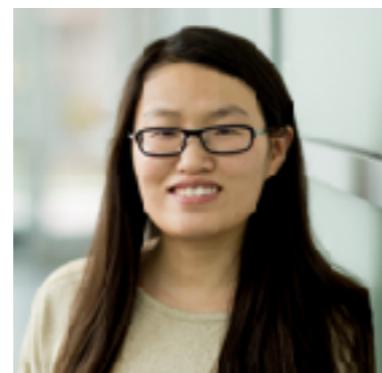


DESIGN AND ANALYSIS OF QUANTITATIVE PROTEOMIC EXPERIMENTS

Introduction to statistical methods
and
practical examples
using Skyline, R and MSstats



Meena Choi
*Northeastern
University*



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*Northeastern
University*



Brendan MacLean
*University
of Washington*



Birgit Schilling
*Buck
Institute for Aging*



Olga Vitek
*Northeastern
University*

SCHEDULE

	March 18	March 19
8:00-9:00		
9:00-9:30	Section1 : Fundamental concepts of statistical experimental design + introduce iPRG data	Skyjam
9:30-10:00		Section6 : Differential Analysis of DDA Data with Skyline
10:00-10:30	break	break
10:30-11:00	Section2 : Introduction to Skyline	Section7 : Hands-on : different abundance analysis with MSstats with iPRG dataset
11:00-11:30	Skyline3 : Processing DDA Data with Skyline	
11:30-12:00		
12:00-12:30	Lunch	Lunch
12:30-13:00		
13:00-13:30	Section4 : Lecture : statistical inference, multiple testing	Section8 : Manual Inspection of Differential Results with Skyline
13:30-14:00		
14:00-14:30	break	break
14:30-15:00		
15:00-15:30	Section5 : Intro R, data exploration, basic statistics	Section9 : Real-World MS1 Filtering with Skyline (Birgit Schilling)
15:30-16:00		

STATISTICAL EXPERIMENTAL DESIGN

Olga Vitek

College of Science
College of Computer and Information Science



Northeastern University

WHY STATISTICS?

- Variation and uncertainty are unavoidable
 - *Technical variation:* sampling handling, storage, processing
 - *Instrumental variation:* elution time, ion suppression
 - *Signal processing:* peak boundaries, identity, intensity
 - *Biological variation:* variation in protein abundance

"Statistics: a body of methods for making wise decisions in the face of uncertainty." (W. A. Wallis)

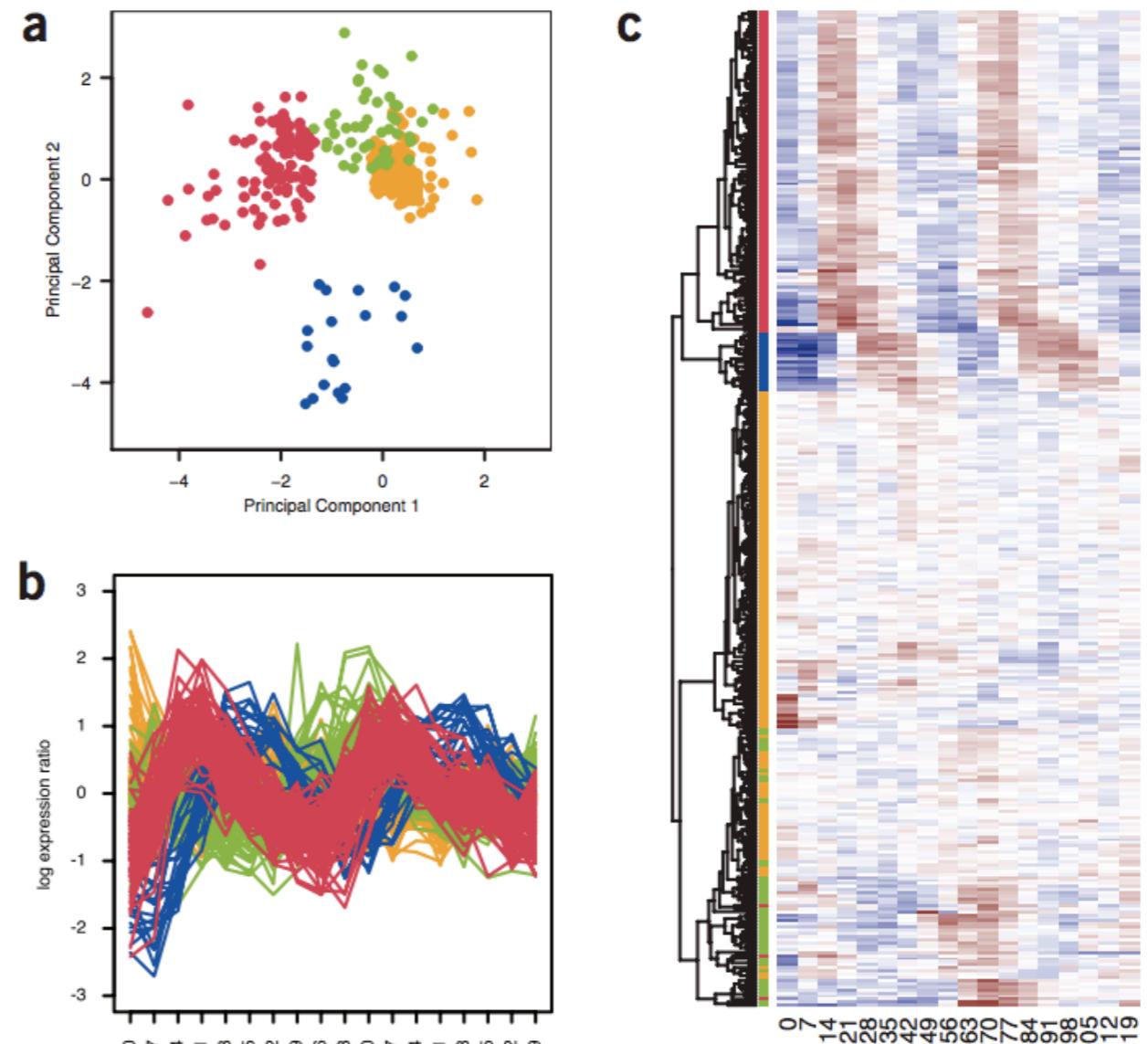
OUTLINE

- Translate scientific question into statistics
 - Statistical terms for ‘biomarker’ (or ‘signature’)
- Experimental design
 - Replication, randomization, blocking
- Case study: iPRG 2015-2016
 - Study design and preliminary analysis

STATISTICAL GOAL I: CLASS DISCOVERY

Discover proteins or subjects with similar patterns

- No known class labels
 - E.g., no ‘healthy’ or ‘disease’
 - All variation treated equally
 - No error rates
- Can’t find something meaningful if unsure what we look for
 - Best used for visualization

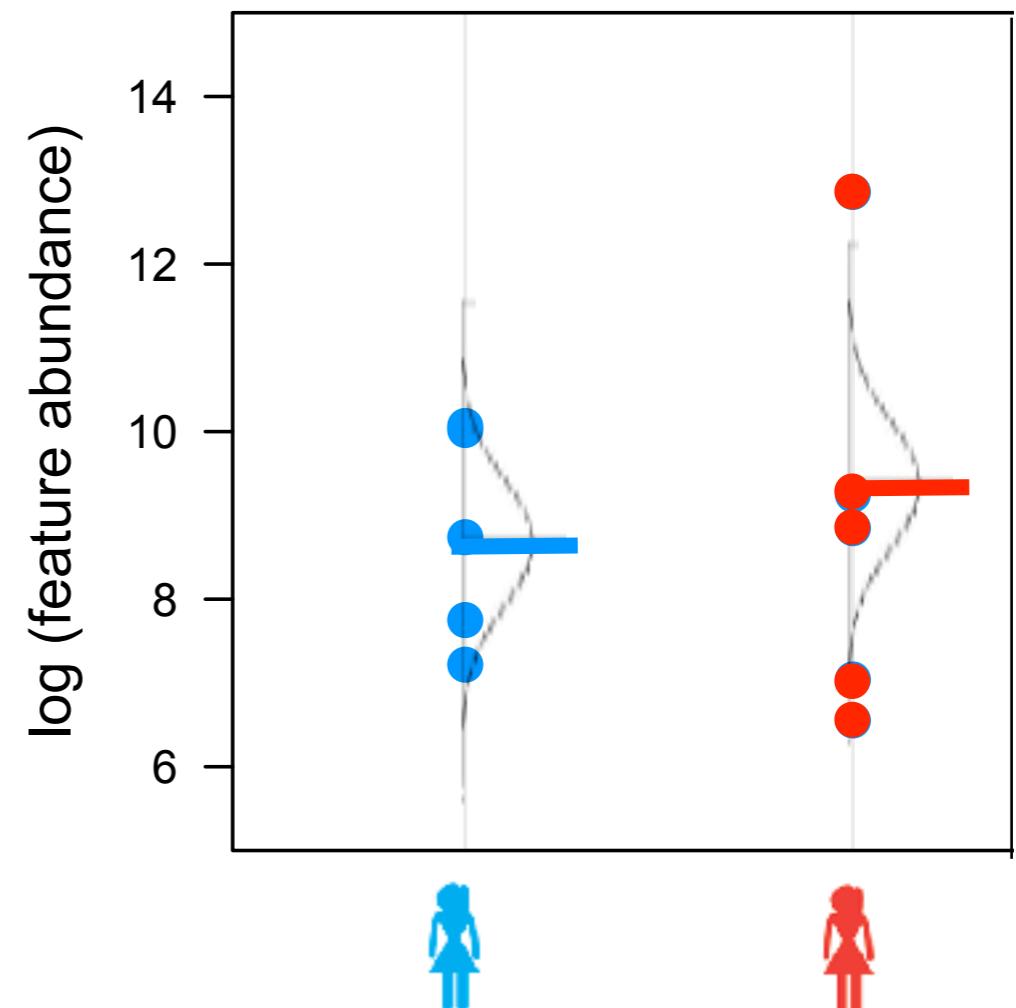


Gehlenborg *et al*, Nature Methods, 2010

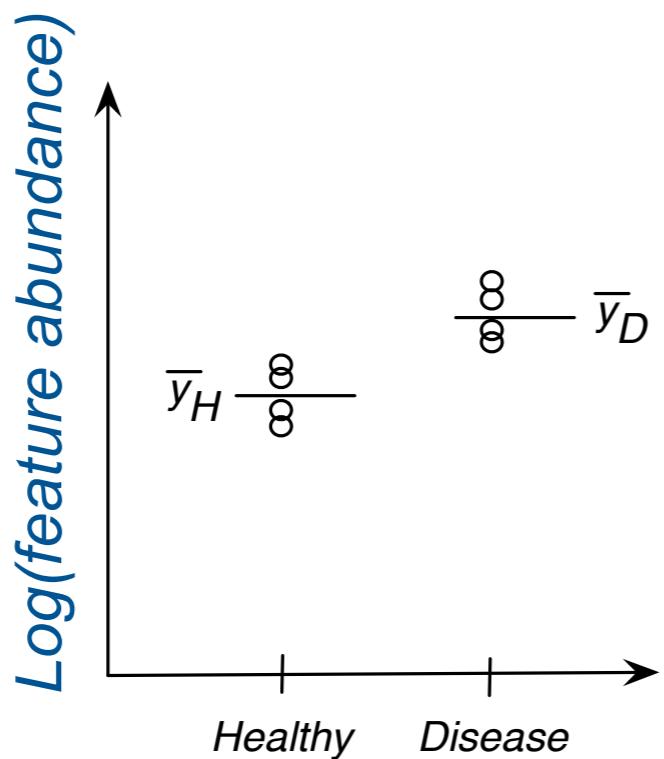
STATISTICAL GOAL 2: CLASS COMPARISON

Compare mean abundances in subject groups

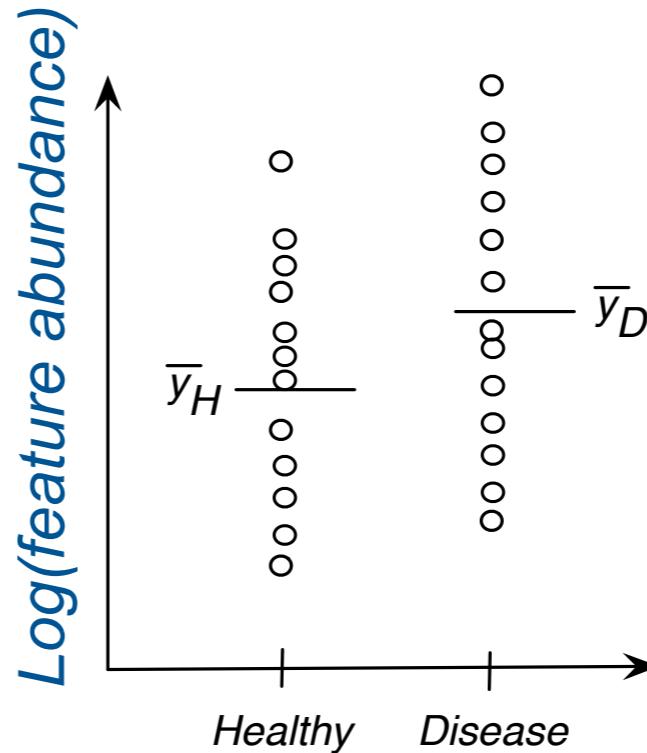
- Known class labels
 - Compare group averages
 - Report p-values, posterior probabilities etc
- Useful when compare groups of subjects
 - Best used for basic biology
 - Initial (Tier III) biomarker discovery screen



DIFFERENTIALLY ABUNDANT PROTEINS ARE NOT ALWAYS BIOMARKERS



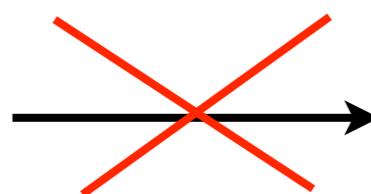
*Differentially abundant
and predictive*



*Differentially abundant
and not predictive*

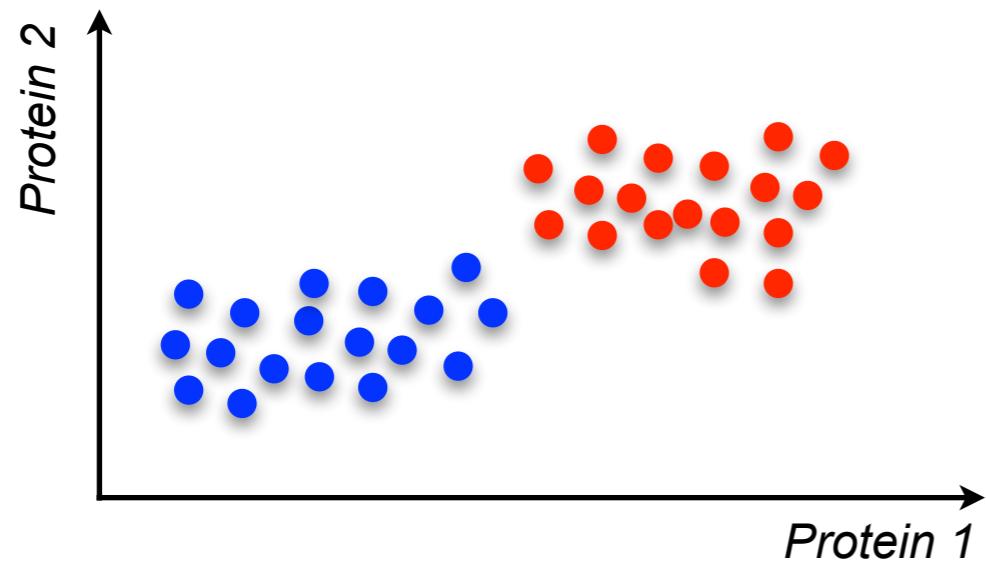
Single protein:

