

Retroactive Image Analysis for Rapid Phenotypic Data Generation

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Introduction

Understanding the relationship between genes and phenotypes is fundamental to biology research. Experiments are used to generate data that can be mined for understanding the expression of specific genes. However, the resources needed for experimentation and the technology used to analyze experiments limit the generation of new phenotypic data. The objective of this study is to demonstrate the fidelity of generating phenotypic data by performing retroactive image analysis using a zebrafish microCT data analysis framework as a model.

Data Organization

- Database of raw image data and quantitative phenotypic data (zebrafish microCT database)
- Other advantages include: decreased data redundancy, increased data security, increased data accessibility
- Having raw image data allows for retroactive analysis, also includes metadata from previous analyses

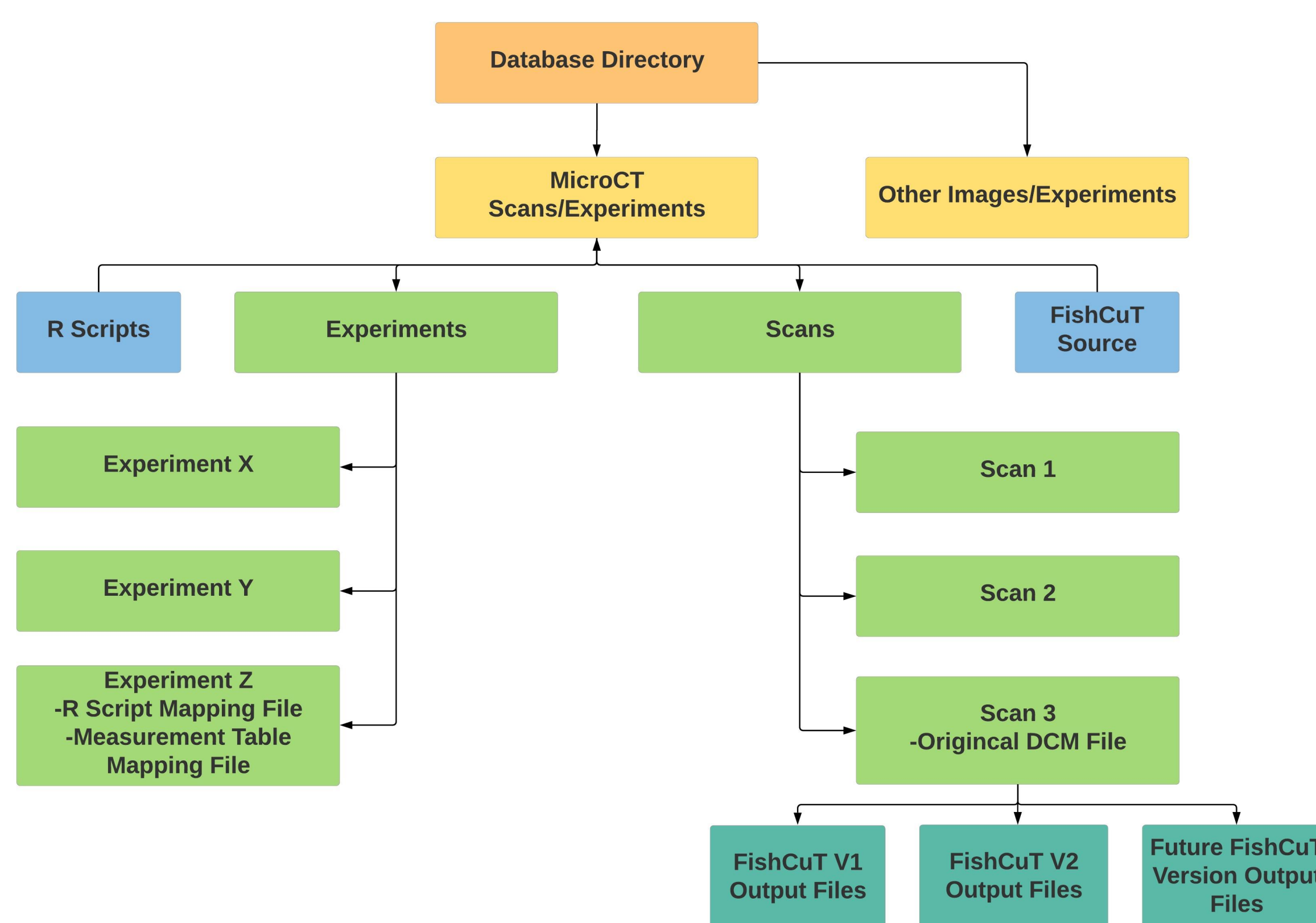


Figure 1: Structure of a zebrafish skeleton microCT database.
FishCuT is the microCT image analysis software.

