

#### **Blessing of Dimensionality – U. Conn.**

# High Dimension Low Sample Size Asymptotics

J. S. Marron
School of Data Science and Society
Dept. of Statistics and Operations Research,
University of North Carolina
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## High Dimension Low Sample Size





Terminology Coined in
Hall, Marron & Neeman (2005)



## 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,  $d \sim 1700$



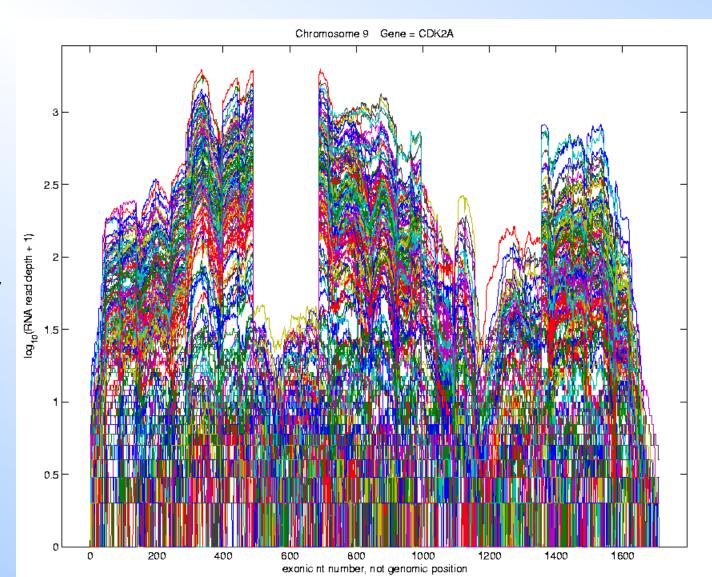
Simple 1st

View:

Curve Overlay

(log scale)

Thanks to Matt Wilkerson





0.015 Scores PC1 Scores Often PC-P.C. 0.005 -50-50-5050 10 20 -10 10 20 30 -1010 20 Useful PC1 Scores PC3 Scores PC4 Scores PC2 Scores Population of the Population o 0.08 Scores Scores 0.06 0.04 0.02 -100 50 -10 10 20 -1010 20 30 10 20 PC1 Scores PC2 Scores PC4 Scores PC3 Scores 30 0.1 PC3 Scores PC3 Scores PC3 Scores 20 20 20 0.05 PCA 10 -50 50 -1010 20 -10 0 20 30 -100 10 20 PC1 Scores PC2 Scores PC3 Scores PC4 Scores Scores PC4 Scores PC4 Scores PC4 Scores 0.1 0.05

10

PC2 Scores

20

-10

10 20

PC3 Scores

-10

0

PC4 Scores

10

20

-50

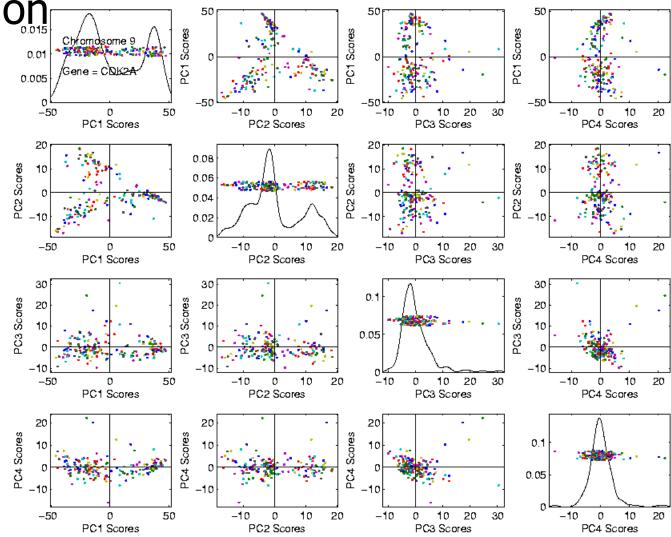
50

PC1 Scores



Suggestion

Of Clusters ???

