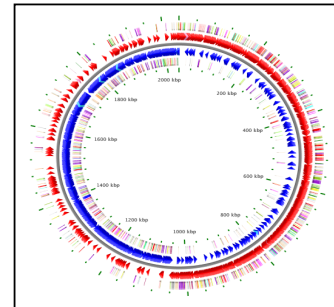
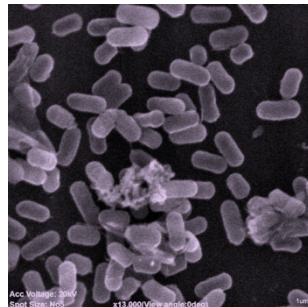


Adding Power to Phenomic Studies: Novel Statistical Approaches for PM Data

Joseph Sturino, Ph.D.

Nutrition and Food Science Department
Texas A&M University



Sodium Chloride Toxicity

Biocatalysts used to produce novel compounds

- Chemostat fermentation (Batch):

ACID ACCUMULATION → Toxicity

- Adjust pH (NaOH)

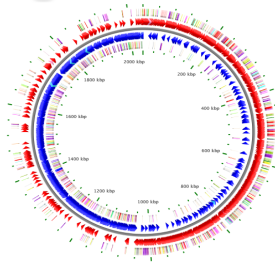
Acid Neutralized, but Toxicity Still Observed

