

Adina S. Wagner^{*1},
 Laura K. Waite^{*1},
 Małgorzata Wierzbna^{*1,2},
 Felix Hoffstaedter^{1,3},
 Alexander Q. Waite¹,
 Benjamin Poldrack¹,
 Simon B. Eickhoff^{1,3}
 & Michael Hanke^{1,3}

FAIRly big: A framework for reproducible processing of large-scale data

 **nencki institute**
of experimental biology

 **JÜLICH**
Forschungszentrum

 **hhu** Heinrich Heine
Universität
Düsseldorf

¹ Institute of Neuroscience and Medicine, Brain & Behaviour INM-7, Research Center Jülich, Germany
² Laboratory of Brain Imaging, Nencki Institute of Experimental Biology, Polish Academy of Sciences, Warsaw, Poland
³ Institute of Systems Neuroscience, Medical Faculty, Heinrich Heine University Düsseldorf, Germany

The framework consists of the following steps. Steps 1-4 are set up by a bootstrap script based on user-input. Its main features are version control, ephemeral workspaces, and computational provenance capture

1. Create a Dataset

```
$ datalad create ukb-vbm
```

2. Link input data

```
$ datalad clone -d . \
  ${datastore}#~ukb-bids
```

3. Link processing pipeline

```
$ datalad clone -d . \
  ${containerstore}#~cat code/cat
$ datalad containers-add \
  code/cat/... --name cat
```

```
# draft a datalad (containers-)run
# command for analysis granularity
# of your choice (e.g., subject) &
# create its ephemeral workspace.
# Pick job scheduler and resources
```

4. Develop compute job

5. Parallel execution

```
# job scheduler
$ condor_submit ...
$ sbatch ...
```

```
Author: Jane Doe <j.doe@fz-juelich.de>
AuthorDate: Wed Feb 10 18:05:30 2021 +0100

{ "chain": [],
  "cmd": "singularity exec -B {pwd} --cleanenv
        code/pipeline[...] sh -e -u -x -c [...]
  "doid": "8938de76-0302-45b5-9825-3c6ce3f3ffe",
  "exit": 0,
  "extra_inputs": ["code/pipeline/datalad/environments/cat/image"],
  "inputs": ["inputs/ukb-sub-6.../ses-2/anat/sub-6..._ses-2_T1w.nii.gz",
            "code/cat_standalone_batch.txt",
            "code/finalize_job_outputs.sh"],
  "outputs": ["sub-6025043/ses-2"],
  "pwd": "." }
```

6. Result consolidation

```
# octopus-merge all "job" branches
$ git merge -m "Merge results" \
  $(git branch -al | grep 'job')
```

