Custom templates for streamlined DAG workflows

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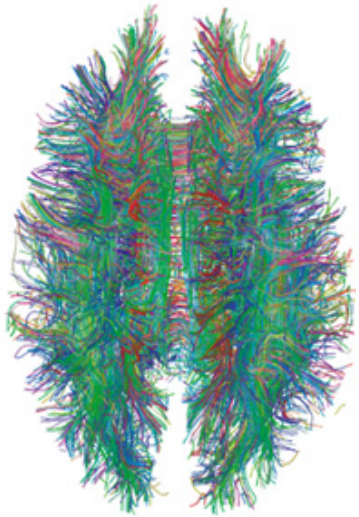
- I am an aspiring Cognitive Neuroscientist.



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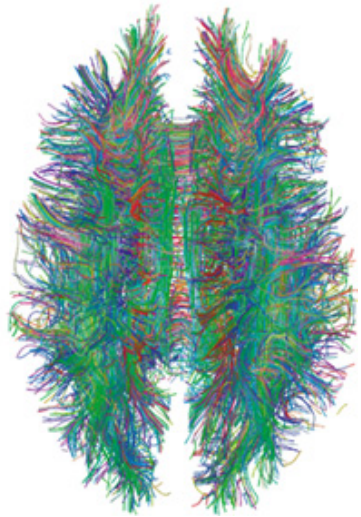

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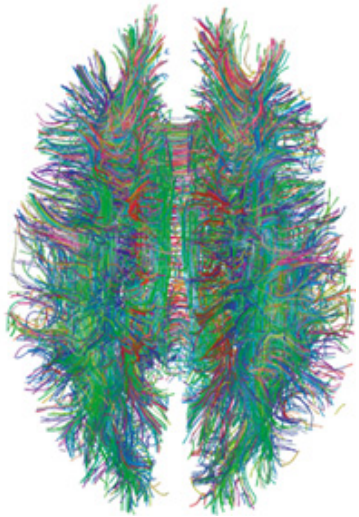
- Studying the brain bases of mental representations is computationally intensive.



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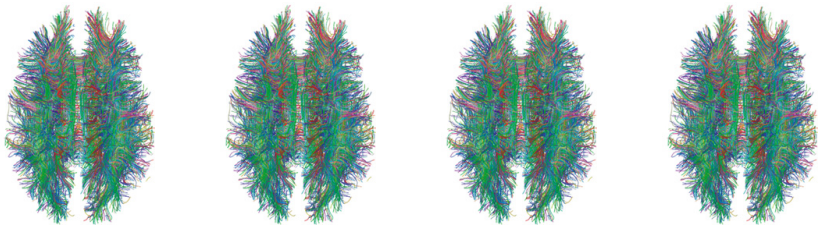

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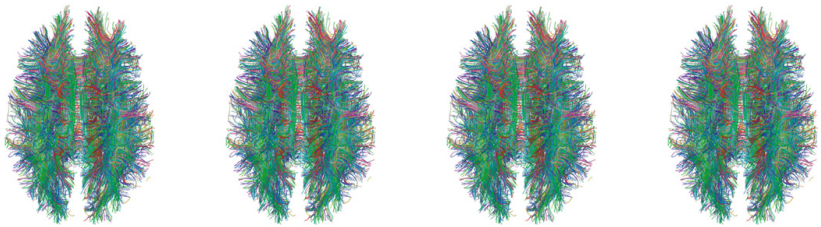

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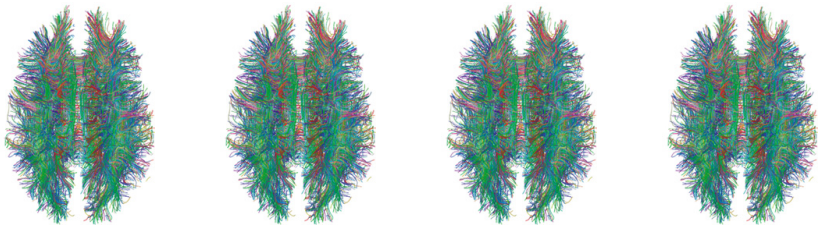

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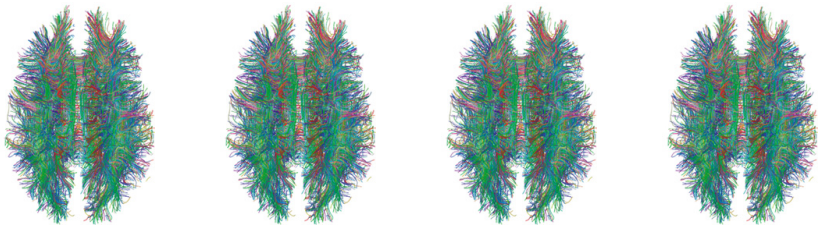

