



Norwegian Winter School – Geilo

UNC, Stat & OR

Object Oriented Data Analysis

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Object Oriented Data Analysis

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What is the “atom” of a statistical analysis?

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



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Examples:

- Medical Image Analysis
 - Images as Data Objects?
 - Shape Representations as Objects
- Gene Expression (Microarrays – RNAseq)
 - Just multivariate analysis?



Principal Component Analysis

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More Than *Dimensionality Reduction*:

- Visualization
 - Relationships Between Objects (Scores)
 - Drivers of Relationships (Loadings)



Principal Component Analysis

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More Than *Dimensionality Reduction*:

- Visualization
 - Relationships Between Objects (Scores)
 - Drivers of Relationships (Loadings)

But \exists Limitations (good to know about)



Principal Component Analysis

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Visualization Limitation:

Finds Directions of Maximal Variation



Principal Component Analysis

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Visualization Limitation:

Finds Directions of Maximal Variation

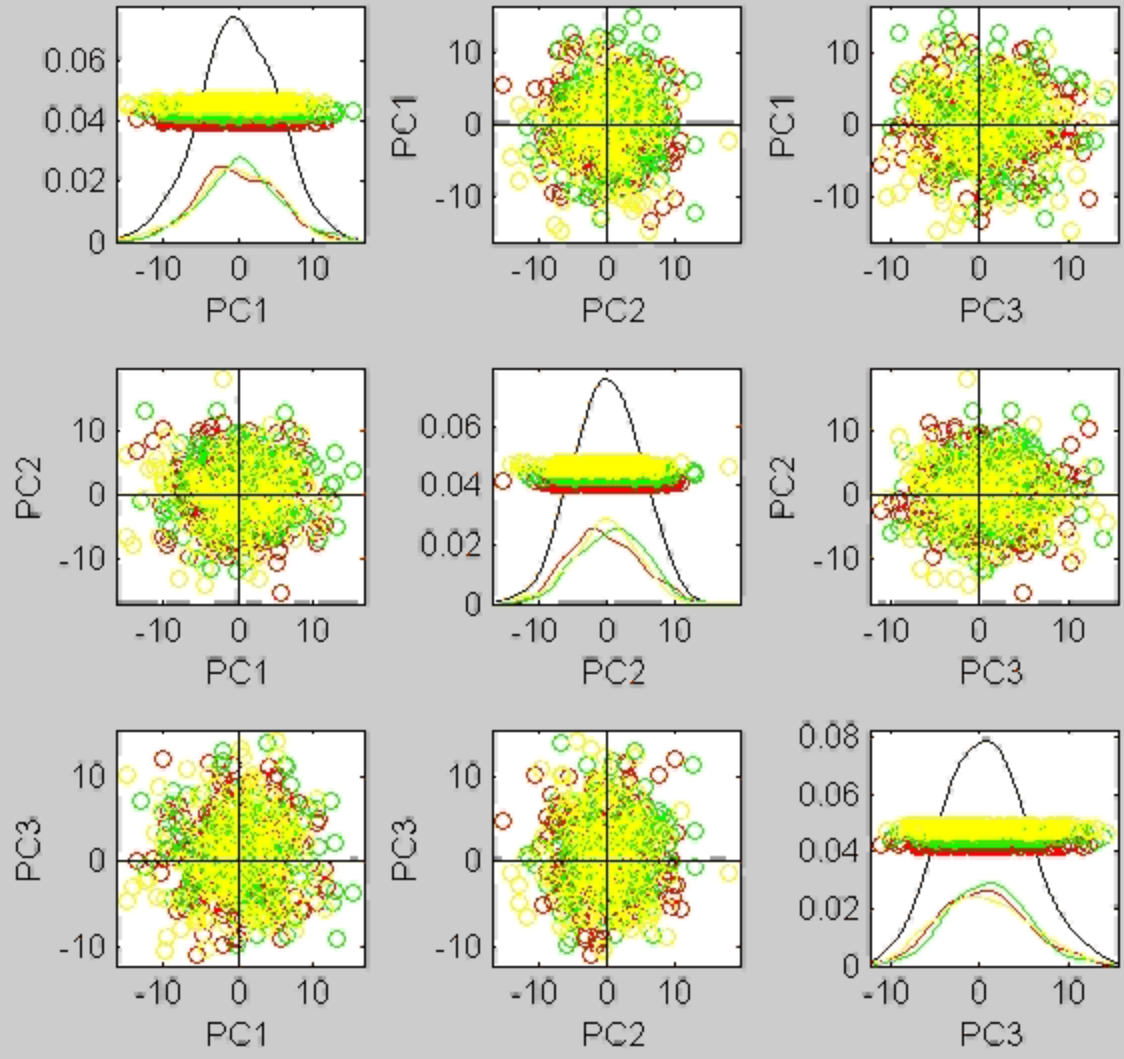
❖ **Apple** – **Banana** – **Pear** Example (6-d)



Apple – Banana - Pear

Apple - Banana - Pear Toy Example

Rotate PC dir'ns to Informative Dir'ns





Apple – Banana - Pear

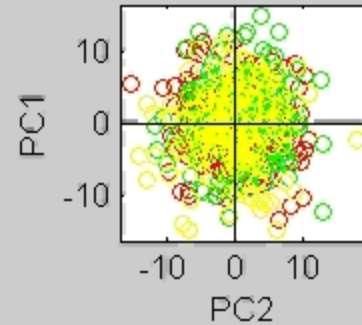
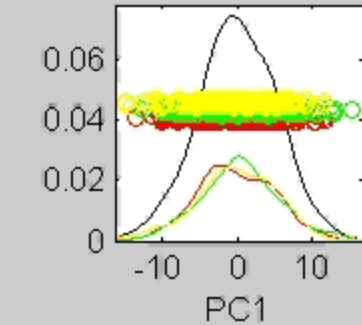
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- Structure in Data Obscured
- 1st 3 PC Dir'ns are Pure Noise
- Rotate Axes to Find Structure

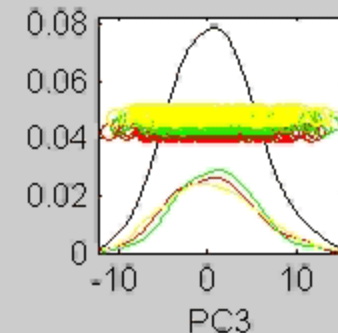
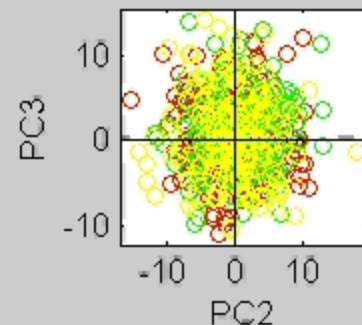
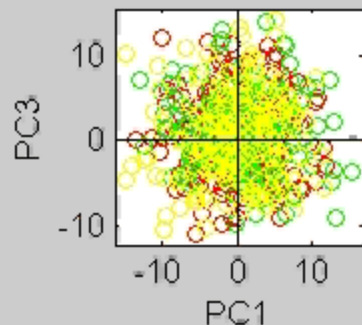
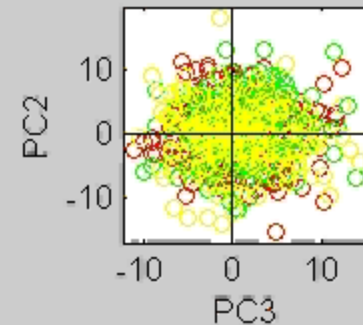
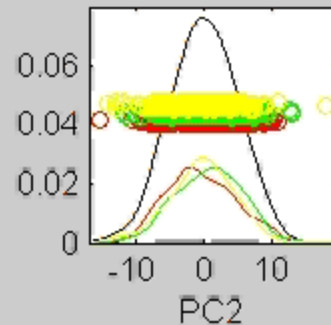
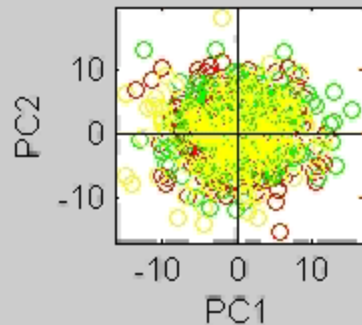
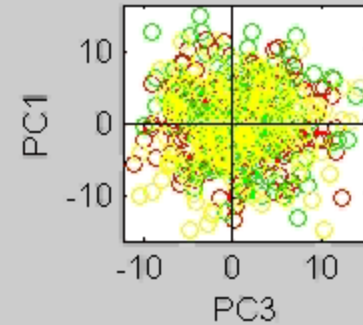


Apple – Banana - Pear

Apple - Banana - Pear Toy Example



Rotate PC dir'ns to Informative Dir'ns





Principal Component Analysis

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Visualization Limitation:

Finds Directions of Maximal Variation

- ❖ **Apple** – **Banana** – **Pear** Example (6-d)
- ❖ Often Doesn't Separate Subgroups



HDLSS Classification (i.e. Discrimination)

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Background: Two Class (Binary) version:

Using “training data” from **Class +1**, and
from **Class -1**

Develop a “rule” for assigning new data to
a Class

Canonical Example: Disease Diagnosis

- New Patients are “Healthy” or “Ill”
- Determined based on measurements



HDLSS Classification (Cont.)

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- Ineffective Methods:
 - Fisher Linear Discrimination
 - Gaussian Likelihood Ratio

- Less Useful Methods:
 - Nearest Neighbors
 - Neural Nets

("black boxes", no "directions" or intuition)



HDLSS Classification (Cont.)

- Currently Fashionable Methods:
 - Support Vector Machines
 - Trees Based Approaches

- New High Tech Method
 - Distance Weighted Discrimination (DWD)
 - Specially designed for HDLSS data
 - Avoids “data piling” problem of SVM
 - Solves more suitable optimization problem

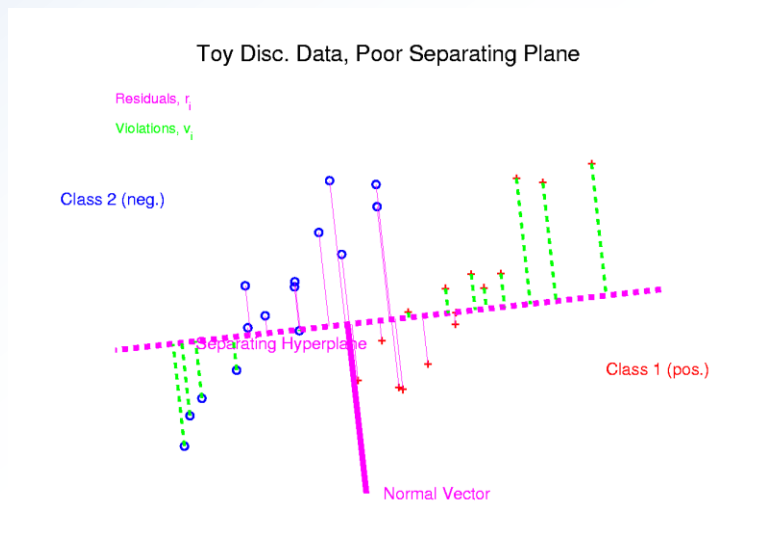


HDLSS Classification (Cont.)

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■ Currently Fashionable Methods:

- Trees Based Approaches
- Support Vector Machines:





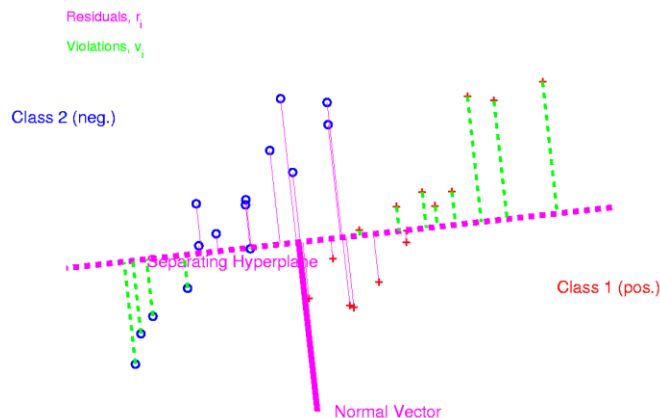
HDLSS Classification (Cont.)

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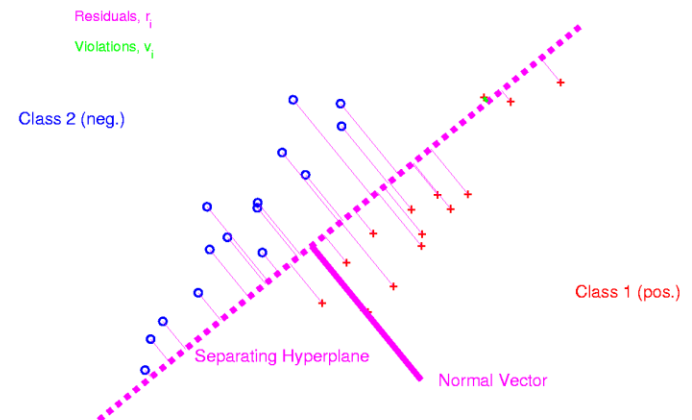
■ Currently Fashionable Methods:

- Trees Based Approaches
- Support Vector Machines:

Toy Disc. Data, Poor Separating Plane



Toy Disc. Data, Better Separating Plane



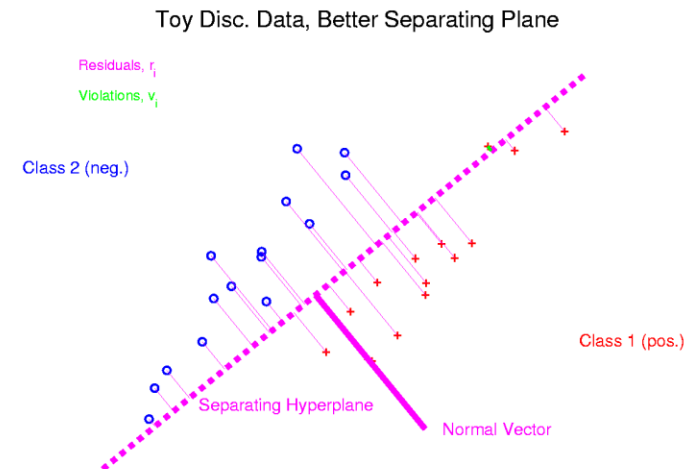
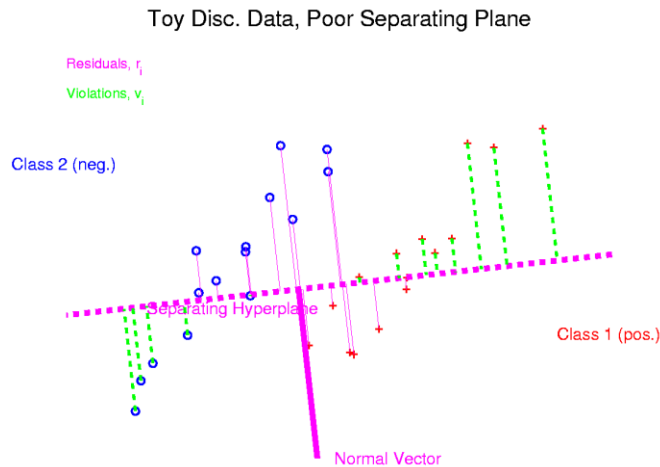
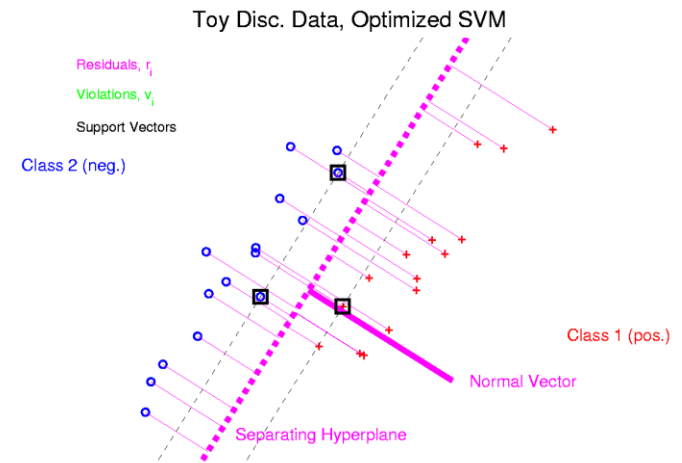


HDLSS Classification (Cont.)

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■ Currently Fashionable Methods:

- Trees Based Approaches
- Support Vector Machines:





Kernel Embedding Idea

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Aizerman, Braverman, Rozoner (1964)

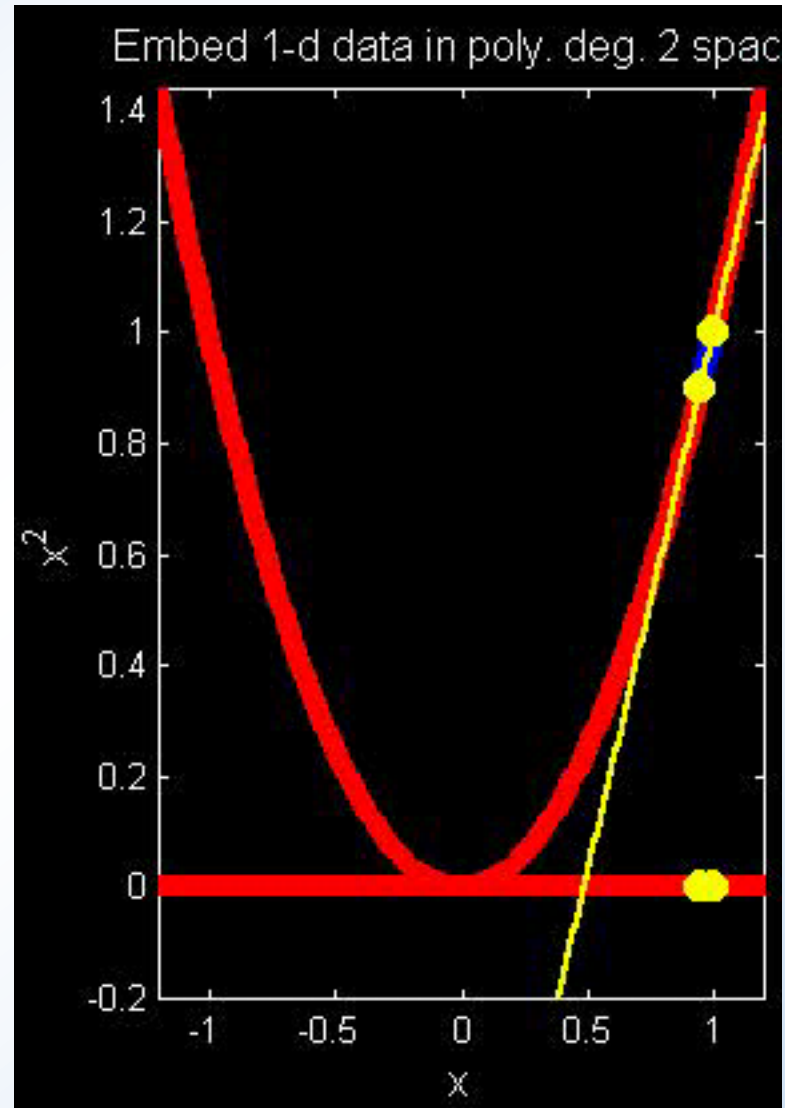
Make data *linearly separable*
by embedding in
higher dimensional space



Kernel Embedding Idea

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Linearly
separable
by
embedding
in
higher
dimensions



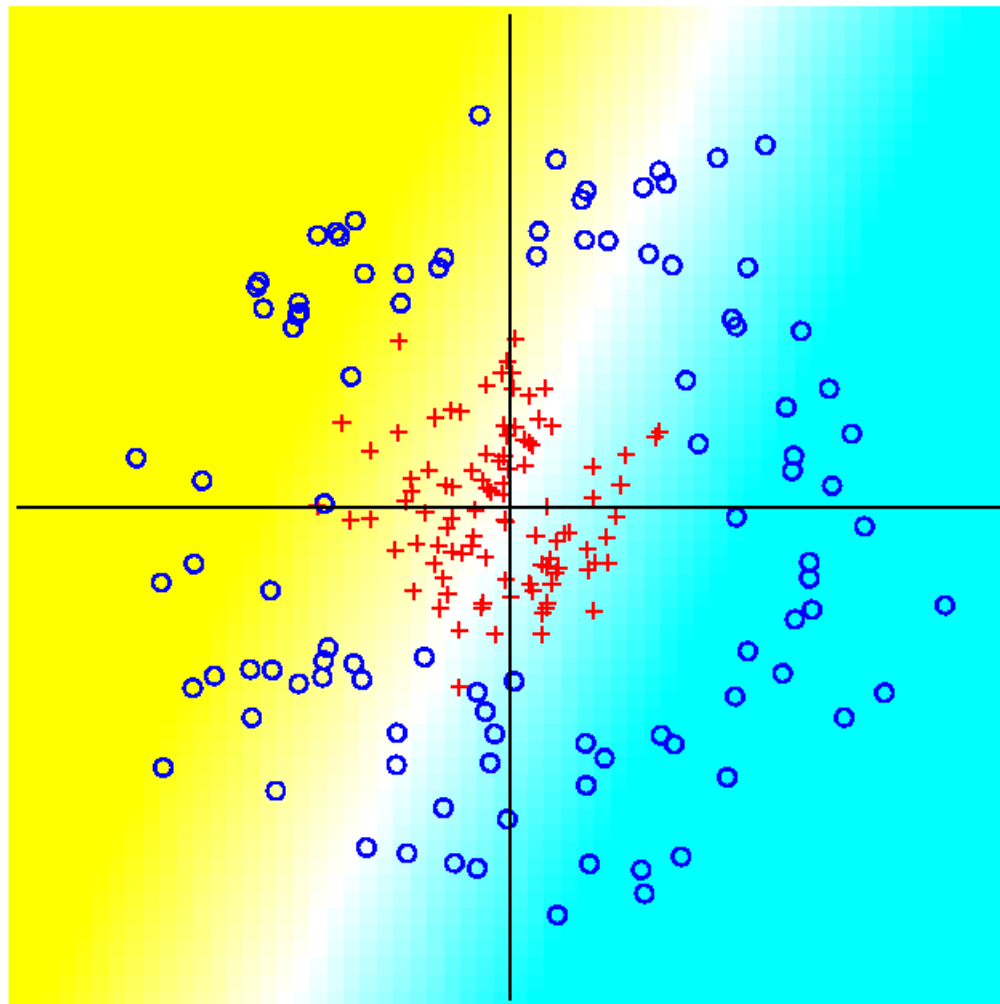


Kernel Embedding Idea

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*Linearly
separable*
by
embedding
in
higher
dimensions

Donut, Disc: FLD, Embed: x_1, x_2 only



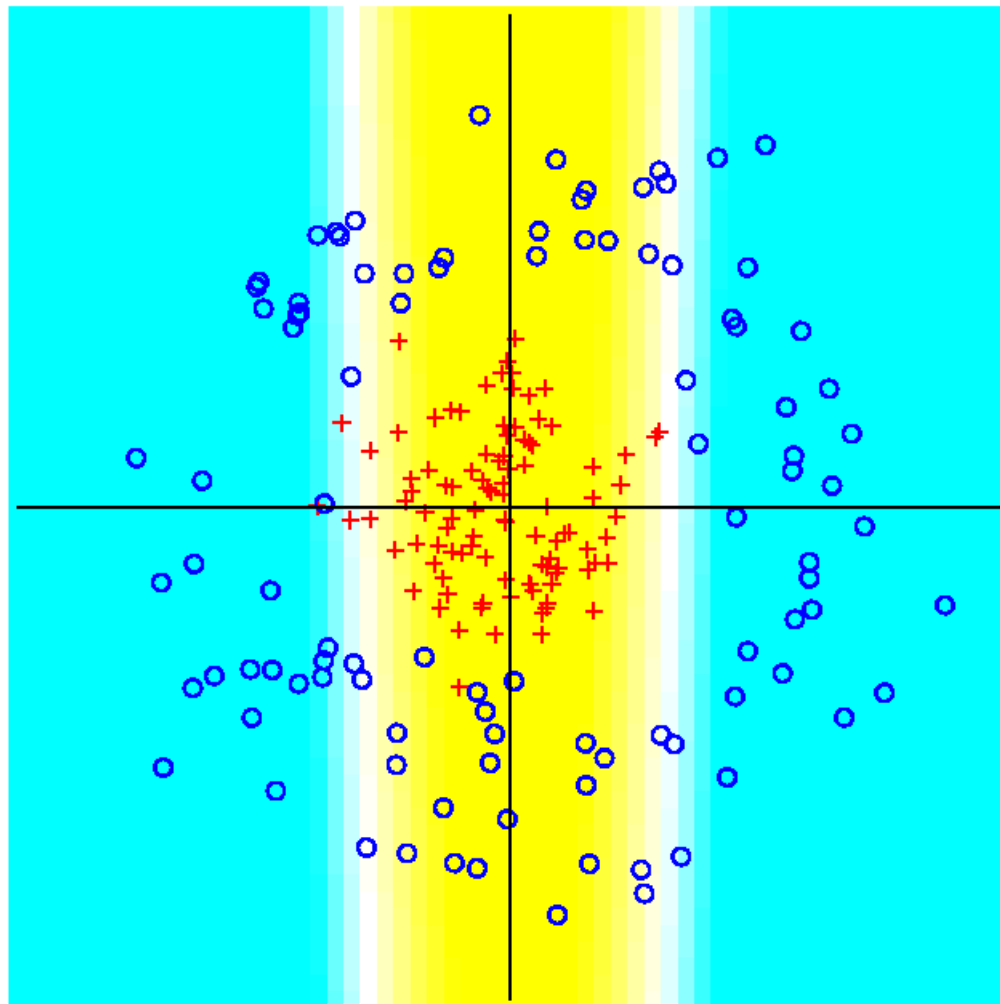


Kernel Embedding Idea

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*Linearly
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Donut, Disc: FLD, Embed: x_1, x_2, x_1^2



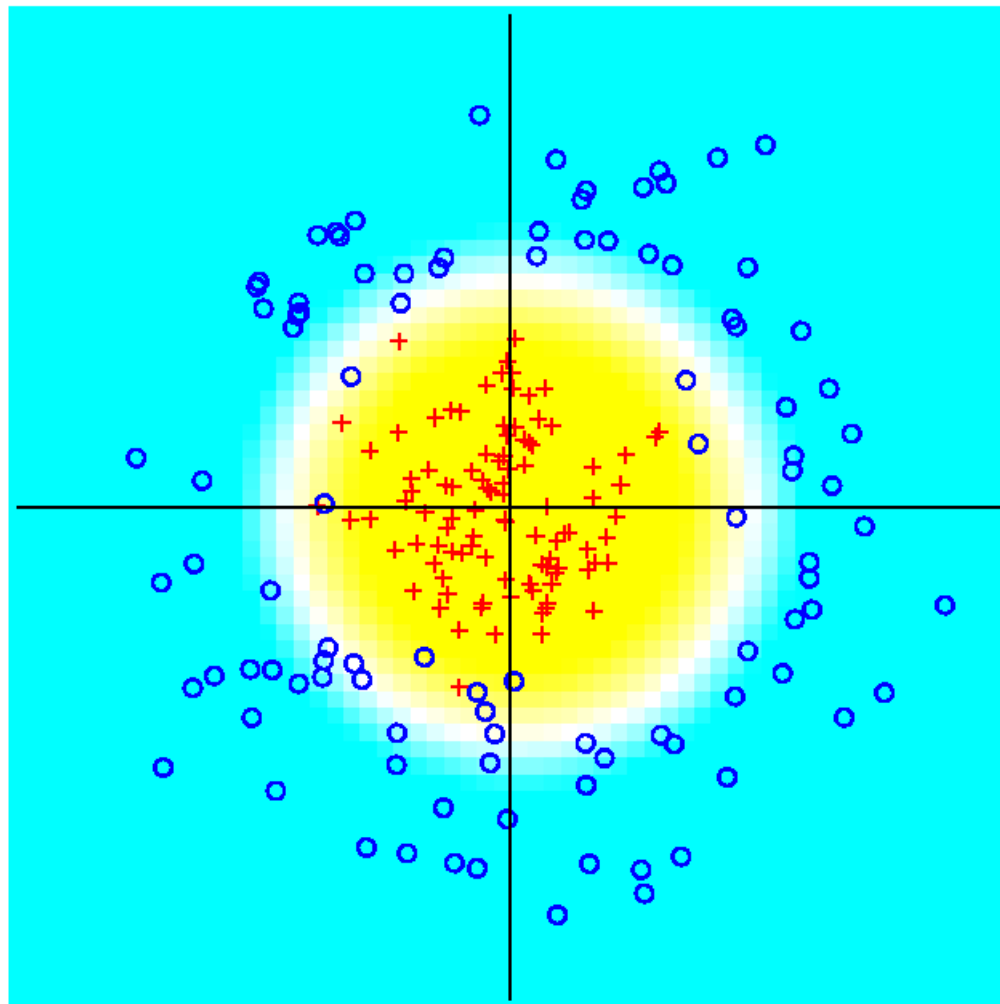


Kernel Embedding Idea

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Donut, Disc: FLD, Embed: x_1, x_2, x_1^2, x_2^2





Kernel Embedding Idea

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*Linearly
separable*
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dimensions

Distributional Assumptions
in Embedded Space?

||
v

Support Vector Machine



HDLSS Classification (Cont.)

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Comparison of Linear Methods (toy data):

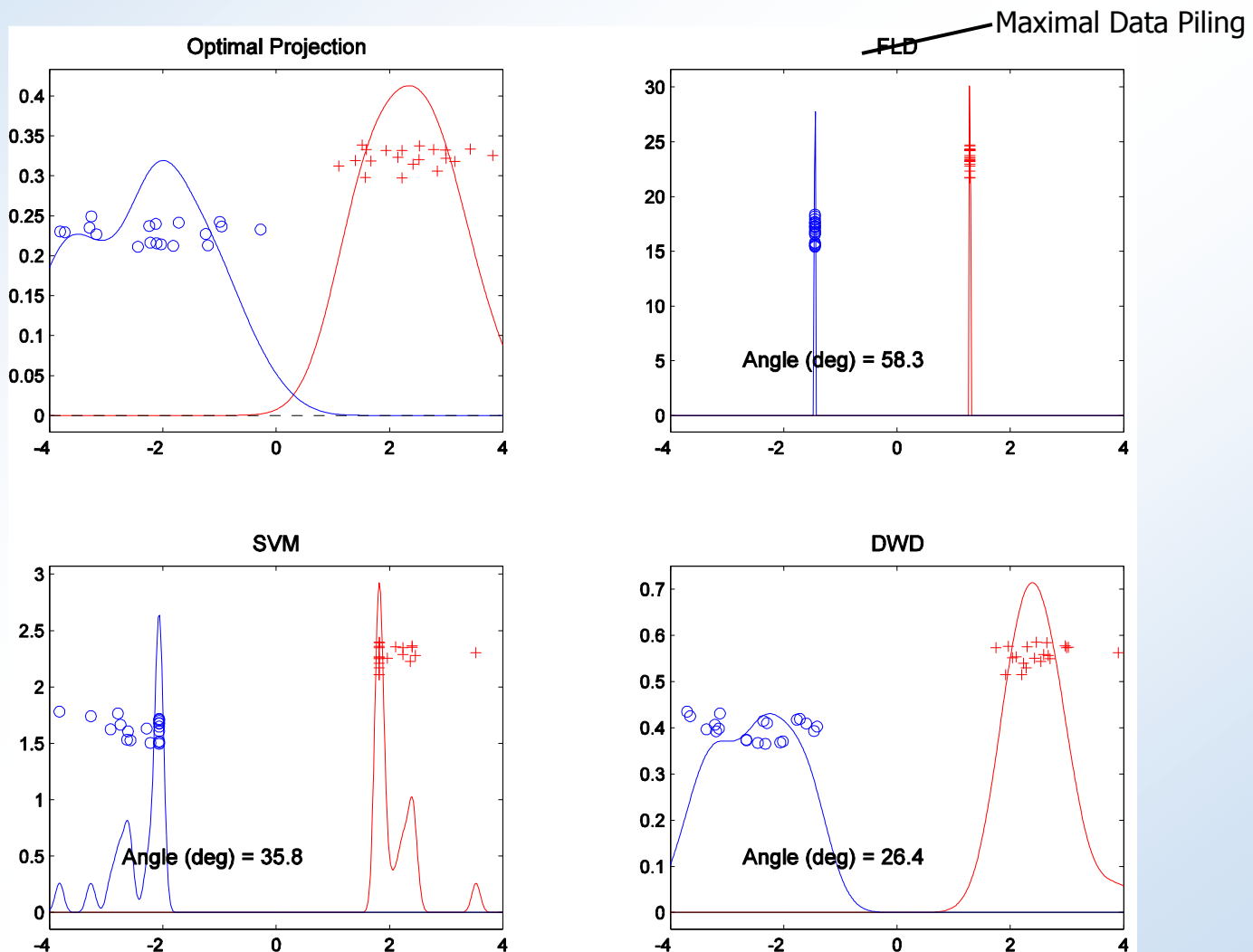
$$N_d(\mu, I), \mu_{1,\pm} = \pm 2.2, n_1 = n_2 = 20, d = 50$$

- Optimal Direction
 - Excellent, but need dir'n in dim = 50
- Maximal Data Piling (J. Y. Ahn, D. Peña)
 - *Great separation*, but generalizability???
- Support Vector Machine
 - More separation, gen'ity, but some data piling?
- Distance Weighted Discrimination
 - Avoids data piling, good gen'ity, Gaussians?



