

# "Time Perturbation" Studies of Somitogenesis Microarray Time Series

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# "Time Perturbation" Studies of Somitogenesis Microarray Time Series

- Purpose
- Background Concepts
- Microarray Analysis Overview
- Numerical Experiments
- Somitogenesis Experiments
- Summary

# Purpose

- Find "best" periodic genes from microarray time series experiments exploring somitogenesis in mouse, chick and zebrafish.
- Develop general methodology that can be applied across all species.

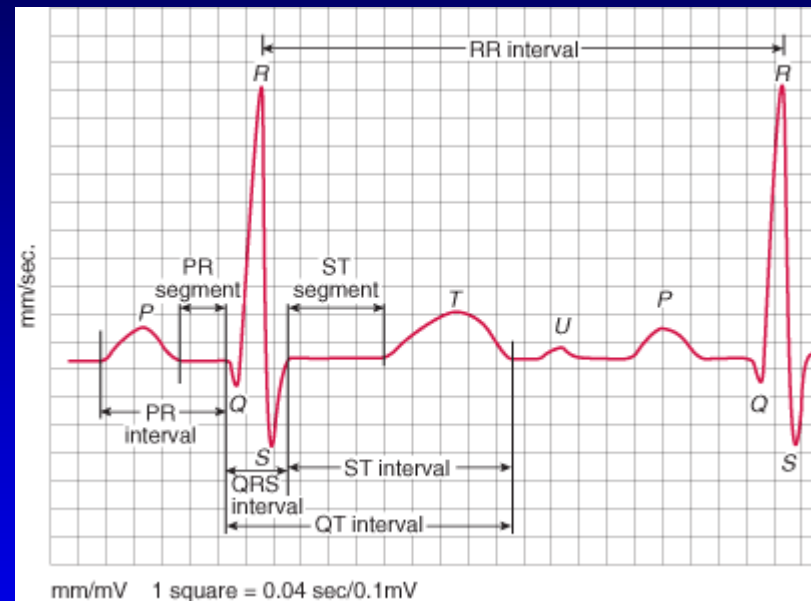
# Background Concepts

- Periodic Time Series in Biology
- Lomb-Scargle Analysis
- Hypothesis Testing with Lomb-Scargle
- Boxplots and "Notches"
- Rank Order and Rank Product

## Background

# Periodic Time Series in Biology

## Electrocardiogram (ECG): QRS Complex



Time

Source: <http://www.merck.com/mmpe/print/sec07/ch070/ch070e.html>

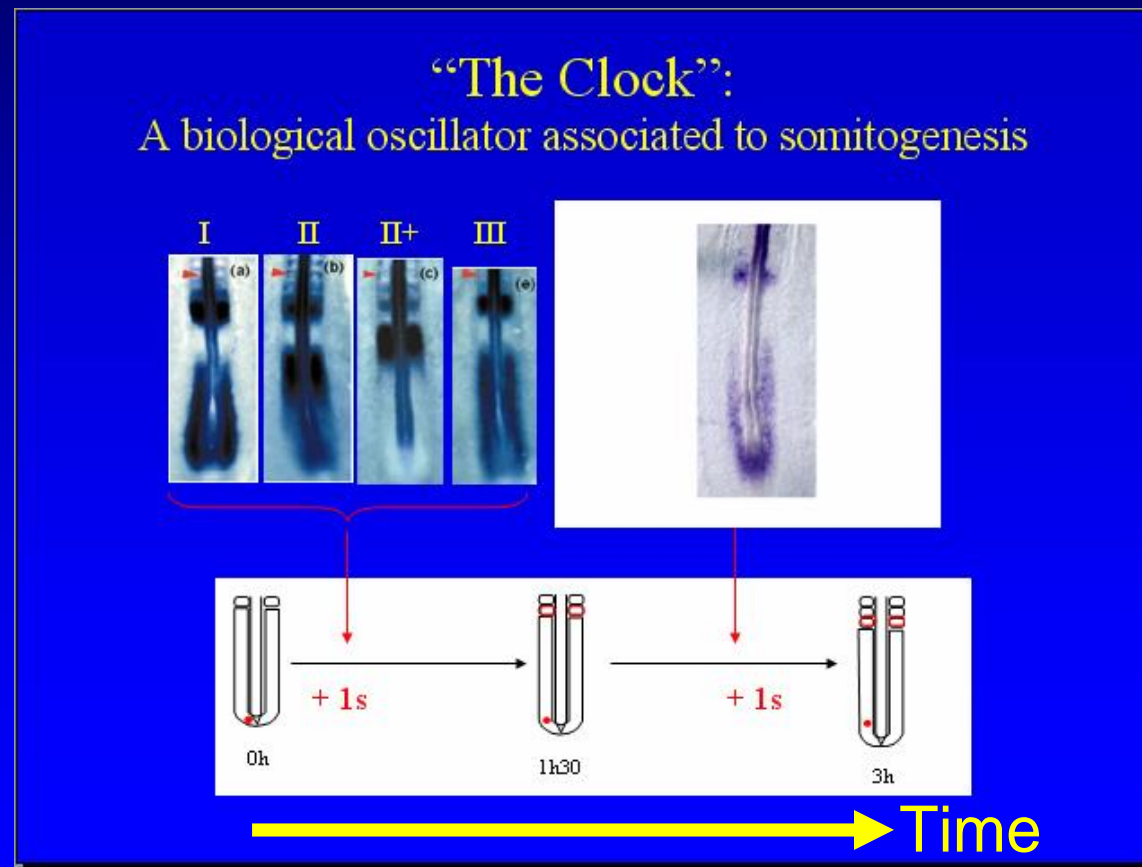
Continuous:  $x(t + T) = x(t)$

Discrete:  $x[n + N] = x[n]$

## Background

# "Periodic" Time Series in Biology

## Segmentation is Established During Somitogenesis



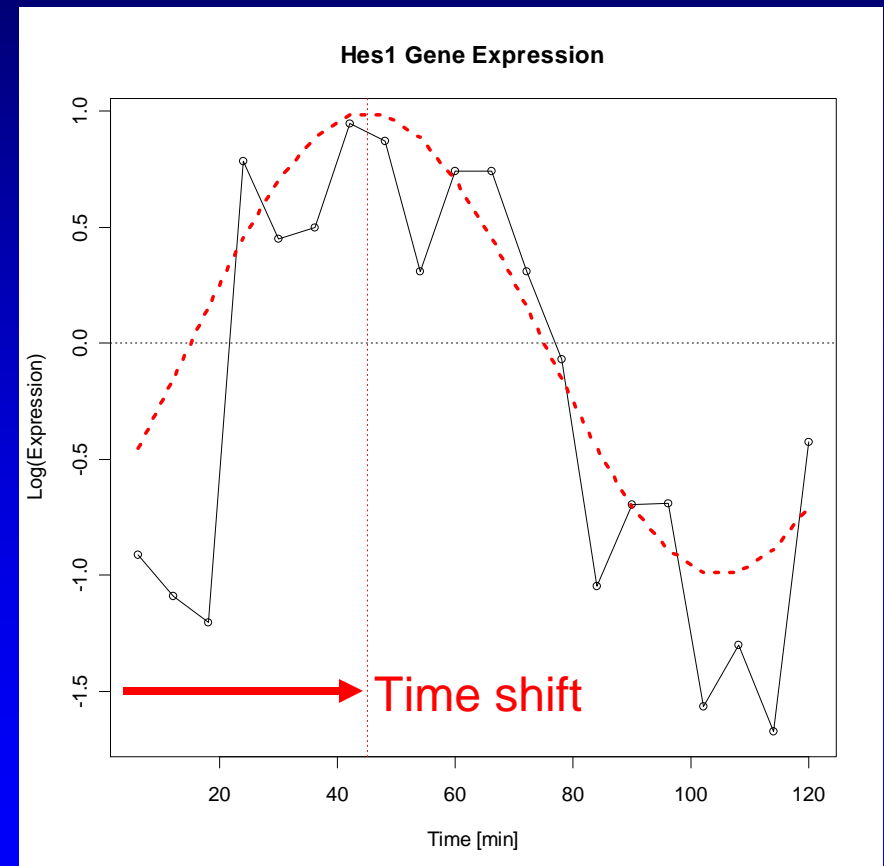
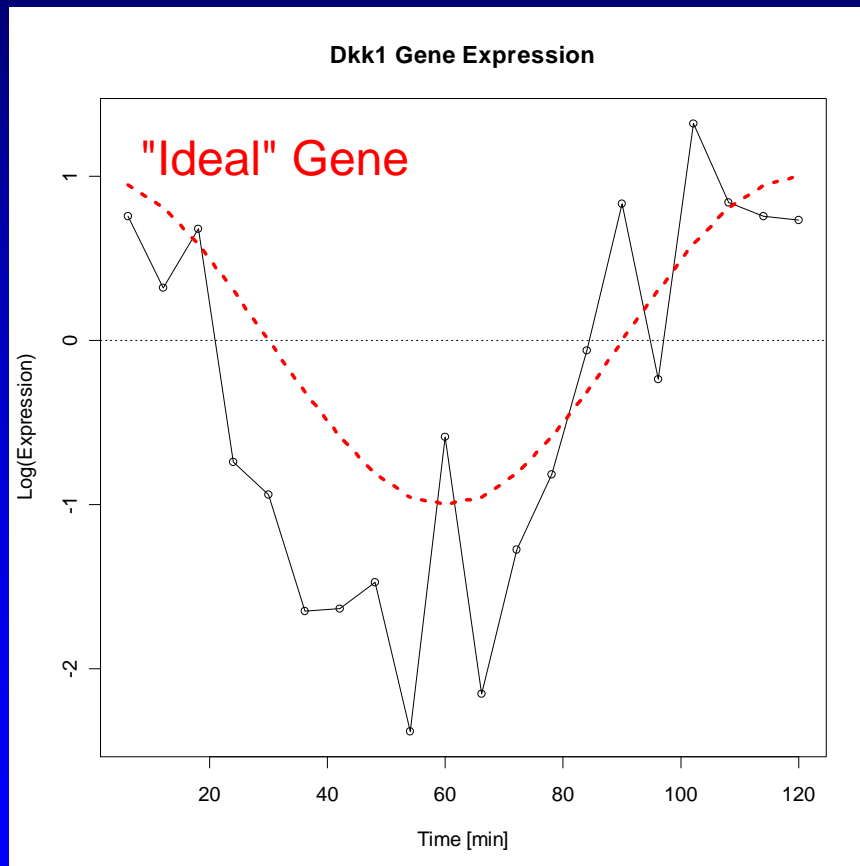
Mouse  
Chick  
Zebrafish

...