Analysis Technology

- Modularized image analysis program allows for easier development
- Developers can follow a template to add modules without needing to know how the core program functions
- As an open source project, researchers can add improvements based on their own needs and interests
- Saves metadata, segmentation data, and quantitative data

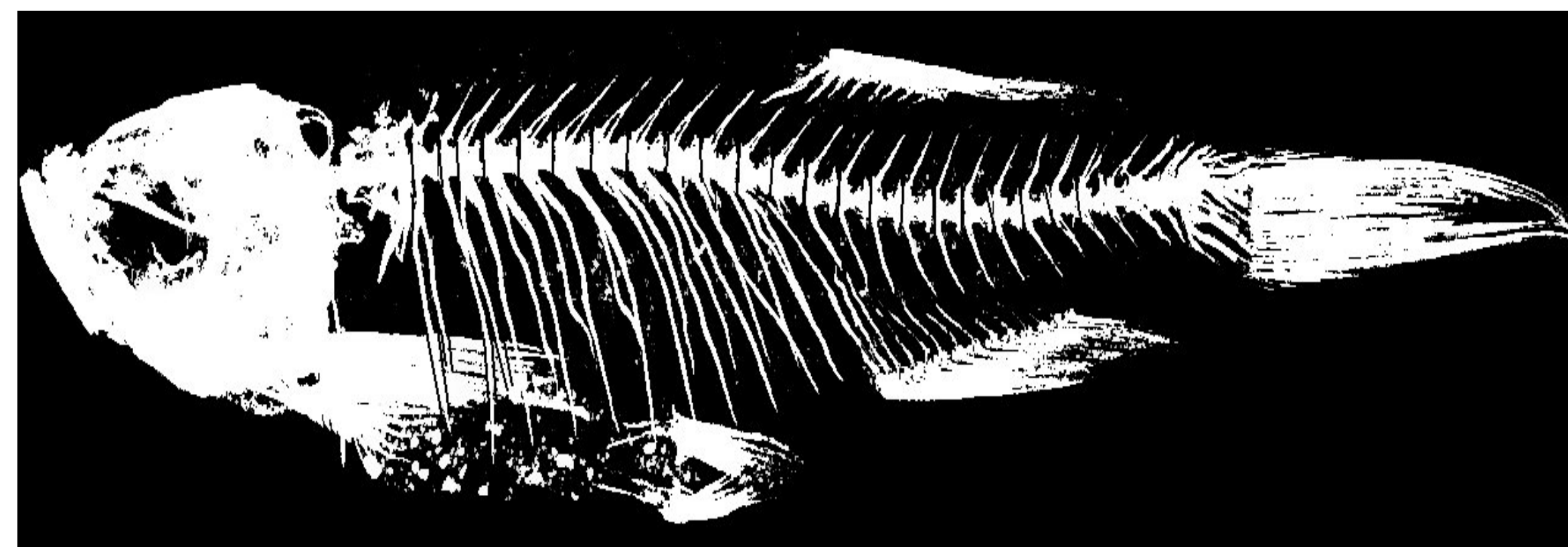


Figure 2: Projection of manually segmented binarized microCT stack of zebrafish skeleton: used for retroactive data analysis

Module Development

- Measurements on the neural arch (superior arch of the vertebra)
- Can be used to detect phenotypes including: neural foramen (hole) area, neural foramen effective major and minor axes, neural arch angle