Distance Weighted Discrimination

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Distance Weighted Discrimination

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Based on Optimization Problem:
$$\min_{w,b} \sum_{i=1}^n \frac{1}{r_i}$$

More precisely work in appropriate penalty for violations

Optimization Method (Michael Todd):

Second Order Cone Programming

- Still Convex gen'tion of quadratic prog'ing
- Fast greedy solution
- Can use existing software

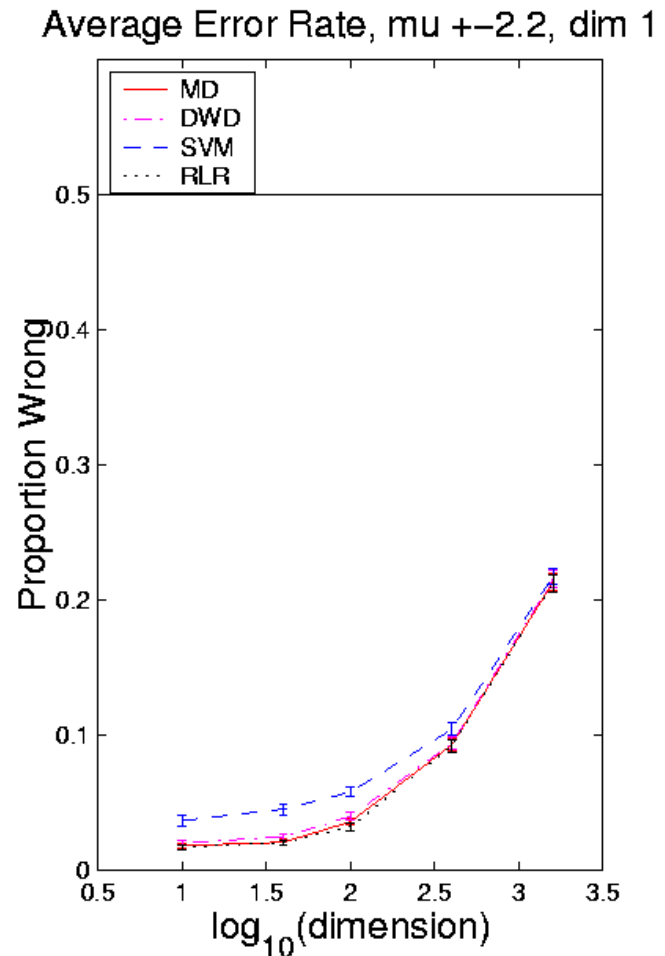


Simulation Comparison

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E.G. Above Gaussians:

- Wide array of dim's
- SVM Subst'ly worse
- MD – Bayes Optimal
- DWD close to MD



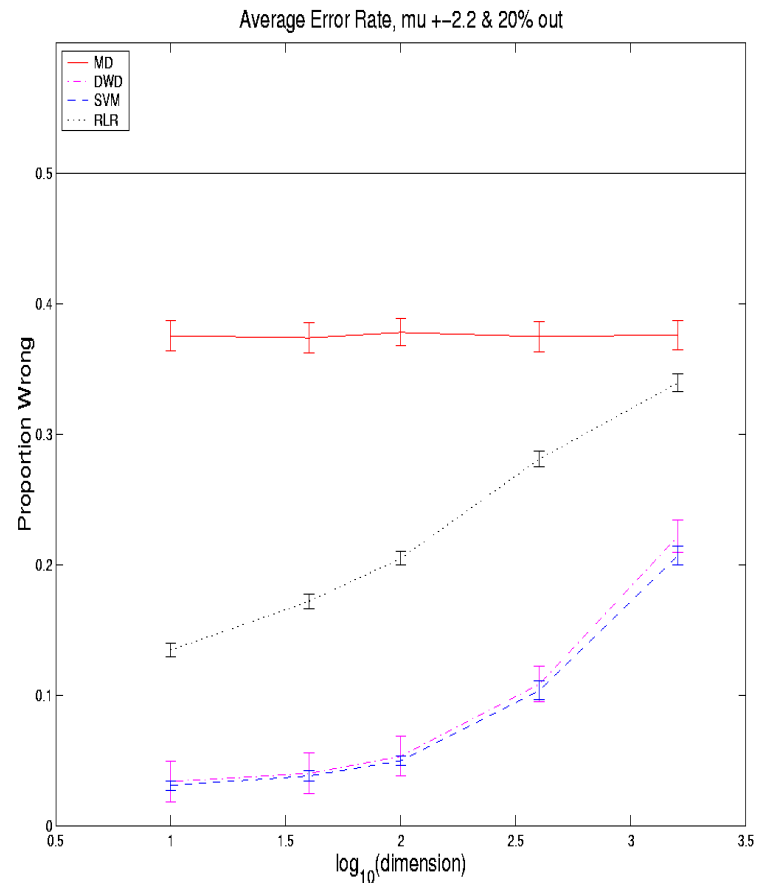


Simulation Comparison

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E.G. Outlier Mixture:

- Disaster for MD
- SVM & DWD much more solid
- Dir'ns are "robust"
- SVM & DWD similar





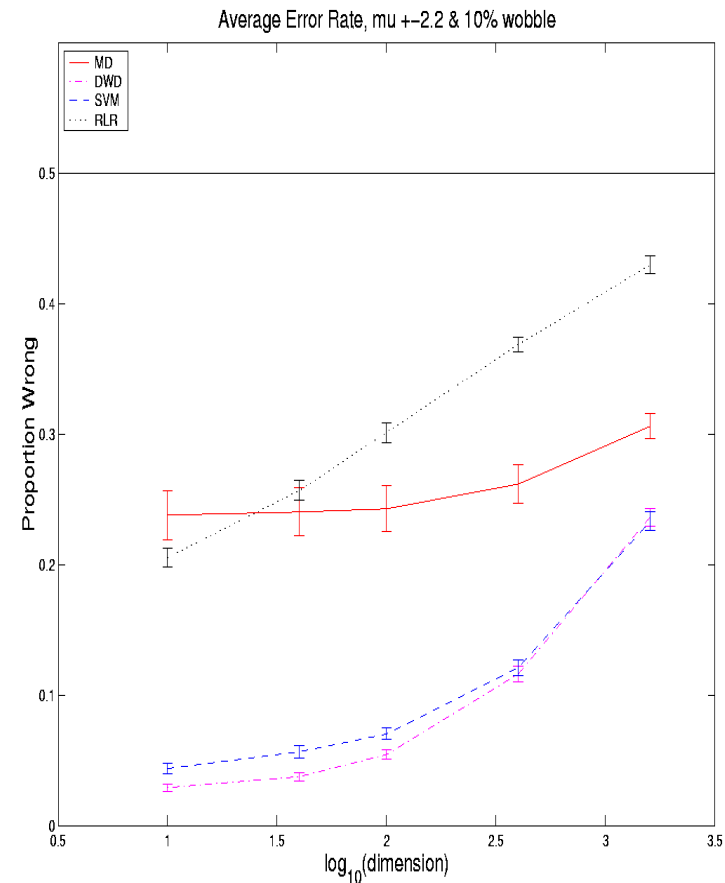
Simulation Comparison

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E.G. Wobble Mixture:

- Disaster for MD
- SVM less good
- DWD slightly better

Note: All methods
come together for
larger d ???





DWD Bias Adjustment for Microarrays

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Microarray data:

- Simult. Measurements of “gene expression”
- Intrinsically HDLSS
 - Dimension $d \sim 1,000s - 10,000s$
 - Sample Sizes $n \sim 10s - 100s$

My view:

Each array is “point in cloud”



DWD Batch and Source Adjustment

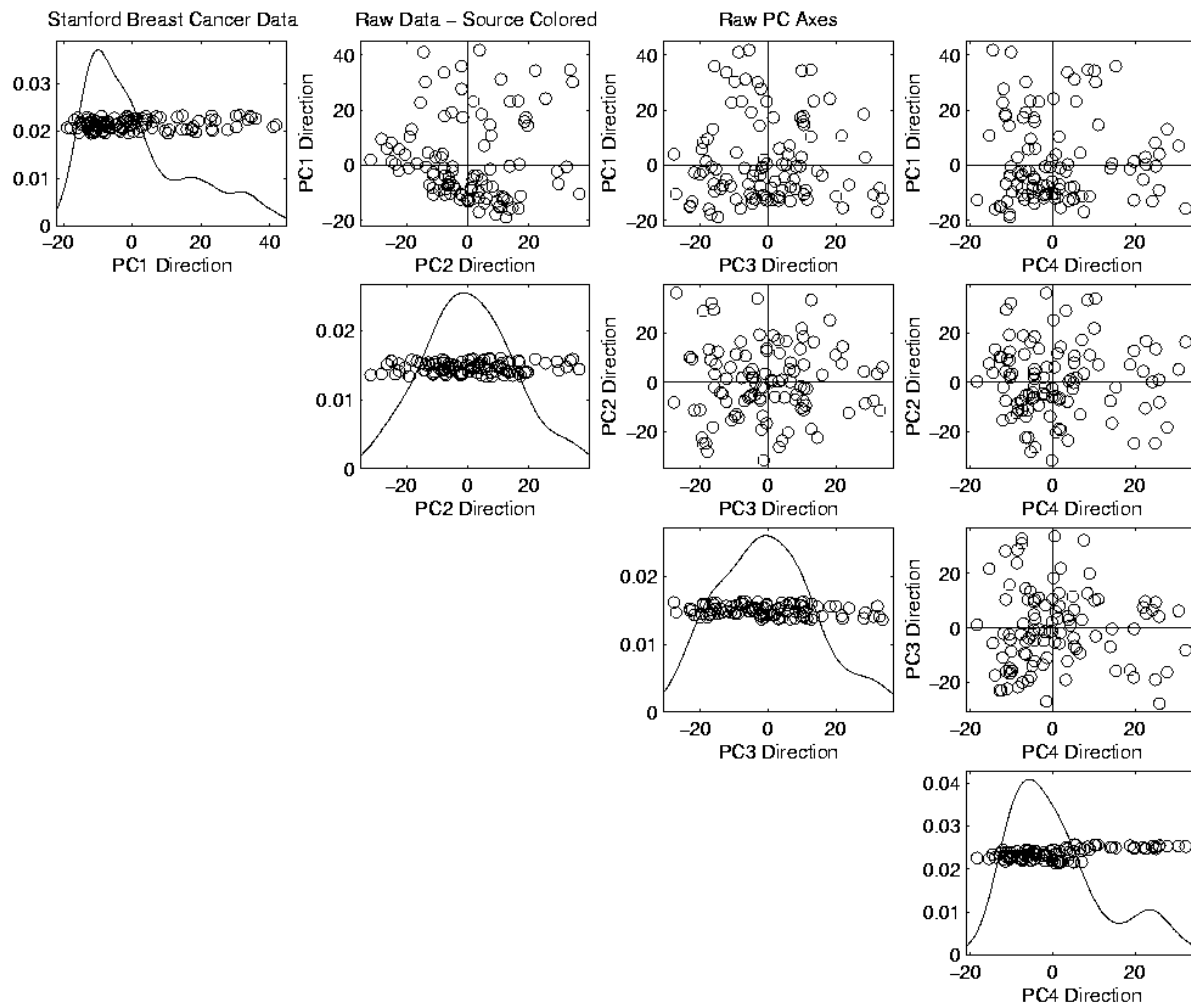
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- For Perou's Stanford Breast Cancer Data
- Analysis in Benito, et al (2004) *Bioinformatics*
<https://genome.unc.edu/pubsup/dwd/>
- Adjust for Source Effects
 - Different sources of mRNA
- Adjust for Batch Effects
 - Arrays fabricated at different times



DWD Adj: Raw Breast Cancer data

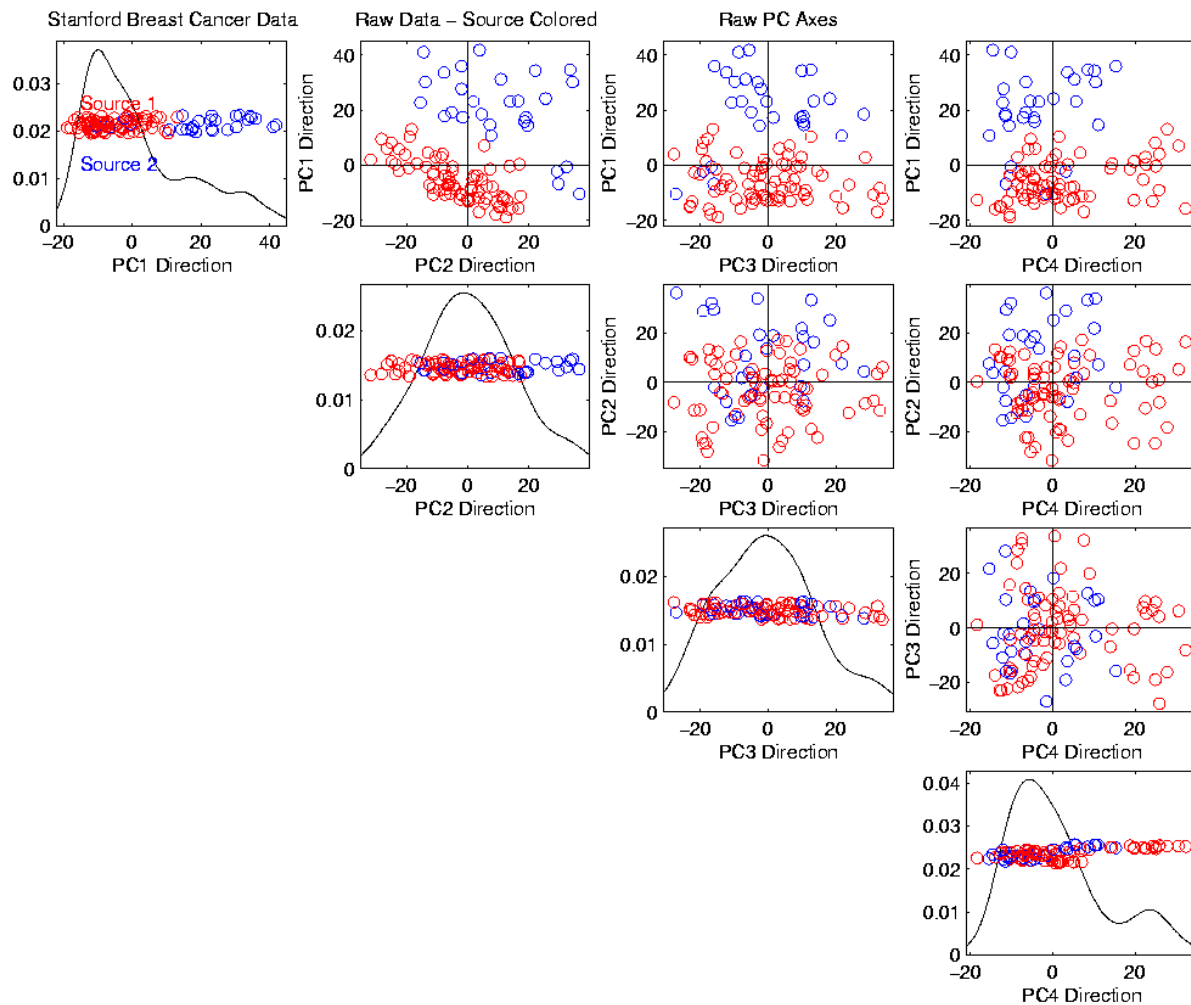
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DWD Adj: Source Colors

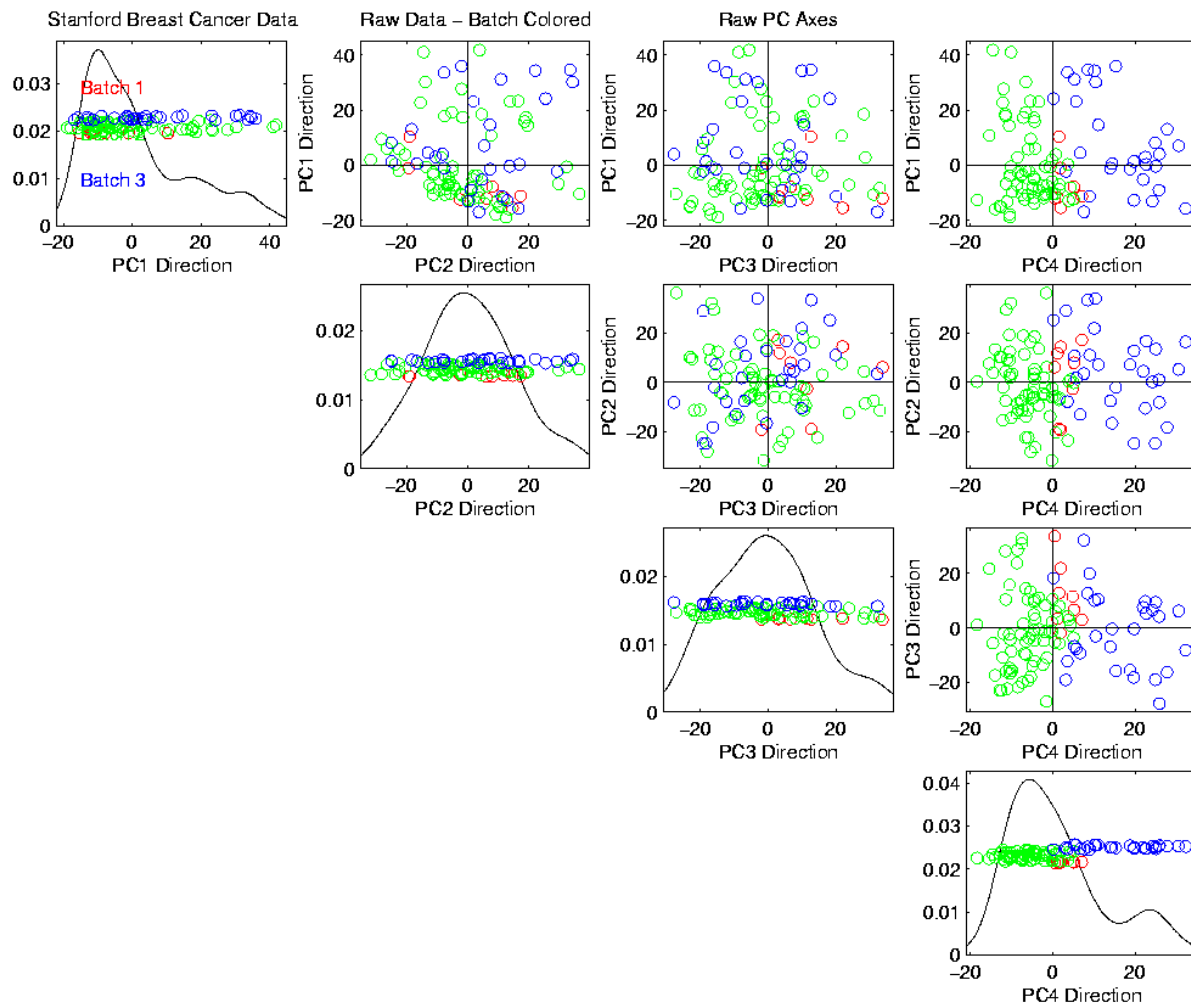
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DWD Adj: Batch Colors

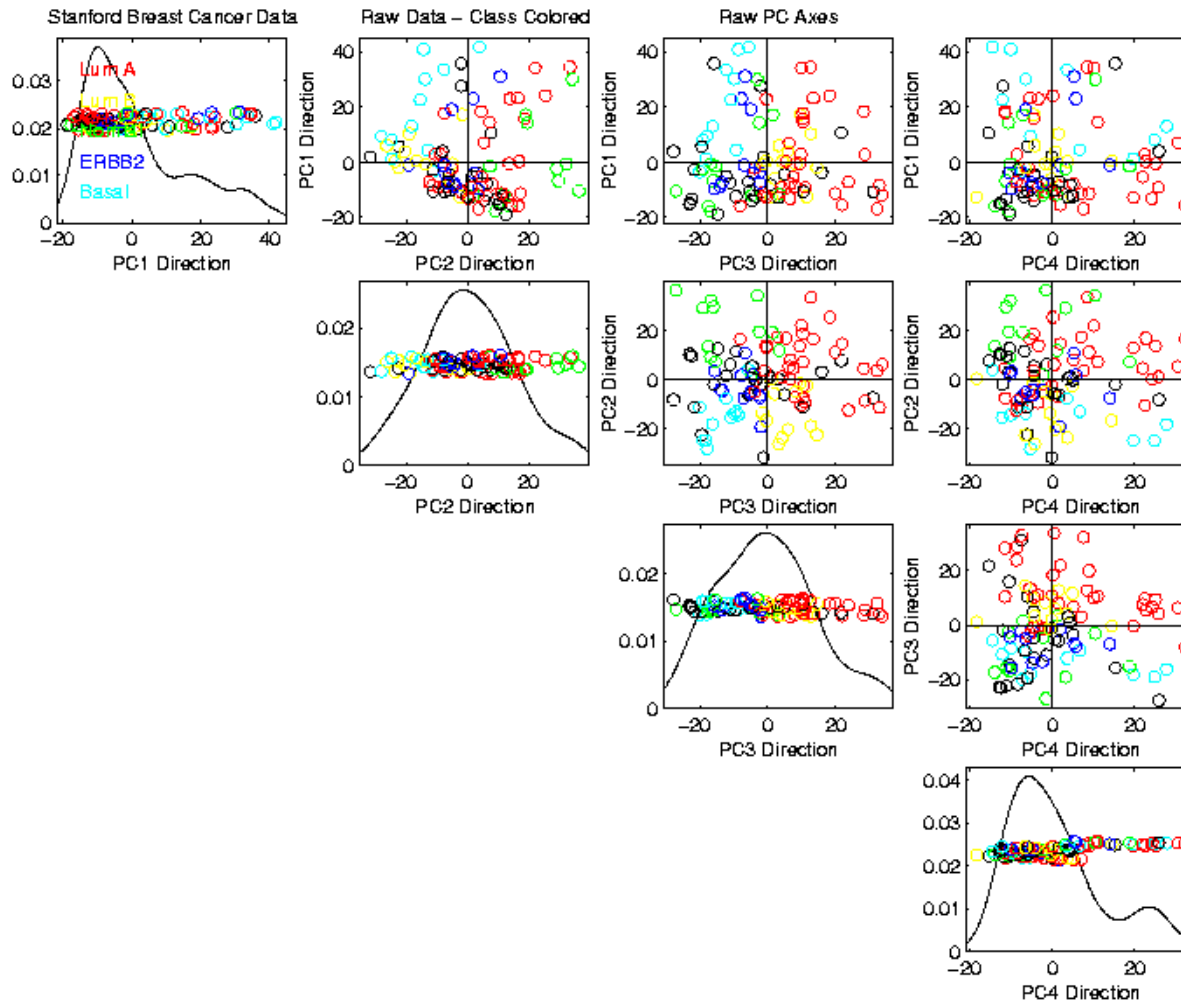
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DWD Adj: Biological Class Colors

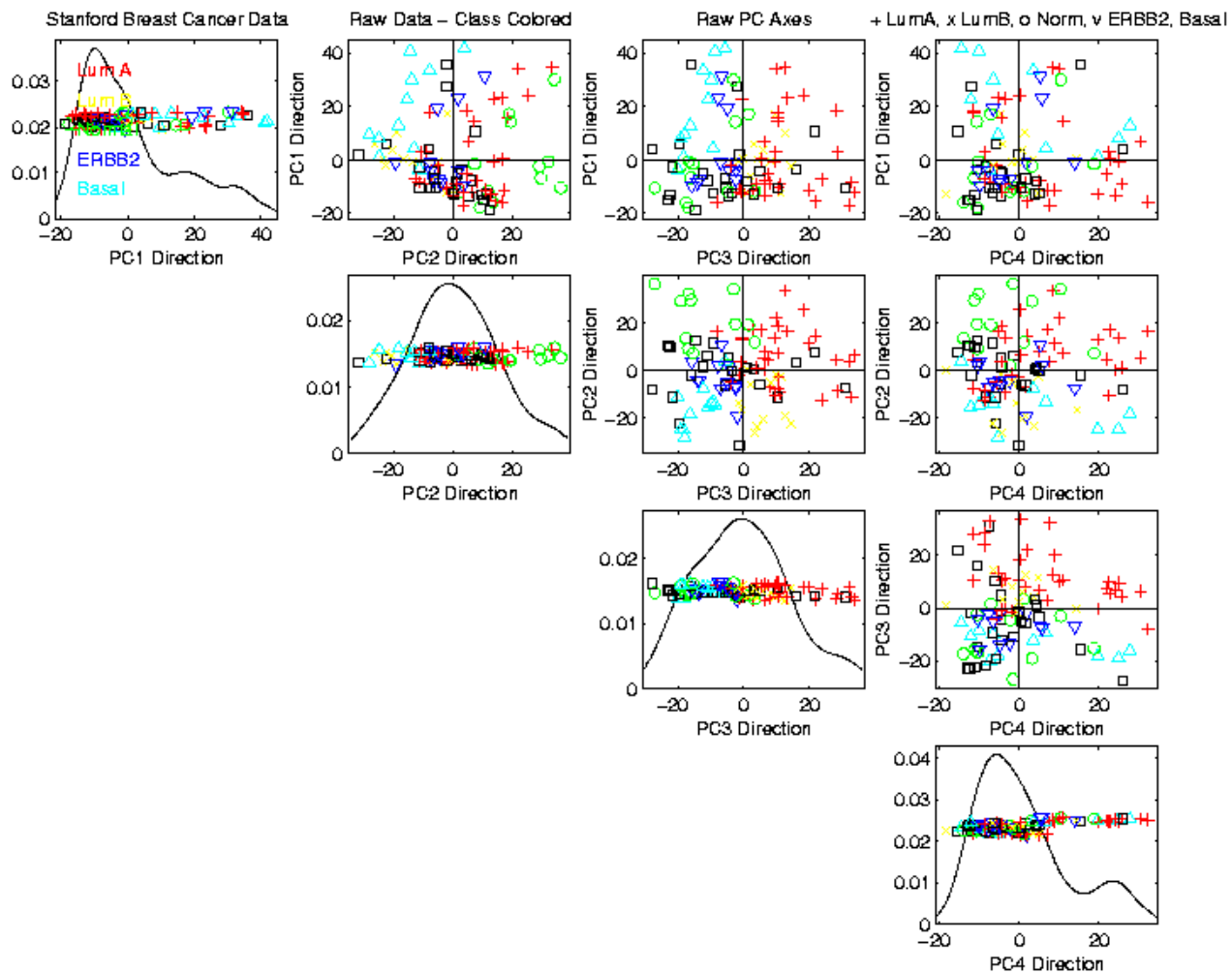
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DWD Adj: Biological Class Colors & Symbols

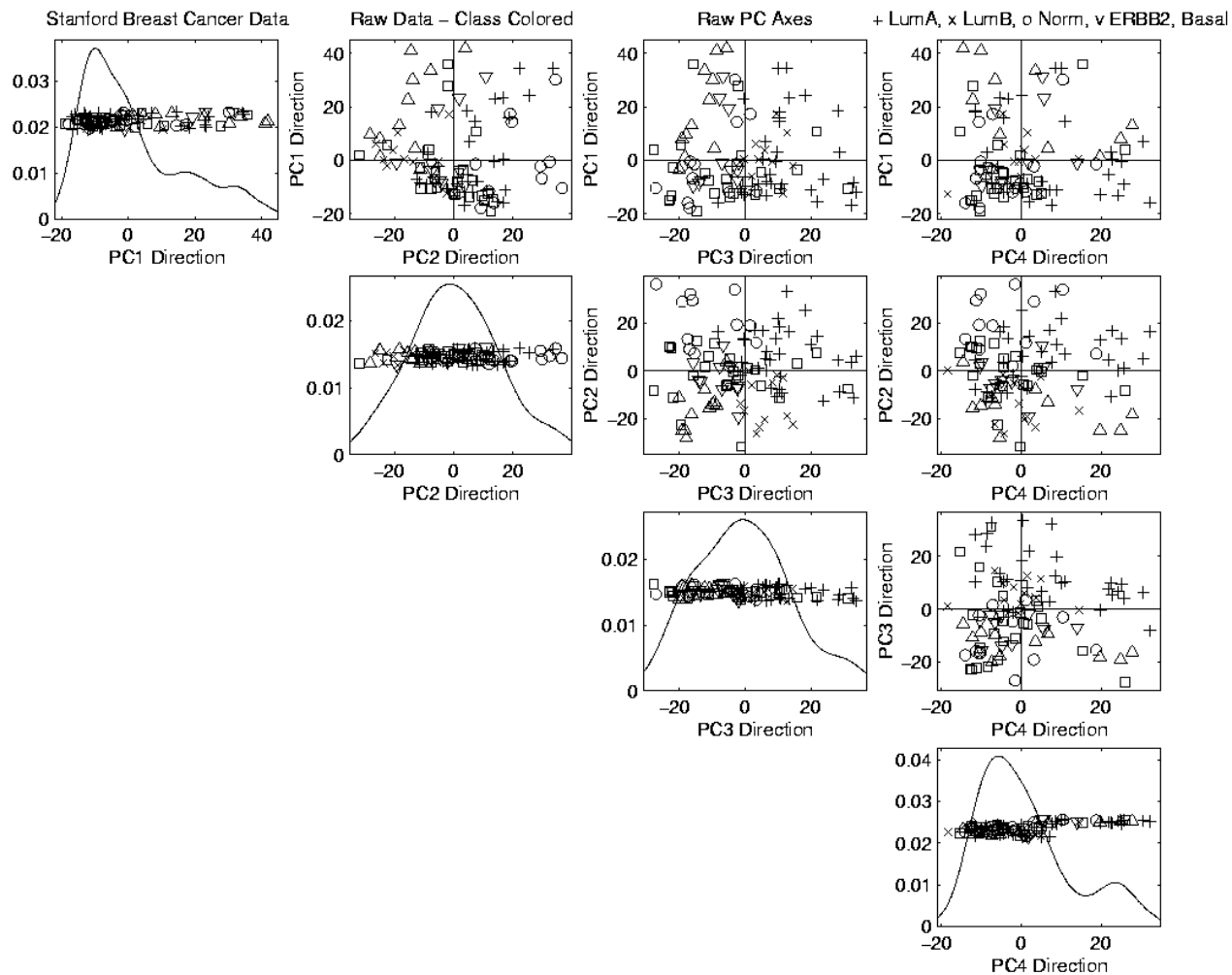
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DWD Adj: Biological Class Symbols

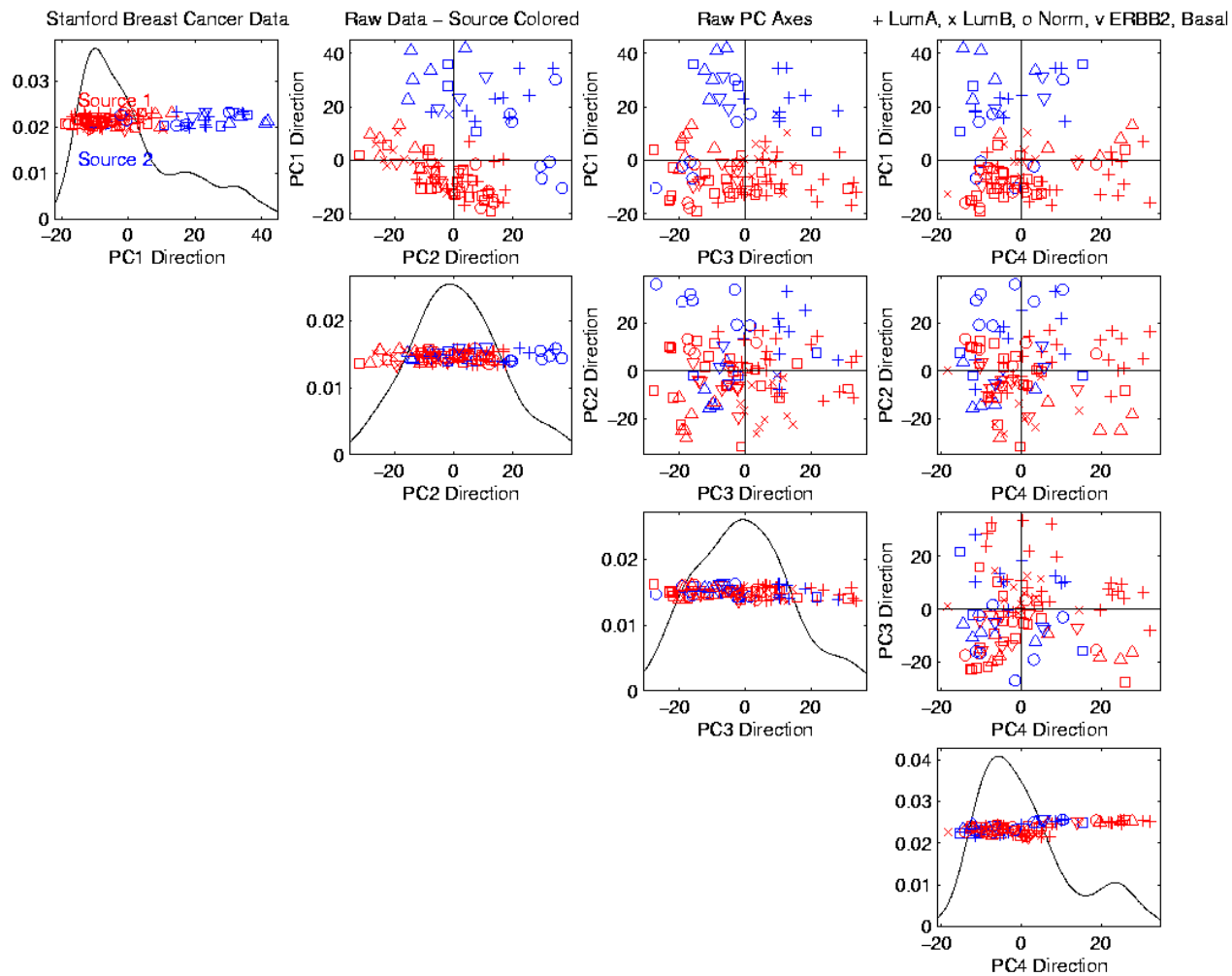
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DWD Adj: Source Colors