Big data? FAIRly difficult

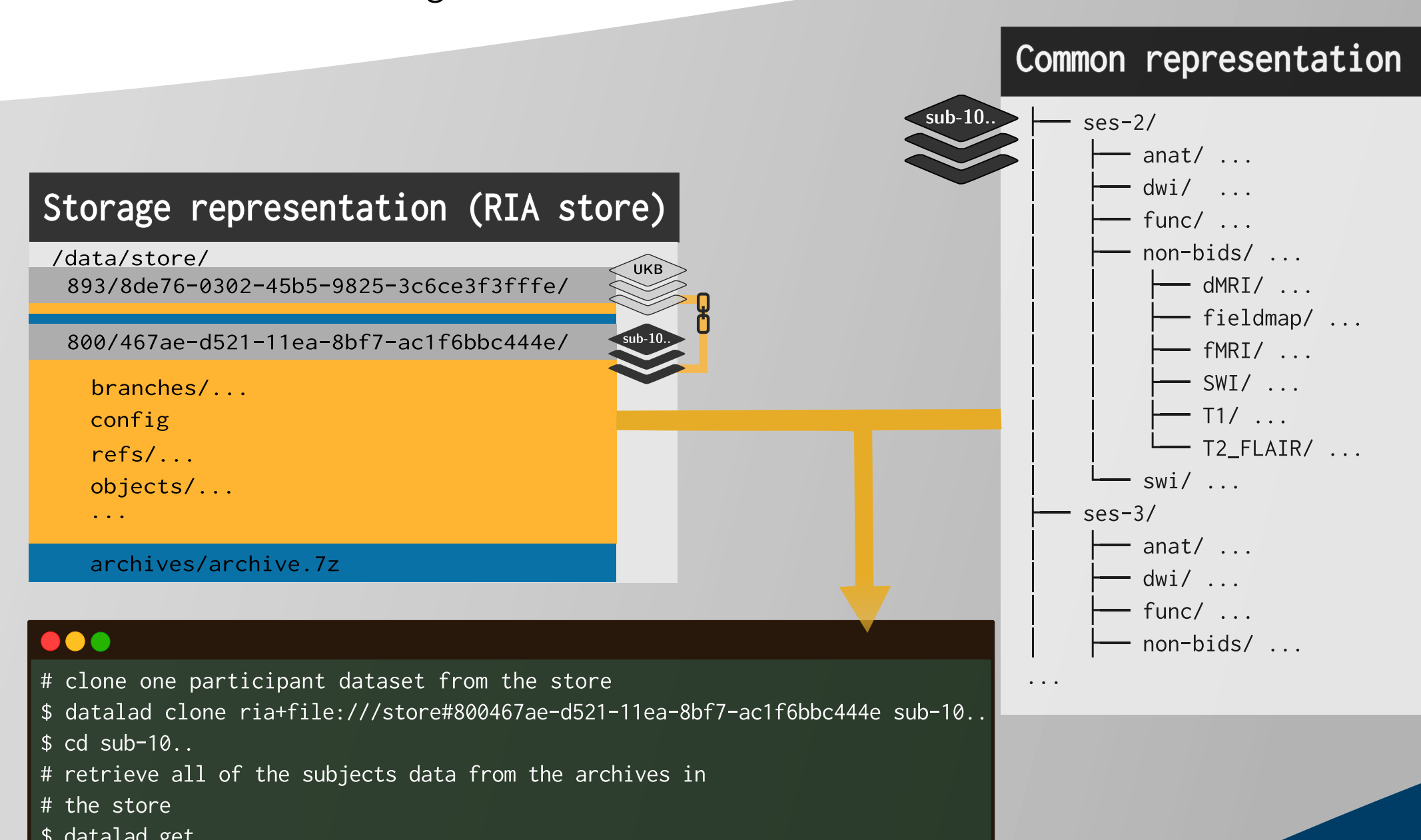
Open **sharing & reusing** derivatives is the most viable way to extend previous work¹. Still, the reproducible processing of **large-scale** or **sensitive** data, or with **proprietary** software poses research data management (**RDM**) **challenges**.

Comprehensive version control

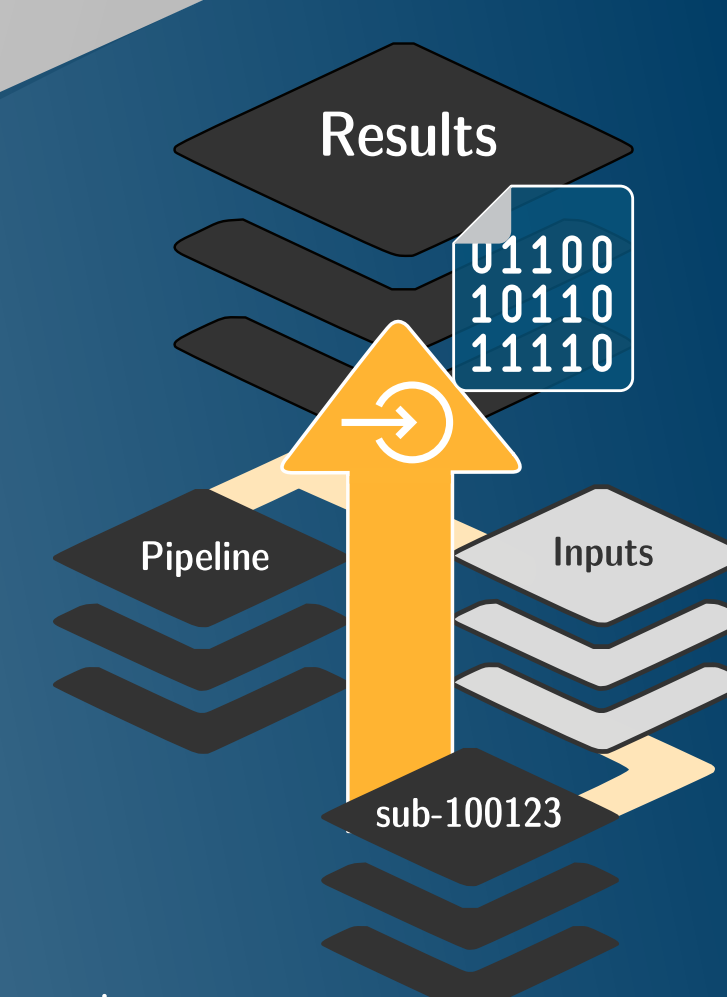
DataLad **datasets**, Git-repository-based overlay structures, version control files of any size or type. They track and transport files in a distributed network of **clones** - lightweight dataset copies linked to their origin dataset - and can retrieve or drop registered, remote file content on demand with single file granularity, enabling data access without permanent storage demands. Datasets can link other datasets in arbitrarily deep hierarchies. Datasets have a **common representation** (a directory tree) familiar to users, and an **internal storage representation** (a RIA store⁴) that can host a dataset of arbitrary size and number of files in fewer than 25 inodes, with minimal server-side requirements, and optional content compression and encryption.

