Normal vs. abnormal: Looking for border value in CT scans of mouse skulls

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Aims

Whole body in-vivo scans of mice (13 weeks old) are used in the Czech Center for Phenogenomics (Vestec, Czech Republic) for standardized morphological phenotyping according to International Mouse Phenotyping Consorcium guidelines. Around 38 mice is scanned on SkyScan 1278 (Bruker, Belgium) with the resolution of 52 μm (0.5 mm Al filter, current = 753 μA, voltage = 54 kV,180° rotation). The scans are reconstructed with NRecon 2 (Bruker, Belgium) and evaluated by a specialist in CT vox (Bruker, Belgium).

The phenotyping is quite time demanding procedure. That's why we are looking for a solution, wich could filter out mice without obvious phenotype. As the first object we were focused on skulls. The crucial point is finding of the boundary value between normal and abnormal mouse skull for automated skull classification.

Method

For comparison were used 6 mice with normal skulls and 3 mice with abnormal skulls.

We decided to use Amira software 2020.2 (Thermo Fisher Scientific). The process contains of three steps: segmentation, alignment, distance calculation.

Segmentation is the first step of preparing the 3D image data. For the segmentation was used Multi-Tresholding Segmentation Algorithm with corresponding thresholds.
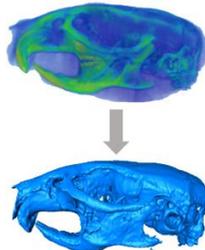

Figure 1: Mouse skull segmentation using Multi-Tresholding Segmentation Algorithm

Second step is skull alignment. For this procedure all segmentated skulls should be transformed into surfaces using Generate Surface Algorithm, that computes a triangular approximation of the interfaces between different regions or materials. The Align Surfaces Method have three methods: Alignment of the Centers of Mass, Alignment of the Principal Axes of the inertia tensor, the final solution is the one with the minimum root mean square distance, Minimization of the Root Mean Square distance between the points of the model surface to corresponding points on the reference surface. The first two methods can be used for approximate alignment prior to using the third method.
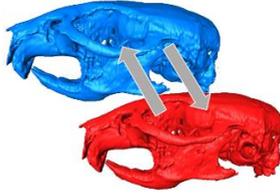
Figure 2: Skull alignment using three methods of Surface Alignment

The last method, that was used to get comparison values was Surface Distance Algorithm. This module computes several different distance measures between two triangulated surfaces. The result of using this method are values of mean distance, standard deviation from the mean distance, root mean square distance, maximum distance (Hausdorff distance), median distance.

Figure 3: Surface Distance Algorithm. Skulls after Surface Alignment Algorithm

Results
At the beginning, were performed paired alignment for normal skulls and than paired alignment between all normal and abnormal skulls. The distance metrics were obtained for the all alignments.
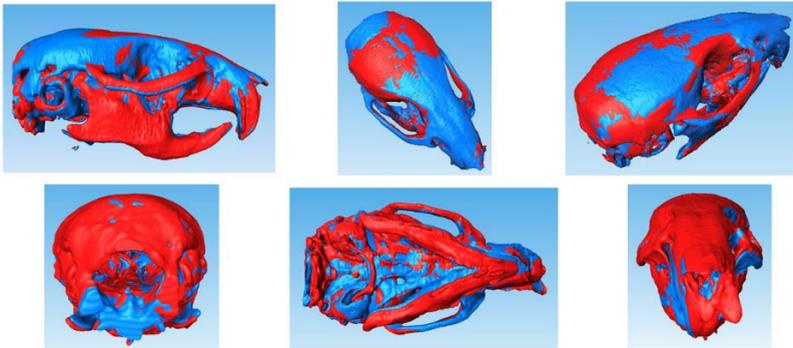
Figure 4: Result of alignment two normal skulls

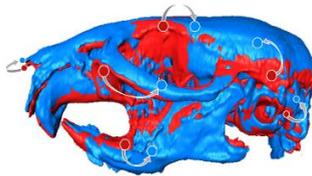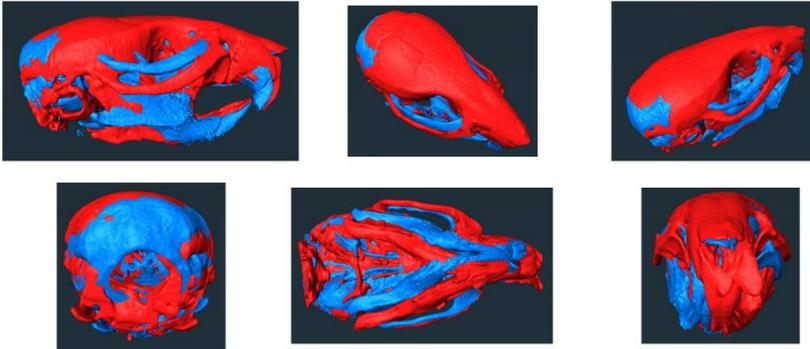Figure 5: Result of alignment normal (red) and abnormal (blue) skull
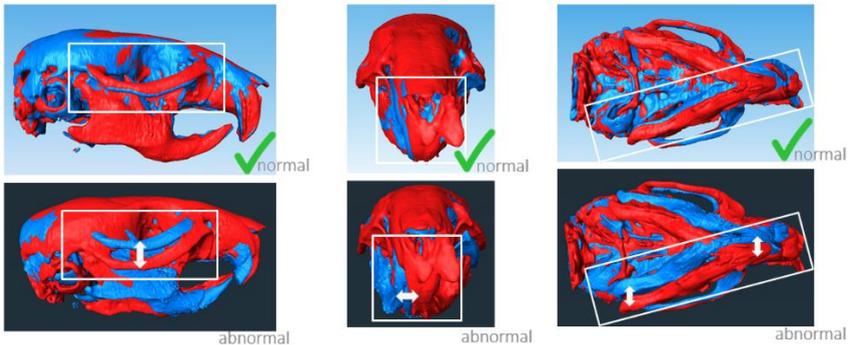
Figure 6: Comparison of normal and abnormal alignments