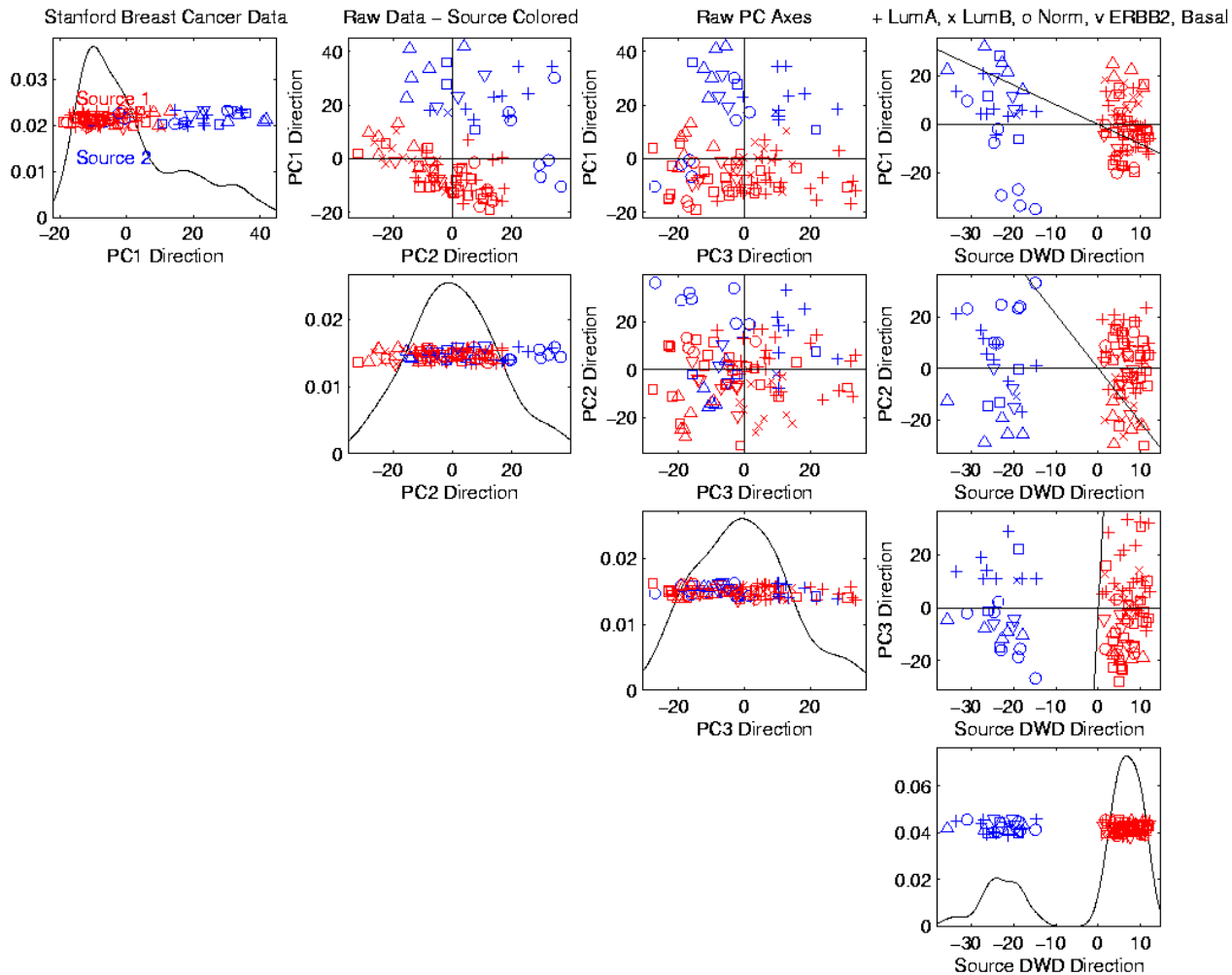
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DWD Adj: PC 1-2 & DWD direction

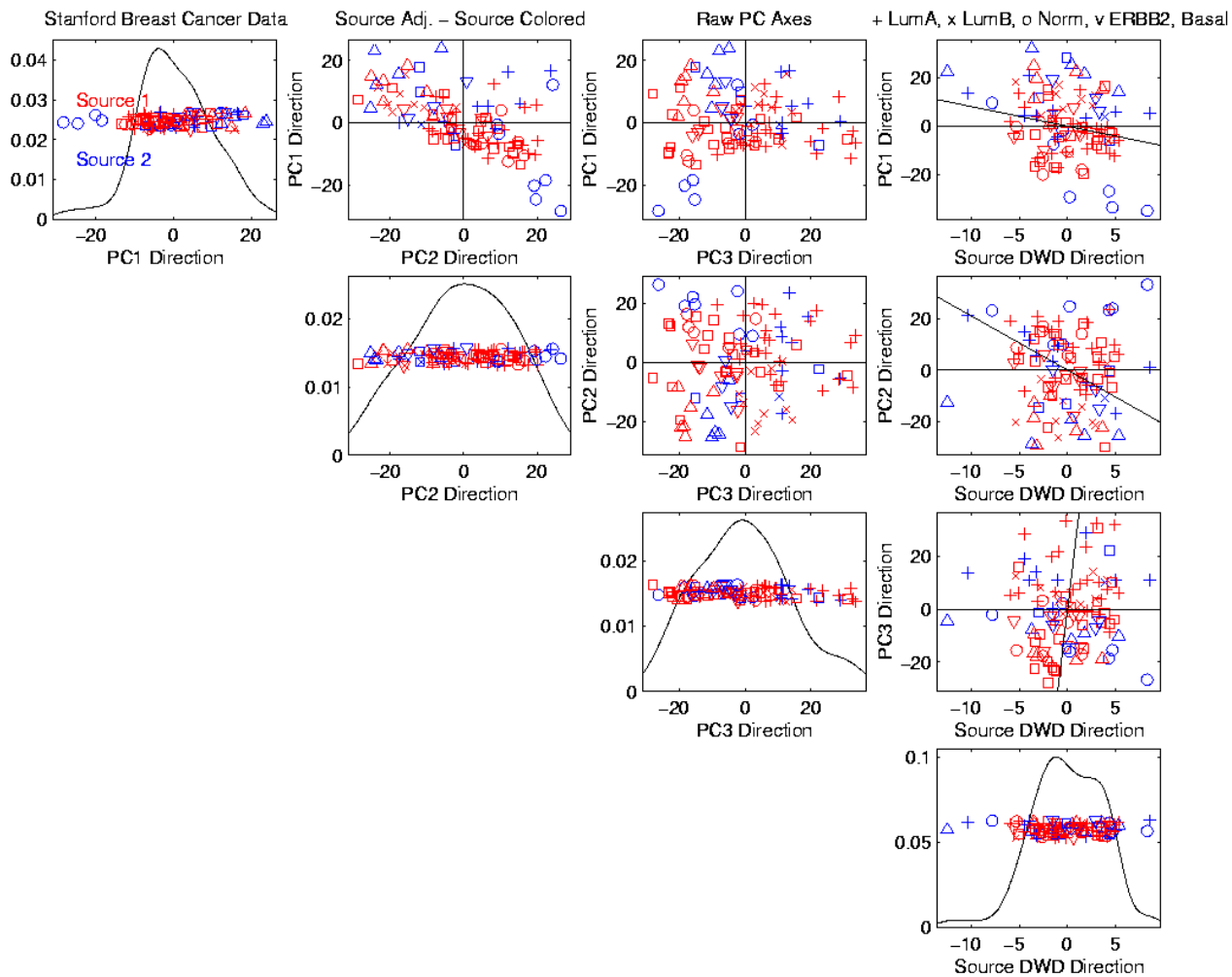
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DWD Adj: DWD Source Adjustment

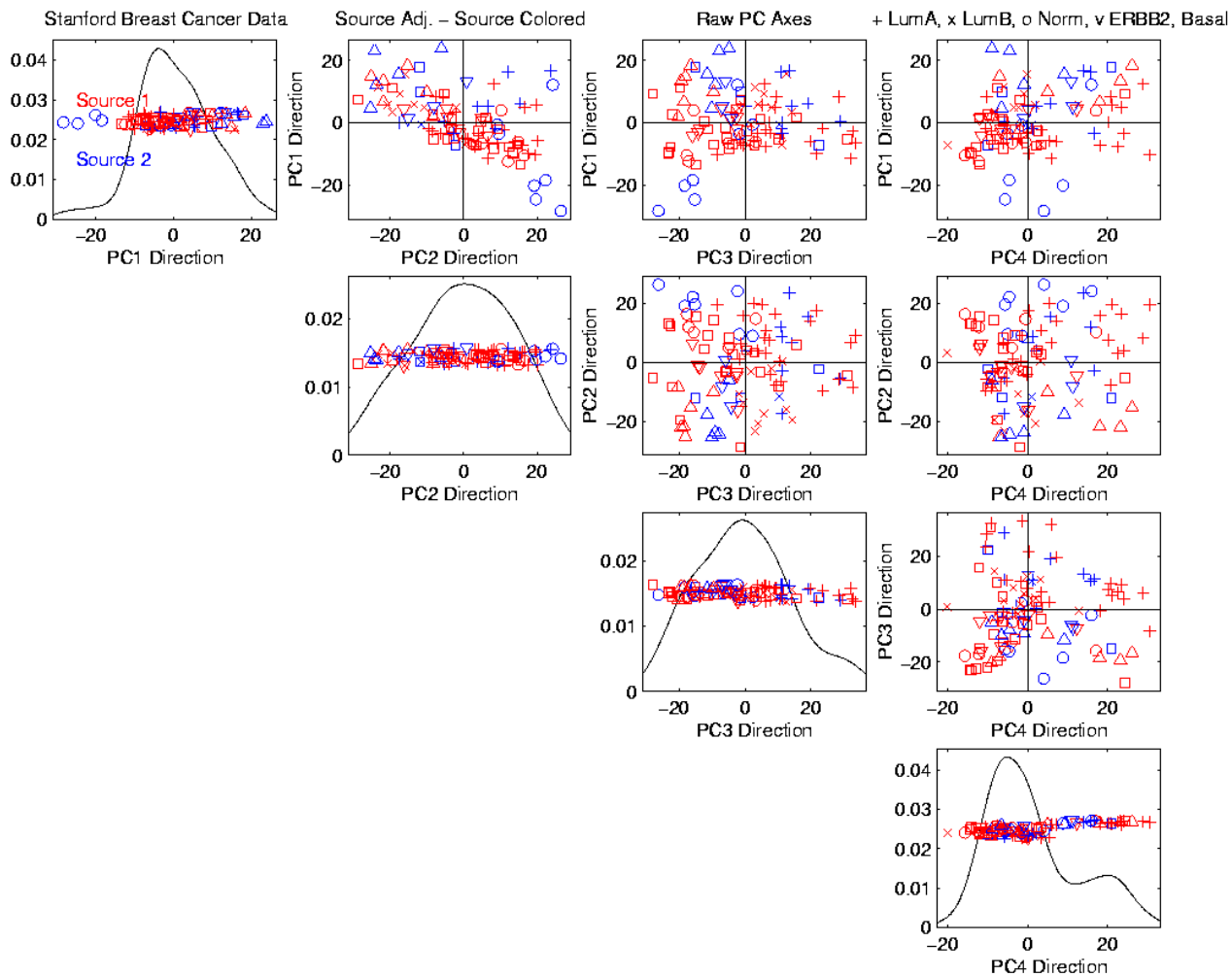
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DWD Adj: Source Adj'd, PCA view

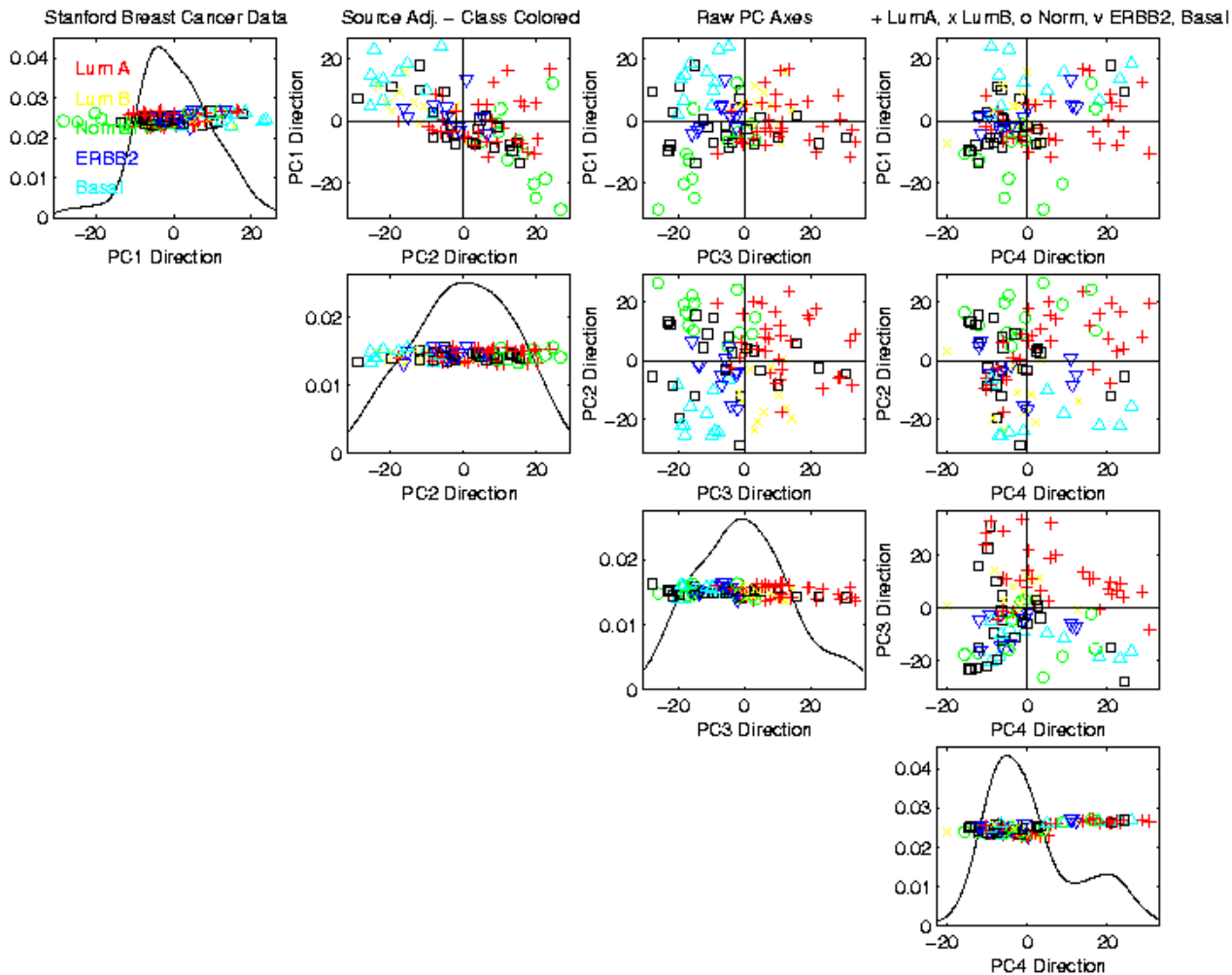
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DWD Adj: Source Adj'd, Class Colored

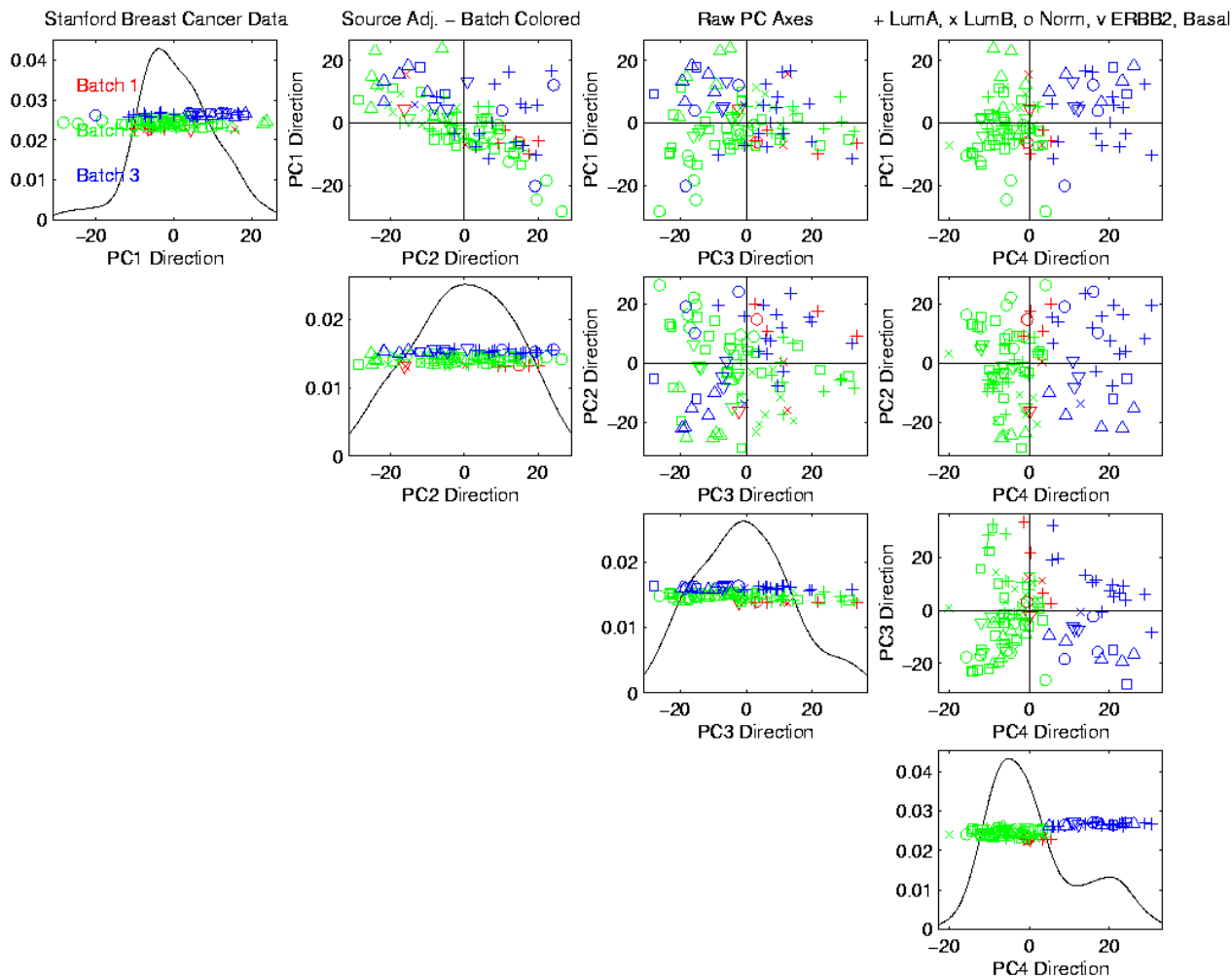
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DWD Adj: Source Adj'd, Batch Colored

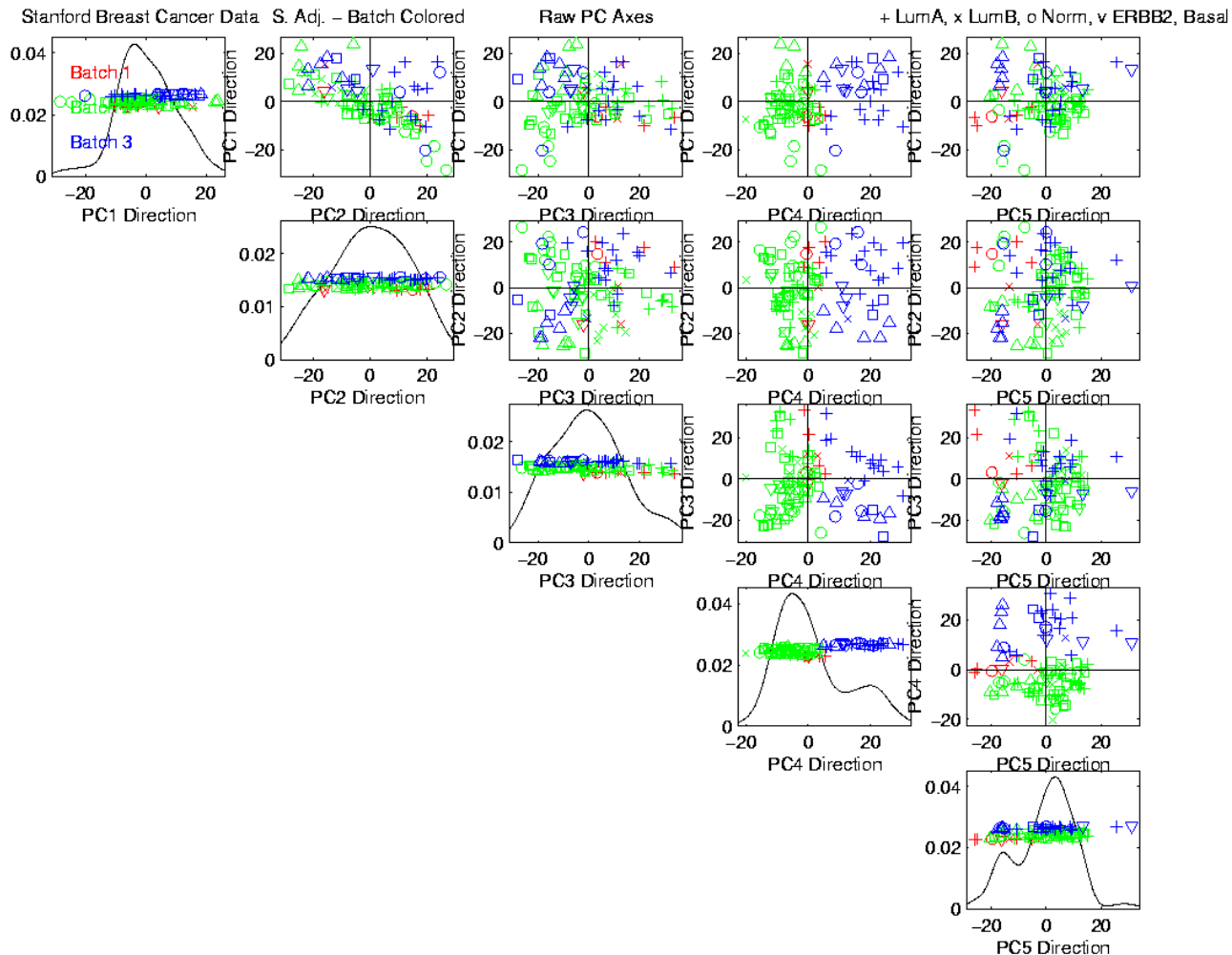
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DWD Adj: Source Adj'd, 5 PCs

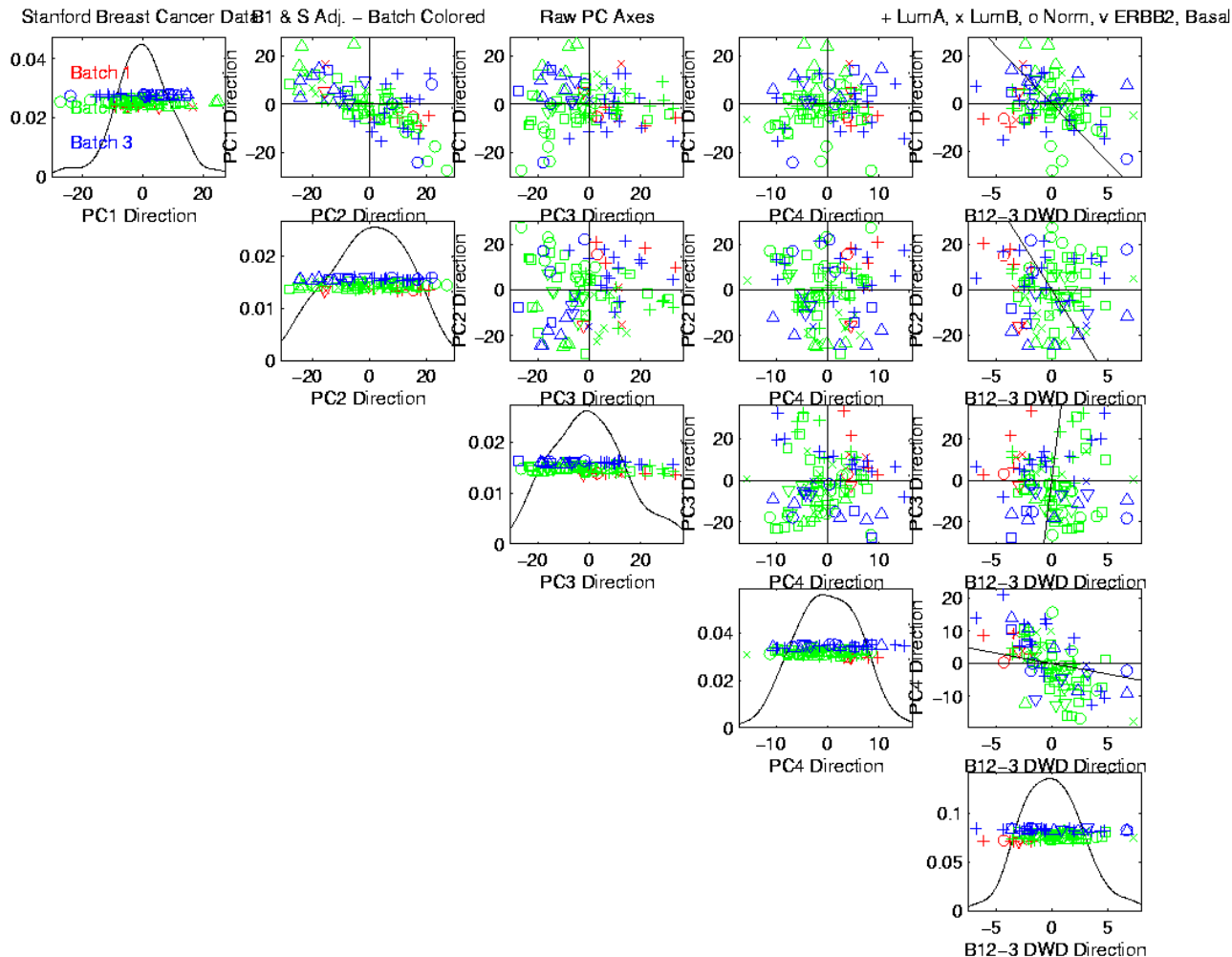
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DWD Adj: S. & B1,2 vs. 3 Adjusted

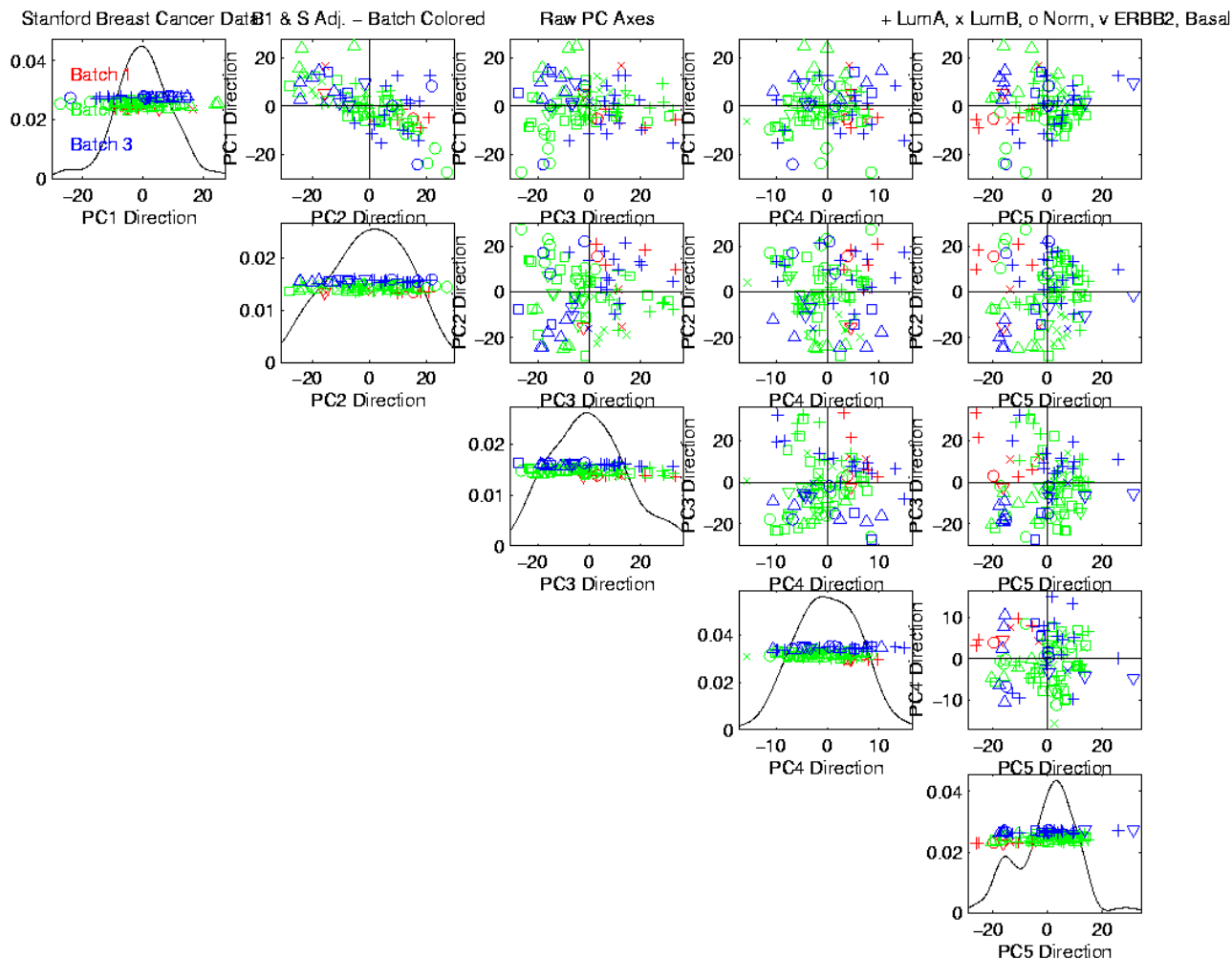
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DWD Adj: S. & B1,2 vs. 3 Adj'd, 5 PCs

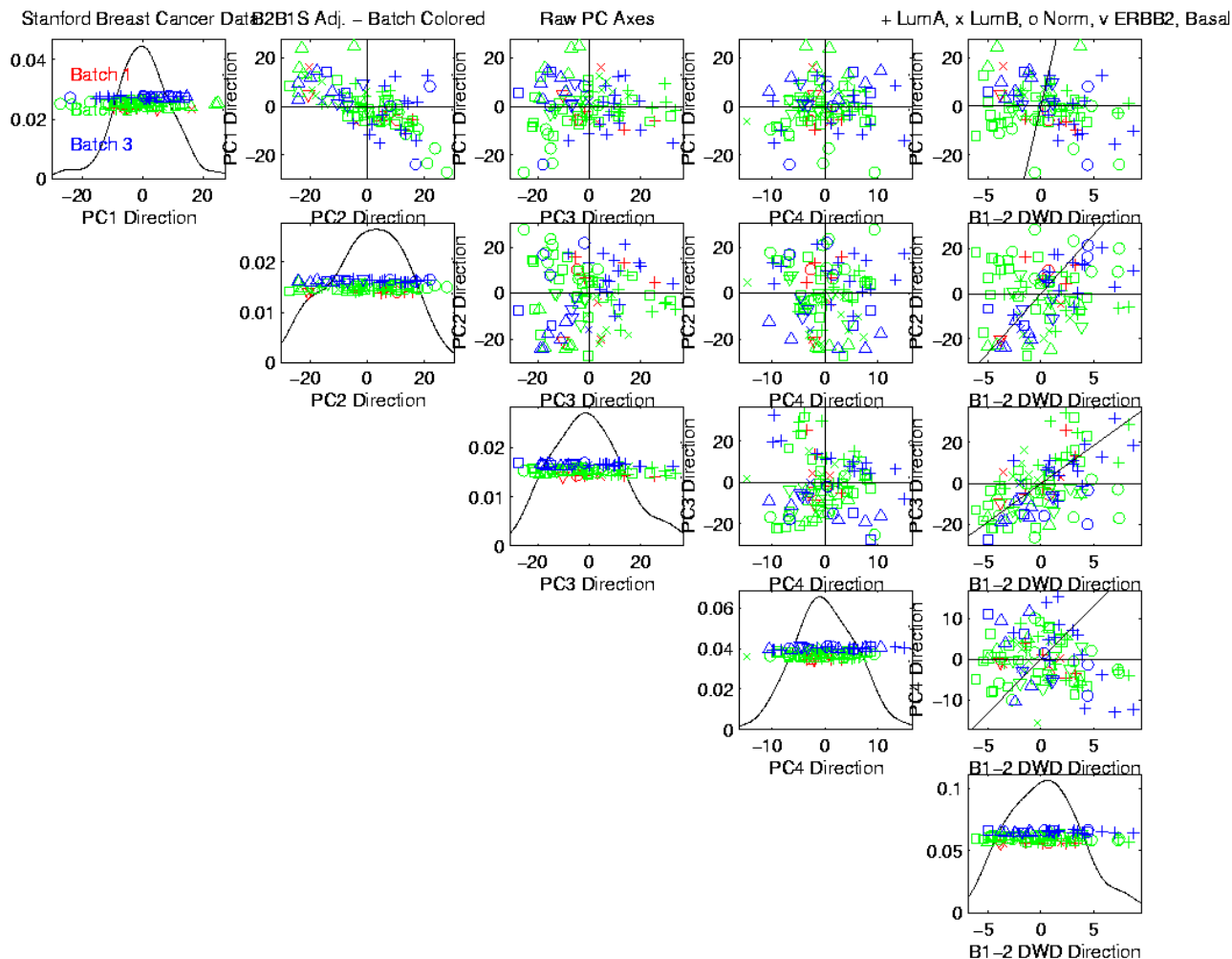
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DWD Adj: S. & B Adj'd, B1 vs. 2 Adj'd