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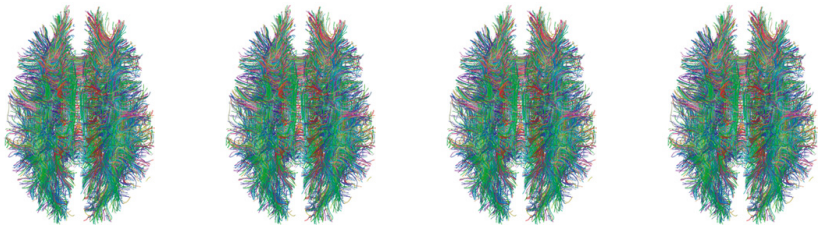
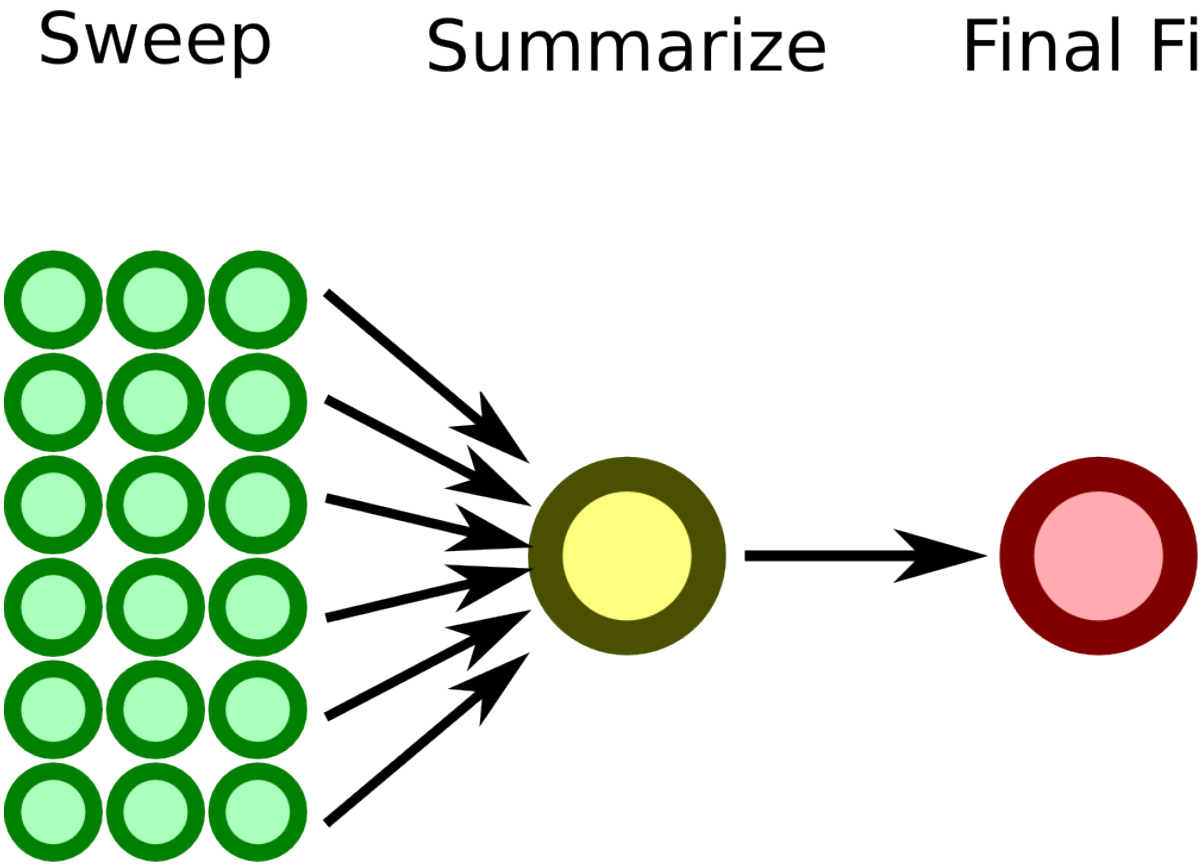


Analyses are complex, and require thousands of different iterations.