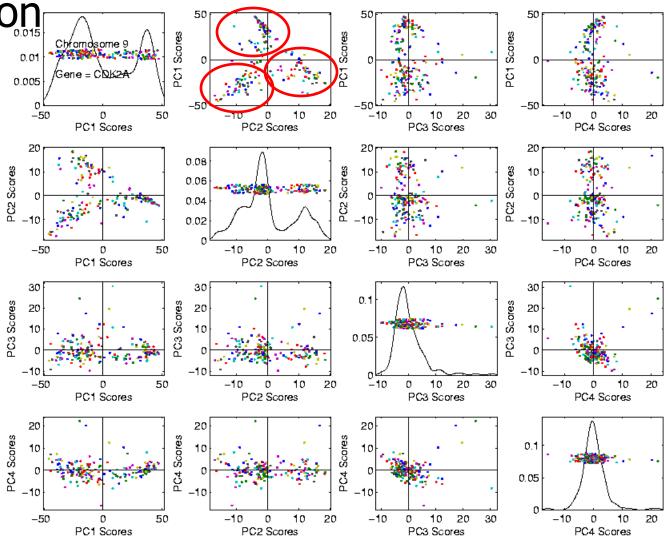




Suggestion

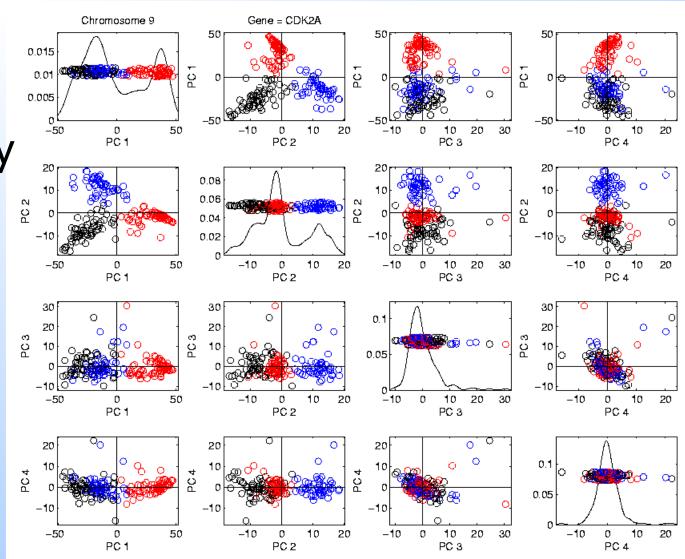
Of Clusters

Which Are These?





Manually Brush Clusters

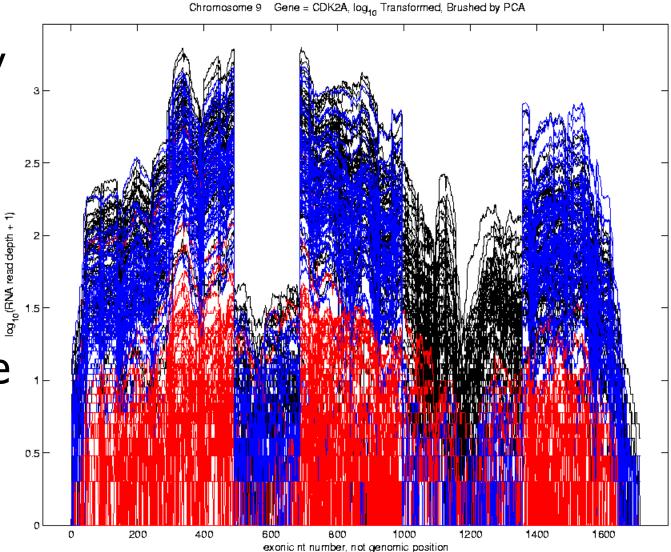




UNC, Stat & OR

Manually Brush Clusters

Clear
Alternate
Splicing





## 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)



## **Important Points**

- ✓ PCA found *Important Structure*
- ✓ In High Dimensional Data Analysis



#### Modern Mathematical Statistics:

- Based on asymptotic analysis
- I.e. Uses limiting operations
- Very often  $\lim_{n\to\infty}$

## Workhorse Method for Much Insight:

- Laws of Large Numbers (Consistency)
- Central Limit Theorems
   (Quantify Errors, Basis of Inference)



#### Modern Mathematical Statistics:

- Based on asymptotic analysis
- I.e. Uses limiting operations
- Very often  $\lim_{n\to\infty}$

Sometimes Ask
Junior Researchers
Why They Do
Asymptotics

- Occasional misconceptions:
  - Indicates behavior for large samples
  - Thus only makes sense for "large" samples
  - Models phenomenon of "increasing data"
  - So other flavors are useless???



#### Modern Mathematical Statistics:

- Based on asymptotic analysis
- Real Reasons:
  - Approximation provides insights
  - Can find simple underlying structure
  - In complex situations
- Thus various flavors are fine:

$$\lim_{n \to \infty} \lim_{d \to \infty} \lim_{n,d \to \infty} \lim_{\sigma \to 0}$$

Even desirable! (find additional insights)



### Which asymptotics?

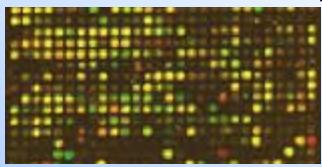
All Interesting "Blessings"

- $n \to \infty \& d \to \infty$ 
  - $n \gg d$ : close to "classical" (Portnoy)
  - $n \sim d$ : random matrices (Johnstone)
  - $d \gg n$ : "ultra high dimension" (Fan)?
- HDLSS asymptotics: n fixed,  $d \rightarrow \infty$



## HDLSS asymptotics: n fixed, $d \rightarrow \infty$

- Follow typical "sampling process"?
  - Microarrays: # genes bounded
  - Proteomics, SNPs, ...





