

# **Neurodevelopmental Disorders**Lessons learned from autism and open brain connectome research

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## Financial disclosure

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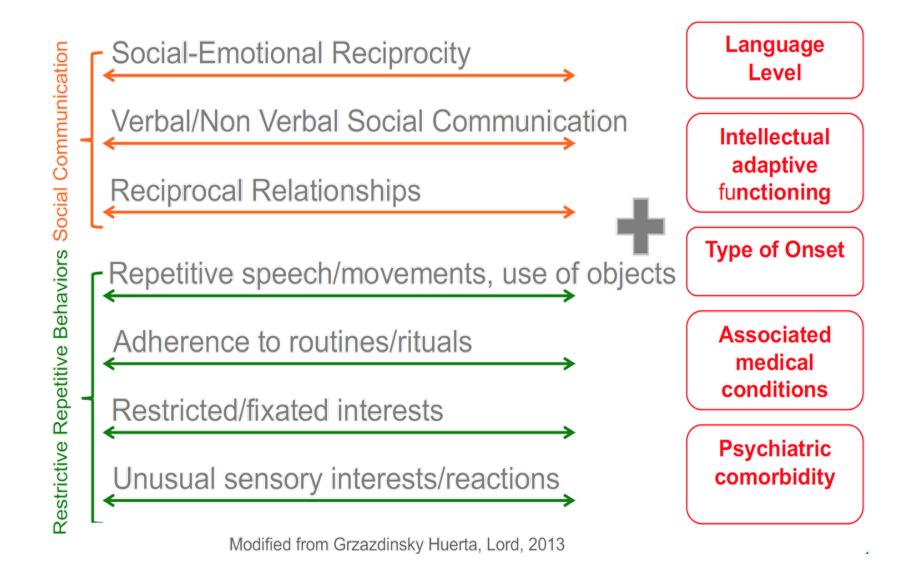
# Neurodevelopmental Disorders share challenges and opportunities for biomarker discovery

- Attention
   Deficit/Hyperactivity
- Autism Spectrum
- Communication
- Motor
- Specific Learning
- Intellectual Disability

- Childhood onset
- Heterogenous presentations
  - Comorbidity rules
- Multifactorial etiopathogenesis
- Brain connectopathies

- 67% neuropsychiatric disorders onset within the first 20 years of life (e.g., Kessler et al 2005)
- Common disorders of childhood can already be diagnosed in preschoolers (~7%) (e.g., Wichstrom et al 2012)
- Continuity of symptom clusters from preschool-age to childhood/adolescence

# Autism heterogeneity- a challenge and an opportunity





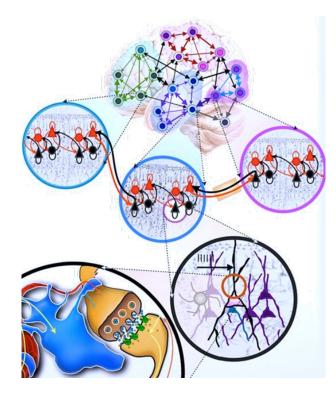
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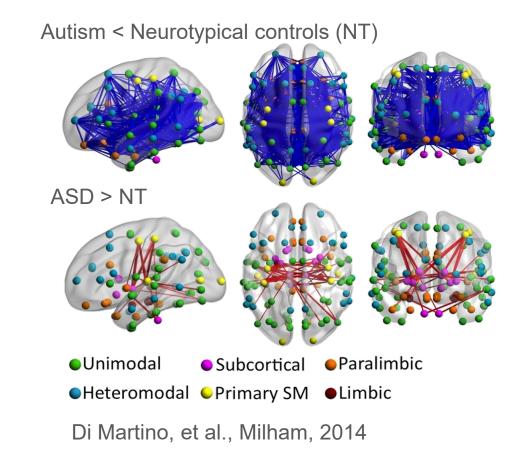
# Developmental brain connectopathy