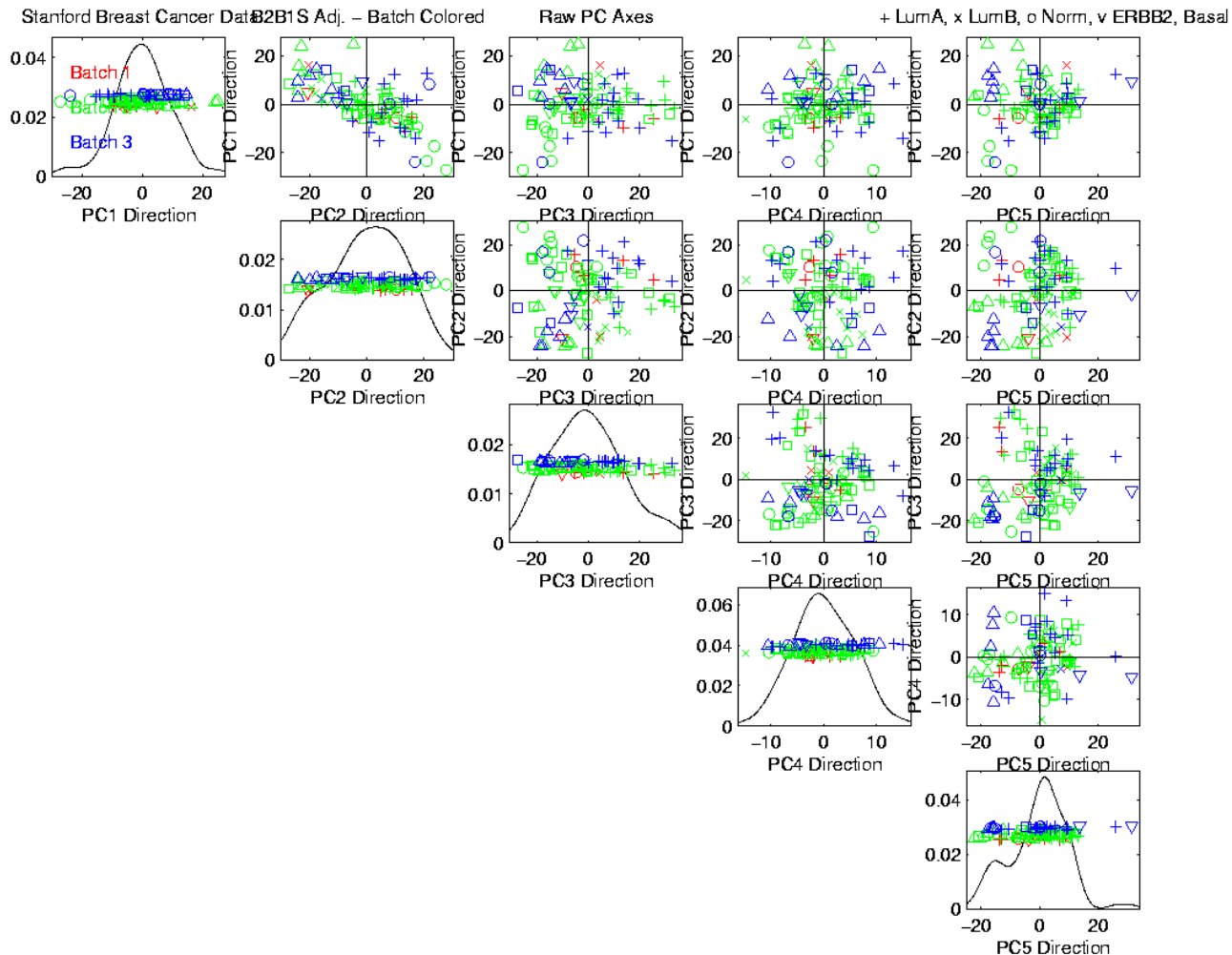
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DWD Adj: S. & B Adj'd, 5 PC view

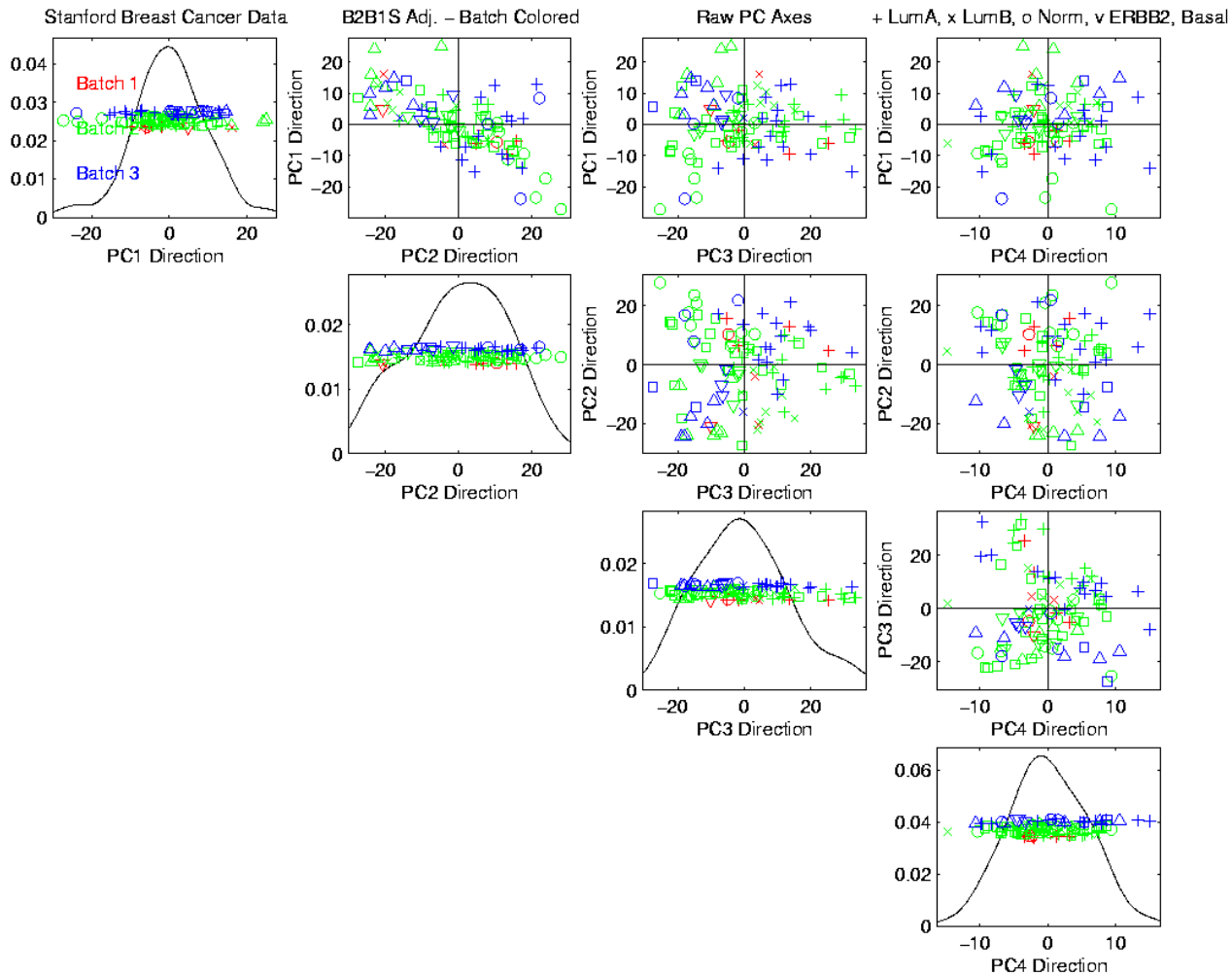
UNC, Stat & OR





DWD Adj: S. & B Adj'd, 4 PC view

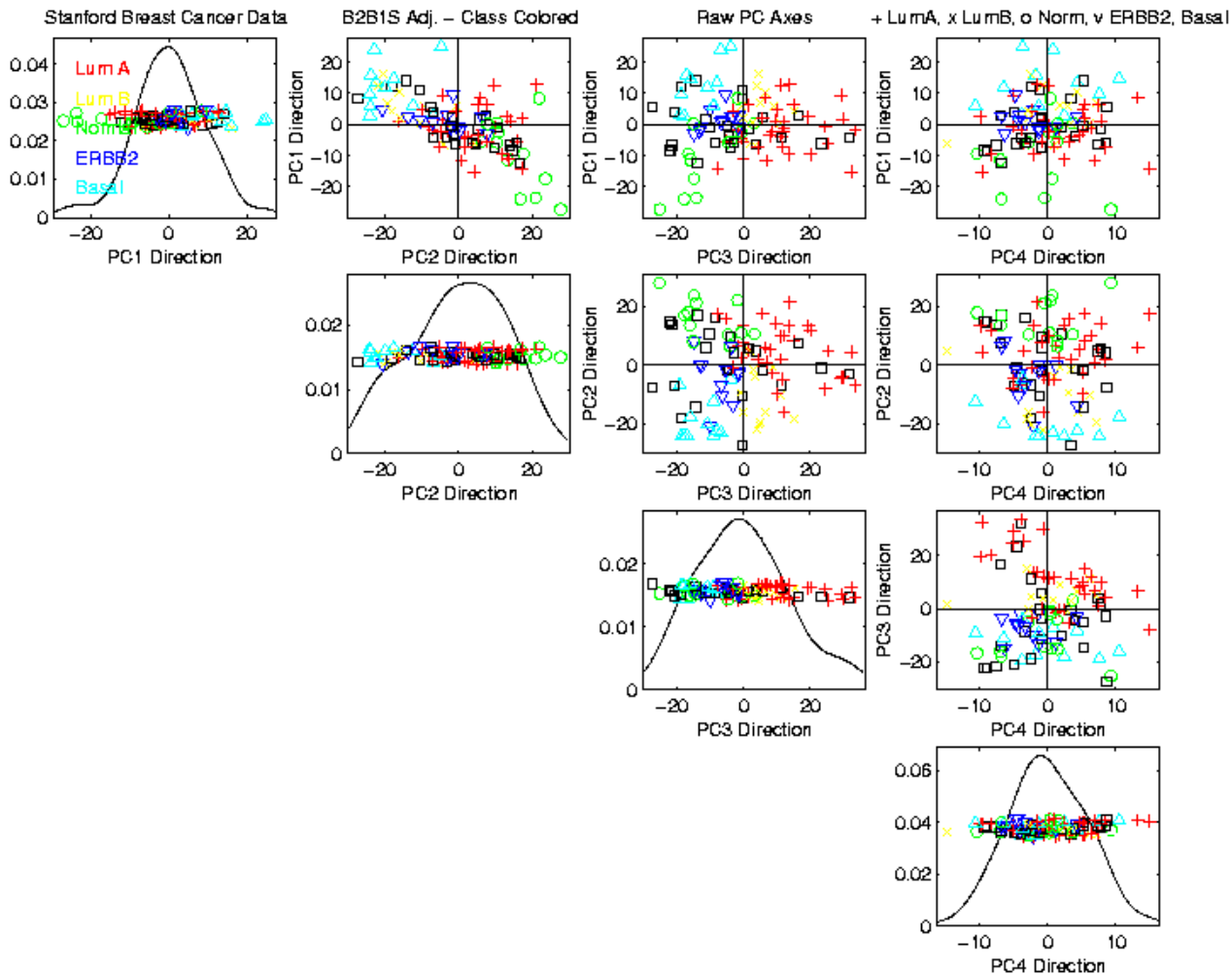
UNC, Stat & OR





DWD Adj: S. & B Adj'd, Class Colors

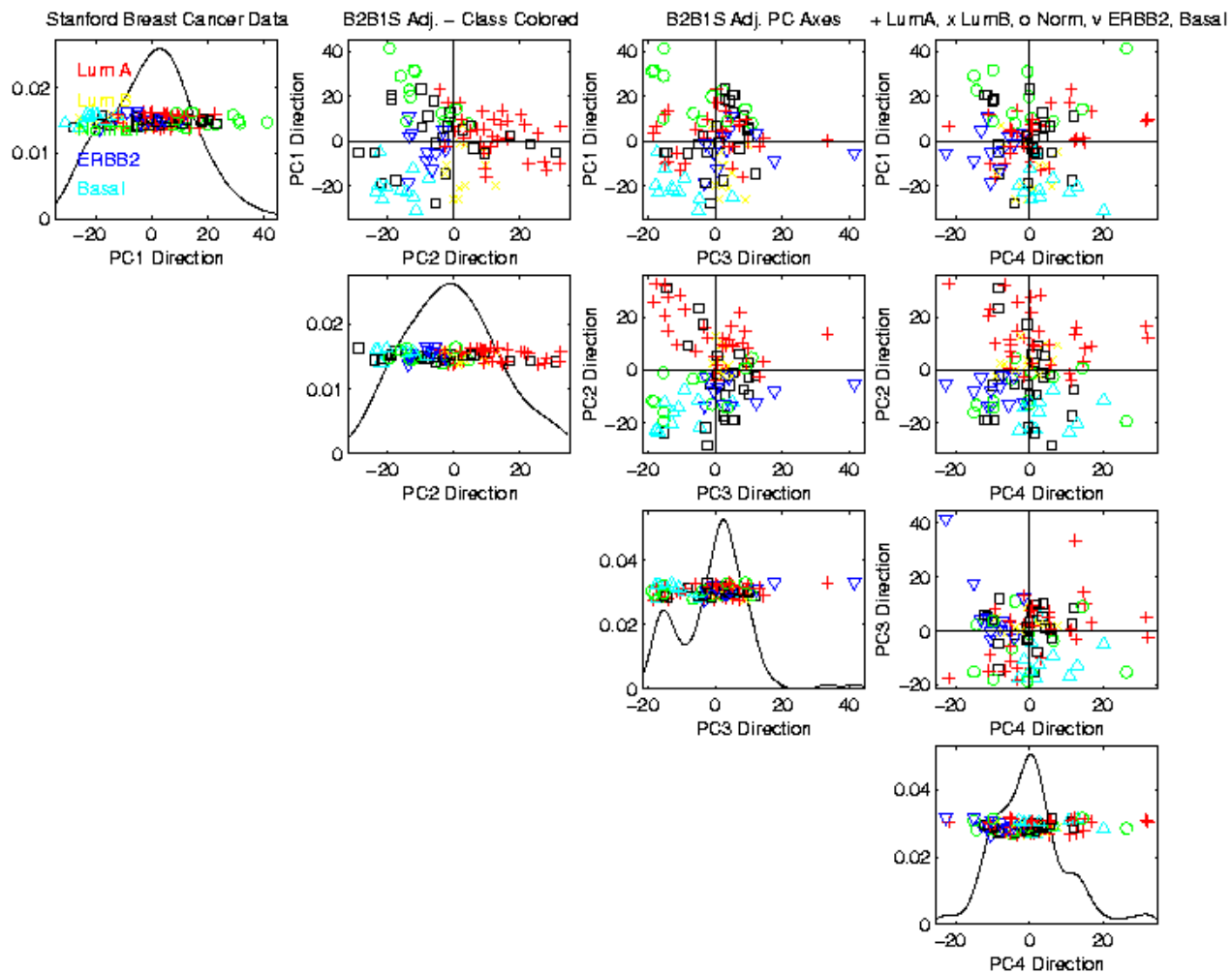
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DWD Adj: S. & B Adj'd, Adj'd PCA

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DWD Bias Adjustment for Microarrays

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- Effective for Batch and Source Adj.
 - Also works for *cross-platform Adj.*
 - E.g. cDNA & Affy
 - Despite literature claiming contrary
- “Gene by Gene” vs. “Multivariate” views
- Funded as part of caBIG
 - “Cancer BioInformatics Grid”
 - “Data Combination Effort” of NCI



Interesting Benchmark Data Set

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- NCI 60 Cell Lines
 - Interesting benchmark, since *same* cells
 - Data Web available:
<http://discover.nci.nih.gov/datasetsNature2000.jsp>
 - *Both* cDNA and Affymetrix Platforms

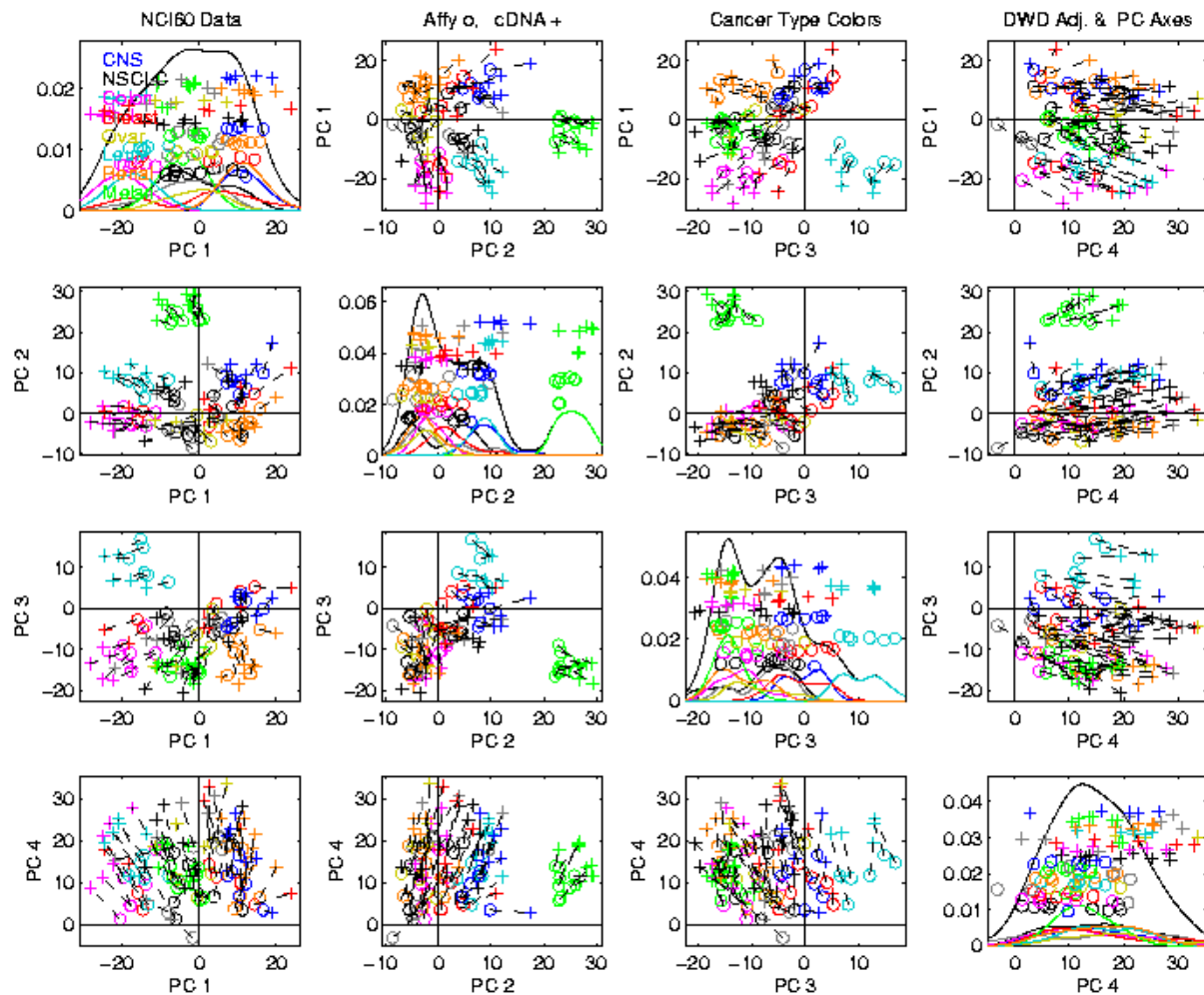
- 8 Major cancer subtypes

- Use DWD now for *visualization*



NCI 60: PCA 1-4 View & Subtype Colors

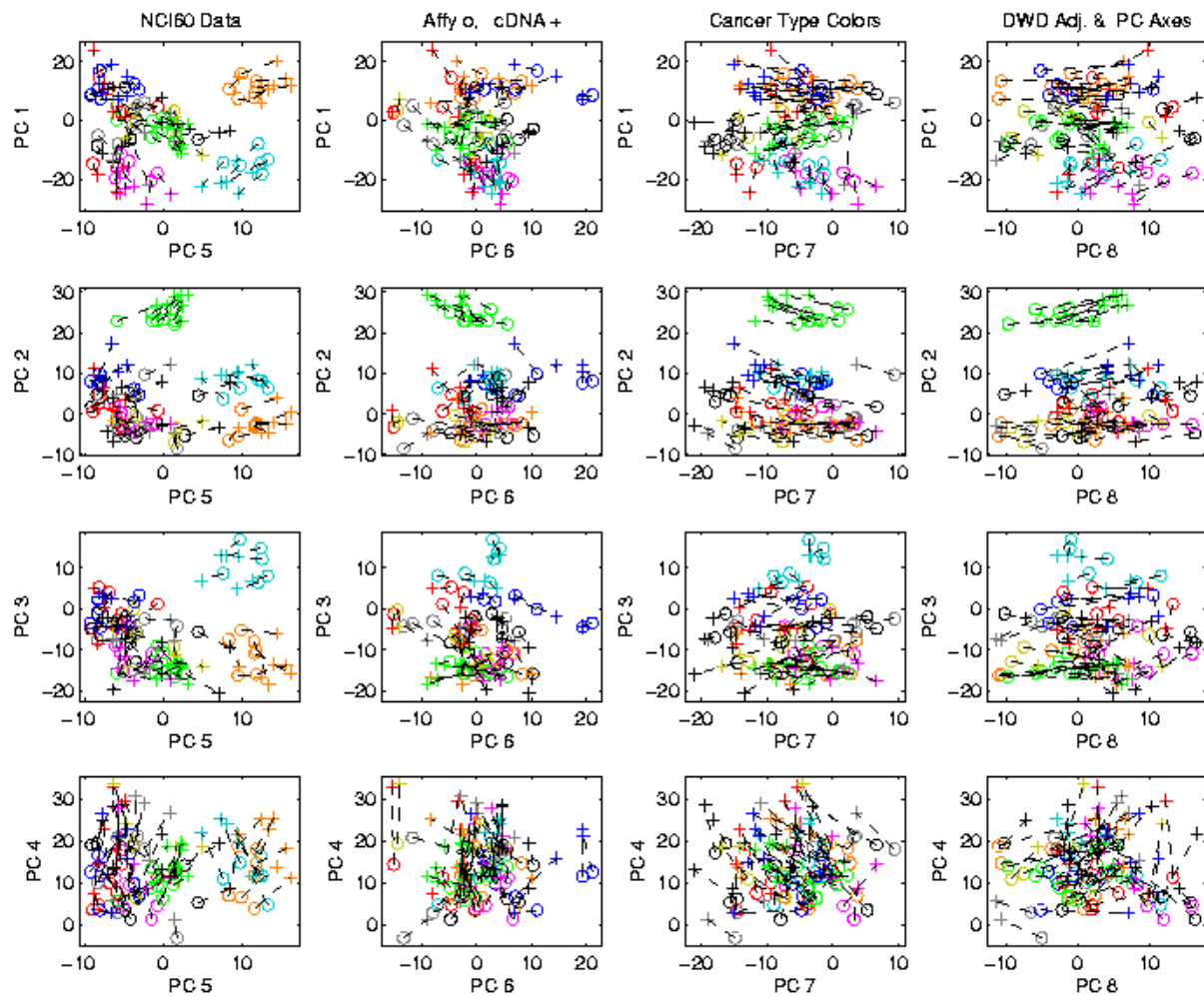
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NCI 60: PCA 1-4 vs. 5-8 View & Subtype Colors

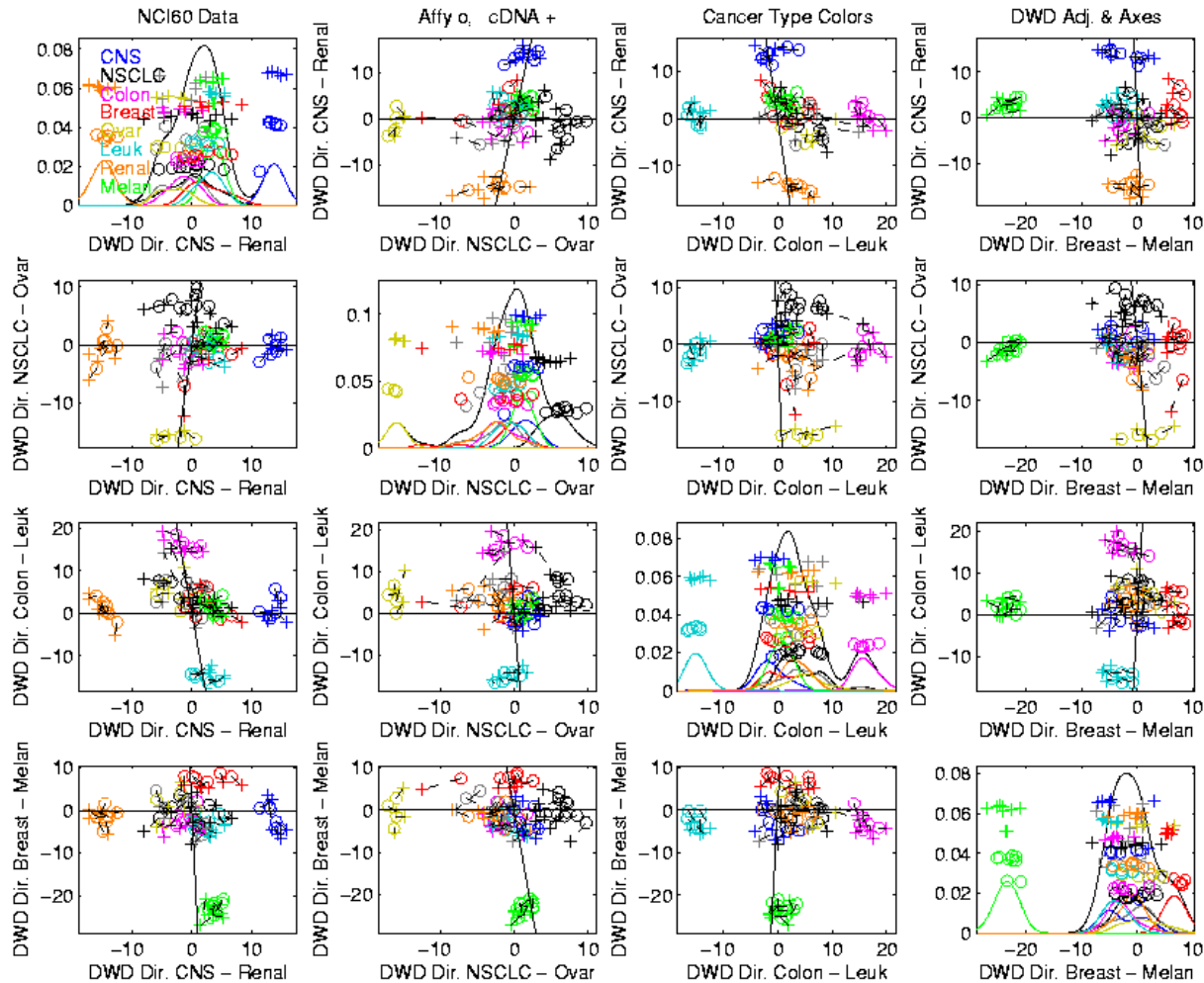
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NCI 60: Views using DWD Dir's (focus on biology)

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Why not adjust by means?

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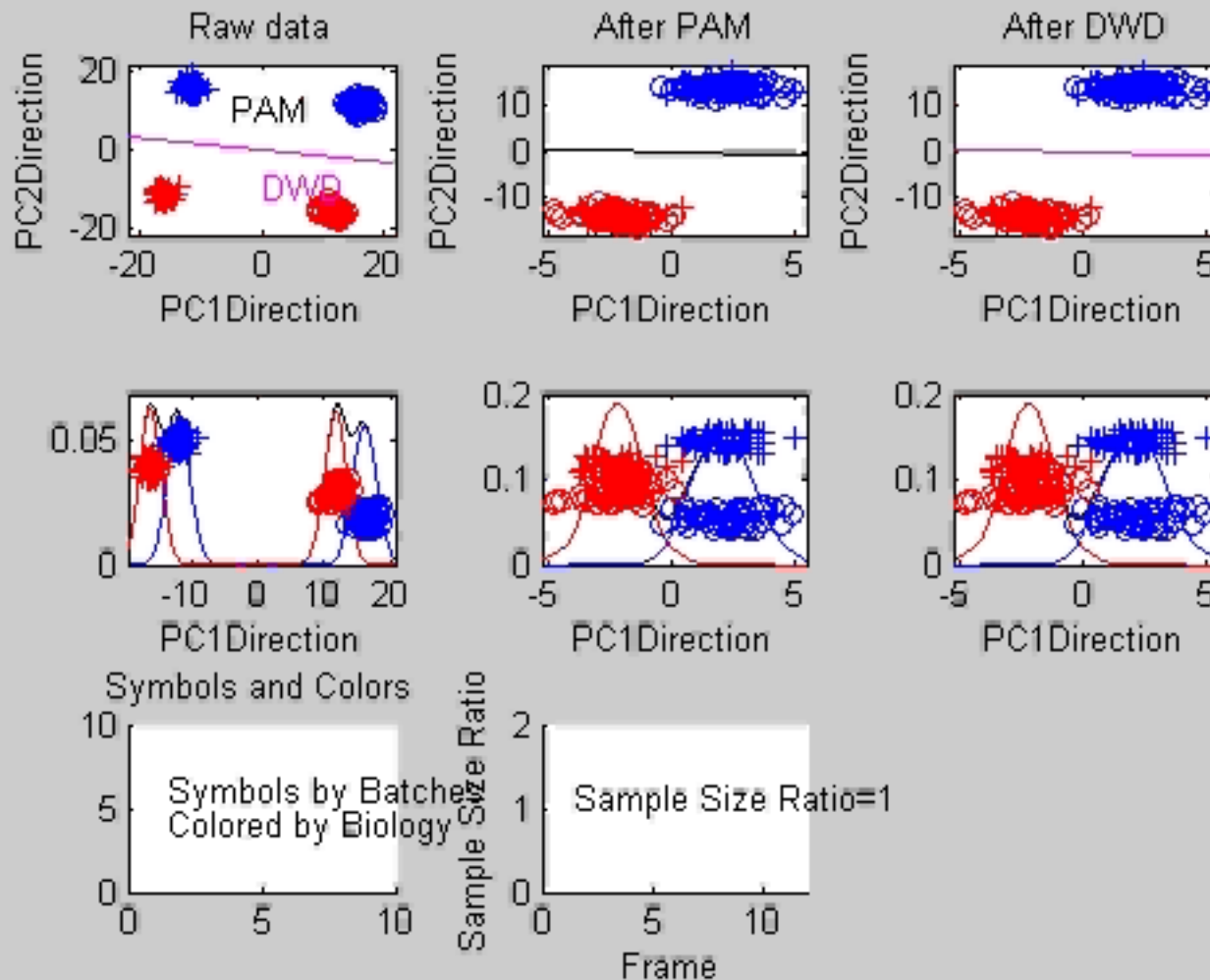
- DWD is complicated: value added?
- Xuxin Liu example...
- Key is sizes of biological subtypes
- Differing ratio trips up mean
- But DWD more robust

(although still not perfect)



Twiddle ratios of subtypes

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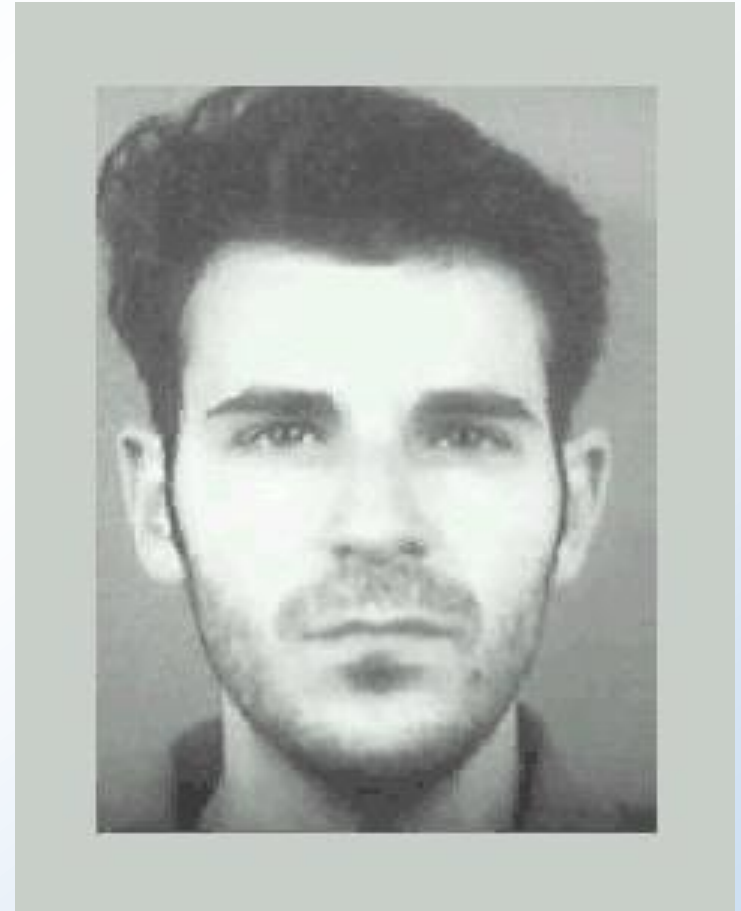




DWD in Face Recognition, I

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- Face Images as Data
(with M. Benito & D. Peña)
- Registered using landmarks
- Male – Female Difference?
- Discrimination Rule?