*Differentially
abundant*

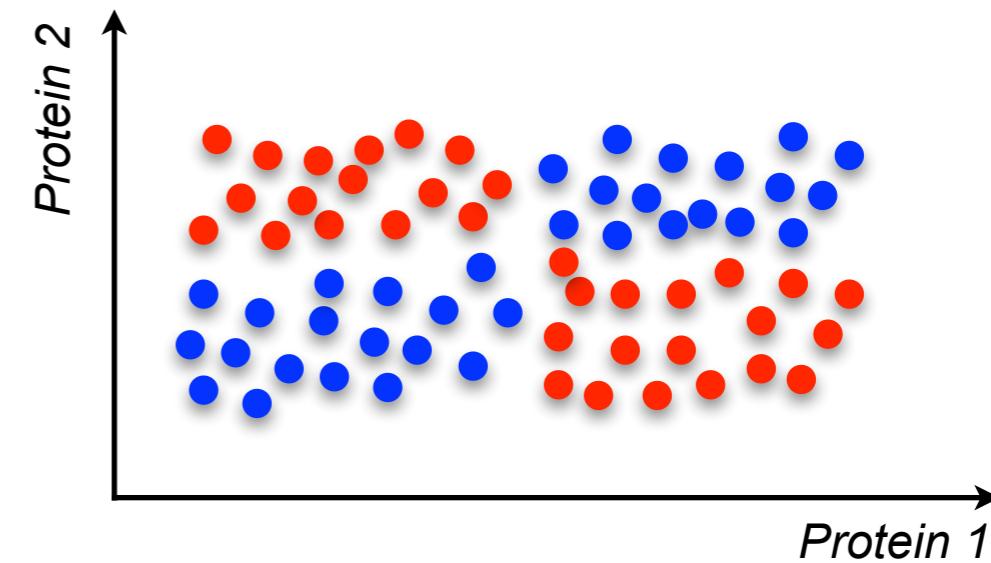


Predictive

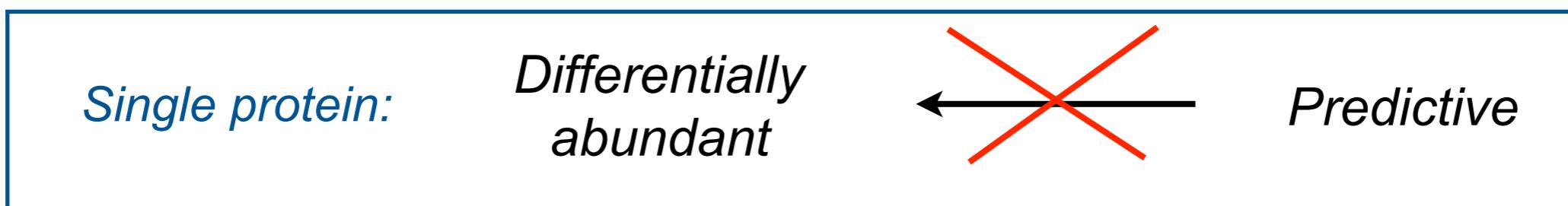
BIOMARKER PROTEINS ARE NOT ALWAYS DIFFERENTIALLY ABUNDANT



*Differentially
abundant and
predictive*



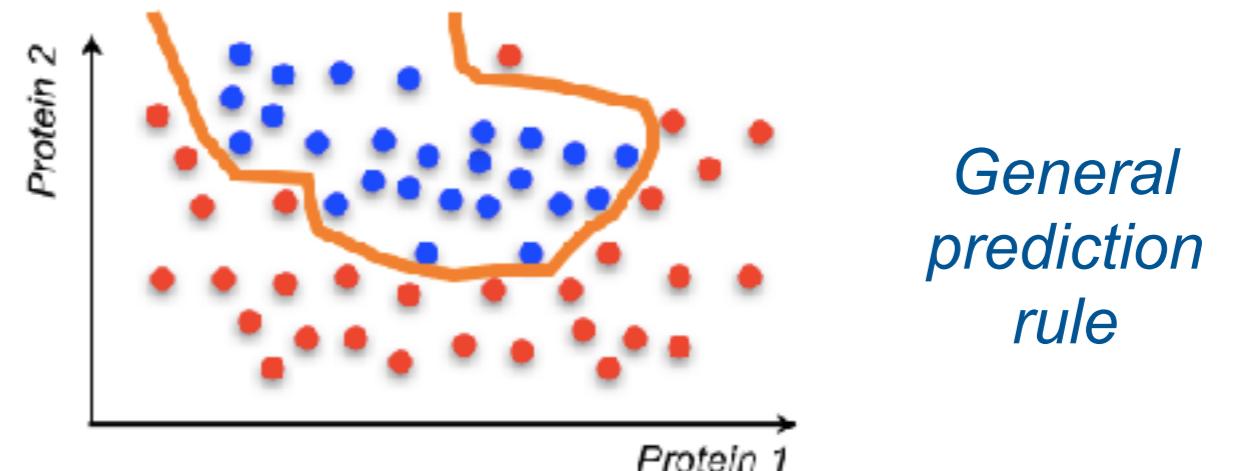
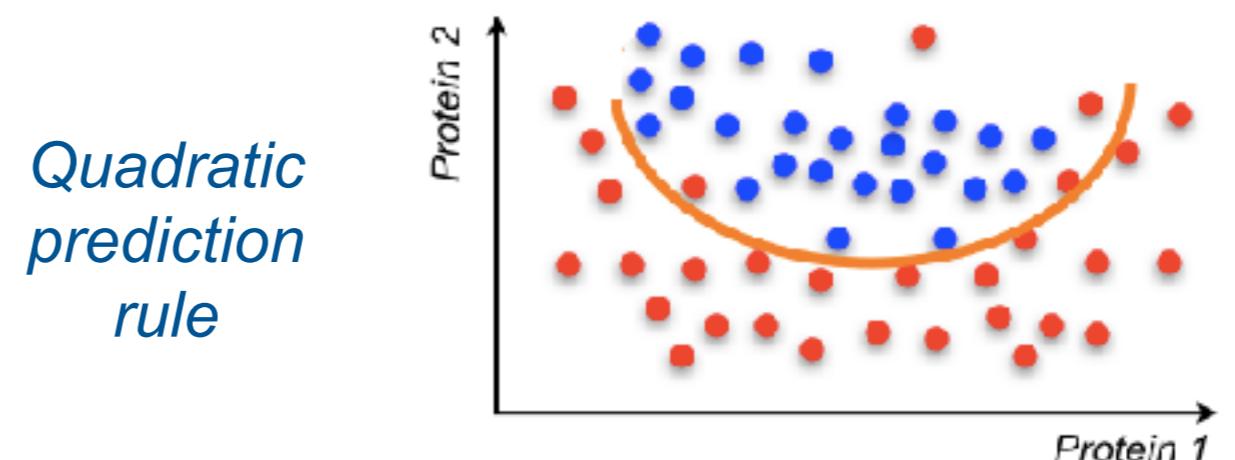
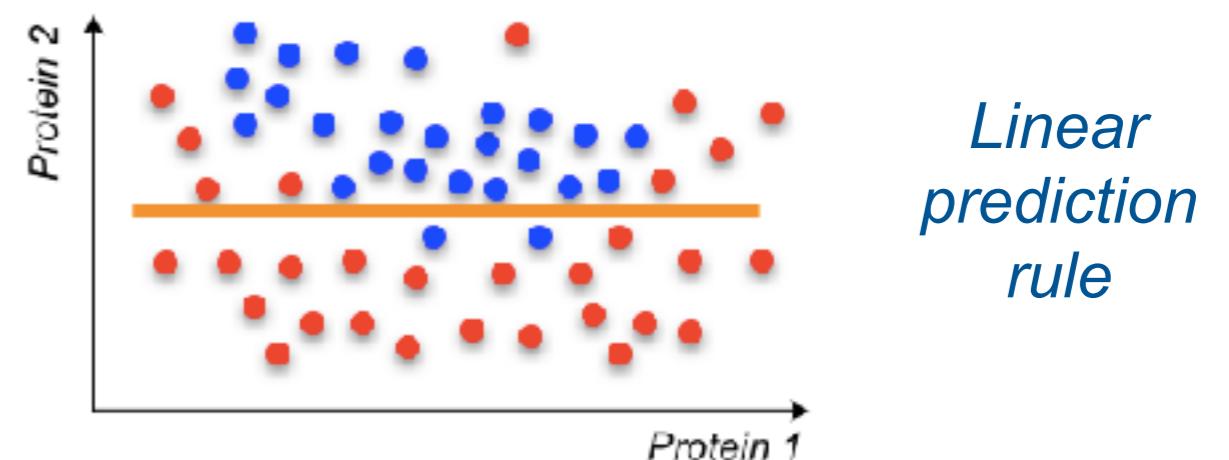
*Not differentially
abundant but
predictive*



STATISTICAL GOAL 3: CLASS PREDICTION

Classify each subject into a known group

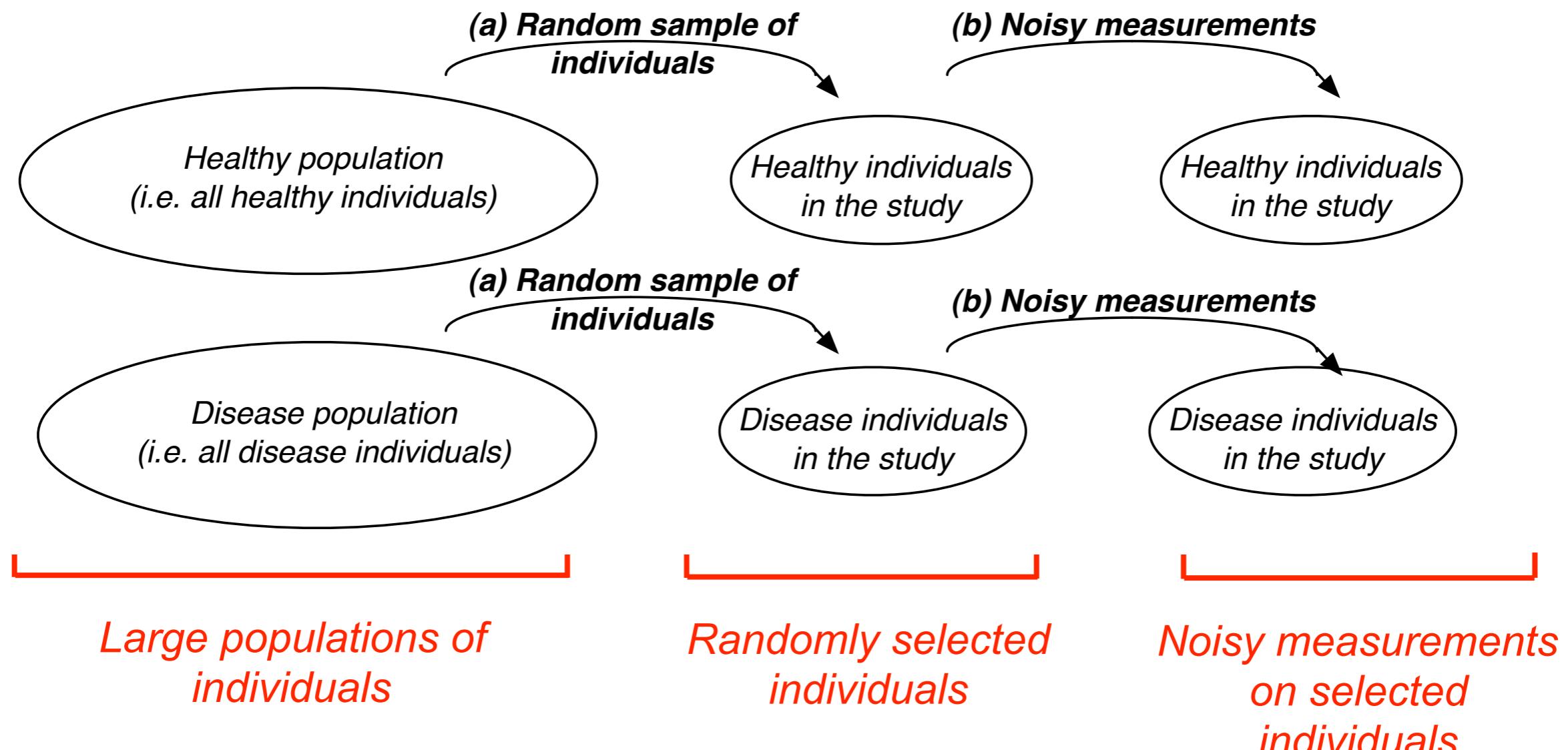
- Known class labels
 - Predict individual subjects
 - Report misclassification error (sensitivity, specificity, predictive value etc)
- Useful when focus on an individual
 - Tier I or Tier II biomarker discovery studies



OUTLINE

- Translate scientific question into statistics
 - Statistical terms for ‘biomarker’ (or ‘signature’)
- Experimental design
 - Replication, randomization, blocking
- Case study: iPRG 2015-2016
 - Study design and preliminary analysis

A STATISTICIAN'S VIEW OF THE EXPERIMENT

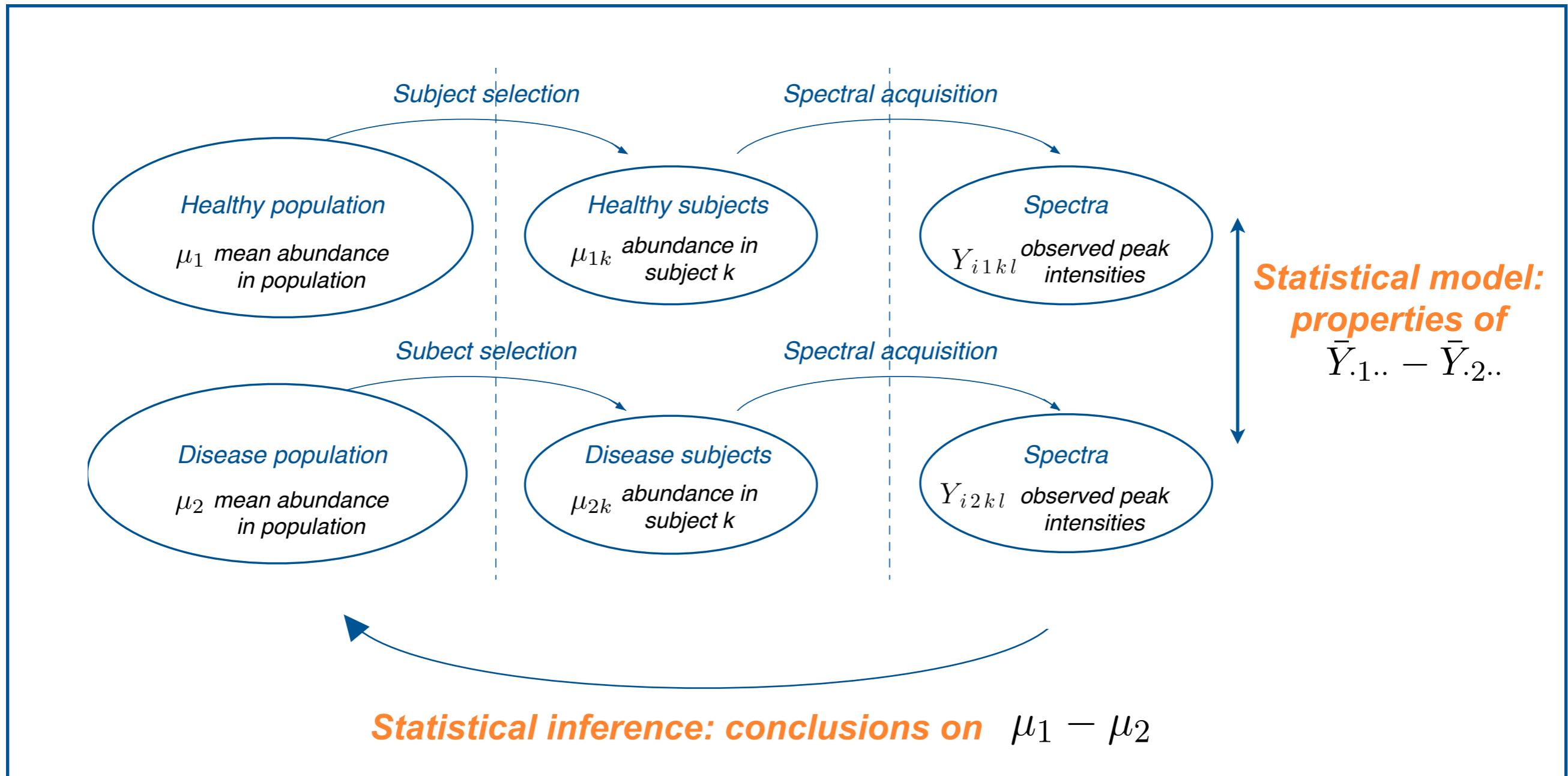


Dangers:

Bias: conclusions systematically differ from truth

Inefficiency: unnecessary variation in the data

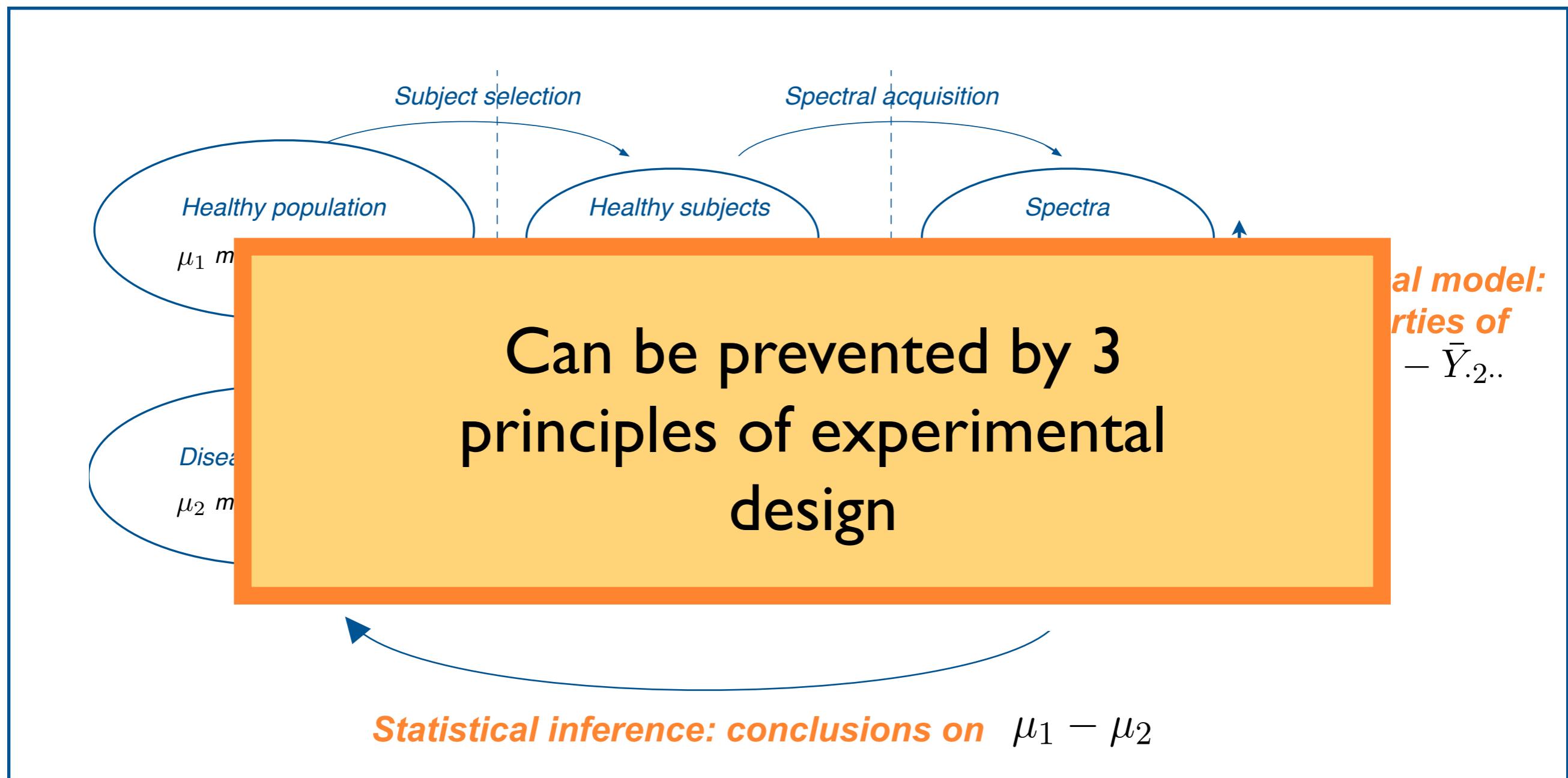
DEFINITION OF BIAS AND INEFFICIENCY



Bias: $\bar{Y}_{.1..} - \bar{Y}_{.2..}$ systematically different from $\mu_{1k} - \mu_{2k}$