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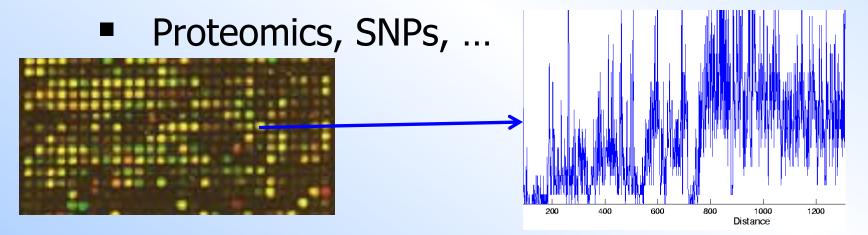


Each gene



HDLSS asymptotics: n fixed,  $d \rightarrow \infty$ 

- Follow typical "sampling process"?
  - Microarrays: # genes bounded



Next Gen Sequencing

Now called "RNA-Seq"



#### HDLSS asymptotics: n fixed, $d \rightarrow \infty$

- Follow typical "sampling process"?
  - Microarrays: # genes bounded
  - Proteomics, SNPs, ...
- A moot point, from perspective:

Asymptotics are a tool for finding *simple* structure underlying complex entities



HDLSS asymptotics: n fixed,  $d \rightarrow \infty$ 

Say anything, as noise level increases????

Yes, there exists simple, perhaps surprising, underlying structure



#### Personal Observations:

HDLSS world is...

Surprising (many times!)

[Think I've got it, and then ...]

- Mathematically Beautiful (?)
- Practically Relevant

Publishable???

Key Point: Must do the Math

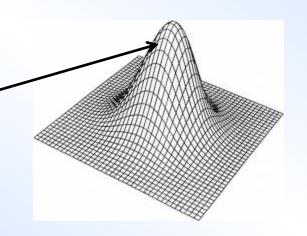


#### For *d* dimensional *Standard Normal* dist'n:

$$\tilde{\mathbf{z}} = \begin{pmatrix} \tilde{z}_1 \\ \vdots \\ \tilde{z}_d \end{pmatrix} \sim N_d(\mathbf{0}, \mathbf{I}_d)$$

Where are the Data?

Near Peak of Density?





For d dim'al "Standard Normal" dist'n:

$$\underline{Z} = \begin{pmatrix} Z_1 \\ \vdots \\ Z_d \end{pmatrix} \sim N_d (\underline{0}, I_d)$$

Euclidean Distance to Origin (as  $d \rightarrow \infty$ ):

$$\left\|\underline{Z}\right\| = \sqrt{d} + O_p(1)$$

- Data lie roughly on surface of sphere of radius  $\sqrt{d}$
- Yet origin is point of "highest density"???
- Paradox resolved by:

"density w. r. t. Lebesgue Measure"



- Paradox resolved by:
  - density w. r. t. Lebesgue Measure
- $\succ$  Consider *Volume of Unit Sphere* in  $\mathbb{R}^d$
- > Find As: Integral In Sph'l Coordinates

$$V_d = \iiint Jd\theta_1 \cdots d\theta_d dr$$



- Paradox resolved by:
  - density w. r. t. Lebesgue Measure
- $\succ$  Consider Volume of Unit Sphere in  $\mathbb{R}^d$
- Find As: Integral In Sph'l Coordinates

$$V_d = \iiint Jd\theta_1 \cdots d\theta_d dr$$

- Look At Integrand w.r.t. r
- $\triangleright$  Can Show: Puts  $\sim$  All Weight Near r=1



- Paradox resolved by: density w. r. t. Lebesgue Measure

- ✓ Lebesgue Measure Pushes Mass <u>Out</u>
- ✓ Density Pulls Data In
- $\sqrt{d}$  Is The Balance Point



As 
$$d \to \infty$$
,  $\|\tilde{\mathbf{z}}\| = \sqrt{d} + O_p(1)$ 

Important Philosophical Consequence:

∄ "Average People"

**Parents Lament:** 

Why Can't I Have Average Children?

Theorem: Impossible (over many factors)!



