TOWARDS INTERACTIVE SUPER-RESOLUTION RECONSTRUCTION OF WHOLE-BODY MRI MOUSE DATA

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PURPOSE: Super Resolution Reconstruction (SRR) is the process of producing a high-resolution (HR) image from a sequence of low-resolution (LR) images, where each LR image transforms and samples the HR scene in a distinct fashion. SRR in MRI is a developing field, and encouraging results have been published showing its potential in resolution enhancement. However, visualization of HR data is often computationally heavy and requires powerful hardware, and the time necessary to reconstruct large volumes (whole-body mice datasets in this case) can be large. To overcome this disadvantage, we make use of recent progress in the areas of articulated atlas-based segmentation of whole-body small animal data [1, 2] and MRI super-resolution reconstruction (SRR) [3]. Here, we present a novel approach for producing highly resolved, localized isotropic volumes-of-interest in whole-body mouse MRI. This enables interactive HR visualization and exploration of anatomical structures in MRI. The idea is similar to that of well-known web-based geographical maps, where it is possible from a global overview image to zoom in on a detail of interest. Such functionality is relevant in a biomedical setting when working with high-resolution volumetric data. Using the method presented in this paper, from a global LR image the user can interactively zoom in on a sub-volume of interest.

METHODS: One post-mortem *C57BL6*, 6 month old, male mouse was scanned on a 7T Bruker Pharmascan system using a fast recovery FSE (frFSE) sequence. TR was 6648 ms, TE was 33 ms, with Navg = 1 and NSP = 1. The 2D slice stack consisted of 64 slices (0.5 mm thick), with a FOV of 50 x 32 mm, and a resulting resolution of 0.125 x 0.125 x 0.5 mm. The scan time per stack was 213 s. The slice stack was rotated 23 times in uniform increments of 180/24 degrees. Due to the scanner's limited FOV, the mouse was scanned in three sections (head, chest, lower abdomen). The final whole-body volume is obtained by using the multiresolution stitching method of Burt and Adelson [4]: see Figure 1(a). To segment the mouse, the semi-automated bone approximation method [1] for whole-body microMRI mouse data was applied on one of the 23 LR datasets. This approach, where the user identifies 16 landmarks, considerably reduces the required user effort compared to a manual segmentation. Using the MOBY mouse articulated atlas (joint locations, anatomically realistic bone dimensions, anatomically realistic degrees of freedom for each joint) and a hierarchical anatomical model of the skeleton, all joints can be labeled and the correspondent bones fitted to the data: see Figures 1(b, c). Next, the Articulated Planar Reformation (APR) algorithm [2] that uses the articulated registration approach mentioned above, was applied to reformat the data into segments specified by the MOBY atlas. With this step, the data is mapped to a standardized atlas space. After applying APR to one of the low-resolution MRI datasets, the user can interactively select any sub-volume of interest for a subsequent SRR of that volume as illustrated in Figure 1(d). The data needed to reconstruct the sub-volume at the requested level of resolution is collected from a database of LR images and the sub-volume is reconstructed on the fly using SRR. These volumes differ in angular shifts in the sampling grid orientation. Our super-resolution technique is then applied to reconstruct the volume on a high-resolution grid. SRR is an inverse problem and involves recovering an HR image given a set of LR images and an acquisition model. Using additional prior knowledge about the solution, *e.g.* its smoothness, the problem can be formulated as a regularized least squares problem. A direct solution of this problem is generally infeasible. Instead, iterative methods are applied. For the purpose of both effective and efficient reconstruction, the method developed in [3] was chosen for our pipeline. This method employs Tikhonov regularization using the L2-norm of the second order derivative of the reconstruction as the regularization term, together with an affine transformation scheme that minimizes aliasing and spectral distortions. This system was solved by the conjugate gradient method.