Inefficiency: Large $Var(\bar{Y}_{.1..} - \bar{Y}_{.2..})$

DEFINITION OF BIAS AND INEFFICIENCY

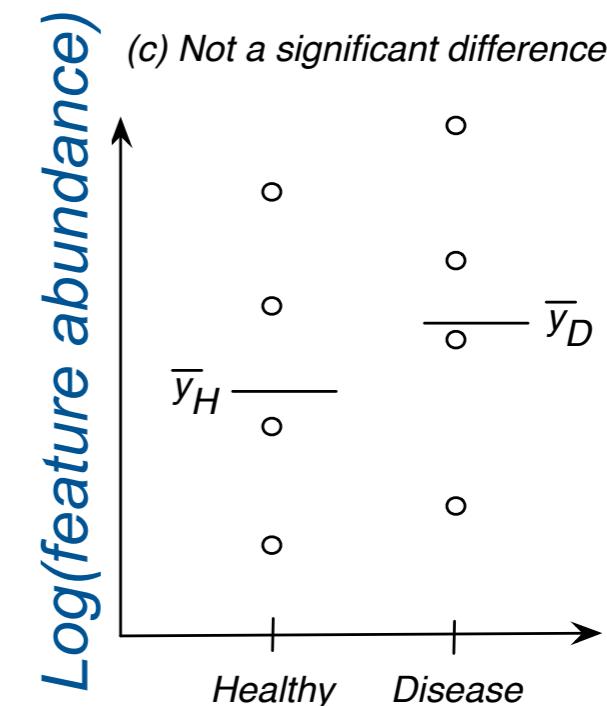
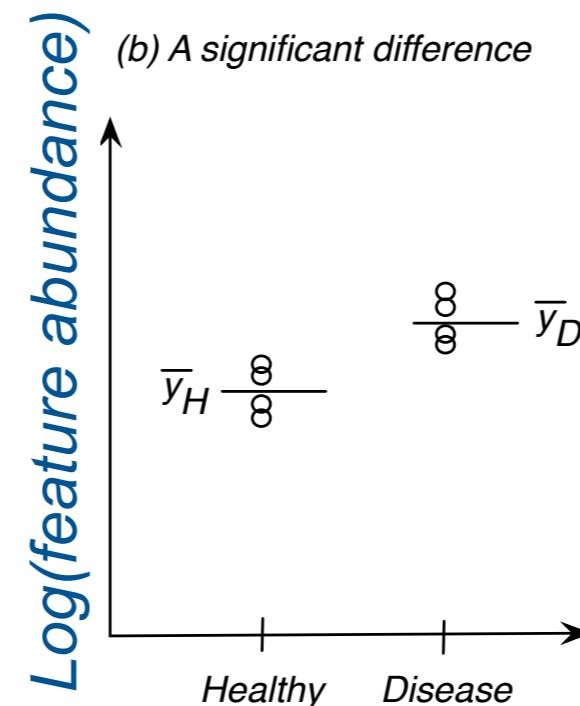
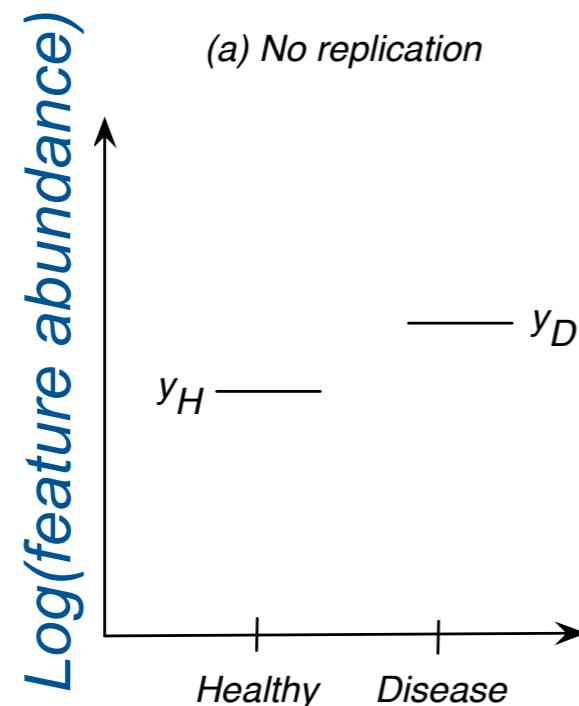
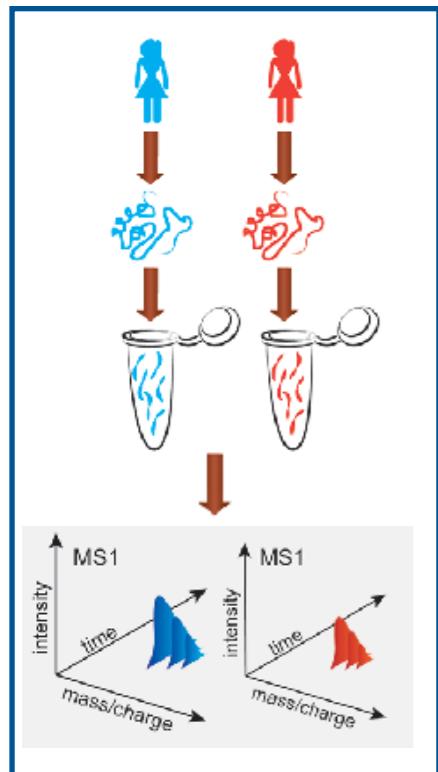


Bias: $\bar{Y}_{.1..} - \bar{Y}_{.2..}$ systematically different from $\mu_{1k} - \mu_{2k}$

Inefficiency: Large $Var(\bar{Y}_{.1..} - \bar{Y}_{.2..})$

PRINCIPLE I: REPLICATION

(1) carries out the inference and (2) minimizes inefficiencies

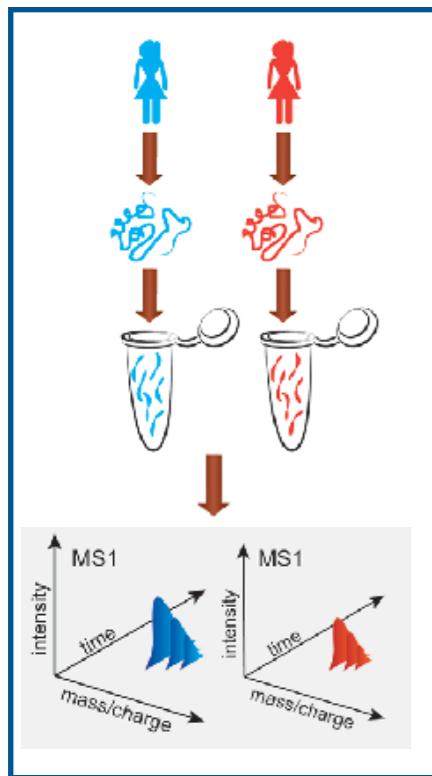


Two levels of randomness imply two types of replication:

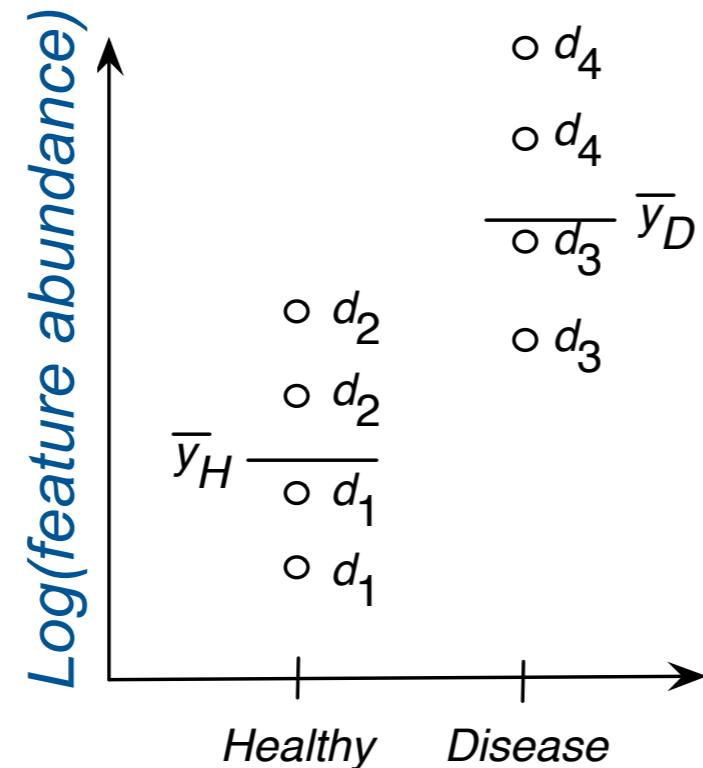
- ◆ *Biological replicates*: selecting multiple subjects from the population
- ◆ *Technical replicates*: multiple runs per subject

PRINCIPLE 2: RANDOMIZATION

Prevents bias

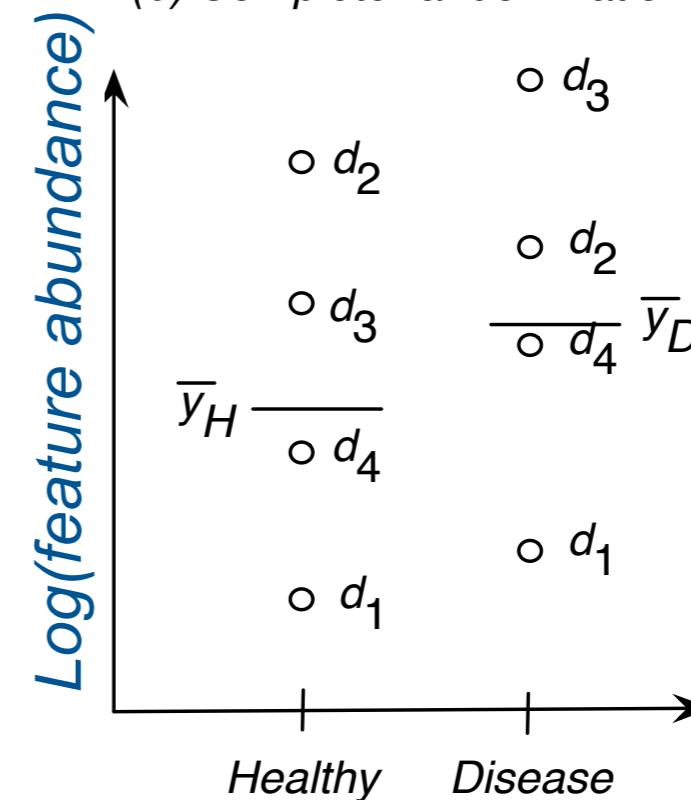


(a) Sequential acquisition



No randomization
= confounding
= bias

(b) Complete randomization



Complete randomization
= no bias

Two levels of randomness imply two types of randomization:

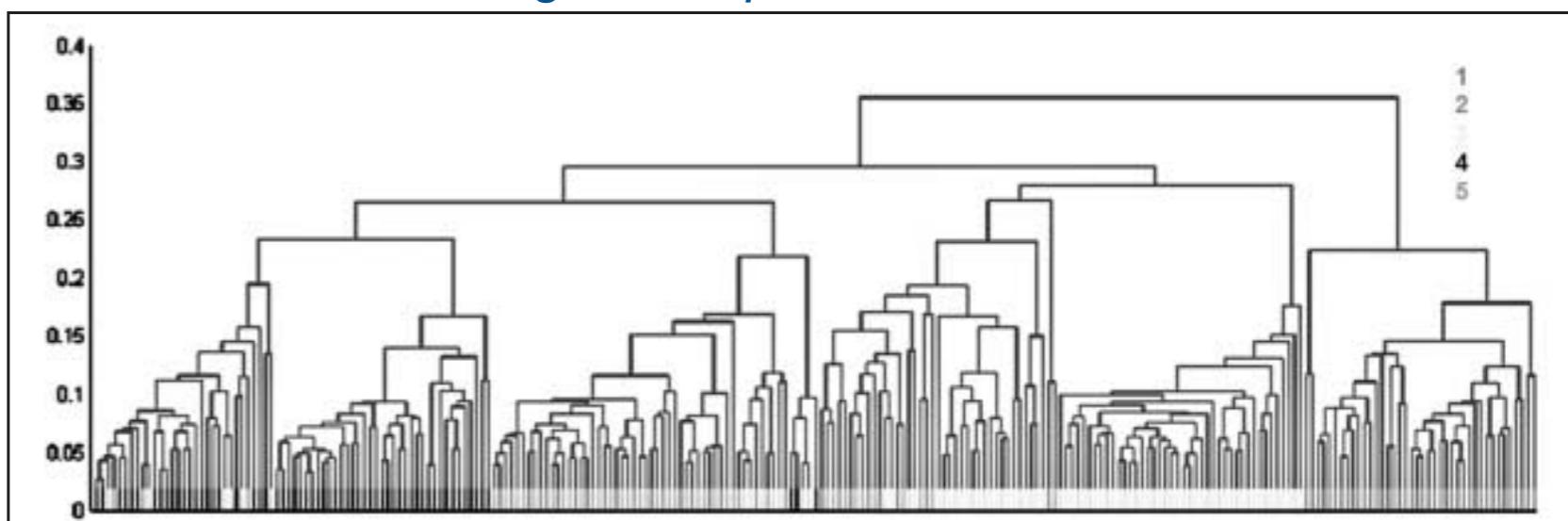
- ◆ *Biological replicates*: random selection of subjects from the population
- ◆ *Technical replicates*: random allocation of samples to all processing steps

EXAMPLE: LACK OF RANDOMIZATION

Hu, Coombes, Morris, Baggerly, *Briefings in Functional Genomics*, 2005

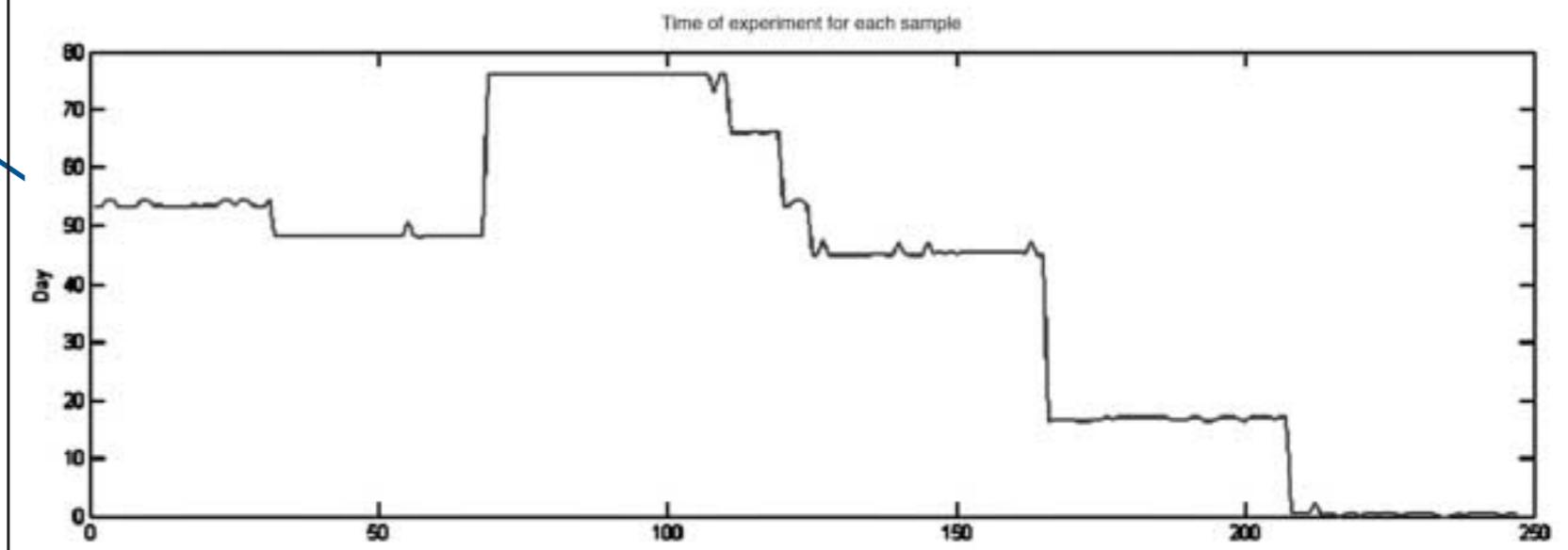
- Serum samples with five types of cancer
- SELDI-TOF MS
 - ◆ normalized, peak picked

Hierarchical clustering of samples



*Cancer subtype
confounded with
time*

*Same time-
based clustering
on the QC
samples!*



BEWARE OF BIG EFFECTS THEY ARE LIKELY TO REFLECT FLAWS OF THE DESIGN

- Study of gene expression between Asians and Europeans
- Found that 78% of genes are differentially
 - Asians were profiles in one year, and Europeans in another
 - The difference therefore likely reflects a batch effect



