Online Method:

Data and Materials

Pre-processing

Statistic Analysis

**Deconvolution**

Network Analysis

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# Deconv\_rlt

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**Importance of deconvolution based genetic association study.**

We are trying to prove the assumption that cell type level analysis is essential and critical in the study of Alzheimer's disease.

To test this hypothesis, we applied deconvolution analysis to test the differential cell type contribution between the samples with AD or without AD.

From the result, we found several celltypes (Ex6, Ex8, In6) have significant celltype contribution in general gene expression between case and control samples. (File.Deconv\_rlt, Tab.'DiffExp by Celltype')

To deep dived this phenomenon in gene level, we test the differential expression cross genes generally as well as in cell type level.

From the result, we provided all the genes with significant differential expression observations in at least one cell-types or in general level. (File.Deconv\_rlt, Tab.'DiffExp by Gene')

Within these genes, 133 could be found significant in general level. Within the 133 genes, 35 could be found also significant cross all cell-types. 275 genes didn't deliver a significant differential expression generally but could be found significant in at least one cell-type. (File.Deconv\_rlt, Tab.'For Venn')

Considerring the impact from experimental error, we also ran the same test with 30% component information excluded.

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# Deconv\_network\_result

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**Importance of deconvolution based net-work analysis.**

For the same goal, we are trying to identify the difference gene-gene expression among different cell-types.

To get the result, we applied the structural equation and search and score algorithm to build the causal network on signaling pathways generally as well as in celltype levels.

We used jaccard score (count of dupplicated edges / count of total edges) to measure the consistency cross different networks. And a range of 24%~98% overlap could be found between networks (Supplementary Table). (File.deconv\_network\_result, Tab.'Network Overlap')

We also tested the stability of each edges (Frequency of occurrence among networks). And a range of 12%~94% stability could be found cross edges. (File.deconv\_network\_result, Tab.'Network Overlap2')

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Rawdata:

Expression data: 447 sample \* 40120 genes

Cell level reference data: 16240 gene \* 4039 cell -> grouped to 17 cell type