

Introduction

MRI brain segmentation is challenging, and typically performed manually by medical experts in a clinical setting. Manual delineation is time-critical, labour intensive, and subject to the skill of the neurologist. In addition, the treatment of pathological data compounds these problems, as the robust and rapid delineation of the damaged and recoverable region is critical for patient rehabilitation.

LOCUS is a software suite, intended for use by clinicians, that provides tools for automatic quantitative measures of brain tissue, structure and lesion volumes. As well as a number of essential tools for preprocessing MRI volumes, LOCUS also contains three powerful segmentation algorithms.

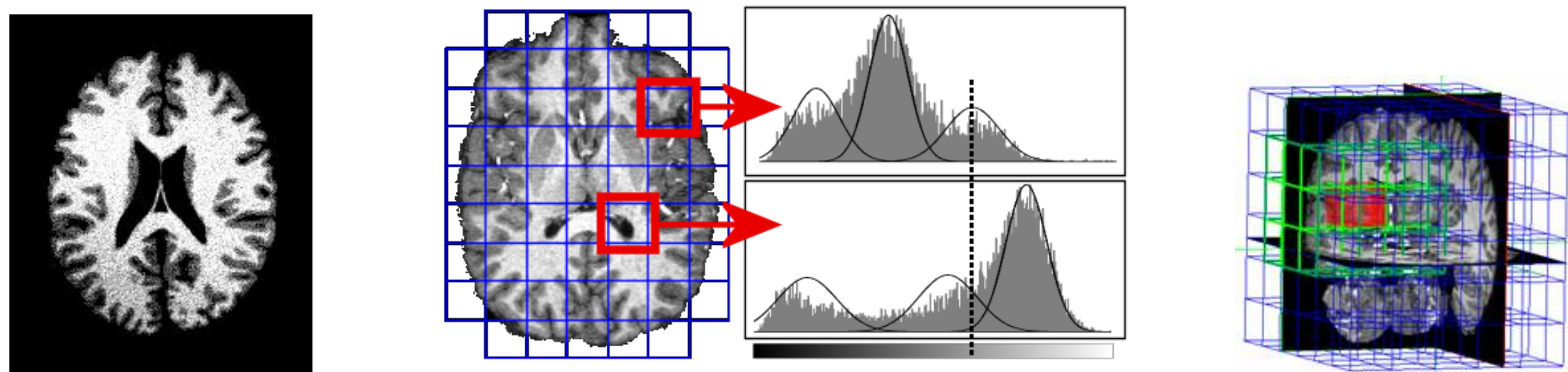
TS-LOCUS Segmentation of normal brain into its respective tissues and sub-cortical structures.

P-LOCUS Vascular Segmentation of vascular pathologies eg. Stroke.

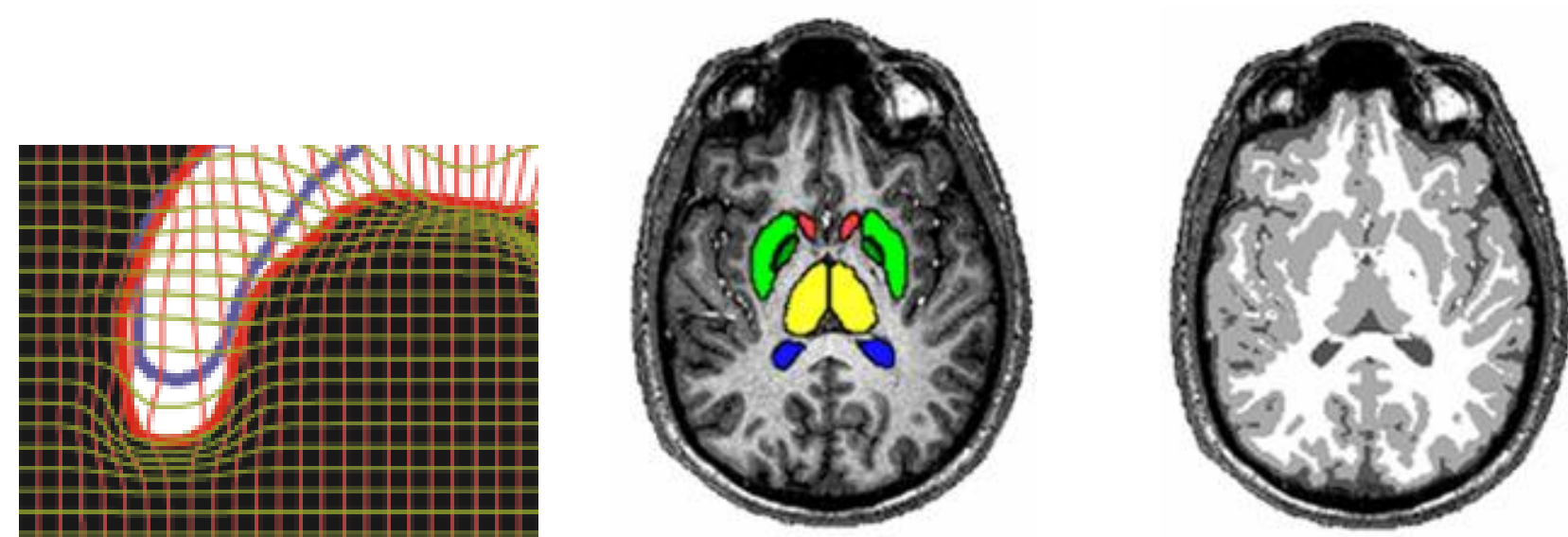
P-LOCUS Non-Vascular Segmentation of non-vascular pathologies eg. Multiple Sclerosis.

