microCT imaging of threespine stickleback

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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
- All log files available here: https://github.com/habi/sticklebacks/tree/main/logfiles

Data analysis

Preparation and handling of tomographic datasets

- Jupyter notebooks [2]
  - Efficiently loading data from disk with `dask` [3]
  - Extract position of single fish (all scanned together), based on the MIP of the scan (see Figure 2).
  - Crop out each fish (with a buffer) and write to cropped dataset (see Figure 4).
    - 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 are saved out as `zarr` [4] and `nrrd` files.

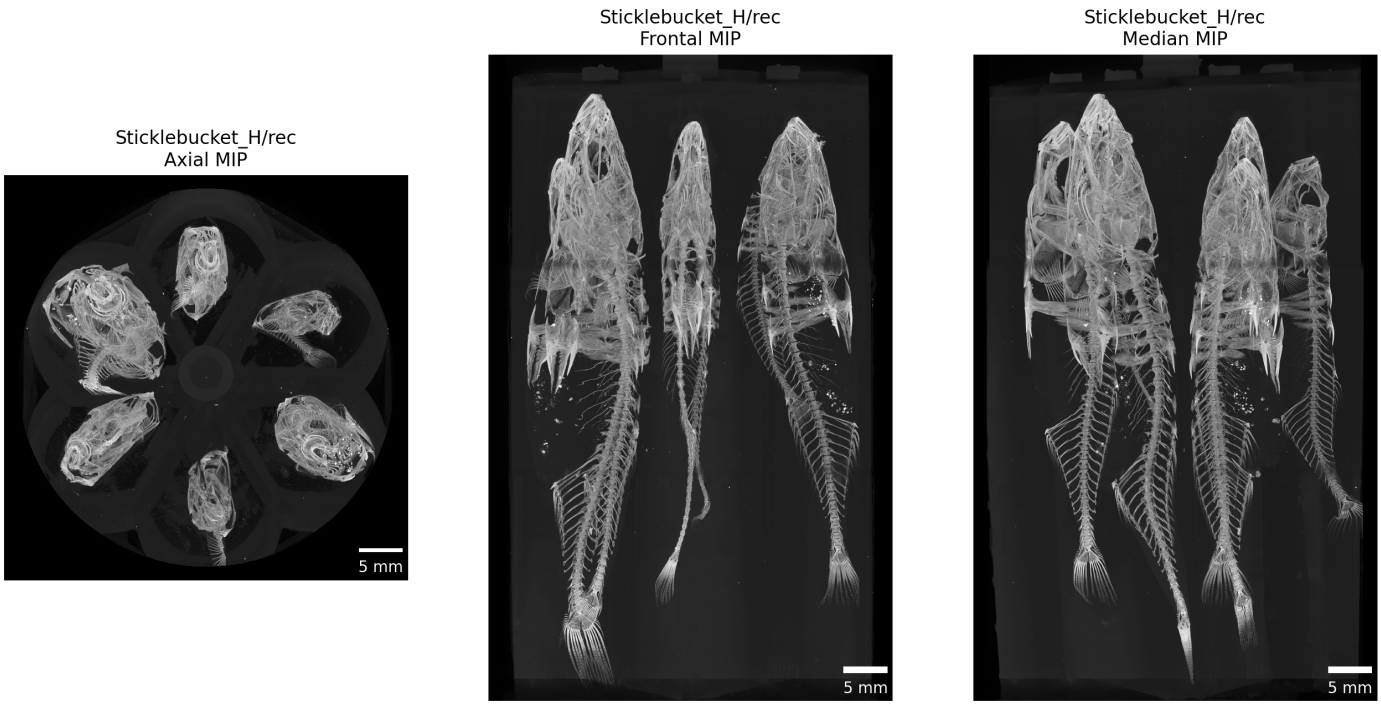

Figure 1: Maximum intensity projections of one acquired dataset along all three cardinal axes.