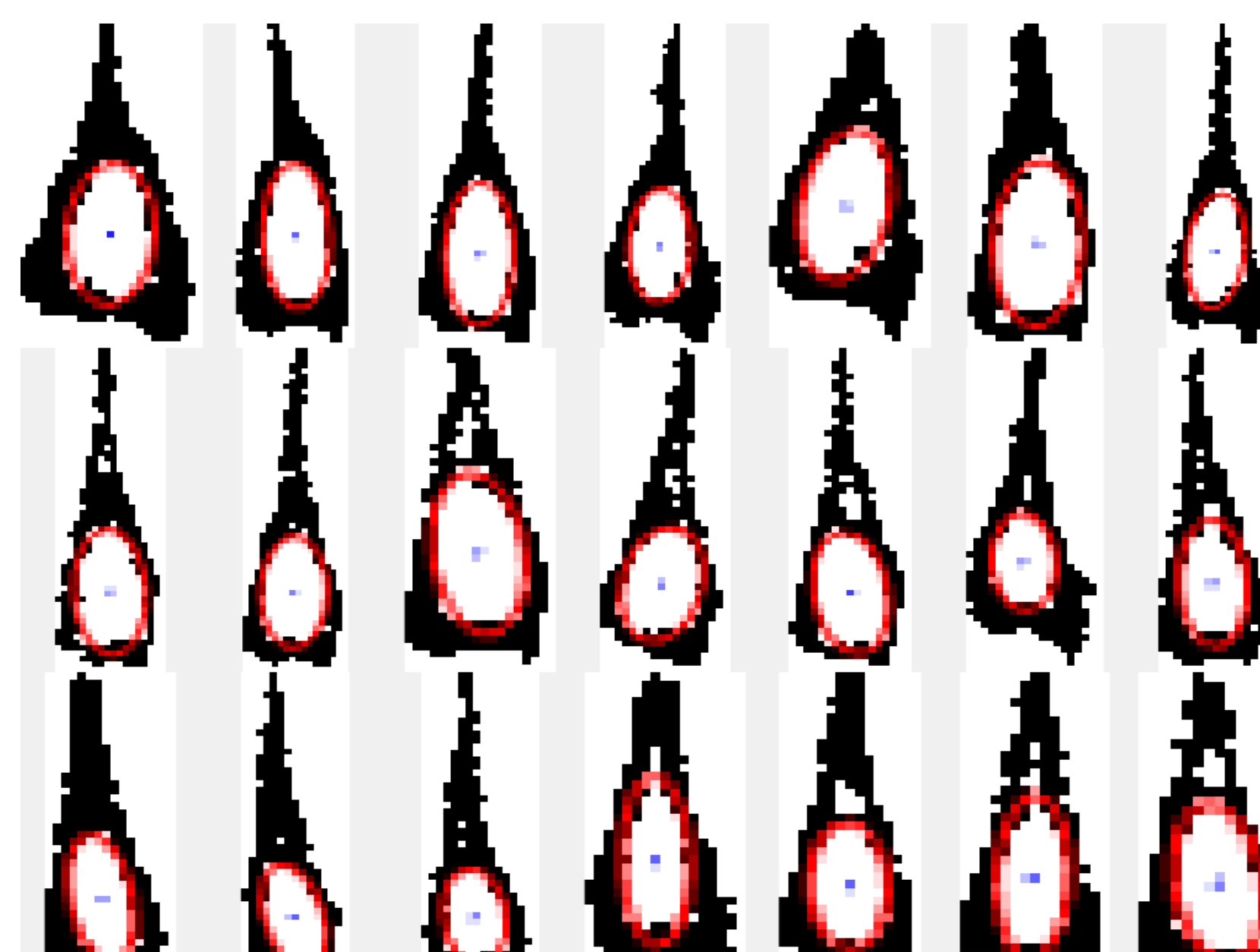


Figure 3: Qualitative data produced by neural arch module – includes projection of the neural arch and automatically fitted ellipse

Module Validation

- Validation data was collected from using an open source volume rendering program called 3D Slicer
- Collected only for effective major axis in 21 vertebra of a control fish

