An Extensible Software for Whole-Skeleton microCT Analysis of Zebrafish

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Introduction

o Zebrafish are a powerful model for rapid throughput skeletal biology [1]

o Previously, the MSBL developed software for microCT-based analysis in zebrafish, FishCuT(v1) [1].

o One limitation of FishCuTv1, due to its architecture, is difficulty in extending analysis to other skeletal structures and traits.

Objectives

o Within FishCuT, incorporate an extensible architecture that facilitates open-source development of new phenotypic algorithms in pursuit of whole-body phenomic analysis.
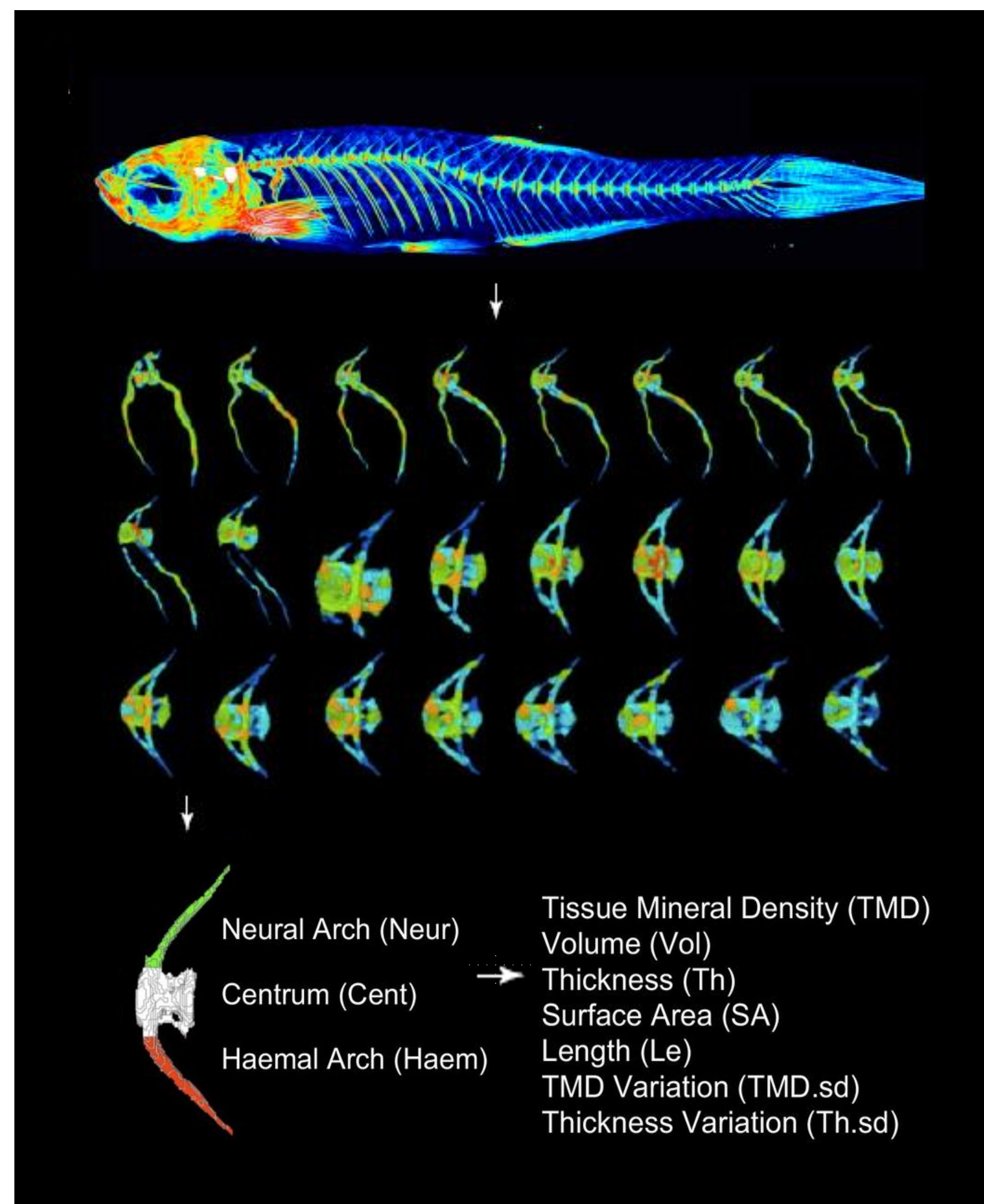

Fig 1: FishCuT isolates individual vertebrae (shown: 24 vertebrae from a single fish), segments each vertebra into three elements (neural arch, centrum, and haemal arch), and computes measures for each element.

