



Czech Centre for Phenogenomics
Phenotyping module
Bioinformatics unit

NORMAL VS. ABNORMAL: LOOKING FOR BORDER VALUE IN CT SCANS OF MOUSE SKULLS

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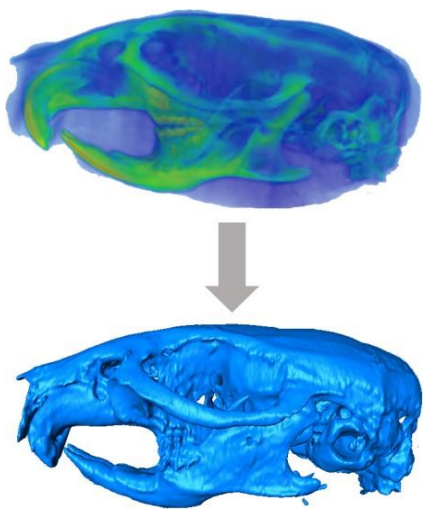
Introduction

The manual analysis of in-vivo scans is a time-consuming procedure, so we develop a more efficient automated image analysis tool. As a starting point, we focused on the mouse skull. We used already phenotyped animals with known normal or abnormal annotation. The crucial point was to find the border, which clearly distinguishes the skull's status.

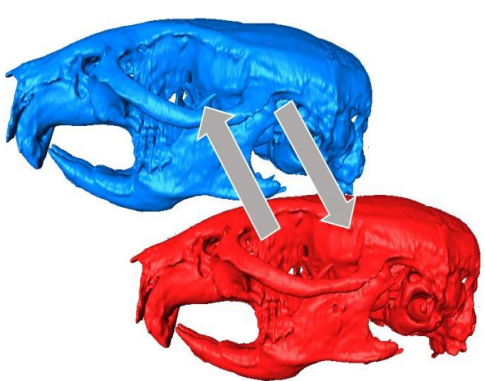
Devices and technologies

- SkyScan 1278 (Bruker, Belgium)
- NRecon 2 (Bruker, Belgium)
- Amira software 2020.2 (Thermo Fisher Scientific)

1 step: segmentation



2 step: skull alignment



3 step: distance calculation

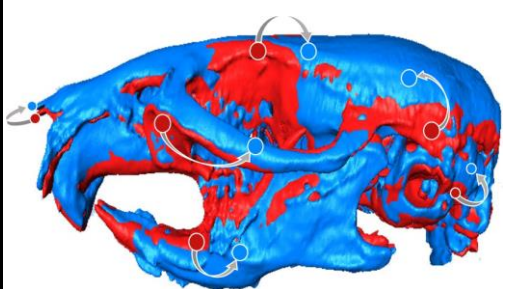


Figure 1: Workflow

Methods:

According to the standard CCP protocol, 13 weeks old mice were scanned using the SkyScan 1278 (Bruker, Belgium) with a resolution of 52 μm (0.5 mm Al filter, current = 753 μA , voltage = 54 kV, 180° rotation). The scans were reconstructed using NRecon 2 (Bruker, Belgium) and evaluated by a specialist in CT vox (Bruker, Belgium). 9 mice were used for this analysis. The automated analysis consists of three main steps: segmentation, alignment, distance calculation (Fig. 1), which were performed using the software AMIRA (Thermofisher). For the segmentation, we used a multi-thresholding segmentation algorithm with a corresponding threshold. As a next step, we used minimalization of the root mean square distance to compute the matrix of Hausdorff distances for the all objects.

Results:

Applying the above-mentioned approach, we confirmed the manual annotation of a normal or abnormal skull (Fig. 2) of 9 cases. In a few cases, there was a discrepancy between automated and manual annotation (Fig.3). There is shown the paired distance between selected aligned skulls. The left table shows a skull with ambiguous annotation, which was expected to be normal but has a possible abnormality, which is highlighted as different position of the yoke arch in the alignment. The right table shows the comparison between normal (rows) and abnormal (columns) skulls. Generally, the skulls annotated as "normal" manually seems to be more similar to each other, than those annotated as "abnormal", although some exceptions from the rule were found.