Storage & computational **demands** of large data strain the capabilities of compute infrastructure; The growing complexity of handling big data threatens the **trustworthiness** of its derivatives. Sensitive data can only be shared as open as its responsible use permits, and proprietary software obstructs recomputation. Sharing large-scale derivatives in bulk can make them as inaccessible as the original raw data due to size.

Data should not only be as **FAIR** as possible, but also handled in a **sustainable** manner that prioritizes **data sharing, transparency & reuse** by appropriate audiences. We present an open source framework built on DataLad² & containerization software³ to **reproducibly process & share** big datasets.



Ephemeral workspaces



In collaborative software development routines, parallel feature development happens in branches. Merging integrates them into main revision history. Similarly, our framework executes jobs in parallel on unique branches, which users merge to aggregate results.

For parallel computations, each compute job bootstraps an ephemeral (shortlived) workspace using job scheduling software (HTCondor, SLURM). Jobs retrieve all relevant elements (e.g., subsets of input data) to their workspace, capture analysis provenance on a unique branch, and push results back. As this potentially expands compressed or archives files on infrastructure with storage constraints, the number of concurrent jobs can be adjusted to fit available resources.

Datasets can **record** and **re-execute** actionable **process provenance** about any file's genesis. It is created as a **machine-readable** record within the compute job, using either a datalad run command (for shell command execution) or datalad containers-run command for container invocations.

```
# perform & capture a container execution in a job
$ datalad containers-run \
  -m "Compute subject ${subid}" \
  -n cat \
  --input "inputs/${subid}/T1w.nii.gz" \
  --output "${subid}" \
  "<arguments for container invocation>"
```

```
# recompute a previous computation
$ datalad rerun e035f896s45c9
```

Computational provenance

Each job adds provenance to its job branch. Ephemeral workspaces ensure its completeness (defining all relevant processing elements), and thus **portability**. Beyond **transparency**, this allows consumers to rerun individual jobs on their own laptops and check for **computational reproducibility**.

