

## Databasing molecular neuroimaging studies

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Positron emission tomography analysis in molecular neuroimaging can either be “voxel-based” or “region-based”. Voxel-based studies are usually reported with reference to the Talairach stereotaxic system and appear with tables listing “hot spot” foci indicating the centers of areas with significant difference between two groups of scans. The voxel-based approach is widely used in the cognitive functional neuroimaging literature. Databasing such studies has been advanced with the BrainMap database (Research Imaging Center, San Antonio, TX). The newest version of this database contains data from over 800 studies with an interface allowing for preprogrammed access to the data. To gain a more flexible access to such studies we have constructed the Brede database which presently records data from 185 studies. Apart from cognitive studies the Brede database also contains data from molecular neuroimaging studies. The experiments in the Brede database are associated with items in an taxonomy. The taxonomy contains items for, e.g., cognitive functions and neuroreceptors. Some of the items are linked with corresponding MeSH terms, items from SenseLab and other biomedical databases. The items are organized in a directed acyclic graph with the most general concepts (e.g., “neuroreceptor”) at the roots of the graph, while more specialized concepts (e.g., the 5-HT<sub>2A</sub> receptor) are at the leafs. The representation of the hot spots centers in standardized coordinate space together with the taxonomy enables the statistical modeling of the distribution of the Talairach coordinates conditioned on, e.g., function and neuroreceptor type. So far we have implemented a line of multivariate analysis methods as well as volume-based similarity metrics that work on these distributions.

Relatively few molecular imaging studies are analyzed and reported with respect to the voxel-based Talairach system, and many studies are region-based where specific variables, such as the “binding potential”, are reported for a series of brain regions. The regions for which variables are reported will typically vary between studies. To handle this variability we have constructed a second taxonomy for brain regions. When results from region-based studies are entered they are annotated with items from this taxonomy. Specially tailored information retrieval and multivariate analysis method such as missing data hierarchical K-means clustering allow us perform data mining on this data set. Based on their differential response in brain regions studies can be clustered, or the brain regions can be clustered based on the their different load over studies.

The published database is available as XML files in the Brain Neuroinformatics Toolbox and on the Internet on the address <http://hendrix.imm.dtu.dk/services/jerne/brede/>. The Internet edition also features results from automated web-page generation and search facilities.