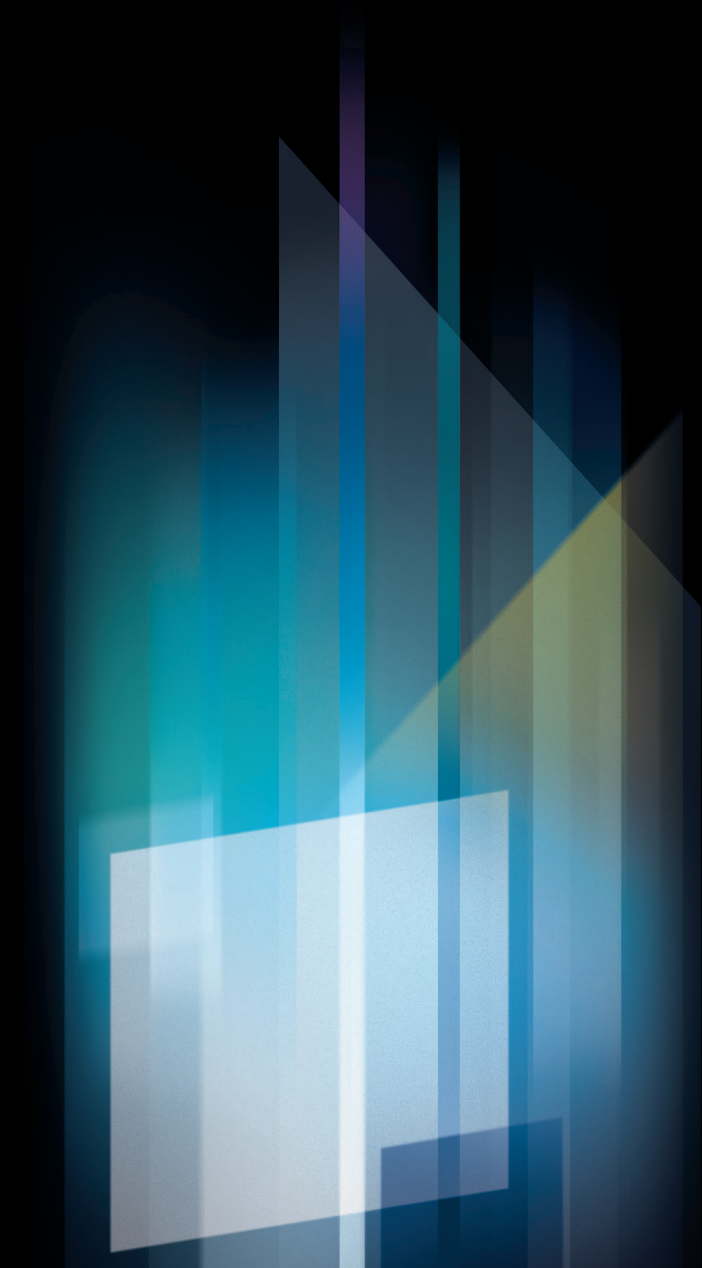




mimneuro®

Increased Confidence





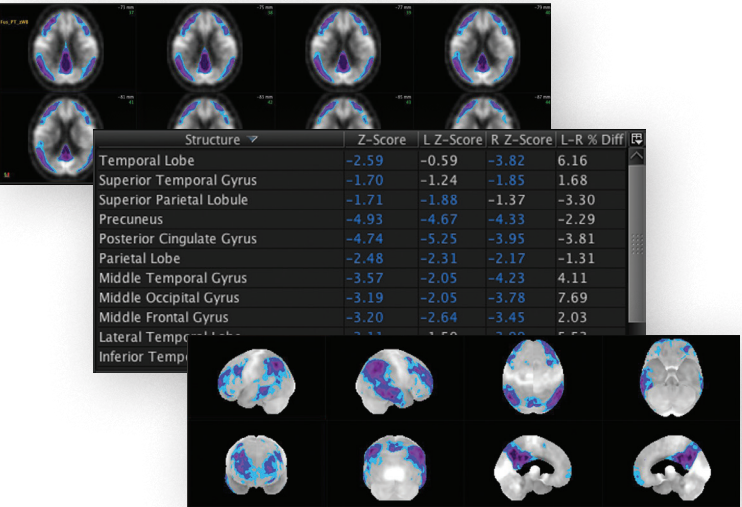
Increased Confidence with Quantitative Analysis

Quantitative analysis provides objective information to aid and complement visual interpretations. MIM Software® addresses the need for quantitation in evaluating neurological disorders with MIMneuro®, an automated analysis solution for PET and SPECT brain scans.

MIMneuro brings together an array of quantitative analytical tools in an automated and easy-to-use package. The software is developed with careful attention to feedback from both radiologists and referring physicians. MIMneuro fits effortlessly into your reading workflow and raises the confidence of both the reader and the referring physician.

