



#### **Functional connectome fingerprinting:** identifying individuals using patterns of brain connectivity Emily S Finn, et al. [Nature 2015]



Data Mining Lab, Big Data Research Center, UESTC Email: junmshao@uestc.edu.cn http://staff.uestc.edu.cn/shaojunming

# Outline



- Introduction
- Fingerprint: brain connectivity
- Cognitive behavior prediction
- Discussion
- Conclusion



### Part 1 Introduction



- Human brain is known as the most sophisticated system in the world
  - 10<sup>11</sup> neurons(神经元)
  - 10<sup>15</sup> synaptic linkages(突触连接)
  - Complex structure connection and functional connection



• Brain anatomical structure





- Neuroimaging lead the way to study the human brain, it includes various techniques:
  - Magnetic resonance imaging(MRI, fMRI, DTI)
  - Computed axial tomography(CT)
  - Electroencephalogram(EEG)



• Neuroimaging towards multidisciplinary sciences





• What is MRI?

Magnetic resonance imaging (MRI) is a medical imaging technique which provides us a Noninvasive (非侵入) and intuitive way to investigate the anatomy (解剖) and physiology of the body



• MRI images look like this





- Advantages of MRI
  - Nonintrusive (非侵入的)
  - No ionising radiation (电离辐射) damage
  - Voxel (三维像素) level analysis
  - Multiple approachs to construct image (T1, T2, proton density...)



• What can we do about MRI?





- fMRI is a category of special MRI which allows to study brain's functional connection
- Detecting changes over time to construct functional connection pattern





- BOLD fMRI(Blood Oxygenation Level Dependent)
  - Blood Oxygenation level changes relating to neuronal activities
  - Oxygenated and deoxygenated hemoglobin (血红蛋白) has different effect on imaging



• BOLD fMRI(Blood Oxygenation Level Dependent)





### Part 2 Fingerprint: brain connectivity



- Biological characteristics
  - Fingerprint
  - Human face
  - Iris (虹膜)
  - Retina



 To quantify brain structure, a brain atlas (defined on Yale data set) consisting of 268 nodes is used in this study



Brain network with 268 nodes



- **Connectivity matrices**: 268 x 268 matrices, calculated by Pearson correlation coefficient
- Similarity measurement: Pearson correlation coefficient between vectors of edge values taken from the target matrix and database matrices



- 268 nodes are further grouped into eight networks
  - 1. Medial frontal



2. Frontoparietal









4. Subcortical-cerebellum





5. Motor



6. Visual I





7. Visual II



8. Visual association







 Data for this study was collected in six fMRI sessions in two different days for each subject



R1: resting-state

WM: working-memory task

Mt: motor task

R2: resting-state

Lg: language task

Em: emotion task



 Identification performed across pairs of scans taken from different days





 Identification process is to find the maximally similar matrix in database compared against target





#### • Experiment result



Black bar: database session

Gray bar: target session

1 + 2: combination of network 1 and 2

All: whole-brain identification



- Experiment result
  - Combination of network 1 and 2 shows high performance





- To find out edge's contribution to identification, used two parameter:
  - **DP**: ability to distinguish subjects
  - $-\phi$ : quantifies the consistency of a connection





Highly unique(DP, top, red)
and highly consistent(φ,
bottom, blue)

L, left hemisphere; R, right hemisphere



 Longer time courses better preserved individual characteristics in connectivity profiles





- Fluid intelligence (gF): the capacity for on-thespot reasoning to discern patterns and solve problems independently of acquired knowledge
- Regression and leave-one-out-cross-validation (LOOCV) was used for the prediction analysis



- Feature selection
  - Pearson correlation was performed between each edge and gF score across subjects in the training set
  - Edges were separated into two group: positively and negatively correlated with gF



- Model building
  - network strength:

[Positive feature network strength]<sub>s</sub> =  $\sum_{i,j} c_{ij} m_{ij}^{(+)}$ 

[Negative feature network strength]<sub>s</sub> =  $\sum_{i,j} c_{ij} m_{ij}^{(-)}$ c: individual *s*'s connectivity matrix

 $m^{(+)}$ : positive correlation matrices between edges and gF  $m^{(+)}$ : negative correlation matrices between edges and gF



- Linear regression
  - Network strength as the explanatory variable and, gF as the dependent variable

 $[Predicted gF score]^{pos} = a^* (Network strength)^{pos} + b$ 

 $[Predicted gF score]^{neg} = a^* (Network strength)^{neg} + b$ 



• Experiment result



a: analysis comparing predicted and observed gF with whole brainb: distribution of positive and negative feature in different network



• Experiment result



c: analysis comparing predicted and observed gF with Frontoparietal networks b: r value of each model in LOOCV analysis

### Discussion



- Brain altas parcellation scheme have effect on identification accuracy
- Longer time series improve identification accuracy
- Task to task, task to rest session identifications are more challenging, additional information improves identification accuracy

## Conclusion



- Individual's functional brain connectivity profile is both unique and reliable, similarly to a fingerprint
- Connectivity profiles can be used to predict the fundamental cognitive trait of fluid intelligence