Journal home > Archive > Letter > Full Text

Journal content
+ Journal home
+ Advance online publication
+ Current issue
+ Archive
+ Focuses and Supplements

Letter

Nature Genetics 39, 226 - 231 (2007)
Published online: 7 January 2007 | doi:10.1038/ng1955

Common genetic variants account for differences in gene expression among ethnic groups

Richard S. Spielman¹, Laurel A. Bastone², Joshua T. Burdick³, Michael Morley³, Warren J. Ewens⁴ & Vivian G. Cheung^{1,3,5}



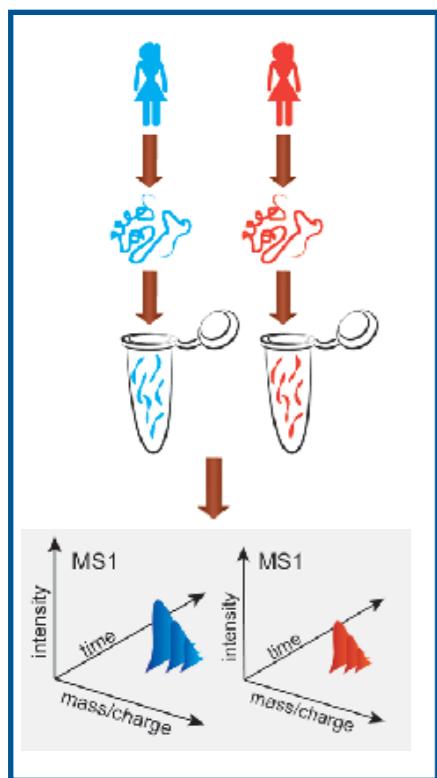
This issue
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Previous article

Source: a blog by Jeff Leek, Biostatistics, John Hopkins University

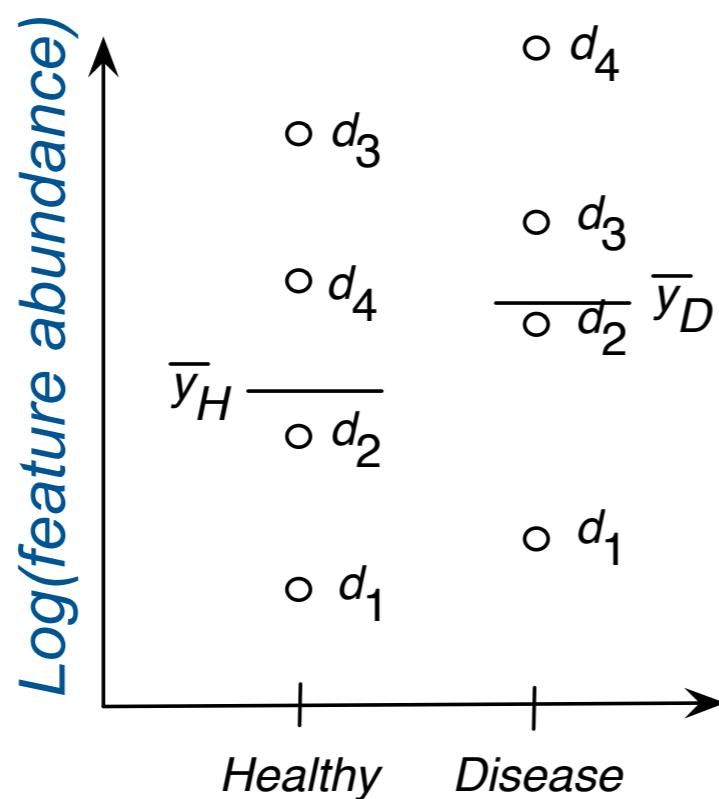
<http://simplystatistics.org/2016/02/01/a-menagerie-of-messed-up-data-analyses-and-how-to-avoid-them/>

PRINCIPLE 3: BLOCKING

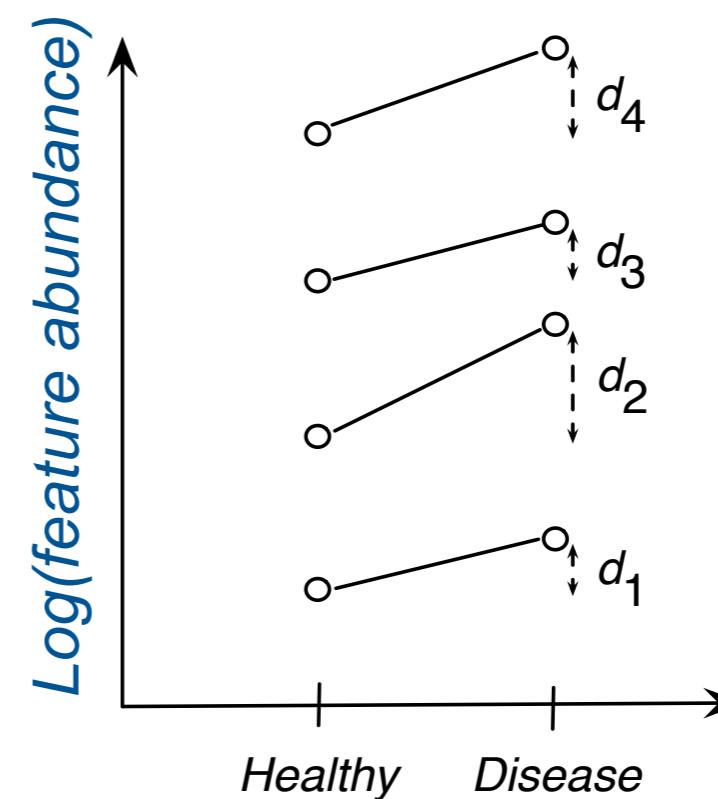
Helps reduce both bias and inefficiency



(b) Complete randomization



(c) Day = block



Complete randomization
= inflated variance

Block-randomization
= restriction on randomization
= systematic allocation

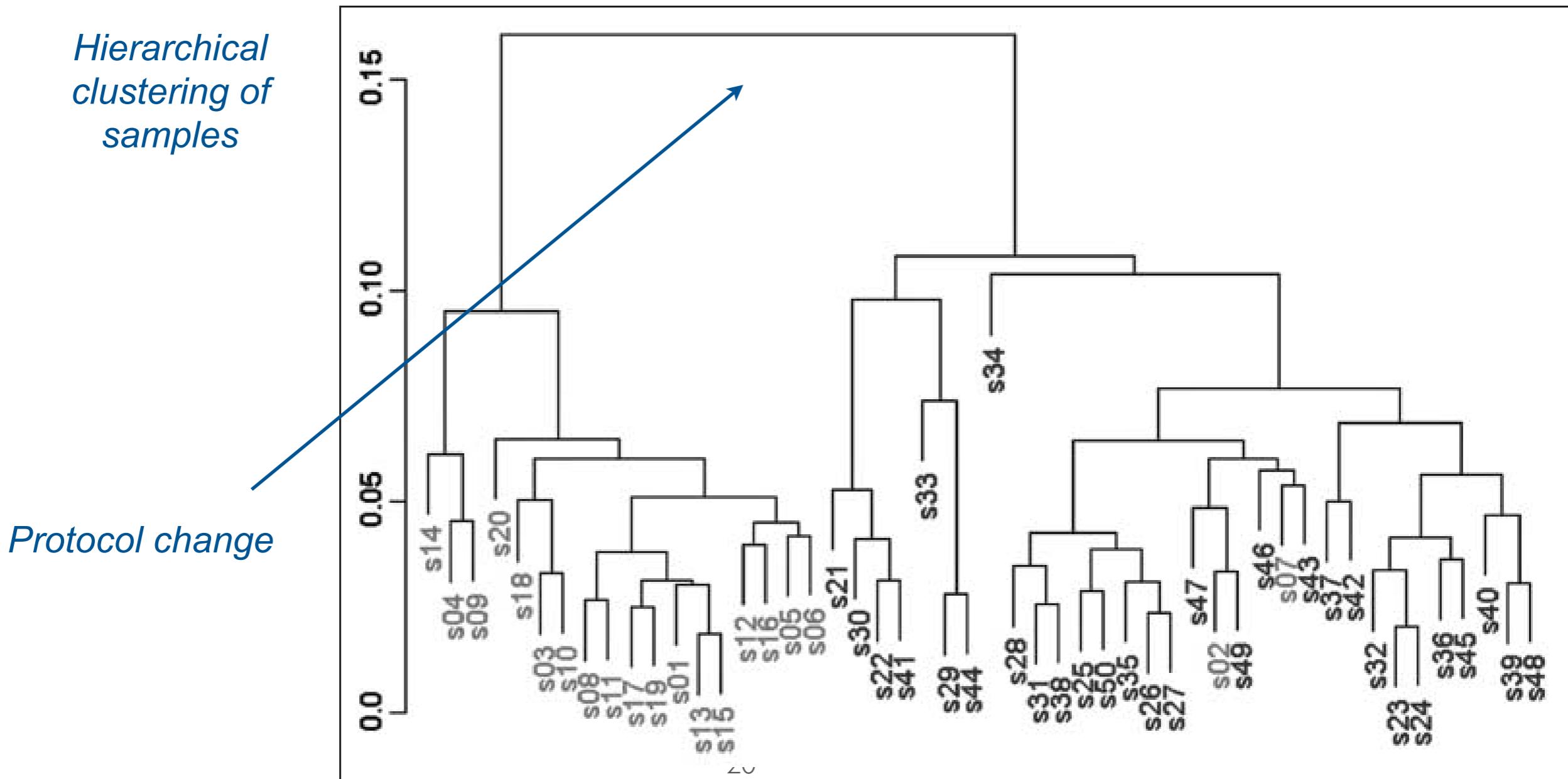
Two levels of randomness imply two types of blocks:

- ◆ *Biological replicates*: subjects having similar characteristics (e.g. age)
- ◆ *Technical replicates*: samples processed together (e.g. in a same day)

EXAMPLE: LACK OF BLOCKING

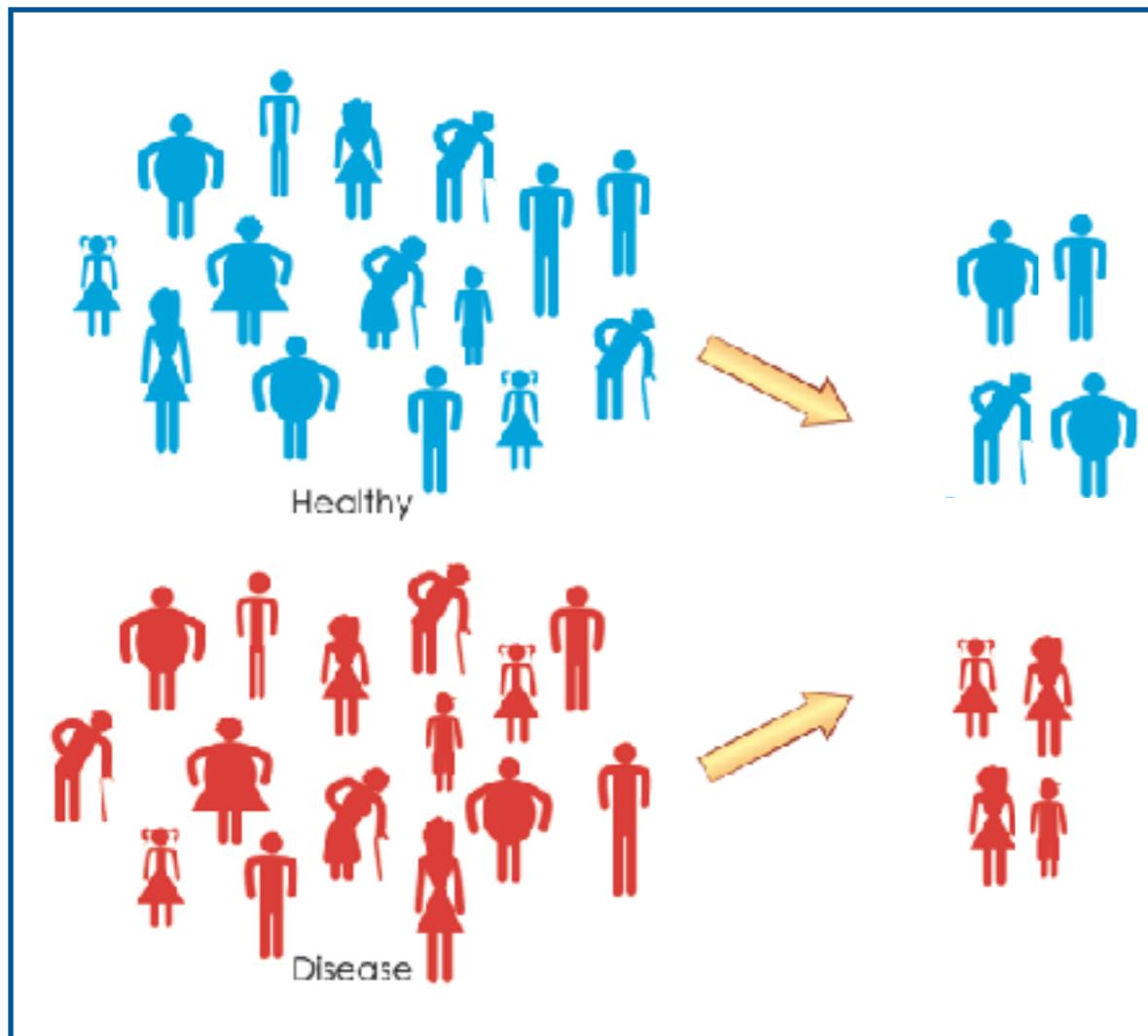
Hu, Coombes, Morris, Baggerly, *Briefings in Functional Genomics*, 2005

- Serum samples with two types of cancer
- SELDI-TOF MS, 3 fractions
 - ◆ normalized, peak picked

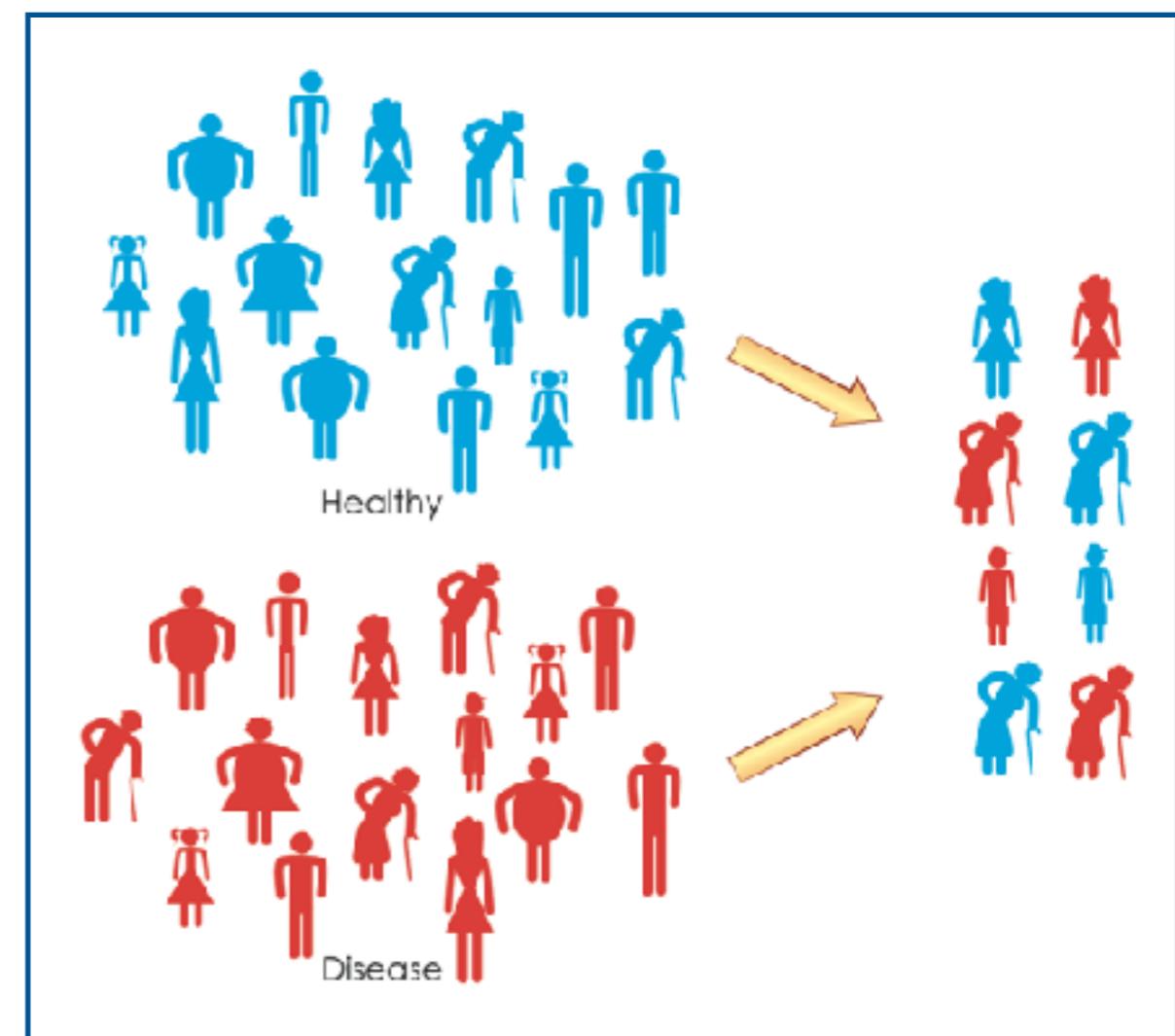


MATCHING

Blocking with respect to biological risk factors



Complete randomization
= inflated variance



Block-randomization
= restriction on randomization
= systematic allocation

EXAMPLE

Block-randomized selection of subjects from repository

		Disease group				
		Control	Stable angina	Unstable angina	NSTEMI	STEMI
Stratification	≥ 58 y.o; Female	354	300	49	39	29
	≥ 58 y.o; Male	701	843	143	86	54
	< 58 y.o; Female	80	56	5	5	8
	< 58 y.o; Male	264	190	34	23	27

