microCT imaging of threespine stickleback

This manuscript ([permalink](#)) was automatically generated from [habi/sticklebacks-manuscript@a0542b5](#) on January 15, 2026.

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Abstract

Introduction

- Embedded into [Alaska Stickleback Restoration Project](#), [Genomics axis](#) where Katie Peichel, Ben Sulser and Sheila Christen are affiliated.

Materials & Methods

Sample preparation

microtomographic imaging

- Scanned on a [Bruker SkyScan 2214](#)
- Sample holder generated with [OpenSCAD](#), available online at [GitHub](#) [1]
  - Scanning several fish toghether to efficiently use machine time
  - Full in Bruker workflow
  - Results in PNG stacks on disk

Data analysis

- [Jupyter notebooks](#)
  - Efficiently loading data from disk with `dask` [2]
  - Extract position of single fish (all scanned together), based on the MIP of the scan
  - Crop out each fish (with a buffer) and write to cropped dataset
    - Cropped datasets are saved to discrete folders for easy handling. In both original gray-scale plus as thresholded dataset, e.g. binarized into bone and "not bone". These sare saved out as `zarr` [**wiki:Zarr_?**(data_format)] and `nrrd` files.

Results

Discussion

Conclusion

Author Contributions

[Contributor Roles Taxonomy (CRediT)](), as defined in [3]:

- [Data curation](): David Haberthür
- [Formal analysis](): David Haberthür
- [Investigation](): David Haberthür
- [Methodology](): David Haberthür
- [Project administration](): David Haberthür
- [Software](): David Haberthür
- [Validation](): David Haberthür
- [Visualization](): David Haberthür
- [Writing – original draft](): David Haberthür
- [Writing – review & editing](): David Haberthür

Competing Interest

Author	Competing Interests	Last Reviewed
David Haberthür	None	2026-01-14
Ben Sulser		
Sheila Christen		
Katie Peichel		
Ruslan Hlushchuk		

Acknowledgements

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