Park and Friston, 2013

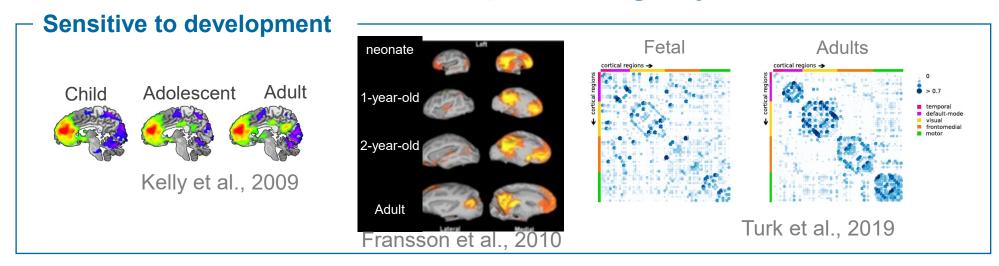
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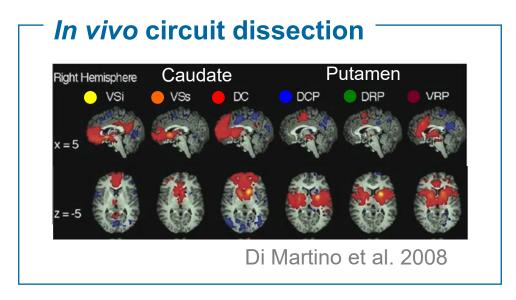
**Brain connectome**: the comprehensive map of brain circuits (i.e., nodes and edges)

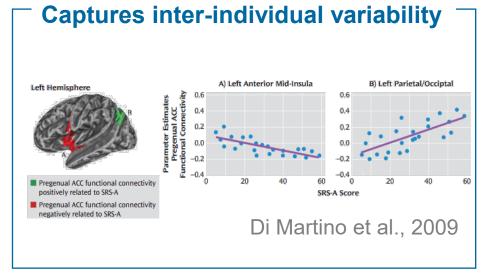


A mosaic of dysconnections: ASDrelated increased and decreased connectivity varying by functional circuitry

# Non-invasive connectome profiling by R-fMRI



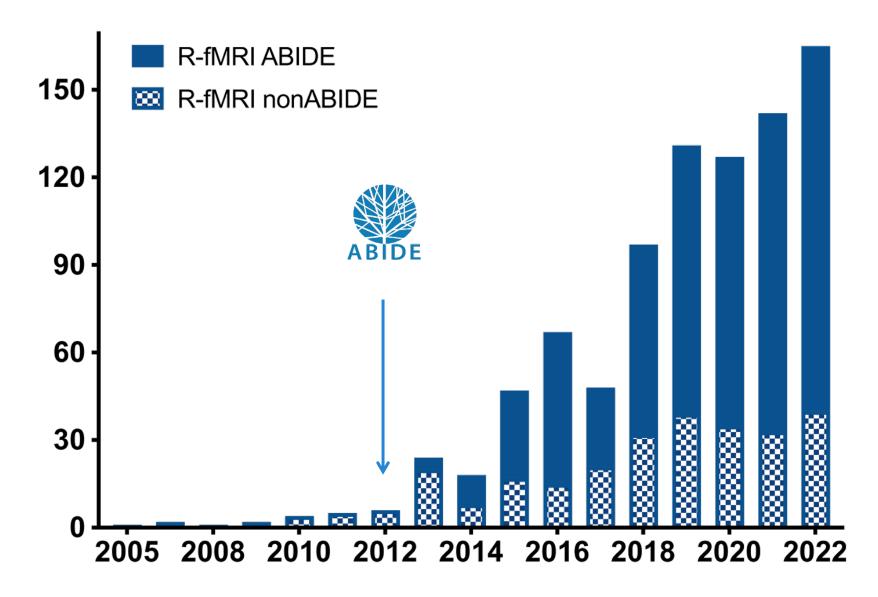






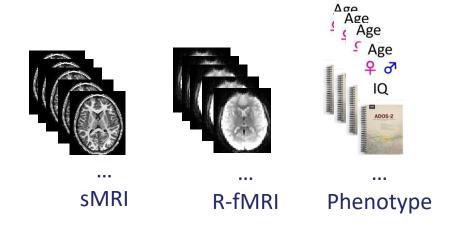


# Resting-state fMRI (R-fMRI) in Autism



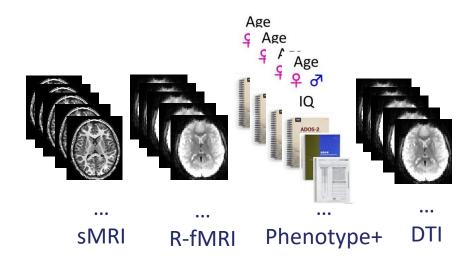


# Autism Brain Imaging Data Exchange - open data sharing



### **ABIDE I**

Released August 2012
N Sites=17
N Collections=20
N Individuals=1112
ASD n=539, TDC n=573
Grass rooted
Di Martino et al., Mol Psych, 2013



