

Object Oriented Data Analysis in Large-scale Medical Studies

University of North Carolina at Chapel Hill

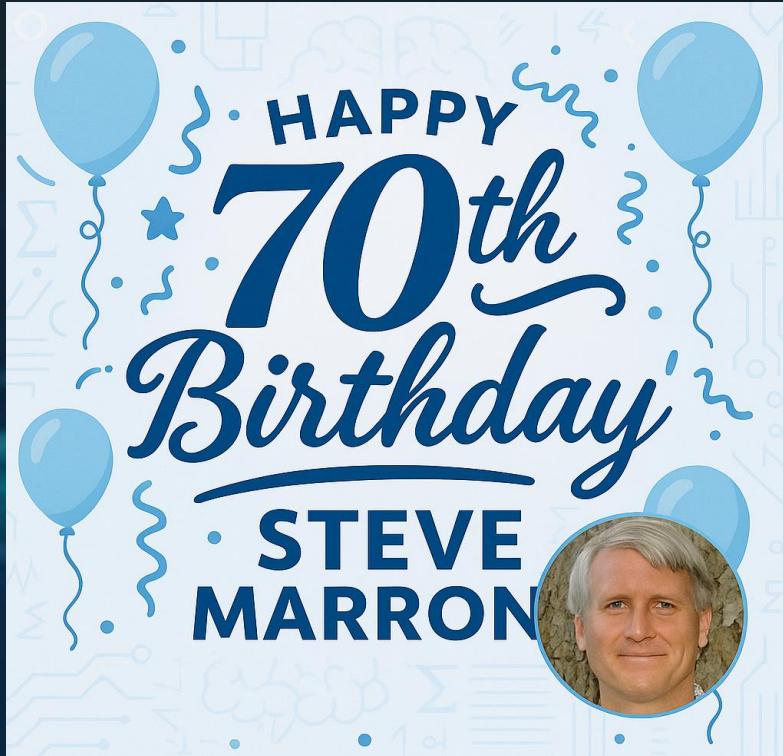
Hongtu Zhu

Joint works with Zhengwu Zhang, Hai Shu, Steve Marron, Di Xiong, Xueqing Wang, Wenliang Pan, Anuj Srivastava, and Joseph Ibrahim

<https://www.med.unc.edu/bigs2/>



Happy 70th Birthday, Steve Marron!
Wishing you a wonderful celebration
and many more joyful years ahead!



Steve Marron has been an outstanding mentor and collaborator to me!

Ying Yuan

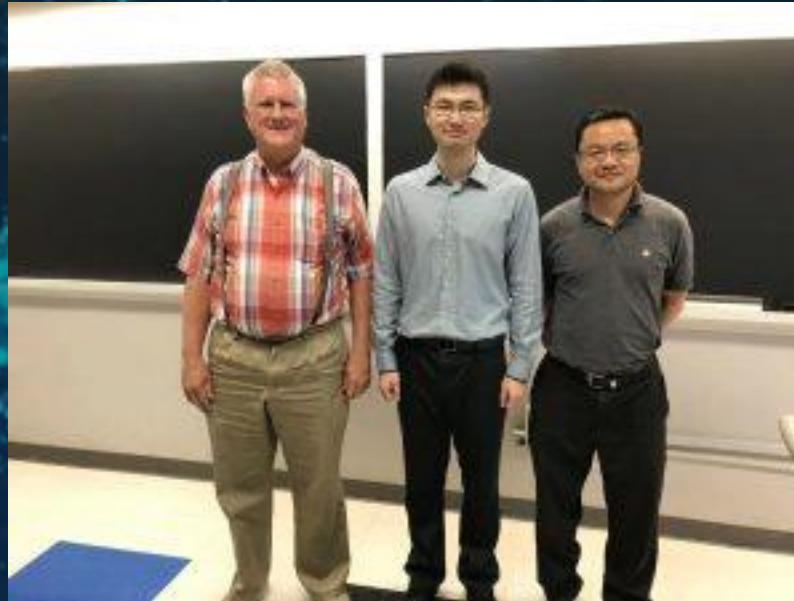
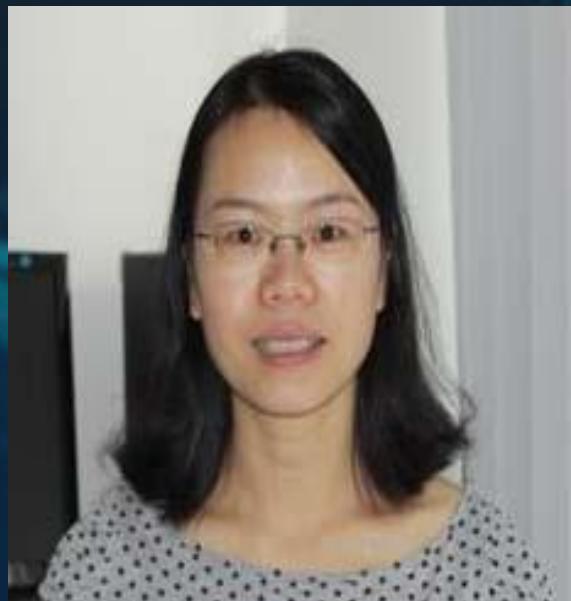
2011

Yang Yu

2017

Liuqing Yang

2019



5 joint papers (2 AOAS,
1 JRSSB, 2 Sinica) +



CONTENTS



Part I

Object Oriented Data Analysis (OODA)



Part II

Case Studies for OODA



Part I

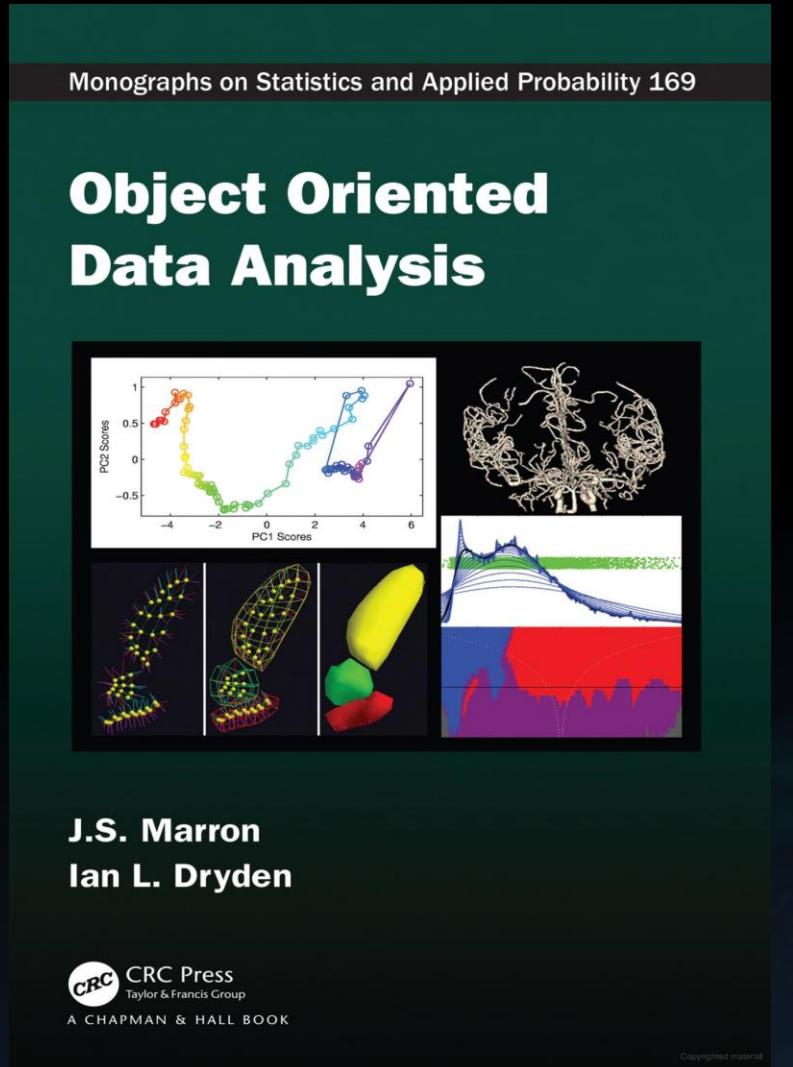
Object Oriented Data Analysis



"Oddly, we are in a period where there has never been such a wealth of new statistical problems and sources of data. The danger is that if we define the boundaries of our field in terms of familiar tools and familiar problems, we will fail to grasp the new opportunities."