FishCuTv2

o We have modularized the architecture of FishCuT to facilitate development of new extensions to measure additional skeletal traits.
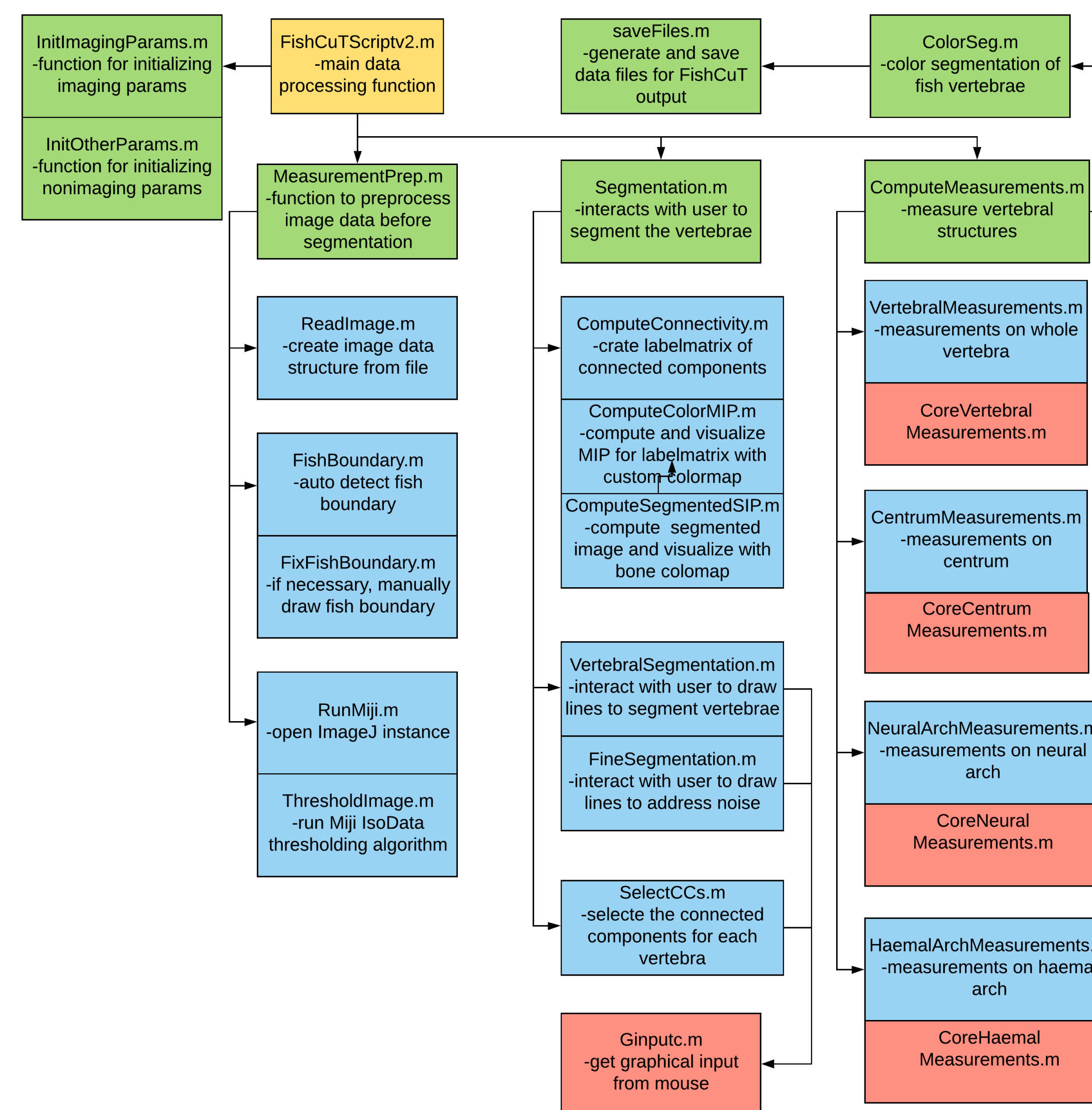

Fig 2: FishCuTv2 is organized in a modular architecture that allows developers to add measurement modules without needing to understand the implementation details image preprocessing, segmentation algorithm, or file Input and output.

o Modules for measuring additional features can be developed and integrated more easily.

o FishCuTv2's new architecture facilitates collaborative development

o New modules can be implemented retroactively to analyze existing microCT data.