### **ABIDE II**

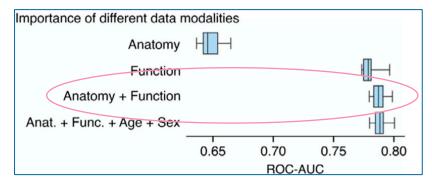
Released June 2016
N Sites=17 (8 from ABIDE I)
N Collections=18 add long
N Individuals=1114
ASD n=521, TDC n=593
NIMH R21MH107045
Di Martino et al., Sci Data, 2017

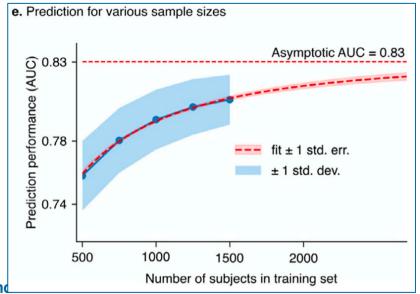


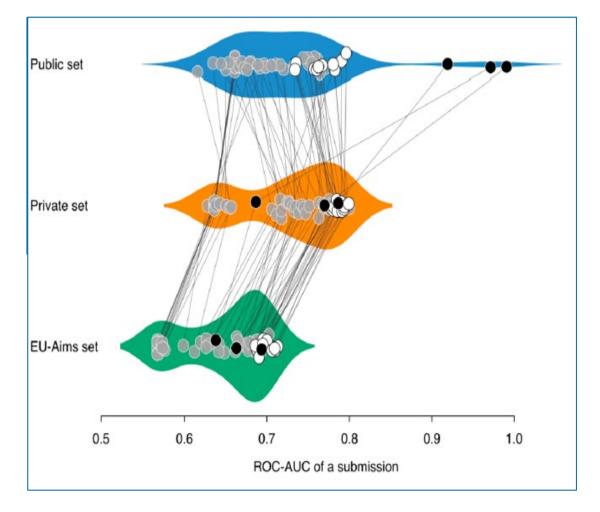
# Insights from an autism imaging biomarker challenge: Promises and threats to biomarker discovery

Nicolas Traut<sup>a,i,†</sup>, Katja Heuer<sup>a,d,i,†</sup>, Guillaume Lemaître<sup>b,c,†</sup>, Anita Beggiato<sup>a,k</sup>, David Germanaud<sup>e</sup>, Monique Elmaleh<sup>f</sup>, Alban Bethegnies<sup>g</sup>, Laurent Bonnasse-Gahot<sup>l</sup>, Weidong Cai<sup>j</sup>, Stanislas Chambon<sup>p</sup>, Freddy Cliquet<sup>a</sup>, Ayoub Ghriss<sup>h</sup>, Nicolas Guigui<sup>e</sup>, Amicie de Pierrefeu<sup>e</sup>, Meng Wang<sup>n,o</sup>, Valentina Zantedeschi<sup>m</sup>, Alexandre Boucaud<sup>b,c</sup>, Joris van den Bossche<sup>b,c</sup>, Balázs Kegl<sup>q</sup>, Richard Delorme<sup>a,k</sup>, Thomas Bourgeron<sup>a</sup>, Roberto Toro<sup>a,+</sup>, Gaël Varoquaux<sup>b,r,+,\*</sup> Neuroimage, 2022

- MRI powerful and reliable for ASD
- MRI modality matters
- Sample size improves accuracy
- Overfitting and sample variations threat discovery