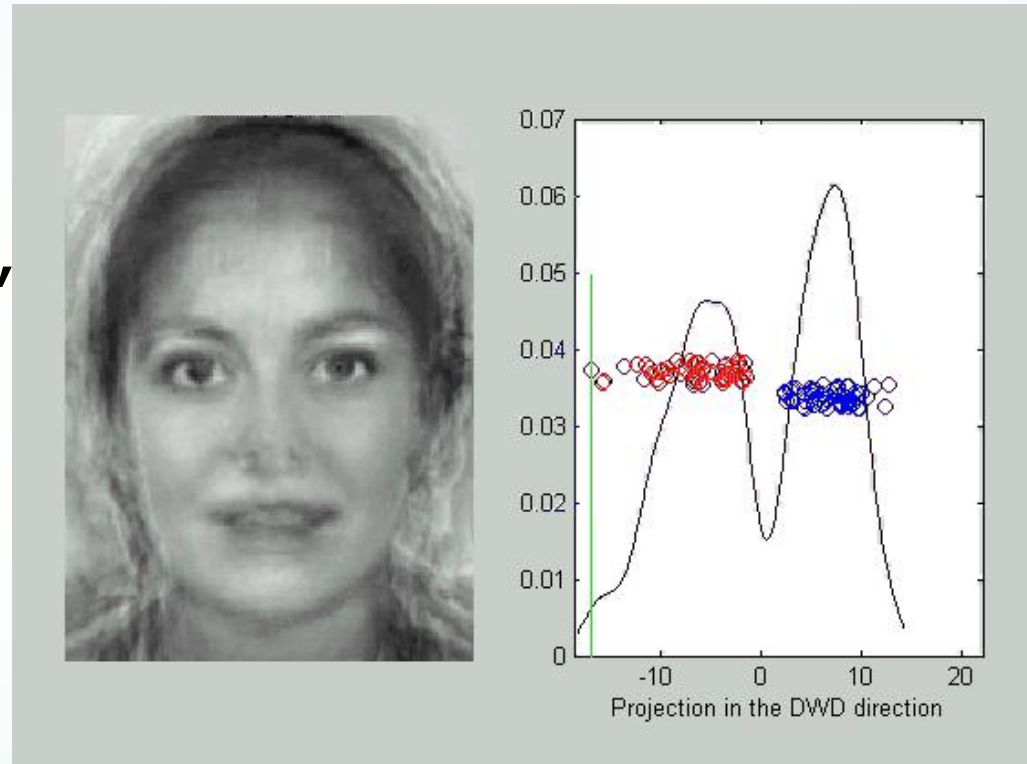




DWD in Face Recognition, II

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- DWD Direction
- Good separation
- Images “make sense”
- Garbage at ends?
(extrapolation effects?)



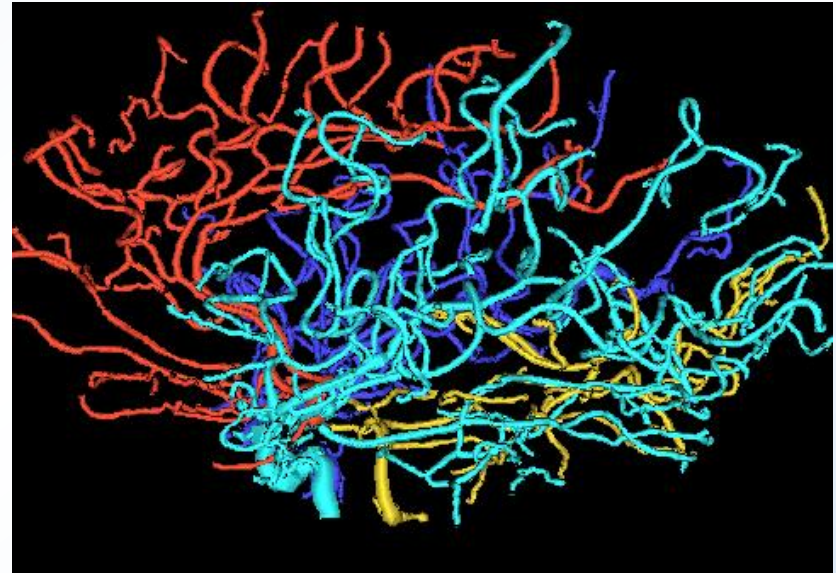


Blood vessel tree data

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Marron's brain:

- Segmented from MRA
- Reconstruct trees
- in 3d
- Rotate to view



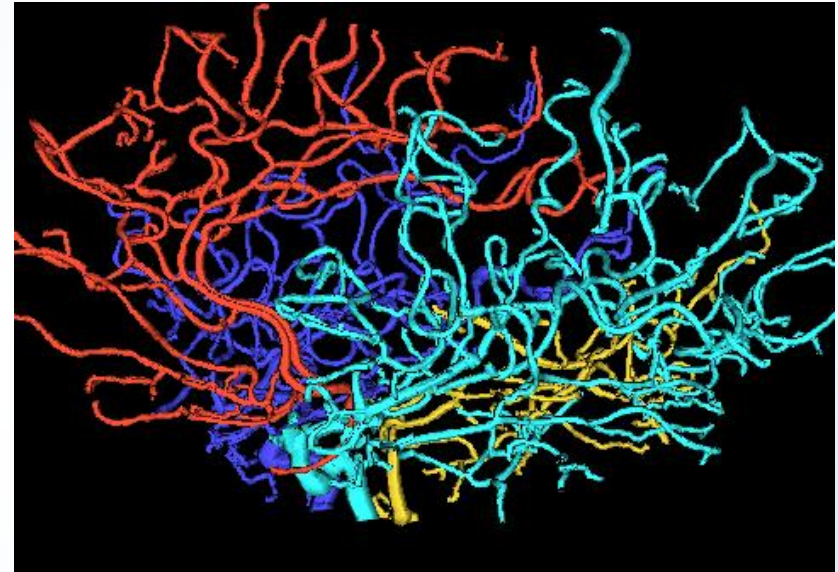


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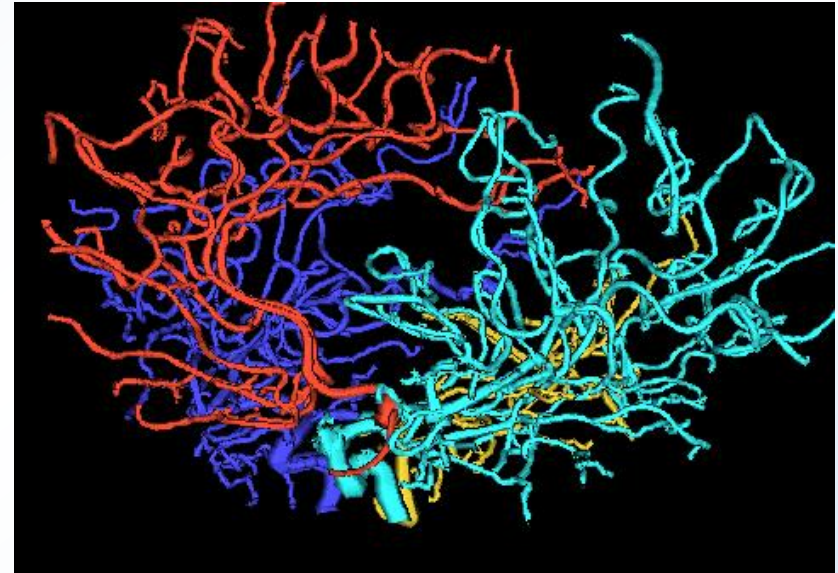


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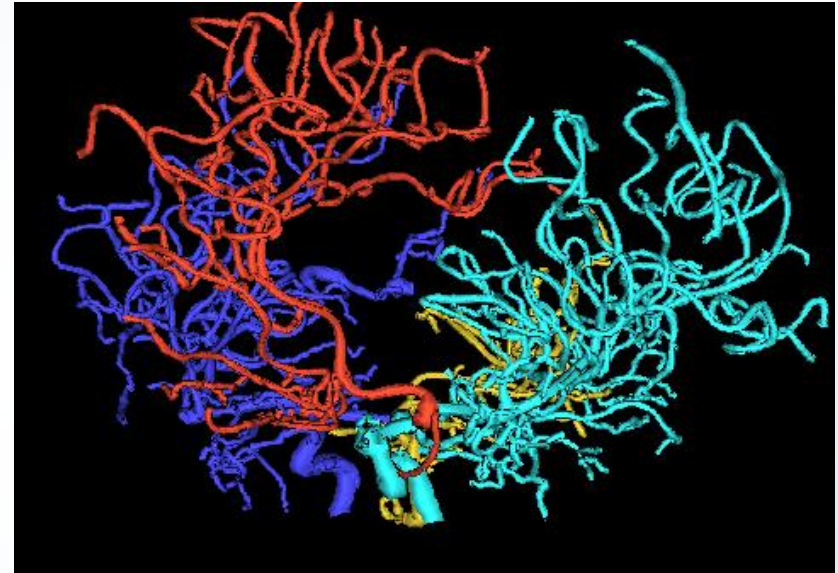


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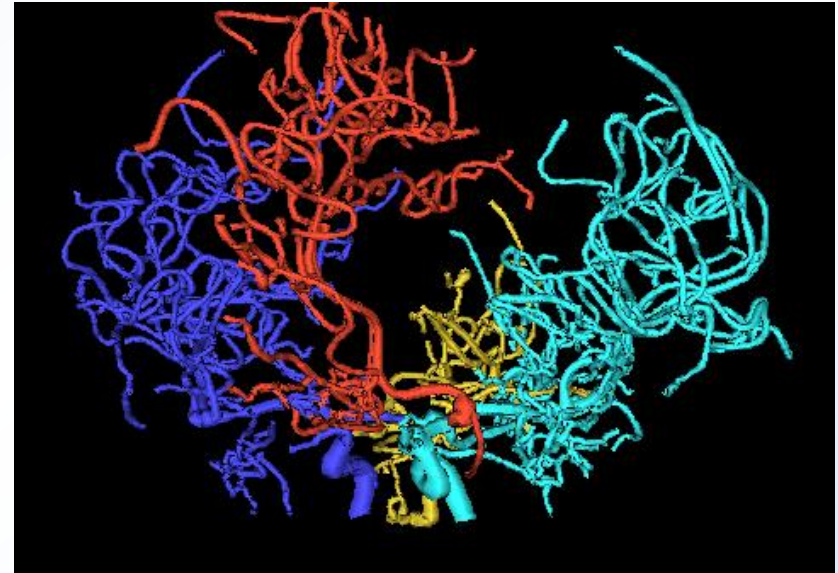


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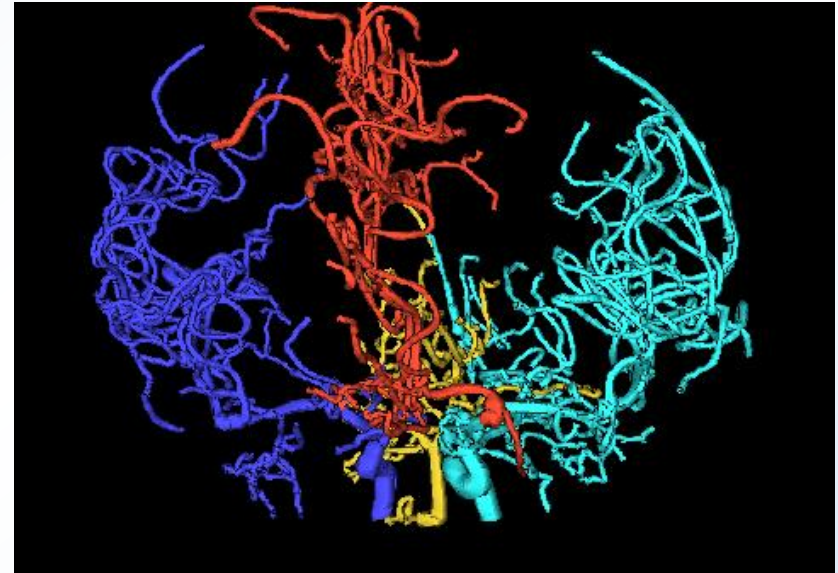


Blood vessel tree data

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Marron's brain:

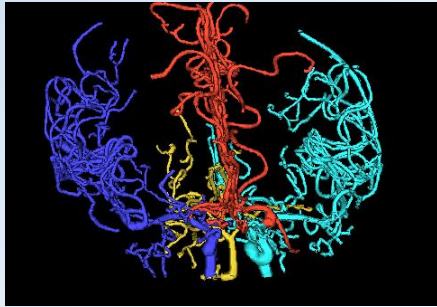
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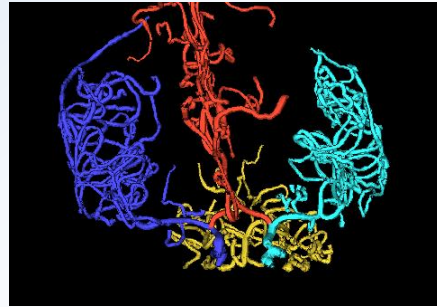


Blood vessel tree data

UNC, Stat & OR



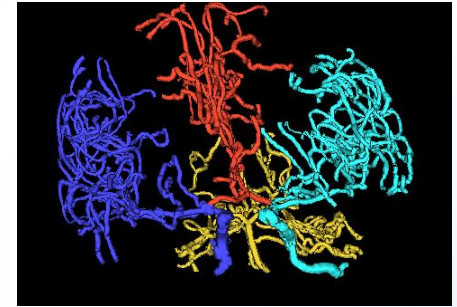
/



/

...

/



Now look over many people (data objects)

Structure of population (understand variation?)

PCA in strongly non-Euclidean Space???



Blood vessel tree data

UNC, Stat & OR

Big Picture: 4 Approaches

1. Purely Combinatorial

2. Euclidean Orthant

3. Harris Correspondence

4. Persistent Homologies



Time Series of Data Objects

UNC, Stat & OR

Mortality Data Illustrates an Important Point:

OODA is more than a “framework”

It Provides a Focal Point

Highlights Pivotal Choice:

What should be the Data Objects?



Time Series of Data Objects

UNC, Stat & OR

Another Interesting Data Set:

- Chemical Spectra
- Evolving over time
- Studying aging of compounds
- Under different conditions
- From Ed Kober, LANL



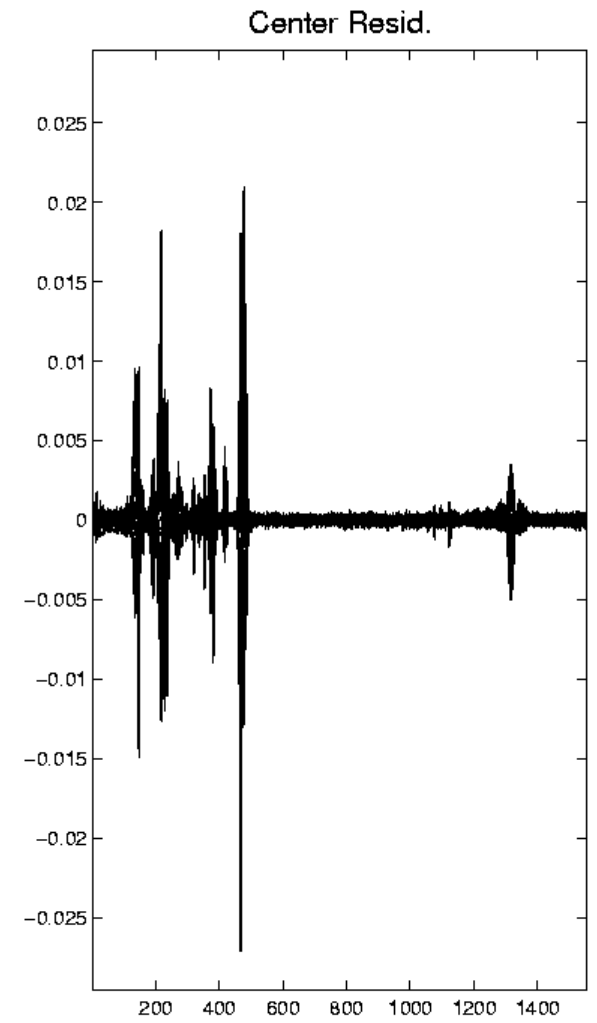
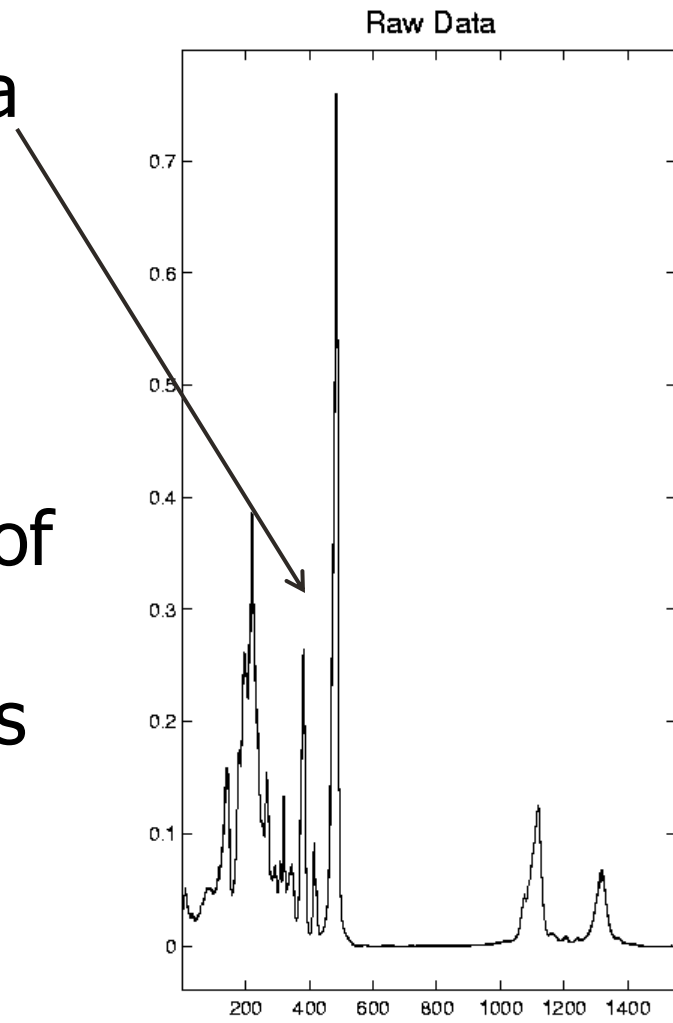
Time Series of Chemical Spectra

UNC, Stat & OR

77 Spectra

Hard to
See Them

(because of
small
differences
and large
dynamic
range)





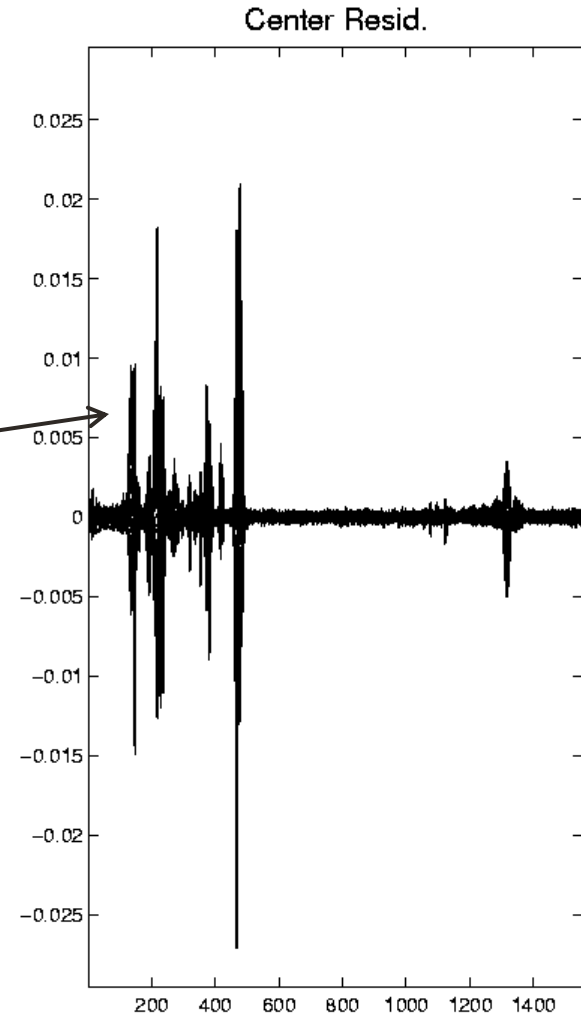
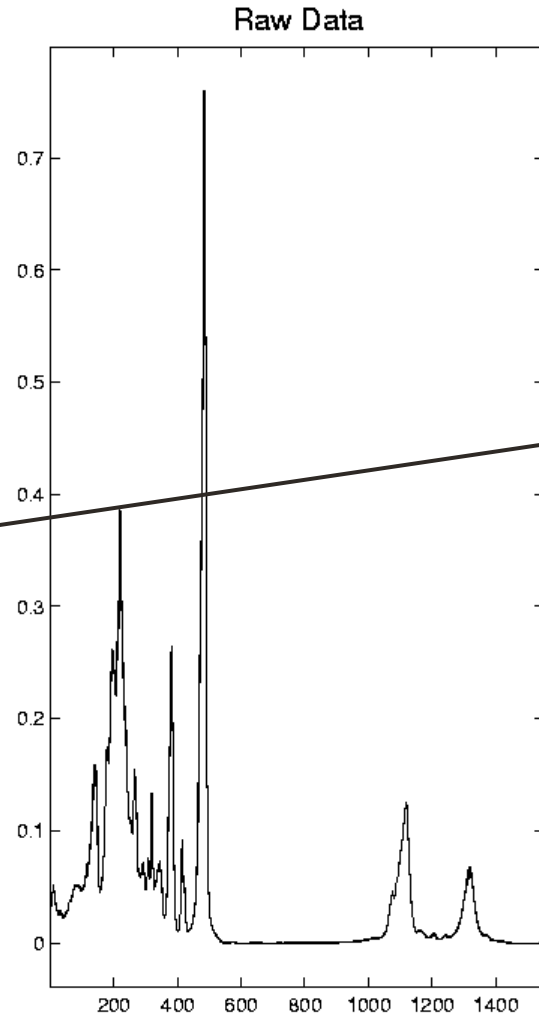
Time Series of Chemical Spectra

UNC, Stat & OR

77 Spectra

Looking at
Mean
Residuals
Helps

(But Not
Much)

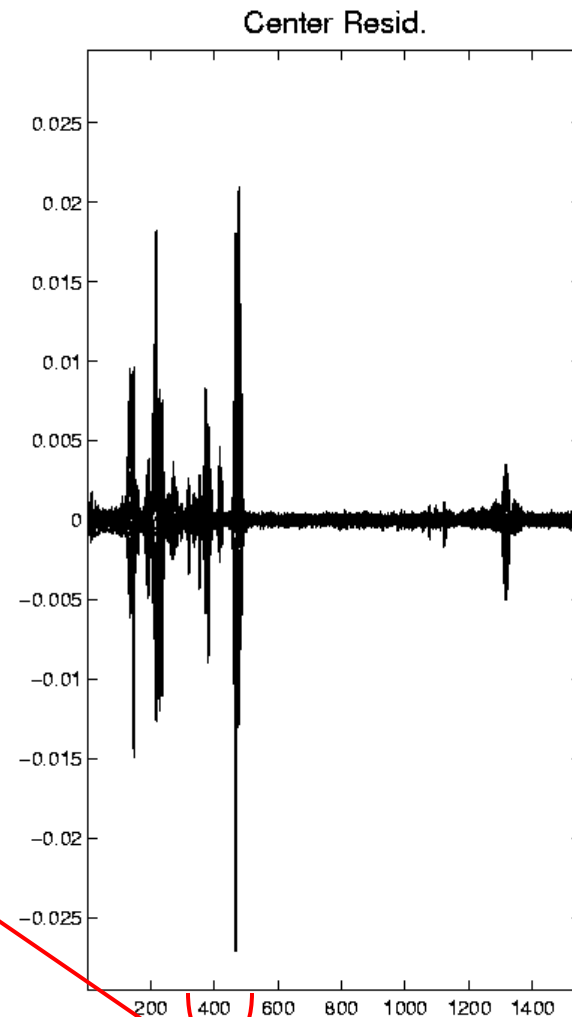
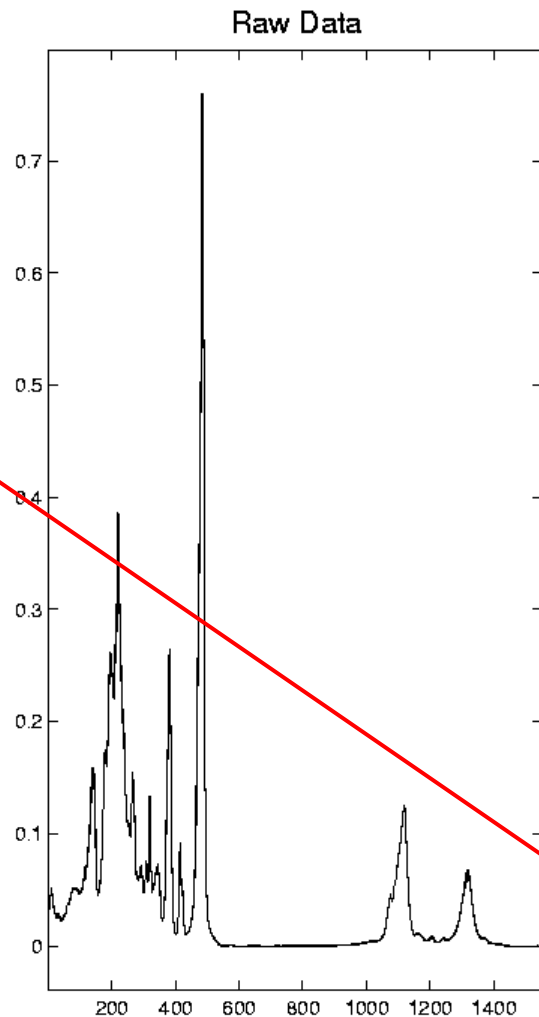




Time Series of Chemical Spectra

UNC, Stat & OR

Try Zooming
In On an
"Interesting
Window"





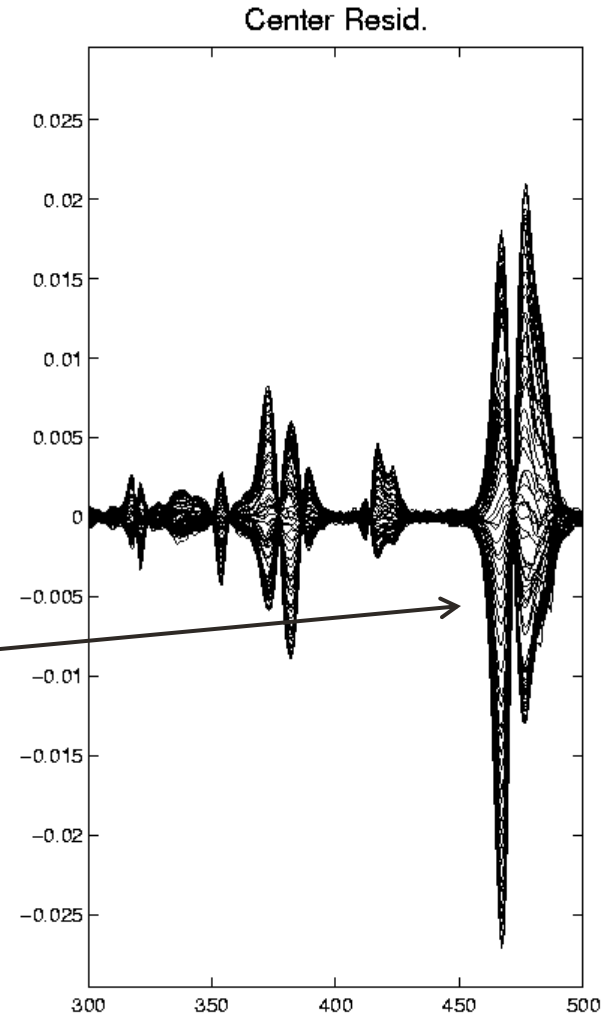
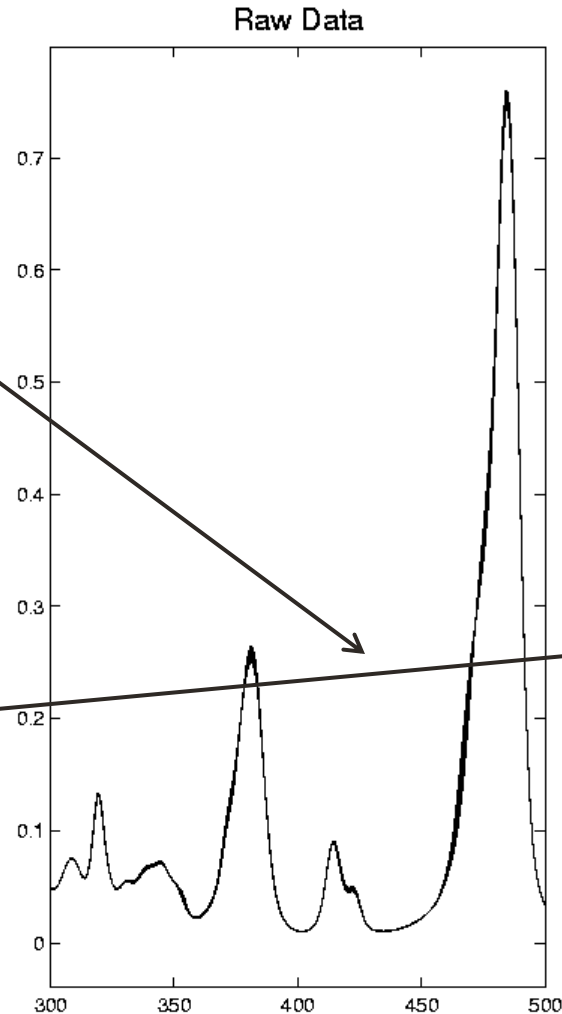
Time Series of Chemical Spectra

UNC, Stat & OR

77 Spectra

Structure
Still Lost in
Dynamic
Range

But Visible
In Mean
Residuals





Time Series of Chemical Spectra

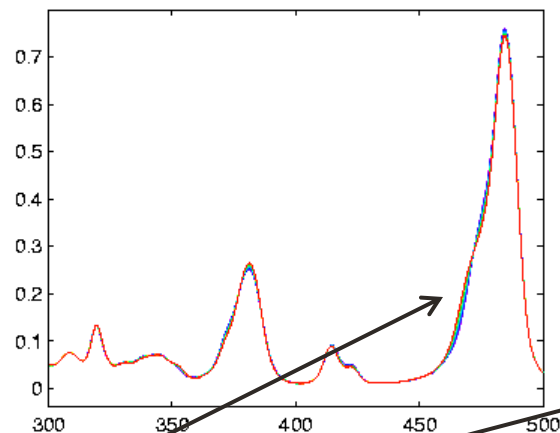
UNC, Stat & OR

Time Colors
Again Very
Helpful

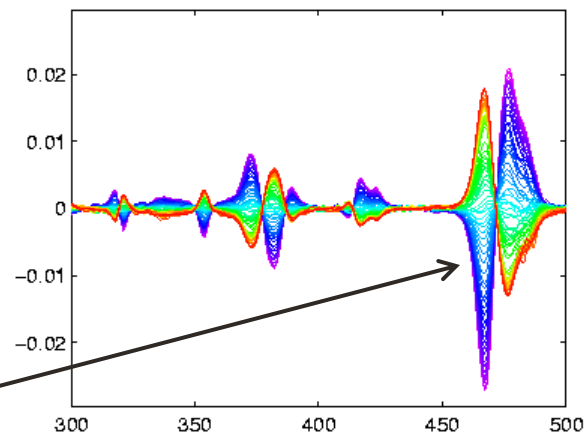
Shows Up
& Down
Behavior

(Movement
Of Mass)

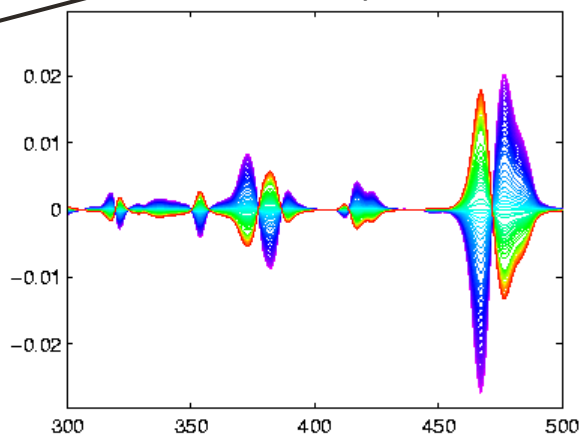
Raw Data



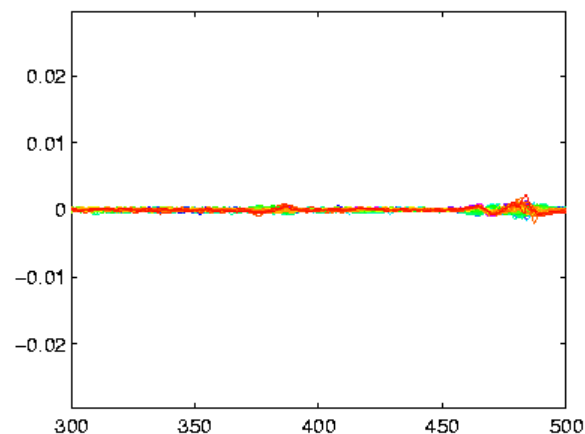
Mean Resid.