Hypothesized: Acid + Base = NaCl Accumulation → **Osmotic Toxicity**

Used comparative phenomics to investigate

Functional Genomic Approach

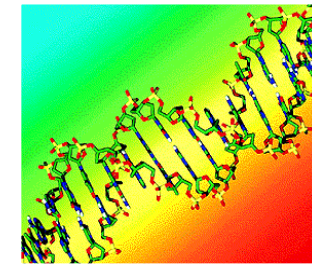
genomics



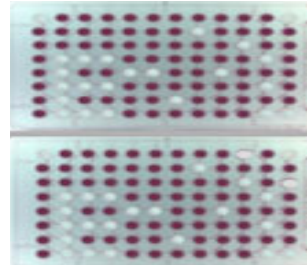
hypothesis



molecular biology



phenomics



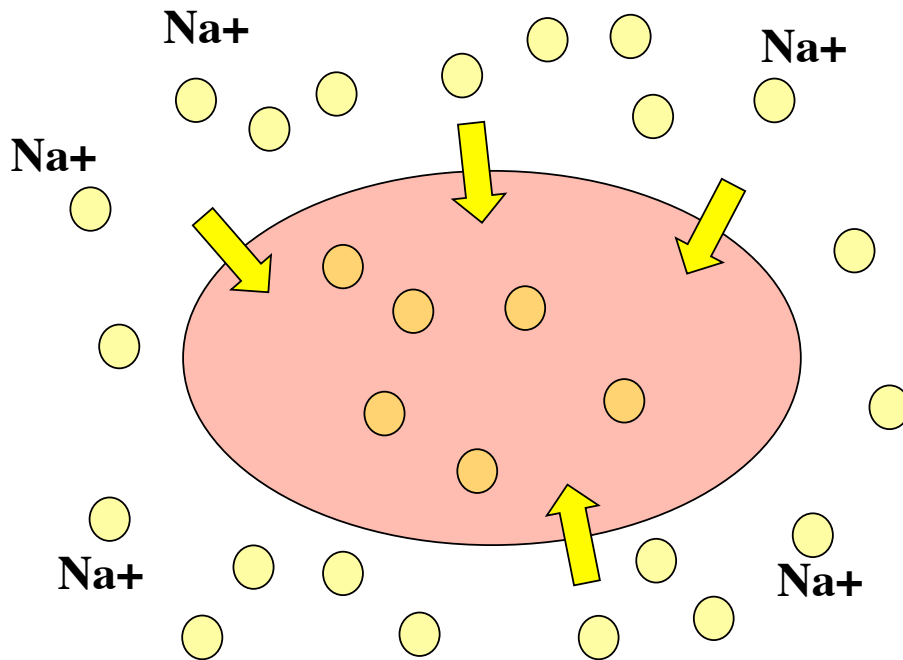
A1	A2	A3	A4	A5	A6	A7	A8	A9	A10	A11	A12
NaCl 1%	NaCl 2%	NaCl 3%	NaCl 4%	NaCl 5%	NaCl 6.5%	NaCl 8%	NaCl 6.5%	NaCl 7%	NaCl 8%	NaCl 9%	NaCl 10%
B1 NaCl 6%	B2 NaCl 6% + betaine	B3 NaCl 6% + 1% (D-threo) glycine	B4 NaCl 6% + Serine	B5 NaCl 6% + (D-threo) aspartyl propanoate	B6 NaCl 6% + UDPH	B7 NaCl 6% + Glucose	B8 NaCl 6% + Choline	B9 NaCl 6% + Phosphoryl choline	B10 NaCl 6% + Creatine	B11 NaCl 6% + Oxadiazole	B12 NaCl 6% + L-Glutamine
C1 NaCl 6% + KCl	C2 NaCl 6% + L-cysteine	C3 NaCl 6% + N-Acetyl-L-glutamine	C4 NaCl 6% + P-D-glutamic acid	C5 NaCl 6% + N-Acetyl-L-aspartic acid	C6 NaCl 6% + D-Glutamine	C7 NaCl 6% + Glycine	C8 NaCl 6% + Trehalose	C9 NaCl 6% + Tryptophan-N-oxide	C10 NaCl 6% + Tryptophan	C11 NaCl 6% + Octadecane	C12 NaCl 6% + Tryptamine
D-1 Potassium chloride 3%	D2 Potassium citrate 6%	D3 Potassium phosphate 6%	D4 Potassium phosphate 6%	D5 Potassium sulfate 2%	D6 Potassium sulfate 2%	D7 Potassium sulfate 2%	D8 Potassium sulfate 2%	D9 Potassium sulfate 2%	D10 Potassium glycol 2%	D11 Potassium glycol 2%	D12 Potassium glycol 2%