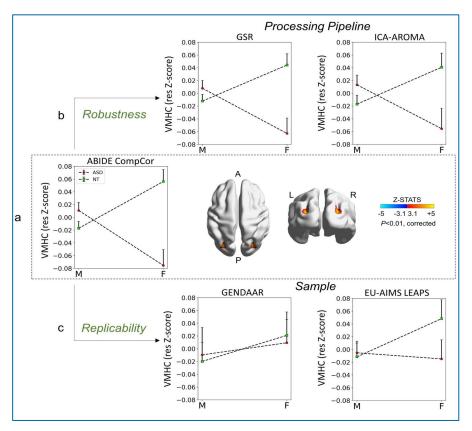




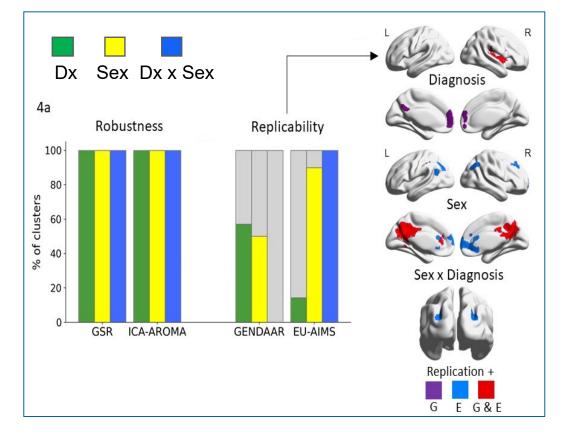
RESEARCH Open Access

# Towards robust and replicable sex Mol Autism, 2021 differences in the intrinsic brain function of autism

Dorothea L. Floris<sup>1,2†</sup>, José O. A. Filho<sup>3†</sup>, Meng-Chuan Lai<sup>4,5,6,7,8</sup>, Steve Giavasis<sup>3</sup>, Marianne Oldehinkel<sup>2</sup>, Maarten Mennes<sup>1</sup>, Tony Charman<sup>9</sup>, Julian Tillmann<sup>9,20</sup>, Guillaume Dumas<sup>10,21</sup>, Christine Ecker<sup>11,12</sup>, Flavio Dell'Acqua<sup>11,13</sup>, Tobias Banaschewski<sup>14</sup>, Carolin Moessnang<sup>15</sup>, Simon Baron-Cohen<sup>7</sup>, Sarah Durston<sup>16</sup>, Eva Loth<sup>11,13</sup>, Declan G. M. Murphy<sup>11,13</sup>, Jan K. Buitelaar<sup>1,2,17</sup>, Christian F. Beckmann<sup>1,2,18</sup>, Michael P. Milham<sup>3,19</sup> and Adriana Di Martino<sup>3\*</sup>

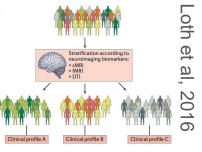


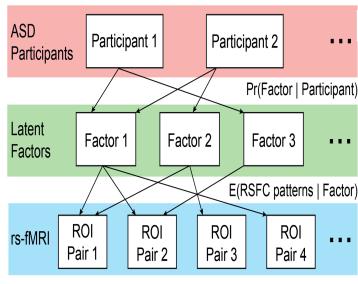
- Diagnostic differences common across the sexes, ASD-specific sex differences
- Results robust to varying analytical choices
- Replicability vary by R-fMRI metric, effects, sample size and sample



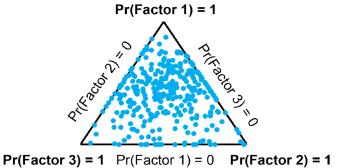
# Neurosubtyping

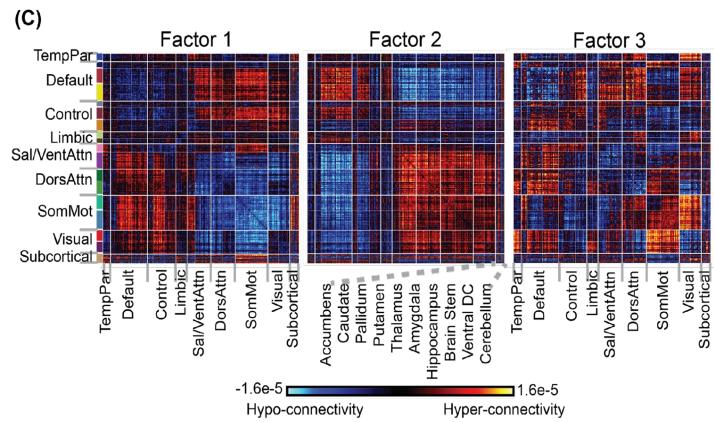
### Mosaic of latent brain connectopathy factors - i.e., neurosubtypes





