

S. C. Big Data Health Sciences Conference

Object Oriented Data Analysis

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From My Elementary Courses:

- Gaining Insight from Numbers Similar to "Data Science" Definitions
- The Science of Managing Uncertainty Where Probability Modeling Is Vital
- This is Why Statistics is Fundamental



More Currently Popular Terminology

Big Data

- Isn't It Just Statistics?
- Yes, But More Needed Too
- Optimization: Machine Learning
- Maybe <u>Bigger</u> Challenge:

Complex Data



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Well Understood Concept:

Great science now done by <u>teams</u> with complementary skill sets

- Biology
- Chemistry
- Engineering
- Quantitative Work

Common Current Idea: 1 Team member



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Extension of this:

- Great *Quantitative Work* needs teams with complementary skill sets
- Statistics
- Imaging
- Optimization
- Data Base







Proposed New Approach:

Team Data Science



- Education of Team Members:
 - Bring Valued (Deep) Skill
 - Know Enough to Communicate
 - Give Opportunities to Practice



What is the "atom" of a statistical analysis?

- 1st Course: Numbers
- Multivariate Analysis Course : Vectors
- Functional Data Analysis: Curves
- More generally: Data Objects



Object Oriented Data Analysis

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Original Thought: OODA = Mathematical Framework

(containing wide variety of interesting cases)



Object Oriented Data Analysis

Original Thought: OODA = Mathematical Framework

Current View: OODA = Focal Point

{For discussions (interdisciplinary)
about tackling serious analyses}



Object Oriented Data Analysis

Original Thought: OODA = Mathematical Framework

Current View: OODA = Focal Point

What should be the Data Objects?



Principal Component Analysis

More Than *Dimensionality Reduction*:

- <u>Visualization</u>
 - Relationships Between Objects (Scores)



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Interesting Real Data Example

- Genetics (Cancer Research)
- RNAseq (Next Gener'n Sequen'g)
- Deep look at "gene components"

Microarrays:Single number (per gene)RNAseq:Thousands of measurements



Interesting Real Data Example

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Interesting Real Data Example

- Genetics (Cancer Research)
- RNAseq (Next Gener'n Sequen'g)
- Deep look at "gene components"
- Gene studied here: CDKN2A
- Goal: Study Alternate Splicing
- Sample Size, n = 180
- Dimension, $d = \sim 1700$

















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Chromosome 9 Gene = CDK2A, log_{1n} Transformed, Brushed by PCA





Consequences of this Visualization:

- Lead to Full Genome Screening Method
 SigFuge
- Important Component: <u>SigClust</u> (Which Clusters are *Really There*?)
- Found New Splices
 (Now Been Biologically Verified)



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Personal Motivating Contexts

Interdisciplinary Areas:

- Cancer Genetics
- Medical Image Analysis
- Evolutionary Biology
- Drug Discovery



Data Object Types:

- Curves (Functional Data Analysis)
- Spectra (Non-Negative!)
- Images
- Shapes
- Trees
- Movies (Functional MRI)


Curves as Data Objects (FDA)

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Generally Euclidean: Use standard methods







Images as Data Objects

Challenge: High Dimension, Low Sample Size









Shapes as Data Objects

Challenge: Data Lie in (Curved) Manifold







Figure 2.2: The Riemannian exponential map.



Challenge: Data Lie in (Curved) Manifold {Tackle With Differential Geometry}

Important General Development: Backwards PCA



Challenge: More Complicated Data Space Manifold Stratified Space







Challenge: More Complicated Data Space Manifold Stratified Space

Surprisingly (?!?) Useful Approach:

Topological Data Analysis Persistent Homology



Advertisement

Short Course on OODA & TDA

International Biometrics Conference Seoul July 2020



Moo K. Chung, U. Wisc.



Yuan Wang, U. S. C.