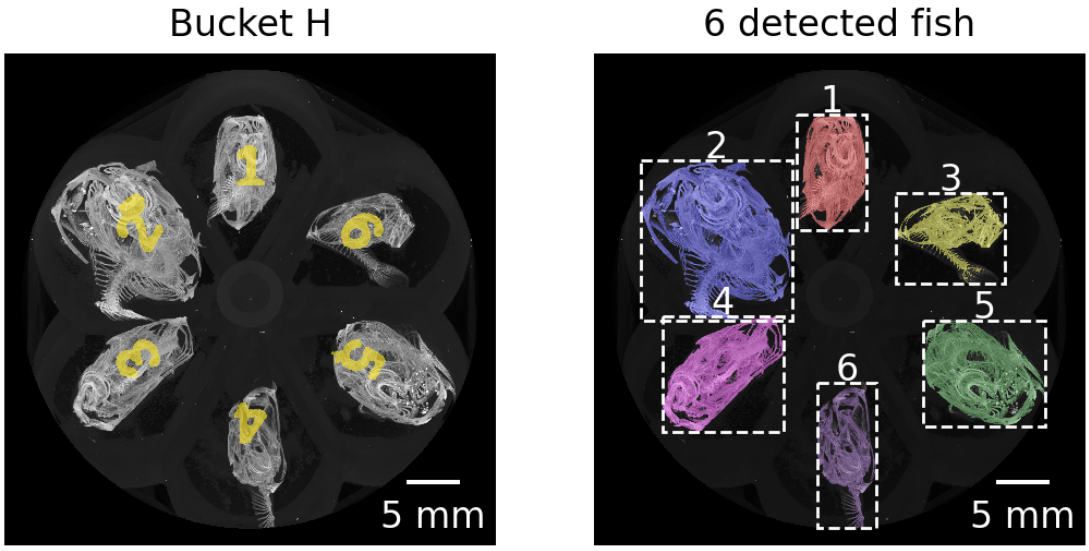

Figure 2: Automatically detected regions based on maximum intensity projection along the rotation axis of the tomographic scan. The regions are numbered consecutively from the top left to the bottom right. These numbers are mapped to the correct fish ID in the next step.

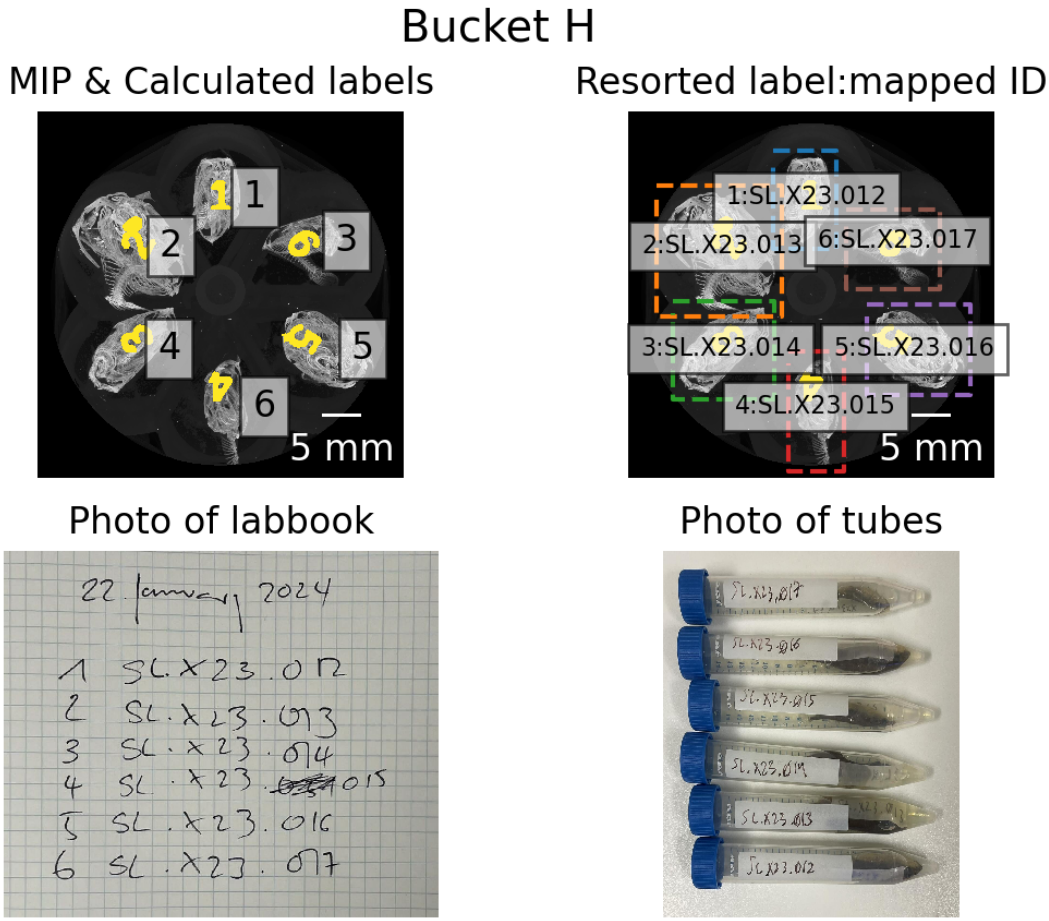

Figure 3: Mapping lab book notes, photos and detected regions to fish ID.

