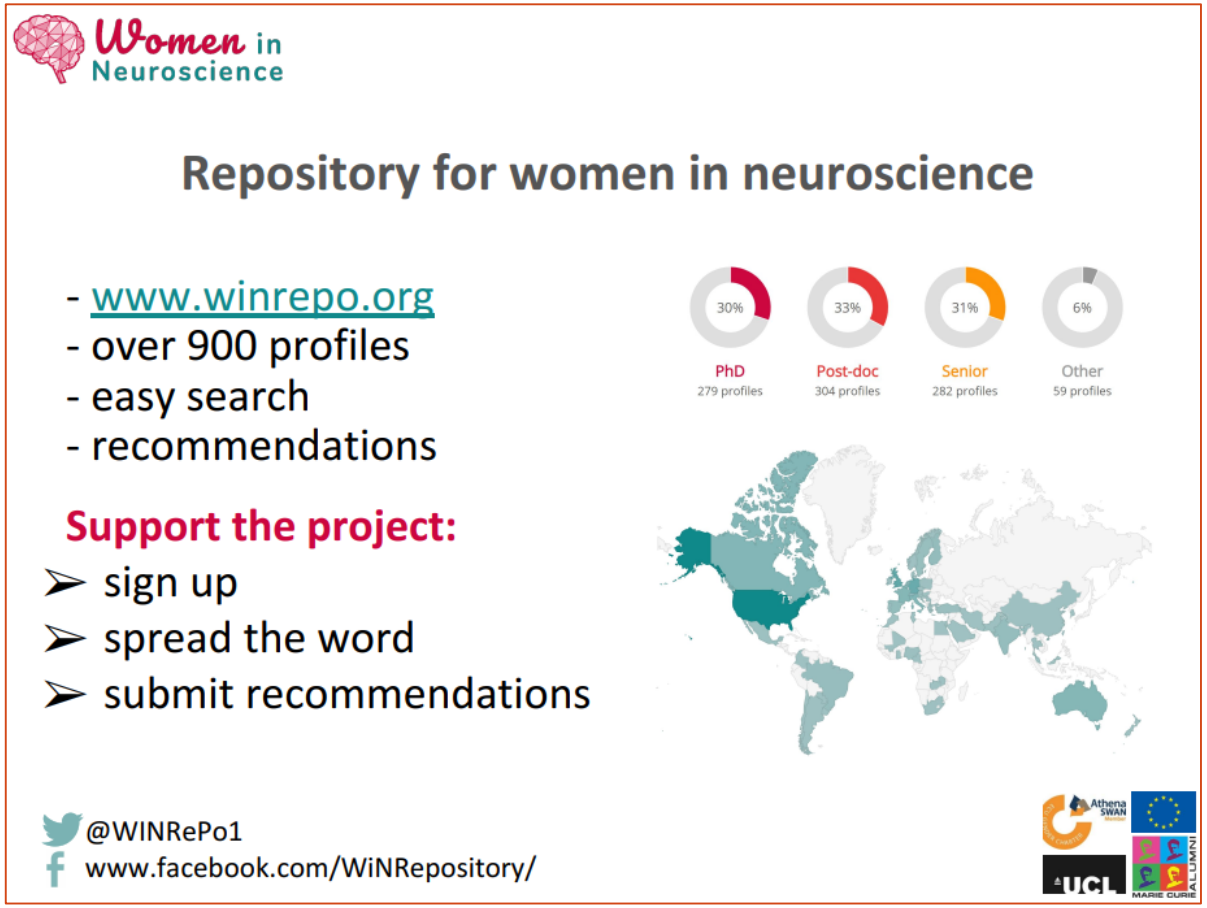
https://wustl.box.com/v/OHBM2019EtzelQC



Can it be useful to minimize error-checking, designing code to fail?

Yes: when the error requires immediate attention.

No: code should always complete, but with warning messages.

Is dynamic report generation only an option if using R?

Yes.

No.

Are control analyses (e.g., of motor responses) good practice for dataset QC?