Yeo et al 2016; Sun et al 2017





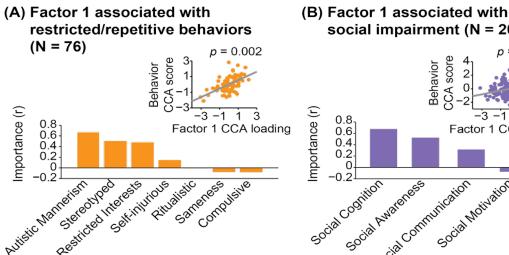
Tang, Sun, Floris, Zhan Di Martino, Yeo., Biol Psych 2020

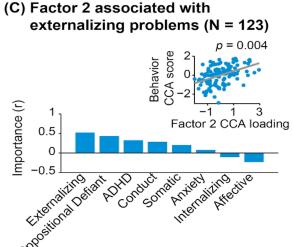


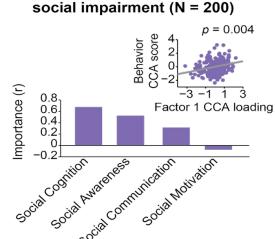
# Phenotypic depth and harmonization have lagged in clinical neuroscience research

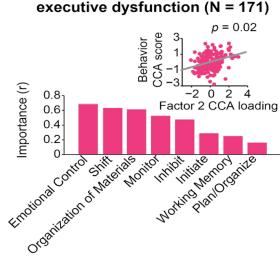


- Across sites depth of multiple phenotyping is limited beyond diagnostics and IQ
- Need prospective harmonized protocols
  - wider and deeper (items-levels) phenotypic data







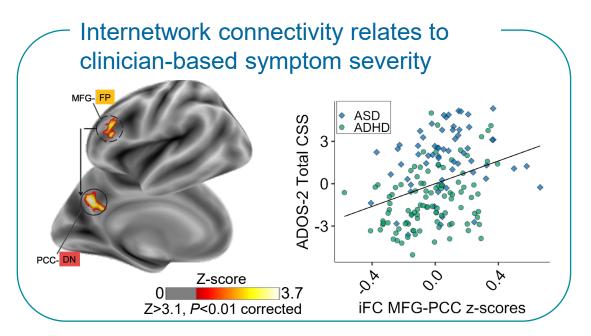


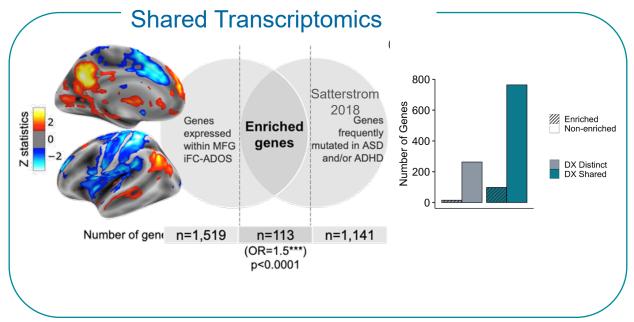
(D) Factor 2 associated with



# Targeting inter-individual differences — transdiagnostic

N=166; n=103 ADHD, N=63 ASD; 6-12 years, 116 males



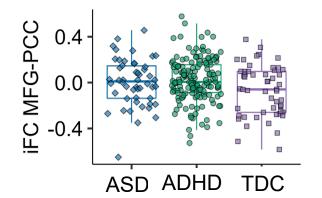


### **Exploring replicability**

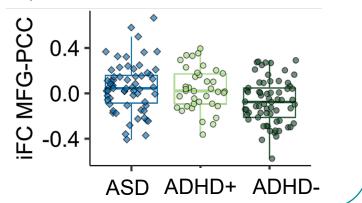
Data Descriptor: An open resource for transdiagnostic research in pediatric mental health and learning disorders Healthy Brain Network

