Manuscript Title

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✉ — Correspondence possible via GitHub Issues

Abstract

Background & Summary

We scanned a *lot* of different mouse strains and so-called hybrids, both male and female. One scan for each strain, each hybrid and each sex gives already 90 samples.

Methods

Sample preparation

- Mice were euthanized and decapitated
- Mouse skulls were stored in EMA
- Separated into 4 batches of approximately 110 animals, labeled as B`batch_number` *`animal number`* *A and B* *`batch_number`* `animal number` B.

Tomographic imaging

- SkyScan 1272 with sample changer
- *All* log files available here: https://github.unibe.ch/david-haberthuer/InMice/tree/main/logfiles
- Report scaning settings and reconstruction parameter data according to[1]
- Use a notebook to pull *all* the relevant data to report directly into the text here, or into a file that is loaded by `manubot`.

QA

- Use a collection of logfile wrangling code[2] to go through *all* the log files of all the aquired scans
  - Use this to surface issues related to aquisition (wrong setting) and reconstruction
- Look at average and maximal brightness of (a subset of) all the projection images aquired
  - Use this to surface issues related to acquisiton, e.g. sometimes the x-ray source inadvertedly shut down, or the counts were too low on the camera, etc.

Image processing

- `Jupyter`[3] notebooks, available here: https://github.unibe.ch/david-haberthuer/InMice/, for reproducible research.
  - Ingest complete, uncropped reconstructions with `dask`[4]/
  - Crop, based on axial MIPs
  - Save cropped data out as `.zarr`-files, ready to be loaded with `n5-ij`[5] in Fiji[6]
  - Save in other formats, to either use 3D Slicer[7]/,[8] or Dragonfly[9]/

Data Records

Technical Validation

Usage Notes

Code Availability

- Jupyter notebooks

References

1. Stock, S. R. & De Carlo, F. Meta-data for absorption tomography measurements. *Tomography of Materials and Structures* **3**, 100015 (2023).

2. David Haberthür. *Habi/BrukerSkyScanLogfileRuminator: First Release for Minting a Zenodo DOI*. (Zenodo, 2025). doi:10.5281/zenodo.15607944.

3. Kluyver, T. *et al.* Jupyter Notebooks – a publishing format for reproducible computational workflows. in (eds. Loizides, F. & Scmidt, B.) 87–90 (IOS Press, 2016). doi:10.3233/978-1-61499-649-1-87.

4. Dask — Dask documentation. https://docs.dask.org/en/stable/.

5. saalfeldlab/n5-ij. Saalfeld Lab (2025).

6. Schindelin, J. *et al.* Fiji: an open-source platform for biological-image analysis. *Nat Methods* **9**, 676–682 (2012).

7. 3D Slicer image computing platform. *3D Slicer* https://slicer.org/.

8. Fedorov, A. *et al.* 3D Slicer as an image computing platform for the Quantitative Imaging Network. *Magnetic Resonance Imaging* **30**, 1323–1341 (2012).

9. Dragonfly Software for Image Processing and Data Analysis - Dragonfly. https://dragonfly.comet.tech/.

10. ANSI/NISO Z39.104-2022, CRediT, Contributor Roles Taxonomy. doi:10.3789/ansi.niso.z39.104-2022.

11. Himmelstein, D. S. *et al.* Open collaborative writing with Manubot. *PLoS Comput Biol* **15**, e1007128 (2019).

Author Contributions

Contributor Roles Taxonomy (CRediT), as defined in[10]:

- Conceptualization: Bernhard Voelkl, Hanno Würbel
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- Formal analysis: David Haberthür, Bernhard Voelkl
- Funding acquisition: Bernhard Voelkl, Hanno Würbel
- Investigation: David Haberthür, Pui Ching Chu, Larisa Petra Kaija
- Methodology: David Haberthür, Pui Ching Chu, Larisa Petra Kaija, Bernhard Voelkl
- Project administration: David Haberthür, Pui Ching Chu, Bernhard Voelkl, Hanno Würbel
- Resources: Pui Ching Chu
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- Validation: David Haberthür, Pui Ching Chu, Larisa Petra Kaija
- Visualization: David Haberthür
- Writing – original draft: David Haberthür
- Writing – review & editing: David Haberthür, Pui Ching Chu, Larisa Petra Kaija, Bernhard Voelkl, Hanno Würbel

Competing Interests

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Larisa Petra Kaija	None	
Bernhard Voelkl	None	2025-08-19
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