Yes: they can help identify problems

No: GLMs should be run on the experimental questions only to avoid double-dipping

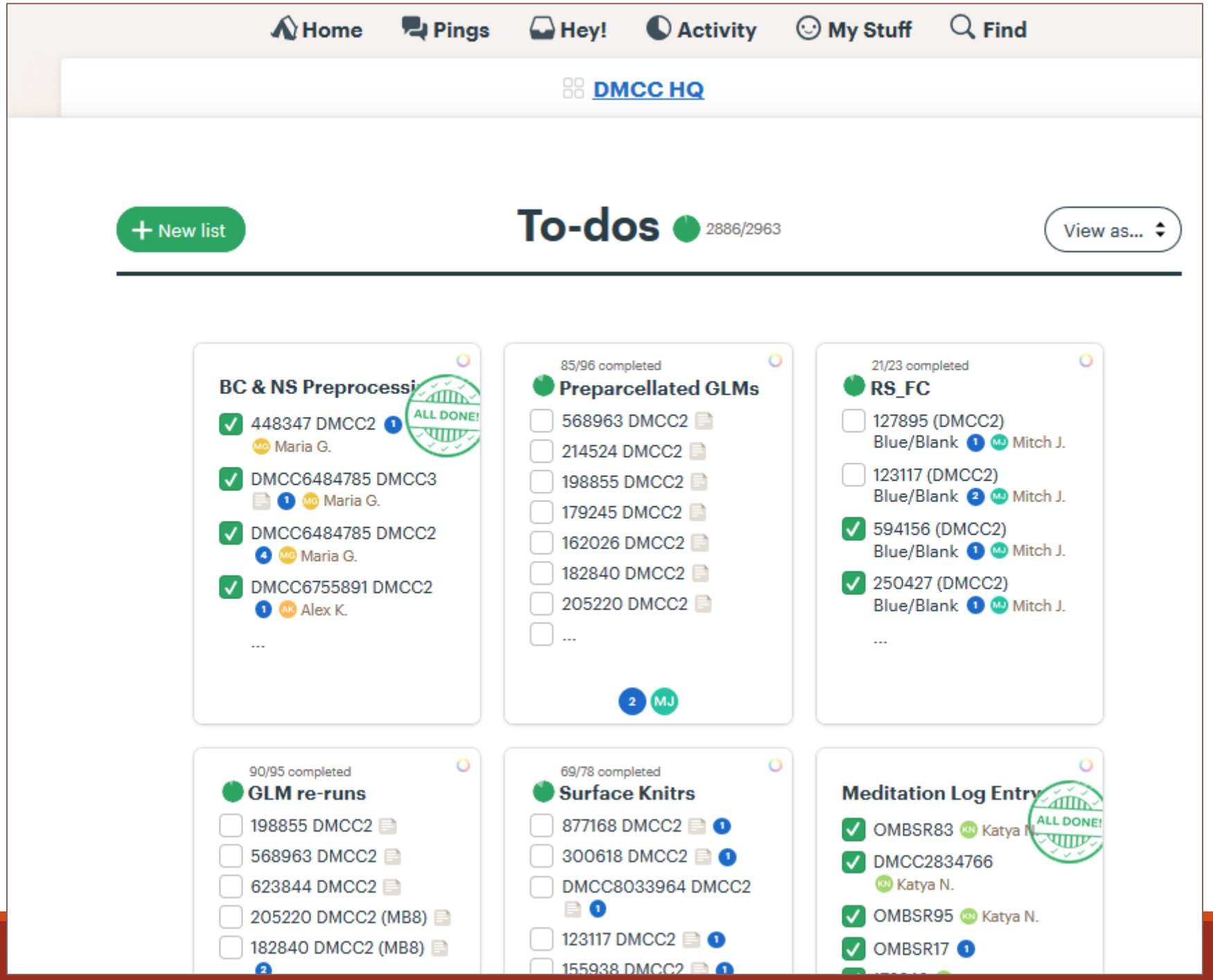
Sometimes: if a problem is suspected

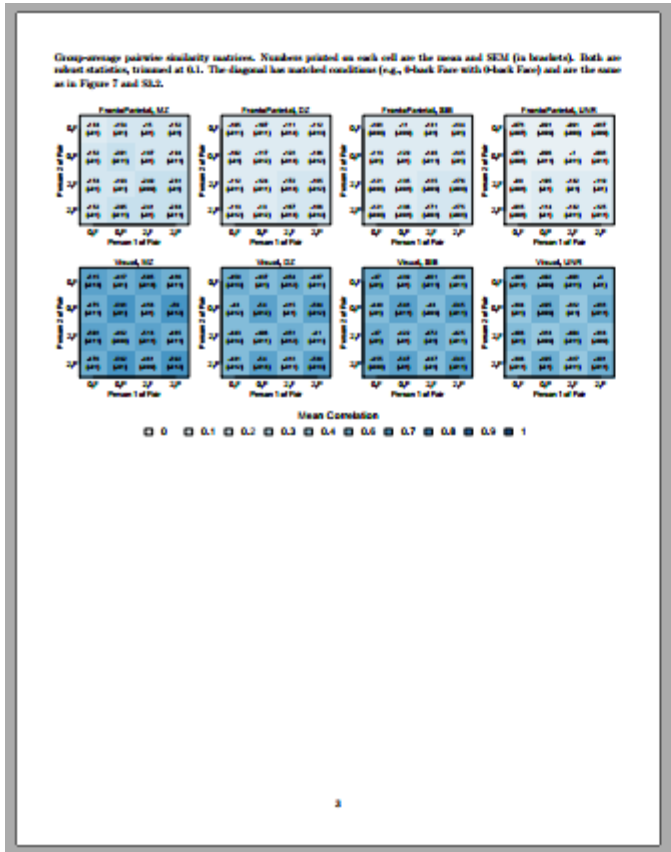
Live Content Slide

When playing as a slideshow, this slide will display live content

Poll: What do you think of dynamic report generation?

basecamp

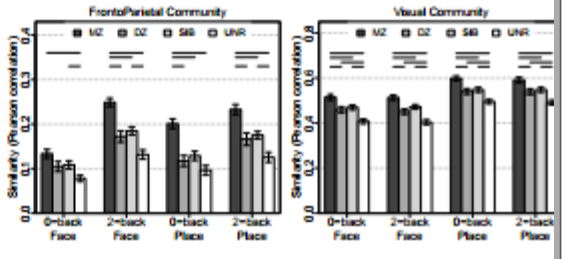

Home
Pings
Hey!
Activity
My Stuff
Find
DMCC HQ
New list
To-dos
2886/2963
View as...
BC & NS Preprocessi
ALL DONE!
448347 DMCC2
Maria G.
DMCC6484785 DMCC3
Maria G.
DMCC6484785 DMCC2
Maria G.
DMCC6755891 DMCC2
Alex K.
...
85/96 completed
Preparcellated GLMs
568963 DMCC2
214524 DMCC2
198855 DMCC2
179245 DMCC2
162026 DMCC2
182840 DMCC2
205220 DMCC2
...
21/23 completed
RS_FC
127895 (DMCC2)
Blue/Blank
Mitch J.
123117 (DMCC2)
Blue/Blank
Mitch J.
594156 (DMCC2)
Blue/Blank
Mitch J.
250427 (DMCC2)
Blue/Blank
Mitch J.
...
90/95 completed
GLM re-runs
198855 DMCC2
568963 DMCC2
623844 DMCC2
205220 DMCC2 (MB8)
182840 DMCC2 (MB8)
69/78 completed
Surface Knitrs
877168 DMCC2
300618 DMCC2
DMCC8033964 DMCC2
123117 DMCC2
Meditation Log Entry
ALL DONE!
OMBSR83
Katya N.
DMCC2834766
Katya N.
OMBSR95
Katya N.
OMBSR17



Group-average pairwise similarity matrices. Numbers printed on each cell are the mean and SEM (in brackets). Both are robust statistics, trimmed at 0.1. The diagonal has matched conditions (e.g., 0-back Face with 0-back Face) and are the same as in Figure 7 and S3.2.

S3.2 Pairwise similarity of matched conditions

Mean similarity of each stimulus type separately; error bars are standard error of the mean (SEM). Both are robust statistics, trimmed at 0.1. Horizontal lines indicate bars that significantly (p <.0083, Bonferroni correction of .05 for 6 comparisons) differ in a t-test; see below for t-test t and p values. Note that the y-axis scaling differs between the two plots.



Mean (SEM) of each stimulus type separately, as plotted above and Figure 7. Both are robust statistics, trimmed at 0.