Counts in the initial repository of samples

		Disease group				
		Control	Stable angina	Unstable angina	NSTEMI	STEMI
Stratification	≥ 58 y.o; Female	3	3	3	3	3
	≥ 58 y.o; Male	3	3	3	3	3
	< 58 y.o; Female	2	2	2	2	2
	< 58 y.o; Male	2	2	2	2	2

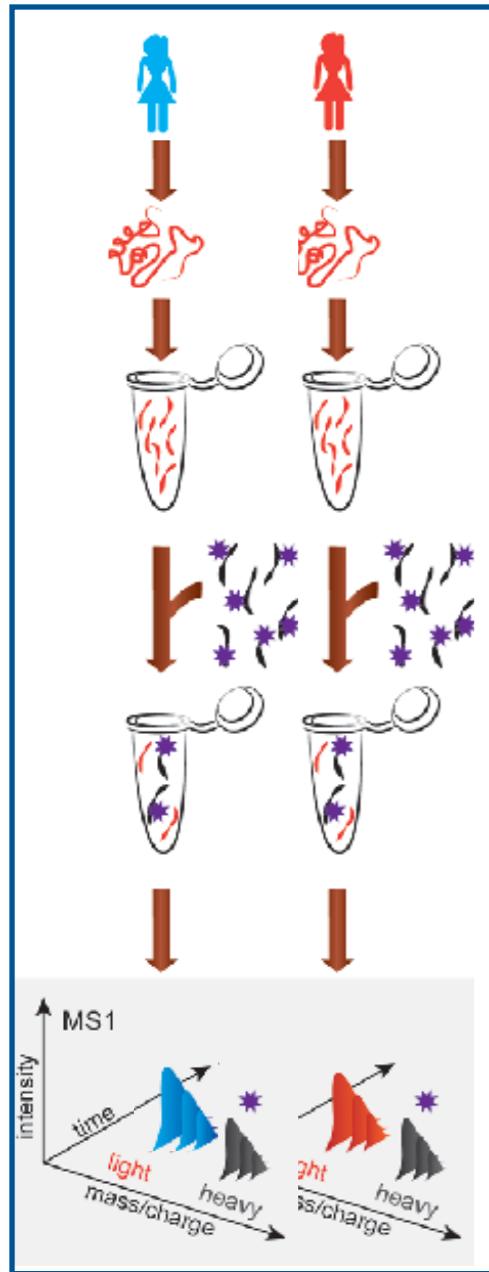
Counts of subjects included in the study

Mass spectra acquired without technical replication

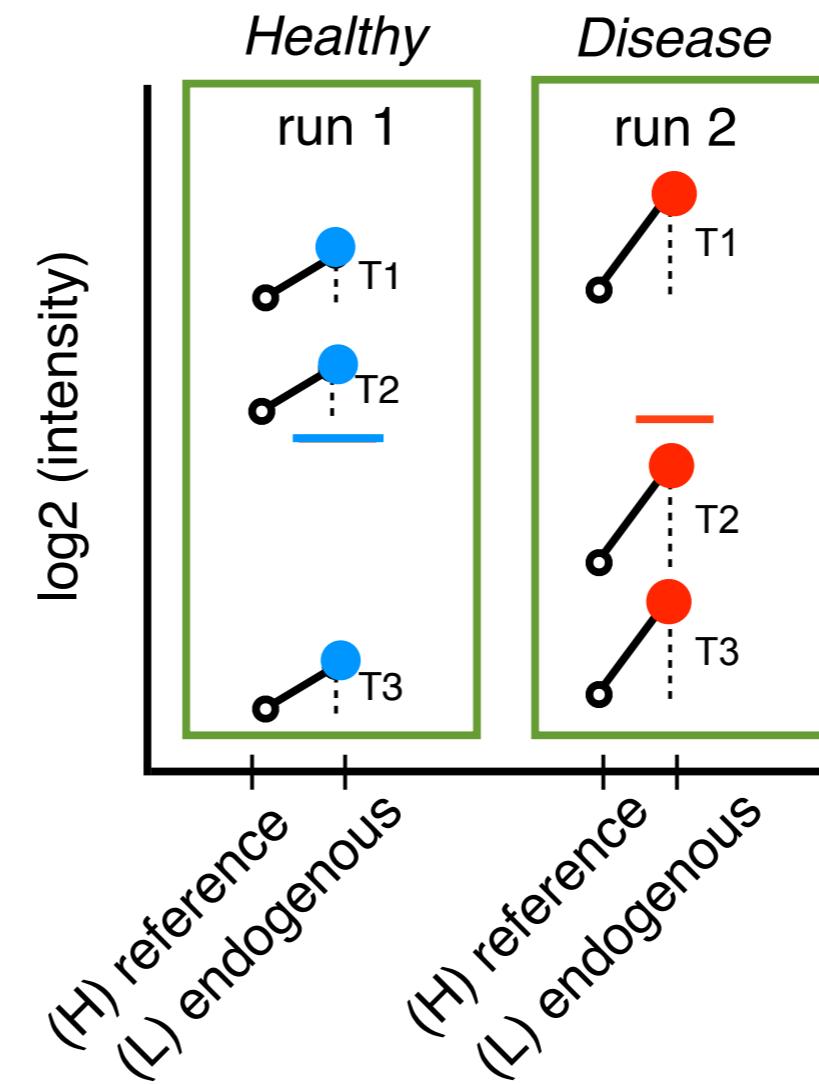
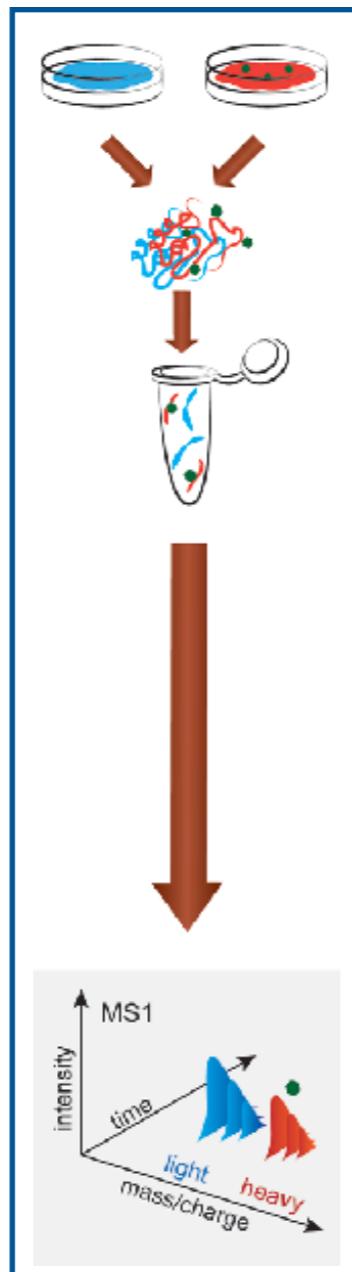
LABELING (=MULTIPLEXING)

Blocking with respect to mass spectrometry run

Synthetic standards



SILAC



- T** transition
- average of log-intensities
- paired log-intensities of L and H
- ⋮** difference of log-intensities of L and H
= log-ratios of L over H
- run

Multiplexing reduces both bias and variance
(assuming that extra sample handling does not introduce extra variation)

Martin Krzywinski & Naomi Altman

nature methods

Techniques for life scientists and chemists

[nature.com](#) ▶ [journal home](#) ▶ [archive](#) ▶ [issue](#) ▶ [this month](#) ▶ [abstract](#)

NATURE METHODS | THIS MONTH

Points of significance: Importance of being uncertain

[Martin Krzywinski & Naomi Altman](#)

[Affiliations](#)

Nature Methods 10, 809–810 (2013) | doi:10.1038/nmeth.2613

Points of significance: Comparing samples—part I

[Martin Krzywinski & Naomi Altman](#)

Points of Significance: Error bars

[Martin Krzywinski & Naomi Altman](#)

[Affiliations](#)

Nature Methods 10, 921–922 (2013) | doi:10.1038/nmeth.2659

Points of significance: Power and sample size

[Martin Krzywinski & Naomi Altman](#)

[Affiliations](#)

Nature Methods 10, 1139–1140 (2013) | doi:10.

Points of significance: Significance, *P* values and *t*-tests

[Martin Krzywinski & Naomi Altman](#)

OUTLINE

- Translate scientific question into statistics
 - Statistical terms for ‘biomarker’ (or ‘signature’)
- Experimental design
 - Replication, randomization, blocking
- Case study: iPRG 2015-2016
 - Study design and preliminary analysis

ABRF IPRG STUDY 2015

Detection of differentially abundant proteins in controlled mixture

Name	Origin	Molecular Weight	Samples			
			1	2	3	4
A Ovalbumin	Chicken Egg White	45KD	65	55	15	2
B Myoglobin	Equine Heart	17KD	55	15	2	65
C Phosphorylase b	Rabbit Muscle	97KD	15	2	65	55
D Beta-Galactosidase	Escherichia Coli	116KD	2	65	55	15
E Bovine Serum Albumin	Bovine Serum	66KD	11	0.6	10	500
F Carbonic Anhydrase	Bovine Erythrocytes	29KD	10	500	11	0.6

Spiked into a constant background: tryptic digests of S. cerevisiae

Choi et al., “ABRF Proteome Informatics Research Group (iPRG) 2015 Study: Detection of differentially abundant proteins in label-free quantitative LC-MS/MS experiments”, *Journal of Proteome Research*, 2017.

EXPERIMENTAL PROCEDURES

● **Background**

- ◆ 200ng of tryptic digests of *S. cerevisiae*

● **Spectral acquisition**

- ◆ *Three technical replicates per sample*
- ◆ *Randomized order*
- ◆ Separation:
 - ◆ Thermo nLC 1000 system
 - ◆ 110-min linear gradient
- ◆ Spectral acquisition:
 - ◆ *DDA profile mode in Orbitrap*
 - ◆ Resolution 70,000 for MS and 17,500 for MS/MS
 - ◆ MSI scan range 300-1650 m/z
 - ◆ Normalized collision energy 27%
 - ◆ Singly charged ions excluded

SPECTRAL PROCESSING

● MS/MS identification

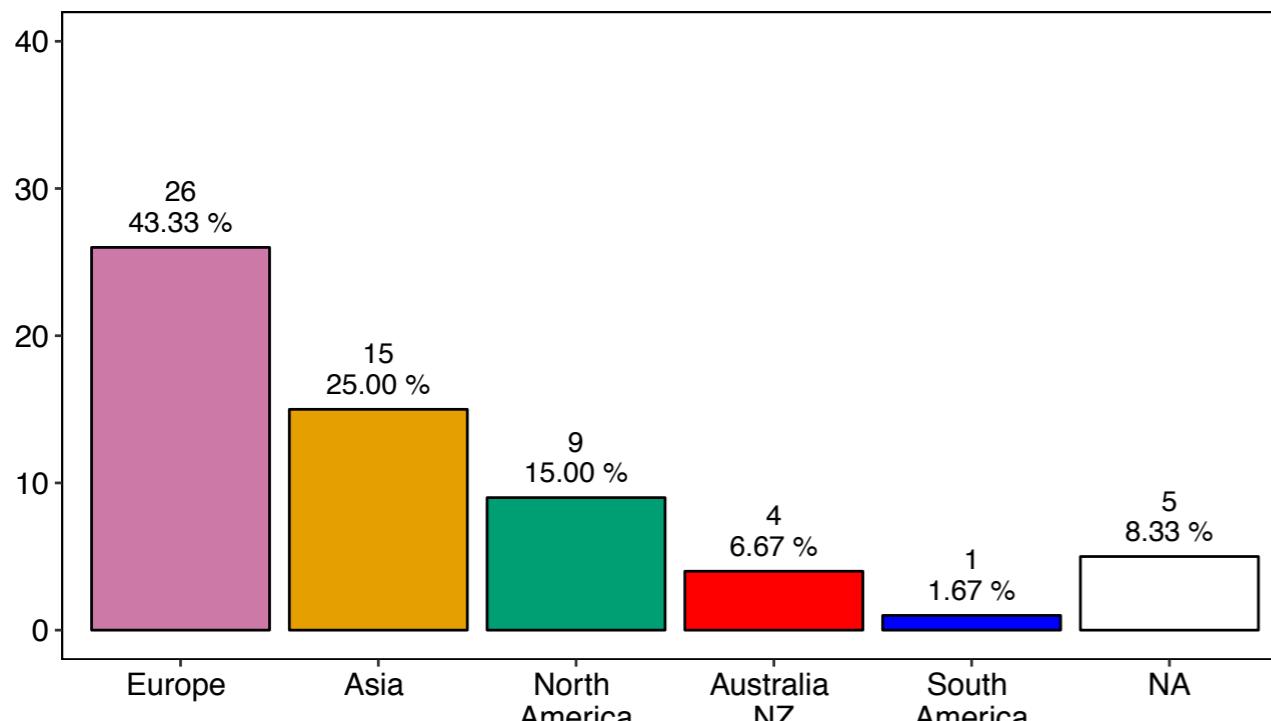
- ◆ Database search: OMSSA7, MS-GF+, Comet
- ◆ Q-value: target-decoy.
 - ◆ No filtering!
- ◆ 5,766 proteins, ~26,242 PSMs/run
- ◆ 48% of proteins had 1 or 2 PSMs
- ◆ 29% of proteins had 15 or more PSMs

● MSI quantification with Skyline

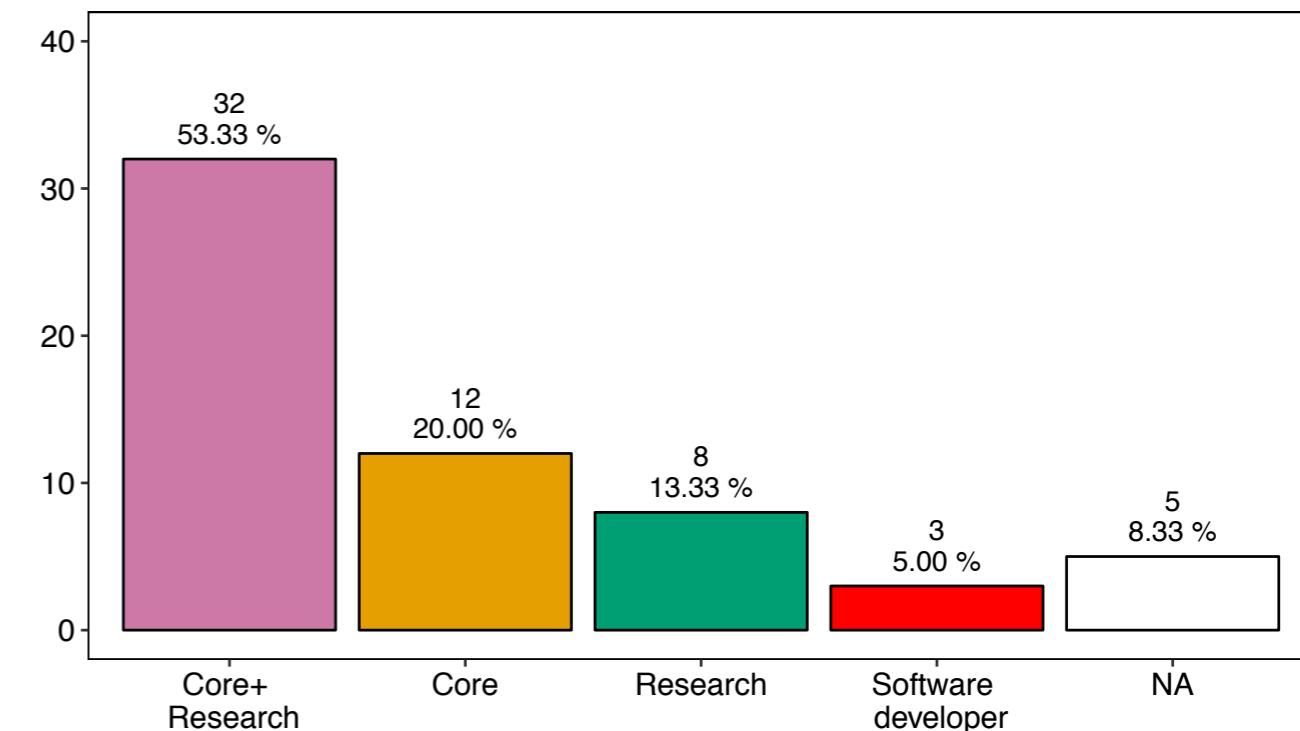
- ◆ Original processing
 - ◆ 3,766 proteins, 29,575 features
 - ◆ median 5 features/protein
- ◆ Post-study processing
 - ◆ 3,027 proteins, 34,783 features
 - ◆ median 7 features/protein