TS-LOCUS [1] [2]

The TS-Locus tool robustly and rapidly segments normal brain volumes into their respective tissues and sub-cortical structures.



The algorithm partitions an MRI image, and invokes a statistical model for each subvolume. The local scope of each model alleviates problems due to intensity inhomogeneity artefacts.

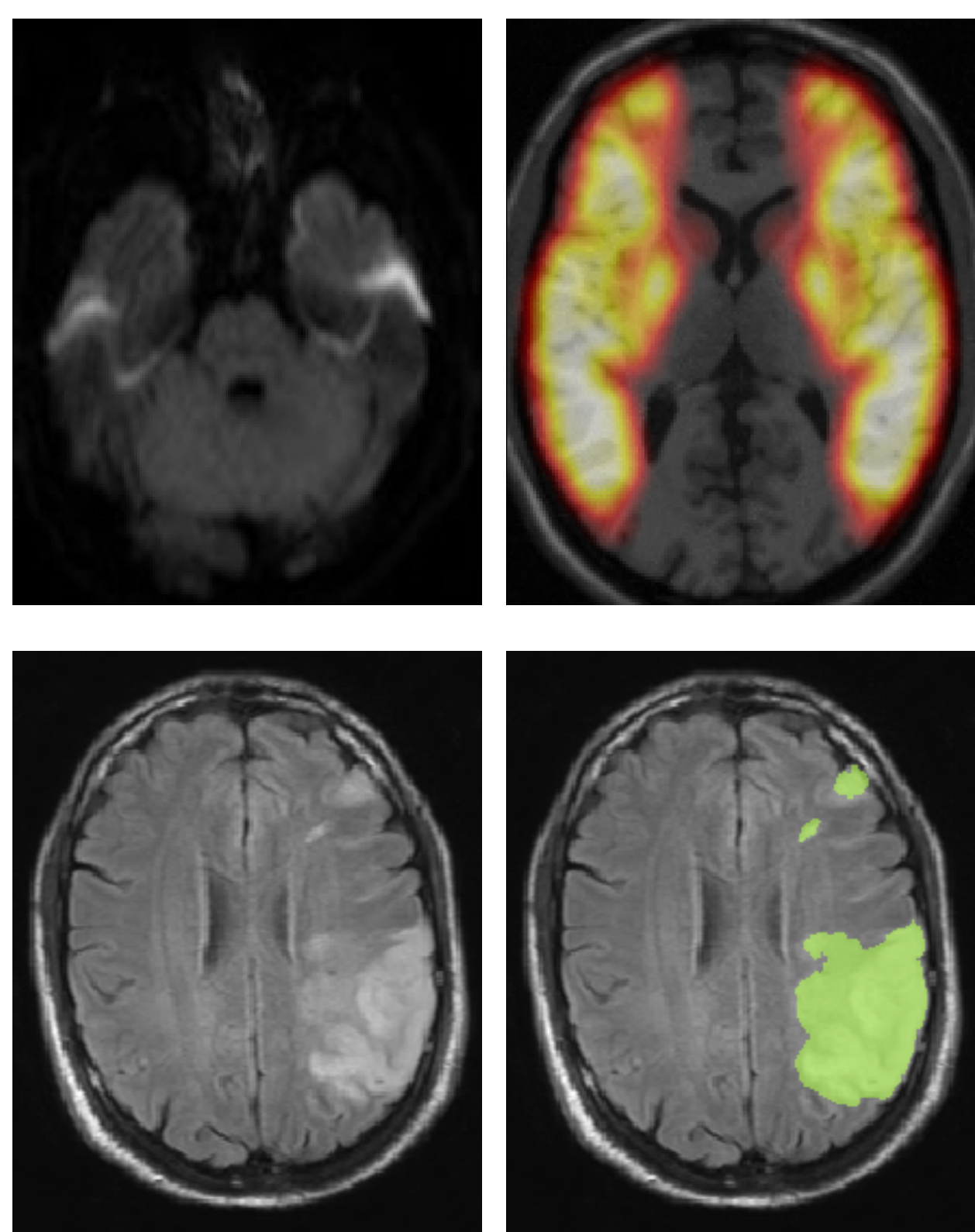


The algorithm includes local affine registration of structure atlases to the data to account for individual variation. Markovian principles are applied to capture the relationship between tissues and structures, to integrate *a priori* anatomical knowledge, and to ensure global consistency. The main innovations are:

- ▶ Robustness to image artefacts