## Background

# "Periodic" Time Series in Biology

## Somitogenesis



Source: Mary-Lee Dequéant, "Mouse 20" dataset, Nov 2004

## Background

# Lomb-Scargle Periodogram Mathematical Details

$$h_i \equiv h(t_i), \quad i = 1, \dots, N$$

$$\bar{h} \equiv \frac{1}{N} \sum_1^N h_i \quad \sigma^2 \equiv \frac{1}{N-1} \sum_1^N (h_i - \bar{h})^2 \quad (13.8.3)$$

Now, the Lomb *normalized periodogram* (spectral power as a function of angular frequency  $\omega \equiv 2\pi f > 0$ ) is defined by

$$P_N(\omega) \equiv \frac{1}{2\sigma^2} \left\{ \frac{\left[ \sum_j (h_j - \bar{h}) \cos \omega(t_j - \tau) \right]^2}{\sum_j \cos^2 \omega(t_j - \tau)} + \frac{\left[ \sum_j (h_j - \bar{h}) \sin \omega(t_j - \tau) \right]^2}{\sum_j \sin^2 \omega(t_j - \tau)} \right\} \quad (13.8.4)$$

Here  $\tau$  is defined by the relation

$$\tan(2\omega\tau) = \frac{\sum_j \sin 2\omega t_j}{\sum_j \cos 2\omega t_j} \quad (13.8.5)$$

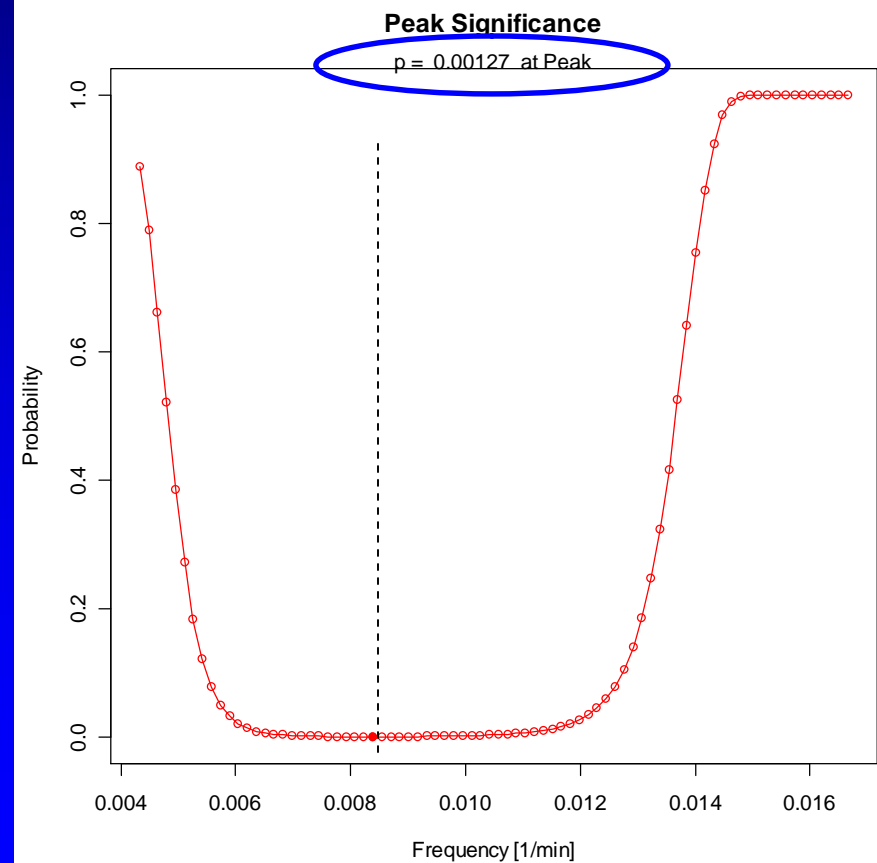
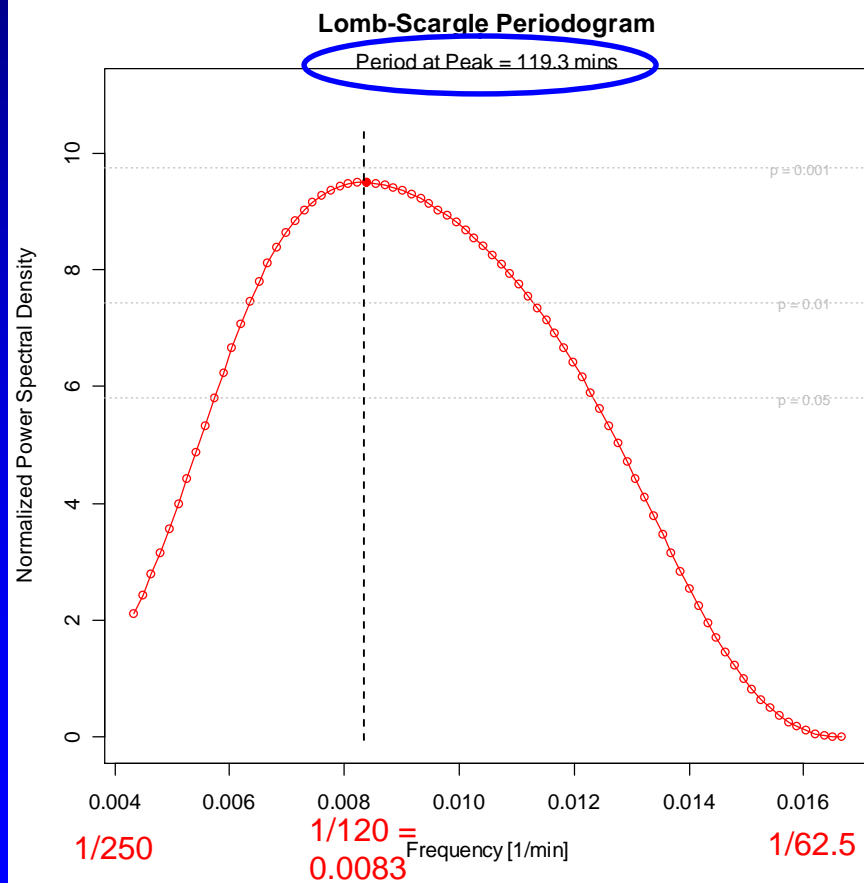
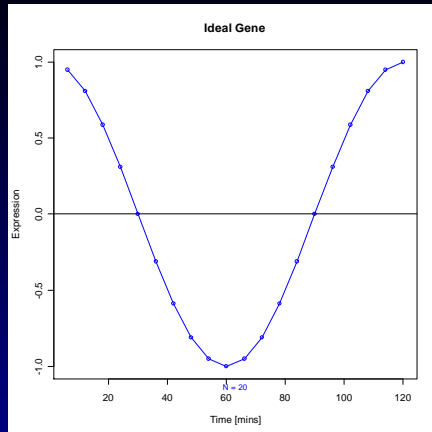
$$P(> z) \equiv 1 - (1 - e^{-z})^M \quad (13.8.7)$$

is the false-alarm probability of the null hypothesis, that is, the *significance level* of any peak in  $P_N(\omega)$  that we do see.

$P_N(\omega)$  has an exponential probability distribution with unit mean.