STUDY PARTICIPANTS

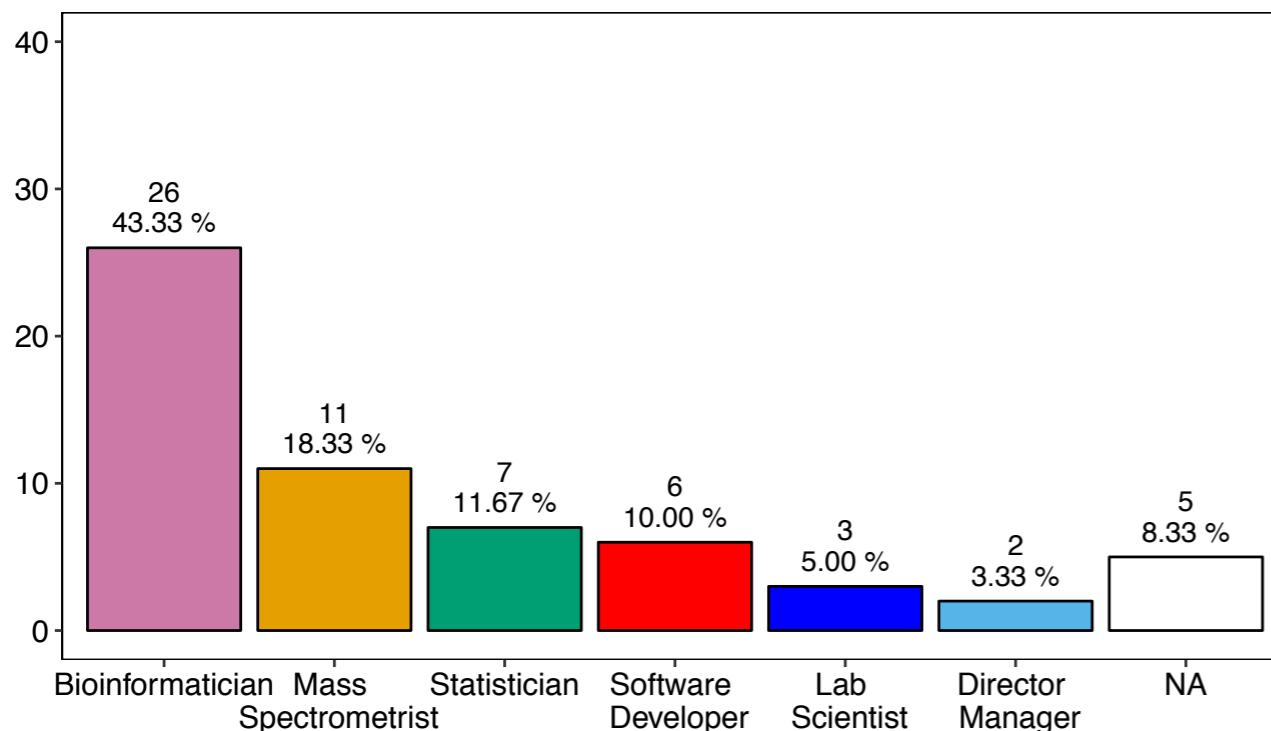
(A) Continent



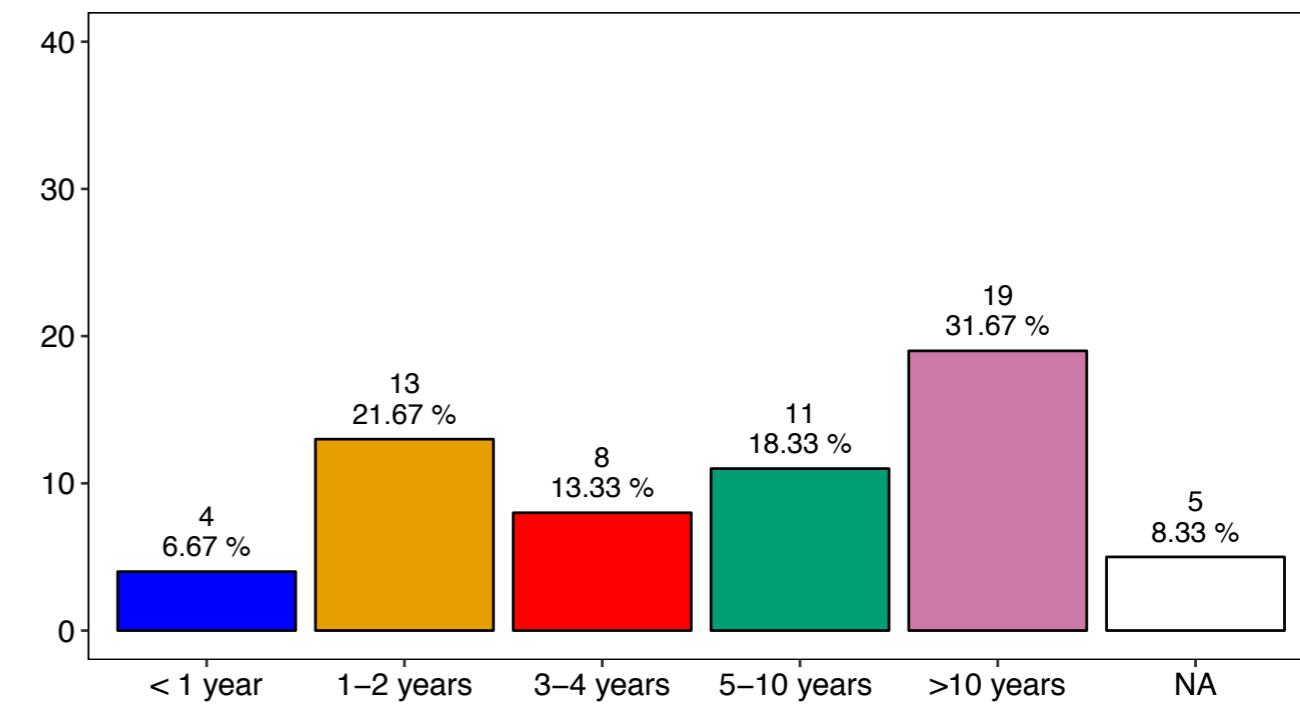
(B) Facility type



(C) Job description

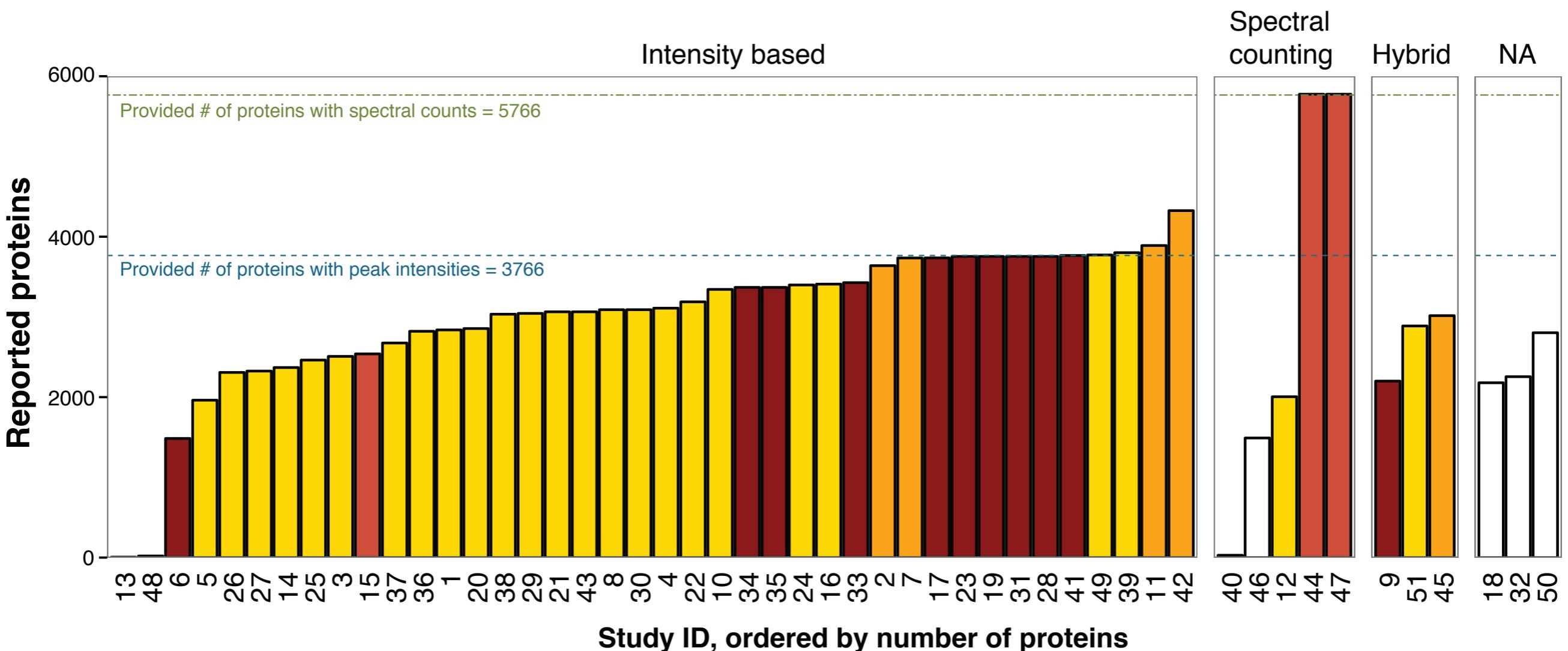
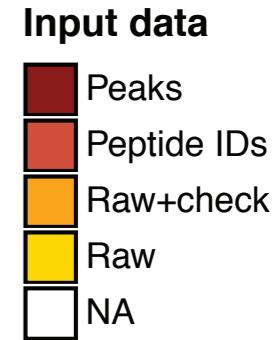