E1 Medium Normal 1%	E2 Sodium formate 2%	E3 Sodium formate 3%	E4 Sodium formate 4%	E5 Sodium formate 5%	E6 Sodium formate 6%	E7 Sodium formate 7%	E8 Sodium formate 8%	E9 Sodium formate 9%	E10 Sodium formate 10%	E11 Urea 6%	E12 Urea 7%
F1 Sodium Lactate 1%	F2 Sodium Lactate 2%	F3 Sodium Lactate 3%	F4 Sodium Lactate 4%	F5 Sodium Lactate 5%	F6 Sodium Lactate 6%	F7 Sodium Lactate 7%	F8 Sodium Lactate 8%	F9 Sodium Lactate 9%	F10 Sodium Lactate 10%	F11 Sodium Lactate 11%	F12 Sodium Lactate 12%
G1 Sodium Phosphate pH 7 100mM	G2 Sodium Phosphate pH 7 50mM	G3 Sodium Phosphate pH 7 100mM	G4 Sodium Phosphate pH 7 100mM	G5 Sodium Phosphate pH 5.2 100mM	G6 Sodium Phosphate pH 5.2 100mM	G7 Sodium Phosphate pH 5.2 100mM	G8 Sodium Phosphate pH 5.2 100mM	G9 Ammonium sulfate pH 8 10mM	G10 Ammonium sulfate pH 8 20mM	G11 Ammonium sulfate pH 8 100mM	G12 Ammonium sulfate pH 8 100mM
H1 Sodium Nitrate 10mM	H2 Sodium Nitrate 20mM	H3 Sodium Nitrate 40mM	H4 Sodium Nitrate 60mM	H5 Sodium Nitrate 80mM	H6 Sodium Nitrate 100mM	H7 Sodium Nitrate 120mM	H8 Sodium Nitrate 140mM	H9 Sodium Nitrate 160mM	H10 Sodium Nitrate 180mM	H11 Sodium Nitrate 200mM	H12 Sodium Nitrate 220mM

PM09: Osmolytes

Osmotic Stress Model System

Escherichia coli

Wild-type
EC25113



Wood. 2006. Osmosensing by Bacteria *Sci. STKE* (357): 43

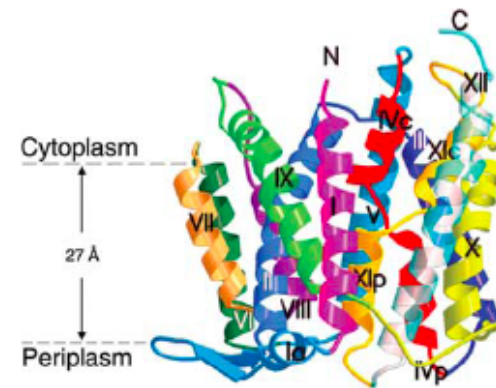
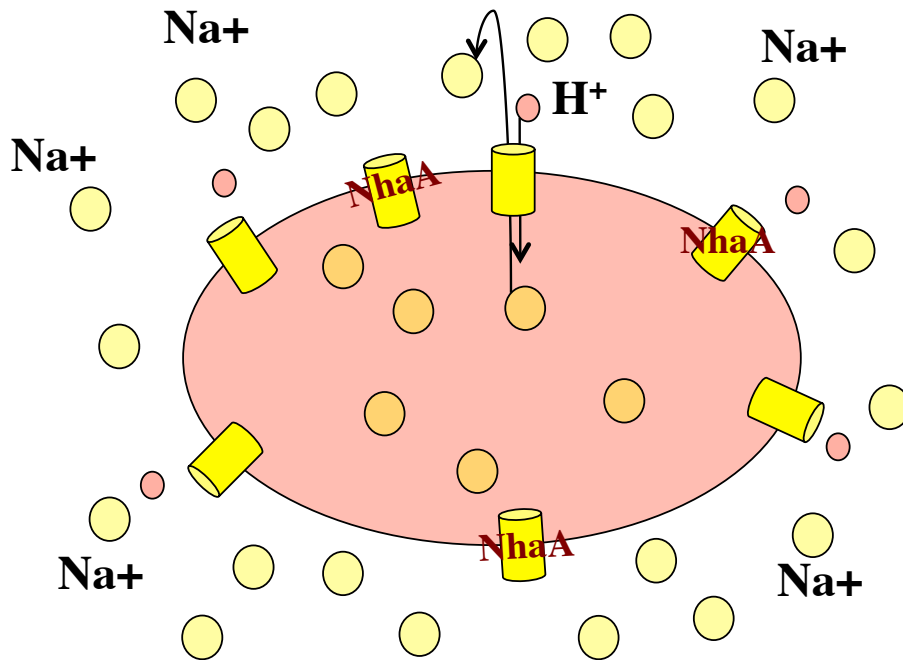
Model System

