# Development of the Expert system for Quantification of Brain Activation (QUBA) in fMR Images: Differential Activation Analysis

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**Synopsis:** In fMRI, labels for brain activation foci are expressed by the x, y, z coordinates of Talairach's brain space using the Talairach Demon software. However, this method needs to use the MNI2TAL function of SPM, which converted MNI brain space to Talairach's brain space, as well as to confirm with comparison of activation maps overlaid on MNI-normalized structural MRI images.

In this study, we developed QUBA software to automatically identify and quantify the activated brain centers using by MNI template images, as well as the common and differential regions from activation maps acquired during two different stimulations.

**Materials and Methods:** The 3-dimensional activation MR images were processed by a statistical parametric mapping program (SPM, The Wellcome Department of Cognitive Neurology, University College London, UK). The QUBA program was coded by Delphi language (version 7.0).

**Results and Discussion:** Standard template images used the high-resolution T1-weighted images (colin holmes 27 of ICBM). Applied groove (<60) and white matter (>104) of Black/White (range 0 to 255) scales to template images, the gray matter (range 60 to 104) were extracted for defining anatomical areas. We confirmed the anatomical areas (AA). The RMS value between the number of pixels covering each anatomical region in Talairach template images and that of the QUBA was 0.823 ($p$<0.0001).

A spmT file, which obtained through t-contrast in SPM, was loaded to QUBA, and interpolated to convert 2mm grid dimension (x:78, y:95, z:68) to 1mm grid dimension (x:181, y:217, z:181) using the trilinear-interpolation algorithm.

Figure 1 shows the screen of QUBA for individual (or a mean) activation which included the resultant t-map images of 1mm grid (a), activation map applied threshold t-value (b), AA template images (c) which we developed in this study, where the image dataset extends from -61mm to 84mm without slice-gab, giving 146 axial images, and were overlaid threshold activation map into AA template images (d).

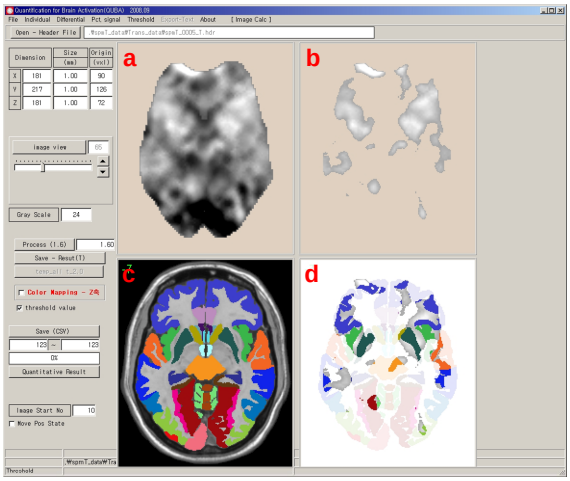


Figure 1. Individual activation analysis: 1mm grid t-map image (a), activation map with an applied threshold t-value (b), AA template image (c) and activation map overlaid into AA template images (d).

Figure 2 demonstrates the screen of QUBA for differential activation analysis. In differential activation from two different activation maps (a, b), we acquired common, dominant and differential activation maps (c), respectively.

The following information were automatically measured the MNI space coordinations and Talairach space coordinations corresponding to maximum t-values, as well as mean t-values and activities (the percentage of the activated pixels of each area) according to each anatomical area. In addition, the regional brain lateralization indices were determined to give hemispheric predominance: the positive (+) and negative (-) indices show left and right predominance, respectively.

**Conclusion:** The QUBA program is capable of providing accurate, informative and quantitative results, including AA labeling of the brain activation areas and lateralization index in about 1 or 2 minute. As well as application of the QUBA to the analysis of fMRI data would be helpful to accurately quantify the brain activations and functions to interpret and assess the human brain function.

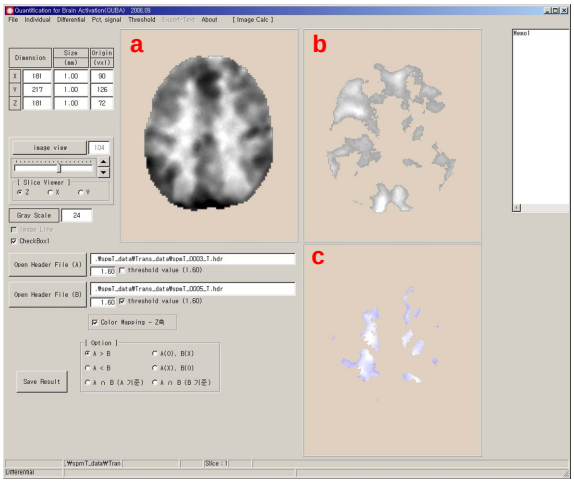


Figure 2. Differential activation analysis: without thresholding map (a) and with thresholding map (b) induced from two different activation maps, and a resultant differential map (c).

**Reference**

1. Tzourio-Mazoyer et al, *Neuroimage*, 2002;15:273–289.
2. Lancaster et al, *Human Brain Mapping*, 2000;10:120–131.
3. Rademacher et al, *Journal of Cognitive Neuroscience*, 1992;4:352–374

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