- Leo Breiman -

Object Oriented Data Analysis



Marron's Teaching Material

OODA:

- STOR 881 – Spring 2024
- STOR 881 – Spring 2022
- STOR 881 – Fall 2019
- STOR 881 – Fall 2017
- STOR 893 – Spring 2016
- STOR 892 – Fall 2014
- STOR 891 – Fall 2012
- STOR 891 – Fall 2007
- STAT 322 – Fall 2005
- Networks – Cornell – Fall 2001
- FDA – Cornell – Spring 2002
- FDA – Spring 2001



Objects are everywhere

Language Translation in Natural Language Processing

Deep learning enhances real-time, accurate translation of languages, as seen in tools like Google Translate. The following picture shows the translation of a webpage from English to Chinese.

Facebook AI is introducing M2M-100, the first multilingual machine translation (MMT) model that can translate between any pair of 100 languages without relying on English data. It's open sourced [here](#).

When translating, say, Chinese to French, most English-centric multilingual models train on Chinese to English and English to French, because English training data is the most widely available. Our model directly trains on Chinese to French data to better preserve meaning. It outperforms English-centric systems by 10 points on the widely used BLEU metric for evaluating machine translations.

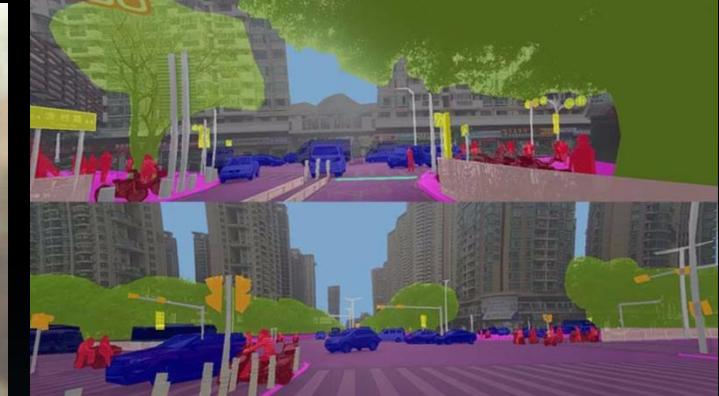
M2M-100 is trained on a total of 2,200 language directions — or 10x more than previous best, English-centric multilingual models. Deploying M2M-100 will improve the quality of translations for billions of people, especially those that speak low-resource languages.

This milestone is a culmination of years of Facebook AI's foundational work in machine translation. Today, we're sharing details on how we built a more diverse MMT training data set and model for 100 languages. We're also [releasing the model, training, and evaluation setup](#) to help other researchers reproduce and further advance multilingual models.

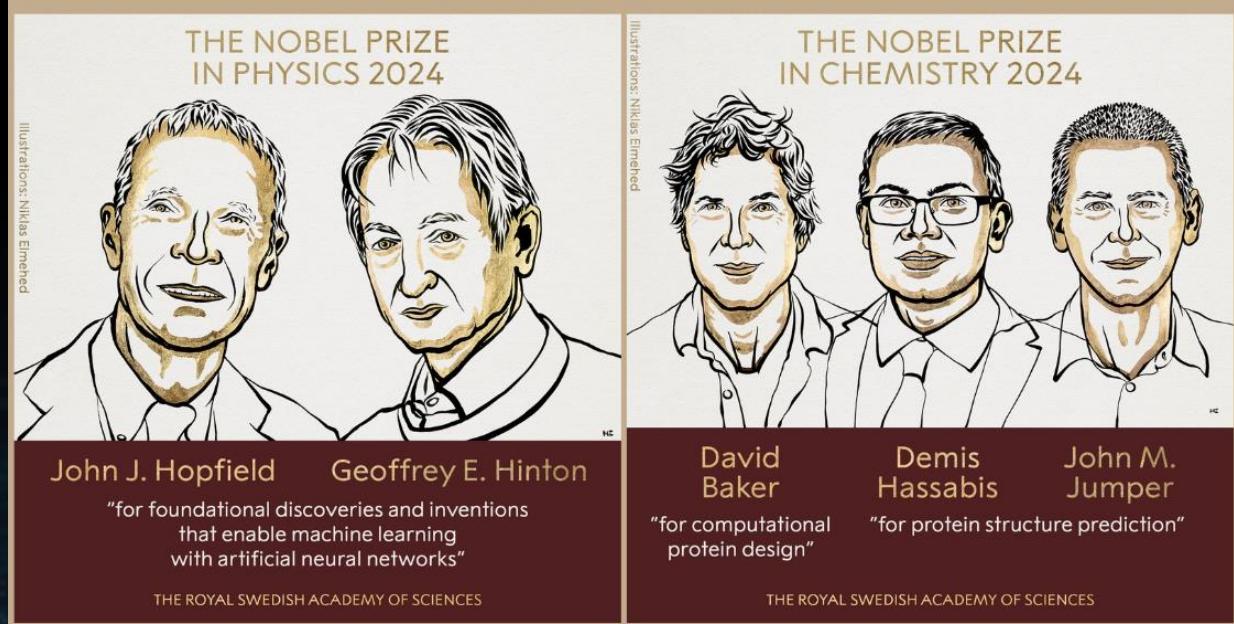
Objects are everywhere



Disease Detection in Healthcare and Medicine



— OODA/ Deep Learning Explosion —



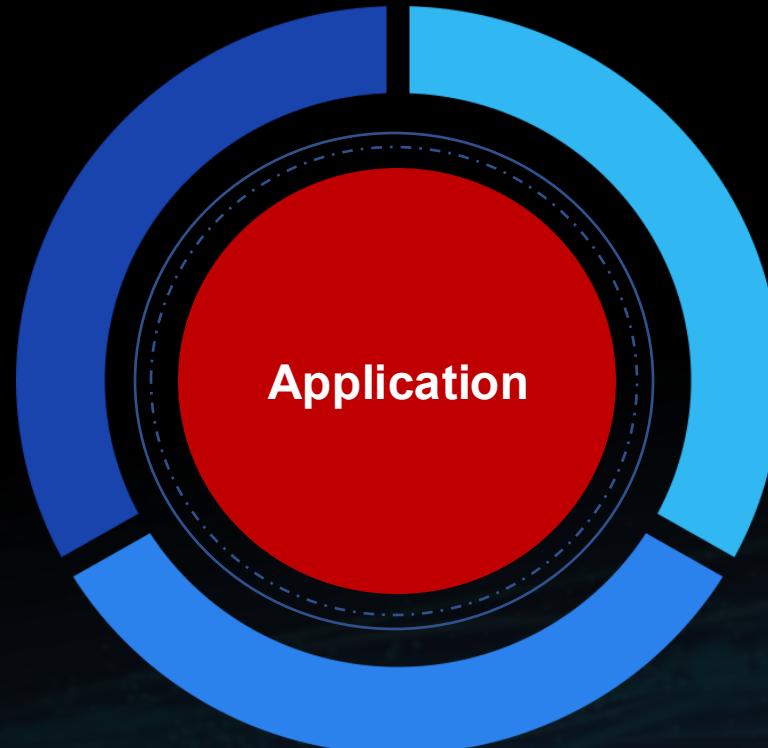
Downloaded from the NSF website and the medium.com

→ Deep Applications and Math/Stat ←



Big Data

<http://medium.com>



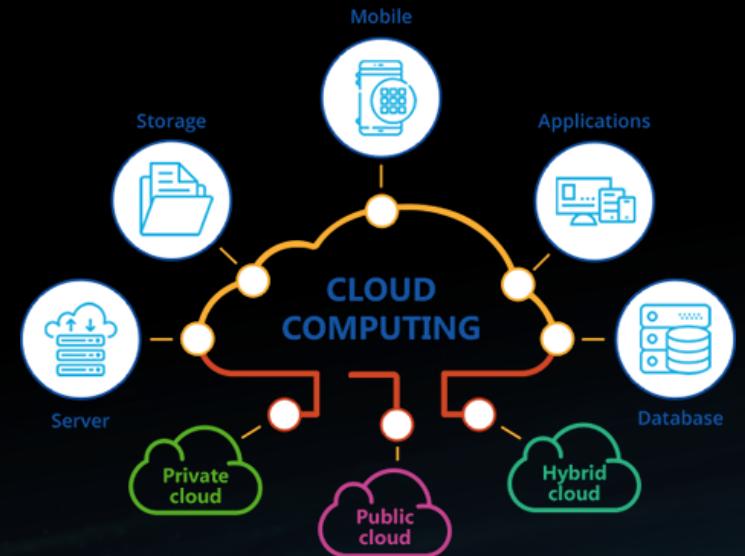
Analytical Tools

Applied
Mathematics

Statistics

Machine
Learning

Engineering



Computing



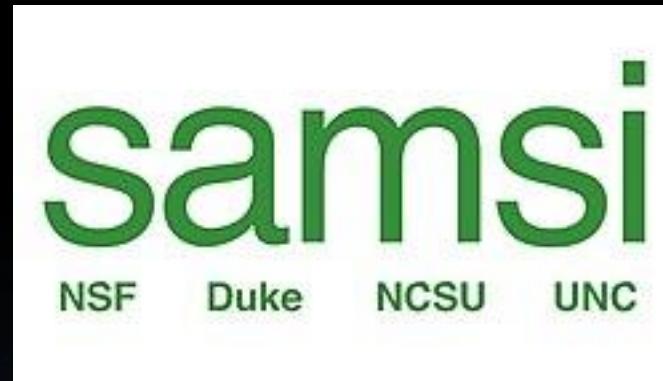
Part II

Case Studies for OODA

"If our goal as a field is to use data to solve problems, then we need to move away from exclusive dependence on data models and adopt a more diverse set of tools."