Escherichia coli

Wild-type
EC25113

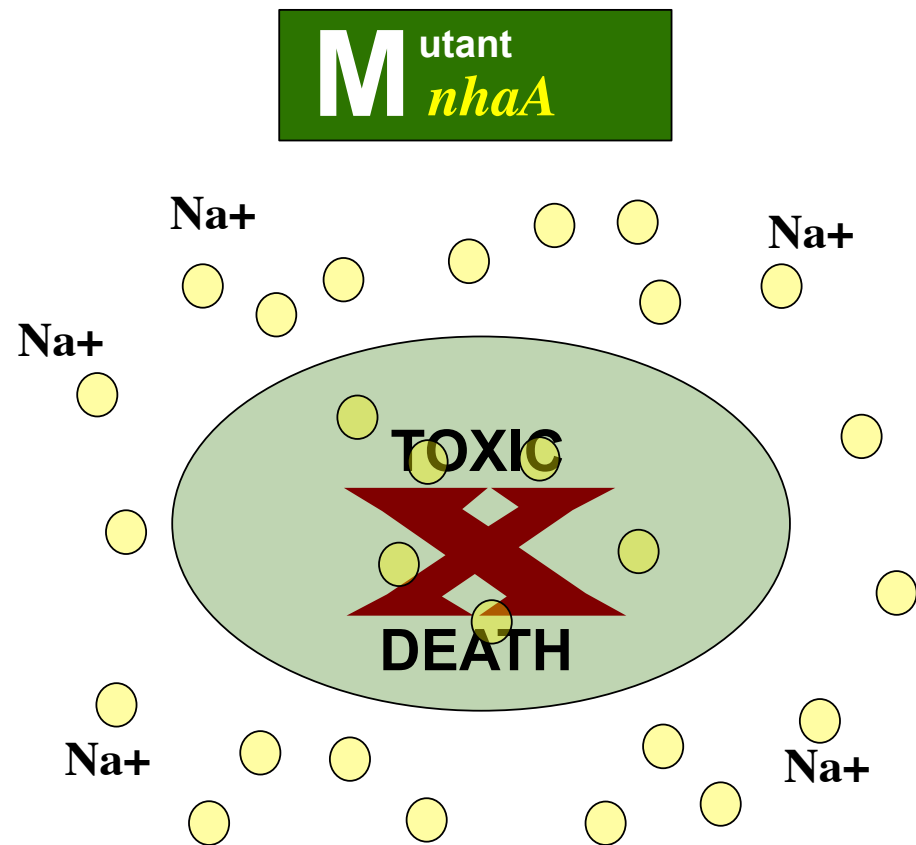
NhaA

Primary (Na⁺-H⁺) Antiporter

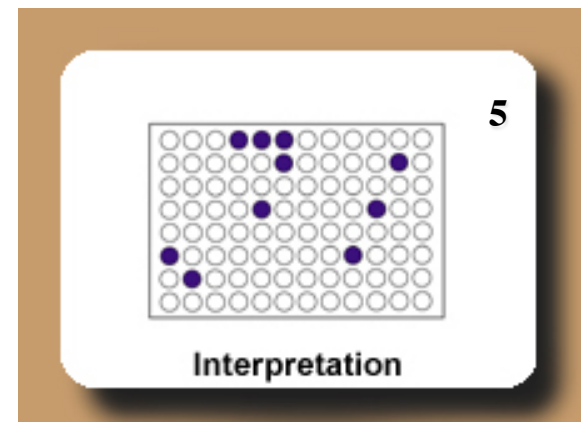
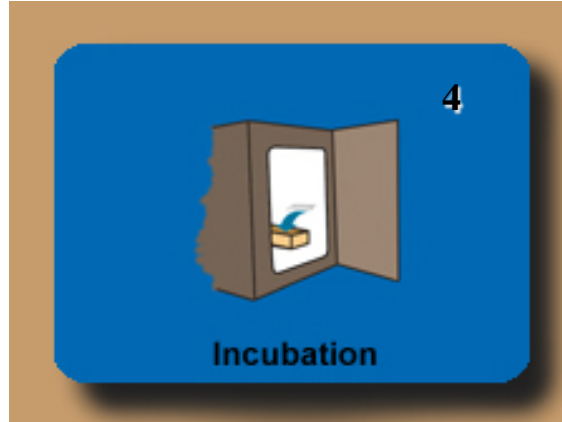
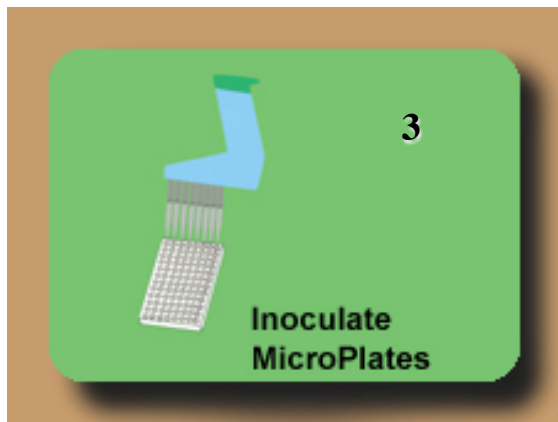
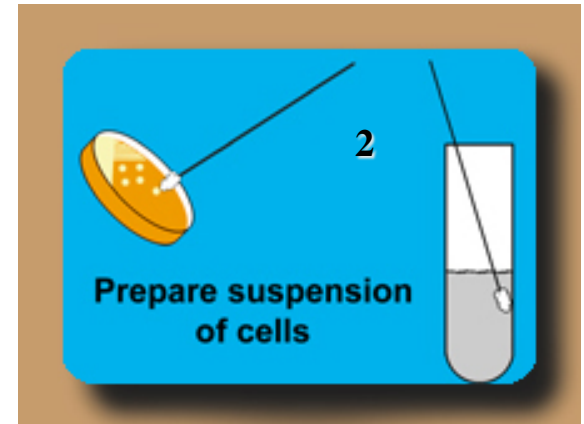
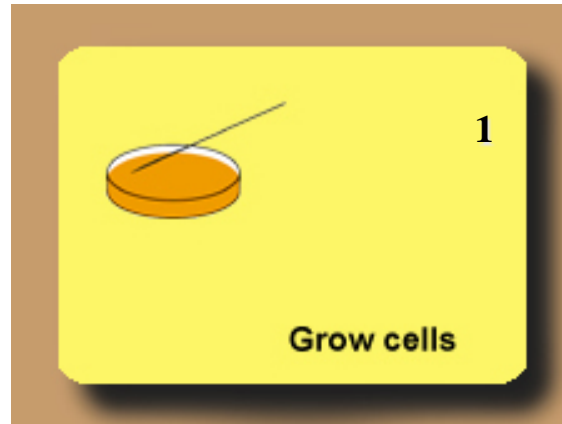
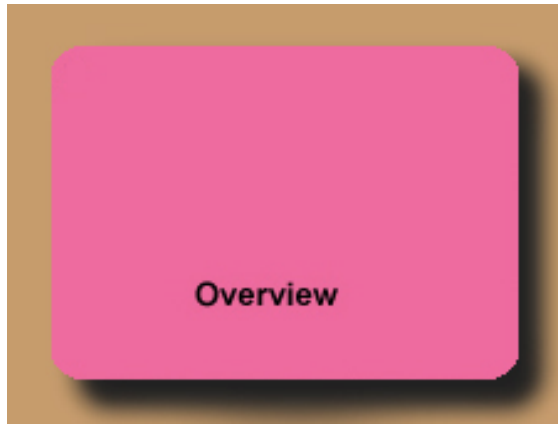


Model System

SENSITIVE TO   [Na⁺]



The Assay



Wild-type
EC25113

PM9
Sodium Chloride (%)