Community	Condition	MZ	DZ	SIB	UNR
FrontoParietal	0-back,Face	.113 (.0096)	.036 (.0112)	.108 (.0092)	.078 (.0090)
FrontoParietal	2-back,Face	.219 (.0092)	.172 (.0120)	.185 (.0092)	.132 (.0093)
FrontoParietal	0-back,Place	.201 (.0109)	.117 (.0122)	.129 (.0101)	.096 (.0098)
FrontoParietal	2-back,Place	.233 (.0113)	.166 (.014)	.175 (.0094)	.125 (.0111)
Visual	0-back,Face	.535 (.0128)	.459 (.0132)	.47 (.0094)	.408 (.0098)
Visual	2-back,Face	.513 (.011)	.451 (.012)	.472 (.0105)	.404 (.0097)
Visual	0-back,Place	.598 (.0102)	.54 (.0123)	.548 (.0108)	.495 (.0094)
Visual	2-back,Place	.592 (.0118)	.539 (.013)	.548 (.0105)	.491 (.0095)


```
sth1 <- subset(mm.th1, mm.th1$community.id == "FrontoParietal" & mm.th1$condition.id == "2,F");
lme.out <- lme(fixed=similarity~pair.group, random="1|pair.id, data=sth1);
#anova(lme.out);
summary(glht(lme.out, mcp(pair.group="Tukey")));

##
##  Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lme.formula(fixed = similarity ~ pair.group, data = sth1, random = "1 |
##     pair.id)
##
## Linear Hypotheses:
##                Estimate Std. Error z value Pr(>|z|)
## MZ - DZ == 0   0.06673    0.01462   4.564  < 0.001 ***
## SIB - DZ == 0  0.01097    0.01481   0.741  0.88033
## UNR - DZ == 0 -0.04000    0.01478  -2.707  0.03455 *
## SIB - MZ == 0 -0.05576    0.01370  -4.069  < 0.001 ***
## UNR - MZ == 0 -0.10673    0.01367  -7.809  < 0.001 ***
## UNR - SIB == 0 -0.05097   0.01387  -3.676  0.00133 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

S3.4 Similarity of matched conditions: ACE modeling

For MZ and DZ.

Community	Condition	h2		c2		e2	
FrontoParietal	0-back,Face	0.05	[0,0.1]	0.08	[0.04,0.12]*	0.87	[0.85,0.89]*
FrontoParietal	2-back,Face	0.16	[0.1,0.21]*	0.09	[0.05,0.14]*	0.75	[0.73,0.77]*
FrontoParietal	0-back,Place	0.16	[0.1,0.22]*	0.04	[-0.01,0.09]	0.8	[0.78,0.82]*
FrontoParietal	2-back,Place	0.13	[0.07,0.19]*	0.1	[0.05,0.15]*	0.76	[0.74,0.78]*
Visual	0-back,Face	0.1	[0.05,0.15]*	0.41	[0.36,0.45]*	0.49	[0.48,0.51]*
Visual	2-back,Face	0.13	[0.07,0.18]*	0.38	[0.34,0.43]*	0.49	[0.47,0.51]*
Visual	0-back,Place	0.12	[0.08,0.16]*	0.48	[0.44,0.51]*	0.41	[0.39,0.42]*
Visual	2-back,Place	0.11	[0.06,0.16]*	0.48	[0.44,0.52]*	0.41	[0.4,0.43]*

For MZ and DZ+SIB.

Community	Condition	h2		c2		e2	
FrontoParietal	0-back,Face	0.04	[0,0.09]	0.09	[0.06,0.12]*	0.87	[0.85,0.89]*
FrontoParietal	2-back,Face	0.14	[0.09,0.18]*	0.11	[0.08,0.14]*	0.75	[0.73,0.77]*
FrontoParietal	0-back,Place	0.15	[0.1,0.2]*	0.05	[0.02,0.09]*	0.8	[0.78,0.82]*
FrontoParietal	2-back,Place	0.12	[0.08,0.17]*	0.11	[0.08,0.15]*	0.76	[0.75,0.78]*