- ▶ Fast execution (typically 3 and 15 minutes for tissue and structures respectively)
- ▶ The segmentation of sub-cortical structures
- ▶ The simultaneous handling of both tissue and structure segmentation and registration to a structure atlas.

P-LOCUS Vascular

The P-LOCUS Vascular tool uses a novel probabilistic vascular territory atlas to model the potential progression and delimitation of vascular accidents, and therefore overcome misclassification due to artefacts.



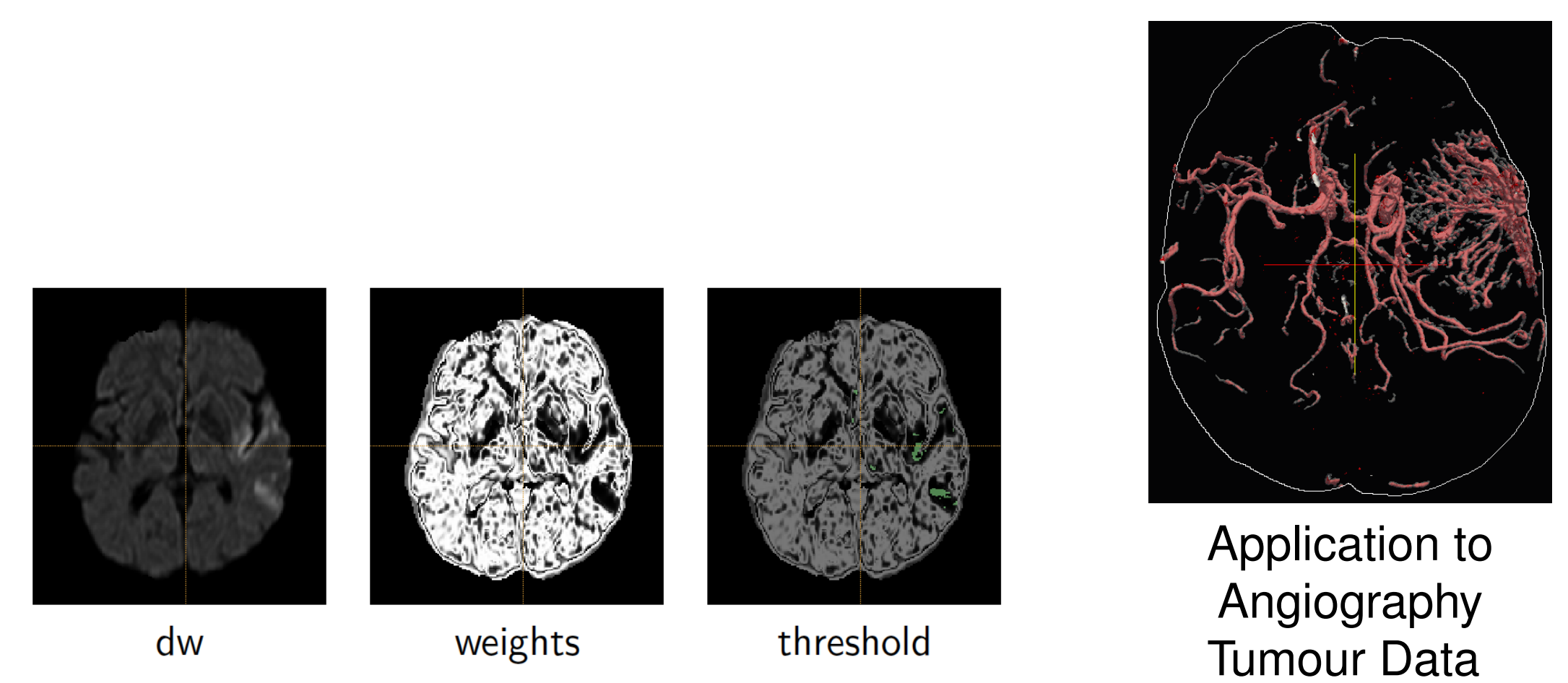
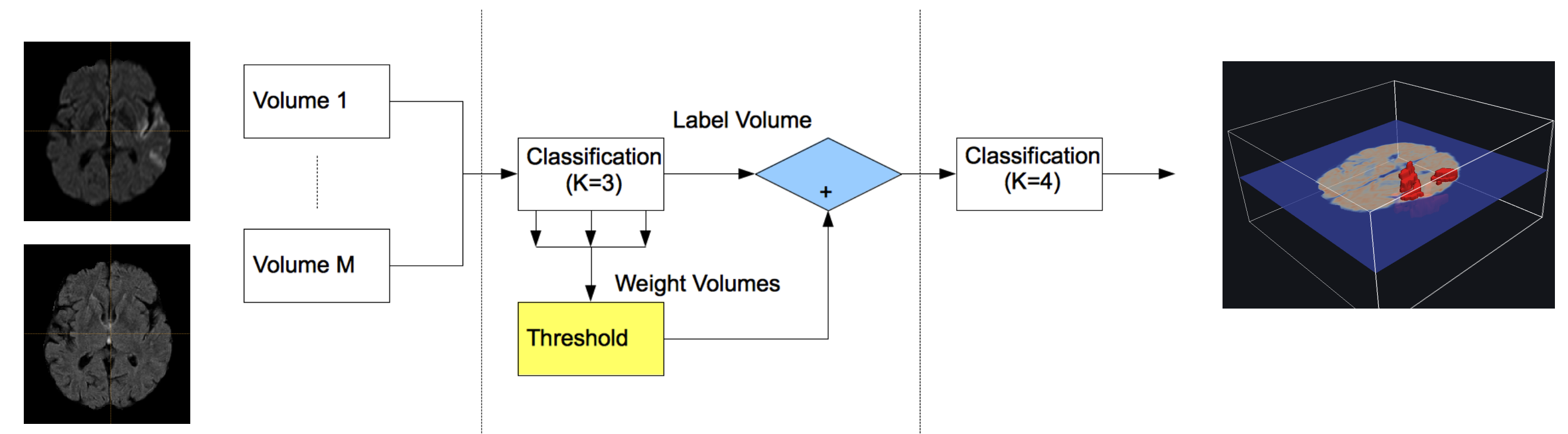
Probabilistic vascular territory atlases can help distinguish stroke lesions from artefacts or historical lesions. Features of this tool include:

- ▶ Robustness to image artefacts
- ▶ Complementary information from multiple MR sequences.
- ▶ Novel incorporation of probabilistic vascular territory atlases.
- ▶ Informative MRF to prevent over-dependence on atlases.

P-LOCUS Non-Vascular [3][4]

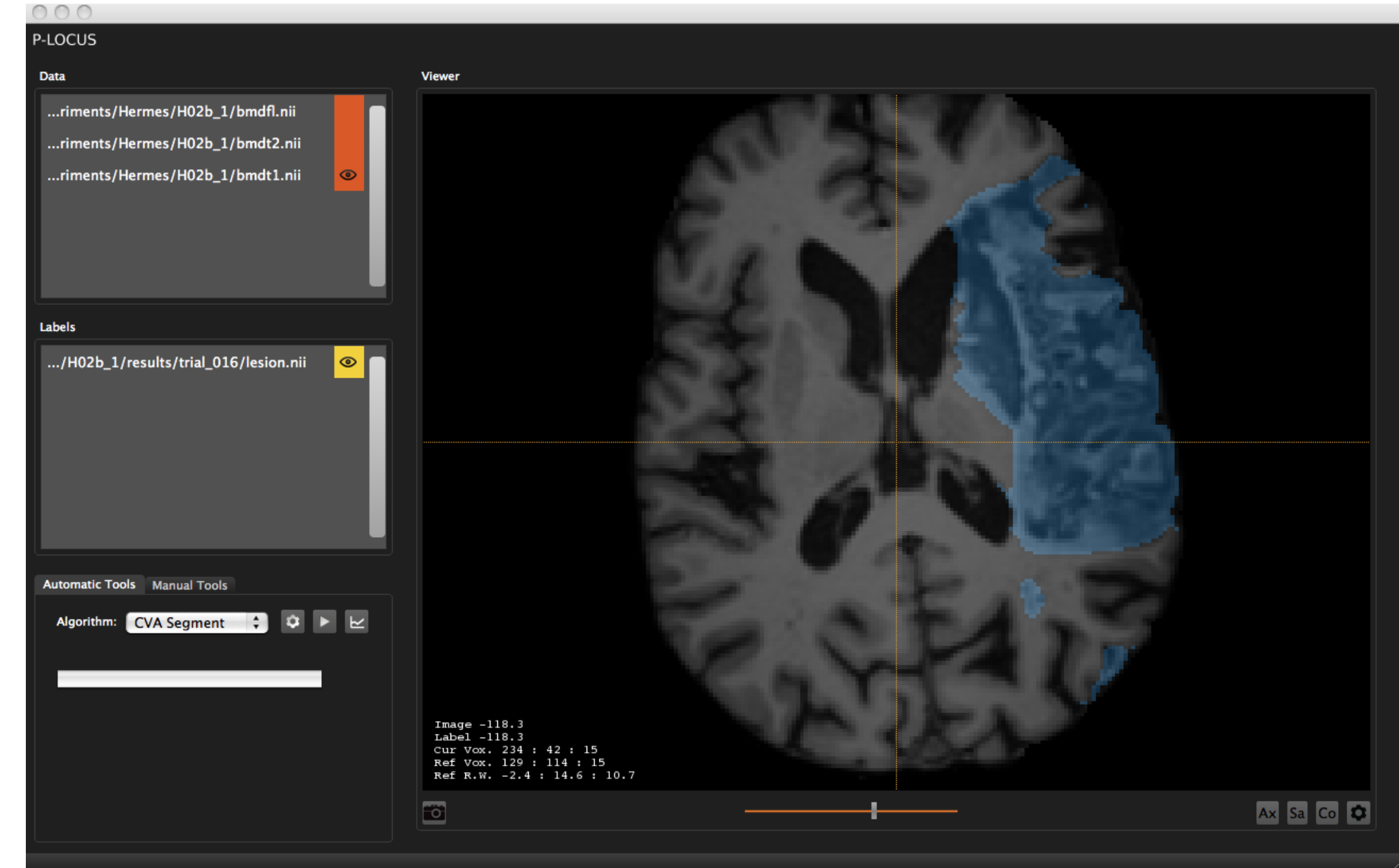
A Bayesian weighted model is used to describe the data from multiple sequences. This model allows for the specification of prior beliefs to describe the relative information content of voxels in each sequence, and consequently resolves delineation problems associated with under-represented and uncharacteristic lesion voxels. The algorithm can operate in a semi-supervised or fully autonomous setting.

- ▶ Include lesion voxels as model inliers.
- ▶ Introduce a weight field to account for possible under-representation of the lesion class, uncharacteristic outliers, and allow complementary information from multiple sequences to be combined axiomatically.
- ▶ Provide an estimation procedure based on a variational Expectation Maximization (EM) algorithm to produce the corresponding segmentation.



LOCUS Software Suite

The software suite provides a user interface that is intuitive and easy to use. Algorithm and display parameters can be modified from the interface. The automatic segmentation tools are supplemented with manual delineation tools, should the user wish to further refine the segmentation.



LOCUS Software Suite

The software will soon be available for testing through the SAYS service <http://www.says-innovation.com>, and for download at our own site.

Conclusion

The LOCUS software suite is an intuitive platform that provides powerful automatic algorithms to identify brain tissues, structures and pathologies. LOCUS tools have been tested on multiple sclerosis, stroke and tumour (angiography) data. Modification and validation of the results is possible with manual delineation tools.

References

- [1] B. Scherrer, F. Forbes, C. Garbay, M. Dojat. *Fully bayesian joint model for MR brain scan tissue and subcortical structure segmentation*. MICCAI 2008
- [2] B. Scherrer, F. Forbes, C. Garbay, M. Dojat. *Distributed Local MRF Models for Tissue and Structure Brain Segmentation*. IEEE TMI 2009
- [3] F. Forbes, S. Doyle, D. Garcia-Lorenzo, C. Barillot, M. Dojat. *Adaptive Weighted Fusion of Multiple MR Sequences for Brain Lesion Segmentation*. IEEE ISBI, 2010.
- [4] F. Forbes, S. Doyle, D. Garcia-Lorenzo, C. Barillot, M. Dojat. *A Weighted Multi-Sequence Markov Model For Brain Lesion Segmentation*. AISTATS, 2010.