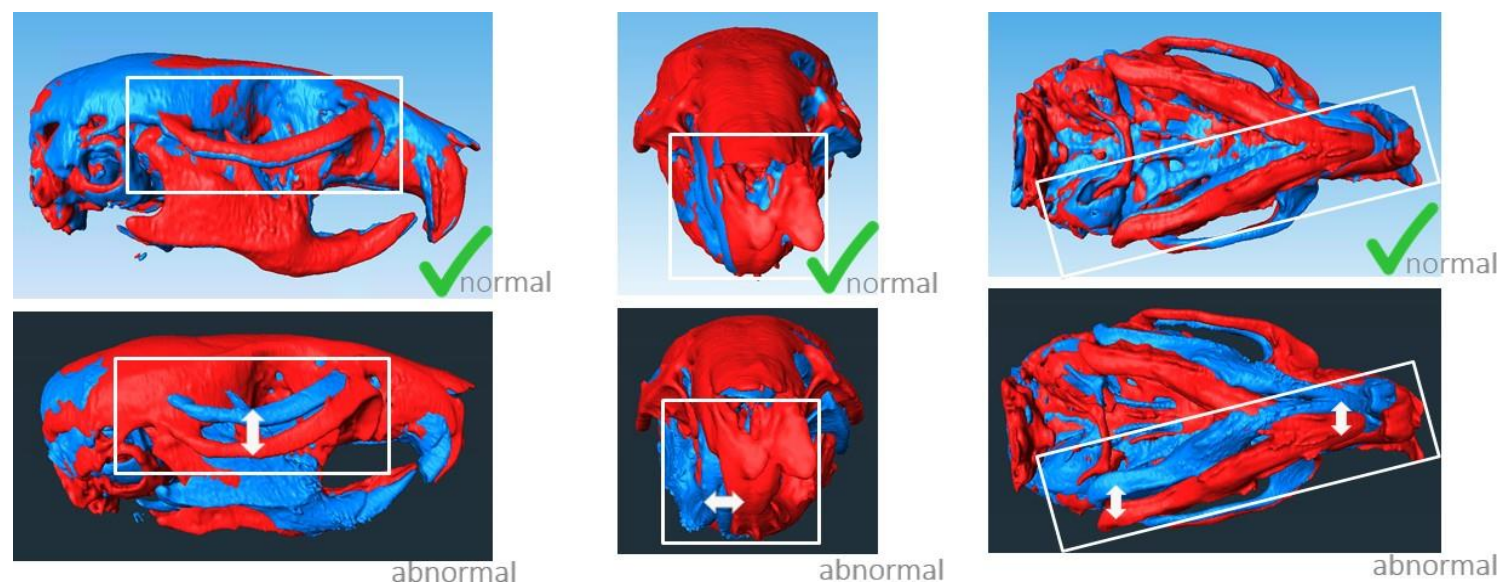


Figure 2: Comparison of normal and abnormal alignments

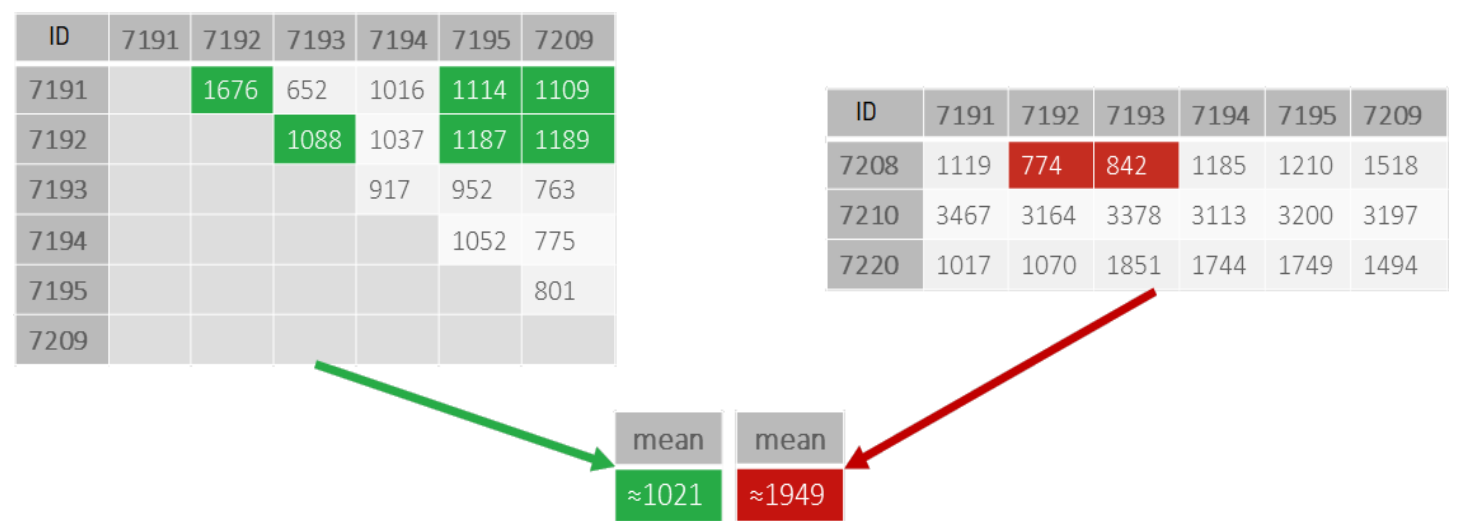


Figure 3: Hausdorff distance

Conclusion:

The calculation of the distance matrix alignment helped us, to establish the border mean square value that separates normal variability from abnormal deviation. Furthermore, three cases showed controversial values when compared with their original annotation, which may indicate that the manual annotation was not correct. We believe, that the combination of automatic and manual approach may better and faster phenotyping of complex 3D objects like mouse skull, where 1) (automatic) identification of abnormality, and 2) its (manual) localization and description are needed.



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