PC1 Proj.



PC1 Resid.





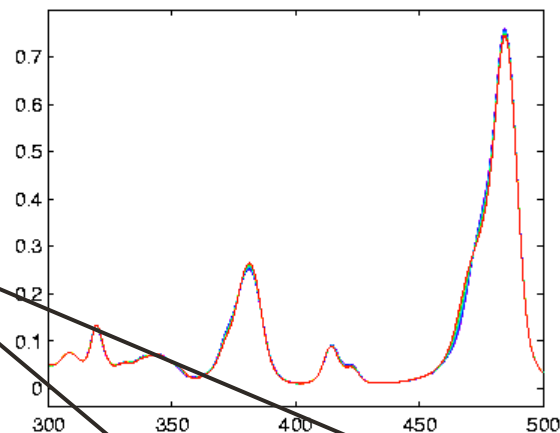
Time Series of Chemical Spectra

UNC, Stat & OR

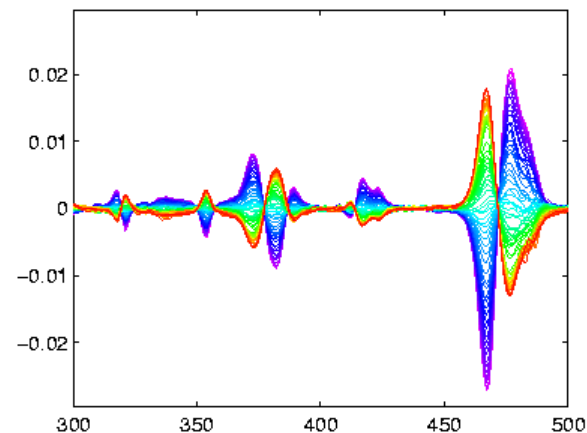
Note PC1
Is Most Of
Variation

(Mostly
Single
Reaction)

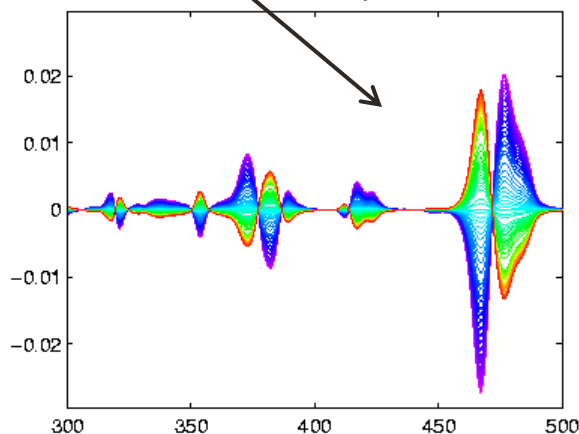
Raw Data



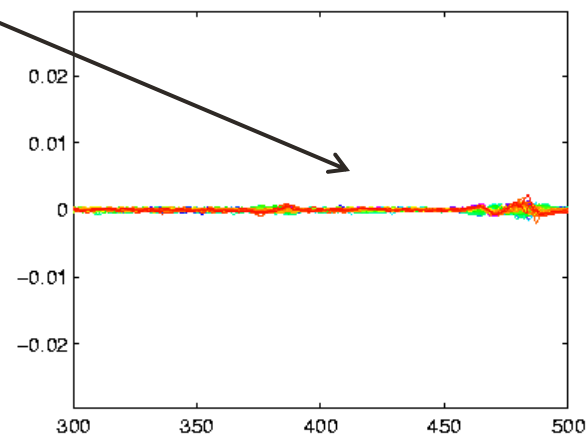
Mean Resid.



PC1 Proj.



PC1 Resid.



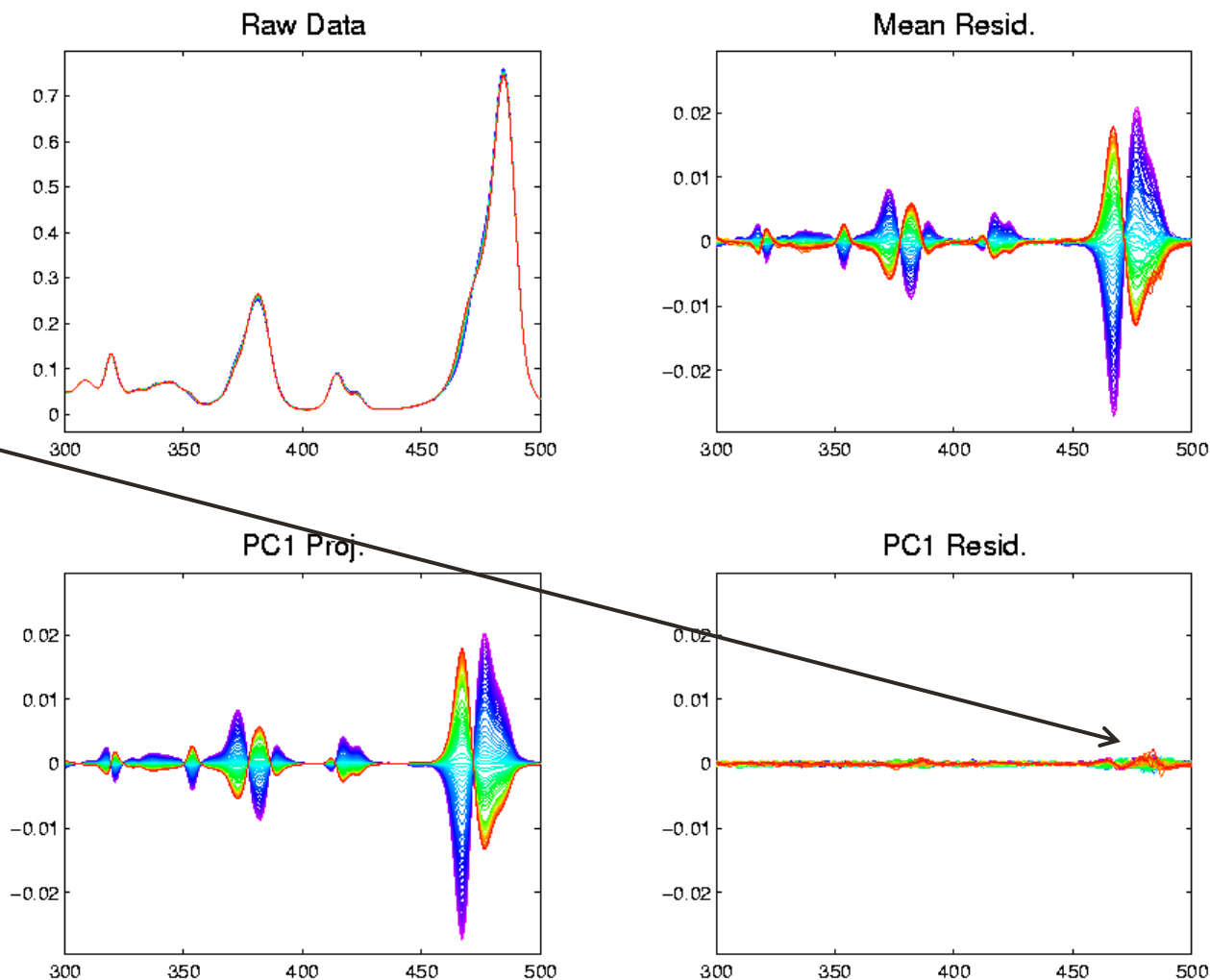


Time Series of Chemical Spectra

UNC, Stat & OR

Anything
Important
Beyond This?

Study Scores
Plot





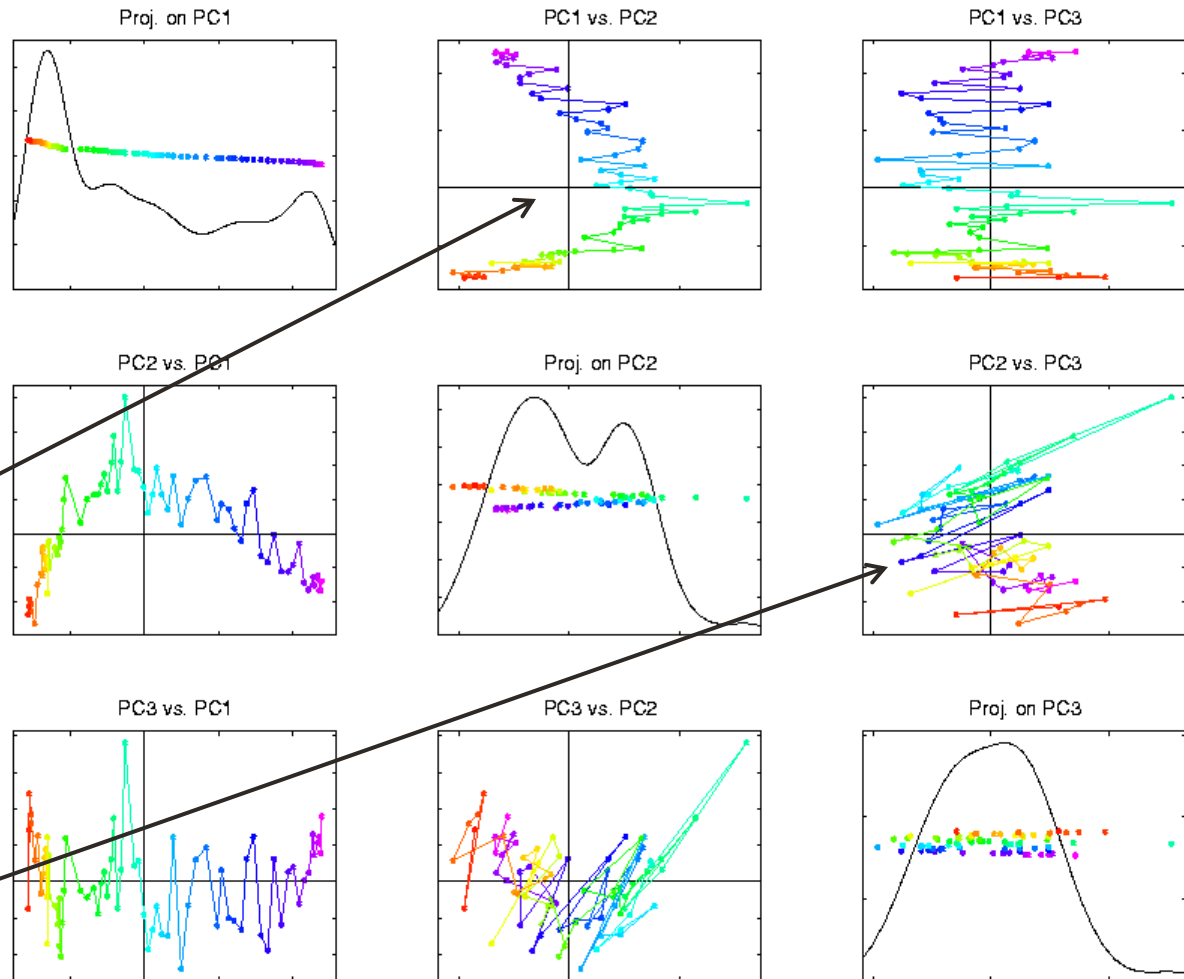
Time Series of Chemical Spectra

UNC, Stat & OR

Study Scores
(Feature Space
Point Cloud)

PC2: (mostly)
Systematic
Variation

PC3: (mostly)
Noise Driven?



Important Trade-Off: Signal vs. Noise

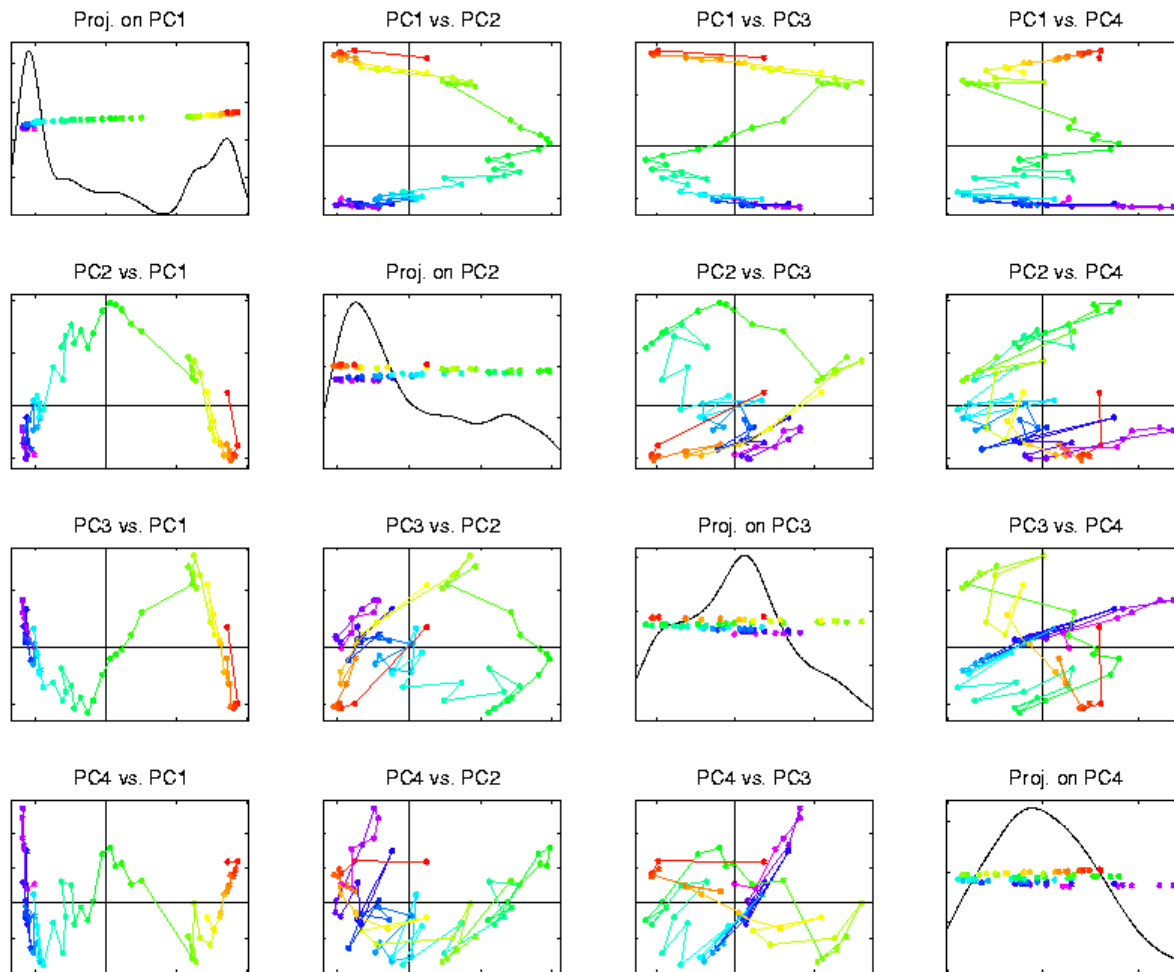


Time Series of Chemical Spectra

UNC, Stat & OR

Another Experiment

(Different Signal vs. Noise Balance)





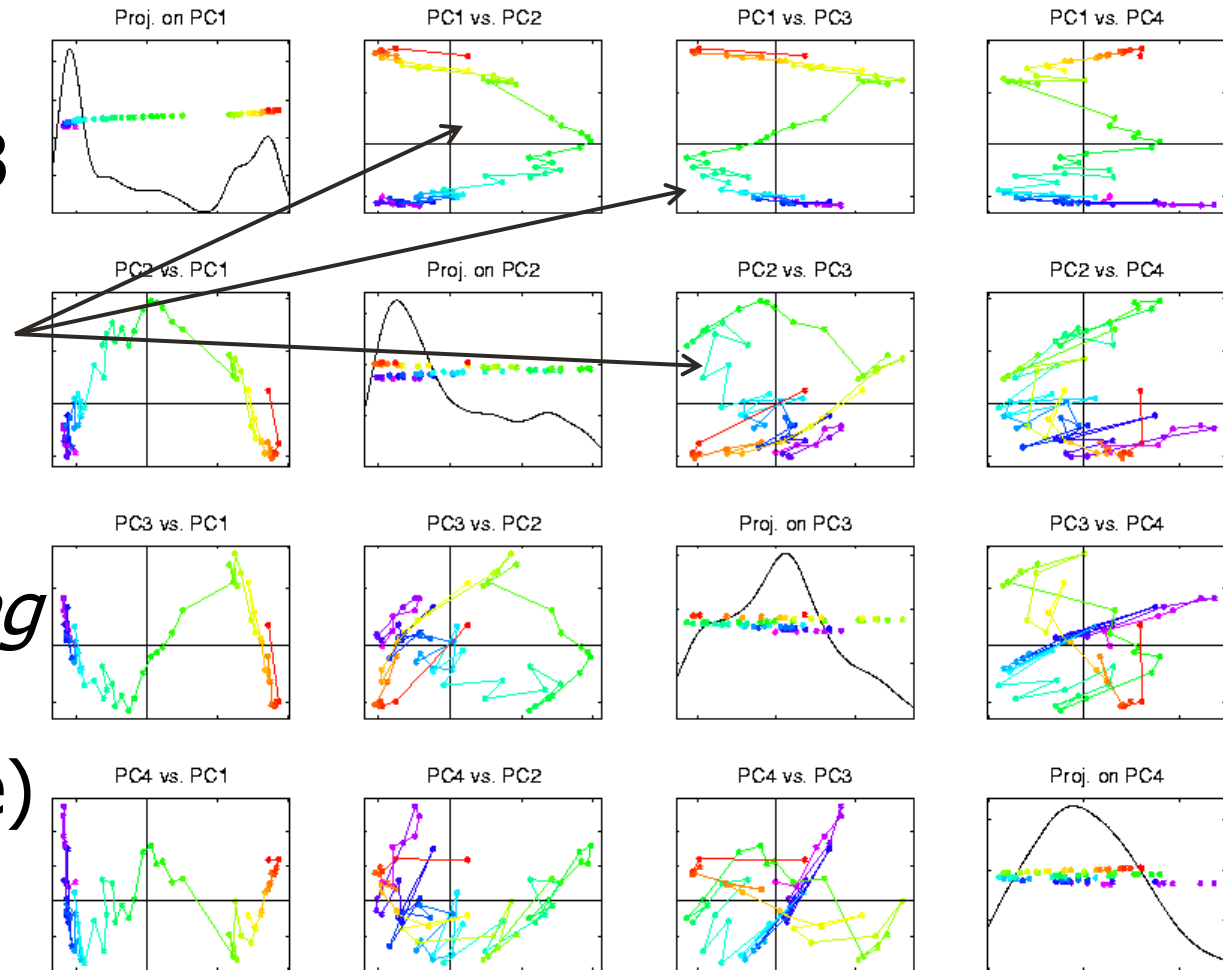
Time Series of Chemical Spectra

UNC, Stat & OR

PC1, PC2, PC3
All Suggest
Important
Patterns

(Think *Bending Curve* in
Feature Space)

Noise Is
Lower Order





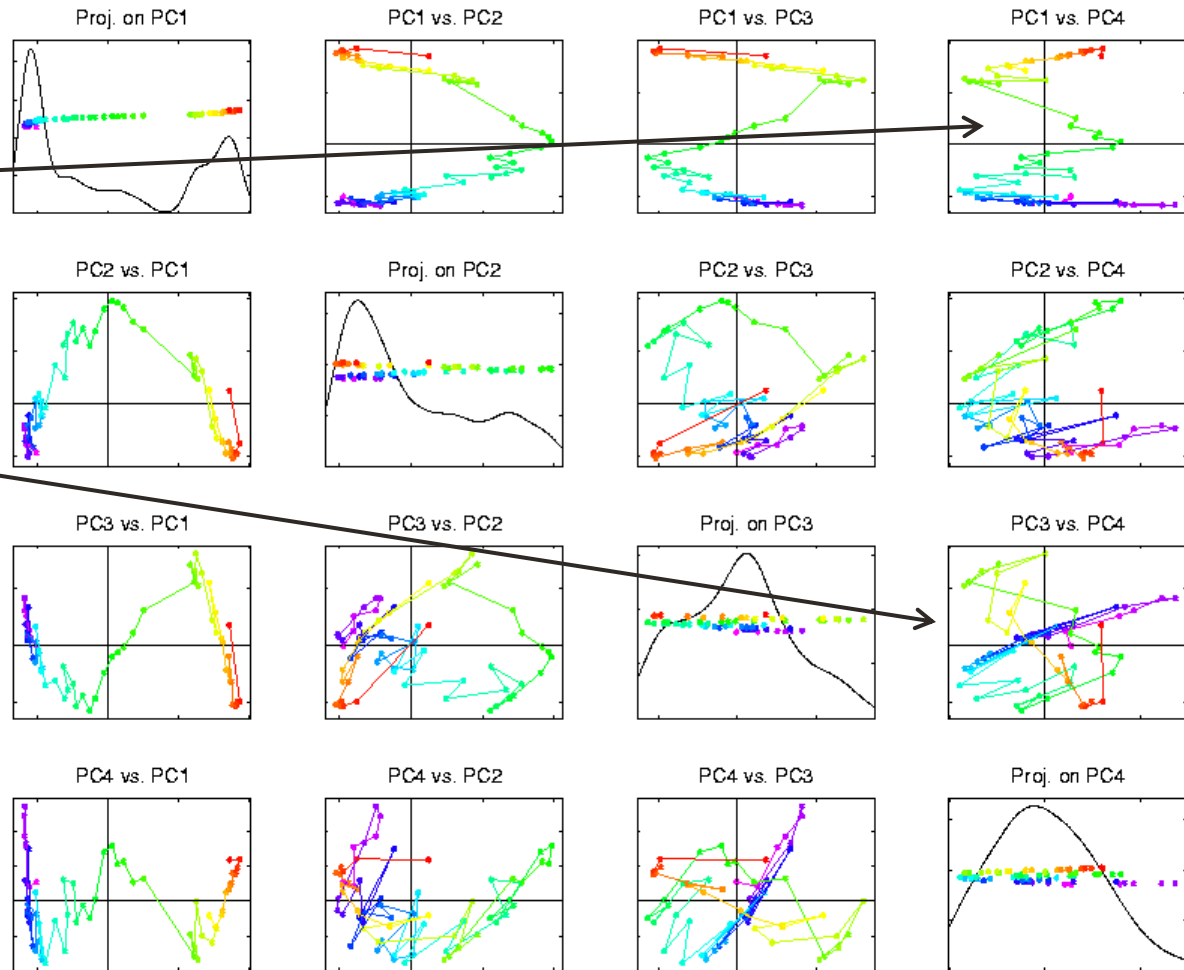
Time Series of Chemical Spectra

UNC, Stat & OR

PC 4?
Systematic?

Or Noise
Dominated?

This Pattern
Appears
Very
General



Interesting Mathematical Question: Why?



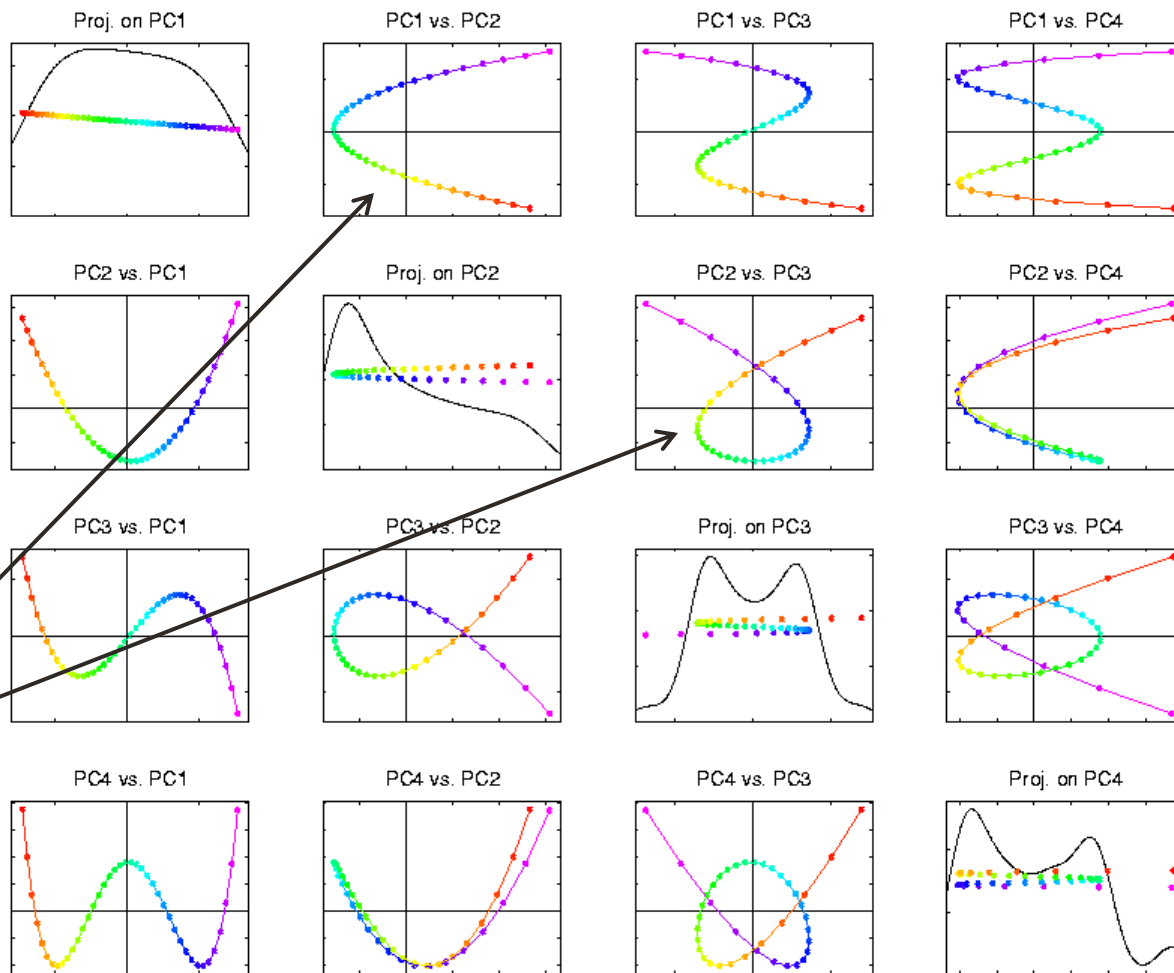
Time Series of Chemical Spectra

UNC, Stat & OR

Simulated
Chemical
Experiment

All Signal,
No Noise

Note
Observed
PC Patterns



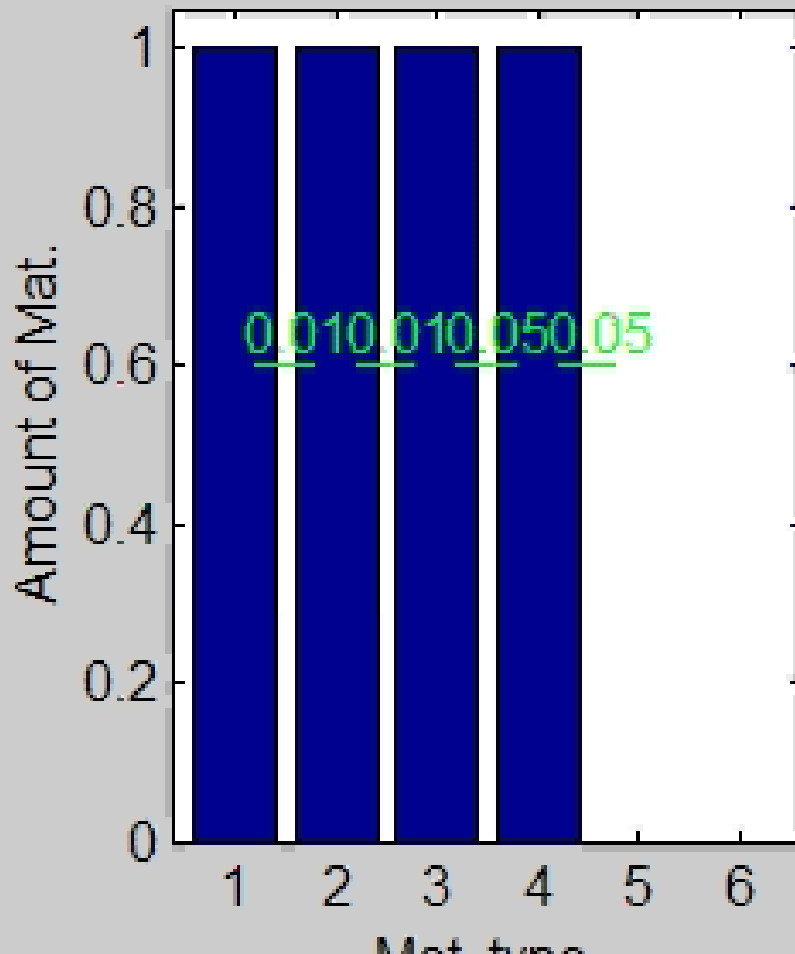


Time Series of Chemical Spectra

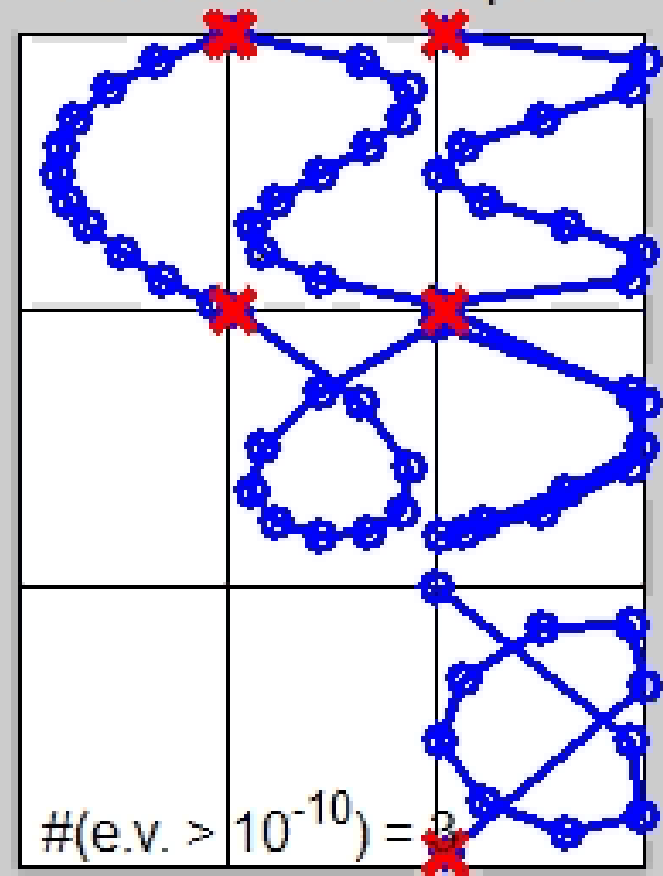
UNC, Stat & OR

Simulated Chemical Experiment

5 Comp, Only



PCA Draftsman's plots



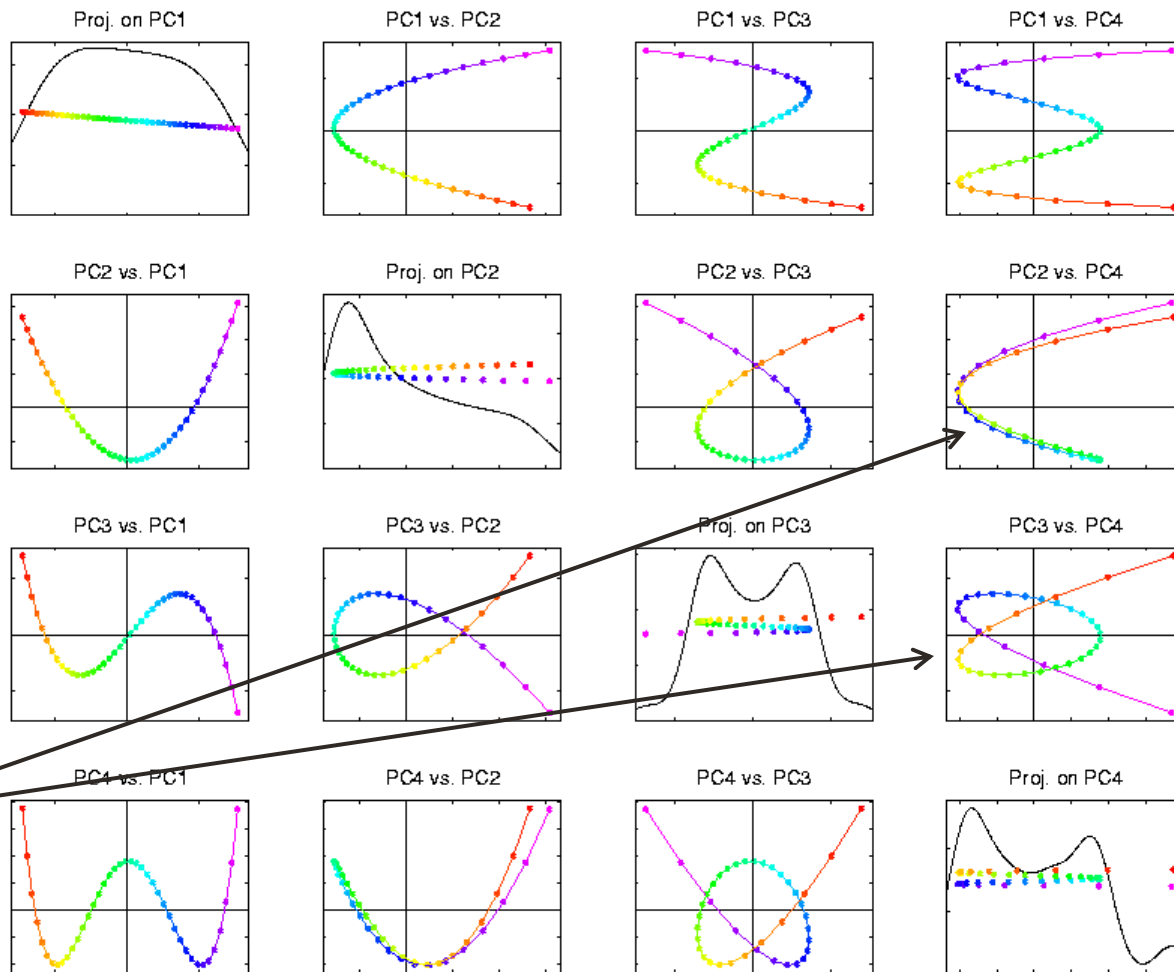


Time Series of Chemical Spectra

UNC, Stat & OR

Simulated
Chemical
Experiment

Higher Order
PC Patterns
Now Clear



See these in real data???