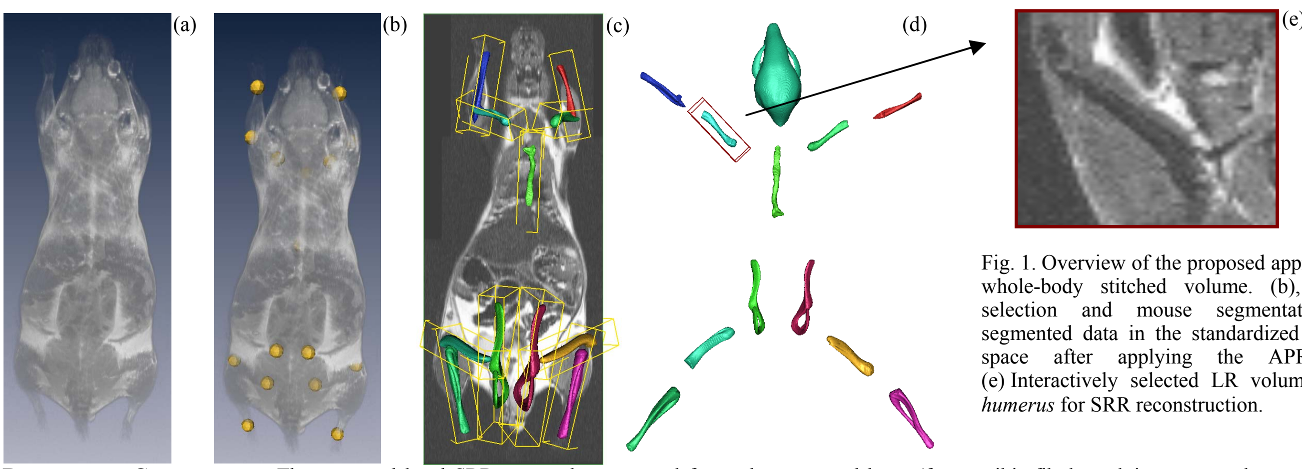

Fig. 1. Overview of the proposed approach: (a) The whole-body stitched volume. (b), (c) Landmark selection and mouse segmentation. (d) The segmented data in the standardized MOBY atlas space after applying the APR algorithm. (e) Interactively selected LR volume of the left *humerus* for SRR reconstruction.

RESULTS AND CONCLUSIONS: The proposed local SRR approach was tested for each segmented bone (femur, tibia-fibula, pelvis, sternum, humerus, ulna-radius), using an increasing number of LR images. The SRR times for each bone experiment were compared with SRR times for the whole-body. SRR time scale approximately linearly with the size of the LR dataset. Since one LR image of the entire mouse contains 322 x 803 x 80 = 20,685,280 voxels, and a typical region of interest (ROI) contains 100 x 100 x 25 = 250,000 voxels, we obtain an increase of approximately a factor 100. Where the entire mouse requires hours to reconstruct, the ROI can be reconstructed within minutes. Figure 2 shows the results of the experiments on the left *humerus* of the post-mortem mouse. The sample axial slices demonstrate that the quality of the reconstructions clearly improves when an increasing number of LR images is used. In agreement with the results of the quantitative experiments, it can be observed that the quality improvement is substantial going from 2 to 8 LR images, while a smaller effect is seen when going from 12 to 23 LR images.

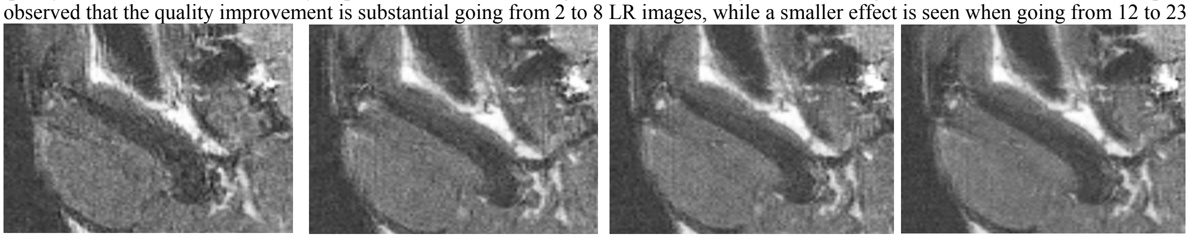

Fig. 2. Result of the SRR reconstruction of the *humerus* using 4, 8, 12 and 23 LR images by that order. The improvement in image quality is especially noticeable when using a high zooming factor.

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