Meta-analytic clustering of molecular neuroimaging studies

Finn Årup Nielsen(1,2), Claus Svarer(1),
Lars Kai Hansen(2), Gitte Moos Knudsen(1)

1: Neurobiology Research Unit, Rigshospitalet;
2: Informatics and Mathematical Modelling,
Technical University of Denmark.

October 15, 2004

Results from molecular neuroimaging studies with single-photon or positron emission tomography are often reported in the form of values of interest across a set of brain regions. The values will vary depending on: 1) the tracer, e.g., altanserin or flumazenil; 3) the value of interest, e.g., 'binding potential', rate constants or correlation between age and binding potential; and 3) the mathematical model used to compute the values. We used K-means to cluster experiments based on the normalized values of interest across brain regions: Molecular neuroimaging studies was entered in a database from published peer-reviewed articles via the Brede Neuroinformatics Toolbox, and an experiments-by-brain-regions data matrix was constructed. There is no standard for the set of brain regions used in molecular neuroimaging and subsequently the regions vary between studies. To manage this discrepancy the regions are linked to items in a taxonomy of brain anatomy when entered in the database and the K-means algorithm was modified to handle 'missing values' in the data matrix. Only regions where more than two experiments report values were included. Furthermore, to account for the variability in the values of interest these values were normalized with 'studentization'. The number of components in the clustering was varied and a graphical technique was used to get an overview of the clusters. With the present database 12 articles resulted in 26 experiments reporting results in 58 different brain regions, i.e., a 26-by-58 matrix. Approximately 16 percent of the elements in this matrix was defined and after excluding columns in the matrix corresponding to brain regions where values were only reported in two or less experiments the matrix appeared with 19 columns. The predominant content of the database was experiments targeting serotonin-2A and benzodiazepine receptors. The K-means algorithm consistently clustered the serotonin-2A studies, performed using altanserin and 5-I-R91150 tracers, into one cluster and benzodiazepine studies using flumazenil and fluoroethylflumazenil into a second. This indicates that molecular neuroimaging is consistent across studies to such an extent that an unsupervised algorithm can group studies according to regional response without the prior knowledge of the target of the study. Our approach is completely automated once the data has been entered in the database.

Acknowledgments

Finn Årup Nielsen is funded by the Villum Kann Rasmussen Foundation.

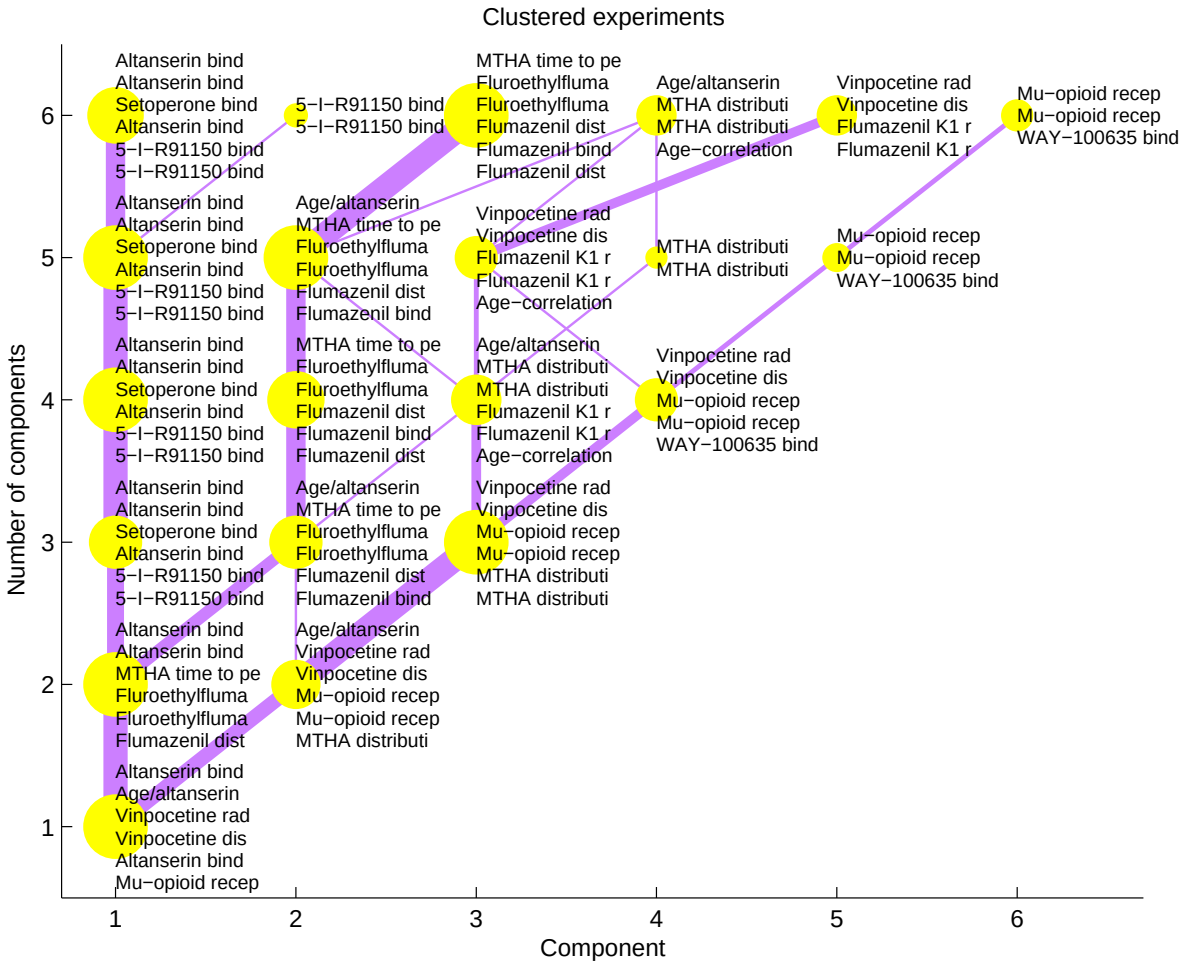

Figure 1: 'Cluster bush' with each cluster displayed as a yellow filled circle. The y-axis is the number of components (K) in the K-means clustering, while the x-axis the individual component in each clustering. The texts on each cluster is a truncated capsule description of the experiment.