- Leo Breiman -

Steve Marron's Contributions to SAMSI and My research



Statistical and Applied Mathematical Sciences Institute (SAMSI)

SAMSI summer workshop on Neuroimaging Data Analysis (NDA) 2013

Program Leader for SAMSI full-year program on Challenges in Computational Neuroscience (CCNS) with five workshops, one short course, and two regular courses 2015-2016

Steve Marron's Contributions to SAMSI and My research

My three SAMSI postdoctoral fellows



Zhengwu Zhang (UNC)



Yize Zhao (Yale)



Benjamin Risk (Emory)



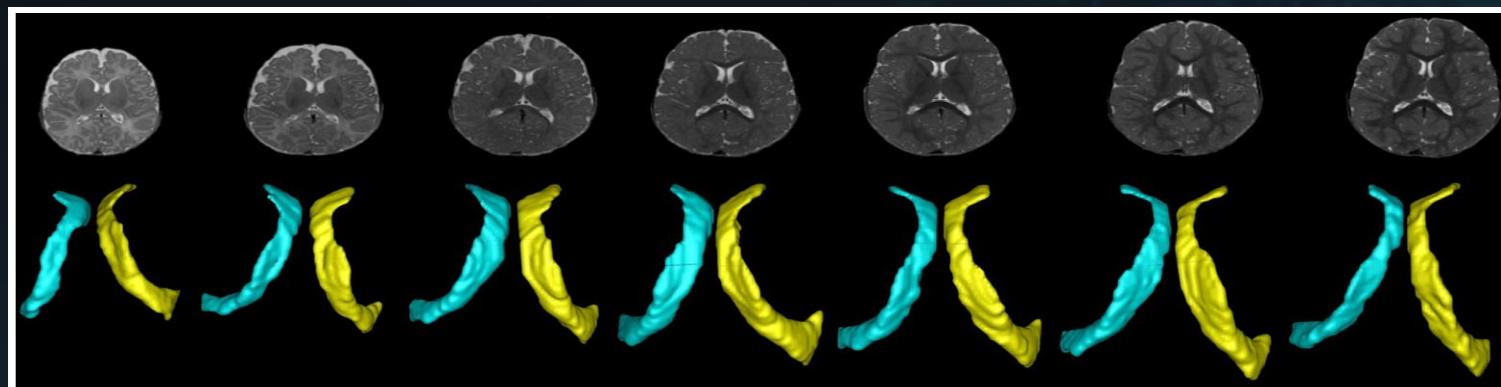
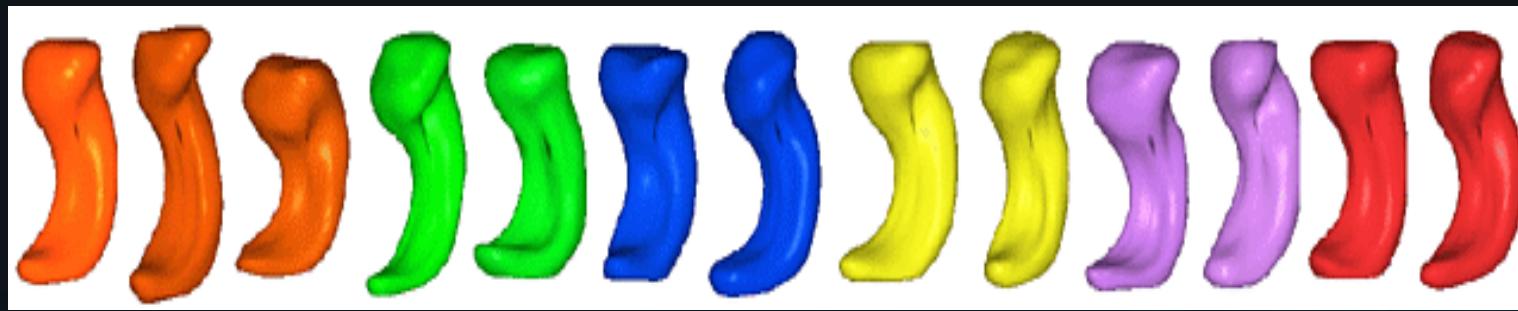
Case Study I

Regression Models for Manifold-value Data

1. Cornea, E., Zhu, H.T., Kim, P. and Ibrahim, J. G. Intrinsic regression model for data in Riemannian symmetric space. *JRSS, Series B*, 79, 463-482, 2017.
2. Shi, XY, Zhu, HT, Ibrahim, J.G., F. Liang, Styner M. Intrinsic regression models for median representation of subcortical structures. *Journal of American Statistical Association*, 107, 12-23, 2012.
3. Yuan, Y., Zhu, H.T., Lin, W. L., and Marron, J. S. Local polynomial regression for symmetric positive definitive matrices. *JRSS, Series B*, 74, 697-719, 2012.

Intrinsic Regression Models

Semiparametric and Nonparametric Regression for
Manifold-valued Response from Cross-sectional,
Longitudinal and Family-based Neuroimaging Studies



