# Functional and deconvolution analysis to identify disease associated genes.

# Key point:

1. Different cell types have different contribution for the pathology of AD
2. Deconvolution based disease association could identify cell-specific pathology related genes and these genes might the truth disease causal genes (Gene ontology anaylsis and gene pathway analysis, gene network analysis)
3. Deconvolution based network analysis better than traditional method and could identify more disease related genes and network.

# Introduction

# Result

1, Which cell types are more related to AD? And which types are less possibility associated with AD?

2, Then focus one AD related cell types and which genes are differential expressed between AD and normal

3, which genes can be identified only with deconvolution method? Which genes could be identified by raw data? What’s the difference between two kinds of genes? (Gene function analysis, my part)

**4, deconvolution based DEG are significantly associated with Neuron Function’s (my part)**

**5，pathway correlation was more significant associated with AD**

# Method

#### **Public dataset**

#### **Deconvolution**

# Discussion

# Abbreviation

# Author’s Contributions

# Reference

Figure legends:

Figure 1.

(a) Schematic overview of data generation and analysis. (a) differential contribution from different neuron cell types in Ads (b) # differential expression genes in relevance AD associated cell types. (c)

Figure 2.