




# JuGEx

Differential gene expression analysis

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 Cytoarchitecture linked to gene expression using probabilistic brain maps

## TECHNOLOGY DESCRIPTION

Decoding the chain from genes to cognition requires detailed insights how areas with specific gene activities and microanatomical architectures contribute to brain function and dysfunction. The [Allen Human Brain Atlas](#) contains regional gene expression data, while the [JuBrain Atlas](#) offers three-dimensional cytoarchitectonic maps reflecting the interindividual variability. JuGEx offers an integrated framework that combines the analytical benefits of both repositories towards a multi-level brain atlas of adult humans. JuGEx is a new method for integrating tissue transcriptome and cytoarchitectonic segregation.

**JuGEx links cytoarchitecture and gene expression to investigate multilevel human brain organization.**

**JuGEx provides a user-friendly workflow directly integrated into the Interactive Atlas Viewer or as a locally installed Matlab or Python version.**

## AREAS

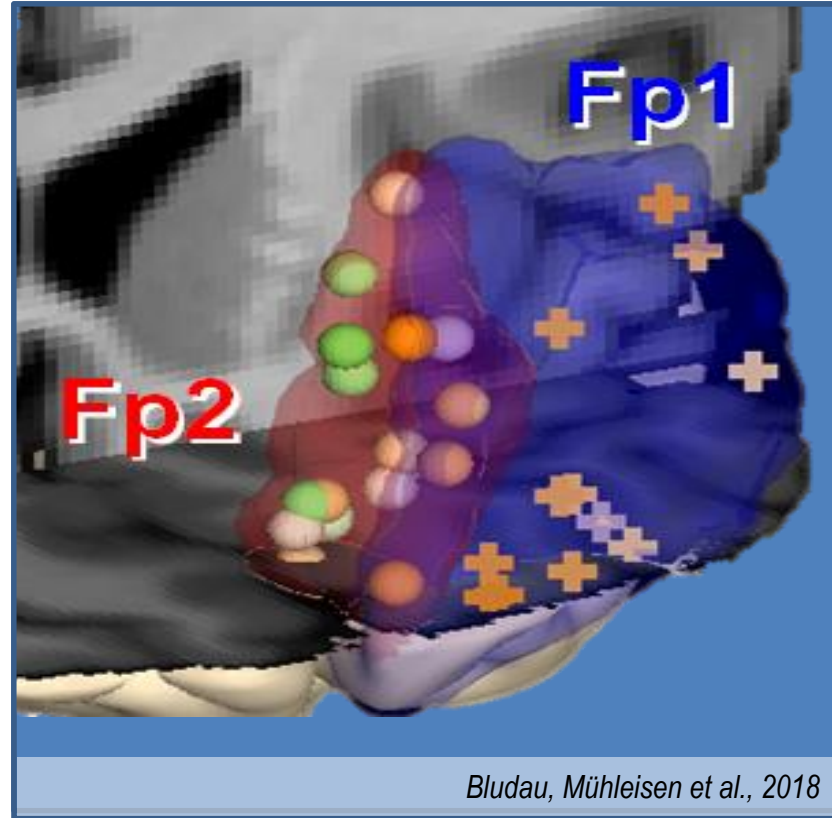
Brain atlases | Neuroanatomy | Genetics | 3D visualization





## COMPETITIVE ADVANTAGES

The added value of JuGex is that different levels of information on brain architecture, e.g. structural and functional connectivity, brain activations, and neurotransmitter receptor density, can now be supplemented by transcriptional information to enlighten biological aspects of brain organization and its diseases, spatially referring to the cytoarchitectonic JuBrain atlas. Such type of analysis properly distinguishes functionally different microstructural areas, going beyond conventional approaches which rely only on the traditional segregation of the brain into sulci and gyri.



Bludau, Mühleisen et al., 2018

Combine the analytical benefits of established scientific platforms  
JuBrain Atlas and AllenBrain  
Microarray data

## TECHNOLOGY READINESS LEVEL



## REFERENCES

JuGEx identified a significant upregulation of risk genes for depression in a region of a neuronal network model which is affected by atrophy and dysfunction in patients (Bludau et al. 2018). In a second use case, JuGEx found evidence for differential expression of candidate genes for phonological processing in two regions which show key roles in language and learning disorders (Unger et al. 2020, under review).

## CONTACT

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## APPLICATION & MARKET POTENTIAL

- JuGEx allows to compare transcriptomic and cytoarchitectonic data from two human brain atlases, ABA and JuBrain, in a common space
- The algorithm is published as a Matlab application, and now accessible as an interactive plugin of HBP's atlas viewer, as well as a Python library
- JuGEx is publicly available to empower research from basic, cognitive and clinical neuroscience in further brain regions and disease models with regard to gene expression.