(D) Experience in label-free proteomics



DIVERSE SUBMISSIONS

*INPUT, PROTEIN NUMBER,
AND CHOICE OF QUANTIFICATION*

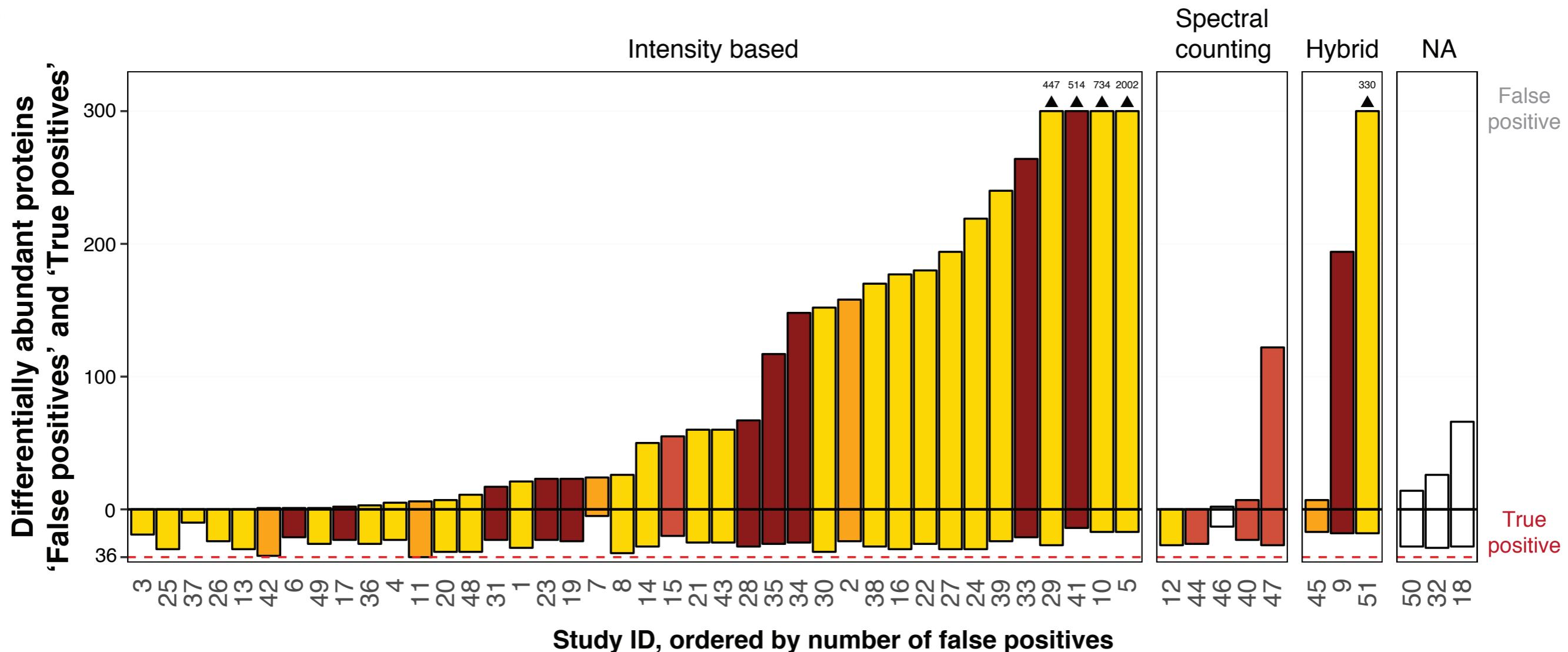


DIVERSE SUBMISSIONS

ACCURACY OF DETECTING DIFFERENTIAL ABUNDANCE

Input data

- Peaks
- Peptide IDs
- Raw+check
- Raw
- NA

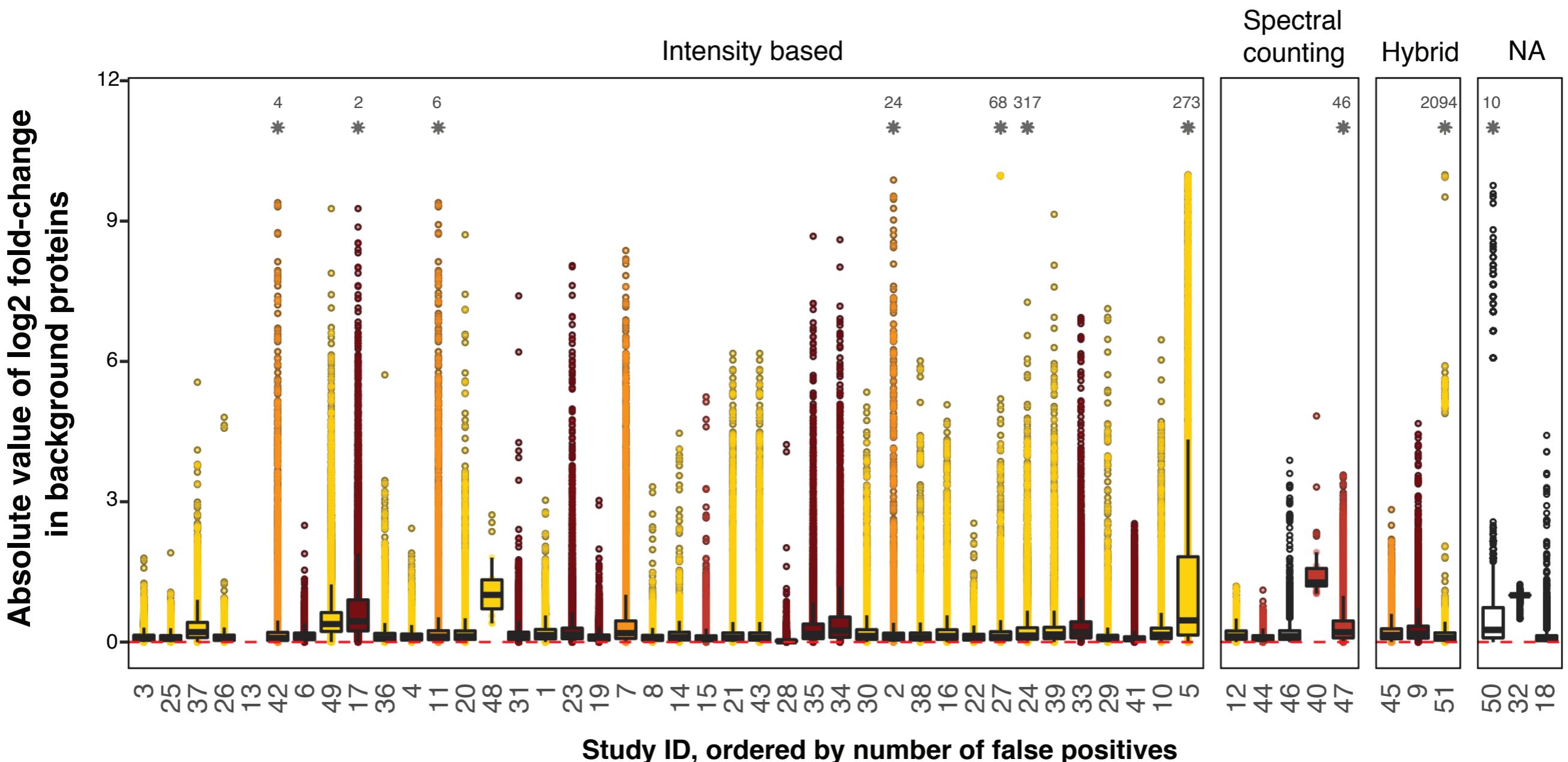


DIVERSE SUBMISSIONS

ACCURACY OF ESTIMATING FOLD CHANGE

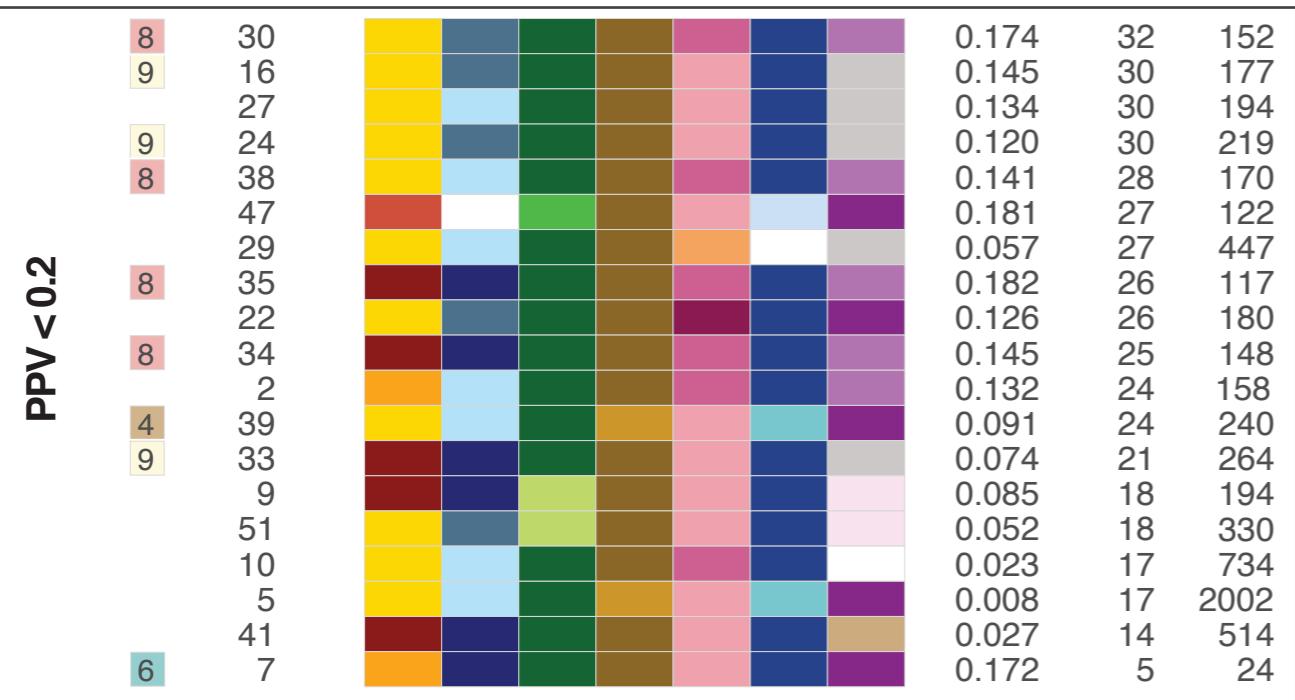
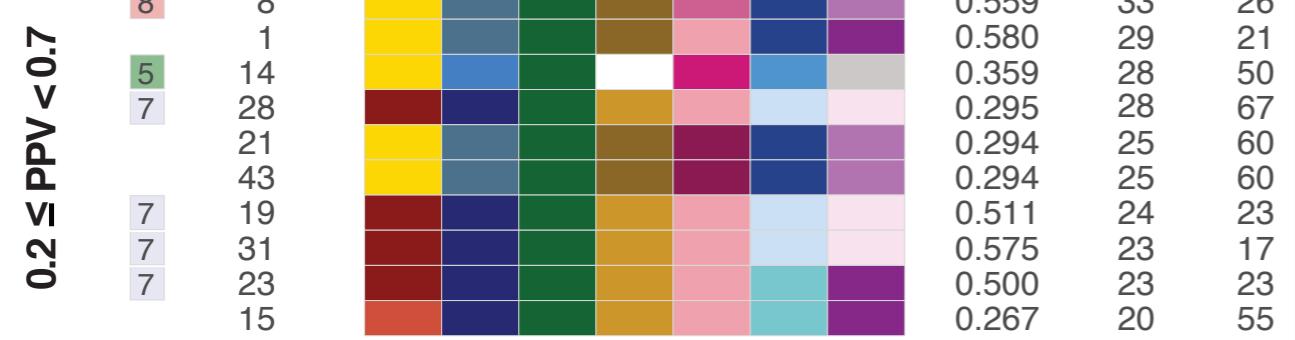
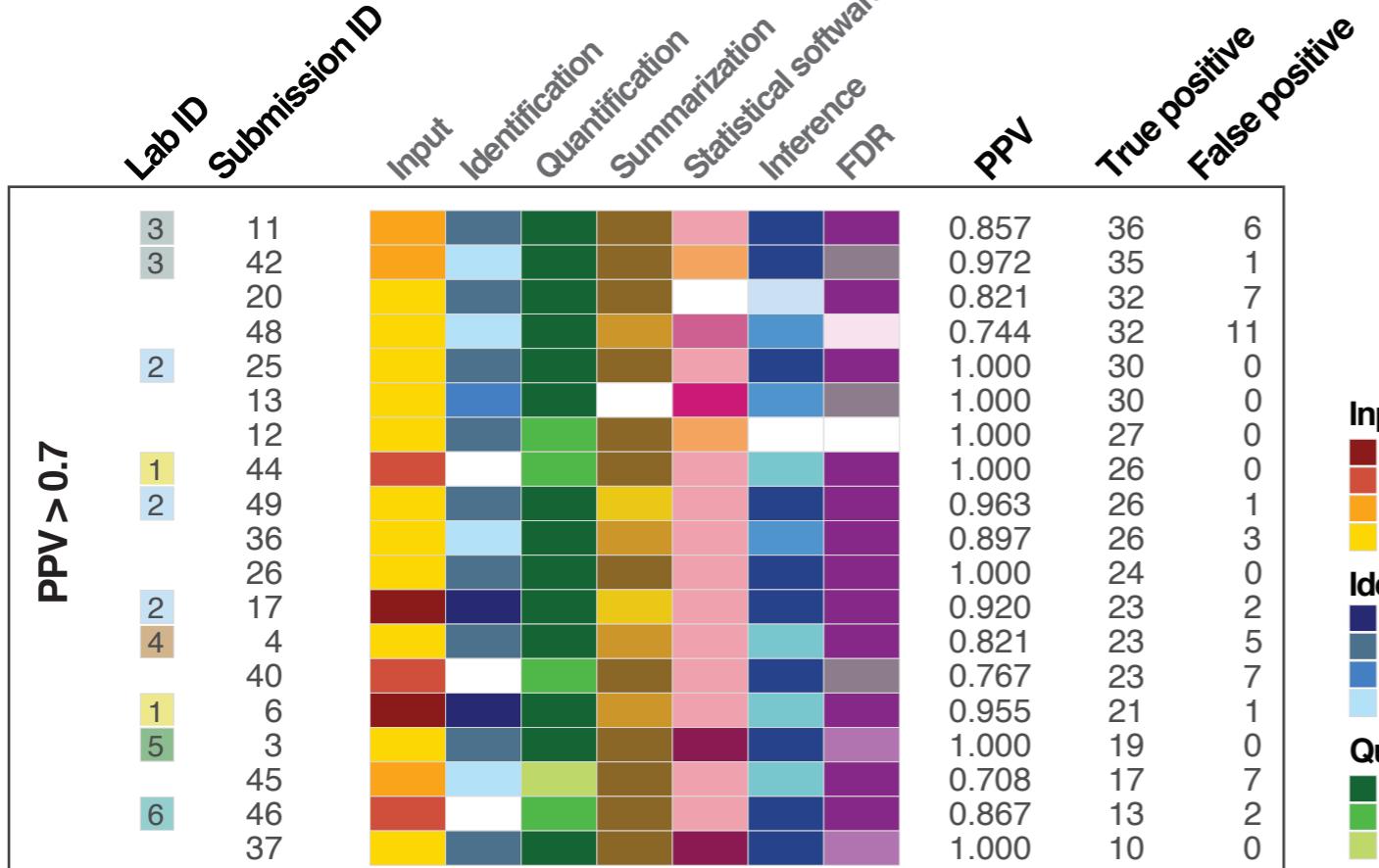
Input data

- Peaks
- Peptide IDs
- Raw+check
- Raw
- NA



SUMMARY OF SUBMISSIONS

USER EXPERTISE IS KEY



Input

- Peaks
- Peptide ids
- Raw+check
- Raw

Identification

- Skyline
- MaxQuant
- Progenesis
- Others

Quantification

- Feature intensity
- Spectral counting
- Hybrid

Summarization

- Protein summarization / Protein-level inference
- Peptide summarization / Protein-level inference
- Peptide summarization / Peptide-level inference

Statistical software

- Persus
- Progenesis QI
- Others
- R, Excel, MatLab, Python
- In-house scripts

Inference

- t-test / SAM's t test
- ANOVA
- Linear (mixed-effects) model
- Others

FDR

- Benjamini Hochberg
- Permutation FDR
- Others
- Manual validation
- FC cutoff
- No adjustment

No information

USER EXPERTISE IS KEY

PPV > 0.7	Lab ID	Submission ID	Process Flow						PPV	True positive	False positive
			Input	Identification	Quantification	Summarization	Statistical software	Inference			
3	11								0.857	36	6
3	42								0.972	35	1
20	20								0.821	32	7
48	48								0.744	32	11
25	25								1.000	30	0
13	13								1.000	30	0
12	12								1.000	27	0
44	44								1.000	26	0
2	49								0.963	26	1
36	36								0.897	26	3
26	26								1.000	24	0
17	17								0.920	23	2
4	4								0.821	23	5
40	40								0.767	23	7
6	6								0.955	21	1
5	3								1.000	19	0
45	45								0.708	17	7
6	46								0.867	13	2
37	37								1.000	10	0

Positive predictive value =

true differentially abundant proteins

claimed differentially abundant proteins

Good

0.2 ≤ PPV < 0.7	Lab ID	Submission ID	Process Flow						PPV	True positive	False positive
			Input	Identification	Quantification	Summarization	Statistical software	Inference			
8	8								0.559	33	26
1	1								0.580	29	21
5	14								0.359	28	50
7	28								0.295	28	67
	21								0.294	25	60
	43								0.294	25	60
7	19								0.511	24	23
7	31								0.575	23	17
7	23								0.500	23	23
	15								0.267	20	55

Bad

PPV < 0.2	Lab ID	Submission ID	Process Flow						PPV	True positive	False positive
			Input	Identification	Quantification	Summarization	Statistical software	Inference			
8	30								0.174	32	152
9	16								0.145	30	177
	27								0.134	30	194
9	24								0.120	30	219
8	38								0.141	28	170
	47								0.181	27	122
	29								0.057	27	447
8	35								0.182	26	117
	35								0.126	26	180
8	22								0.145	25	148
	34								0.132	24	158
2	2								0.091	24	240
4	39								0.074	21	264
9	33								0.085	18	194
	51								0.052	18	330
10	10								0.023	17	734
5	5								0.008	17	2002
6	41								0.027	14	514
	7								0.172	5	24

Very bad

USER EXPERTISE IS KEY

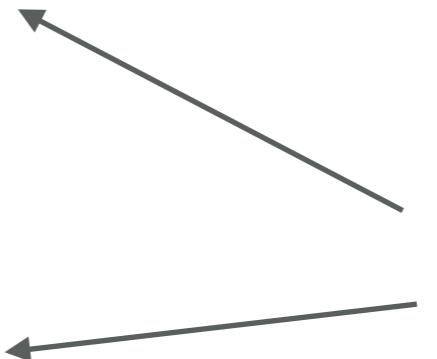
	Lab ID	Submission ID	Input	Identification	Quantification	Summarization	Statistical software	Inference	FDR	PPV	True positive	False positive
PPV > 0.7												
3	11									0.857	36	6
3	42									0.972	35	1
20										0.821	32	7
48										0.744	32	11
2	25									1.000	30	0
13										1.000	30	0
12										1.000	27	0
1	44									1.000	26	0
2	49									0.963	26	1
36										0.897	26	3
2	26									1.000	24	0
4	17									0.920	23	2
4	4									0.821	23	5
40										0.767	23	7
1	6									0.955	21	1
5	3									1.000	19	0
6	45									0.708	17	7
6	46									0.867	13	2
6	37									1.000	10	0
0.2 ≤ PPV < 0.7												
8	8									0.559	33	26
	1									0.580	29	21
5	14									0.359	28	50
7	28									0.295	28	67
	21									0.294	25	60
7	43									0.294	25	60
7	19									0.511	24	23
7	31									0.575	23	17
7	23									0.500	23	23
	15									0.267	20	55
PPV < 0.2												
8	30									0.174	32	152
9	16									0.145	30	177
	27									0.134	30	194
9	24									0.120	30	219
8	38									0.141	28	170
	47									0.181	27	122
8	29									0.057	27	447
8	35									0.182	26	117
8	22									0.126	26	180
8	34									0.145	25	148
	2									0.132	24	158
4	39									0.091	24	240
9	33									0.074	21	264
	9									0.085	18	194
51										0.052	18	330
10										0.023	17	734
5										0.008	17	2002
6	41									0.027	14	514
6	7									0.172	5	24

MaxQuant and Perseus

USER EXPERTISE IS KEY

	Lab ID	Submission ID	Input	Identification	Quantification	Summarization	Statistical software	Inference	FDR	PPV	True positive	False positive
PPV > 0.7												
3	11									0.857	36	6
3	42									0.972	35	1
20										0.821	32	7
48										0.744	32	11
2	25									1.000	30	0
13										1.000	30	0
12										1.000	27	0
1	44									1.000	26	0
2	49									0.963	26	1
36										0.897	26	3
2	26									1.000	24	0
4	17									0.920	23	2
4	4									0.821	23	5
40										0.767	23	7
1	6									0.955	21	1
5	3									1.000	19	0
6	45									0.708	17	7
6	46									0.867	13	2
6	37									1.000	10	0
0.2 ≤ PPV < 0.7												
8	8									0.559	33	26
	1									0.580	29	21
5	14									0.359	28	50
7	28									0.295	28	67
	21									0.294	25	60
7	43									0.294	25	60
7	19									0.511	24	23
7	31									0.575	23	17
7	23									0.500	23	23
	15									0.267	20	55
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8	30									0.174	32	152
9	16									0.145	30	177
	27									0.134	30	194
9	24									0.120	30	219
8	38									0.141	28	170
	47									0.181	27	122
8	29									0.057	27	447
8	35									0.182	26	117
8	22									0.126	26	180
8	34									0.145	25	148
	2									0.132	24	158
4	39									0.091	24	240
9	33									0.074	21	264
	9									0.085	18	194
51										0.052	18	330
10										0.023	17	734
5										0.008	17	2002
6	41									0.027	14	514
6	7									0.172	5	24

Skyline and linear modeling in R



USER EXPERTISE IS KEY

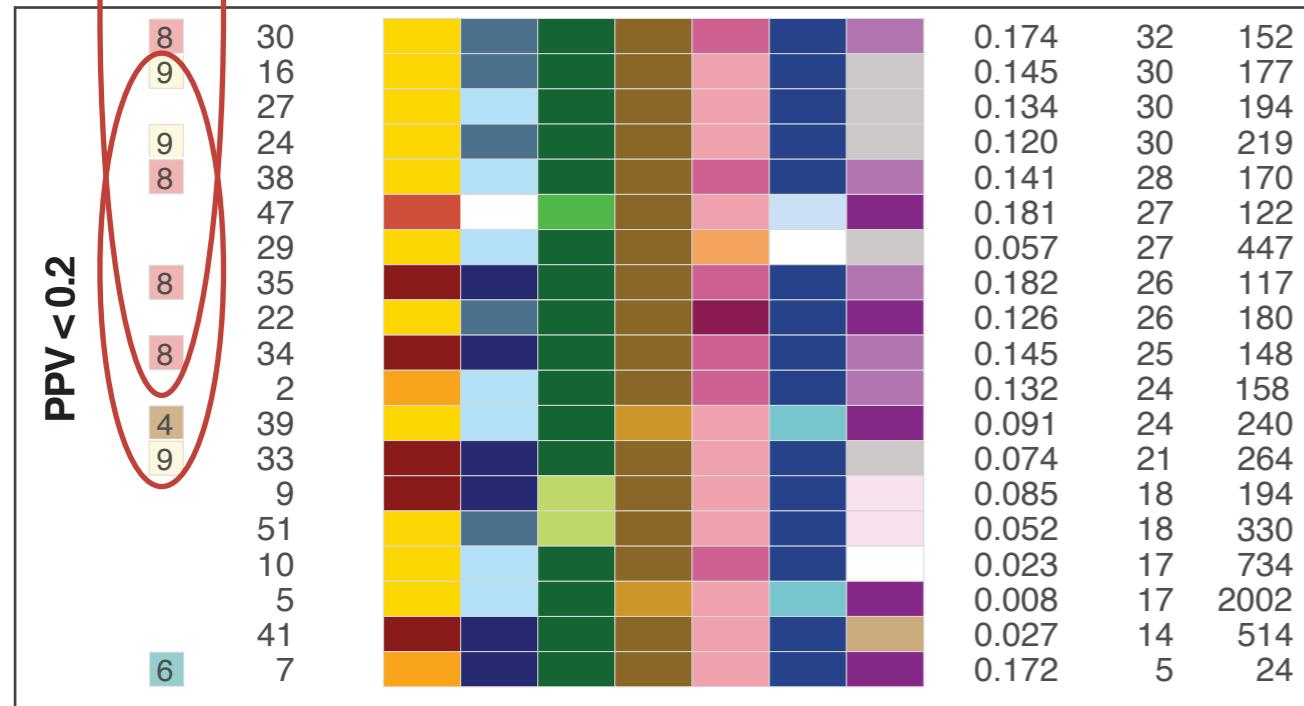
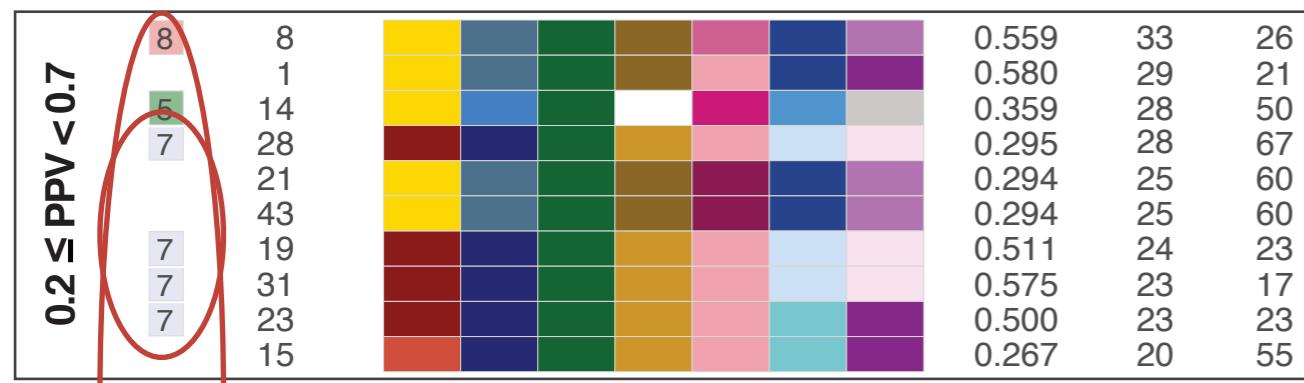
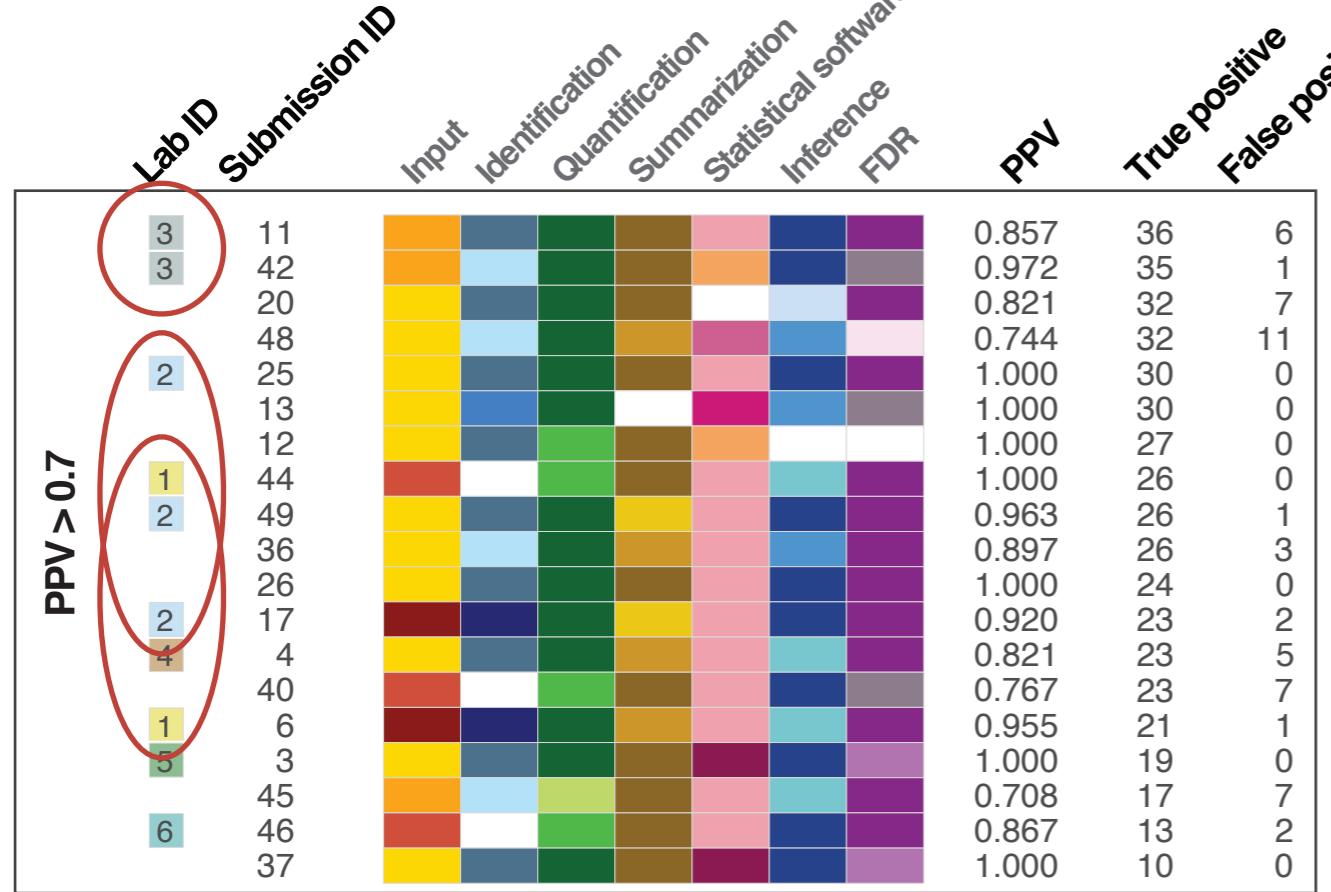
Lab ID	Submission ID	Input	Identification	Quantification	Summarization	Statistical software	Inference	FDR	PPV	True positive	False positive
3	11								0.857	36	6
3	42								0.972	35	1
20	20								0.821	32	7
48	48								0.744	32	11
2	25								1.000	30	0
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36	36								0.897	26	3
2	26								1.000	24	0
4	17								0.920	23	2
4	4								0.821	23	5
40	40								0.767	23	7
1	6								0.955	21	1
5	3								1.000	19	0
45	45								0.708	17	7
6	46								0.867	13	2
	37								1.000	10	0