Measured vs Predicted Neural Foramen Maj Axis

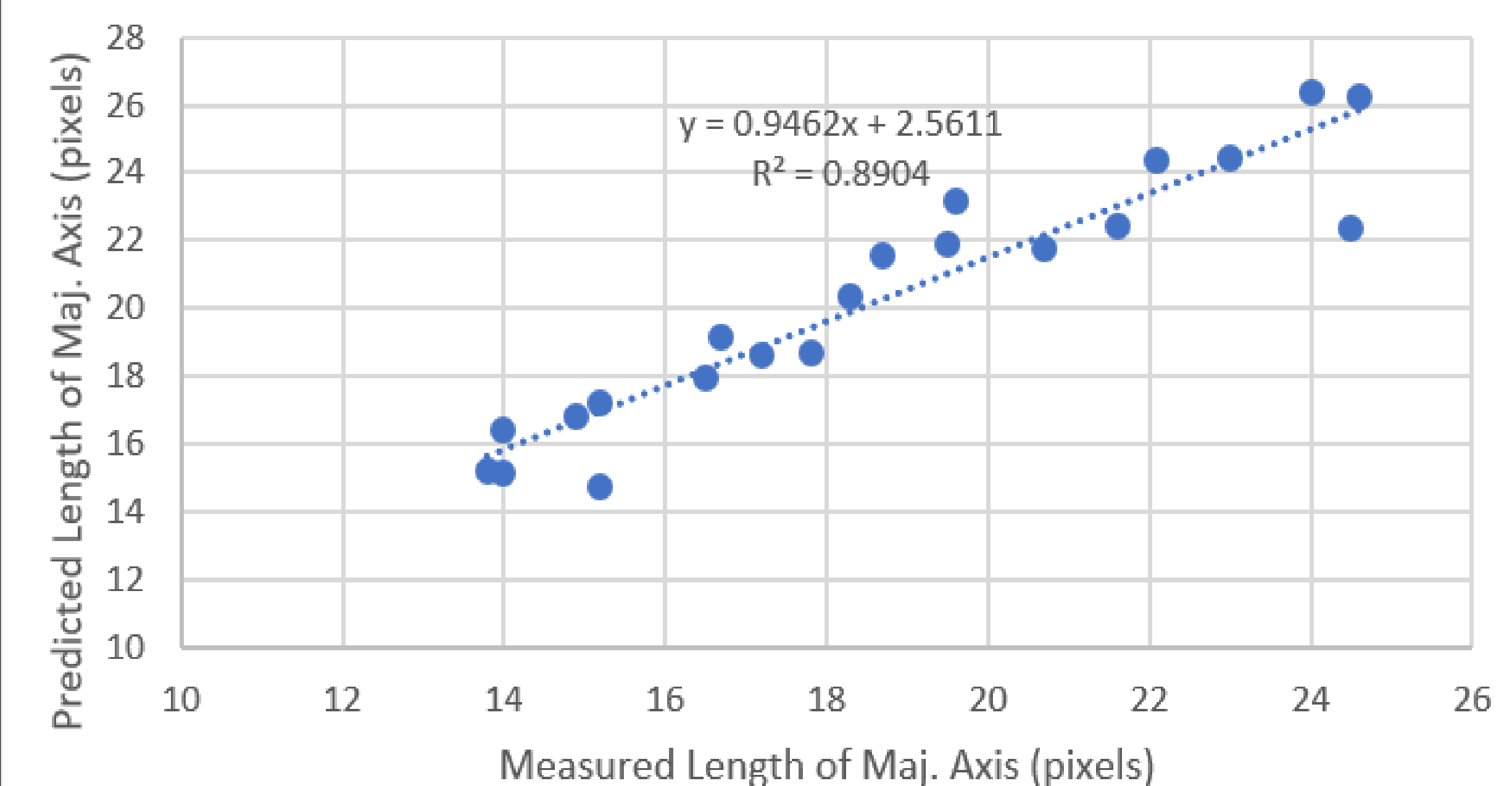


Figure 4: Quantitative analysis of validation data - manually measured data compared with module predicted data

Discussion

- A data analysis framework was developed for compatibility with retroactive image analysis
- The first non-core module of the zebrafish microCT analysis software is in development
- Further steps include: finishing and validating the neural arch module, implementing the module through retroactive analysis to discover new phenotypes

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