$$= g(x, \theta, f) \oplus \varepsilon$$

$$x \in R^k, \theta \in \Theta \subset R^p, f \in F$$

$$g : R^k \times R^p \times F \rightarrow M$$

Intrinsic Regression Models

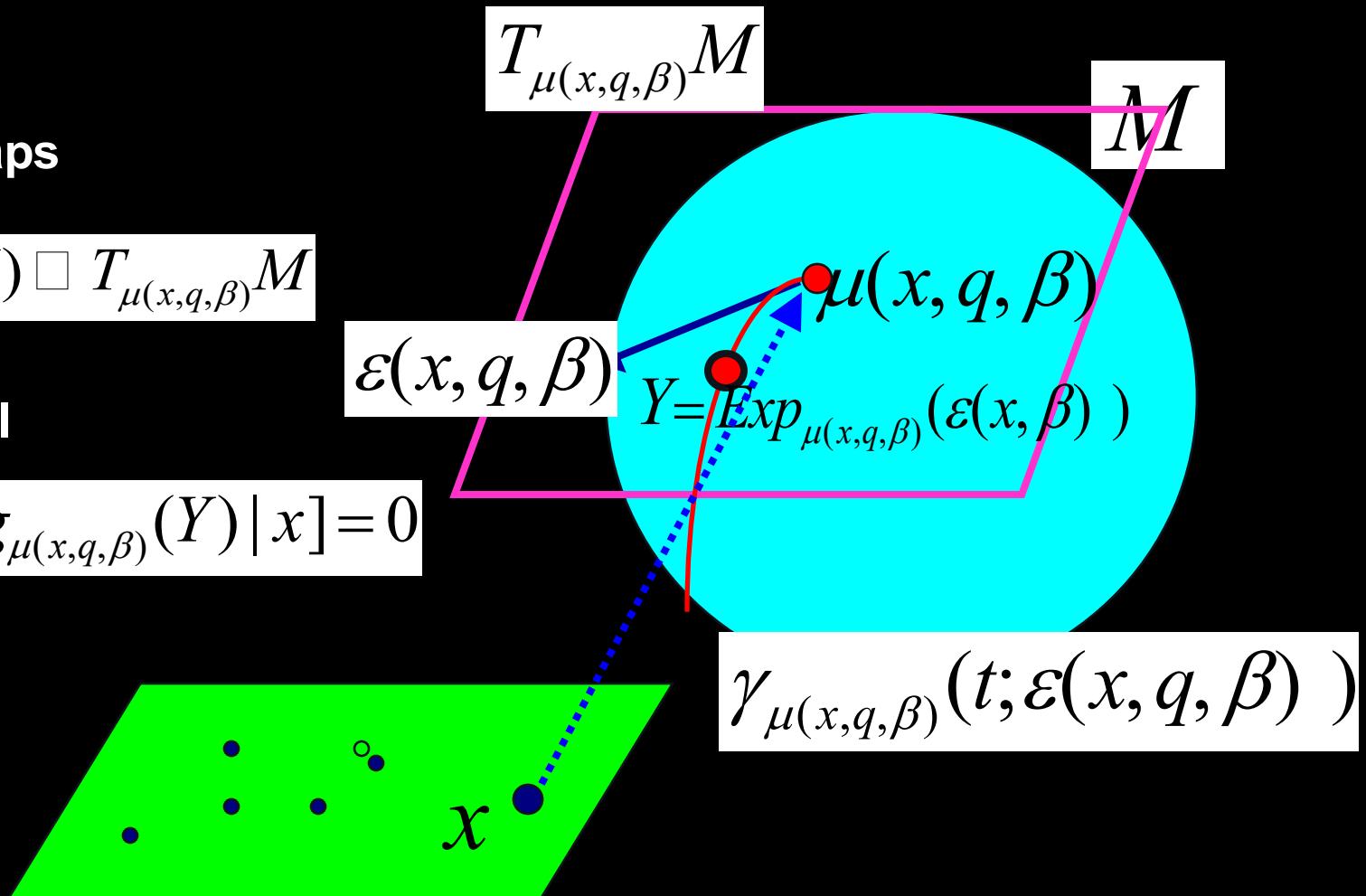
Conditional Mean

Riemannian logarithm maps

$$\mathcal{E}(x, q, \beta) = \text{Log}_{\mu(x, q, \beta)}(Y) \square T_{\mu(x, q, \beta)}M$$

Conditional Moment Model

$$E[\varepsilon(x, q, \beta) | x] = E[Log_{\mu(x, q, \beta)}(Y) | x] = 0$$



Intrinsic Regression Models

Rotated Residuals at the common tangent space

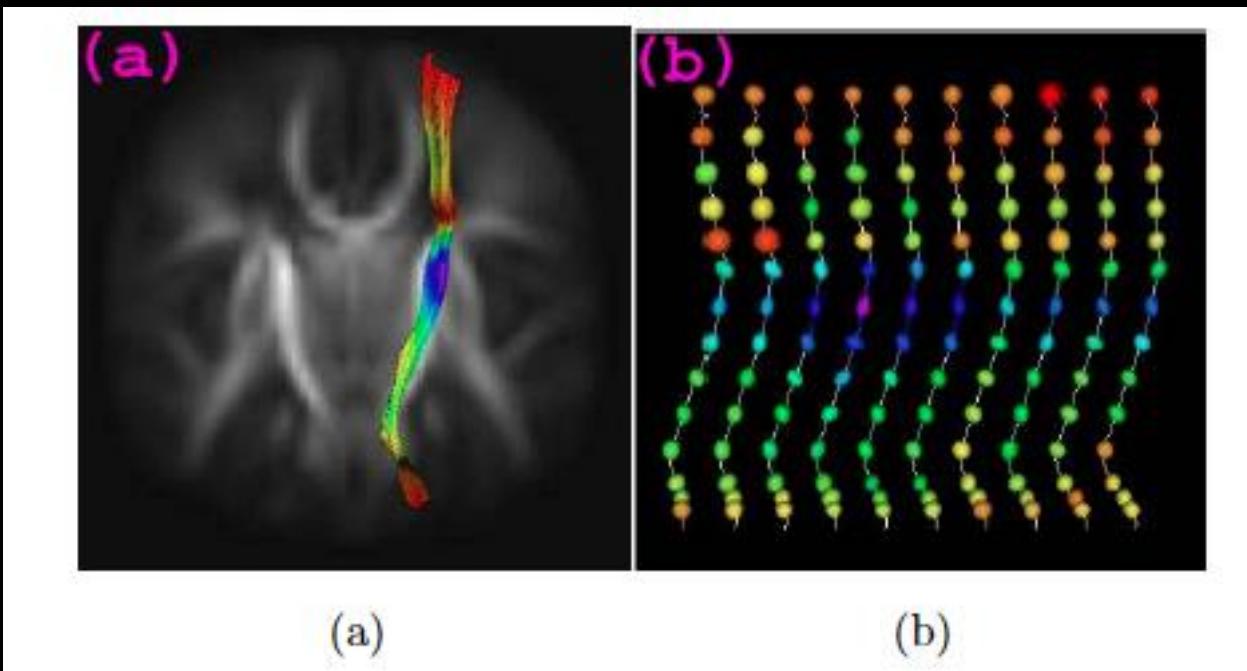
$$\mathcal{E}(y_i, \mathbf{x}_i; \mathbf{q}, \boldsymbol{\beta}) = \mathcal{E}_i(\mathbf{q}, \boldsymbol{\beta}) := \text{Log}_{\mathbf{p}} \left(c(1; \mathbf{x}_i, \mathbf{q}, \boldsymbol{\beta})^{-1} \cdot y_i \right) \in T_{\mathbf{p}} M \quad \text{for } i = 1, \dots, n,$$

Geodesic: $\gamma(t; q, \boldsymbol{\beta}) = c(t; q, \boldsymbol{\beta}) \square p$

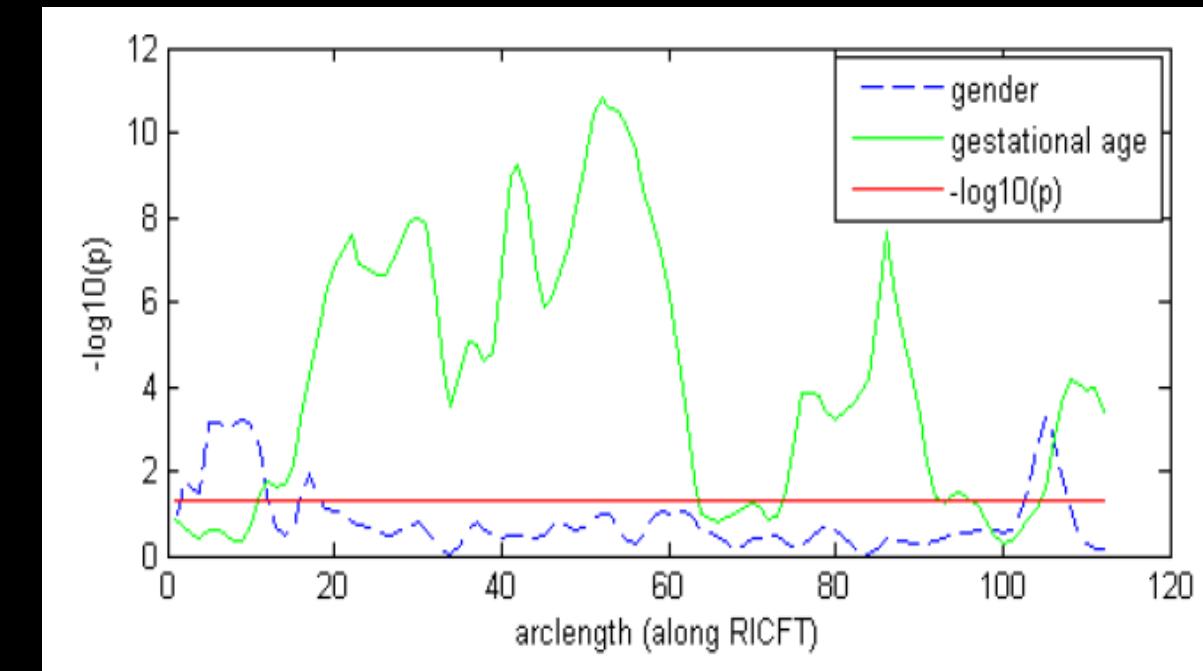
connecting base point: $p \square M$ and $\mu(x; q, \boldsymbol{\beta})$

$$\begin{aligned} L_{c(1; \mathbf{x}_i, \mathbf{q}, \boldsymbol{\beta})^{-1}}^{-1} (\text{Log}_{\mu(\mathbf{x}_i, \mathbf{q}, \boldsymbol{\beta})} (y_i)) &= L_{c(1; \mathbf{x}_i, \mathbf{q}, \boldsymbol{\beta})^{-1}}^{-1} (\text{Log}_{\mu(\mathbf{x}_i, \mathbf{q}, \boldsymbol{\beta})} (y_i)) \\ &= \text{Log}_{\mathbf{p}} (L_{c(1; \mathbf{x}_i, \mathbf{q}, \boldsymbol{\beta})^{-1}} (y_i)) = \text{Log}_{\mathbf{p}} (c(1; \mathbf{x}_i, \mathbf{q}, \boldsymbol{\beta})^{-1} \cdot y_i) \in T_{\mathbf{p}} M. \end{aligned}$$