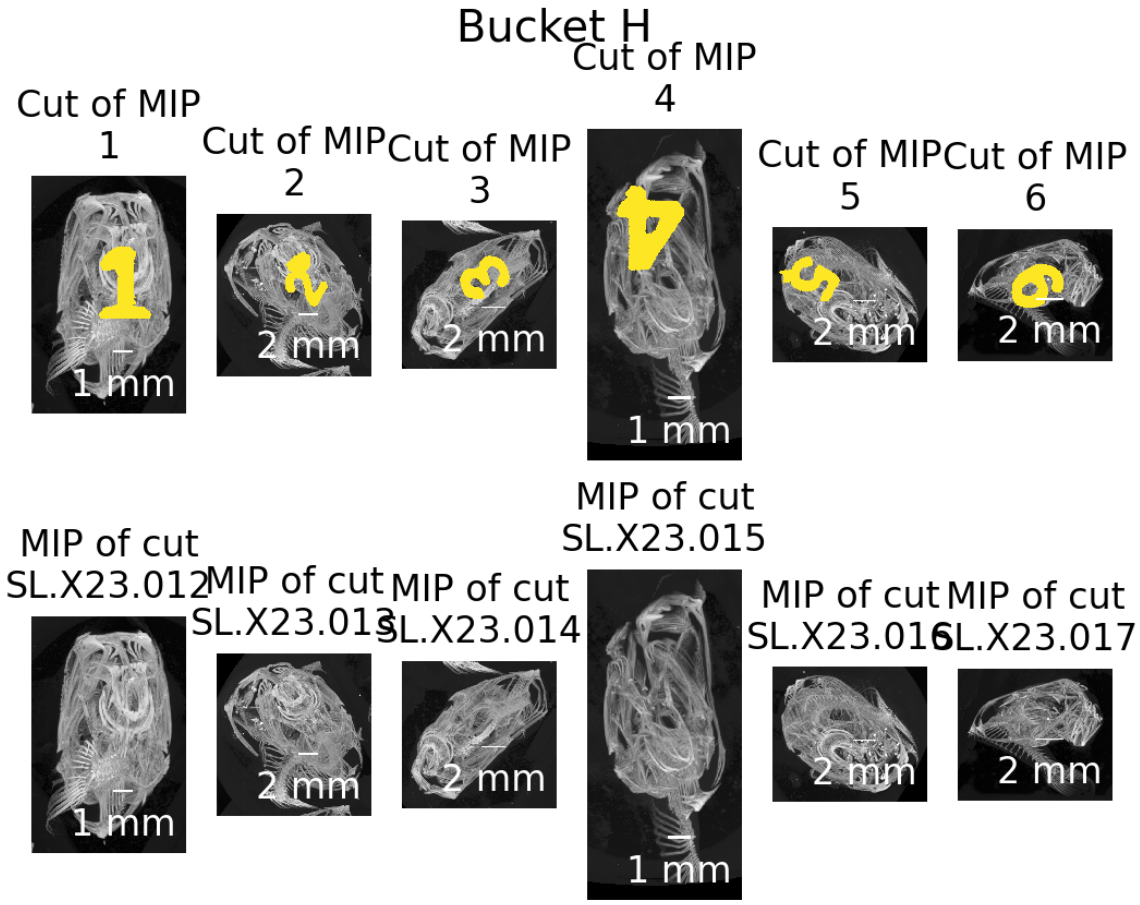

Figure 4: Doublechecking crop extent and fish ID.

Extraction of features of interest

- Biomedisa [5]

Results

- 3D shape variation on internal pharyngobranchial bone. Only possible to get this information in 3D.

Discussion

- Both *repeatable* and *reproducible* research
- Automated cropping out of single fish from combined scan very efficiently uses machine time. Several fish can be scanned together, splitting is performed after the fact, reproducibly and without manual input.
- Combination of methdes cust down on time **a lot**.
- Biomedisa makes more “extraction” possible. Other biological questions can be answered, too.

Conclusion

Author Contributions

Contributor Roles Taxonomy (CRediT), as defined in [6]:

- 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		

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