1% 2% 3% 4% 5% 5.5% 6% 6.5% 7% 8% 9% 10%

Bio1
rep

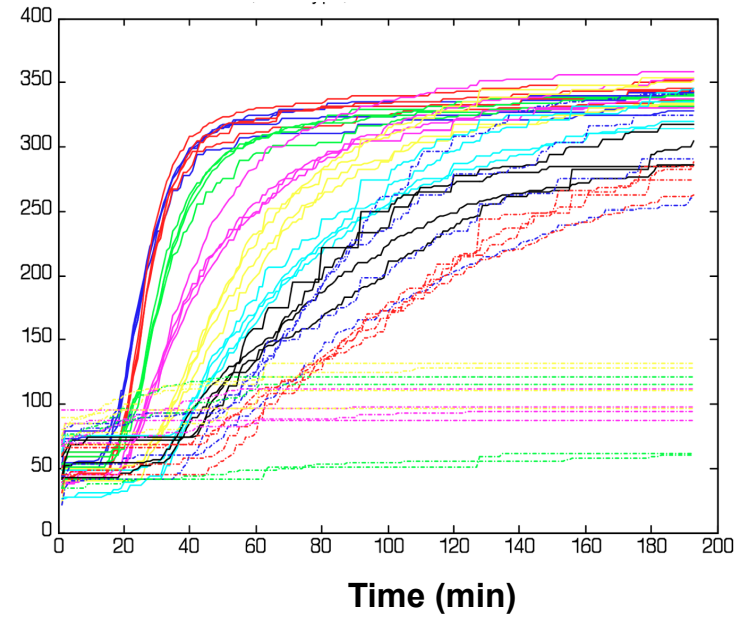
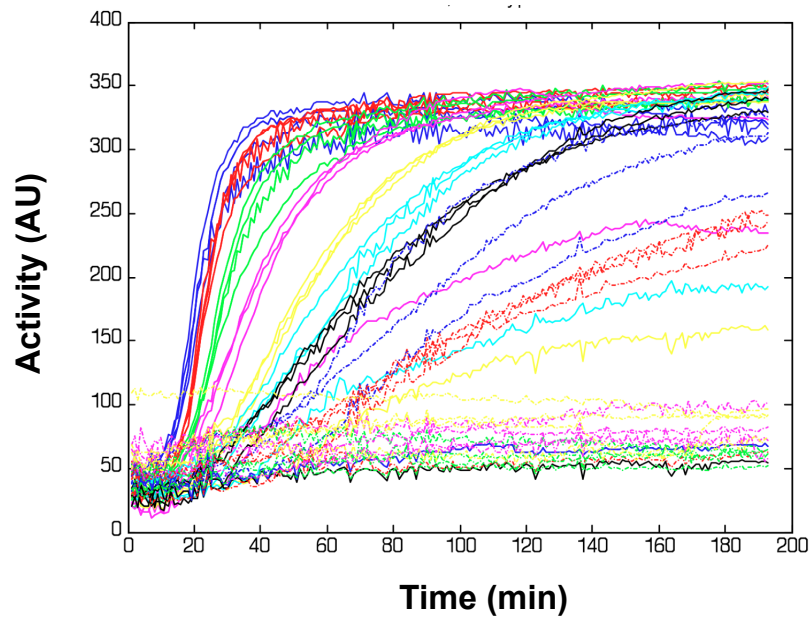
3 tech
reps

5.7×10^5
CFU ml⁻¹

Bio2
rep

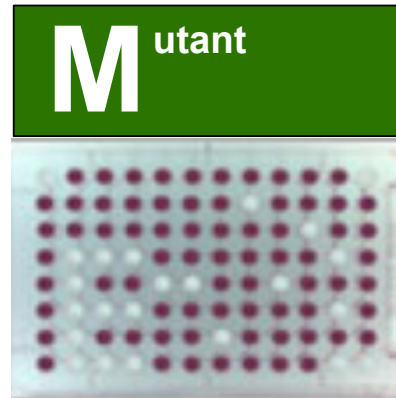
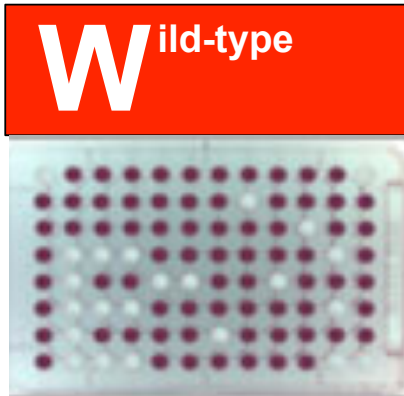
3 tech
reps

7.2×10^5
CFU ml⁻¹



Robust, but inter-replicate differences found

Parametric Module



- Compare two microorganisms
- Calculates summary values
 - Area under the curve
 - Min/maximum signal intensity
 - Maximum slope
 - Lag time