Real Data Analysis



Right internal capsule



$$48 = 18(m) + 30(f)$$



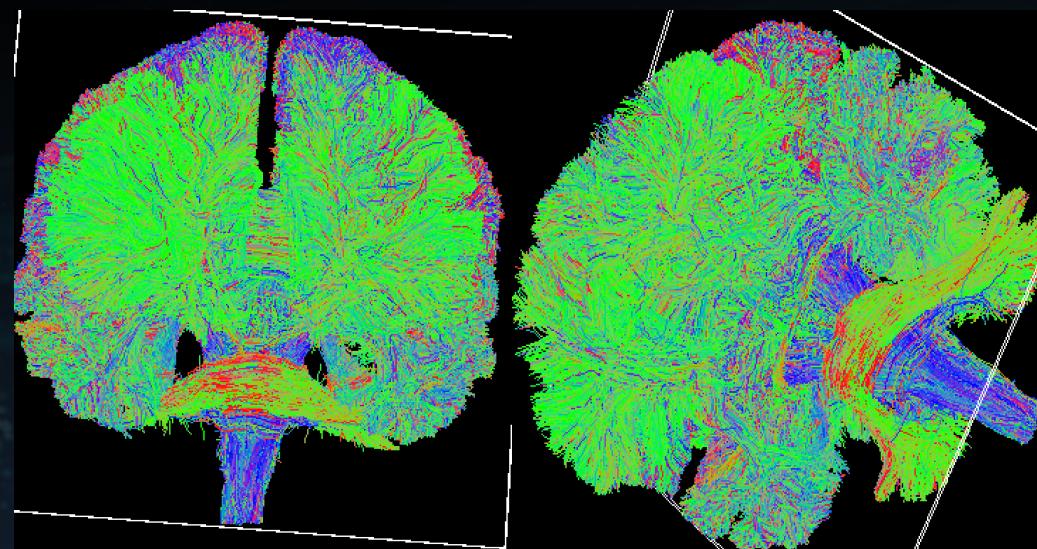
Case Study II

PSC: Population Structural Connectome Analysis

1. **Z. Zhang**, M. Descoteaux, J. **Zhang**, G. Girard, M. Chamberland, D. Dunson, A. Srivastava, and **H. Zhu**. (2018). Mapping Population based Structural Connectomes. *NeuroImage*, 172, 130-145.
2. Wang, X. F. (2021). *Statistical Learning Methods for Diffusion Magnetic Resonance Imaging*. *Ph.D. Dissertation*.

Brain Imaging Genetics Paradigm

- Extract the connectome using dMRI and T1 image
- Use tractography algorithm proposed in *Girard et al. 2015*
 - Step1. Construct HARDI
 - Step 2. Fiber tracking (incorporate anatomical info):
 - Step 3. Final output:
 - . More than a million streamlines
 - . Each streamline has hundreds 3D points
 - 3. Each subject takes > 3 GBs



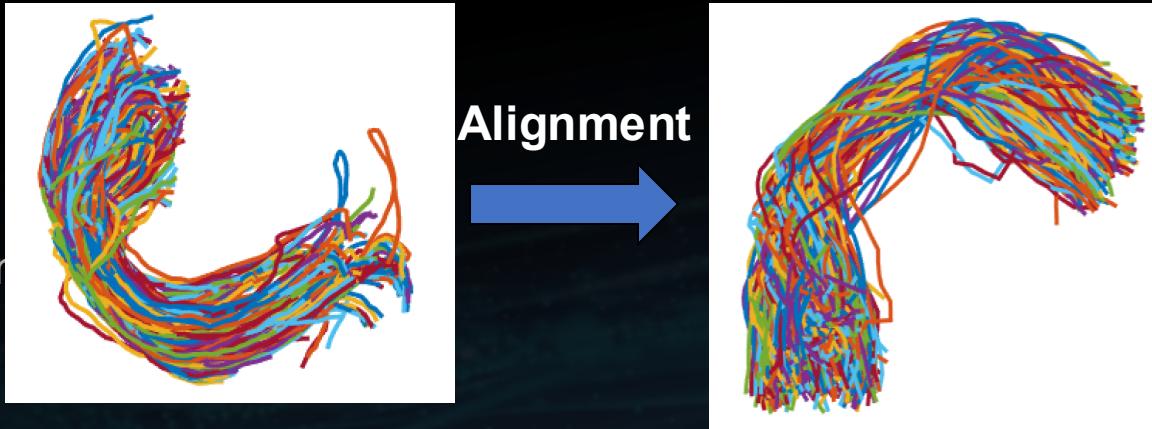
Efficient Representation of Streamlines

- Represent the streamlines through basis and coefficients
- Basis can be learnt from data to increase its representing power

Step 1. Generate atlas for streamlines connecting each pair of regions

Step 2. Alignment using the **Elastic Shapes Analysis** framework (Srivastava et al. 2012)