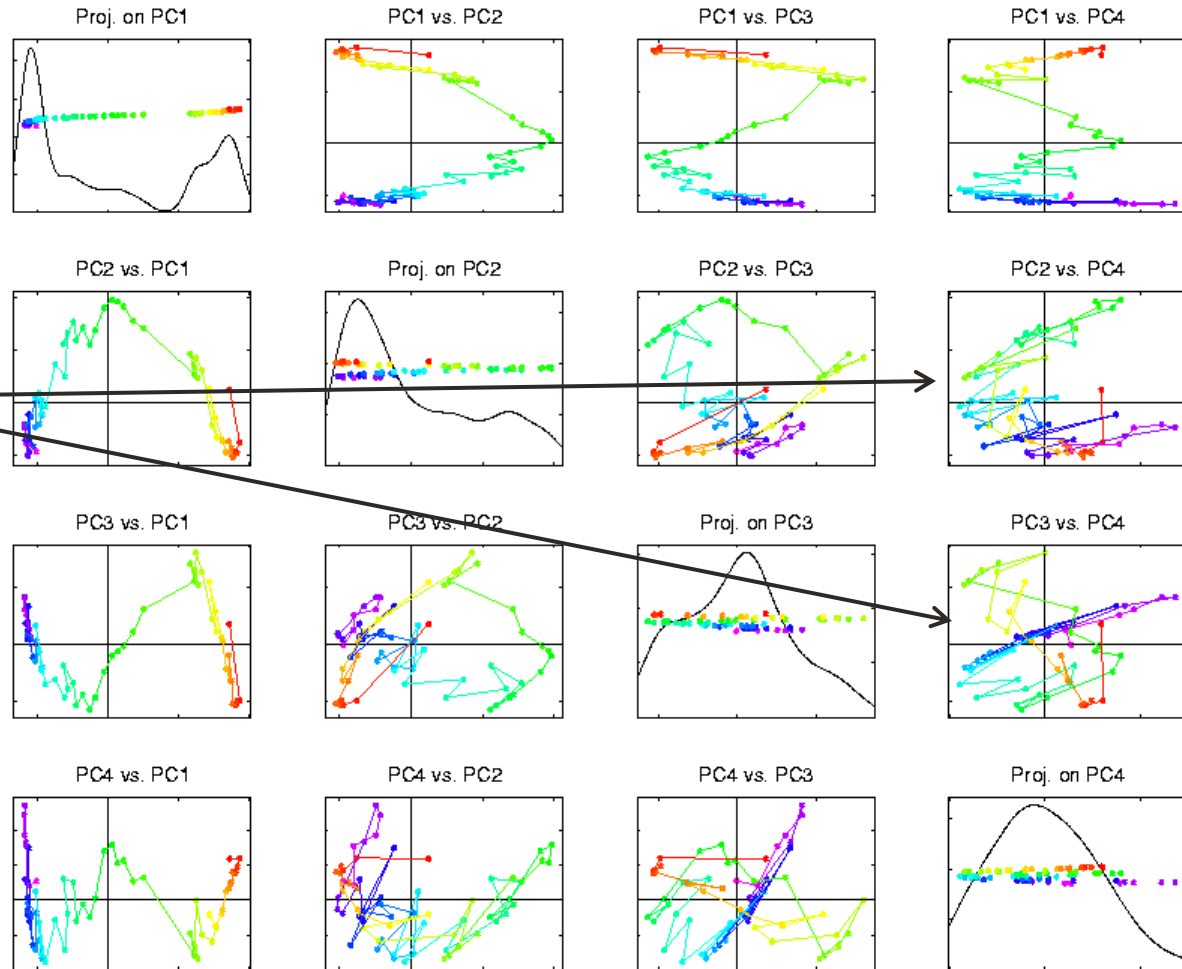
Time Series of Chemical Spectra

UNC, Stat & OR

Revisit
Real Data

Same
Patterns

Plus Noise





HDLSS Hypothesis Testing

UNC, Stat & OR

Context: 2 – sample means

$$H_0: \mu_{+1} = \mu_{-1} \quad \text{vs.} \quad H_1: \mu_{+1} \neq \mu_{-1}$$



HDLSS Hypothesis Testing

UNC, Stat & OR

Context: 2 – sample means

$$H_0: \mu_{+1} = \mu_{-1} \quad \text{vs.} \quad H_1: \mu_{+1} \neq \mu_{-1}$$

Challenges:

- Distributional Assumptions
- Parameter Estimation



HDLSS Hypothesis Testing

UNC, Stat & OR

Context: 2 – sample means

$$H_0: \mu_{+1} = \mu_{-1} \quad \text{vs.} \quad H_1: \mu_{+1} \neq \mu_{-1}$$

Challenges:

- Distributional Assumptions
- Parameter Estimation
- **HDLSS** space is slippery

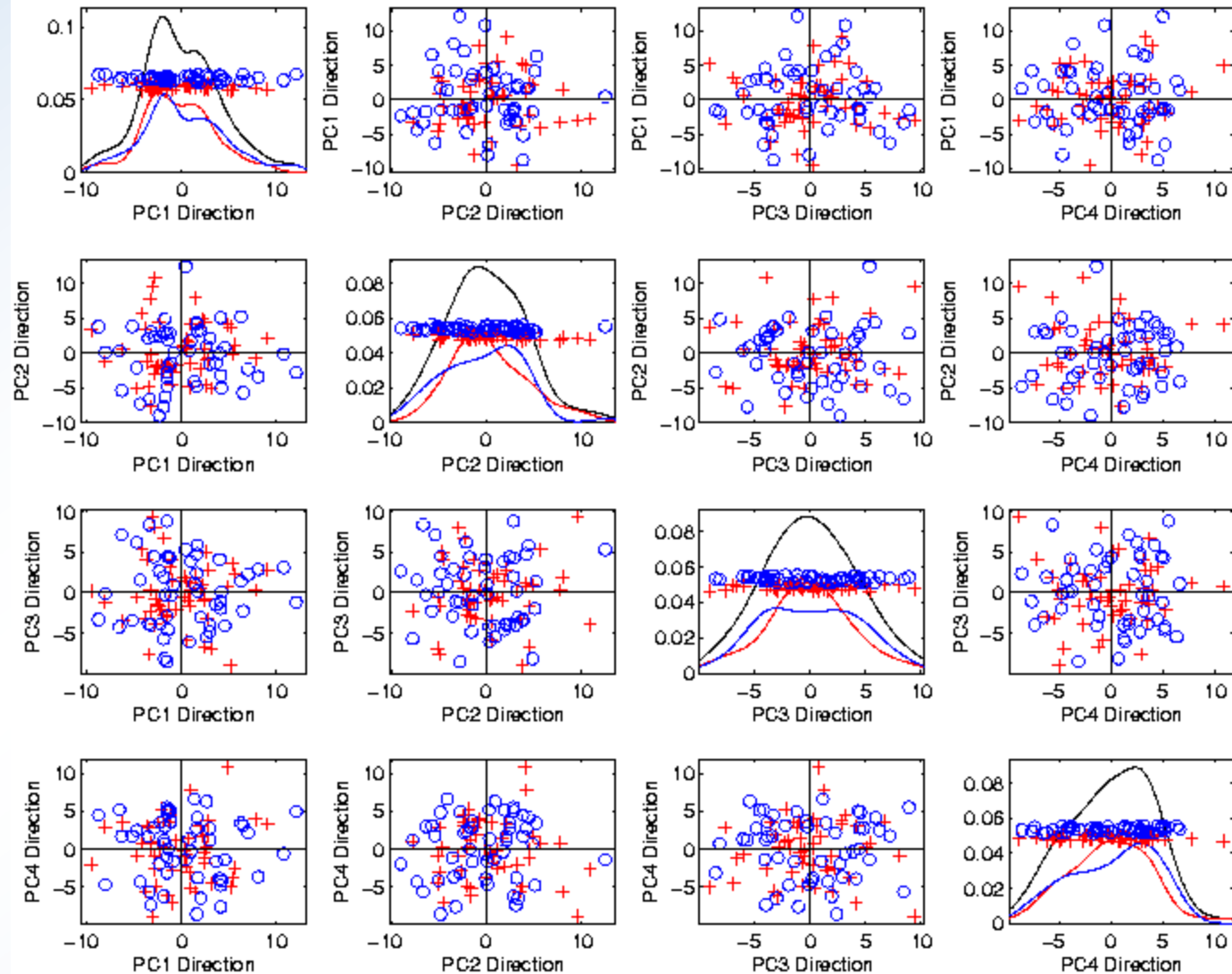


HDLSS Hypothesis Testing

UNC, Stat & OR

Toy 2-Class Example

See
Structure?





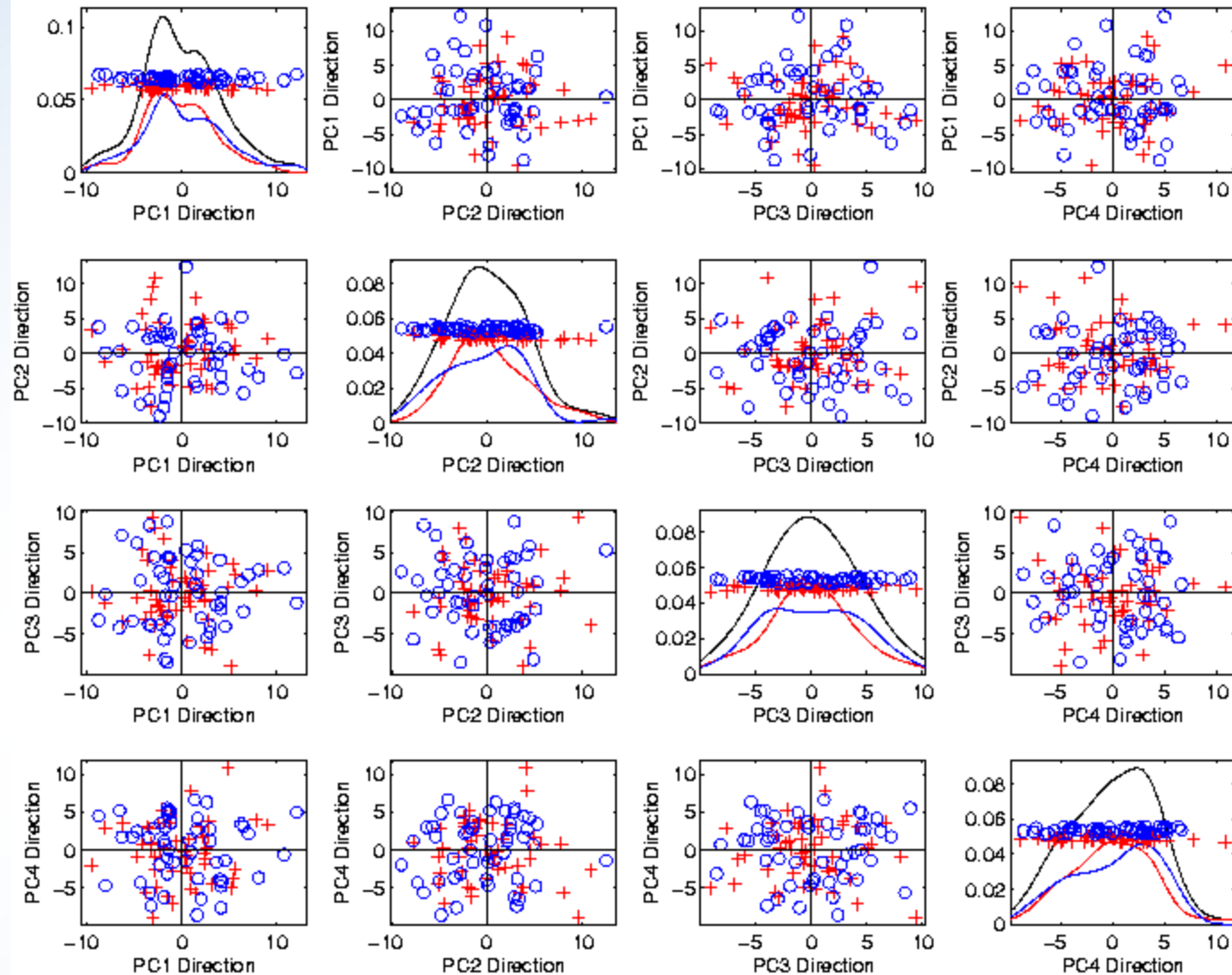
HDLSS Hypothesis Testing

UNC, Stat & OR

Toy 2-Class
Example

See
Structure?

Careful,
Only PC1-4

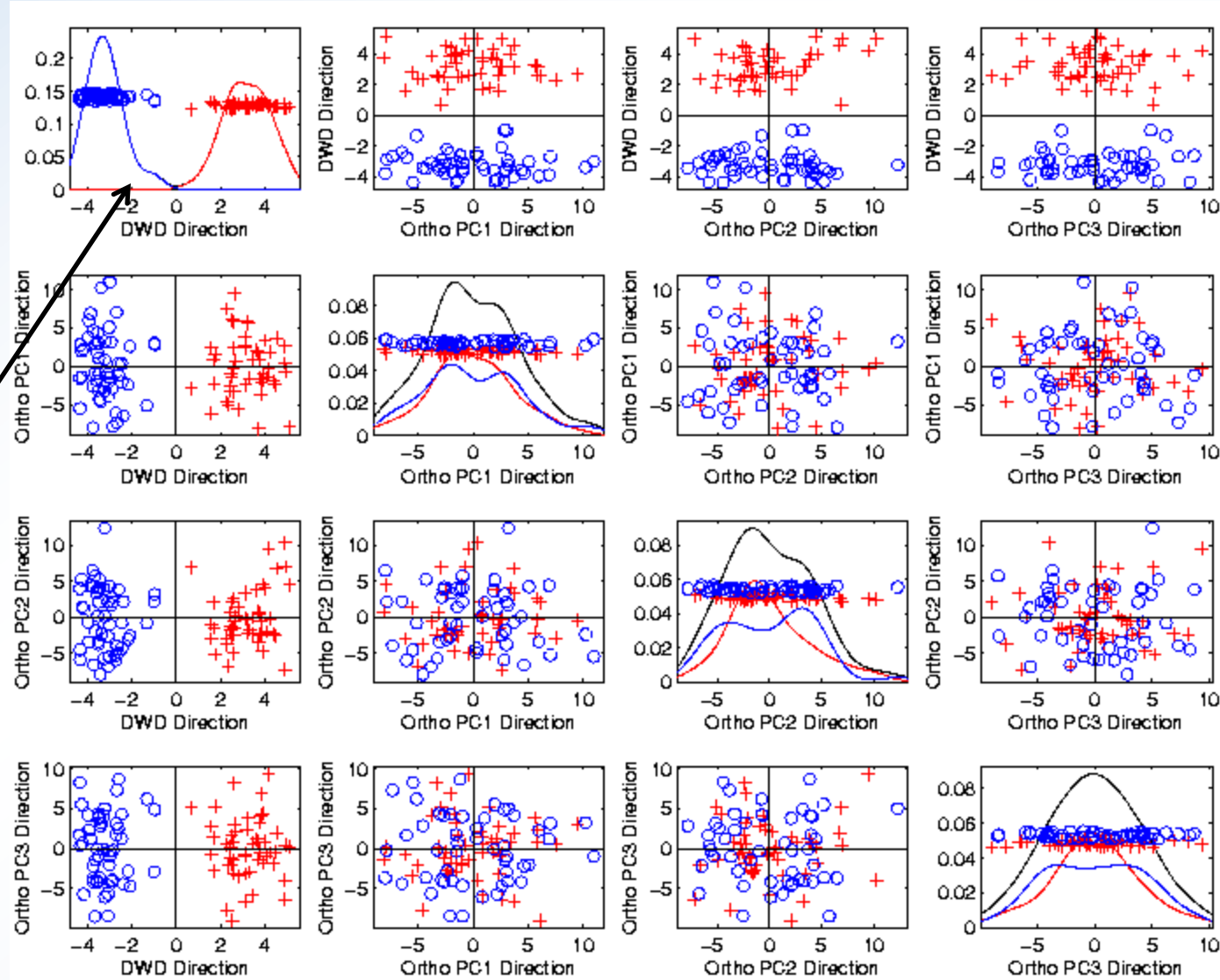




HDLSS Hypothesis Testing

UNC, Stat & OR

Toy 2-Class Example



Structure
Looks
Real???



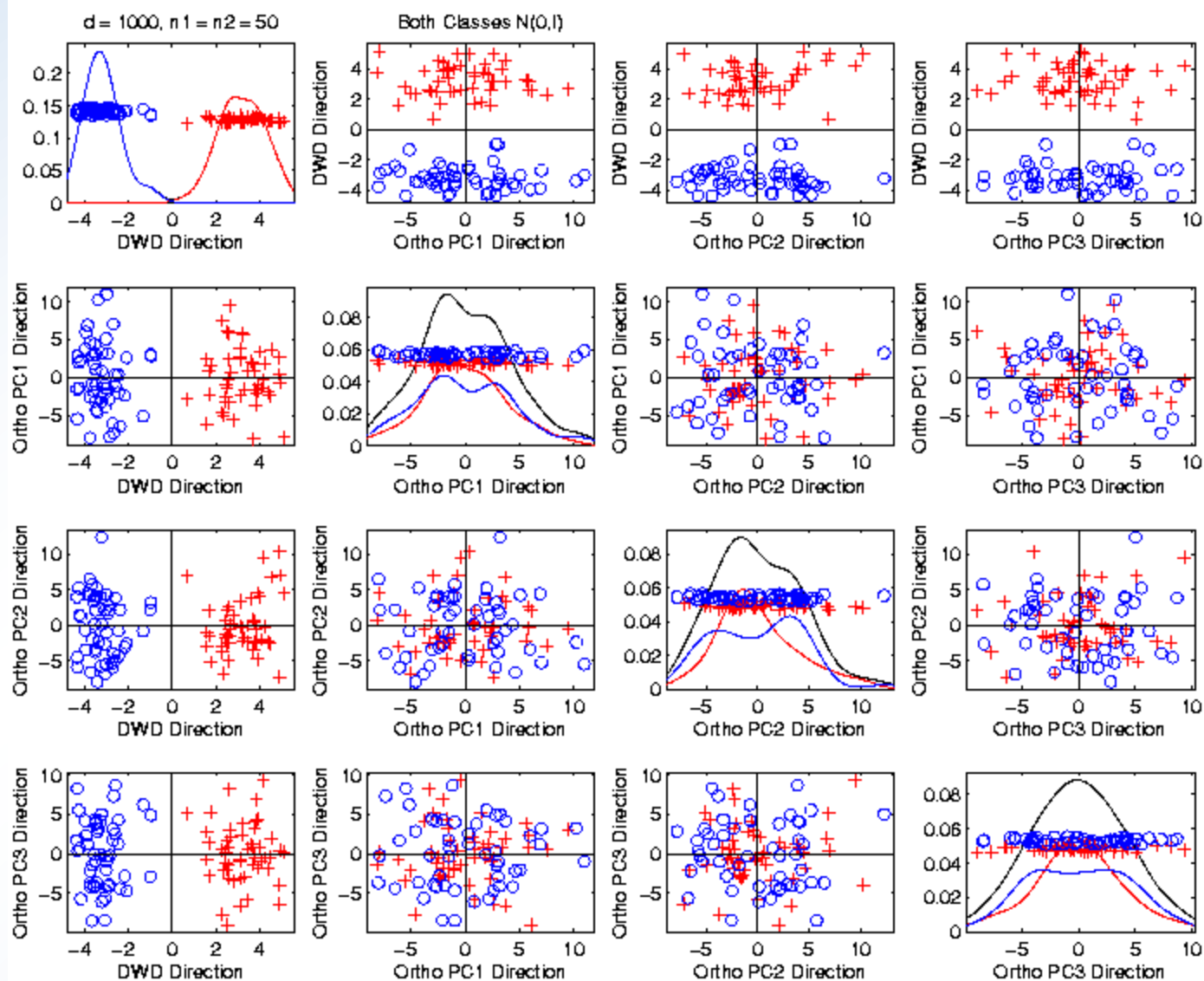
HDLSS Hypothesis Testing

UNC, Stat & OR

Toy 2-Class Example

Actually
Both
Classes

Are $N(0, I)$,
 $d = 1000$





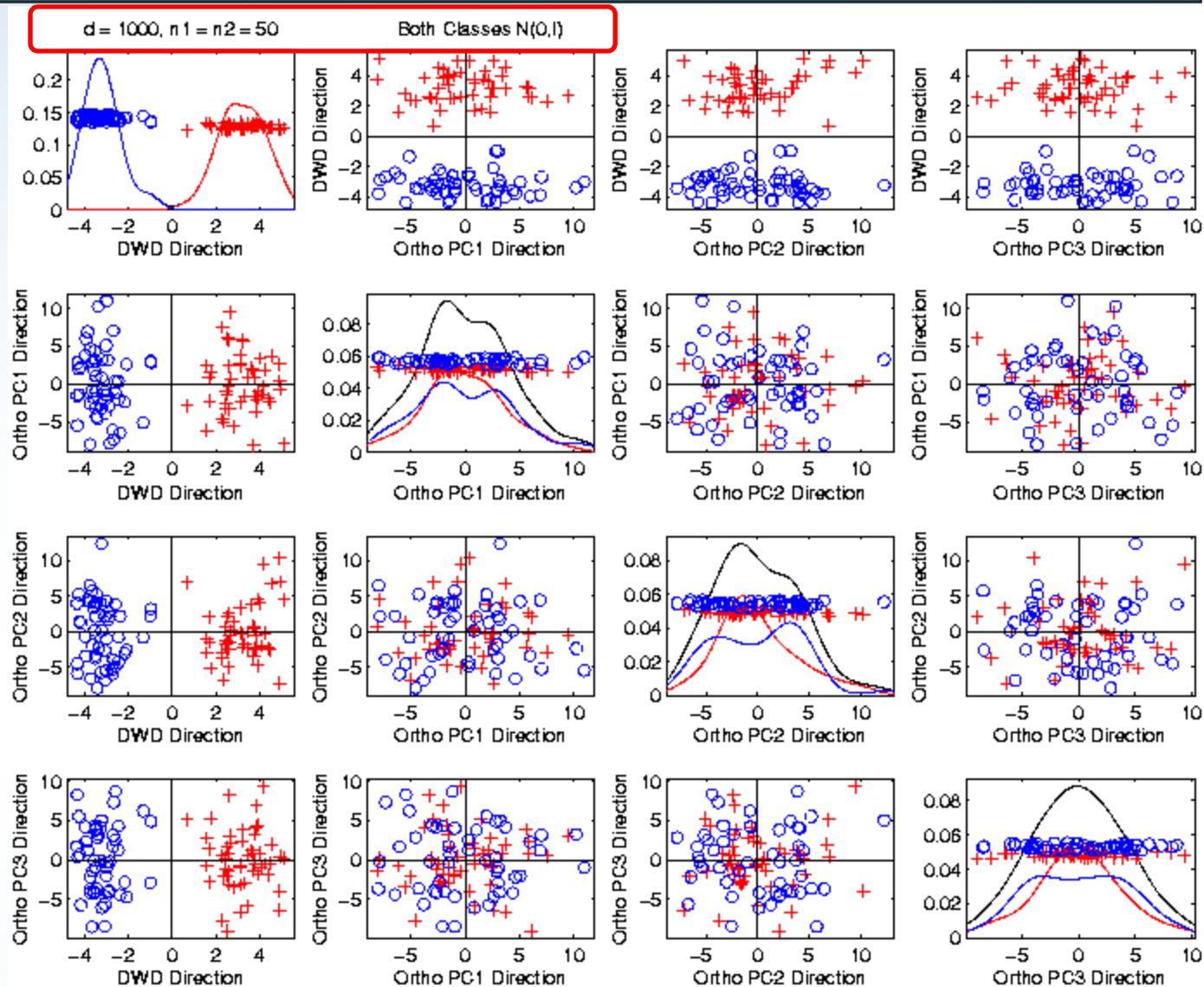
HDLSS Hypothesis Testing

UNC, Stat & OR

Toy 2-Class Example

Actually Both Classes

Are $N(0, I)$, $d = 1000$



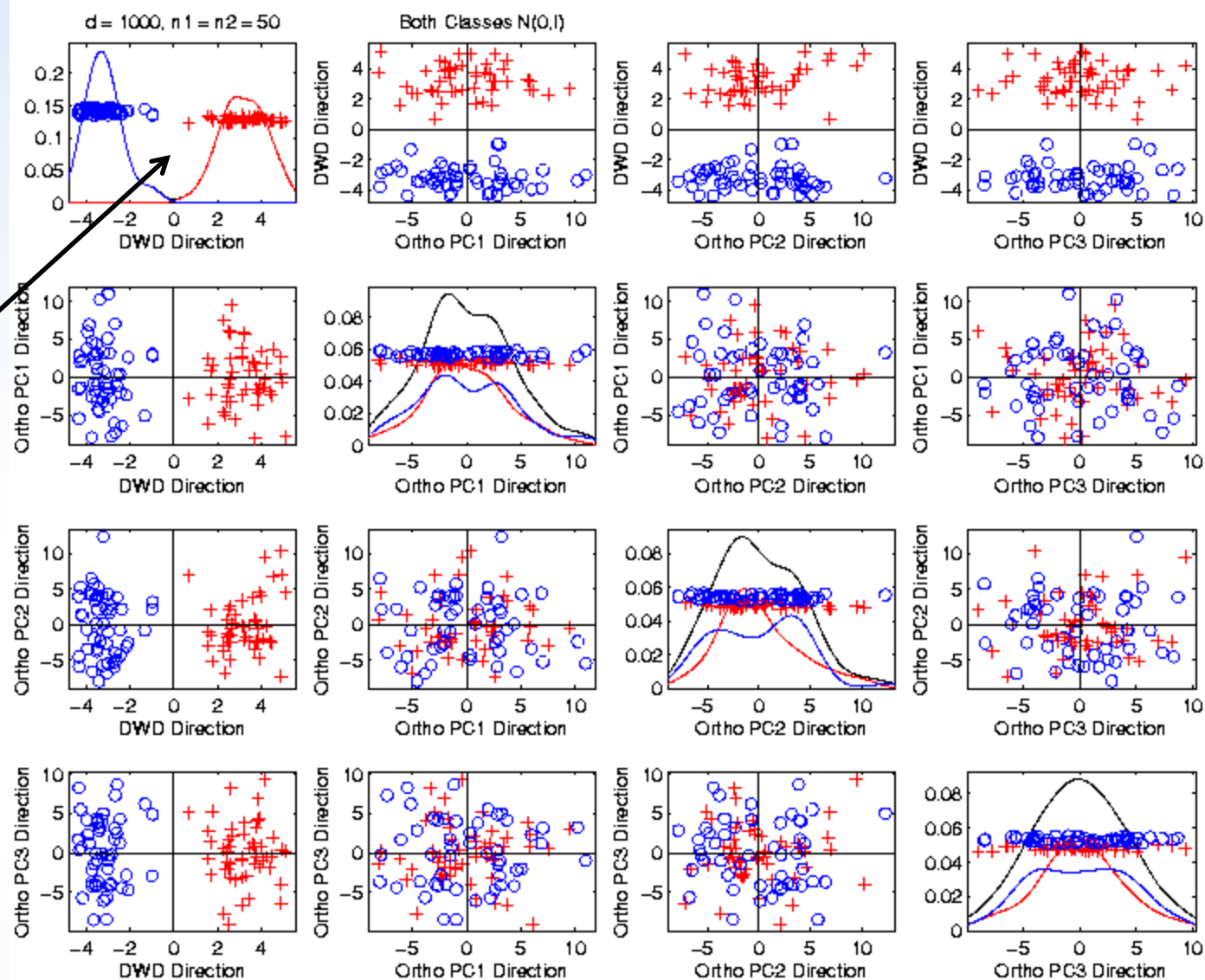


HDLSS Hypothesis Testing

UNC, Stat & OR

Toy 2-Class Example

Separation
Is *Natural*
Sampling
Variation





HDLSS Hypothesis Testing

UNC, Stat & OR

Context: 2 – sample means

$$H_0: \mu_{+1} = \mu_{-1} \quad \text{vs.} \quad H_1: \mu_{+1} \neq \mu_{-1}$$

Challenges:

- Distributional Assumptions
- Parameter Estimation
- **HDLSS** space is slippery



HDLSS Hypothesis Testing

UNC, Stat & OR

Context: 2 – sample means

$$H_0: \mu_{+1} = \mu_{-1} \quad \text{vs.} \quad H_1: \mu_{+1} \neq \mu_{-1}$$

Challenges:

- Distributional Assumptions
- Parameter Estimation

Suggested Approach:

Permutation test



HDLSS Hypothesis Testing - DiProPerm

UNC, Stat & OR

Suggested Approach:

✓ Find a DIrection

(separating classes)



HDLSS Hypothesis Testing - DiProPerm

UNC, Stat & OR

Suggested Approach:

✓ Find a DIrection

(separating classes)

✓ PROject the data

(reduces to 1 dim)



HDLSS Hypothesis Testing - DiProPerm

UNC, Stat & OR

Suggested Approach:

- ✓ Find a DIrection

(separating classes)

- ✓ PROject the data

(reduces to 1 dim)

- ✓ PERMute

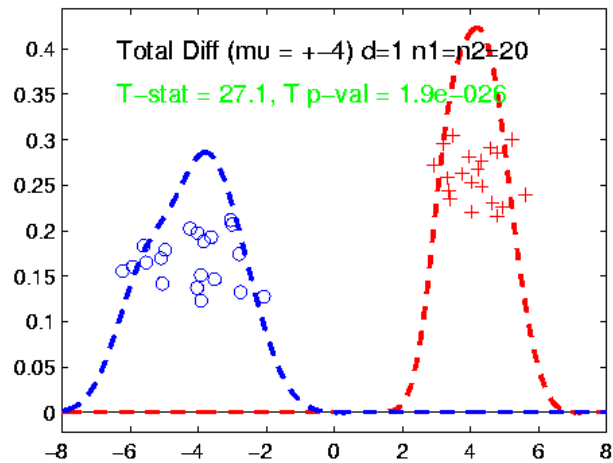
(class labels, to assess significance,
with recomputed direction)



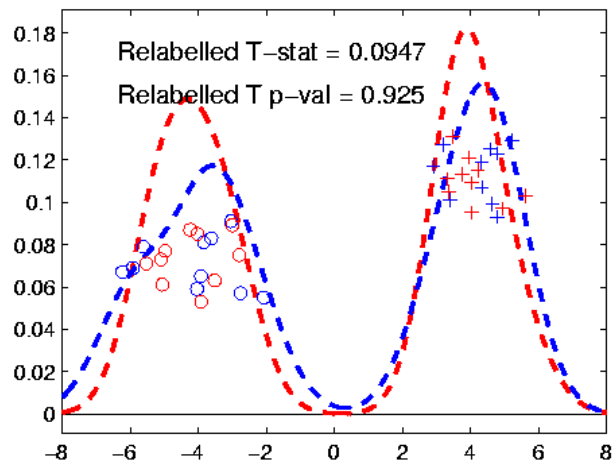
HDLSS Hypothesis Testing - DiProPerm

UNC, Stat & OR

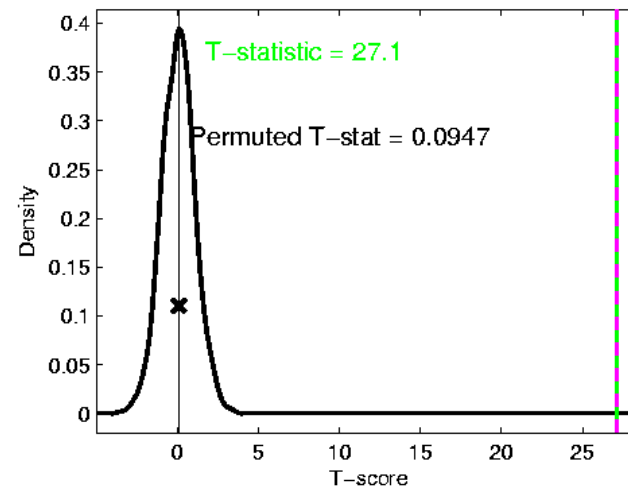
True Labelling, Total Diff.



