Automatic Detection of Histological Artifacts in Mouse Brain Slice Images

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MOTIVATION & CONTRIBUTION

Reconstruction and analysis of annotated virtual 3D mouse brain models with neuronal structures require automatic registration of mouse brain slice images. However, automation of registration process becomes difficult if the brain slices have histological artifacts such as cuts, tears, and missing regions. Conventional brain slicing and processing techniques often introduce such artifacts in brain tissue slices, which makes it extremely difficult for further processing such as automatic alignment of adjacent slices and annotation of regions of the slices. **We propose a novel geometric algorithm to automatically detect major histological artifacts such as tears and tissue loss (missing data) in high-resolution mouse brain slice images without using any information from neighbouring slices.** We not only provide qualitative analysis but also perform quantitative evaluation of registration of 52 conventionally processed mouse brain slice images (from different datasets) with major histological artifacts to their corresponding annotated atlas slice images from Allen Reference Atlas.
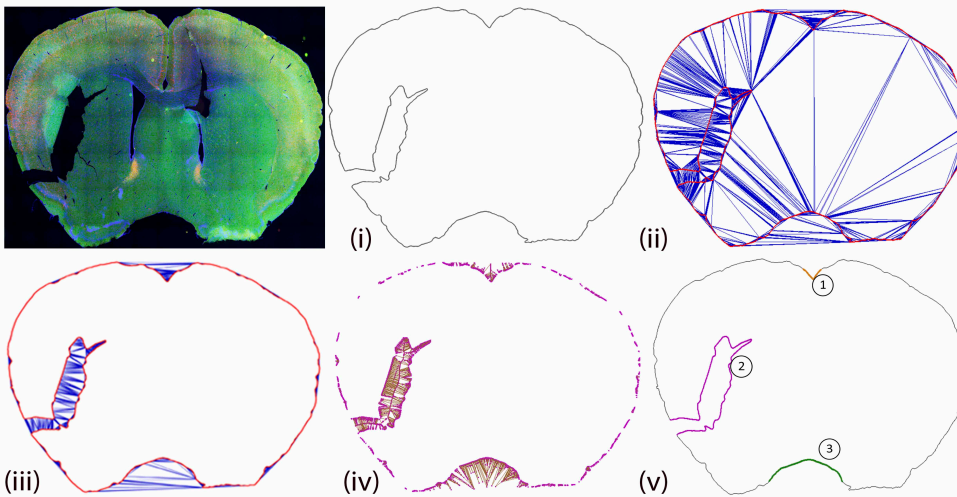
METHOD

i. Input to the algorithm−Outermost contour of the microscopic slice image.

ii. Constrained Delaunay Triangulation (CDT) of the vertices V & edges E using the outermost contour.

iii. Exterior Delaunay Triangles. Also removed skinny triangles (cleaning).

iv. Dual graph− Voronoi vertices (magenta) & edges (brown).

v. Three candidate damage regions whose **medial axis length** (Voronoi edge sequence) was above threshold α.

Points corresponding to **only the 2nd candidate** region classified as damage region (artifacts) as they are vertically asymmetric.
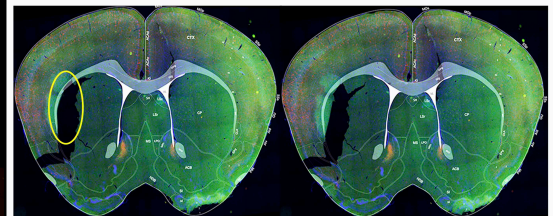
RESULTS
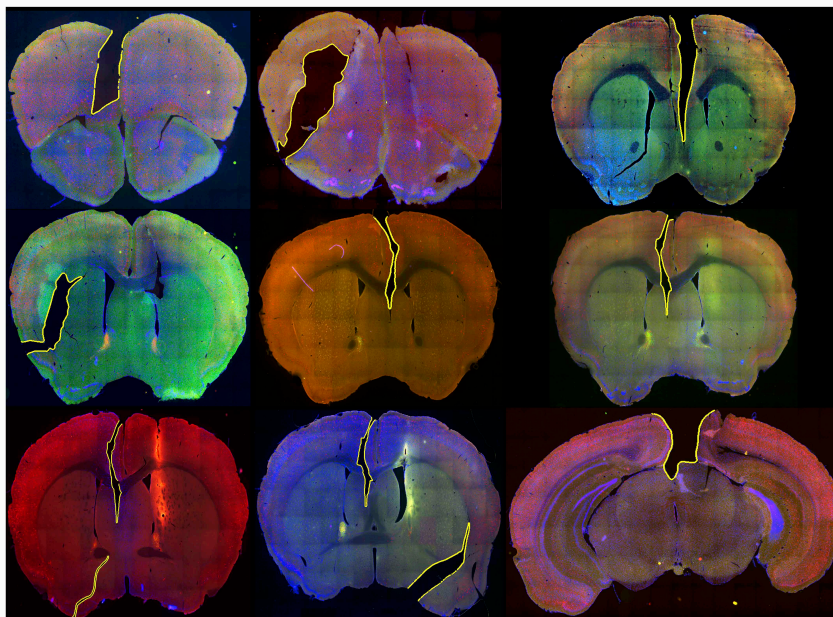
FEATURE BASED REGISTRATION
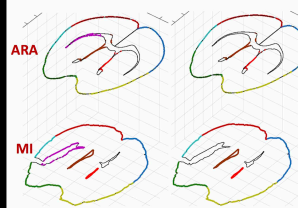
A comparison of non-linear registration of mouse brain microscopic slice images (MI) with the Allen Reference Atlas (ARA) with & without our algorithm. Points classified as damaged regions are removed from the correspondence finding steps.

Errors (in pixels)	With Our Algorithm			Without Our Algorithm		
	Average RMSE	Average MEE**	Average MAE	Average RMSE	Average MEE	Average MAE
After Affine Transformation	13.37	10.66	25.27	16.28	13.30	30.79
After Non-Linear Transformation	3.91	2.53	4.36	5.51	4.47	11.90

**RMSE – root mean square error; MEE – median error; MAE – maximum error

CONCLUSIONS

➤ We present a completely automatic algorithm to **identify & locate** slice-specific histological artifacts (tissue tears & tissue loss).

➤ Our approach is independent of neighbouring slices. Hence can be scaled to large non-homogeneous datasets.

➤ We can detect multiple such artifacts, thereby facilitating extremely thin tissue sectioning.

FUTURE WORK

➤ Detection of other extreme histological artifacts i.e. tissue folding, tissue overlap, displacement of tissues etc.

➤ Validating our approach on larger datasets & comparing its performance on registration.

➤ A complete 3D reconstruction of mouse brain slices from conventional processing techniques with major histological artifacts.

ACKNOWLEDGEMENTS

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