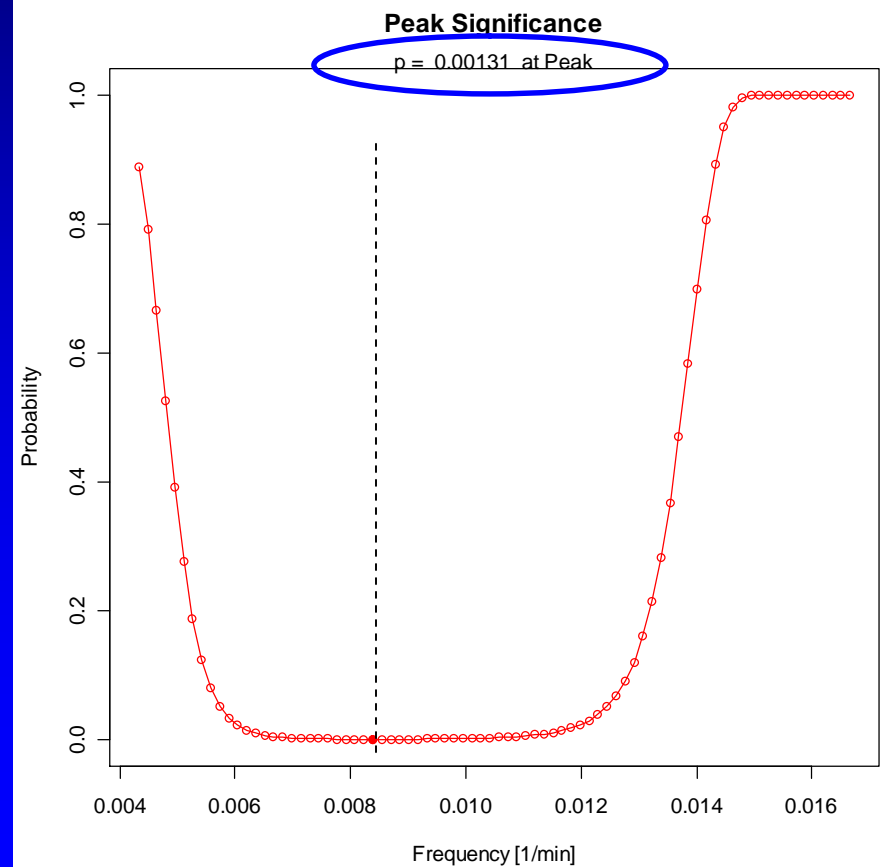
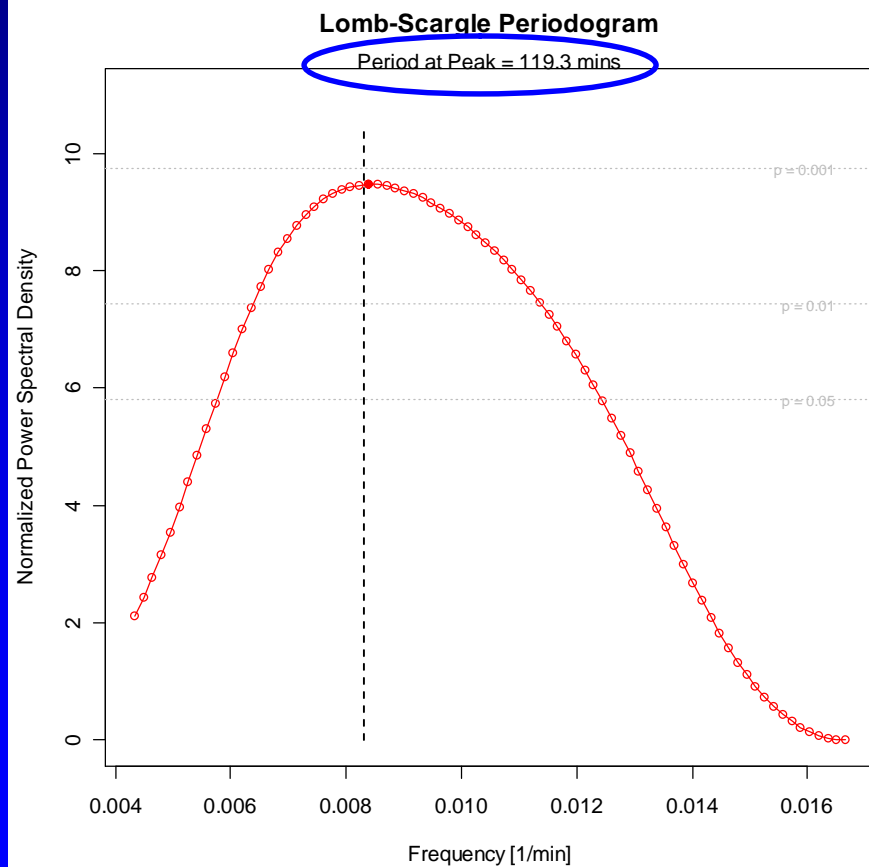
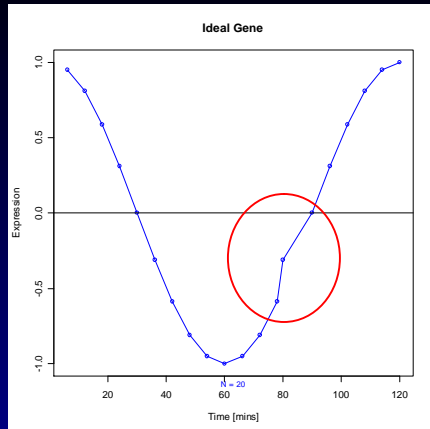


# Lomb-Scargle Analysis: "Ideal Gene"



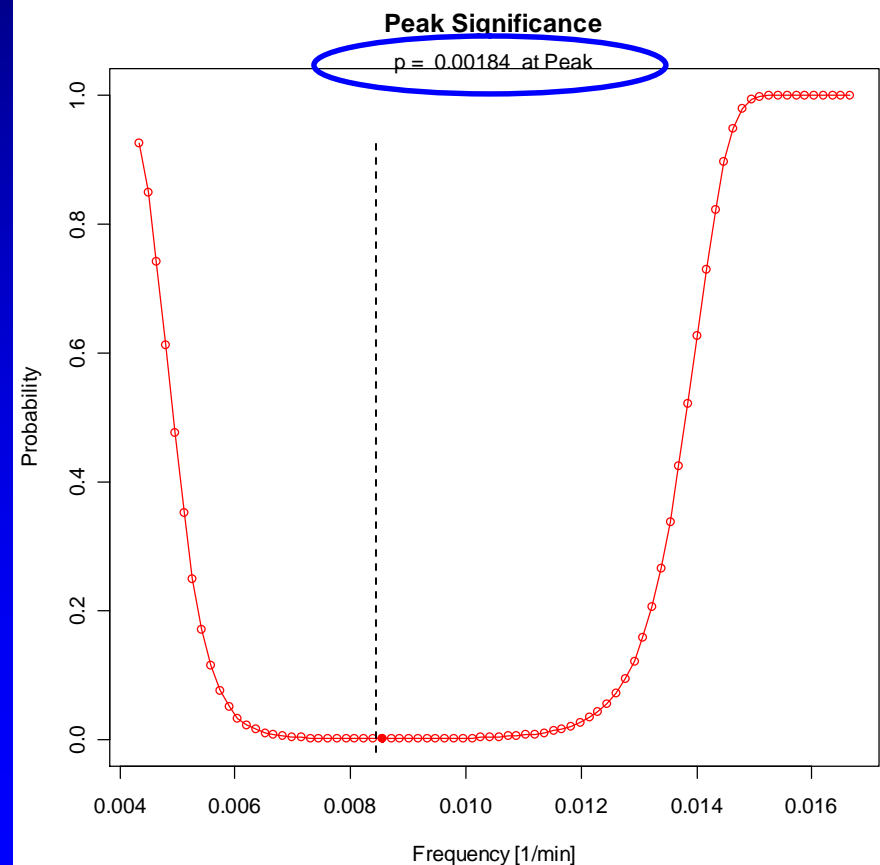
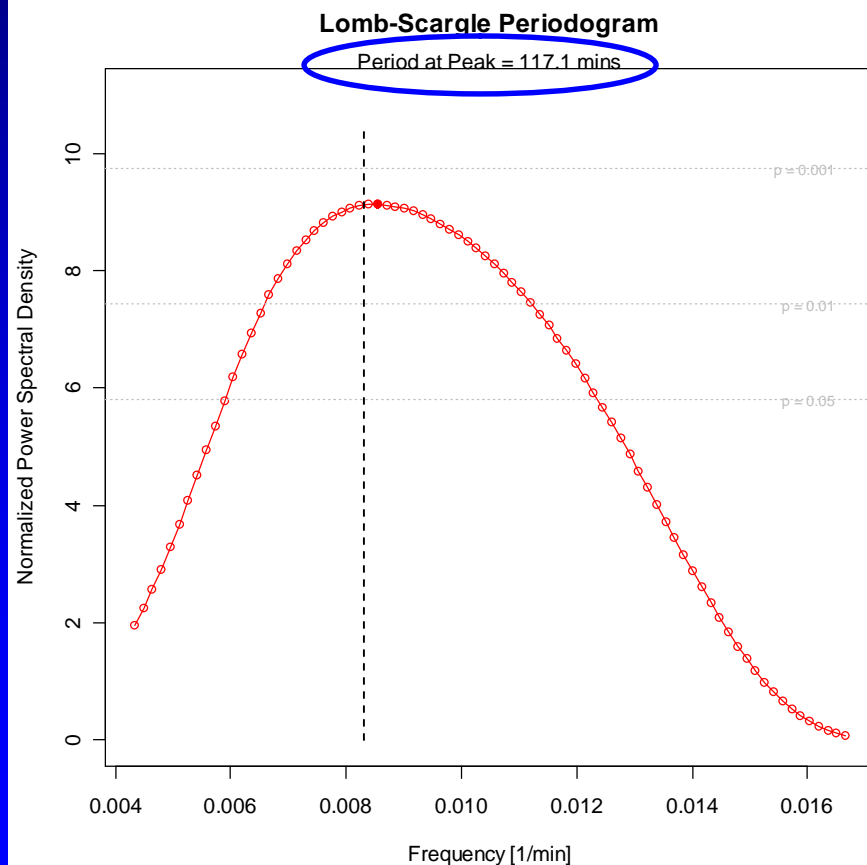
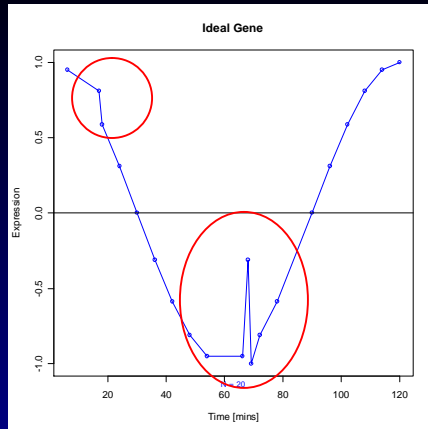
# Lomb-Scargle Analysis: "Ideal Gene" with one "bad" time point

$p = 0.00127$  for "perfect"



# Lomb-Scargle Analysis: "Ideal Gene" with three "bad" time points

$p = 0.00127$  for "perfect"



# Lomb-Scargle Analysis

## Hypothesis Testing

SIGNIFICANCE TESTING OF PERIODOGRAM ORDINATES

CHRIS KOEN

Institute of Physics and Astronomy, National Central University, Republic of China

THE ASTROPHYSICAL JOURNAL, 348: 700–702, 1990 January 10

### III. HYPOTHESIS TESTING

The theory developed above can now be used to test hypotheses. Two hypotheses are relevant:

$H_1$ : the observations do not constitute noise

$H_2$ : the data contain a specific periodicity .