Random Labelling # 1



1 T-stats, from random relab's

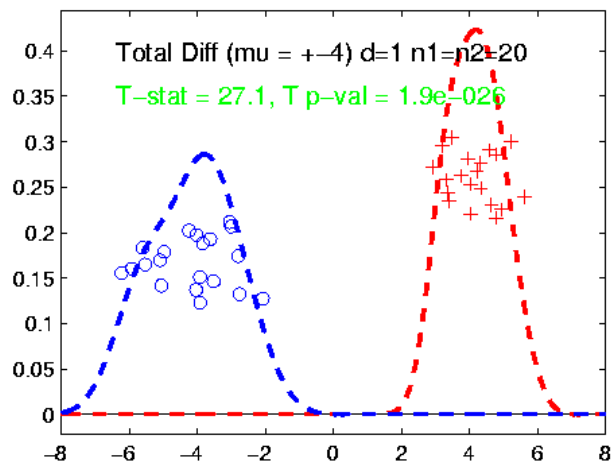




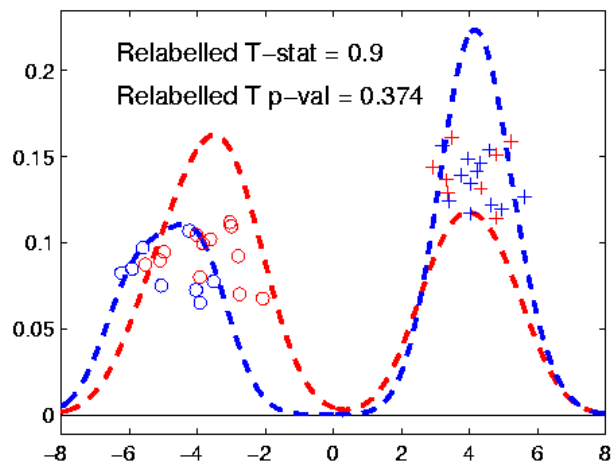
HDLSS Hypothesis Testing - DiProPerm

UNC, Stat & OR

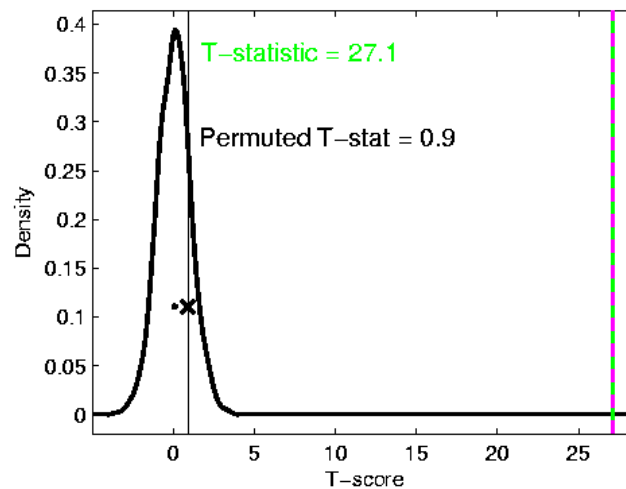
True Labelling, Total Diff.



Random Labelling # 2



2 T-stats, from random relab's

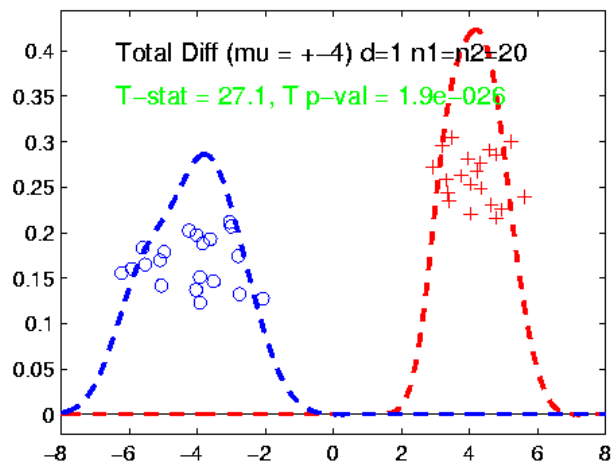




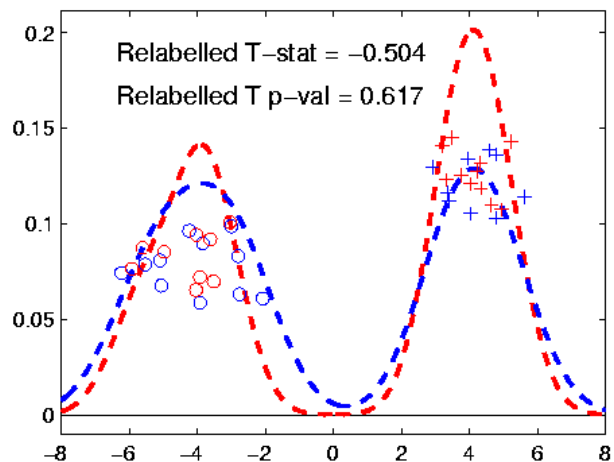
HDLSS Hypothesis Testing - DiProPerm

UNC, Stat & OR

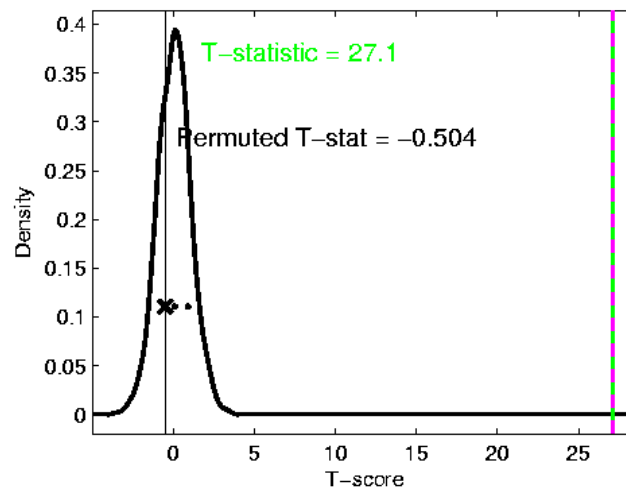
True Labelling, Total Diff.



Random Labelling # 3



3 T-stats, from random relab's

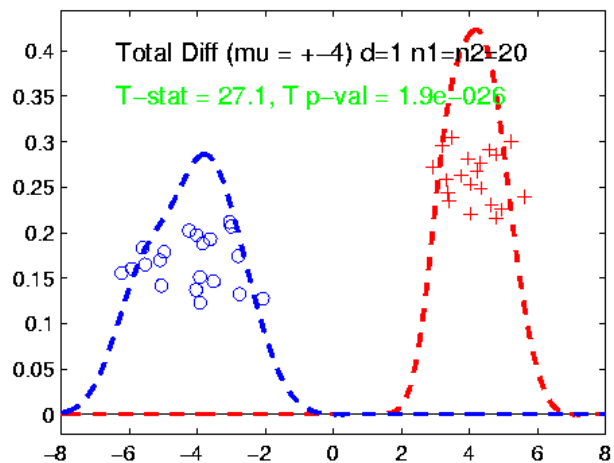




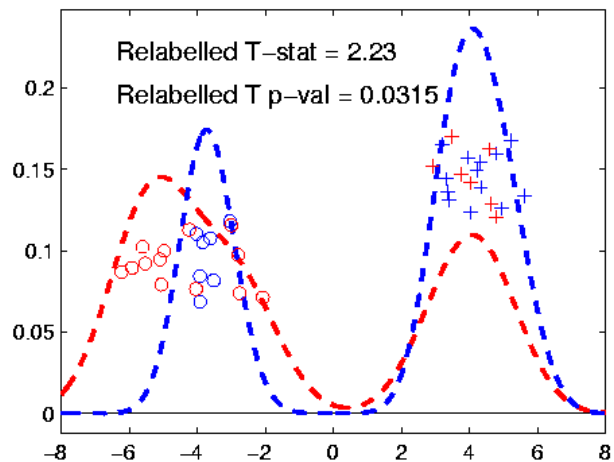
HDLSS Hypothesis Testing - DiProPerm

UNC, Stat & OR

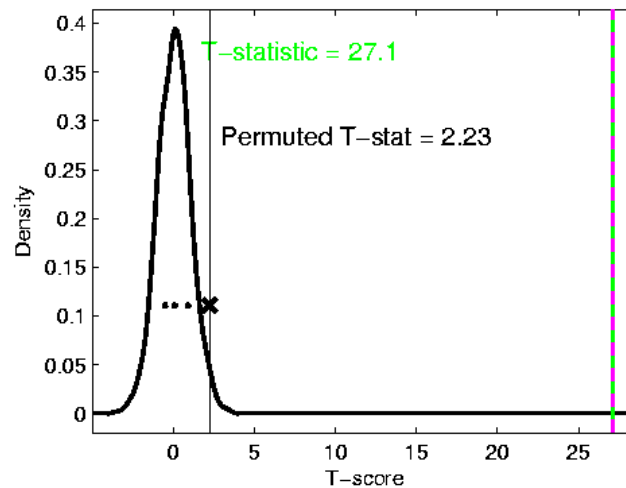
True Labelling, Total Diff.



Random Labelling # 4



4 T-stats, from random relab's





HDLSS Hypothesis Testing - DiProPerm

-
-
-

Repeat this 1,000 times

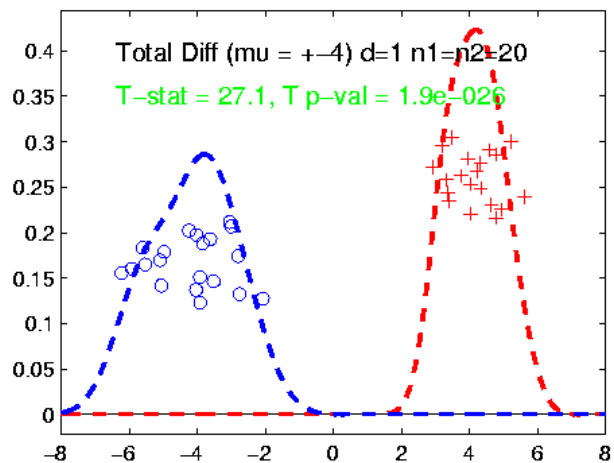
To get:



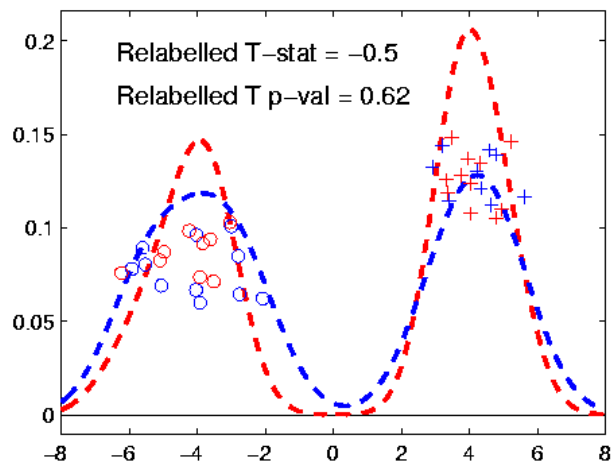
HDLSS Hypothesis Testing - DiProPerm

UNC, Stat & OR

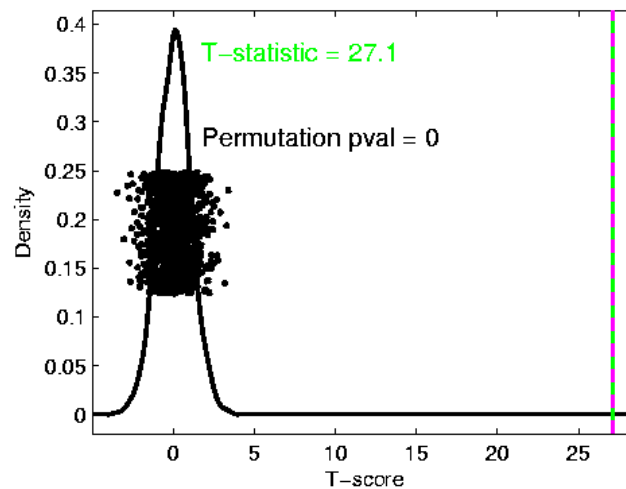
True Labelling, Total Diff.



Random Labelling # 1000



1000 T-stats, from random relab's



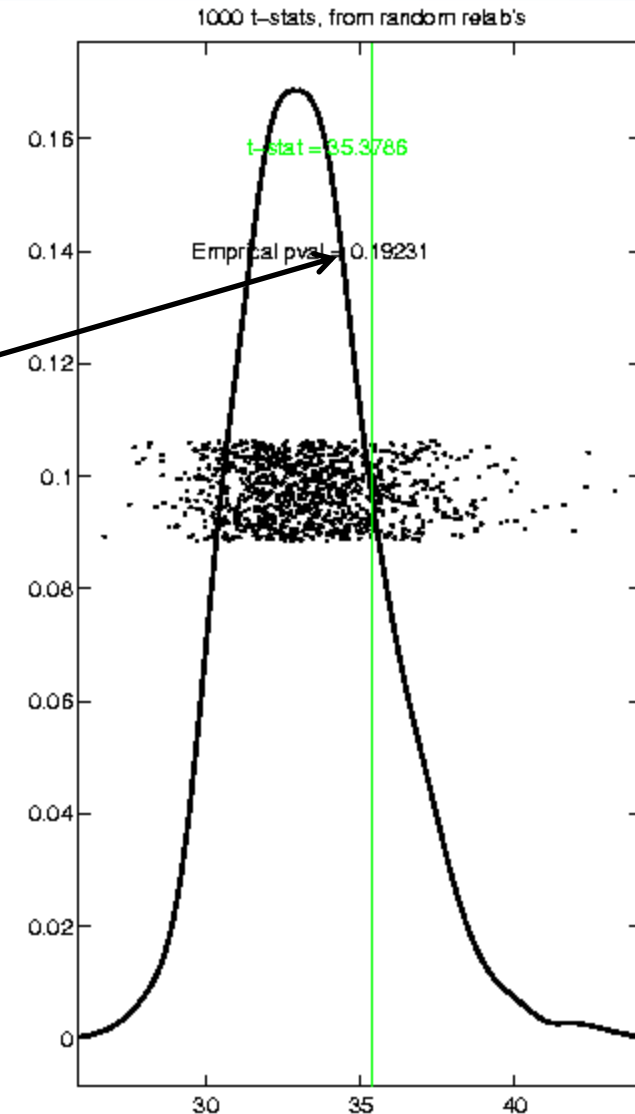
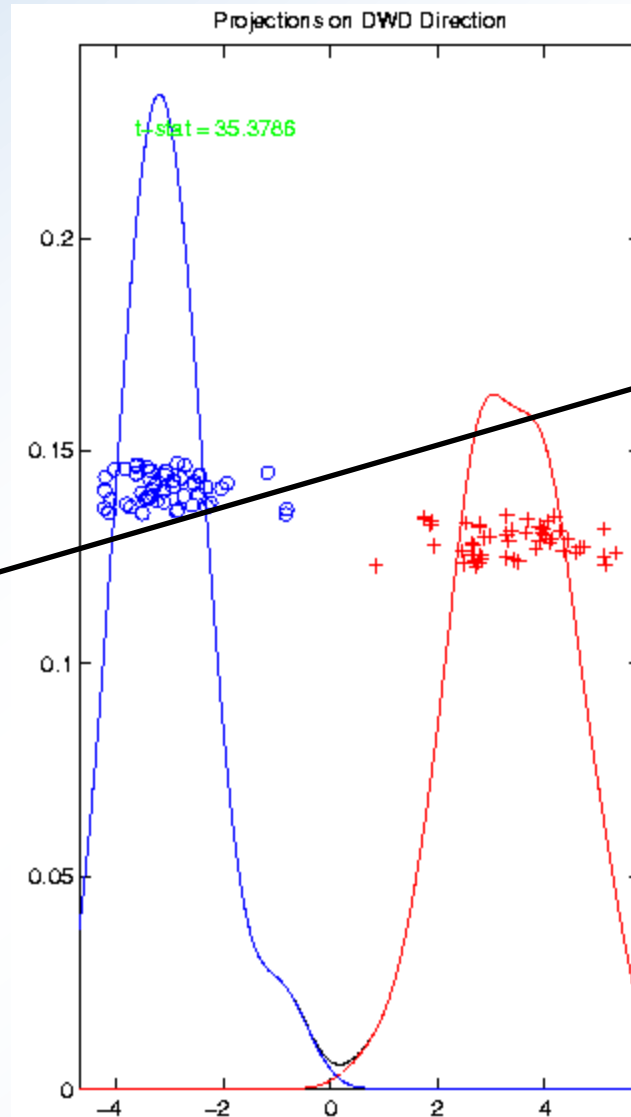


HDLSS Hypothesis Testing

UNC, Stat & OR

Toy 2-Class Example

p-value
Not
Significant





HDLSS Hypothesis Testing - DiProPerm

UNC, Stat & OR

Real Data Example: Autism

Caudate Shape

(sub-cortical brain structure)

Shape summarized by 3-d locations of 1032
corresponding points

Autistic vs. Typically Developing



Autism Data - DiProPerm

UNC, Stat & OR

Finds

Significant

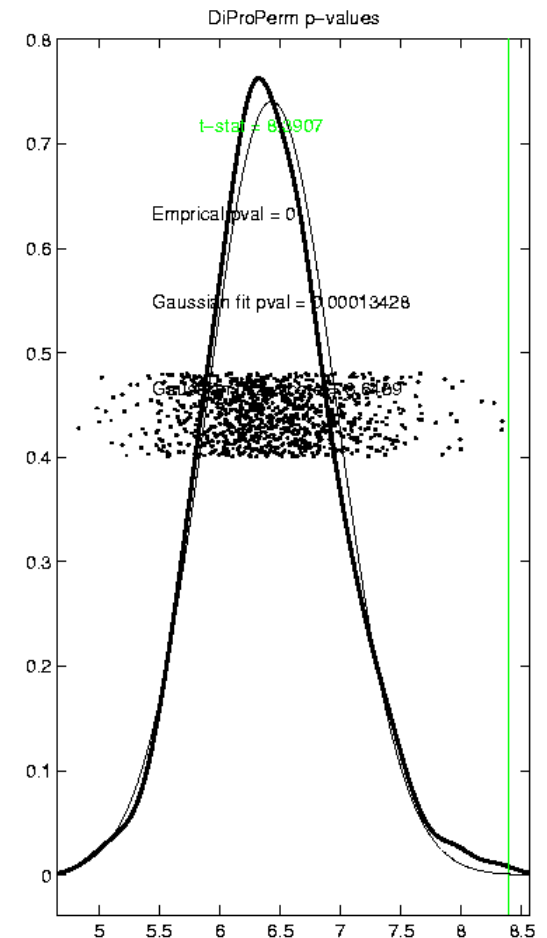
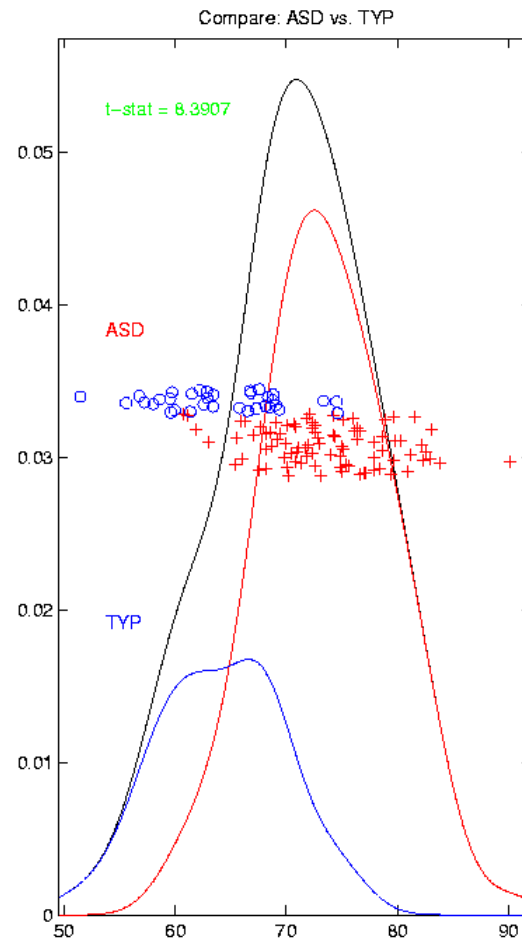
Difference

Despite Weak

Visual

Impression

Thanks to Josh Cates





Autism Data - DiProPerm

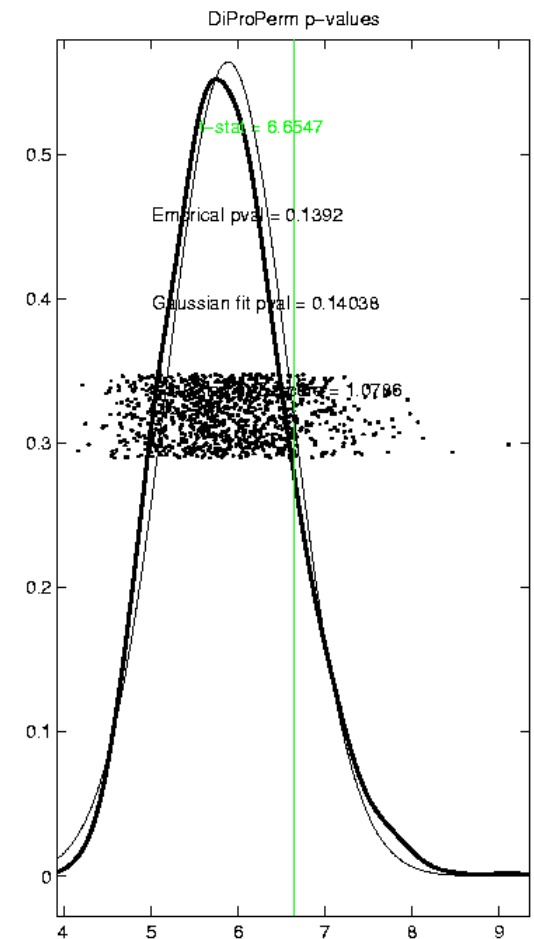
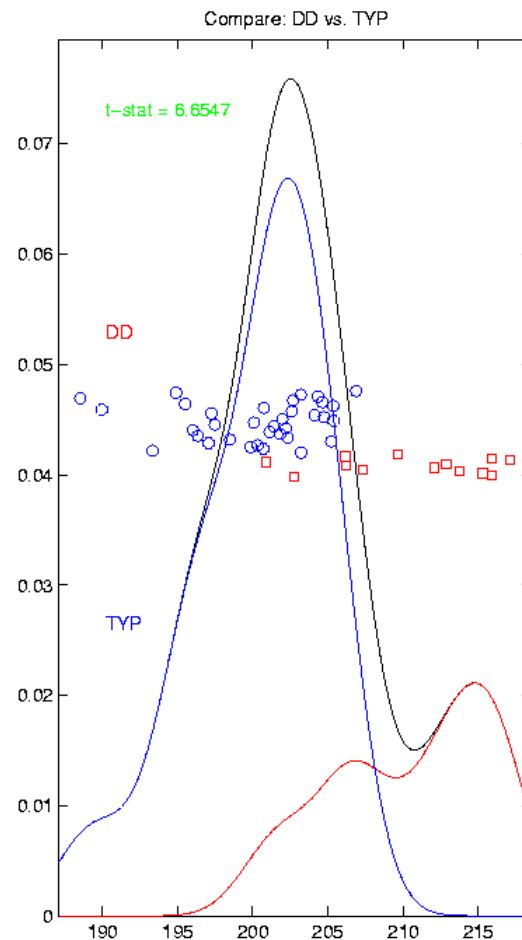
UNC, Stat & OR

Also Compare: Developmentally Delayed

No
Significant
Difference

But Strong
Visual
Impression

Thanks to Josh Cates



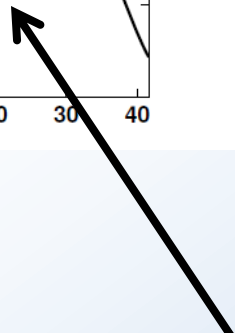
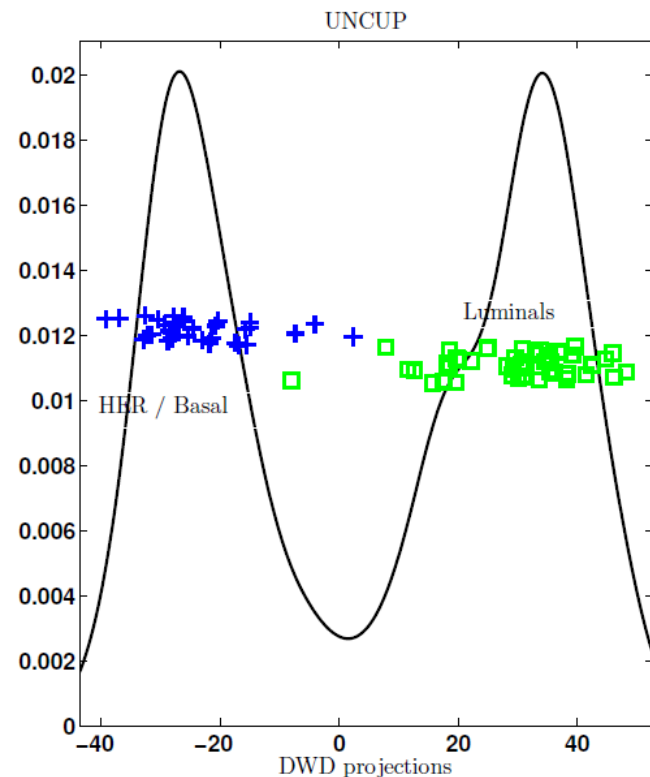
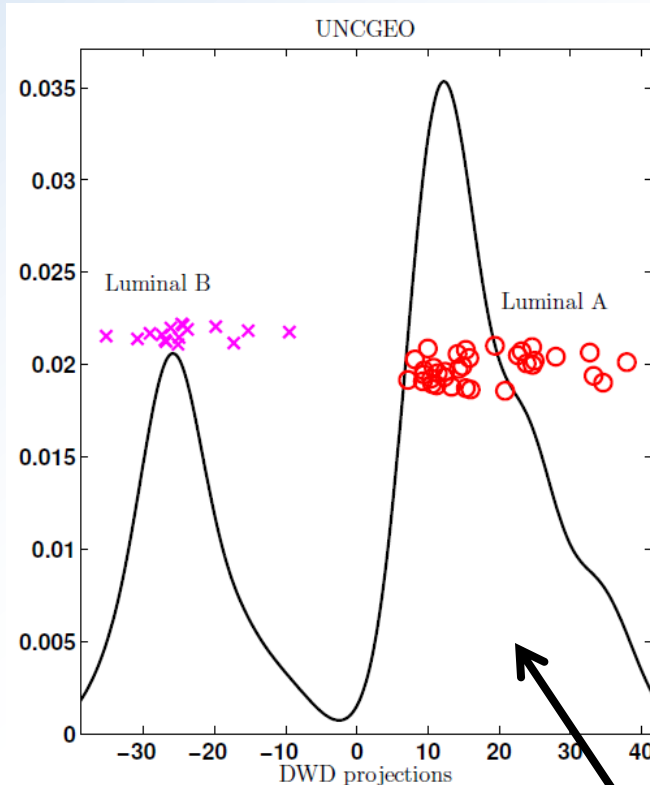


Breast Cancer Microarray Data - DiProPerm

UNC, Stat & OR

Two
Examples

Which Is
"More
Distinct"?



Visually *Better Separation*?

Thanks to Katie Hoadley



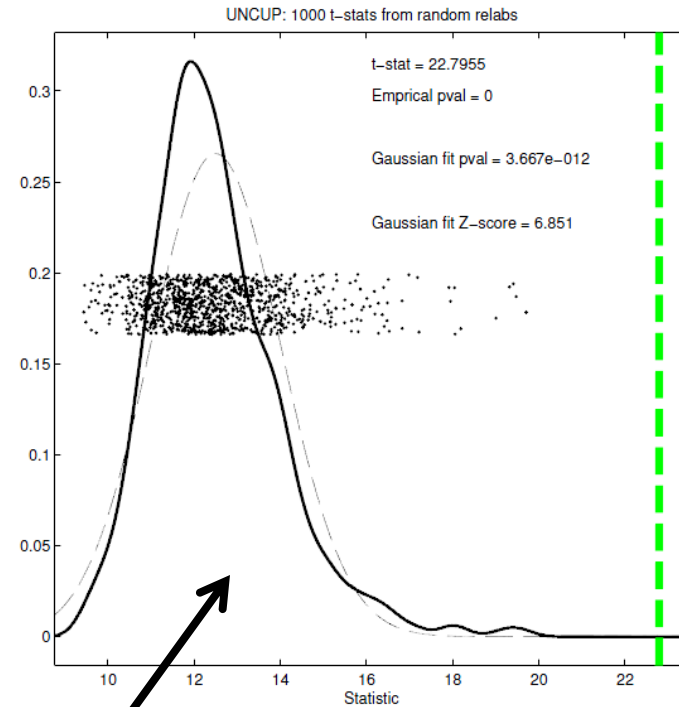
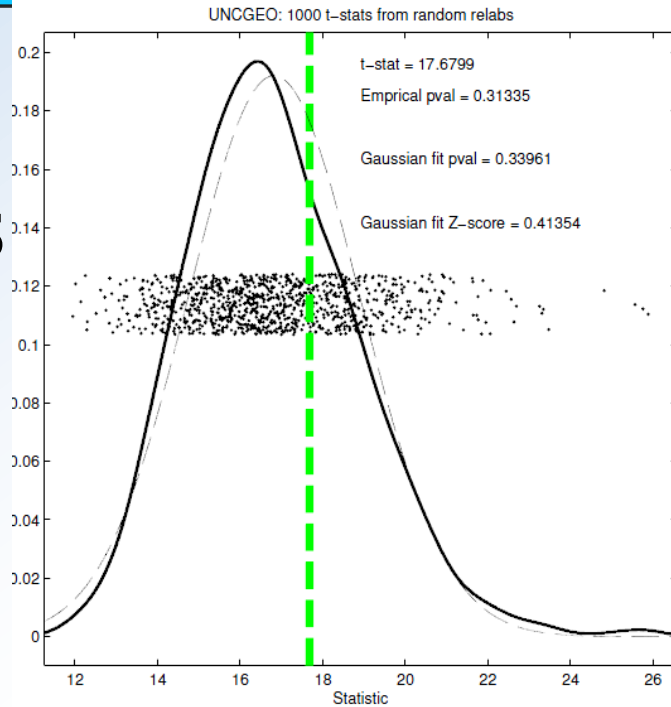
Breast Cancer Microarray Data - DiProPerm

UNC, Stat & OR

Two
Examples

Which Is
"More

Distinct"?



Stronger *Statistical Significance*

Thanks to Katie Hoadley



HDLSS Hypothesis Testing - DiProPerm

UNC, Stat & OR

Value of DiProPerm:

- ❑ Visual Impression is Easily Misleading
(onto HDLSS projections,
e.g. Maximal Data Piling)
- ❑ Really Need to Assess Significance
- ❑ DiProPerm used routinely
(even for variable selection)



HDLSS Hypothesis Testing - DiProPerm

UNC, Stat & OR

Choice of Direction:

- ❖ Distance Weighted Discrimination (DWD)
- ❖ Support Vector Machine (SVM)
- ❖ Mean Difference
- ❖ Maximal Data Piling
-
-
-



HDLSS Hypothesis Testing - DiProPerm

UNC, Stat & OR

Choice of 1-d Summary Statistic:

- 2-sample t-stat
- Mean difference
- Median difference
- Area Under ROC Curve
-
-
-



Carry Away Concept

UNC, Stat & OR

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?