Lindsay M. Alexander<sup>2</sup>, Jasmine Escalera<sup>3</sup>, Lei Ai<sup>3</sup>, Charissa Andreotti<sup>3</sup>, Karina Febre<sup>3</sup>, Alexander Mangone<sup>1</sup>, Natan Yega-Potler<sup>3</sup>, Nicolas Langer<sup>12</sup>, Alexis Alexander<sup>3</sup>, Meagan Kovacs<sup>2</sup>, Shannon Litke<sup>3</sup>, Bridget O'Hagan<sup>1</sup>, Jennifer Andersen<sup>1</sup>, Batya Bronstein<sup>3</sup>, Anastasia Bui<sup>3</sup>, Marijayne Bushey<sup>3</sup>, Henry Butler<sup>3</sup>, Victoria Castagna<sup>3</sup>, Nicolas Camacho<sup>3</sup>, Lilsha Chan<sup>3</sup>, Danielle Citera<sup>3</sup>, Jon Clucas<sup>3</sup>, Samantha Cohen<sup>3</sup>, Sarah Dufek<sup>3</sup>, Megan Eaves<sup>3</sup>, Brian Fradera<sup>3</sup>, Judith Gardner<sup>5</sup>, Natalei Grant-Villegas<sup>3</sup>, Bobriella Green<sup>3</sup>, Camille Gregopo<sup>3</sup>, Emily Hart<sup>3</sup>, Shana Harris<sup>3</sup>, Megan Horton<sup>6</sup>, Danielle Kahn<sup>3</sup>, Katheine Kabotyanski<sup>3</sup>, Bernard Karmel<sup>3</sup>, Simon P. Kelly<sup>7</sup>, Kayla Kleinman<sup>3</sup>, Bonhwang Koo<sup>5</sup>, Eliza Kramer<sup>3</sup>, Elizabeth Lennon<sup>5</sup>, Catherine Lord<sup>4</sup>, Ginny Martello<sup>3</sup>, Amy Margolis<sup>5</sup>, Kathleen R. Merikangas<sup>30</sup>, Judith Milham<sup>13</sup>, Giuseppe Minniti<sup>3</sup>, Rebecca Neuhaus<sup>3</sup>, Alexandra Levine<sup>5</sup>, Yael Osman<sup>5</sup>, Lucas C. Parra<sup>3</sup>, Ken R. Pughi<sup>12</sup>, Amy Racanello<sup>3</sup>, Anita Restrepo<sup>3</sup>, Tian Saltzman<sup>3</sup>, Alexandra Levine<sup>5</sup>, Taus Guba<sup>3</sup>, Raselle Waltz<sup>3</sup>, Anna Williams<sup>3</sup>, Anna Yeo<sup>5</sup>, Francisco X. Castellanosi<sup>5,1,3</sup>, Amo Klein<sup>5</sup>, Tomas Paus<sup>2,16,17</sup>, Bennett L. Leventhal<sup>1,18</sup>, R. Cameron Craddock<sup>1,13</sup>, Harold S. Koplewicz<sup>1</sup> &

### Independent sample – HBN (n=232)



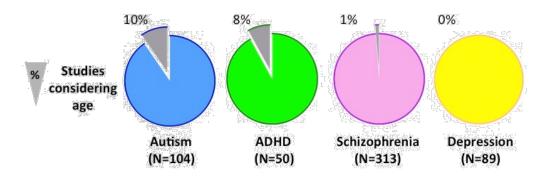
### Primary sample (n=166)



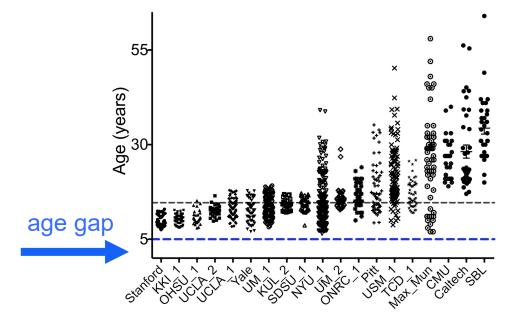


# Remaining challenges

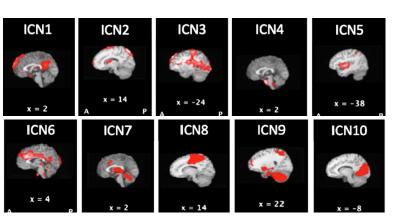
## Developmental perspective to developmental disorders



