# Visual Mining of Neuro-Metaspaces

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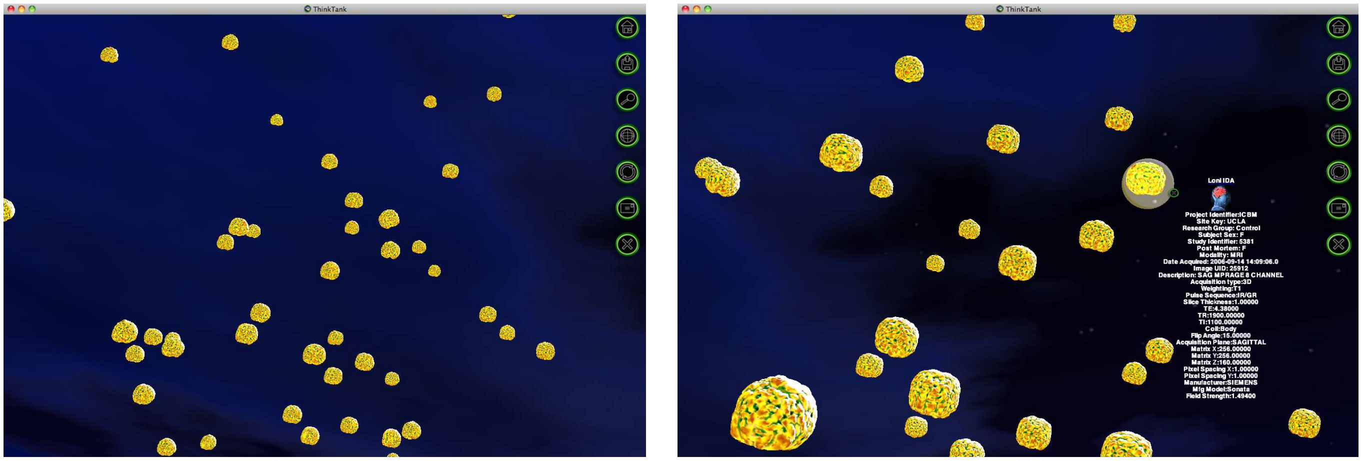

**Figure 1:** *Two views of cortical representations of brains distributed in a meta-space.*

## 1 Introduction

Large scale neuroimaging data archival protocols are gradually becoming ubiquitous in both research as well as clinical settings. Current user-database interfaces are limited to textual searches and often require data-specific knowledge for performing queries. This is proving to be an obstacle for researchers who wish to obtain a holistic view of the data before designing pilot neuroscientific studies or even formulating statistical hypotheses. Instead of providing a restricted, unidimensional view of the data, we seek to place a multi-dimensional view of the entire neurodatabase at the user's disposal. With the aim of visual navigation of complete neuro-repositories, we introduce the concept of brain meta-spaces. The meta-space models the implicit nonlinear manifold where the neurological data resides, and encodes pair-wise dissimilarities between all individuals in a population. Additionally, the novelty in our approach lies in the user ability to simultaneously view and interact with many brains at once but doing so in a vast meta-space that encodes (dis)similarity in morphometry.

## 2 Method

The mining environment is composed of three primary stages, i) input-processing stage consisting of feature extraction, and representation, ii) data-analytics stage consisting of modeling, regression, and clustering, and finally iii) visualization stage that gives unrestricted, multi-faceted, 3D navigable and selectable views [Joshi et al. 2009] of the neuroimaging data. The input data comprises of structural neuroimaging acquisitions that are generated from 3D MRI scanners. The primary source of visualization is a surface geometry representation of the cortex, obtained after pre-processing, skull removal, segmentation, cortical extraction, and topology correction. All of these steps are automated and executed without user intervention on a grid [Dinov et al. 2009], and are only performed once, when new data is added into the repository. After preprocessing, we calculate several features on cortical surfaces, for e.g. shape foldedness index, principal curvatures, curvedness etc. Additionally we also incorporate several volumetric features such as cortical thickness, and gray matter volumes, thereby defining a feature $n-$dimensional vector at each point on each cortex. The analytics component is now responsible for constructing the meta-space by approximating the underlying manifold, purely based upon discriminative models on the above feature vectors. Finally, for visualization purposes, we project distances between features vectors in the Euclidean space after approximation by multi-dimensional scaling. The visualization environment is a dynamic view of the meta-space, enabling the user to navigate, discover, and verify the brain surface geometry simultaneously in relation to it's neighbors. Each brain surface is accompanied by an XML description of its meta-data that can be quickly displayed on the screen to get more information about the individual brain.

## 3 Conclusion and Future Work

We foresee the development of graphical visualization tools that enable and enhance scientific interaction with large-scale databases, as the next step in neuroimaging informatics. Though some basic image viewing tools exist, we have argued for a need for a next generation visual interaction framework. We have also demonstrated a content-based solution that can be applied to any such archive in order for researchers to more easily examine dissimilarity between brains and to dynamically visualize patterns in the degree of proximity between brains. This may further be indicative of the demographic and clinical attributes of the data themselves. In fact, all throughout our approach, we have made as few assumptions about the data as possible, and really let the data segregate itself based upon the characteristics of regional shape and geometry.

## References

Dinov, I., Van Horn, J. D., and et al. 2009. Efficient, distributed and interactive neuroimaging data analysis using the loni pipeline. *Frontiers in Neuroinformatics*, 38.

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SIGGRAPH 2010, Los Angeles, California, July 25 – 29, 2010.
ISBN 978-1-4503-0210-4/10/0007