In this paper only a special case of  $H_2$  will be considered, namely,

$H_2$ : the largest periodogram ordinate is significant .

Koen suggests Lomb-Scargle evaluates  $H_1$ , while a Fisher test is needed for  $H_2$ , but ...

## Background

# Box Plots and Notches

Means

a = 0.0

b = 0.0

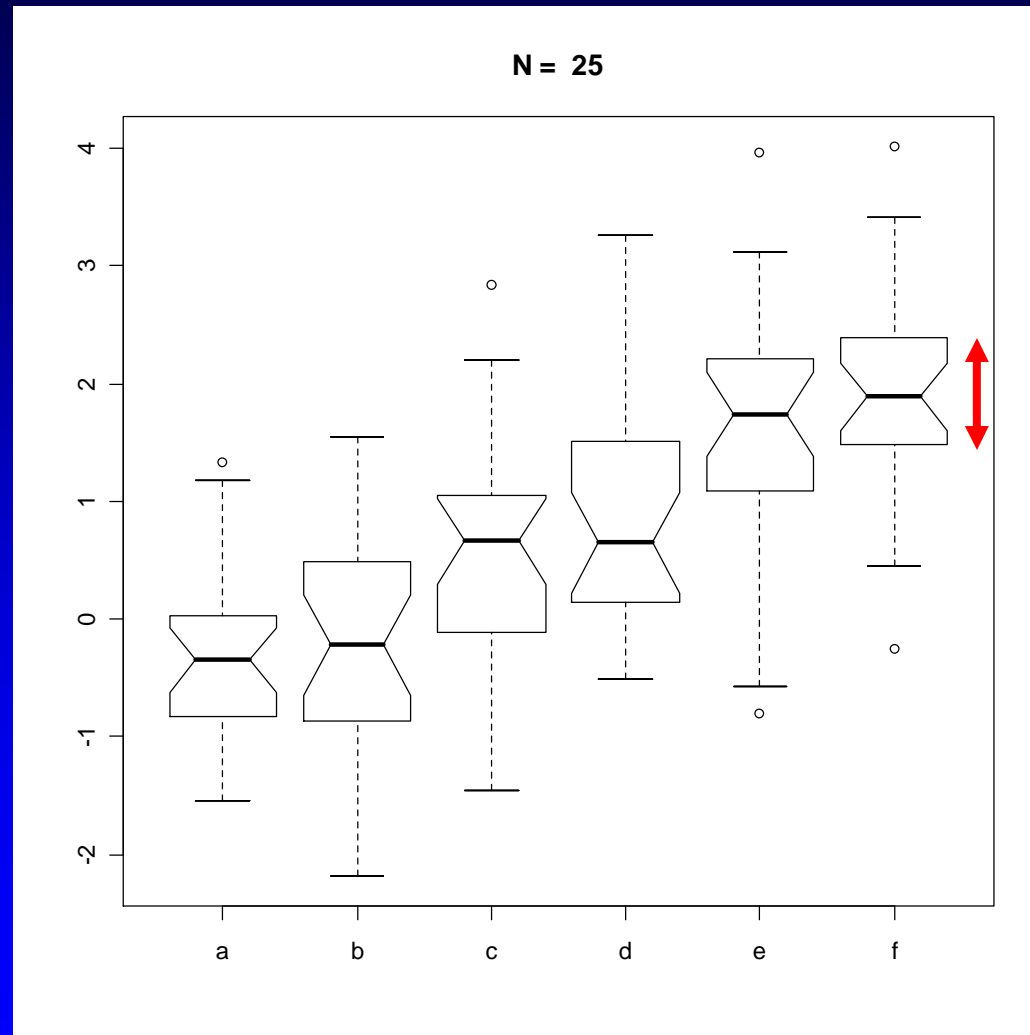
c = 0.5

d = 1.0

e = 1.5

f = 2.0

S.D. = 1.0



Significant difference at 5% level when notches do not overlap

## Background

# Box Plots and Notches

Means

a = 0.0

b = 0.0

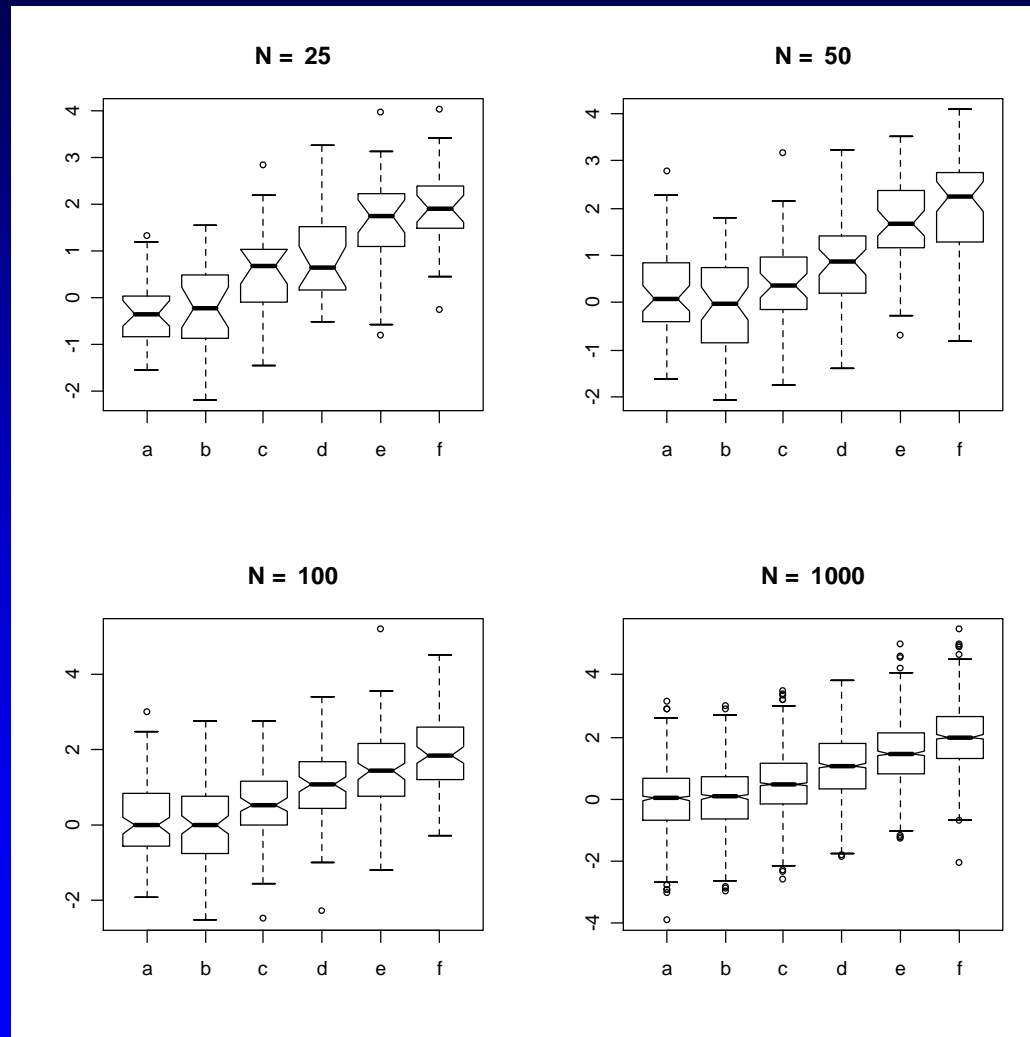
c = 0.5

d = 1.0

e = 1.5

f = 2.0

S.D. = 1.0



## Background

# Box Plots

Means

a = 0.0

b = 0.0

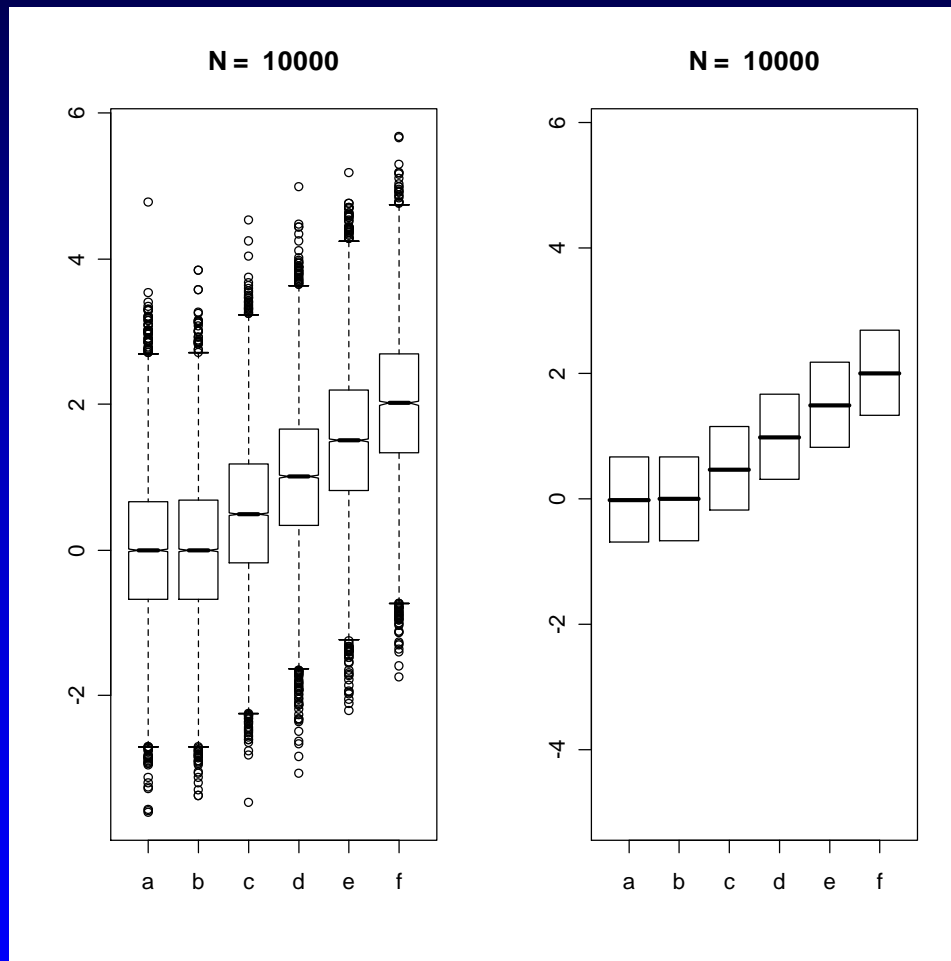
c = 0.5

d = 1.0

e = 1.5

f = 2.0

S.D. = 1.0



Most boxplots on slides to follow have N=10,000.  
Notches, "whiskers," outliers will usually not be shown.