- rotation
- translation
- scaling
- re-parameterization

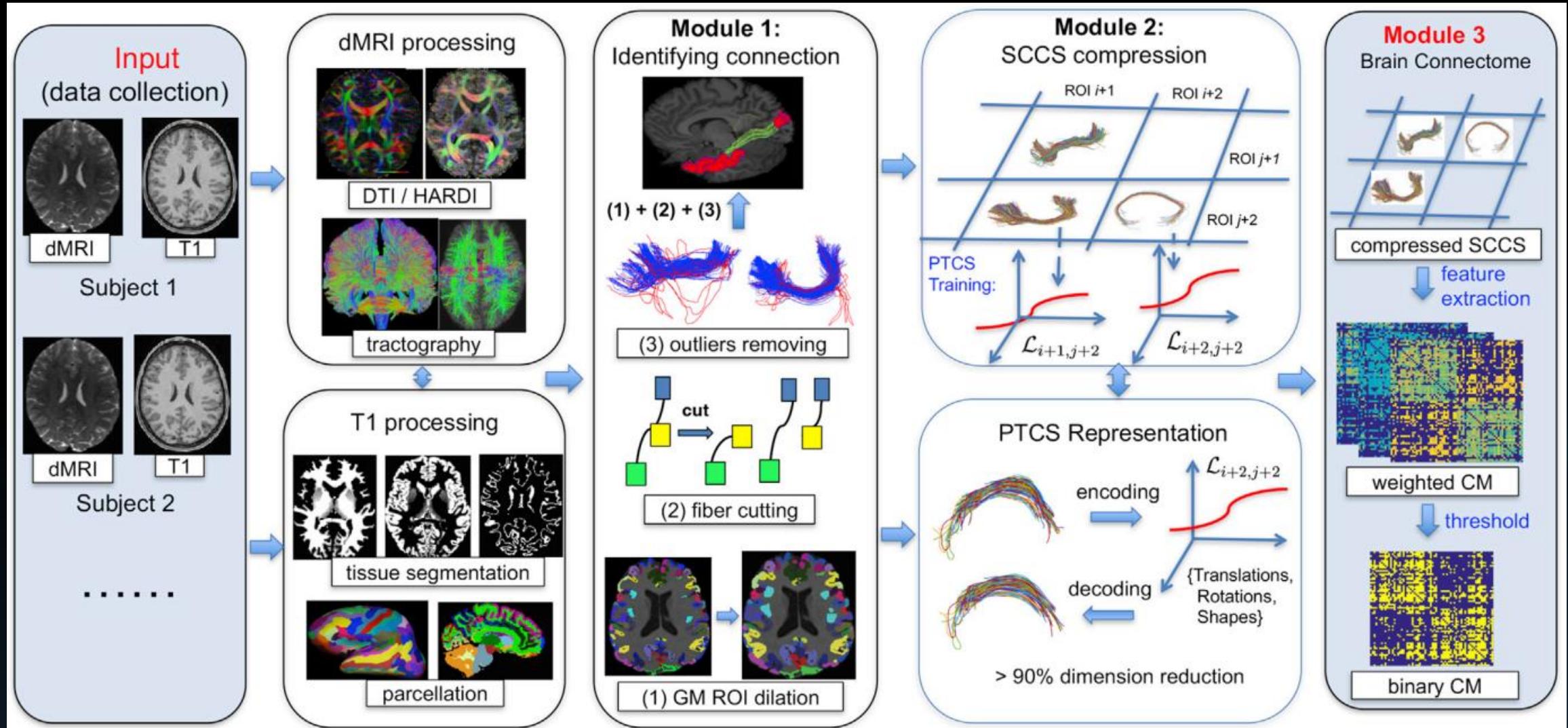


*K-means clustering may be used if these streamlines have different shapes

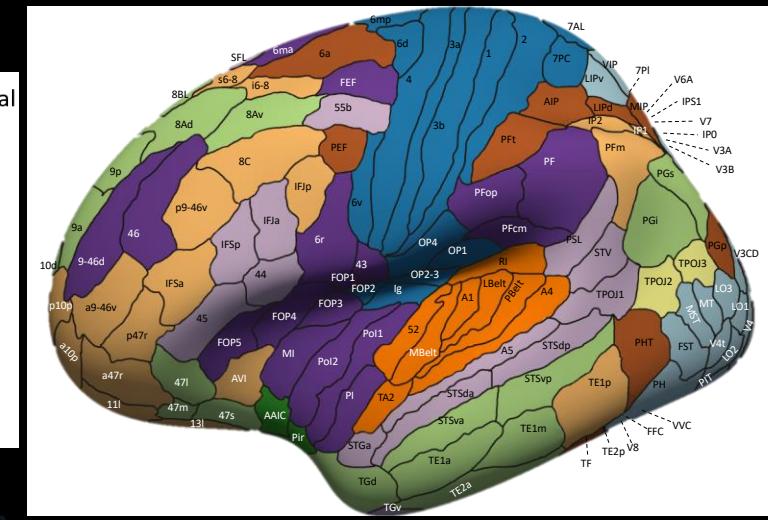
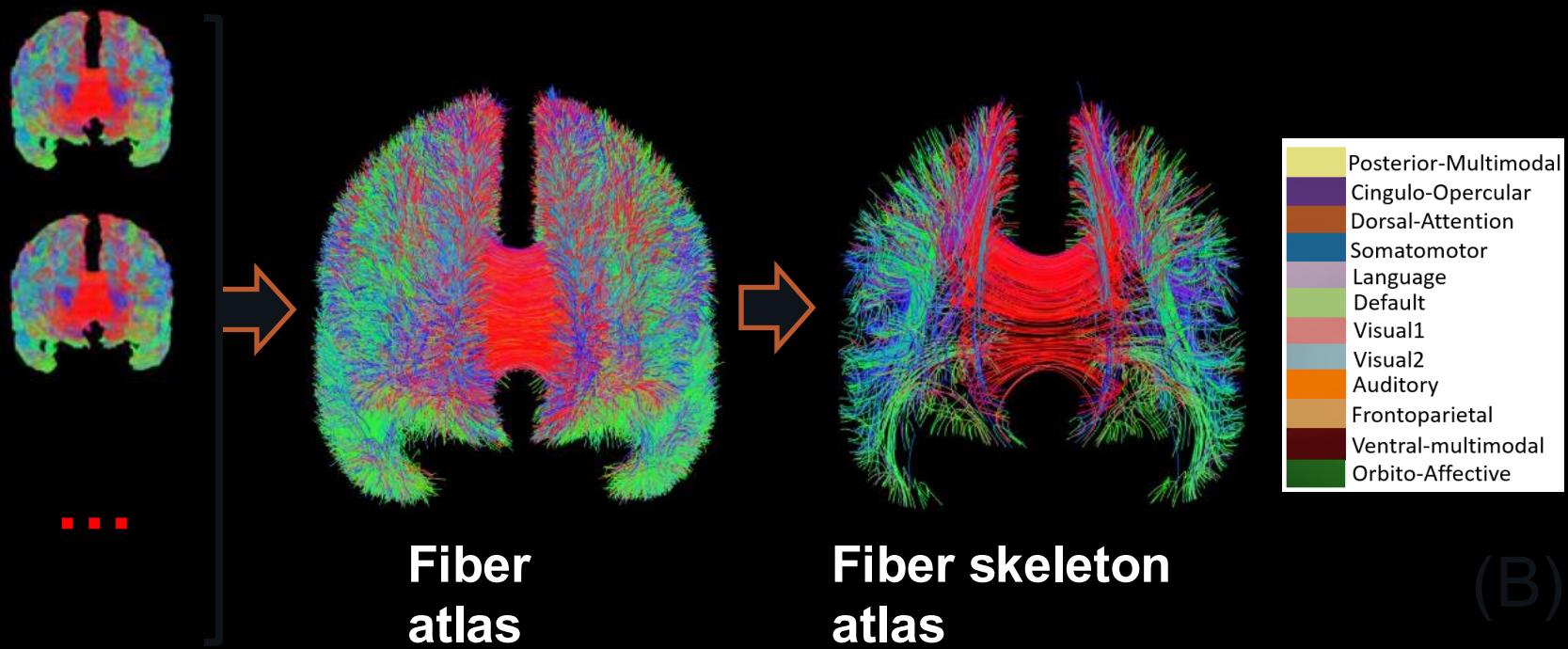
Square-root velocity function (SRVF) and Fisher-Rao metric

Srivastava, A. and Klassen, E. P. (2017) Functional and Shape Data Analysis.
Springer.

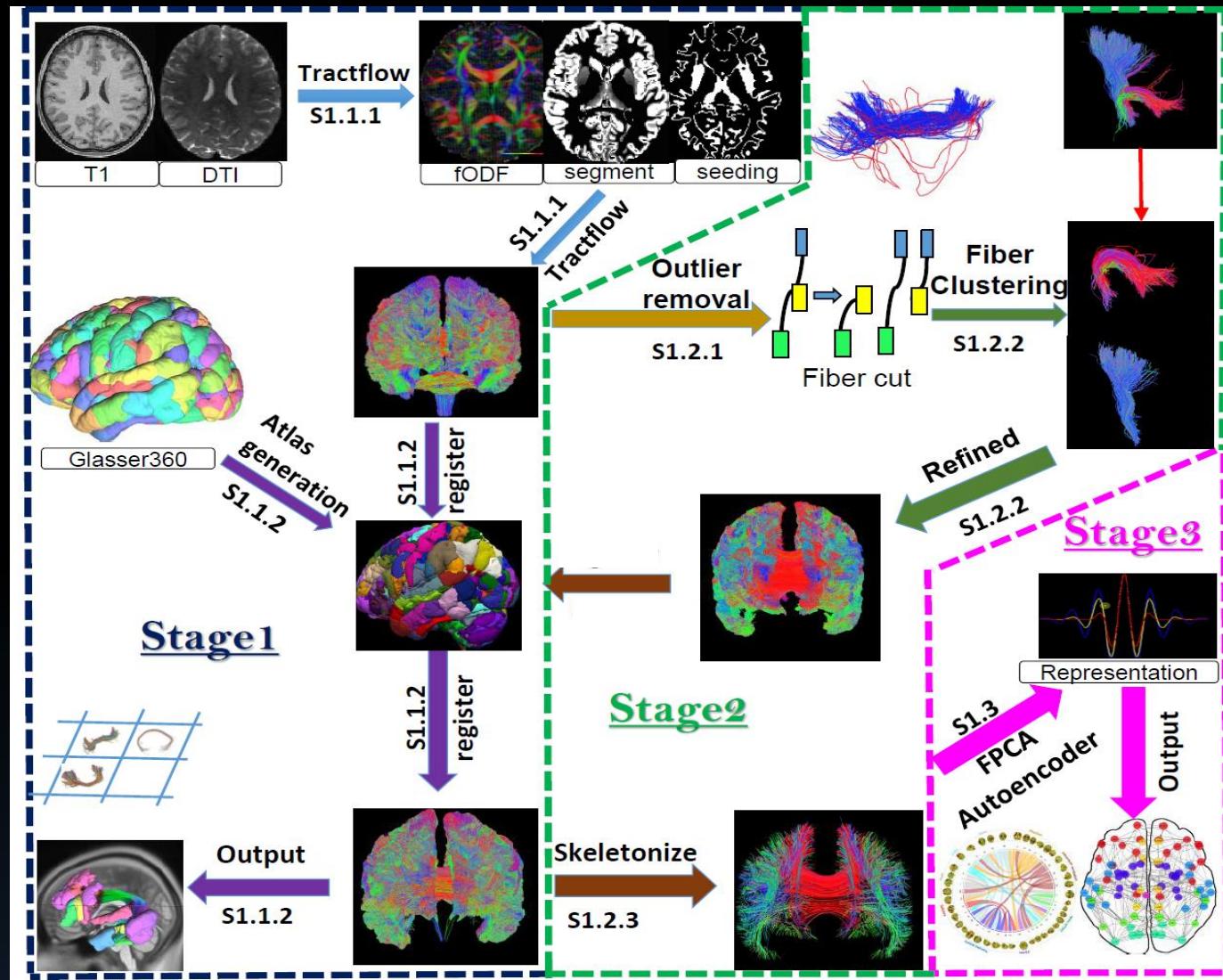
Population Structural Connectome



Brain Function-based Structural Connectome Atlas



Brain Function-based Structural Connectome Atlas



2.

Stage 1:

Whole-brain Structural Connectome

3.

Stage 2:

Creation of Fiber Skeleton

4.