Visual	0-back,Face	0.09	[0.05,0.14]*	0.41	[0.38,0.45]*	0.49	[0.48,0.51]*
Visual	2-back,Face	0.11	[0.06,0.15]*	0.4	[0.37,0.44]*	0.49	[0.47,0.51]*
Visual	0-back,Place	0.11	[0.07,0.15]*	0.48	[0.46,0.51]*	0.41	[0.39,0.42]*
Visual	2-back,Place	0.1	[0.06,0.13]*	0.49	[0.47,0.52]*	0.41	[0.4,0.43]*

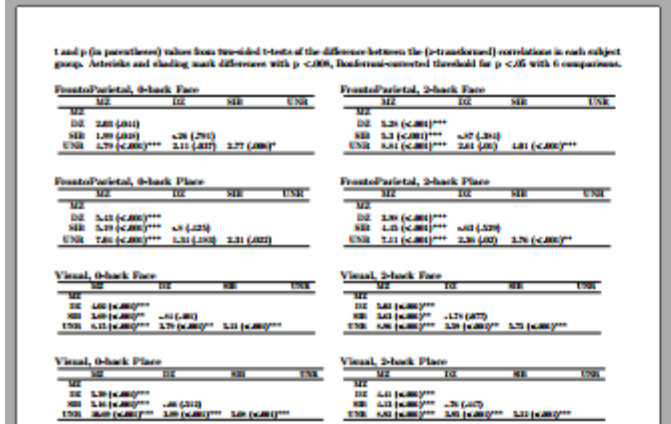
S3.5 Comparison of variance components with other studies

Reference	Mean Age	MZ... similarity (Npairs)	DZ... similarity (Npairs)	UNR similarity (Npairs)	a2	c2	e2	Reference table or figure
Etzel FPN	22-36 Avg 29.2	.13-.25 (105)	.11-.19 (78+99 SIB)	.08-.13 (100)	5-15%**	5-15%	75-87%	Figure 7, S3.2, S3.4
Etzel Visual	22-36 Avg 29.2	.35-.60 (105)	.26-.55 (78+99 SIB)	.46-.55 (100)	9-11%**	40-49%**	41-49%**	Figure 7, S3.2, S3.4
Polk (2007)	18-29	~.73 (13)	~.63 (11)	~.62 (22)	20%*	53%*	27%*	Figure 2 (faces)
Pinel (2015)	Avg 21.7	~.40 (16)	~.25 (13)	~.27#	30%*	10%*	60%*	Figure 6 (faces)
Pinel (2015)	Avg 21.7	.489 (16)	.302 (13)	-	55%** [9-82%]	0%** [0-47%]	45%** [18-100%]	Tables 3, 4 (OFAface, L-L)
Bloklund (2008)	21-27	.39-.42 (29)	~.26-.30 (31)	-	11-36.5%**	0-19.3%	63.5-81.4%	Table 2
Bloklund (2011)	20-30	Fig2b (75)	Fig2b (66)	-	33%** (average across regions)	-	67%	Figure 2b, 3
Bloklund (2017)	16-30	.39-.54 (110)	.05-.33 (138)	-	41%** (average across regions)	-	59%	Supplement Table 1

N.B. MZ and DZ similarity coefficients (typically, correlations) prefaced by a ~ represent approximations from Figures where a precise estimate of the correlation was not provided; similarly, the * in the estimate of additive genetic (a2), common environment (c2) and individual-specific environment (e2) denotes that those estimates were computed for the purpose of this table, based on: e2=1-rMZ; a2=2(rMZ-rDZ); and c2=rMZ-a2, and were not provided in the study either using such equations or via formal model-fitting (latter denoted by **); # study does not specify number of unrelated pairs.

The table above outlines variance components estimates for brain activation during a working memory task across multiple studies of MZ and DZ twins. The current study (Etzel) is among the largest. Based the table above, we see similarities and distinctions across the studies with regards to each variance component:

- Individual-specific environment: The estimate of individual-specific environment (e2) is roughly derived from subtracting the MZ correlation from unity; this estimate is typically estimated with reasonable power even in smaller samples and includes an estimate of measurement error. With the exception of Polk (2007), which includes the fewest MZ pairs and thus may have derived a higher rMZ (the feature selection procedure may also have increased the rMZ), estimates of e2 are >40%, and often >60%, although less so for Visual in the current study. The observation that e2 estimates are the highest for FPN also support our hypothesis of that this network's structure is more idiosyncratic (and so has additional sources of person-specific variance).
- Additive genetics, or heritability: Despite the larger sample size of the current study, estimates of heritability (a2) were lower for both FrontoParietal (FPN) and Visual in the current study, although when compared to Bloklund (2011), heritability of behavioral performance (accuracy and mean reaction time, see Table 2 in Bloklund and SI.6 in current study) were quite comparable especially for the 2-back in Bloklund (2011) suggesting that the lower heritability in our study may be attributed to our analytic approach and our communities of interest.
- Common environment: Importantly, unlike a majority of the other studies, we were able to parse familial effects (i.e., rMZ) into its heritable and common environmental sources, where the latter reflects those environments that are received or perceived equivalently by members of MZ and DZ pairs (and, in our case, non-twin siblings as our analyses did not reveal any evidence for special twin environment). The only other study to hint at common environmental influence is Polk (2007) although we arrive at this estimate via approximation based on the relative magnitude of their MZ and DZ correlations where the latter appears considerably greater than half the former. Interestingly, our choice to contrast the FPN and Visual communities further underscored the role of c2. For instance, while familial effects (i.e., MZ similarity) on Visual were greater than those on FPN, the greater familiality in Visual was primarily attributable to common environment. We might speculate that our estimates deviate from those reported by other studies due to



t and p (in parentheses) values from two-sided t-tests of the difference between the (z-transformed) correlations in each subject group. Asterisks and shading mark differences with p <.008, Bonferroni-corrected threshold for p <.05 with 6 comparisons.

FrontoParietal, 0-back Face

	MZ	DZ	SIB	UNR
MZ				
DZ	2.03 (.044)			
SIB	1.99 (.05)	+.26 (.794)		
UNR	5.79 (<.001)***	3.11 (.017)	2.77 (.006)*	

FrontoParietal, 2-back Face