On the pictures we can see a big difference between normal skulls alignments and between normal and abnormalskulls alignments. Calculation of distance metrics depends on alignment. So, we have all distance metrics and can compare their values. Tables to the left show paired distances and green cells indicate controversial values between normal skulls alignments. Tables to the right show paired distances and red cells indicate controversial values between normal (horizontally) and abnormal (vertically) skulls alignments.

Hausdorf distance

ID	7191	7192	7193	7194	7195	7209
7191		1676	652	1016	1114	1109
7192			1088	1037	1187	1189
7193				917	952	763
7194					1052	775
7195						801
7209						

ID	7191	7192	7193	7194	7195	7209
7208	1119	774	842	1185	1210	1518
7210	3467	3164	3378	3113	3200	3197
7220	1017	1070	1851	1744	1749	1494

mean	mean
≈1021	≈1949

Figure 7: Hausdorf distance

Root Mean Square distance

ID	7191	7192	7193	7194	7195	7209
7191		160	101	136	162	188
7192			176	191	234	245
7193				145	135	154
7194					152	150
7195						138
7209						

ID	7191	7192	7193	7194	7195	7209
7208	189	129	204	208	251	277
7210	367	424	338	324	297	275
7220	207	240	383	370	349	324

mean ≈ 164   mean ≈ 286

Figure 8: Root Mean Square distance

Standard deviation

ID	7191	7192	7193	7194	7195	7209
7191		104	63	89	112	120
7192			111	126	160	162
7193				95	91	100
7194					100	94
7195						84
7209						

ID	7191	7192	7193	7194	7195	7209
7208	121	82	125	136	171	186
7210	263	304	238	226	206	188
7220	130	152	269	255	243	226

mean ≈ 107   mean ≈ 195
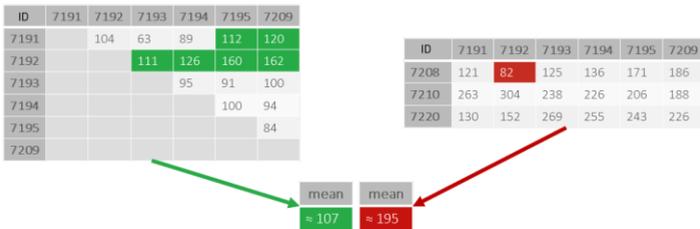
Figure 9: Standart deviation

Mean distance

ID	7191	7192	7193	7194	7195	7209
7191		120	78	103	117	144
7192			136	143	171	184
7193				109	100	117
7194					114	116
7195						108
7209						

ID	7191	7192	7193	7194	7195	7209
7208	145	99	160	157	184	206
7210	257	296	240	231	312	200
7220	161	185	272	267	251	233

mean ≈ 124   mean ≈ 208

Figure 10: Mean distance

Median distance

ID	7191	7192	7193	7194	7195	7209
7191		97	65	83	86	116
7192			110	111	124	138
7193				86	78	91
7194					88	95
7195						91
7209						

ID	7191	7192	7193	7194	7195	7209
7208	115	79	133	120	133	154
7210	171	192	167	159	151	147
7220	132	146	187	185	177	162

mean ≈ 97   mean ≈ 150
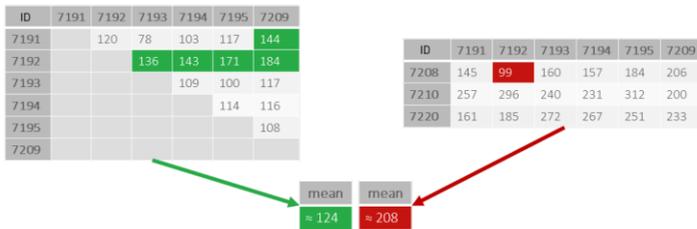
Figure 11: Median distance

Conclusion

After alignments, we can see:

- that distances between normal skulls are less than distances between normal and abnormal skulls,

- it means, that we have boundary value. So this value allows to realize the automatic skull classification.

- two normal and one abnormal mice have controversial values, it may indicate that the mice were not manually classified correctly(normal mouse was classified as abnormal and abnormal mice were classified as normal), because they can have internal changes in the structure of the skull that cannot be seen visually.

References:

1. Thermo Fisher Scientific, "Auto Threshold for Multi-Thresholding" Xtra Library for Thermo Scientific Amira, 2020
2. Thermo Fisher Scientific, "Module: Generate Surface (Avizo Lite)" Avizo User's Guide, 2020
3. Hege H.-C., Seebass M., Stalling D., and Zockler M, "A generalized marching cubes algorithm based on non-binary classifications", Zuse Institute Berlin, 97-05, 1997
4. Thermo Fisher Scientific, "Module: Align Surfaces (Avizo XMesh Extension)" Avizo User's Guide, 2020
5. Thermo Fisher Scientific, "Module: Surface Distance (Avizo Lite)" Avizo User's Guide, 2020