MIMneuro's industry-leading tools provide support for multiple tracers including DaTscan™, FDG, Amyvid™, NeuraCeq™, VizamyI™ and HMPAO. Statistically significant differences in tracer uptake are highlighted in color-coded overlays and in a data table of brain regions. Statistical results can also be fused with MR or CT for easier localization of abnormalities.

At the very core of any neuro quantitative analysis software is the registration method. MIMneuro’s **BrainAlign™** deformation algorithm provides accuracy by matching the size, shape, and orientation of a patient's brain scan to a database of normal controls for comparison.



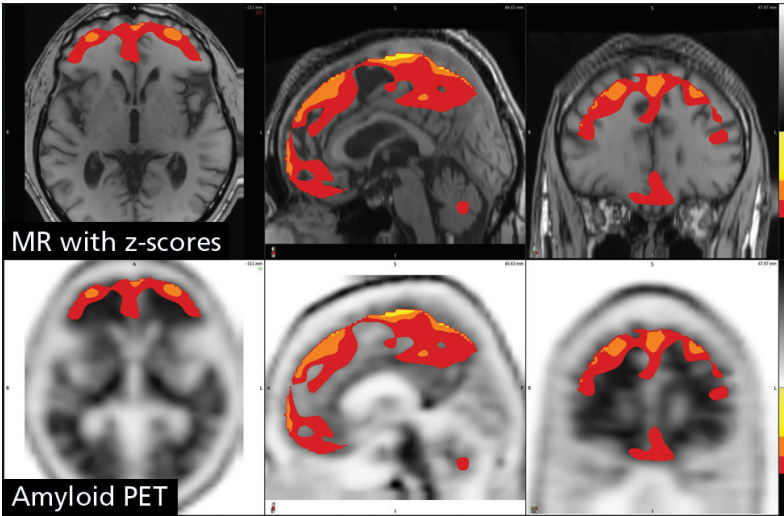
Although often overlooked, quantitative neuroimaging software is only as good as its registration algorithm. Without a sound registration technique to ensure anatomical correspondence across multiple patients, you cannot be certain that any regional or voxel-level comparison is truly apples-to-apples.

BrainAlign™ is MIMneuro's landmark-based deformation algorithm which meticulously registers each brain to a standard template, allowing for increased accuracy in quantitative comparisons. Some algorithms seek to match intensity values, which minimizes real differences and leaves registered brains looking unrecognizable. Alternatively, affine registration alone is insufficient to accurately account for local shape differences in patient brains. In contrast, with more than 700 landmarks identified throughout the brain, BrainAlign has sufficient degrees of freedom to correct for local differences without changing the relative distribution of tracer uptake.

The most recent enhancement to BrainAlign is multiple template registration, which allows for accurate registration of highly-specific tracers such as Amyvid. Unique to MIM®, this method performs simultaneous registration to multiple templates, removing the bias present with single template or one-at-a-time template registrations.



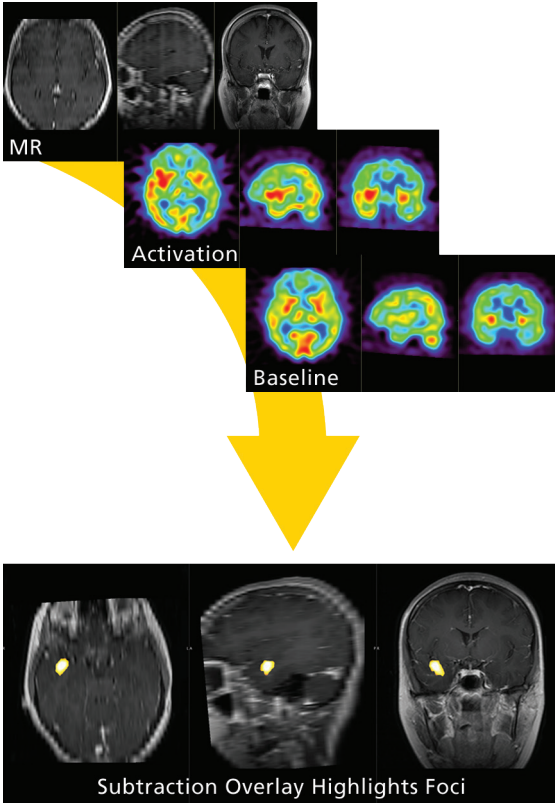
Voxel-based analysis, which compares tracer uptake between a patient and normal controls on a voxel-by-voxel basis, highlights areas of statistically significant differences with color-coded overlays. Cool colors indicate areas of decreased tracer uptake such as FDG hypometabolism. Warm colors indicate increased tracer accumulation in patients with amyloid plaques when using a tracer such as Amyvid.