Di Martino et al., Neuron 2014



- Longitudinal approaches are needed to assess traits vs state-related biomarkers
- Focus on younger ages
  - e.g., IBIS >>infants likely to develop autism
- Natural sleep resting state fMRI is feasible



Manning et al 2013





# Summary and moving forward

- Aggregation of openly-shared increasingly large MRI dataset is feasible and necessary to facilitate:
  - Replicability assessments (should be the norm)
  - Leverage heterogeneity
    - A priori focus on known sources of variation (e.g., sex at birth, comorbidity...) and underrepresented subgroups
    - Neurosubtyping
    - Inter-individual variability across dimensional metrics
  - Connectome-based fMRI markers are promising candidate for Multimodal BioM discovery but clinical utility of BM depends on phenotyping depth
  - Need for harmonization efforts focusing on reliable and specific measures
  - Measurement-invariance analyses
- Transdiagnostic and longitudinal large-scale efforts needed



### **CMI**

Michael P Milham Seok-Jun Hong Ting Xu Alex Franco Marco Pagani Lindsay Alexander Phoebe Thomson Diego Perez **Steve Giavasis** Patricia Segura Margaret Dyson Cynthia Martin **Bethany Vibert Bennet Leventhal** 

# NYU Child Study Center F Xavier Castellanos Eva Petkova

# **Acknowledgments**



Transforming Children's Lives childmind.org

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Cathy Lord

### NKI

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### **UCSF**

Somer Bishop

University of Singapore Thomas Yeo

MNI, MIC

**Boris Bernhardt** 

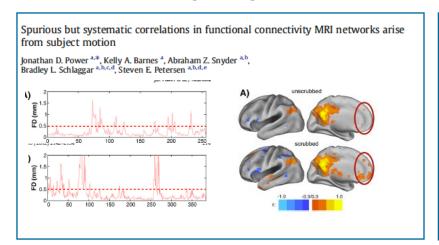
**ABIDE Consortium** 



### IIT

Alessando Gozzi Michael Lombardo

## Drawbacks and proposed solutions...



A comprehensive assessment of regional variation in the impact of head micromovements on functional connectomics

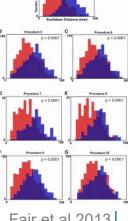
Chao-Gan Yan <sup>a,b,c</sup>, Brian Cheung <sup>b</sup>, Clare Kelly <sup>c</sup>, Stan Colcombe <sup>a</sup>, R. Cameron Craddock <sup>b,d</sup>, Adriana Di Martino <sup>c</sup>, Qingyang Li <sup>b</sup>, Xi-Nian Zuo <sup>e</sup>, F. Xavier Castellanos <sup>a,c</sup>, Michael P. Milham <sup>a,b,\*</sup>

#### Mitigating head motion artifact in functional connectivity MRI

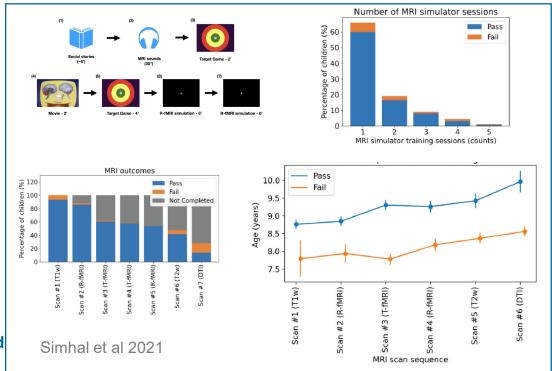
Rastko Ciric<sup>1</sup>, Adon F. G. Rosen<sup>1</sup>, Guray Erus<sup>2</sup>, Matthew Cieslak<sup>1,2</sup>, Azeez Adebimpe <sup>0,1,2</sup>, Philip A. Cook<sup>3</sup>, Daniel H. Wolf<sup>1,2</sup>, Theodore D. Satterthwaite 012\*

