# Automatic workflow for the analysis of large batches of micro-tomographic scans of human teeth

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# Abstract

The abstract will be written at the end, here are some key points

- Python
- Only free and open-source software
- Image analysis
- Fully reproducible research
- Efficiently done, already during scan of parts of the batch. New scans are just dumped on the script to process.
- Probably not possible manually in the needed time-frame or extremely cumbersome (huge batch-process).
- Everyone can do/check it, show it in Binder!

# Introduction

Successful endodontic treatments require a precise knowledge of the external and internal morphology of the teeth [**???**]. For both surgical and non-surgical interventions it is necessary to know both the complex three-dimensional root canal system with its configurations as well as the details of the apical region of the tooth. This knowledge is necessary to select the correct instruments and materials and thus make important treatment decisions. It also helps to avoid errors that can occur during various steps of clinical endodontic treatment, such as preparation of the access cavity, rinsing, shaping and filling of the root canal system [1]. The errors include, for example, frequently occurring perforations during trepanation or failure in preparing the root canals. A detailed description and understanding of the root canal system are essential for the clinical practitioner. Nowadays, in the literature there are numerous imaging methods for the morphological description of teeth, such as clearing technique [2], optical microscopy [3], two-dimensional radiography, scanning electron microscopy, or three-dimensional imaging techniques such as cone beam computer tomography and micro-computed tomography (micro-CT) [4].

# Materials & Methods

## Teeth

Describe how the teeth have been collected and stored.

## X-ray microtomography

After preparation of the teeth, the 104 samples were imaged on a Bruker SkyScan 1272 high-resolution microtomography machine (Control software version 1.1.19, Bruker microCT, Kontich, Belgium). To facilitate the scanning of this large batch of samples, we used the automatic sample changer to enable us to scan batches of 16 teeth without manual intervention. In addition to the sample changer, the machine is equipped with a Hamamatsu L11871_20 X-ray source and a XIMEA xiRAY16 camera.

We used a custom-made sample-holder to scan the teeth on the sample changer. The sample holder has been 3d printed and is freely available online (https://git.io/JJbAZ) as part of a library of sample holders [5].

The X-ray source was set to a tube voltage of 80.0 kV and a tube current of 125.0 µA, the x-ray spectrum was filtered by 1mm of Aluminium prior to incidence onto the sample. For each sample, we recorded a set of either 4 or 5 stacked scans overlapping the sample height, each stack was recorded with 482 projections of 1632 x 1092 pixels at every 0.4° over a 180° sample rotation. Every single projection was exposed for 950 ms, 3 projections were averaged to one to greatly reduce image noise. This resulted in a scan time of approximately 40 minutes per stack and between 2 hours and 40 minutes to 3 hours and 15 minutes per sample. In total, we thus scanned for approximately 13 days. The projection images were then subsequently reconstructed into a 3D stack of axial images spanning the whole length of each tooth with NRecon (Version 1.7.4.6, Bruker microCT, Kontich Belgium) using a ring artifact correction of 14. The whole process resulted in datasets with an isometric voxel size of 10.0 µm.

We recorded on average 8.17 GB of raw data for each tooth, totalling to 849.59 GB for all the 104 teeth.

## Image analysis

Already during scanning the first items of the batch, we wrote a Jupyter [**???**] notebook with Python code which permitted to check the already performed scans as soon as they were reconstructed. Reruns of the notebook added newly scanned and reconstructed teeth to the analysis, facilitating preliminary checks and analysis of already scanned teeth. The notebook we used for the analysis presented in this manuscript is freely available online [6]. The important steps of the analysis steps are described in detail below.