	MZ	DZ	SIB	UNR
MZ				
DZ	5.26 (<.001)***			
SIB	5.3 (<.001)***	+.07 (.941)		
UNR	6.81 (<.001)***	2.61 (.03)	1.81 (<.001)***	

FrontoParietal, 0-back Place

	MZ	DZ	SIB	UNR
MZ				
DZ	5.13 (<.001)***			
SIB	5.19 (<.001)***	+.8 (.425)		
UNR	7.01 (<.001)***	1.31 (.193)	2.31 (.022)	

FrontoParietal, 2-back Place

	MZ	DZ	SIB	UNR
MZ				
DZ	3.99 (<.001)***			
SIB	4.25 (<.001)***	+.63 (.529)		
UNR	7.11 (<.001)***	2.36 (.02)	3.76 (<.001)**	

Visual, 0-back Face

	MZ	DZ	SIB	UNR
MZ				
DZ	4.66 (<.001)***			
SIB	5.03 (<.001)***	+.82 (.41)		
UNR	8.15 (<.001)***	3.76 (<.001)**	3.21 (<.001)***	

Visual, 2-back Face

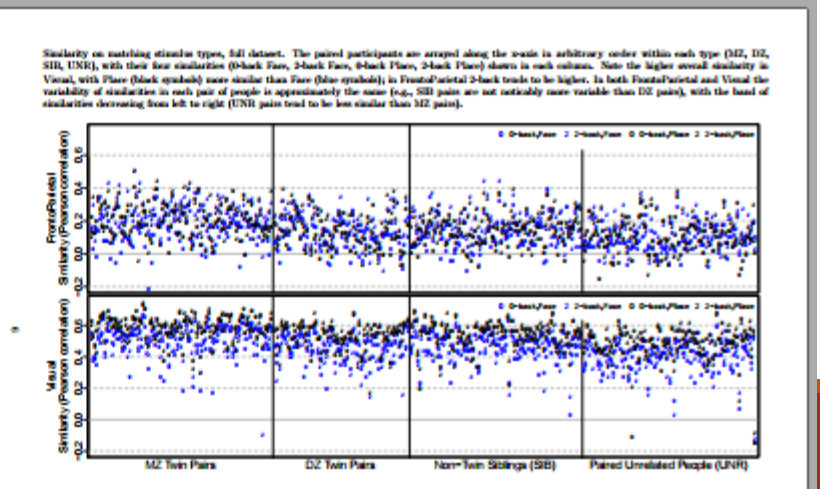
	MZ	DZ	SIB	UNR
MZ				
DZ	5.62 (<.001)***			
SIB	5.63 (<.001)***	+.179 (.857)		
UNR	8.56 (<.001)***	3.59 (<.001)**	3.75 (<.001)***	

Visual, 0-back Place

	MZ	DZ	SIB	UNR
MZ				
DZ	5.39 (<.001)***			
SIB	5.56 (<.001)***	+.46 (.651)		
UNR	10.69 (<.001)***	5.99 (<.001)***	5.69 (<.001)***	

Visual, 2-back Place

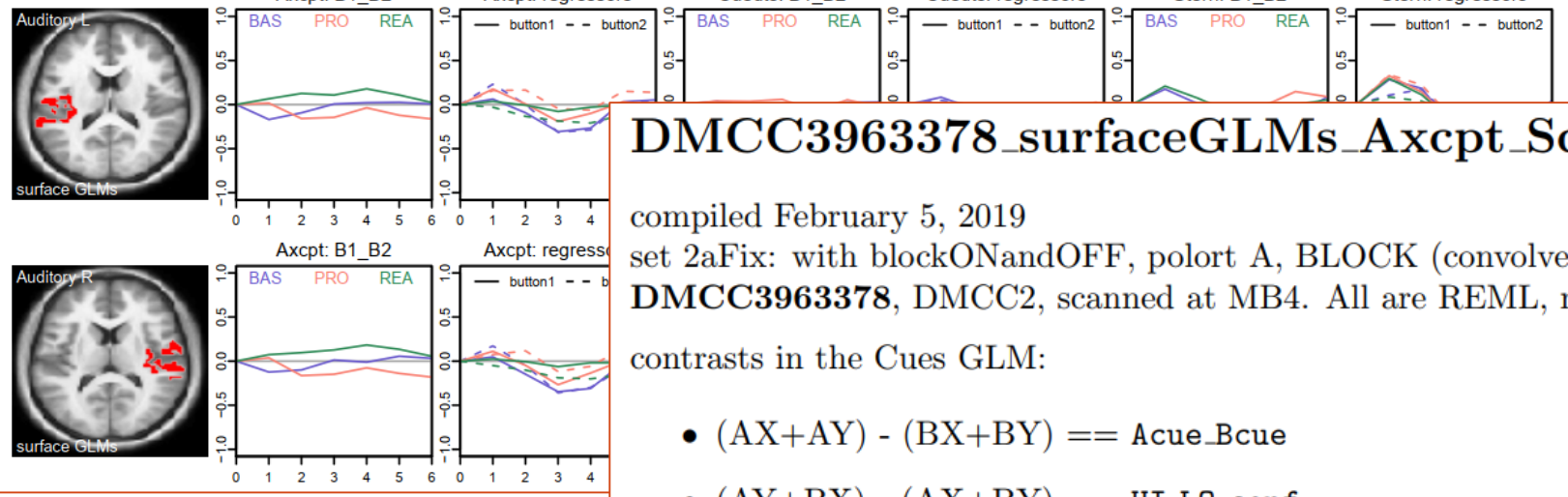
	MZ	DZ	SIB	UNR
MZ				
DZ	6.31 (<.001)***			
SIB	6.53 (<.001)***	+.76 (.457)		
UNR	9.82 (<.001)***	3.95 (<.001)**	3.31 (<.001)***	



Similarity on matching stimulus types, full dataset. The paired participants are arrayed along the x-axis in arbitrary order within each type (MZ, DZ, SIB, UNR), with their four similarities (0-back Face, 2-back Face, 0-back Place, 2-back Place) shown in each column. Note the higher overall similarity in Visual, with Place (black symbols) more similar than Face (blue symbols); in FrontoParietal 2-back tends to be higher. In both FrontoParietal and Visual the variability of similarities in each pair of people is approximately the same (e.g., SIB pairs are not noticably more variable than DZ pairs), with the band of similarities decreasing from left to right (UNR pairs tend to be less similar than MZ pairs).

more example knitrs: syntax coloring, formatted tables, rotated pages for longer graphs, itemized lists of text, captions, …

Gordon communities



more example knitrs: parcel-average TENT GLM results, with brain images to show parcel locations.

DMCC3963378_surfaceGLMs_Axcpt_Schaefer_censored.rnw

compiled February 5, 2019
set 2aFix: with blockONandOFF, polort A, BLOCK (convolved block); durations fixed.
DMCC3963378, DMCC2, scanned at MB4. All are REML, not ICA-FIX, 2 TRs for each TENT knot for MB4.

contrasts in the Cues GLM:

- (AX+AY) - (BX+BY) == `Acue_Bcue`
- (AY+BX) - (AX+BY) == `HI_LO_conf`
- (Ang+Bng) - (AX+AY+BX+BY) == `Nogo_Go` (calculated, but replaced here with BX - BY)