**Does Not Include
Hypothesis Testing**

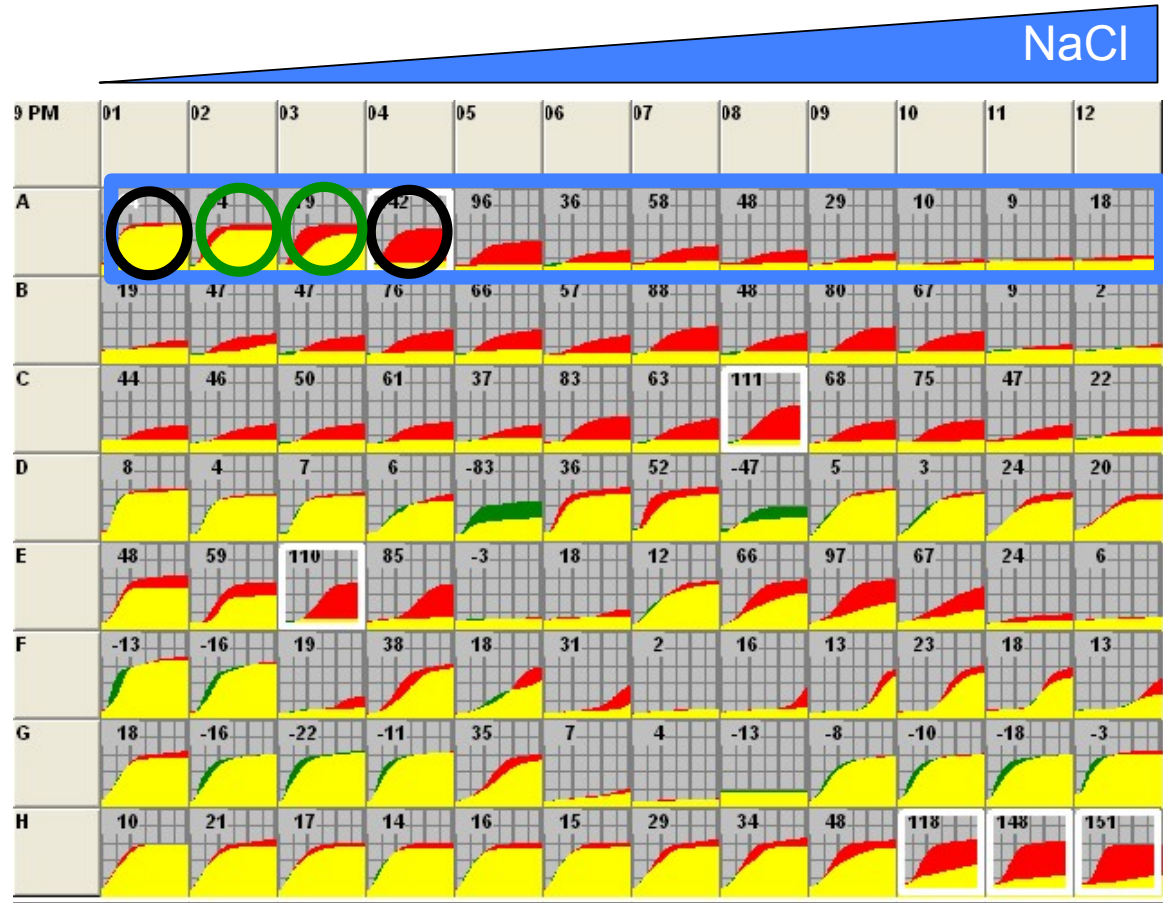


Gradient Differences Unclear

Wild-type
EC25113

Mutant
nhaA

OVERLAP
BOTH



W

WM

?

Two strains under same conditions

Study Objective



Dr. Raymond Carroll
Texas A&M University

Develop simple but robust statistical methodologies

Enable sound biological inferences from PM data

*The International Journal of
Biostatistics*

Volume 6, Issue 1

2010

Article 29

Sturino *et al.*, 2010

Statistical Methods for Comparative
Phenomics Using High-Throughput Phenotype
Microarrays



Dr. Ivan Zorych
Columbia University



Dr. Nikolay Bliznyuk
University of Florida

(www.r-project.org)

Hypothesis Testing

Permutation-based statistics:

H₀ NULL

$$f_1(t) = f_2(t) \text{ for all } t$$

**2 Organisms
have
exchangeable
phenotypes**

H₁ ALT

$$f_1(t) \neq f_2(t) \text{ for all } t$$

Nonparametric Permutation

$Y_{ij}(t)$ defined as observed phenotype curve for:

Organism $i = 1, \dots, I = 2$ and

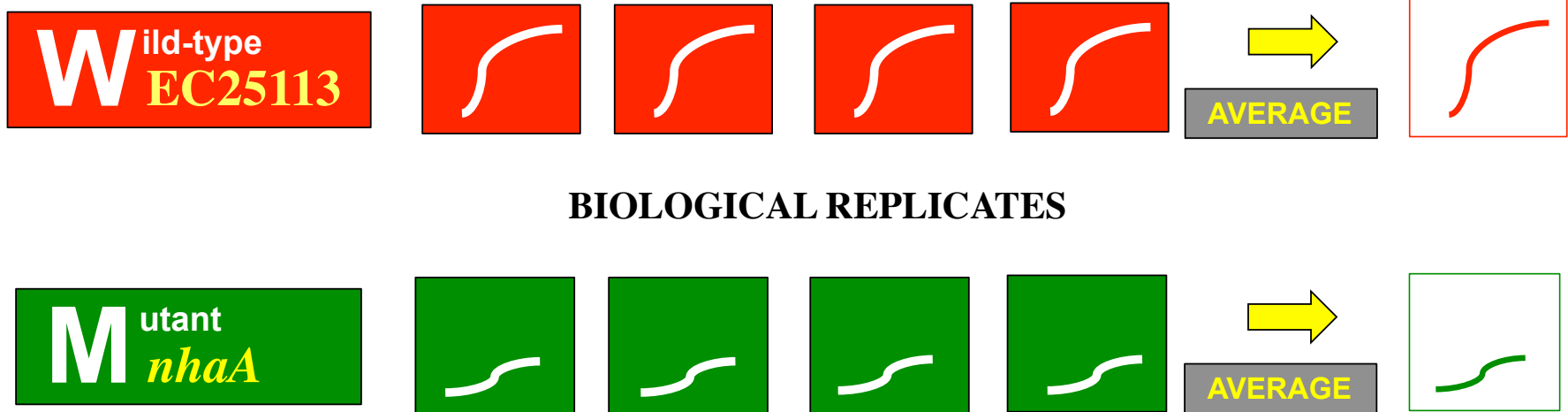
Replicate $j = 1, \dots, J,$

Sample curve (mean) in organism i is:

**MEAN
CURVES**

$$\hat{f}_i(t) = J^{-1} \sum_{j=1}^J \{Y_{ij}(t)\}$$

Nonparametric Permutation



Calculate overall *squared difference* between mean curves:

$$S = \int \{\hat{f}_1(t) - \hat{f}_2(t)\}^2 dt.$$

Permutation Device

Take all permutations of the indices (i, j) such that:

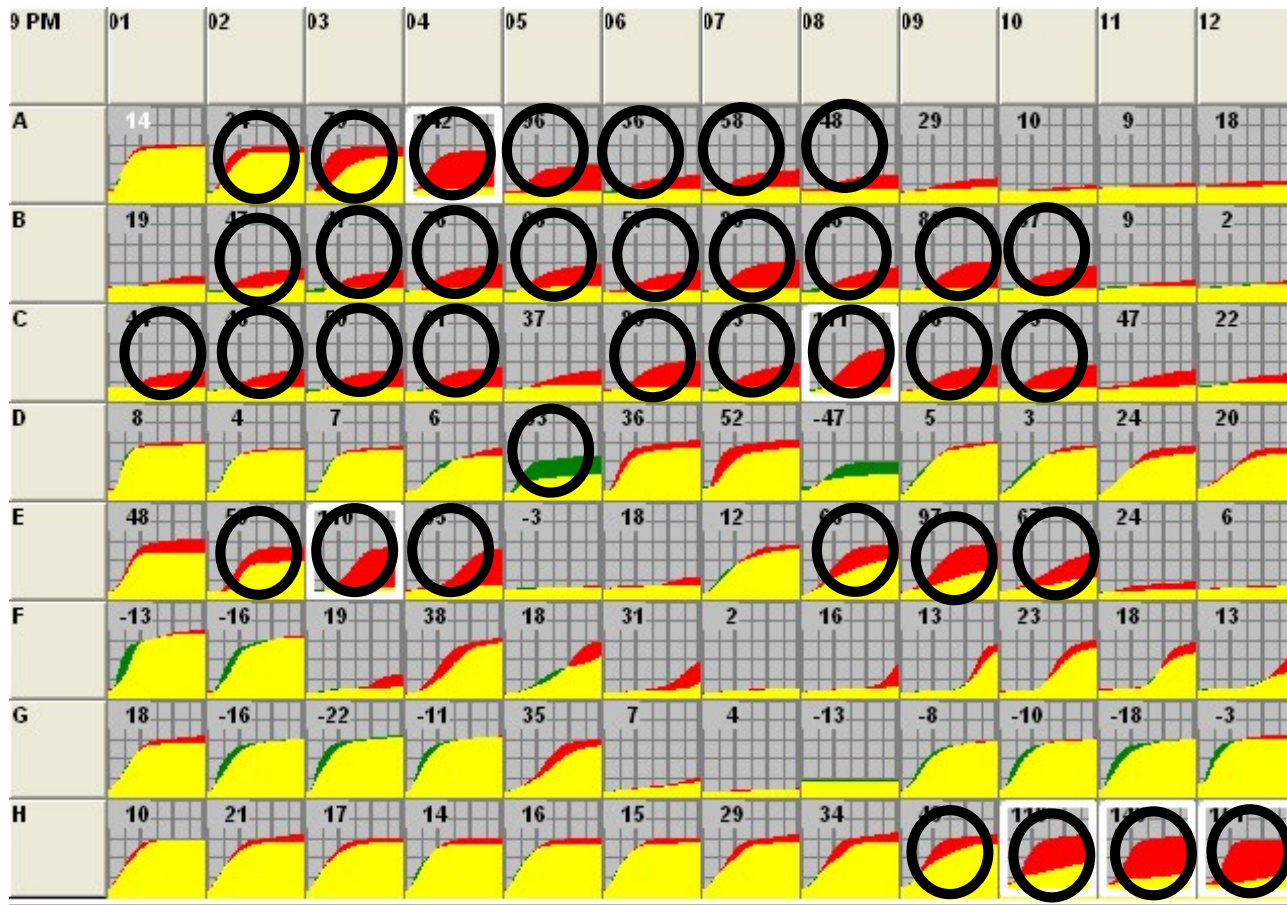
Let the number of unique permutations be **B**.