Cluster analysis can be used to remove distracting areas that are not large or abnormal enough to be considered statistically significant. For subtle changes, or for readers with less experience in neuroimaging, this visual aid plays an important role in assisting the qualitative interpretation.

Using an integrated anatomical brain atlas, tracer uptake can also be compared region-by-region by calculating either Z-scores or SUV Ratios (SUVR). Appropriate regions such as the posterior cingulate gyrus and precuneus, are included for all approved tracers including amyloid PET, FDG, and perfusion SPECT agents.

Brain images can be also viewed as cortical surface projections (or stereotactic surface projections), allowing for quick localization of abnormalities and providing an easily understood view for your referring physicians.



“The neuro subtraction workflow significantly reduces processing time by our technologist from an hour to minutes. I can even quickly process the data myself, so that I can read the study when I’m ready, not when it’s ready. Also, the cluster analysis increases my diagnostic confidence.”

PETER FAULHABER, MD
Director, Clinical PET
University Hospitals Case Medical Center
Case Western Reserve University
Cleveland, Ohio

Integrated Anatomical Atlases

One of the most powerful and unique features of MIMneuro is its integration of three anatomical atlases. These atlases provide a solid basis for regional statistical comparisons, SUVR calculations, and normalization for voxel-based and cortical analyses.

The single-brain atlas is an anatomically complete atlas developed as a coordinated effort between several radiologists and a neuroanatomist. It is integrated deeply into the software, allowing the reader to simply hover over any part of the image to reveal an automatic indication of the anatomical area of interest. This allows for more conclusive and even faster qualitative reads.

The probabilistic atlases are each built from 10 individuals, allowing for increased anatomical sensitivity and specificity when performing region-based analysis or computing SUVR. One of these probabilistic atlases is provided for perfusion and metabolism tracers, while the other is ideal for amyloid analysis.

Visualize the Difference

Automated subtraction workflows facilitate the processing of serial brain exams in evaluating treatment response or disease progression. Workflows also allow for comparing baseline and activation PET and SPECT exams and ultimately make the process faster and more consistent. At many sites, subtraction workflows have reduced the processing time for studies from an hour to minutes.

Image intensities are matched through auto-normalization so that normal areas will have similar intensities on both exams. The areas of difference are then highlighted through cluster analysis, which removes statistically insignificant, distracting differences. The resulting difference image can be fused to an MR or CT, which helps to localize the abnormality and provides a result that can be easily communicated to your neurology or neurosurgery colleagues.

Advanced Applications

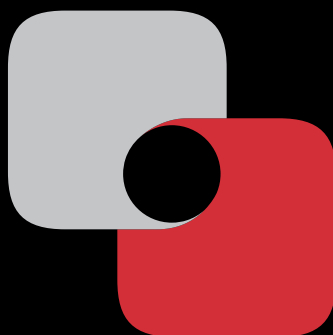
For advanced research, MIM has incorporated sophisticated tools into MIMneuro, allowing researchers to take advantage of the same flexible and easy-to-use tools that are available to clinicians.

For example, the *Neuro Group Comparisons* tool compares groups of patients. Patterns of disease can be analyzed by comparing groups of diseased patients with healthy patients. The effects of treatment on a population can also be analyzed by comparing pre- and post-therapy scans. Both t-scores and p-values are calculated on a voxel-by-voxel basis and across brain regions, highlighting statistically significant differences.

MIMneuro also provides the ability to create *Custom Brain Regions* for analysis. Whether it is a new anatomical region or a combined region created by adding together several regions, *Custom Brain Regions* can be saved for use in future quantitative analyses.

“We are doing twice as many Neuro PET exams as we did a year ago. This is a direct result of the quantitative capability of MIMneuro, which allows us to generate more definitive reports that increase our clinicians' confidence. In my opinion, MIMneuro is an obligatory tool for neuro PET.”

LARRY MCNAMEE, MD
Medical Director
Specialty Teleradiology
Westlake, Ohio



To learn more, call **866-421-2536** or visit mimsoftware.com/contact to schedule a presentation of MIM.



MIM SOFTWARE INC.

25800 Science Park Drive - Suite 180
Cleveland, OH 44122
866-421-2536
www.mimsoftware.com
info@mimsoftware.com

MIM SOFTWARE

Beijing Co., Ltd.
北京明维视景医疗软件开发有限公司
地址: 北京市海淀区学院路51号首享科技大厦809室
邮编100191
电话 86-10-82626960
邮箱 info@mimsoftware.com



MIM SOFTWARE

Brussels BVBA
Drukpersstraat 4
1000 Brussel
Belgium
info@mimsoftware.com

© MIM Software Inc.
2023 All Rights Reserved

TD-218
21 Aug 2023



Emergo Europe

Westervoortsedijk 60
6827 AT Arnhem
The Netherlands



MedEnvoy Switzerland

Gotthardstrasse 28
6302 Zug
Switzerland