Carolina Breast Cancer Study

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The Carolina Breast Cancer Study

Phase III: The Jeanne Hopkins Lucas Study



Thanks to: **Lain Carmichael** (Deep Learning, AJIVE) Melissa Troester (Head, CBCS) Joseph Geradts, Benjamin Calhoun (Pathology) Katie Hoadley, Chuck Perou (Genomics)





Clinical Diagnosis of Cancer:

Pathologist Views Tissue Under Microscope,

Tissue Stained with Hematoxylin & Eosin (H&E)



Thanks to BBC.CO.UK

and Reseachgate.net











Joint & Individual Variation Explained

(Angle Based)



JIVE Collaborators

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Eric Lock

Qing Feng





Andrew Nobel

Jan Hannig





JIVE Data Structure

JIVE Organizational Model: Multiple Matrices

(Data Types, i.e. "Blocks")

With <u>common</u> Columns as Data Objects









JIVE Analytic Goals

Explore & Quantify Variation

In spirit of PCA (Principal Component Analysis)





Tissue Micro Array Data:

Extract Small

(1mm diam.)

"Cores"

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Carolina Breast Cancer Study

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Experimental Design: n = 1191 people

For Each: 1 - 4 TMA Cores



PAM 50 Gene Expression:





Carolina Breast Cancer Study

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PAM 50 Gene Expression:

Set of 50 Genes

Early Technology, More Recent RNAseq → 10,000s Genes

- Measured mRNA Expression Level
- Good at Separating SubTypes
 - Basal
 - Her2
 - Luminal A
 - Luminal B



Perou Discovery: No Benefit From Chemo-Therapy



500

1000

1500

2000 2500

500

1000

2000

2000

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Deep Learning Image Representation

Each Core:

Randomly

Select 100

 224×224

Patches





Deep Learning Image Representation

Reduce Each Patch to 512 Features

Using Transfer Learning From VGG16:

(Trained on Many

Natural Images)



Thanks to pyimagesearch.com



Deep Learning Image Representation

For Each Core:

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Aggregate Patches by Averaging (Damps Out "Location" Information)

Then Average Cores For Each Person



UNC, Stat & OR JIVE: Common Nor

Look at Extremes

Negative End

Top Person

Top 16 Patches

Fat Cells & Stroma



















1500

33363, group





JIVE: Common Nor

Look at Extremes

Positive End

Top Person

Top 16 Patches Highly "Cellular" Markedly Atypical Cell





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JIVE: Common Nor

Look at Extremes

Negative, Top

Top 16 Patches

High Nuclear Grade

Atypical Cells







Positive, Top

Top 16 Patches

Lower Nuclear Grade

Stroma, Sclerosis







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JIVE, Genes, Individua

Overall Up & Down

Together

Not Subtype Related!









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JIVE, Images, Indiv

Negative

Mostly Fat Cells

Few Nuclei





UNC, Stat & OR

JIVE, Images, Indiv

Positive

Reactive Stroma,

Few Nuclei

Little Gene Connected





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JIVE, Images, Indiv

Negative

Mucinous & Micro-

Papillary Carcinoma

Not PAM50 Related







1816 -

1922

1345

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JIVE, Images, Indiv

Positive

Fat Cells

Common Endpoint?

"Center"?



Data Integration Via Subspace Analysis (DIVAS)



DIVAS / JIVE Collaborators

Jan Hannig

Meilei Jiang

Xi Yang



Iain Carmichael

Jack Prothero







DIVAS Improves JIVE

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1. Partially Shared Blocks



DIVAS Improves JIVE

UNC, Stat & OR

1. Partially Shared Blocks JIVE




DIVAS Improves JIVE

UNC, Stat & OR

1. Partially Shared Blocks DIVAS





DIVAS Motivation

The Cancer Genome Atlas

Multiple Blocks

People <u>Common</u> Across Blocks



Figure : The Cancer Genome Atlas Research Network, Weinstein, J.N., Collisson, E.A., Mills, G.B., Shaw, K.M., Ozenberger, B.A., Ellrott, K., Shmulevich, I., Sander, C., and Stuart, J.M. (2013)



DIVAS on TCGA Data

Breast Cancer

- Gene Expression (GE) [16615 x 616]
- Copy Number (CN) [24174 x 616]
- Protein Exp. (RPPA) [187 x 616]
- Mutation Status (MU) [18256 x 616]







OODA is more than a "framework"

It Provides a Focal Point

Highlights Pivotal Choices:

What should be the Data Objects?

How should they be Represented?