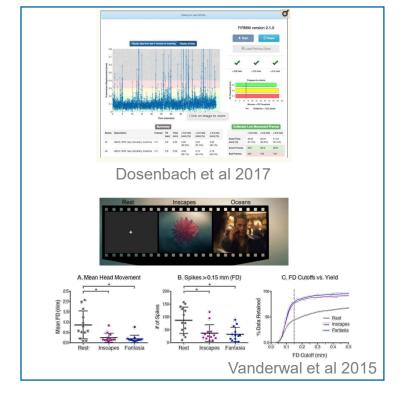
An evaluation of the efficacy, reliability, and sensitivity of motion correction strategies for resting-state functional MRI

Linden Parkes\*, Ben Fulcher, Murat Yücel, Alex Fornito

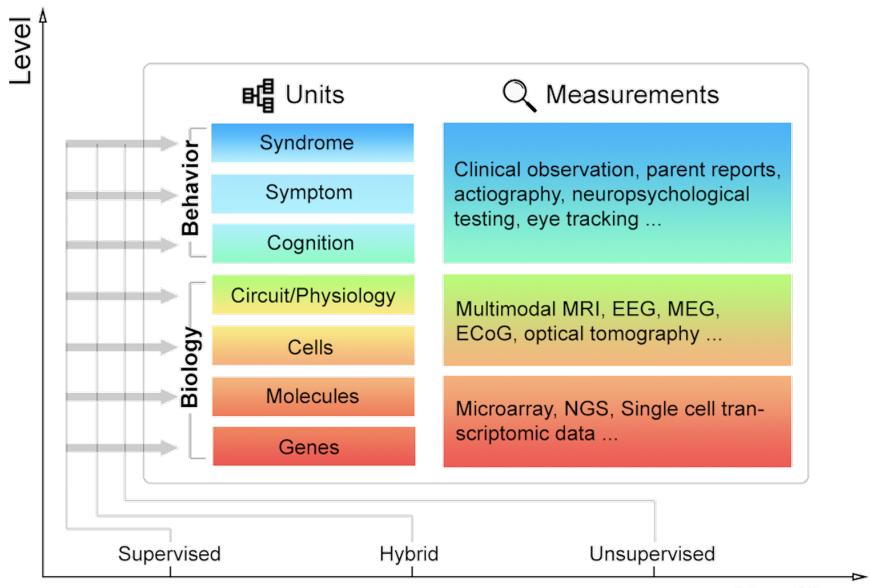


Fair et al 2013





## Approaches to Autism

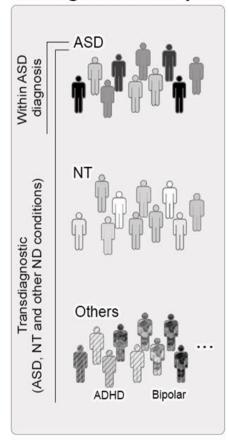




Algorithms

## Data driven neurosubtyping in autism

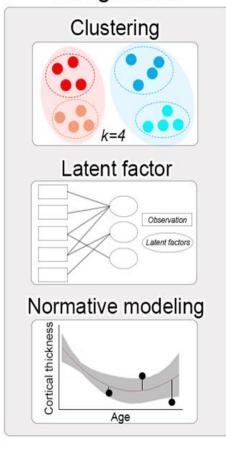
### A. Diagnostic samples



### **B.** Features

 Feature selection - A priori selection Quantitative selection (e.g., Filter, Wrapper methods) Structural Functional BOLD topine, of them time-series Source Target Dimensionality reduction (e.g. PCA, NMF) Data fusion (e.g. Multi-viewing learning - SNF, JIVE) Data harmonization (e.g. Combat, Significance-weighted PCA)

### C. Algorithms



### D. Validation

- · Goodness of fit
  - Silhouette, Davies-Bouldin index
- Stability
  - Cross-method validation, Bootstrapping
- Independent validation
  - Clinical (e.g., symptom severity -ADOS, ADI-R)
  - Cognitive (neuropsychological scores)
  - Biological (genetics profile CNV, common/rare variants)
- Replicability
  - Bootstrap aggregation (Bagging)
  - Cross-modal validation (e.g., functional connectivity or structural metrics)