## Rank Order and Rank Product

Gene	Trial 1 Rank	Trial 2 Rank	Trial 3 Rank	Rank Product	Overall Rank
gene 1	1	2	1	2	1
gene 2	2	3	3	18	3
gene 3	3	1	2	6	2

Ranks may be more robust with weak signals.



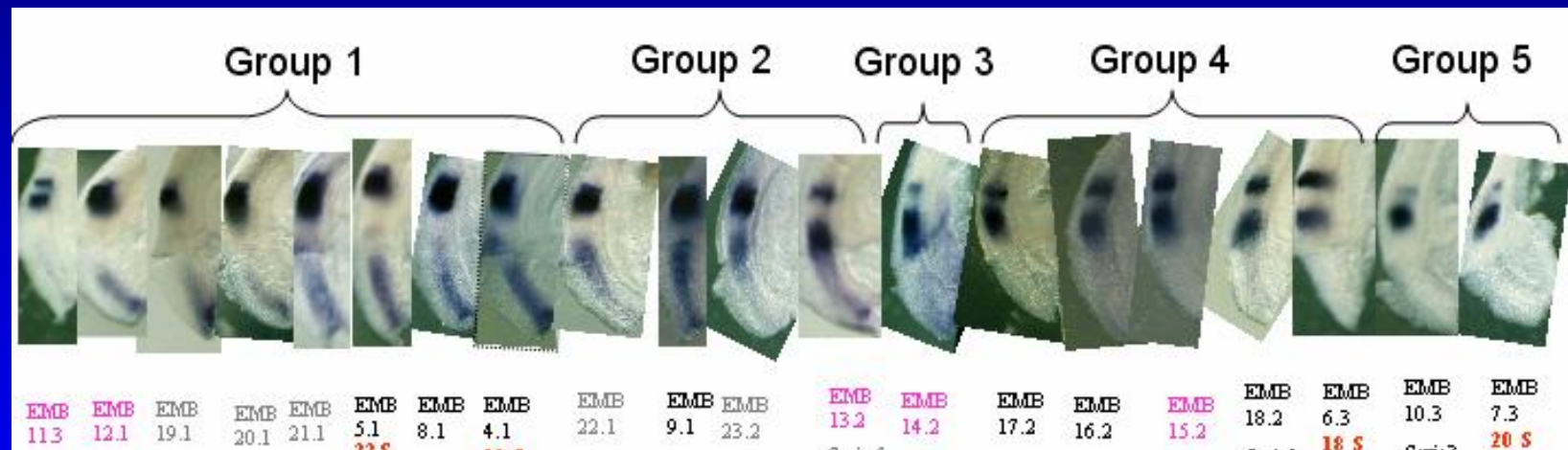
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- Somitogenesis Experiments
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# Microarray Analysis Overview

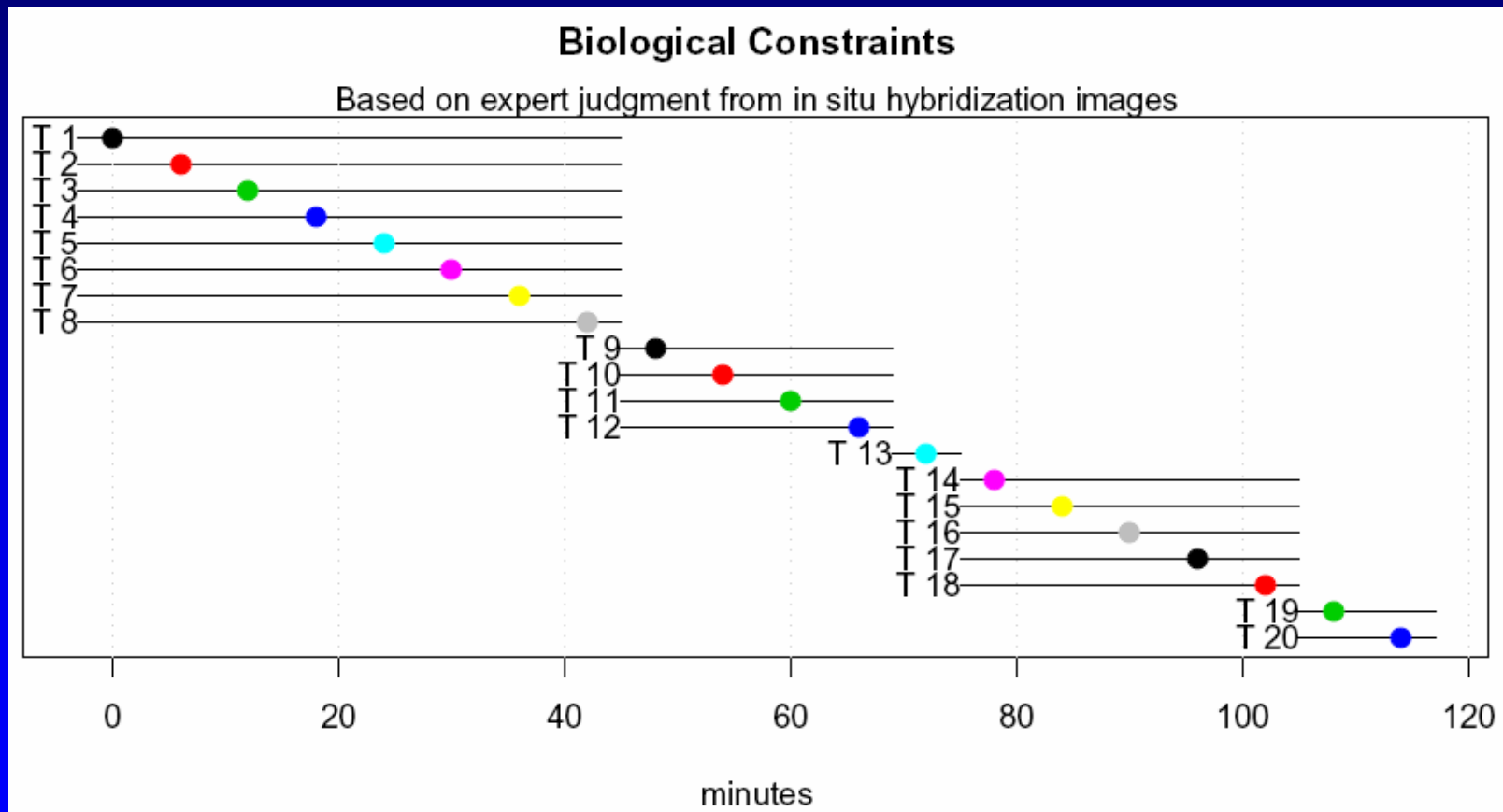
Somitogenesis Datasets: Mouse, Chick, Zebrafish

