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ALLEN INSTITUTE *for* BRAIN SCIENCE

FAQ: Human Cortex Study

General

What is the goal of this project?
The goal of this project is to provide the scientific community with a free, open resource for accessing human cortical brain gene expression information with cellular resolution.

What features are available in this application?
Users will find a searchable dataset of ISH images organized by gene, cortical region, donor and tissue characteristics. A toggle feature allows viewing of raw ISH images and pseudo-color gene expression masks, and images can be viewed as sets or individually with zoom and pan features. Nearest Nissl data are available for each image or image set. An alphabetically organized gene list is available for browsing. Users can click the "?" to access Help for all features on each application page.

Project Methods

Where can I get in-depth methods information for this project?
Please visit the documentations page (http://humancortex.alleninstitute.org/has/help/main.html to access a technical white paper describing methods and references for probe design, tissue and RNA quality characterization, ISH processes, image acquisition, data processing and quality control. Acknowledgements and answers to FAQ may also be found on the documentations page.

How are cases selected for gene expression characterization?
Postmortem human brain samples from subjects with no evidence of micro- or macro-neuropathology and no known history of neuropsychiatric disease or drug use are selected to provide baseline characterization of gene expression.

How are tissue samples obtained?
Tissue samples are obtained from established tissue repositories that provide well-characterized frozen postmortem tissue samples. Applicable regulatory guidelines governing human subjects research are adhered to, and at no time is any information that could identify a subject (e.g. first or last name) requested or received by the Allen Institute.

Will this be a genome-wide dataset?
Approximately 1,000 genes will be characterized in multiple individuals during the course of this project and several data releases are planned as data are generated. The genes cover a range of families, including ion channels, GPCRs, transporters, synaptic proteins, cortical and cell type markers, disease related genes and genes of interest in the comparative genomics field.

What is a RIN number?
RNA integrity number, or RIN, is a metric commonly used to indicate quality of RNA extracted from tissue samples and is assumed to reflect the quality of RNA in tissue sections used for ISH. RINs range from 1 to 10, with 10 indicating intact RNA. RIN may vary due to sample specific characteristics and may be influenced by assay parameters for RNA extraction and RIN measurement. Additional information may be accessed via the documentation page.
http://humancortex.alleninstitute.org/has/help/main.html.

What is PMI?
PMI is an acronym for 'postmortem interval', the duration of time (expressed in hours) between actual or estimated time of death and time that tissue samples are frozen. PMI is often reported in the literature as one indication of tissue quality. It has also been reported that postmortem interval has at most a modest effect on RNA quality. Additional information may be accessed via the documentation page. http://humancortex.alleninstitute.org/has/help/main.html.

What does pH information tell me?
Brain tissue pH may be an indicator of RNA integrity by virtue of its relationship to agonal state. Tissue samples used in this dataset have a cerebellar pH of 6 or higher. Additional information may be accessed via the documentation page. http://humancortex.alleninstitute.org/has/help/main.html.

Are any criteria in place for tissue samples?
Standard criteria that reflect the range of criteria in the literature are in place. PMI, pH, and RIN are presented to allow users to assess data according to user-specific needs. Additional information may be accessed via the documentation page. http://humancortex.alleninstitute.org/has/help/main.html.

What probes are used?
Digoxigenin-labeled riboprobes for target mRNA are made using cDNA clones or pooled cDNA prepared from pooled total human brain RNA as templates. All probes are designed with specific criteria to minimize cross-hybridization with non-target mRNA but are pan-specific for alternative splice variants. Where applicable, probes are designed to match corresponding Allen Brain Atlas mouse orthologs. Additional information may be accessed via the documentation page.
http://humancortex.alleninstitute.org/has/help/main.html.

How are images generated?
ISH and Nissl slides are digitized using either the image capture system (ICS) created by the Allen Institute or the ScanScope system from Aperio Technologies, Inc. The ICS system creates images with the desired resolution (~ 1 µm per pixel) by stitching individual tiles to form a composite image of the entire section. The ScanScope system currently being used creates images at the same 1 µm/pixel resolution using line scanning technology that results in more consistent focus and greater image acquisition speed.

Is there anything I can do to better visualize lightly stained tissue?
The addition of an acid wash step enhances data quality by greatly reducing background and also produces lightly stained tissue, particularly when gene expression is sparse. When viewing image sets, a slider bar is available to adjust the darkness of both ISH and pseudo-color images. Contrast and brightness settings are adjustable in the single image viewer. Zooming to higher resolution on a specific region on the image is also effective for better visualization of the data.

Citation and Use

What is the appropriate way to cite this resource?
Details on appropriate citation of this resource are available in the Allen Institute's Citation Policy at http://www.alleninstitute.org/content/citation_policy.htm

What are your terms of use?
The Allen Institute provides this dataset as a free, open resource for the scientific community. Users are encouraged to use this resource to support, for example, research, teaching, grant applications, publications and presentations, as per the Terms of Use, available at:
http://www.alleninstitute.org/content/terms_of_use.htm.

What is your privacy policy?
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http://www.alleninstitute.org/content/privacy_policy.htm.