

Growth Charting of Brain Connectivity Networks and the Identification of Attention Impairment in Youth

Published in JAMA Psychiatry, 2016 (Kessler, Sripada, &
Angstadt)

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Outline

1 Introduction

2 Methods

3 Results

4 Discussion

5 Acknowledgements

Motivation

Pediatric Growth Charts

- Long history for height, weight, etc

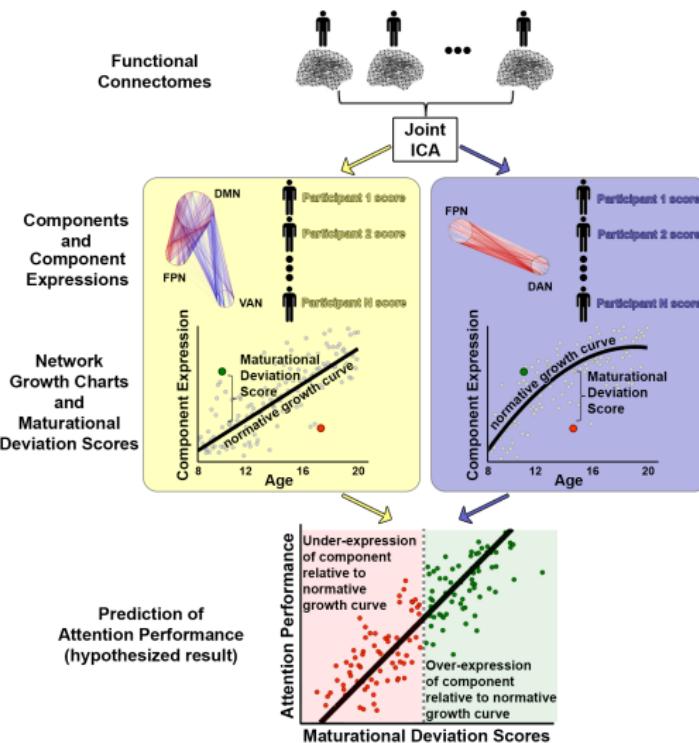
Intrinsic Connectivity Networks

- Attention & ADHD connection
- DMN vs TPN balance

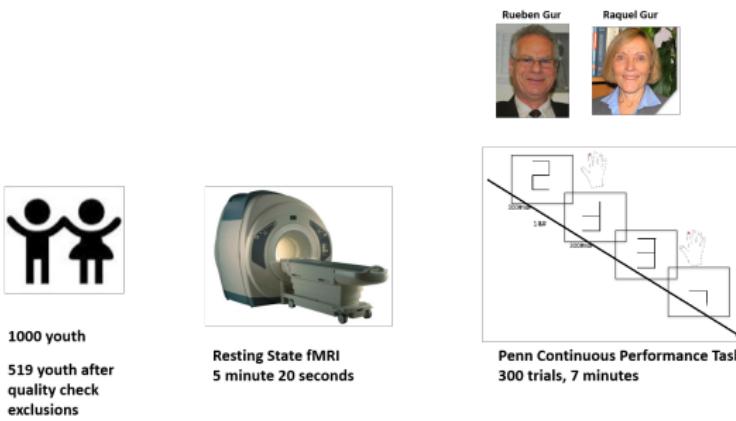
Background

- Focus today: processing pipeline, modeling, and analysis
- Slides: linked from <http://dankessler.me>
- Paper: Kessler, Angstadt, & Sripada. JAMA Psychiatry 2016

Method Overview



Sample



- Philadelphia Neurodevelopmental Cohort
 - Resting state fMRI
 - Penn Continuous Performance Task
 - N = 519 (after QC & exclusions)

Task: PCPT

- Penn Continuous Performance Test
- 1s to respond
- "Go" on digit/letter (varies by phase)
- Measure: Acc (corrected for age with quadratic model)

Clinical Interview

- Assesses psychopathology dimensions
- ADHD Module
- Symptom endorsement -> pseudo ADHD "diagnosis"

MRI Measures

- T1-weighted image (structural contrast)
- Resting State fMRI

T1 Image

- Structural contrast
- Ventricles are black, "gray matter" is darker, "white matter" is brighter

Resting state fMRI

- 4D Image (Multiple "Volumes"): X*Y*Z*time
- T2* contrast captures BOLD (blood oxygenation, coupled to neural activity)

fMRI Preprocessing Overview

Lots of quality-control steps throughout

- ① Slice-time Correction
- ② Motion Correction
- ③ Normalization
- ④ Smoothing

Preproc: Slice-time Correction



- Each fMRI volume is acquired sequentially in slices
- Volume not acquired simultaneously
- Correct (through interpolation) s.t. all slices w/in volume temporally aligned

Preproc: Motion Correction

- Participants move their head over the scan
- Estimate affine realignment to common volume (e.g. V_0)
- Alignment is progressive (rigid body transforms)
 - realign V_1 to V_0 using affine matrix Q_1
 - align V_2 to V_0 , initialize solution with Q_1
 - and so on
- Store Q_i
- Process Q_i 's to capture summary displacement information for each frame
 - this will be used later in preprocessing