For d dim'al "Standard Normal" dist'n:

$$\underline{Z}_1$$
 indep. of  $\underline{Z}_2 \sim N_d(\underline{0}, I_d)$ 

Euclidean Dist. between  $\underline{Z}_1$  and  $\underline{Z}_2$  (as  $d \to \infty$ ):

Distance tends to *non-random* constant:

$$\left\|\underline{Z}_1 - \underline{Z}_2\right\| = \sqrt{2d} + O_p(1)$$

Can extend to  $Z_1, \dots, Z_n$ Where do they all go???

(We can only perceive 3 dimensions)



#### Reason For This

- Perceptual System from Ancestors
- They Needed to Find Food
- Food Exists in 3-d World

(We can only perceive 3 dimensions)



For d dim'al "Standard Normal" dist'n:

$$\underline{Z}_1$$
 indep. of  $\underline{Z}_2 \sim N_d(\underline{0}, I_d)$ 

High dim'al Angles (as  $d \to \infty$ ):

$$Angle(\underline{Z}_1, \underline{Z}_2) = 90^{\circ} + O_p(d^{-1/2})$$

- "Everything is orthogonal"????
- Where do they all go???
   (again our perceptual limitations)
- Key Point: 1st order structure is non-random



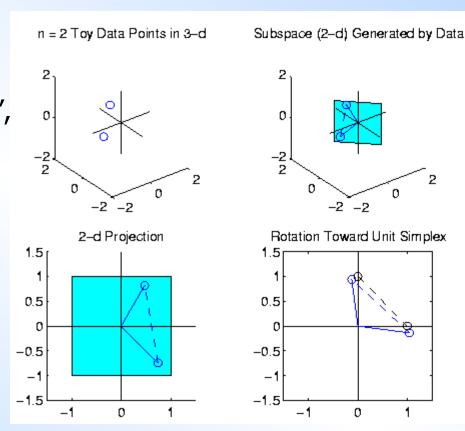
#### **HDLSS Asy's: Geometrical Representation, I**

Assume  $\underline{Z}_1, \cdots, \underline{Z}_n \sim N_d(\underline{0}, I_d)$ , let  $d \to \infty$ 

Study Subspace Generated by Data

- $\triangleright$  Hyperplane through 0, of dim'n n
- Points are "nearly equidistant to 0", & dist  $\sqrt{d}$
- Within plane, can "rotate towards  $\sqrt{d} \times$  Unit Simplex"
- All Gaussian data sets are "near Unit Simplex Vertices"!!!

"Randomness" *appears only in rotation* of simplex



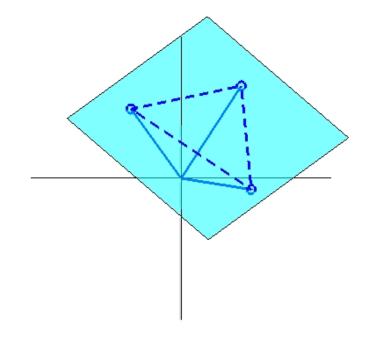
With P. Hall & A. Neeman



#### **HDLSS Asy's: Geometrical Representation, II**

Assume  $\underline{Z}_1, \dots, \underline{Z}_n \sim N_d(\underline{0}, I_d)$ , let  $d \to \infty$ Study Hyperplane Generated by Data

- $\triangleright n-1$  dimensional hyperplane
- Points are pairwise equidistant, dist  $\sim \sqrt{2d}$
- Points lie at vertices of " $\sqrt{2d}$  × regular n hedron"
- Again "randomness in data" is only in rotation
- Surprisingly rigid structure in data?

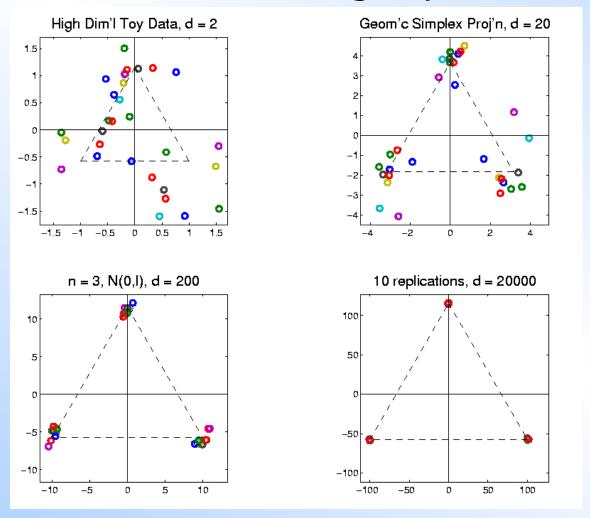


Key Point: Must do the Math



#### **HDLSS Asy's: Geometrical Representation, III**

Simulation View: shows "rigidity after rotation"





#### **HDLSS** Asy's: History & Assumptions

Hall, Marron and Neeman (2005)

