3D Registration of MR Mouse Images

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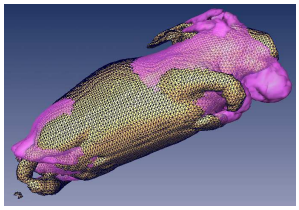
Objective. Development of a methodology for three-dimensional (3D), non-linear registration of articulate objects. More specifically, the objective is to develop an algorithm for automatic registration of high resolution anatomical MR images of whole mice.

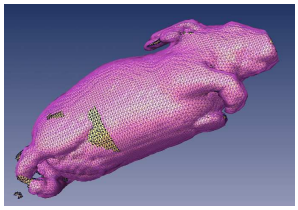
Motivation. Morphological assessment and mouse phenotyping are the main motivation for the development of high throughput imaging techniques at the Mouse Imaging Centre. High resolution (2.4 gigabytes per image) coupled with high throughput requires development of automatic procedures for anatomical assessment. For example, in the context of random mutagenesis, where large numbers of mice from the same inbred strain are exposed to random mutations, we would like to develop tests for detecting anatomical malformations. Such tests will be based on a statistical atlas of normal (non-mutant) mouse anatomy, which in turns requires 3D registration of mouse images.

Problem Definition.

Given two mouse images, source and target, find a 3D deformation field *F*, so that the source mouse when transformed by *F* assumes the posture of the target mouse. Alignment of all inner anatomical structures is required.



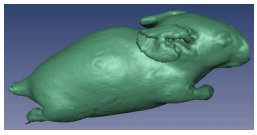
Target mouse is shown as yellow wireframe. Source mouse is shown as pink transparent surface.



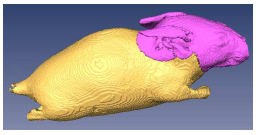
Deformation field recovered by the registration process repositions the source mouse into the space of the target mouse.

Method. An image of a representative normal mouse is chosen as a reference image (R). Manual anatomical labeling is performed so that every voxel in the reference image is assigned to one of a finite number of anatomical structures. Labels are organized in a hierarchical tree based on a "part-of" concept.
The problem is then reformulated as follows: **given an arbitrary sample mouse image (S), find a deformation field F so that F(S) is a aligned with the reference image R.**

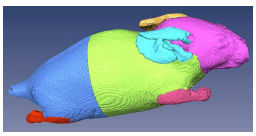
Stage 0. The entire reference mouse is considered as a single region. Registration is performed on downsampled images and corrects for global misalignments only.



Stage 1. The reference mouse is decomposed into 2 large regions: head and body. Each region is registered independently. Both regional transformations are initialized from their parent transformation found in Stage 0.



Stage 2. Regions from Stage 1 are further decomposed into smaller regions according to the hierarchical anatomical tree. For example, the body is decomposed into 4 limbs, thorax and abdomen. Once again, independent regional registrations are performed with an initialization provided by the parent regions of the previous stage.



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The registration process is scheduled as a succession of stages increasing in anatomical decomposition complexity paralleled by an increase in image resolution.

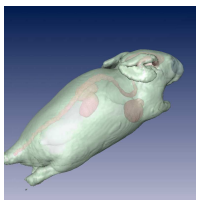
At any given stage, regional alignments are mutually independent giving rise to a "natural" parallelization of the algorithm.

UCLA's AIR package provides a robust core alignment algorithm. Their methodology has been originally developed for the purpose of human brain image registrations. It has proven to be a robust method for many purposes, especially when transformations are limited to affine ones (rotations, translations scales and shears, total = 12 parameters).
Given a region of interest, A, in the reference image and its approximately corresponding region B in the sample image, an affine transformation which maps A into B is required. Assuming the same image modality, the scaled least square is a good choice for a similarity function, so that intensity scaling is added as an additional parameter.

The correspondence between anatomical regions in two images is enforced through the hierarchical approach.

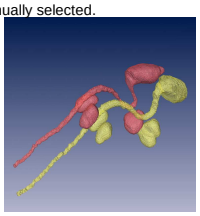
The end transformation for the whole mouse body is therefore piecewise affine.

Example. Effect of the registration process on a set of selected inner organs.

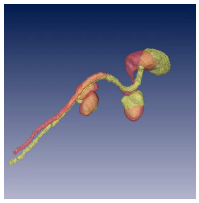


Red surface inside of the reference mouse represents the outer surface of the brain, spine, heart and two kidneys

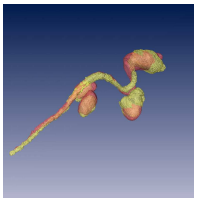
Red surface represents organs of interest in the reference mouse and yellow surface represents the corresponding surface in the sample image. Both surfaces have been manually selected.

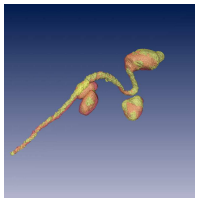


Initially, the two mice are misaligned.



After Stage 0, large scale translational and rotational misalignments have been corrected.





Further stages provide piecewise affine transformations with increasing number of "pieces" (degrees of freedom). Note how two surfaces exhibit reasonable overlap in the last image.

Open Questions.

How small can regions become before the core regional alignment algorithm starts failing?

What is the stopping criterion? It is known that even mice with identical genotype, age and sex exhibit anatomical variations (e.g., vascular trees have different topology).

Do piecewise affine transformations allow enough degrees of freedom? If not, how robust would piecewise polynomial models be?