PPV > 0.7	PPV ≤ 0.7	PPV < 0.2
8	8	30
1	1	16
5	14	27
7	28	24
	21	38
	43	47
7	19	29
7	31	35
7	23	35
	15	22

PPV < 0.2	PPV > 0.7	PPV ≤ 0.7
8	30	8
9	16	16
	27	27
9	24	24
8	38	38
	47	47
8	29	29
8	35	35
8	35	35
8	22	22
8	34	34
2	2	2
4	39	39
9	33	33
	9	9
51	51	51
10	10	10
5	5	5
41	41	41
6	7	7

Compared peak intensity vs spectral counts

USER EXPERTISE IS KEY



Input

- Peaks
- Peptide ids
- Raw+check
- Raw

Identification

- Skyline
- MaxQuant
- Progenesis
- Others

Quantification

- Feature intensity
- Spectral counting
- Hybrid

Summarization

- Protein summarization / Protein-level inference
- Peptide summarization / Protein-level inference
- Peptide summarization / Peptide-level inference

Statistical software

- Persus
- Progenesis QI
- Others
- R, Excel, MatLab, Python
- In-house scripts

Inference

- t-test / SAM's t test
- ANOVA
- Linear (mixed-effects) model
- Others

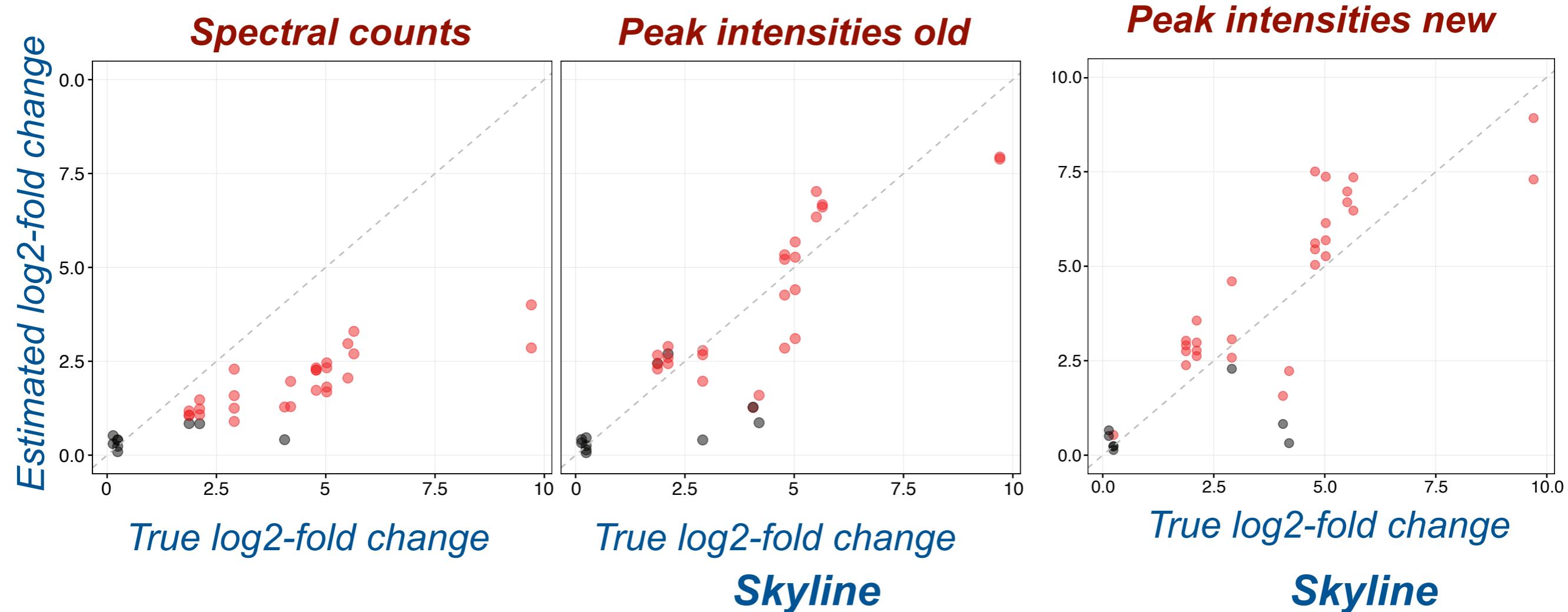
FDR

- Benjamini Hochberg
- Permutation FDR
- Others
- Manual validation
- FC cutoff
- No adjustment

No information

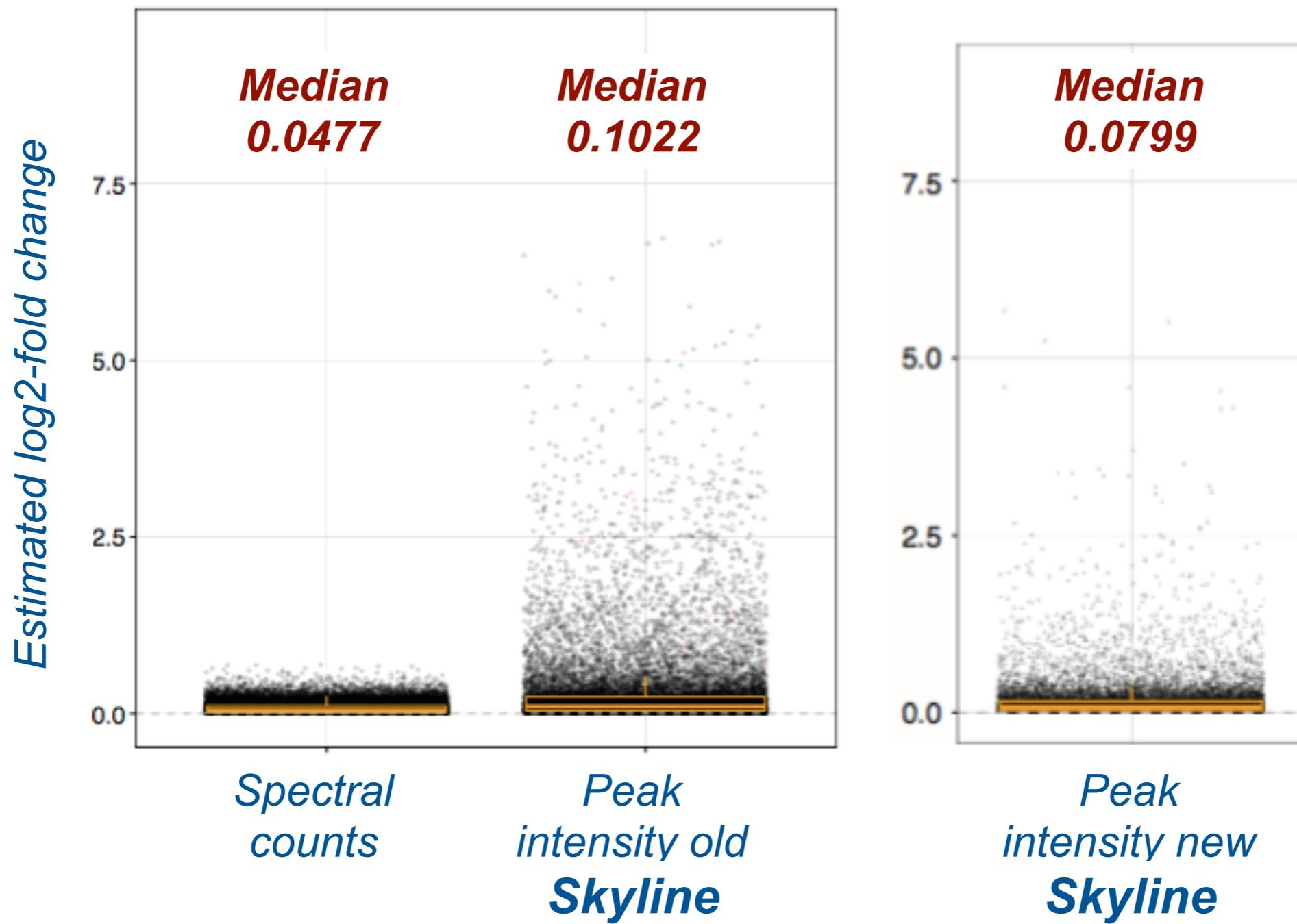
DATA PROCESSING MATTERS

IMPROVES ACCURACY OF QUANTIFICATION

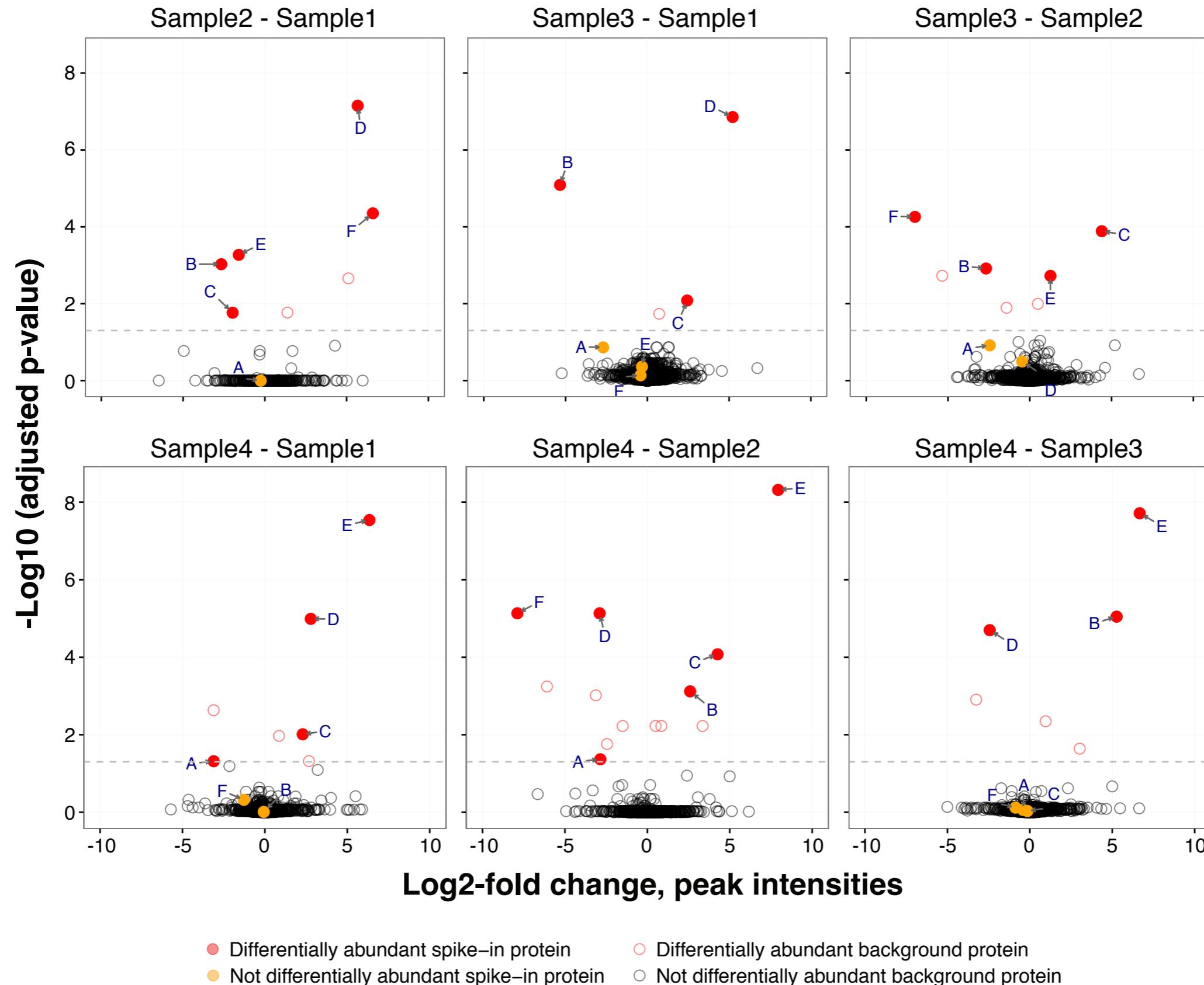


DATA PROCESSING MATTERS

IMPROVES ACCURACY OF QUANTIFICATION



DETECTION OF DIFFERENTIALLY ABUNDANT PROTEINS



CHOICES OF SIGNAL PROCESSING AFFECT THE RESULTS

Statistical analysis with MSstats, using varying inputs

- No single-hit proteins
- Sum 3 isotopic peaks

	ID QUALITY (Q-VALUE CUTOFF)			
	0.05	0.15	0.5	0.95
True positives	29	28	28	28
Total positives	34	29	31	29
Positive predictive value	0.852941176	0.965517241	0.903225806	0.965517241

- No single-hit proteins
- Monoisotopic peak

	ID QUALITY (Q-VALUE CUTOFF)			
	0.05	0.15	0.5	0.95
True positives	28	29	29	30
Total positives	42	34	37	35
Positive predictive value	0.666666667	0.852941176	0.783783784	0.857142857

- Single-hit proteins
- Sum 3 isotopic peaks

	ID QUALITY (Q-VALUE CUTOFF)	
	0.15	0.95
True positives	29	29
Total positives	56	53
Positive predictive value	0.517857143	0.547169811

Positive predictive value =
$$\frac{\text{# true differentially abundant proteins}}{\text{# claimed differentially abundant proteins}}$$

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ABRF Proteome Informatics Research Group (iPRG) 2015 Study: Detection of Differentially Abundant Proteins in Label-Free Quantitative LC-MS/MS Experiments

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J. Proteome Res., 2017, 16 (2), pp 945–957

DOI: 10.1021/acs.jproteome.6b00001

Publication Date (Web): December 19, 2016

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