Time series from in situ hybridization images



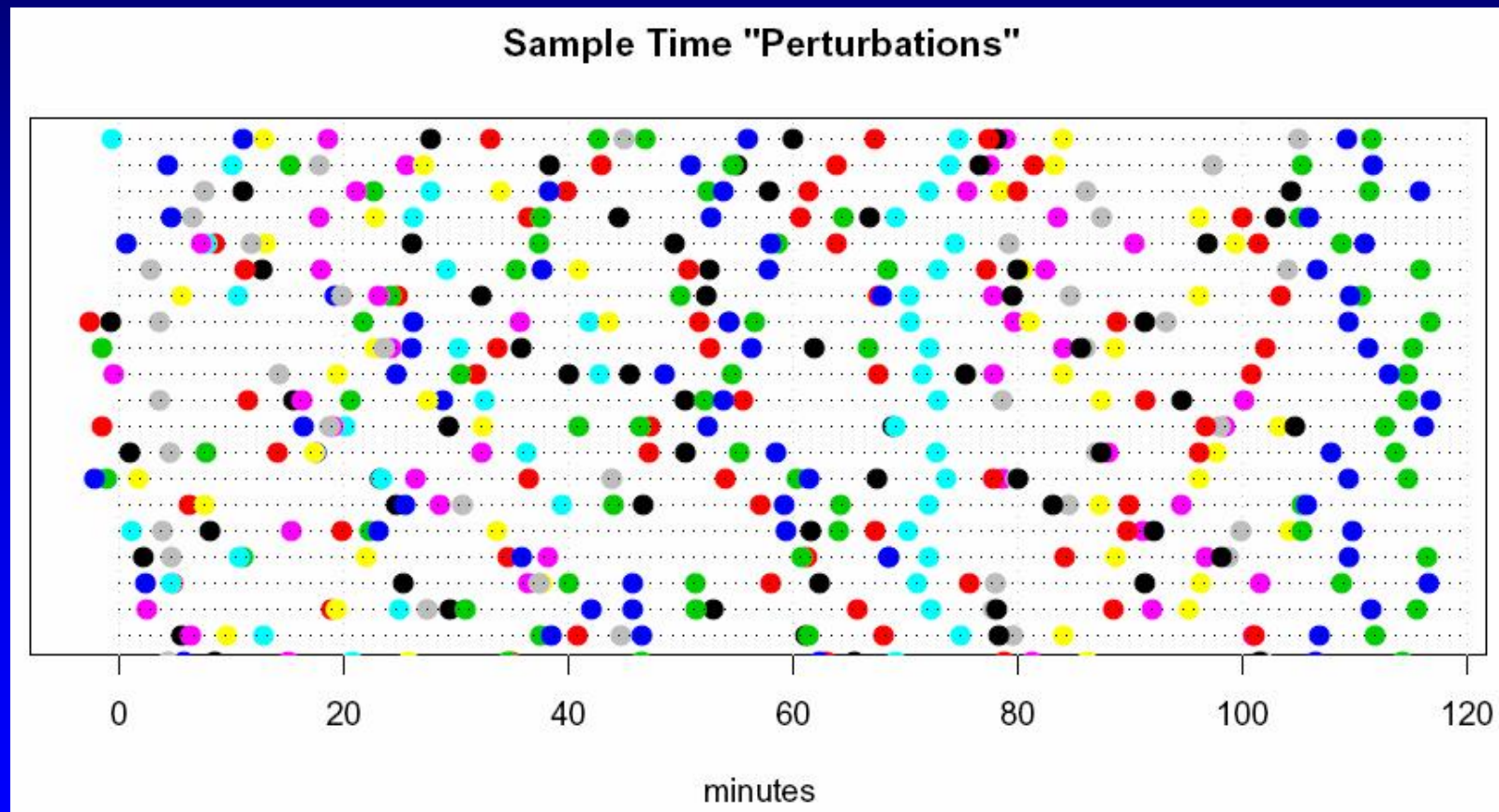
- Time
- What time values should be used in time series?
  - What biological constraints define groups?

# Time Perturbations



Dots show position of "baseline" times.

# Time Perturbations



Each row of dots represents one time ordering. 20

# Somitogenesis Datasets

Time Perturbations

Affymetrix Chips

Mouse

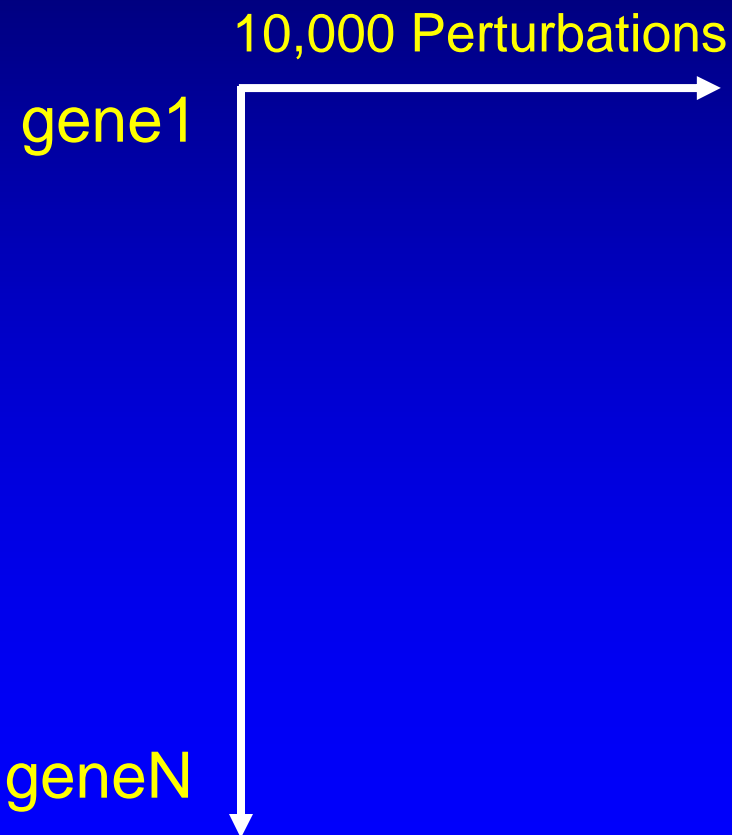
N=22,690 or 45,101

Chick

N=38,535

Zebrafish

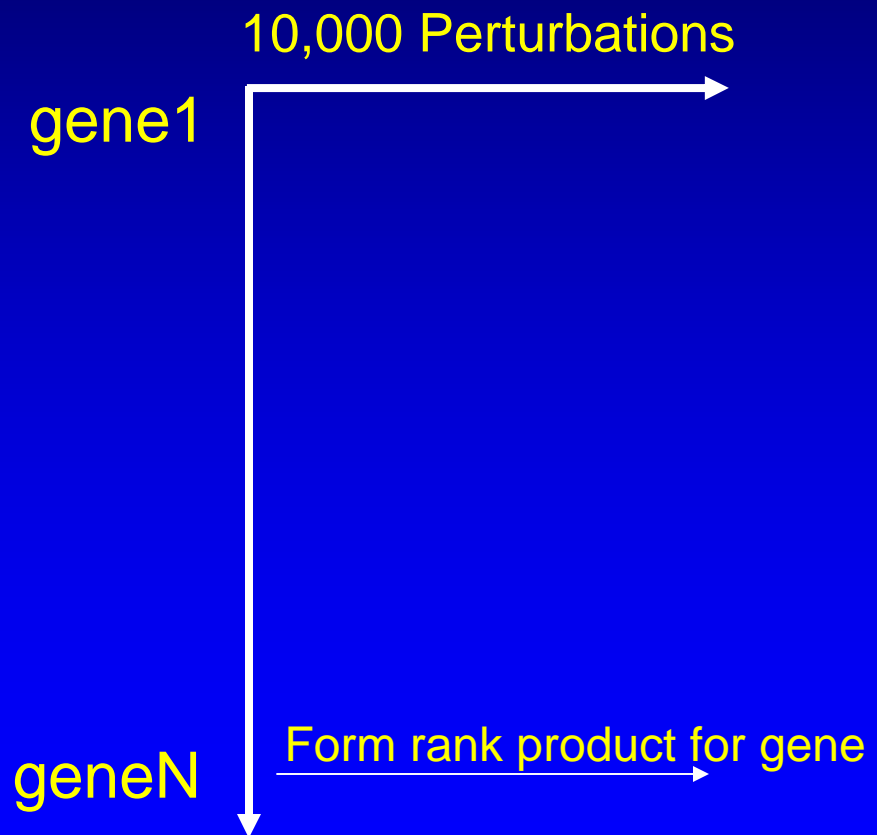
N=15,618



# Somitogenesis Datasets

## Time Perturbations

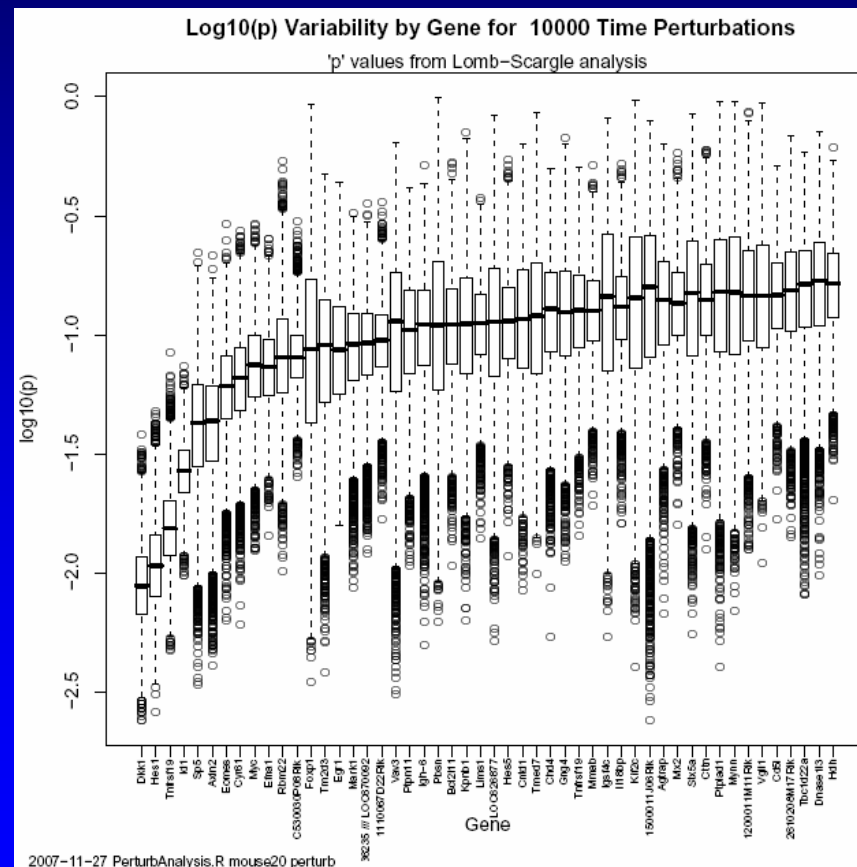
1. Perform Lomb-Scargle analysis on each of 10,000 perturbations for each gene.  
[Cluster problem]
2. For given perturbation, rank order genes based on Lomb-Scargle p-value.
3. Form rank product for each gene for overall ranking.