My typical workflow



My typical DAG

workflow.dag

```
SPLICE A A/sweep.dag
SPLICE B B/summarize.dag
SPLICE C C/finalfit.dag
PARENT A CHILD B
PARENT B CHILD C
```

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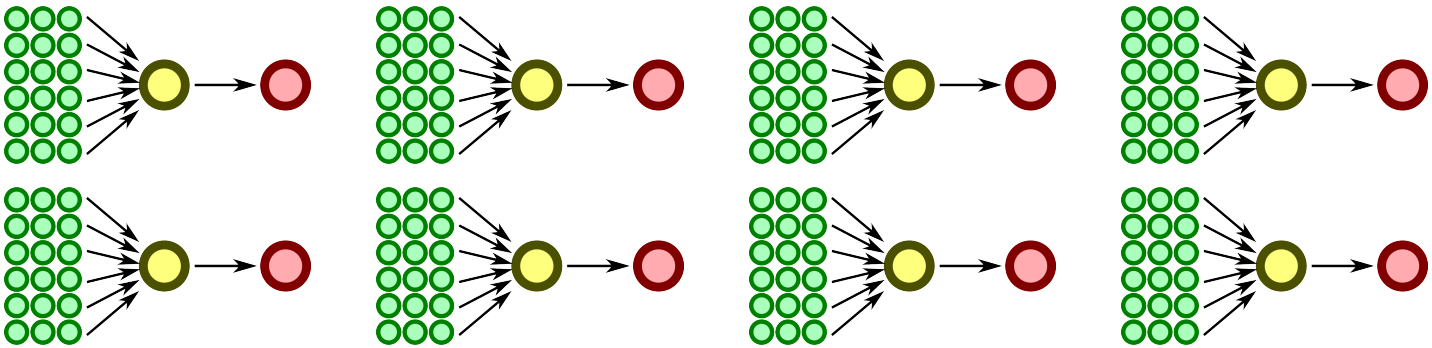

My pitch

Much of this can be **easily automated** in a way that is **easy to maintain** and **intuitive to work with**.

Perl and `Text::Template`

Requirements

1. *Basic* working knowledge of Perl. (I'm proof that you don't need to know much.)
2. Getting comfortable with `JSON` (and/or `YAML`).
3. The `Text::Template` module for Perl.

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This is the same way some dynamic web pages are constructed.

Example (YAML) parameter file

```
# If your jobs are less than 4 hours
# long, "flock" them ...
FLOCK: "false"
# If your jobs are less than ~2 hours
# long, "glide" them ...
GLIDE: "false"
# Specify in KB, MB, or GB.  No space
# between numbers and letters.
request_memory: "4GB"
request_disk: "10GB"
```

Example template

```
# If your jobs are less than 4 hours
# long, "flock" them ...
+WantFlocking = <% $FLOCK %>
# If your jobs are less than ~2 hours
# long, "glide" them ...
+WantGlidein = <% $GLIDE %>
# Tell Condor how many CPUs (cores), how
# much memory (MB) and how much
# disk space (KB) each job will need:
request_cpus = 1
request_memory = <% $MEM_MB %>
request_disk = <% $DISK_KB %>
```

Example header for Perl program[1]

```
#!/usr/bin/env perl
use strict;
use warnings;
use YAML::XS; # or JSON::Parse
use Text::Template;
```

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#!/usr/bin/env perl
use strict;
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```

Optional, but often useful:

```
use String::Scanf;
use Data::Dumper;
use Path::Tiny qw( path );
```

`Data::Dumper` lets you print hashes to the screen, and `Path::Tiny` contains a function for composing absolute paths.

[1] https://github.com/crcox/condortools

expandStub.py and expandStub_yaml.py

Ok, but what about all the parameter files you need to write?

[2] https://github.com/crcox/condortools

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Ok, but what about all the parameter files you need to write?
I have written a couple Python tools that can help with this.[2]

[2] https://github.com/crcox/condortools

expandStub_yaml.py demo

If I have a file called stub.yaml that contains:

```
lambda: [1,2,3,4]
targets: "animals"
Gtype: "L1L2"
ExpandFields:
  - lambda
```

`expandStub_yaml.py stub.yaml` will produce a file named `master.yaml` that contains:

```
--- {Gtype: L1L2, lambda: 1, targets: animals}
--- {Gtype: L1L2, lambda: 2, targets: animals}
--- {Gtype: L1L2, lambda: 3, targets: animals}
--- {Gtype: L1L2, lambda: 4, targets: animals}
```

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- These basic tools can be combined to automate the creation of files that every project needs.
- A stub file can be expanded into a "master" file where all combinations of flagged parameters will be expanded into an easily looped form.
- Such a loop can be implemented within a Perl program to generate files based on a template.

Thank you

https://github.com/crcox/condortools