Stage 3:

Sparse Representation



Case Study III

LESA: Longitudinal Elastic Shape Analysis

Zhang, Z. W., Yuexuan Wu, Di Xiong, Joseph G. Ibrahim, Anuj Srivastava, and Hongtu Zhu. LESA: Longitudinal elastic shape analysis of brain subcortical structures (with discussion). *Journal of the American Statistical Association, Application and Case Studies*.

Shape Changes of Brain Subcortical Structures

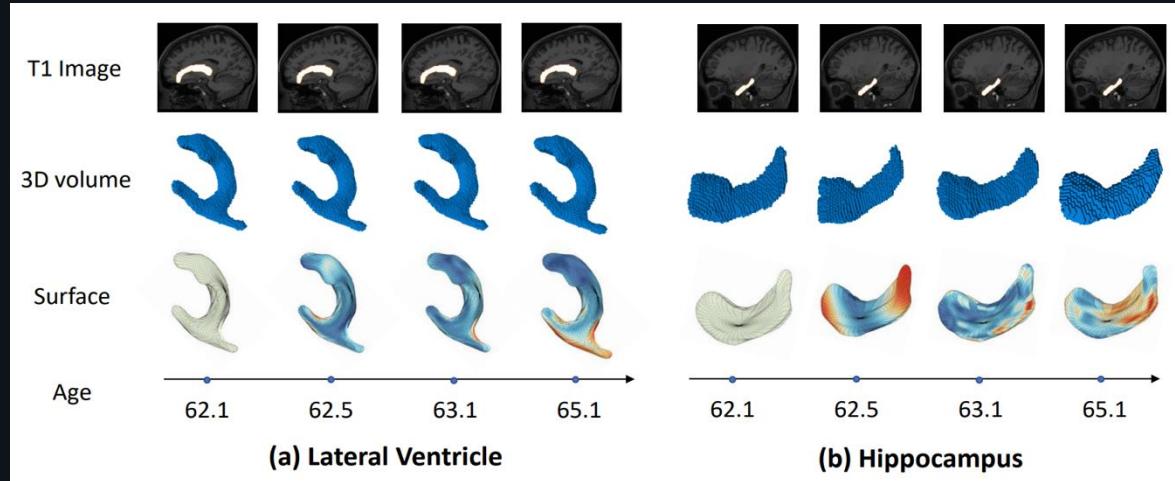


Figure 1: An example of three different representations of lateral ventricle and hippocampus across four time points for a randomly selected subject.

(Q1) How to measure developmental changes in the shape of subcortical regions?

(Q2) How to quantify the effect of disease or other covariates on subcortical shape changes?

Longitudinal Elastic Shape Analysis

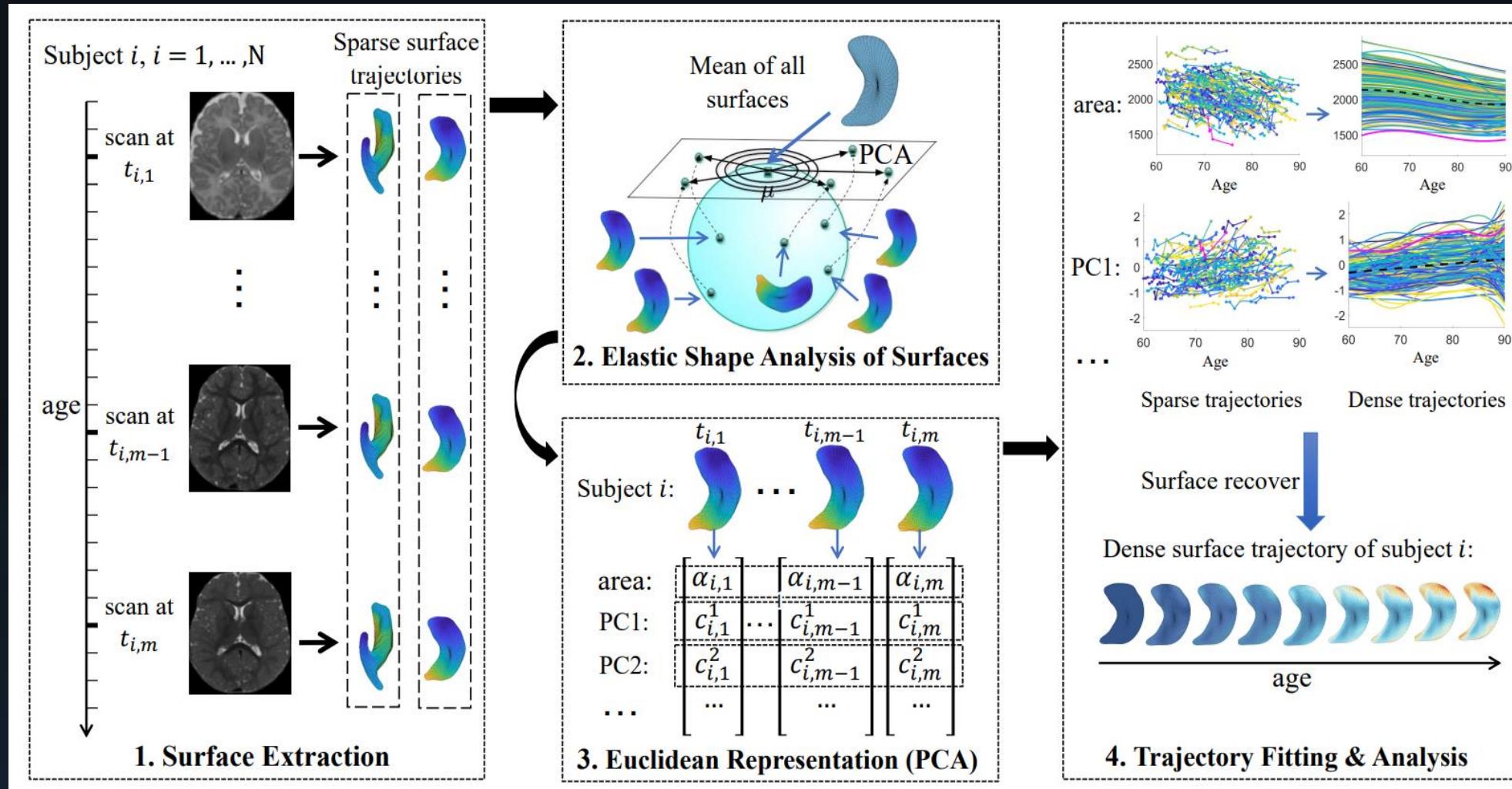
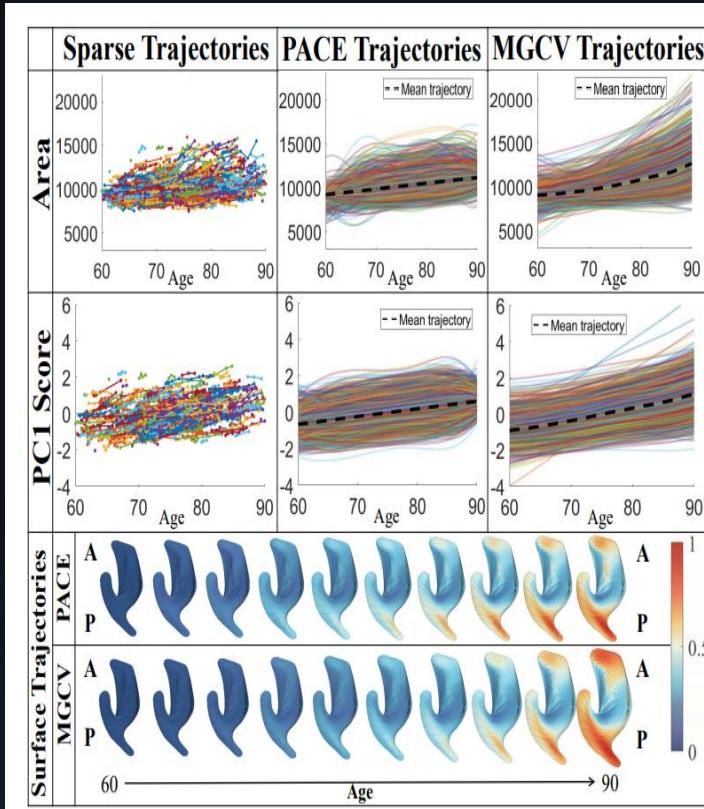
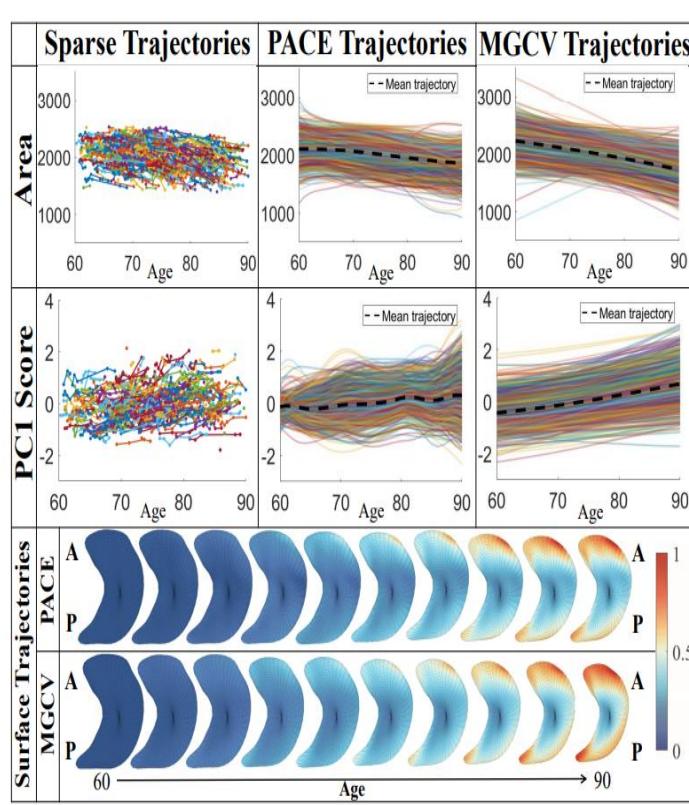