## Somitogenesis Datasets

### Lomb-Scargle p-values

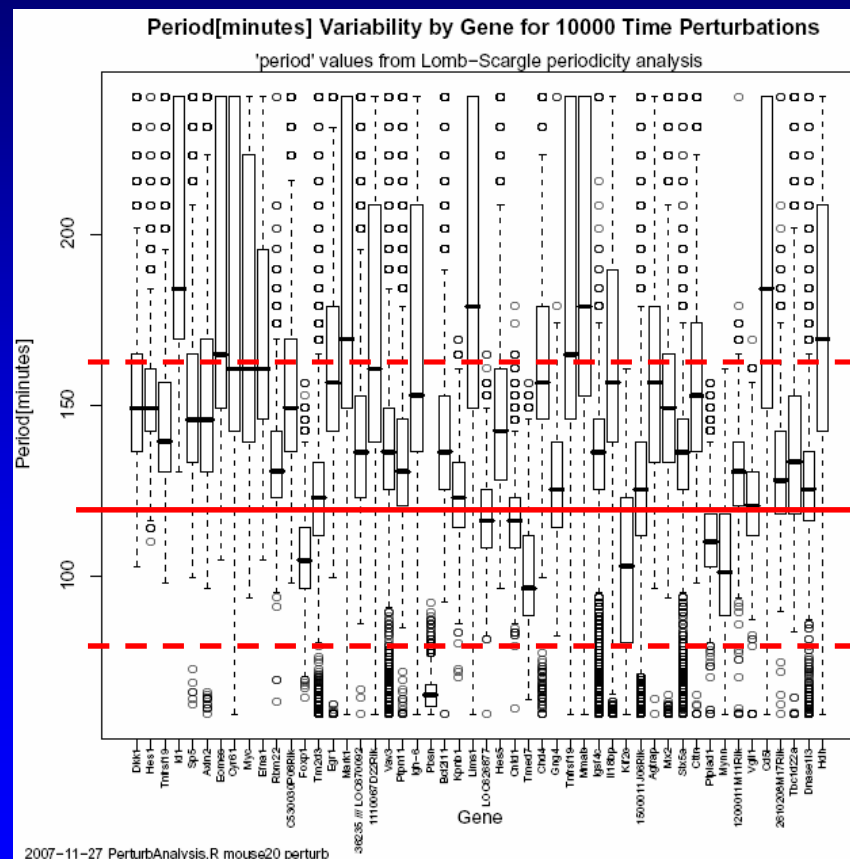
Ordered by  
"Overall Rank"  
(i.e., Rank product  
of 10,000 ranks  
from Lomb-Scargle  
p-values.)



Looks "good" but need to know how to interpret results.

# Somitogenesis Datasets

## Lomb-Scargle Periods



Mouse somite period is assumed to be 120 minutes

Need to filter results for period of biological interest. 24



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# Numerical Experiments

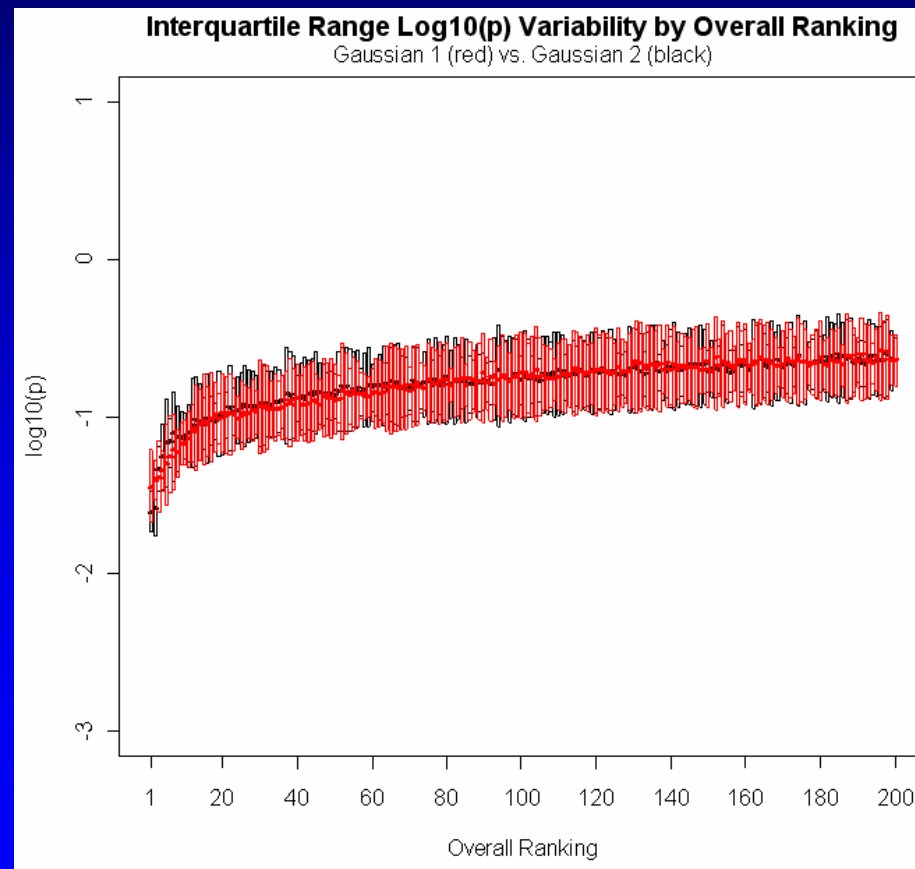
"Controlled Experiments"

- Gaussian Noise vs. Gaussian Noise
- 2.5% "perfect" periodic genes
- 20 genes with signal-to-noise gradient
- 16 genes, half good, half not so good

## Numerical Experiment

# Gaussian Noise vs. Gaussian Noise

**Assume GeneChip experiments once normalized are roughly Gaussian.**



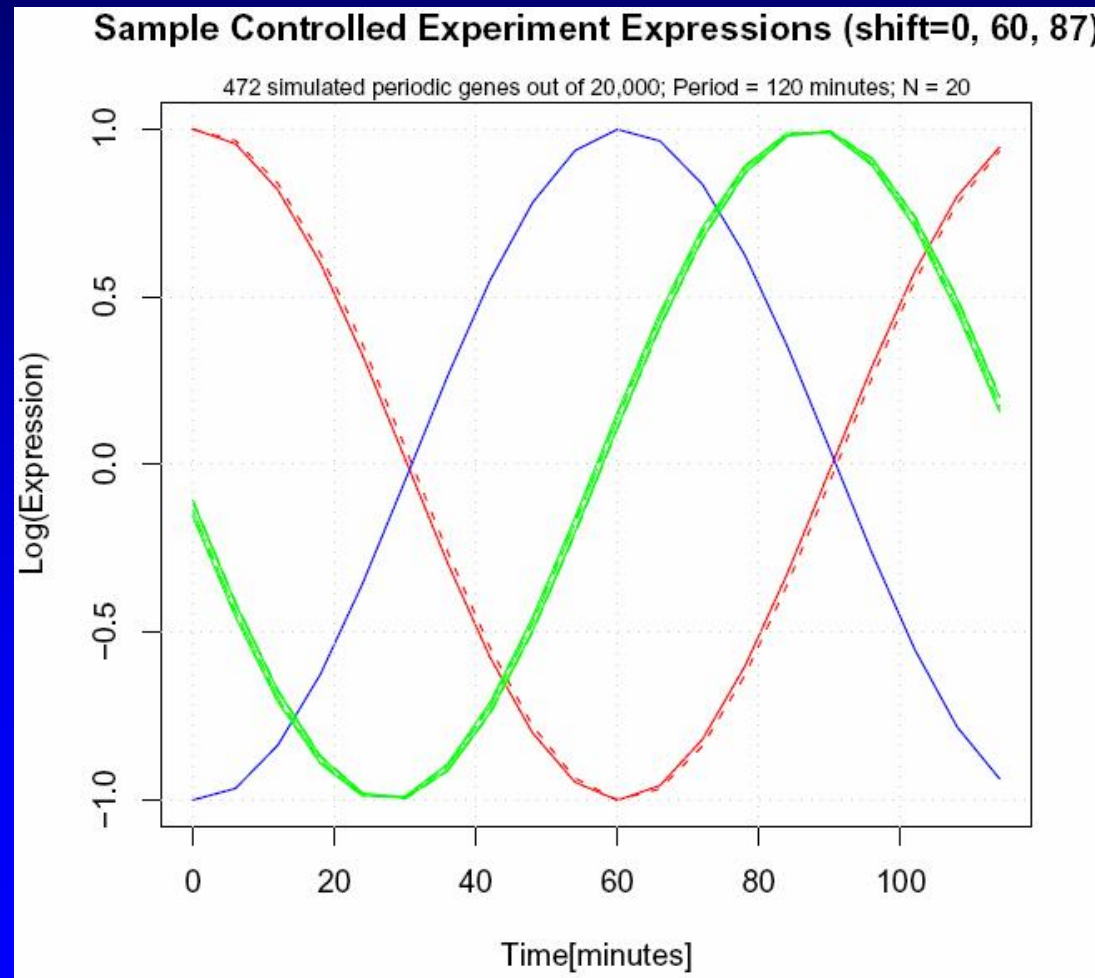
Compare signal rank with "noise" rank.

Numerical Experiment (mouse)

## 2.5% "perfect" periodic genes

What if many strong periodic genes are involved in somitogenesis?