- Above  $\tilde{x} \sim N_d(\mathbf{0}, \mathbf{I}_d)$  is too strong
- So Assumed ρ Mixing Condition
   Common in Time Series

Far Apart Entries Uncorrelated

In  $\lim_{d\to\infty}$ 



#### **HDLSS** Asy's: History & Assumptions

Hall, Marron and Neeman (2005)

**Publication History:** 

Rejected by Biometrika

" $\rho$ -Mixing Along Vector Not Practical"

Hence Published in JRSS-B



#### **HDLSS** Asy's: History & Assumptions

Hall, Marron and Neeman (2005)

Later Realization:

This Mixing is Very Natural in

**Genome Wide Association Studies** 

1<sup>st</sup> such: Klein et al (2005)



#### **HDLSS** Asy's: History & Assumptions

Genome Wide Association Study

Data Objects: Vectors of Genetic Variants, at <a href="https://known.chromosome.nc/">known</a> chromosome locations (Called SNPs)

Discrete (takes on 2 or 3 values)

Dimension d as large as ~5 million (can be reduced, e.g. d~20000)



#### **HDLSS** Asy's: History & Assumptions

Genome Wide Association Study

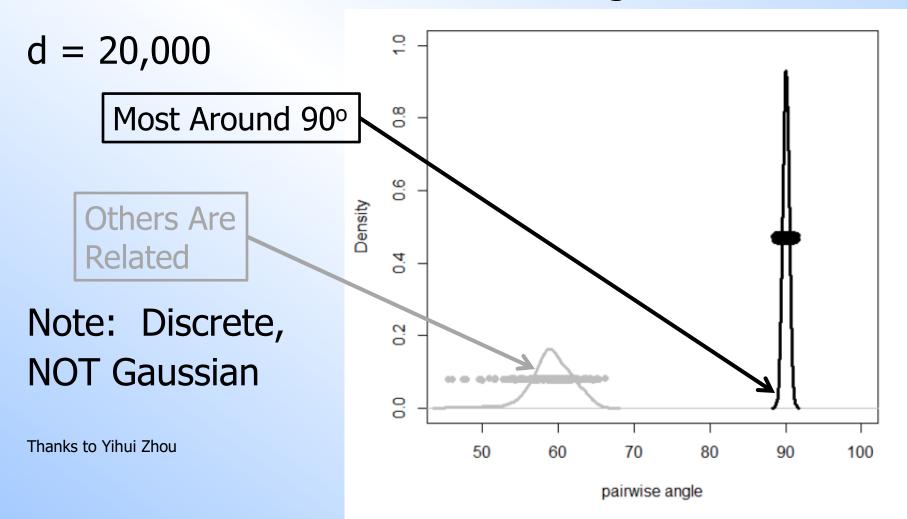
Data Objects: Vectors of Genetic Variants, at <a href="https://known.chromosome.nc/">known</a> chromosome locations (Called SNPs)

Sexual Reproduction  $\Rightarrow \rho$  - Mixing Actually Very Natural "In Practice"



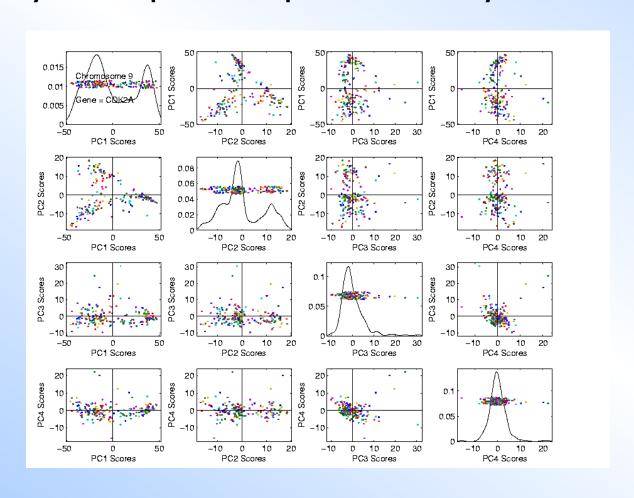
#### **HDLSS** Asy's: History & Assumptions

View of GWAS data: Pairwise Angles





#### Next Study Principal Component Analysis





Next Study Principal Component Analysis

For Centered  $d \times n$  Data Matrix, SVD is

$$m{X} = m{U}m{S}m{V}^t = m{\sum}_{k=1}^r m{u}_k s_k m{v}_{k}^t$$
Loadings Scores (Directions) (Projection Vectors Coefficients)

Equivalent to Eigen-Analysis of Cov. Matrix



Consistency & Strong Inconsistency:

Spike Covariance Model (Johnstone & Paul)

For Eigenvalues:  $\lambda_{1,d} = d^{\alpha}$ ,  $\lambda_{2,d} = 1, \dots, \lambda_{d,d} = 1$ 

1<sup>st</sup> Eigenvector:  $u_1$ 

How good are empirical versions,  $\hat{\lambda}_{1,d}, \cdots, \hat{\lambda}_{d,d}, \hat{u}_1$  as estimates?