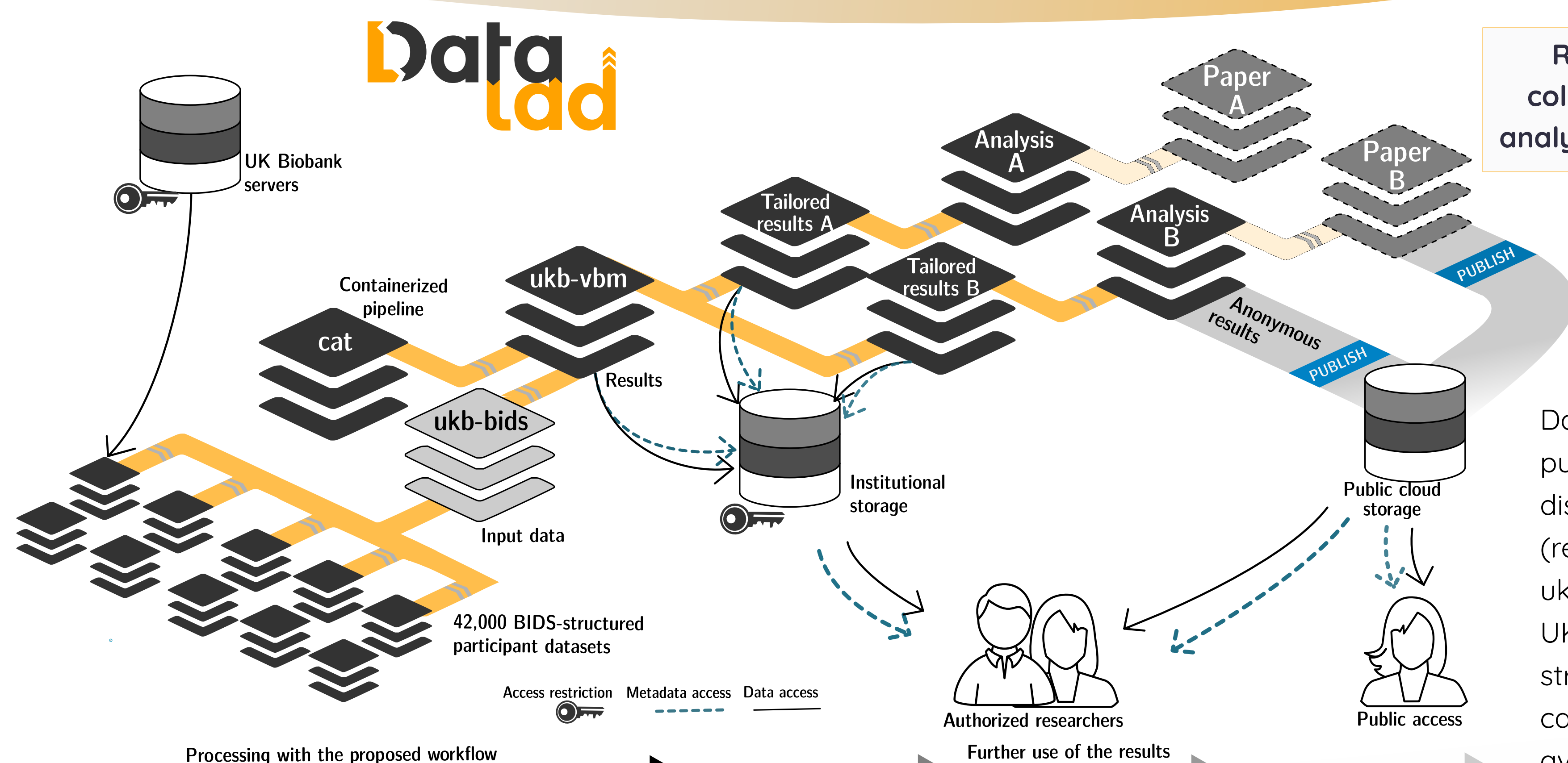
UK-Biobank use case

Key workflow metrics:

- 41.180 T1-weighted brain images. Each compute job:
- processed one image for voxel-based morphometry⁵
- required one CPU hour
- needed 5 GB disk space
- needed 4 GB RAM
- created 4 output archives

Key computing metrics:

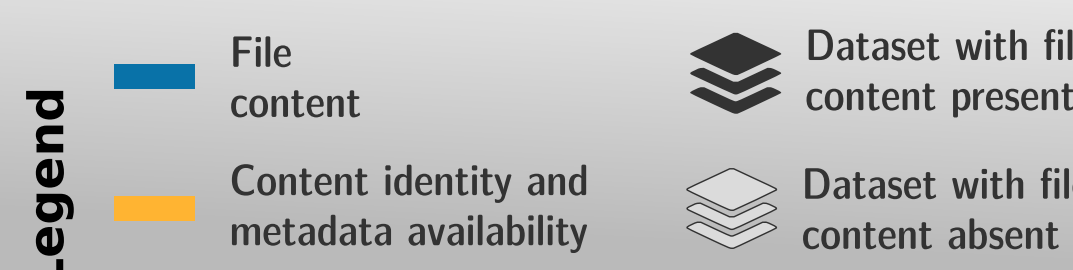
- Low disk space **HTC**:
 - up to 600 jobs at a time
 - Processing time: 6 weeks
 - Node-constrained **HPC**:
 - 3125 jobs at a time
 - Processing time: 10 hours
- Recomputations yielded >50% binary identical results with the exception of cortical projections.



Recompute your colleagues' multi-TB analysis - on your laptop!

Re-Use

DataLad Datasets ease public or private data distribution. Access to raw (retrieved by datalad-ukbiobank⁶) & processed UKB data is restricted, but streamlined. If legal, data can be made publicly available easily.



References

- Craddock, C. et al. (2013). doi 10.3389/conf.fninf.2013.09.00041
- Halchenko, Y. O. et al. (2021). doi: 10.21105/joss.03262
- Kurtzer et al. (2017). doi: 10.1371/journal.pone.0177459
- Poldrack et al. (2021). doi: 10.7490/f1000research.1118494.1
- Gaser & Dahnke, http://www.neuro.uni-jena.de/cat
- Hanke et al. (2021) doi: 10.5281/zenodo.4773629

