Allen Institute for Brain Science launches Allen Human Brain Atlas

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The Allen Institute for Brain Science announced today that it has launched the Allen Human Brain Atlas, a publicly available online atlas charting genes at work throughout the human brain. The data provided in this initial data release represent the most extensive and detailed body of information about gene activity in the human brain to date, documenting which genes are expressed, or "turned on" where. In the coming years, the Atlas will be expanded with more data and more sophisticated search, analysis and visualization tools to create a comprehensive resource useful to an increasingly wide range of scientists and research programs worldwide.

The Allen Human Brain Atlas, available at www.brain-map.org, is a unique multi-modal atlas of the human brain that integrates anatomic and genomic information to create a searchable, three-dimensional map of gene activity in the brain. Data modalities in this resource include magnetic resonance imaging (MRI), diffusion tensor imaging (DTI) and histology—providing information about gross neuroanatomy, pathways of neural connections, and microscopic anatomy, respectively—as well as gene expression data derived from multiple approaches.

"The launch of the Allen Human Brain Atlas is a significant milestone for the Allen Institute," said Allan Jones, Ph.D., chief executive officer of the Allen Institute. "This is the largest and most challenging project we have undertaken to date, and after over two years of planning and nine months of data generation, we are delighted to now be able to get this first, significant dataset into the hands of the research community."

The data in this inaugural release provide both a broad survey of gene activity throughout the entire adult human brain using microarrays, in which the entire genome can be analyzed in a single experiment, as well as more focused cellular-resolution analyses of the expression of individual genes in specific brain regions using in situ hybridization (ISH), a technique that provides images of where genes are expressed at high microscopic resolution and that was used for all earlier Allen Brain Atlas resources.

New data in this release include:

- Whole Brain Microarray Survey: This "all genes, all structures" survey represents the largest component of this initial data release. It includes MRI, histology and microarray data from a single adult male control ("normal") brain, all integrated into a unified 3D framework. Specifically, the gene expression data include spatially mapped microarray data for over 700 distinct anatomic locations throughout the brain and containing information for over 62,000 gene probes with 93% of known genes represented by at least 2 probes—in all, providing nearly 50 million gene expression measurements from a single brain. Data from brainstem and additional brains will be added in the future.

- Subcortex Study: This ISH study characterizes 55 genes in subcortical regions extending from the front of the caudate through posterior substantia nigra, and a smaller set of 10 genes through the hypothalamus. The 55-gene set focuses on the glutamatergic and GABAergic systems. The 10-gene set includes useful markers for anatomic delineation.

In addition, existing data from what was previously available as the Allen

Human Cortex Study have now been integrated into the Allen Human Brain Atlas. These data include:

- 1,000 Gene Survey in Cortex: This ISH study characterizes approximately 1,000 genes in visual and temporal cortex of multiple control cases. Genes included in this dataset represent several categories of broad scientific and clinical interest: cortical cell type markers, gene families important to neural function, disease-related genes and genes important in the comparative genomics field.

- Schizophrenia Study: This ISH study examines 60 genes in a region of the cortex implicated in neuropsychiatric disorders—the dorsolateral prefrontal cortex (DLPFC)—in over 50 control and schizophrenia (SCZ) cases. Genes covered in this dataset include cell-type markers, cortical layer-specific markers and SCZ candidate genes culled from the literature.

Provided by Allen Institute for Brain Science

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