Then for each of the $b = 1, \dots, B$ unique permutations,

Recompute the test statistic (1) and record it as S_b .

p-value:
$$p = B^{-1} \sum_{b=1}^B I(S_b > S).$$

Effective Differentiation



○ $P < 0.05$

Alternative Tests

**MEDIAN
CURVES**

$$\tilde{f}_i(t) = \text{median}_{j \in J} \{Y_{ij}(t)\}$$

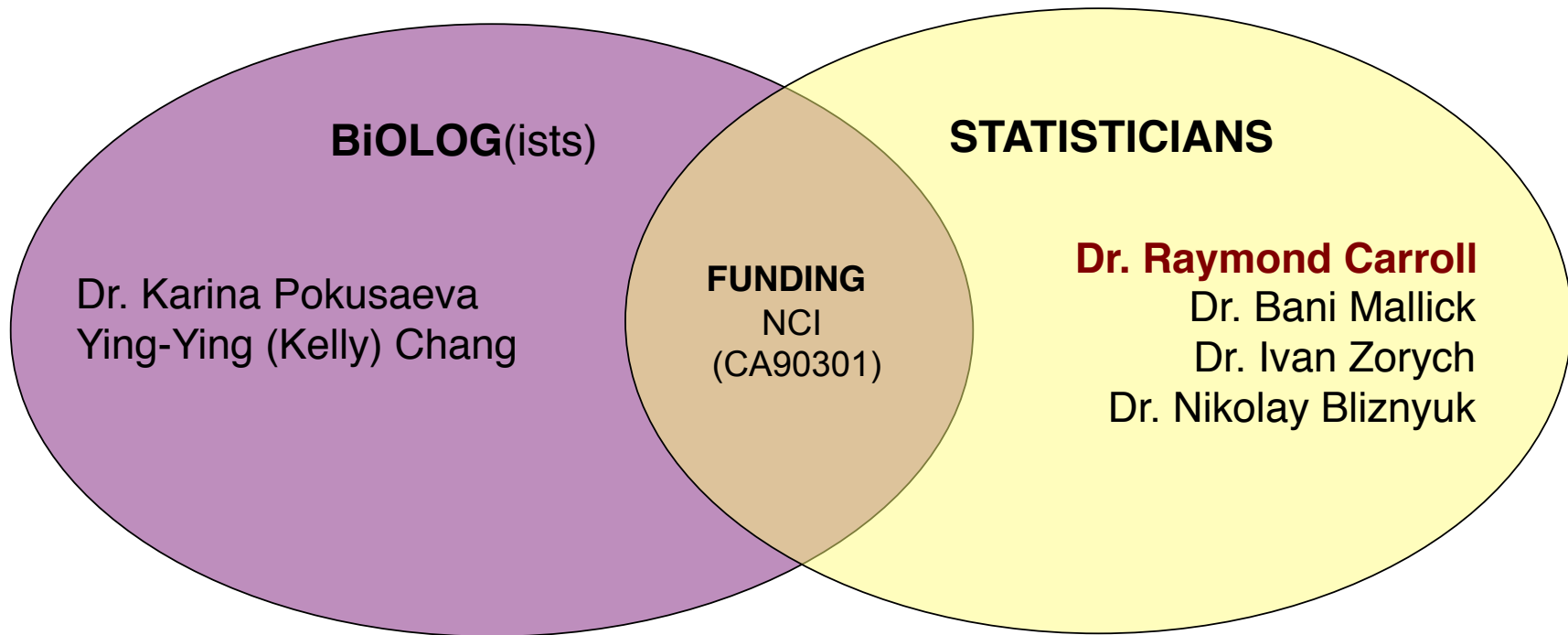
When error-adjusted, test can be carried out as with mean curves

Effective for high data skewness

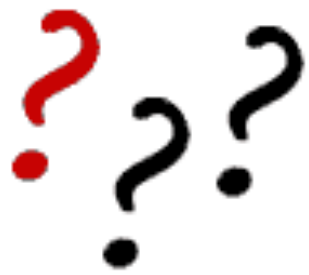
**CURVES
AREA**

fPCA

Acknowledgments



joseph.sturino@tamu.edu



Questions