Consistency (big enough spike):

For 
$$\alpha > 1$$
,

$$Angle(u_1, \hat{u}_1) \rightarrow 0$$

Strong Inconsistency (spike not big enough):

For 
$$\alpha < 1$$
,

$$Angle(u_1, \hat{u}_1) \rightarrow 90^{\circ}$$



Intuition: Random Noise  $\sim d^{1/2}$ 

For  $\alpha > 1$  (recall on scale of variance), Spike pops out of *noise sphere* 

For  $\alpha < 1$ ,

Key Point: Must do the Math

Spike contained in *noise sphere* 



## Consistency of Eigenvalues?

$$\hat{\lambda}_{1,d} \stackrel{L}{\to} \frac{\chi_n^2}{n} \lambda_{1,d}$$

- Eigenvalues Inconsistent
- But Known Distribution
- Unless  $n \to \infty$  as well



#### Careful look at:

■ PCA Consistency -  $\alpha > 1$  spike

Independent of Sample Size,

So true for n = 1 (!?!)



#### Careful look at:

■ PCA Consistency  $-\alpha > 1$  spike

Independent of Sample Size,

So true for n=1 (!?!)

Absurd, shows assumption too strong

for practice ???



# **Motivation of HDLSS Asy's**

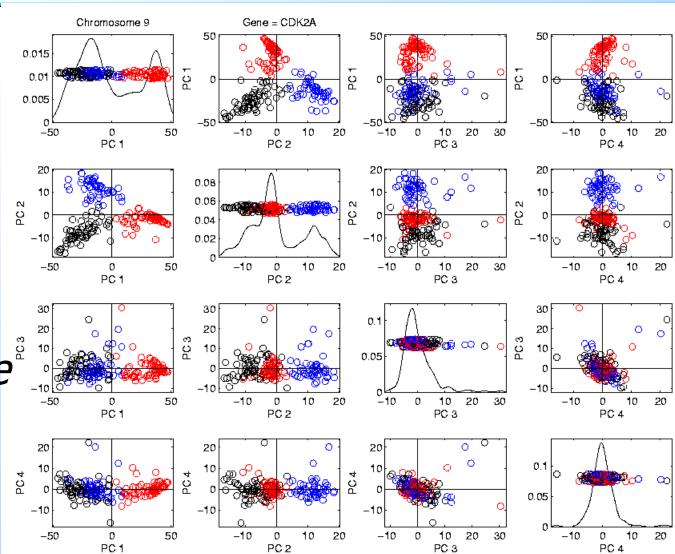
UNC, Stat & OR

#### **HDLSS**

**PCA** Often **Finds Signal** 

Not Pure

Noise





## Recall Theoretical Separation:

- Strong Inconsistency  $\alpha$  < 1 spike
- Consistency  $\alpha > 1$  spike

**Mathematically Driven Conclusion:** 

Real Data Signals Are This Strong



# An Interesting Objection:

Should not Study Angles in PCA

Recall, for 
$$\alpha > 1$$
, 
$$Angle(u_1, \hat{u}_1) \rightarrow 0$$

For 
$$\alpha < 1$$
, 
$$Angle(u_1, \hat{u}_1) \rightarrow 90^{\circ}$$



## An Interesting Objection:

Should not Study Angles in PCA

Because PC Scores (i.e. projections)

**Not Consistent** 



## An Interesting Objection:

Should not Study Angles in PCA

Because PC Scores (i.e. projections)

**Not Consistent** 

For Scores 
$$(\hat{s}_{i,j} = P_{\hat{v}_j} x_i)$$

What we study in PCA scatterplots



# An Interesting Objection:

Should *not Study Angles* in PCA

Because PC Scores (i.e. projections)

## **Not Consistent**

For Scores 
$$\hat{s}_{i,j} = P_{\hat{v}_j} x_i$$
 and  $s_{i,j} = P_{v_j} x_i$ 

Can Show  $\frac{\hat{s}_{i,j}}{s_{i,j}} \to R_j \neq 1$  (Random!)



PC Scores (i.e. projections)

**Not Consistent** 

So how can PCA find *Useful Signals* in Data?