Preproc: Normalization

- Everybody's brain is unique
- This is problematic for group analyses
- Standard Brain/Space: MNI (Montreal Neurological Institute)
- Steps
 - ① Rigid body registration of T1 scan to T2* scan
 - ② Estimate nonlinear warp (affine + splines) b/w T1 and MNI template
 - ③ Apply estimated warp to each volume of T2* scan

Preproc: Smoothing

- Normalization isn't perfect
- Brains are plastic and diverse even when perfectly aligned anyway
- Smooth with Gaussian kernel (3D, 8mm FWHM)

Resting Processing & Connectome Generation

Processing

- Linearly detrended
- COMPCor: PCA-based nuisance regression (CSF & WM)
- Bandpass Filtering (0.01 to 0.1 Hz)
- Motion Scrubbing: Delete volumes with large displacement/motion

Connectome Generation

- Isomorphic grid, 12mm spacing
- 1068 Regions of Interest (ROIs)
- Calculate pairwise correlation, then R-to-Z transform
- Vector embedding: Each participant contributes $\binom{1068}{2}$ edges

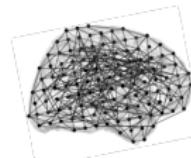
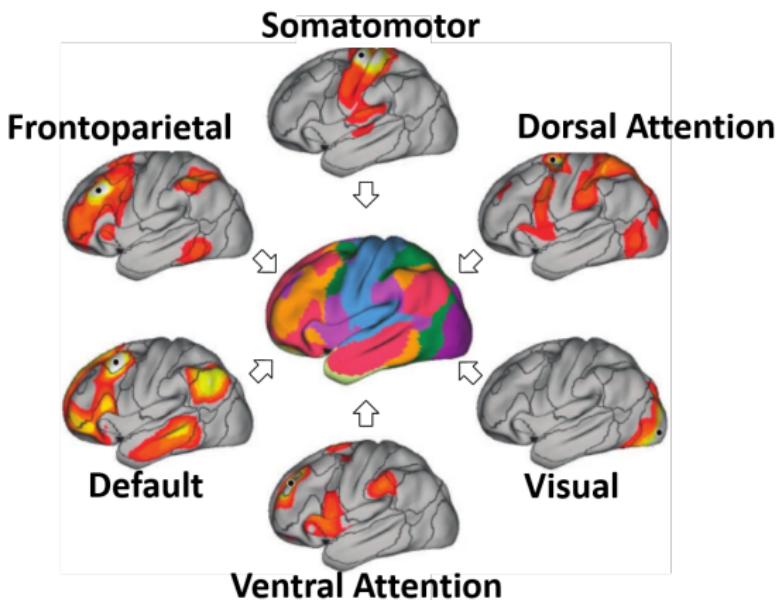
Data Cleansing

- Intersubject nuisance effects may manifest at edge level
- e.g.: left handers have > connectivity at edge i
- Concatenate vector embeddings into matrix X
- estimate with OLS $X = Y\hat{\beta} + \hat{\epsilon}$
- Reestimate data as $X^\dagger = Y^\dagger\hat{\beta}$
- Y is ideal design matrix where nuisance fx are flat
- Induce eigenvector selection through augmentation: add $\hat{\beta}$ for fx of interest at each edge

Independent Components Analysis

- reduce rows of X^\dagger through PCA (DX) (retain top 15 eigenvectors)
- ICA-decomposition using FastICA $X = AS$
- A: mixing matrix 15 by 15
- S: source matrix: 15 by $\binom{10^{68}}{2}$
- Unreduce $A^\dagger = D^{-1}A$
- A^\dagger is # of subjects by 15
- The i,j element indicates the expression of component j for subject i