## Preparation

In a first step we extract all wanted parameters from the log file of each scan to store into a Pandas [7] dataframe for comparing and double-checking all the necessary scan parameters of each tooth scan with all the others. Afterwards, we loaded the preview image of each scan and then generated an overview image of all the scans (see Figure 1).
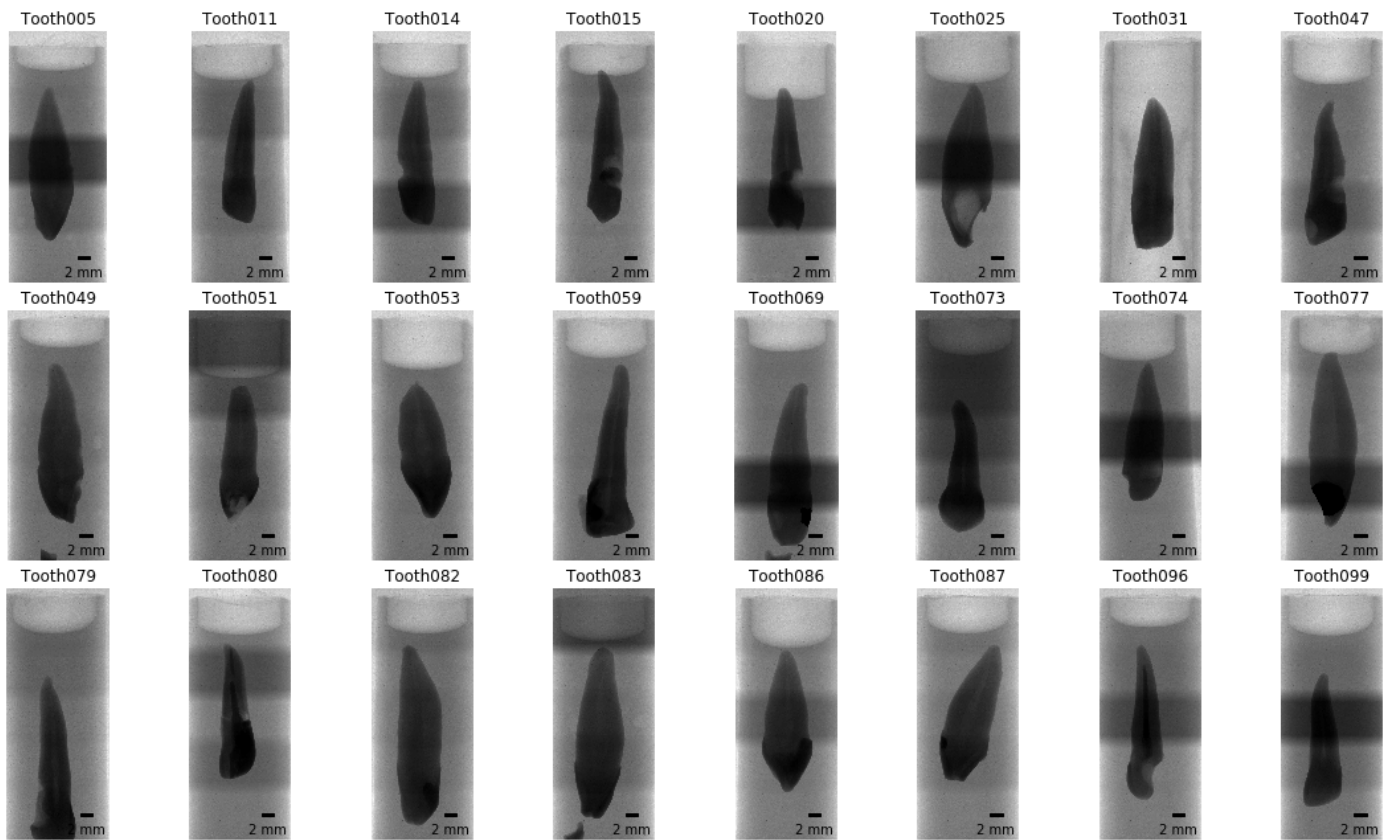
**Figure 1:** Overview images for each of all the teeth we scanned. It is immediately visible that several teeth slipped down in the holder. Since we were particularly interested in the bottom part of the teeth this poses no problem for further analysis. The irregular illumination stems from the rudimentary stitching process and is not visible in the reconstructed slices.

And here's some more text.

# Introduction

Hereby we present a method to efficiently and reproducibly analyze large batches of teeth.

# Conclusions

The presented method offers an efficient approach to scan, check and preview micro-computer tomographic datasets of a large amount of teeth. We describe a helpful, free and open-source software tool to prepare datasets for precise description and characterization of the internal morphology of human permanent teeth using automated segmentation of features of interest. Due to the high reproducibility and standardization of the presented method, datasets of large cohorts and populations can be investigated easily and rapidly.

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# Contributions

- DH scanned the teeth, wrote the analysis notebook and the original draft of the manuscript.
- RH contributed with discussion during the development of the method and reviewed the manuscript.
- TGW contributed with ideas and discussion for developing the method, discussed the results, edited and reviewed the manuscript.

All authors read and approved the final manuscript.

# Conflict of interest statement

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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