# **Motivation of HDLSS Asy's**

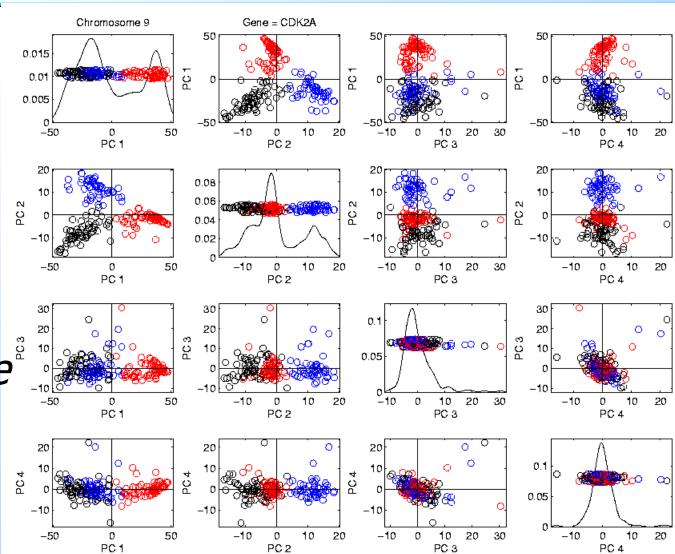
UNC, Stat & OR

#### **HDLSS**

**PCA** Often **Finds Signal** 

Not Pure

Noise





PC Scores (i.e. projections)

### **Not Consistent**

So how can PCA find *Useful Signals* in Data?

Key is "Proportional Errors" 
$$\frac{\hat{s}_{i,j}}{s_{i,j}} \rightarrow R_j \neq 1$$

Axes have Inconsistent Scales,

But Relationships are Still Useful

Key Point: Careful About Interpreting the Math



## **Direct Solution:**

- Aoshima & Yata
- Consistent Scores Estimates
- Based on Dual Space (Gram Matrix) Ideas







# **HDLSS Deep Open Problem**

## In PCA Consistency:

- Strong Inconsistency  $\alpha$  < 1 spike
- Consistency  $\alpha > 1$  spike

What happens at boundary (  $\alpha = 1$  )???



# **HDLSS Deep Open Problem Result**

# In PCA Consistency:

- Strong Inconsistency  $\alpha$  < 1 spike
- Consistency  $\alpha > 1$  spike

What happens at boundary (  $\alpha = 1$  )???

3 interesting Limit Distn's (Sen et al)



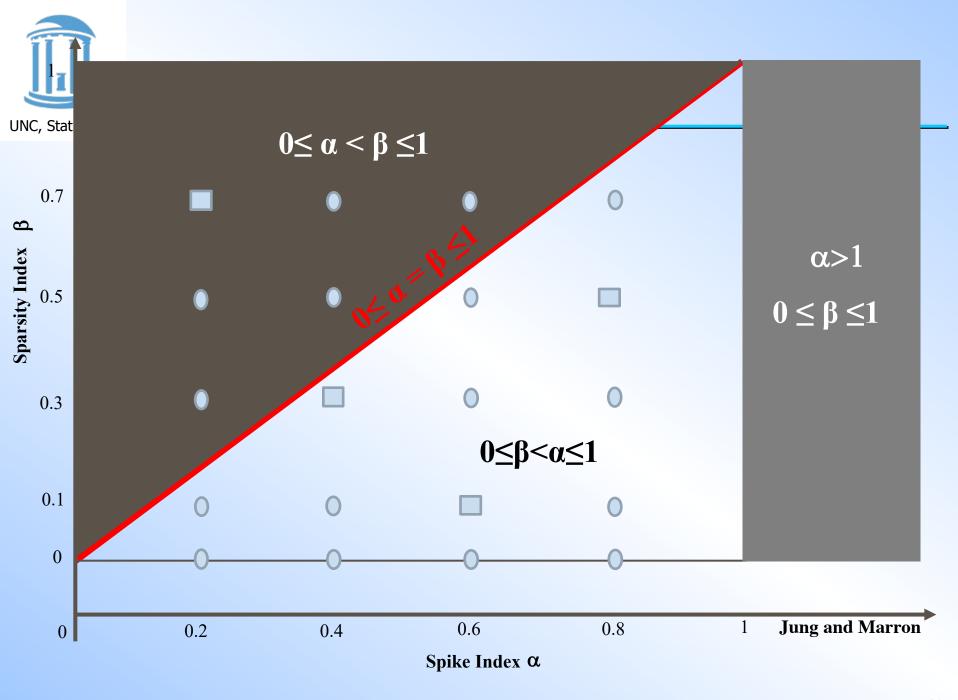
# **HDLSS & Sparsity**

New Area Opened in PhD Work by Dan Shen

- $\Box$  Uses Spike Index,  $\alpha$
- $\square$  And Sparsity Index,  $\beta$
- Explores Consistency