Network Assignment & Visualization

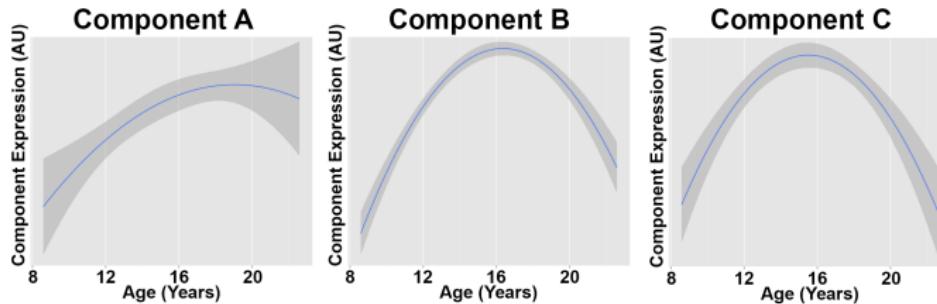


Network Growth Charting Analyses

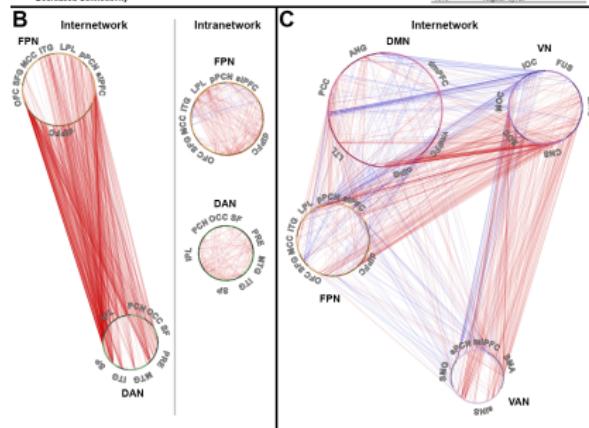
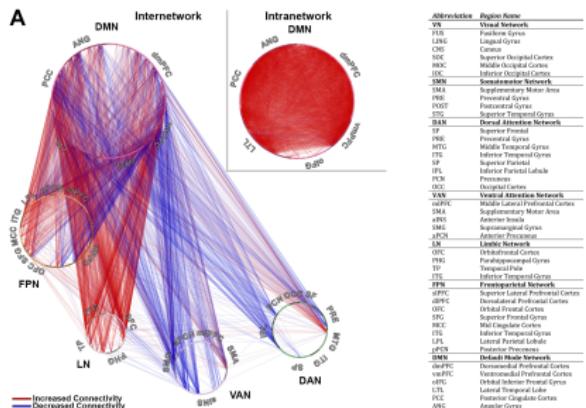
- Growth charts obtained from OLS population-level estimates
- Predict each column of A with OLS $A_i^\dagger = \text{age} + \text{age}^2$
- Residuals from these models are **deviation scores** reflecting over- or under-expression of a component relative to age
- Use **deviation scores** to predict
 - Accuracy on PCPT (age-corrected)
 - ADHD status

Network Growth Charting to Predict Task Accuracy

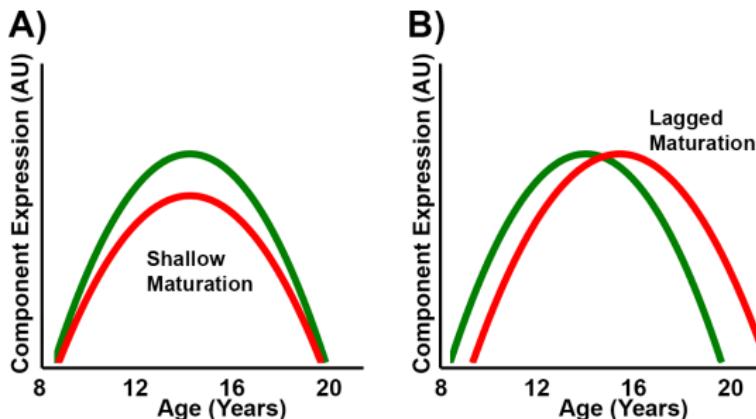
- Deviation scores predict accuracy very well ($R^2 = 0.287$)
- A subset of just 6 components' deviation scores do most of the work ($R^2 = 0.240$)
- Of these, 5 show vigorous maturational profiles
- Split half analysis, OLS with all 15 deviation scores: $R^2 = 0.176$



DMN-TPN Shifts in Maturing Components



Shallow vs Lagged Dysmaturation and Task Accuracy



Shallow Dysmaturation

Dysmaturation yields consistent underexpression of components

Lagged Dysmaturation

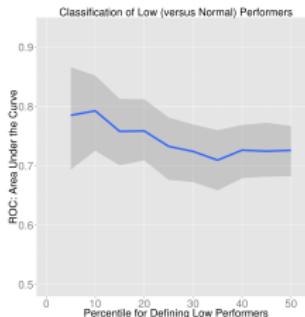
Dysmaturation yields comparable, but right-shifted, peak

Strong Evidence for Shallow Dysmaturation over Lagged

Likelihood Ratio $> 10^{26}$

Biomarker of Attention Dysfunction from Network Growth Charting

- Goal: Binary Classification of Attention Dysfunction
- Binarize task performance into *low* and *normal* performers (split by %ile cutoff)
- Vary %ile cutoff for binning
- LOOCV of Logistic Regression, performance assessed with ROC AUC, error bars from permutations



Biomarker of ADHD from Network Growth Charting

- Goal: Binary Classification of Pseudo ADHD Diagnosis
- Logistic regression predicting dx using 6 components IDed earlier
- Model is significant, but effect size weak compared to attention prediction
- $\chi^2_6 = 13.00; P = 0.043$

Discussion

- Recent review paper calls for developmental approaches to connectomic imaging
- We link dysmaturation of ICN topology to attention dysfunction
- DMN-TPN intra- and inter-relationships implicated
- Shallow vs lagged dysmaturation provides better predictive fit

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