Measurement Module

o We developed a module to quantify neural arch area, height, and width to demonstrate FishCuTv2's extensibility.
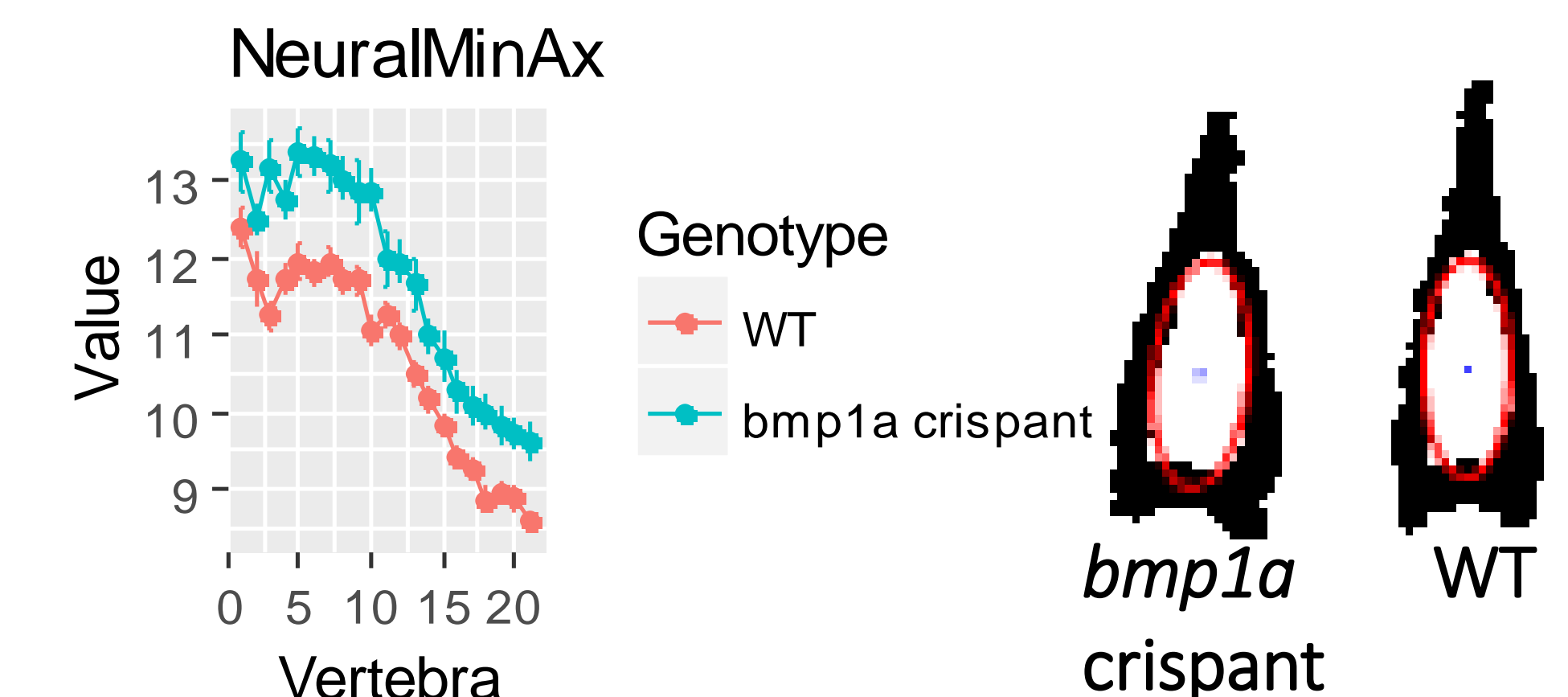

Fig 3: Quantitative and qualitative analysis of neural arch area and effective minor axis for bmp1a somatic mutants

o In *bmp1a* crispants, we detected a statistically significant ($p < 0.05$) increase in neural arch width (NeuralMinAx) (Fig 3). This was consistent with previous studies showing increased neural arch area in *bmp1a* germline mutants [2].

Discussion

o We improved FishCuT's architecture and prototyped new phenotypic modules for higher content descriptions of whole-body microCT datasets.

o FishCuTv2 facilitates collaborative development and retroactive screening of microCT data to identify new gene-to-phenotype relationships.

References

[1] Hur et.al., eLife 2017, [2] Charles et.al., Bone 2017.

Acknowledgments