& Strong mconsistency

Sparsity Gives Broad New Region





# **HDLSS & Other Asymptotics**

Larger Context: PhD Work by Dan Shen

Explores PCA Consistency under all of:

Classical: d fixed,  $n \to \infty$ 

Portnoy:  $d, n \to \infty, d \ll n$ 

Random Matrices:  $d, n \rightarrow \infty$ ,  $d \sim n$ 

HDMSS:  $d, n \to \infty$ ,  $d \gg n$ 

HDLSS:  $d \to \infty$ , n fixed



# **HDLSS & Other Asymptotics**

Larger Context: PhD Work by Dan Shen

Explores PCA Consistency under all of:

Classical: d fixed,  $n \to \infty$ 

Interesting and Surprising Case

Portnoy:  $d, n \to \infty$ ,  $d \ll n$ 

Random Matrices:  $d, n \to \infty$ ,  $d \sim n$ 

HDMSS:  $d, n \to \infty$ ,  $d \gg n$ 

HDLSS:  $d \to \infty$ , n fixed



#### **HDMSS**

Asymptotics:  $d, n \rightarrow \infty$   $d \gg n$ 

# **Leading Groups:**

- > Fan, et al (Princeton)
- Aoshima, Yata (Tsukuba)



# **HDMSS**, Fan View

Asymptotics:  $d, n \rightarrow \infty$   $d \gg n$ 

"Ultra High Dimension" (Fan & Lv 2008):

1. Driver:  $n \to \infty$ 

(Classical Viewpoint)

2. Follower:  $d \sim e^n$ 

(Perhaps Impressive?)



# **HDMSS**, Aoshima View

Asymptotics:  $d, n \rightarrow \infty$   $d \gg n$ 

1. Driver:  $d \rightarrow \infty$ 

(New Viewpoint)

2. Follower:  $n \sim \log(d)$ 

(Mathematically Equivalent?)



# **HDMSS**, Personal Choice

#### **Aoshima View:**

1. Driver:  $d \to \infty$ 

2. Follower:  $n \sim \log(d)$ 

Since this allows <u>easy interface</u> with HDLSS:

 $d \to \infty$ , with n fixed



# **HDLSS Asymptotics**

# Publishability???

PCA Consistency for n = 1Inconsistent, but Useful Scores

- Basic Ideas Developed as "Concentration of Measure" by Talagrand (1990s)
- Many are Corollaries of "Concentration Inequalities", Massart, Lugosi, van der Vaart, Kolchinski, Tsybakov, ...
- Value (: pub'able) of HDLSS asymptotics:

Statistical Insights



## **HDLSS Asymptotics**

#### Personal Observations:

HDLSS world is...

Surprising (many times!)

[Think I've got it, and then ...]

- Mathematically Beautiful (?)
- Practically Relevant

Publishable???

Key Point: Must do the Math



# The Future of HDLSS Asymptotics?

- Address your favorite statistical problem...
- 2. HDLSS versions of classical optimality results?
- Continguity Approach (~Random Matrices)
- 4. Rates of convergence?
- 5. Improved Discrimination Methods?

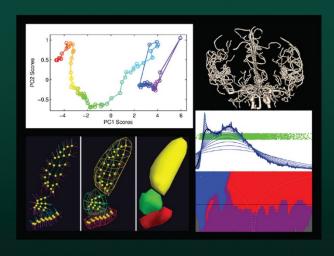
It is early days...



# **My Current Research**

Monographs on Statistics and Applied Probability 169

# Object Oriented Data Analysis



J.S. Marron lan L. Dryden



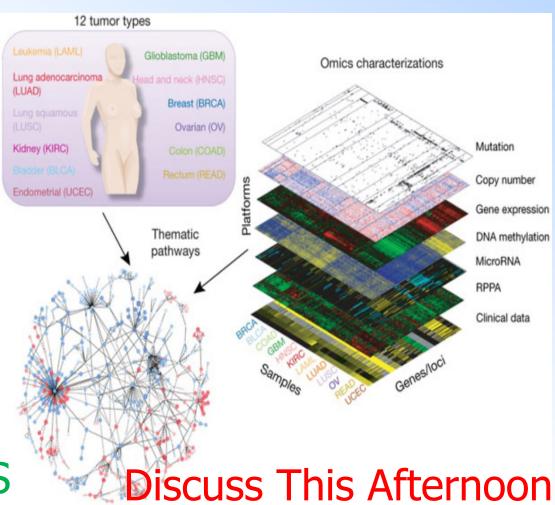




# **My Current Research**

Data Integration:

Important
New Methods:
JIVE
DIVAS



**Interesting HDLSS** 

Asy. Challenges

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)

The Cancer Genome Atlas Pan-Cancer analysis project.