Figure 2: A schematic overview of LESA.

Longitudinal Shape Data Analysis



(i) Left ventricle



(ii) Left hippocampus



Figure 4: Trajectory fitting results of LESA from the observed sparse data in ADNIGO2

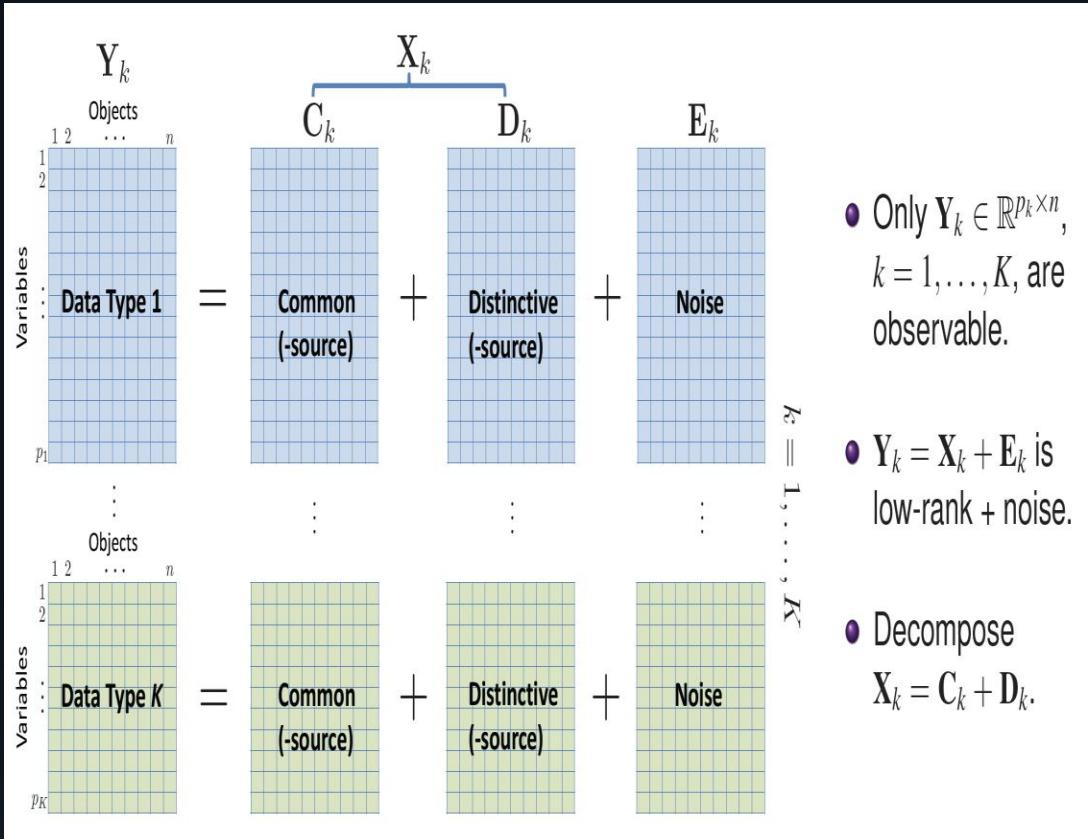


Case Study IV

Data Integration via D-CCA

1. H. Shu, & H. Zhu (2025). D-CDLF: Decomposition of Common and Distinctive Latent Factors for Multi-view High-dimensional Data. Draft note available on arXiv:2407.00730v2
2. H. Shu, & H. Zhu (2025). Comments on: Data integration via analysis of subspaces (DIVAS), Test.
3. H. Shu, Z. Qu, & H. Zhu (2022). D-GCCA: Decomposition-based generalized canonical correlation analysis for multi-view high-dimensional data. *Journal of Machine Learning Research*. 23(169):1–64.
4. H. Shu, X. Wang, & H. Zhu (2020). D-CCA: A decomposition-based canonical correlation analysis for high-dimensional datasets. *Journal of the American Statistical Association*, 115(529): 292-306.

Low-rank Plus Noise Models



"Low-rank plus noise" model:

$$Y_k = X_k + E_k = C_k + D_k + E_k, \quad k = 1, \dots, K$$

All common-source matrices

$\{C_k\}_{k=1}^K$: from the **common latent factors** of the K data views.

k -th distinctive-source matrix

D_k : from the **distinctive latent factors** of the k -th data view.

Steve's Contributions

Assume the columns of $\mathbf{Y}_k = \mathbf{X}_k + \mathbf{E}_k = \mathbf{C}_k + \mathbf{D}_k + \mathbf{E}_k \in \mathbb{R}^{p_k \times n}$
are n i.i.d. samples of mean-zero $\mathbf{y}_k = \mathbf{x}_k + \mathbf{e}_k = \mathbf{c}_k + \mathbf{d}_k + \mathbf{e}_k \in \mathbb{R}^{p_k}$.

Existing methods: different in defining the common & distinctive latent factors.

JIVE

Lock et al. (2013)

R.JIVE

O'Connell & Lock (2016)

AJIVE

Feng et al. (2018)

OnPLS

Löfstedt & Trygg (2011)

DISCO-SCA

Schouteden et al. (2014)

COBE

Zhou et al. (2016)

SLIDE

Gaynanova & Li (2019)

D-GCCA

Shu et al. (2022)

DIVAS

Prothero et al. (2024)

Drawback

Assume the columns of $\mathbf{Y}_k = \mathbf{X}_k + \mathbf{E}_k = \mathbf{C}_k + \mathbf{D}_k + \mathbf{E}_k \in \mathbb{R}^{p_k \times n}$
are n i.i.d. samples of mean-zero $\mathbf{y}_k = \mathbf{x}_k + \mathbf{e}_k = \mathbf{c}_k + \mathbf{d}_k + \mathbf{e}_k \in \mathbb{R}^{p_k}$.

In the (L^2, E) space of **mean-zero** real-valued random variables, $x \perp y \Leftrightarrow \text{cov}(x, y) = 0$

Drawback: Fail to well consider the **orthogonality** (i.e., **uncorrelatedness**) among the common latent factors (CLFs) and distinctive latent factors (DLFs).

- Some only consider the **orthogonality between CLFs and DLFs** (OnPLS, DISCO-SCA, COBE, JIVE, AJIVE, DIVAS).
- Some only consider the **orthogonality btwn DLFs from different data views** (D-GCCA).
- Some consider both the two types of orthogonality, but either sacrifice unexplained signal as noise (R.JIVE) or offer an asymmetrical decomp. for identically distributed signals (SLIDE).

Acknowledgement



UNC

GILLINGS SCHOOL OF
GLOBAL PUBLIC HEALTH

Brain Imaging Genetics Knowledge Portal (BIG-KP)

Genetics Discoveries in Human Brain by Big Data Integration

bigkp.org

Funding: U.S. NIH Grants R01AG082938, 1R01AG085581, 1R01MH136055, and R01AR082684.

Pictures: Copyrights belong to their own authors and/or holders.

Data: We thank Bingxin Zhao, Tengfei Li and other members of the **UNC BIG-S2 lab** (<https://med.unc.edu/bigs2/>) for processing the neuroimaging data.

UK Biobank resource application number: 22783.