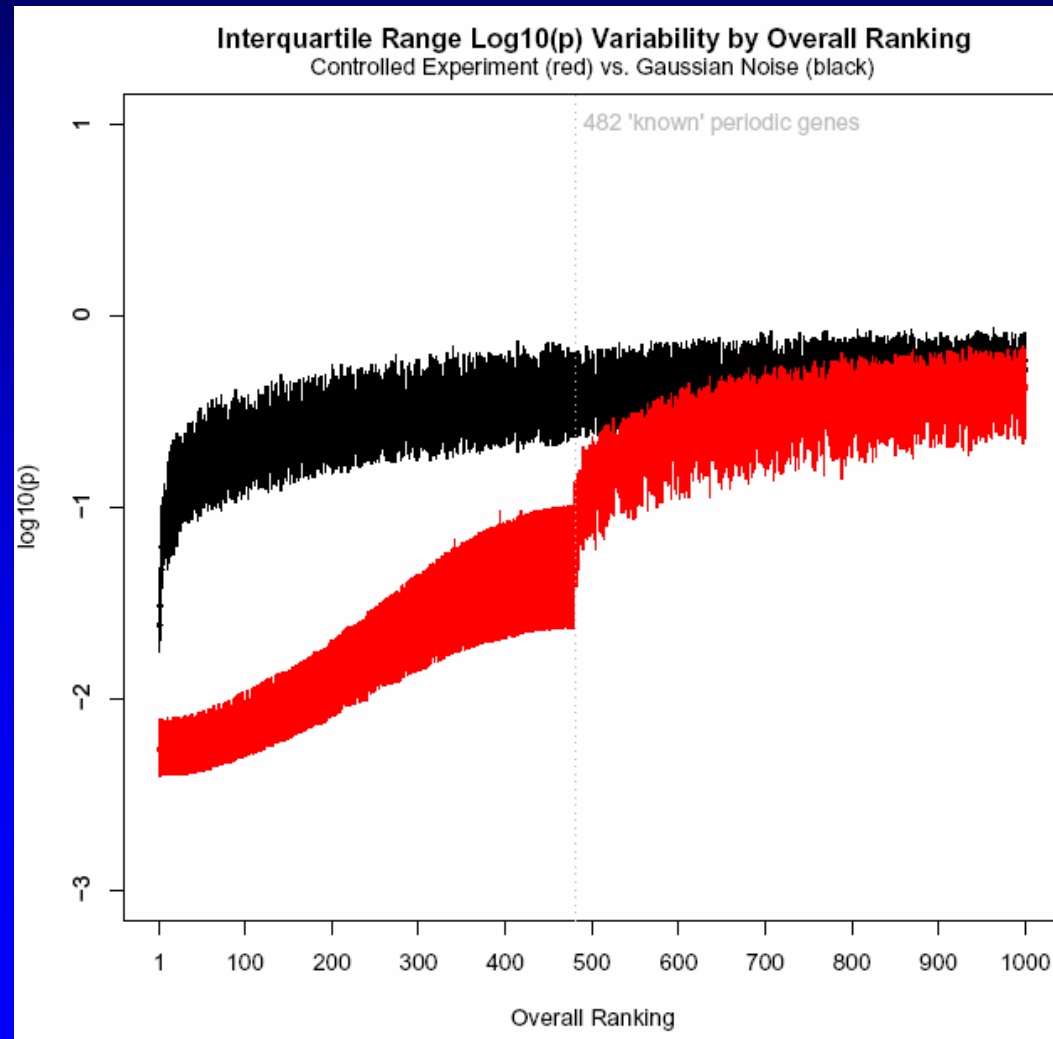
482 synthetic genes out of 20,000 were defined as sinusoids with various phase shifts



Numerical Experiment (mouse)

## 2.5% "perfect" periodic genes

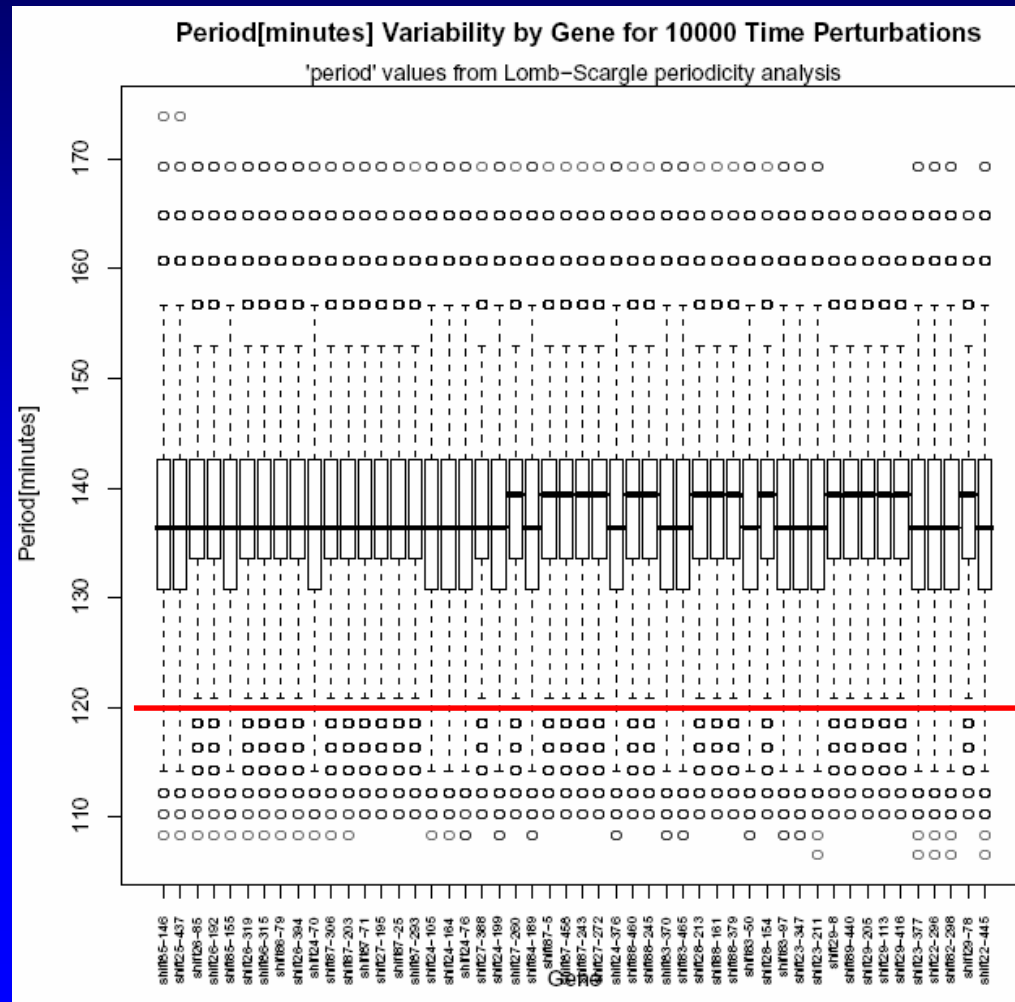
What if many strong periodic genes are involved in somitogenesis?



## Numerical Experiment (mouse)

# 2.5% "perfect" periodic genes

Are all periods this same?

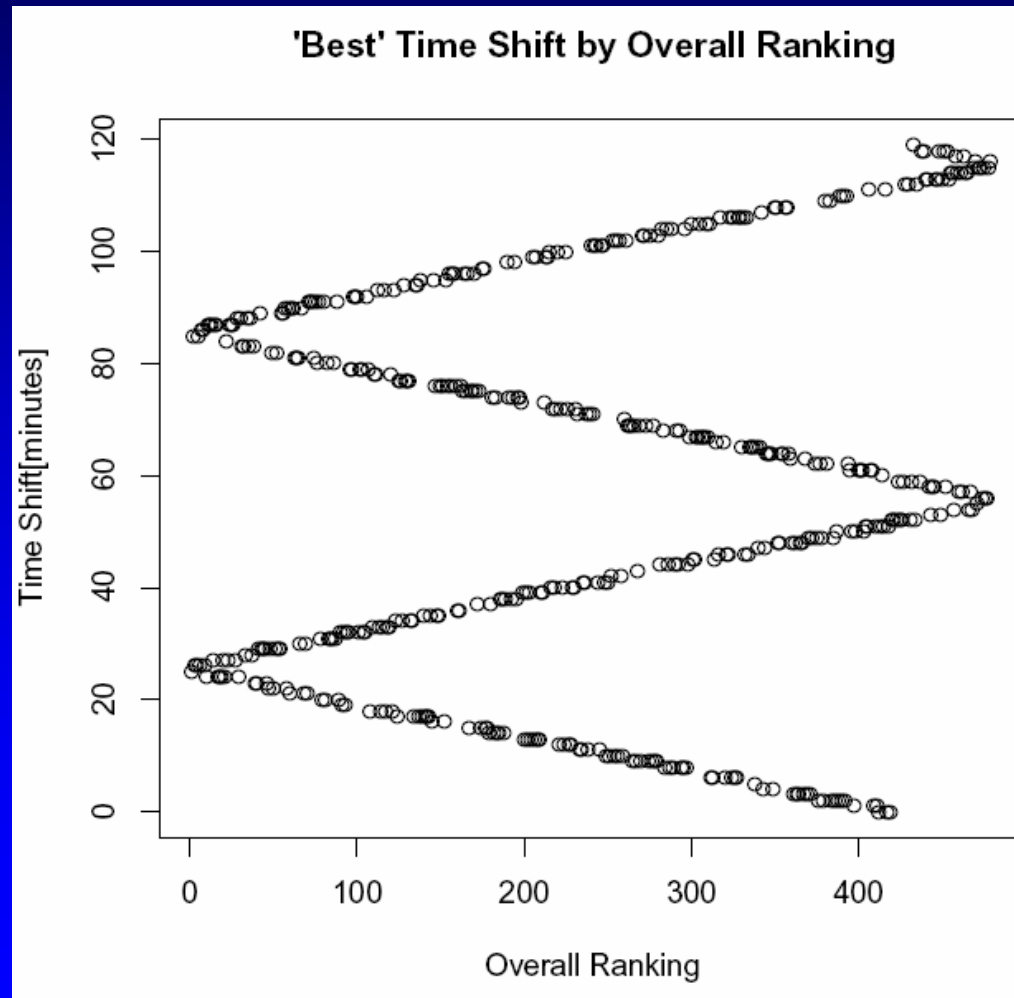


Mouse somite period is assumed to be 120 minutes

Numerical Experiment (mouse)

## 2.5% "perfect" periodic genes

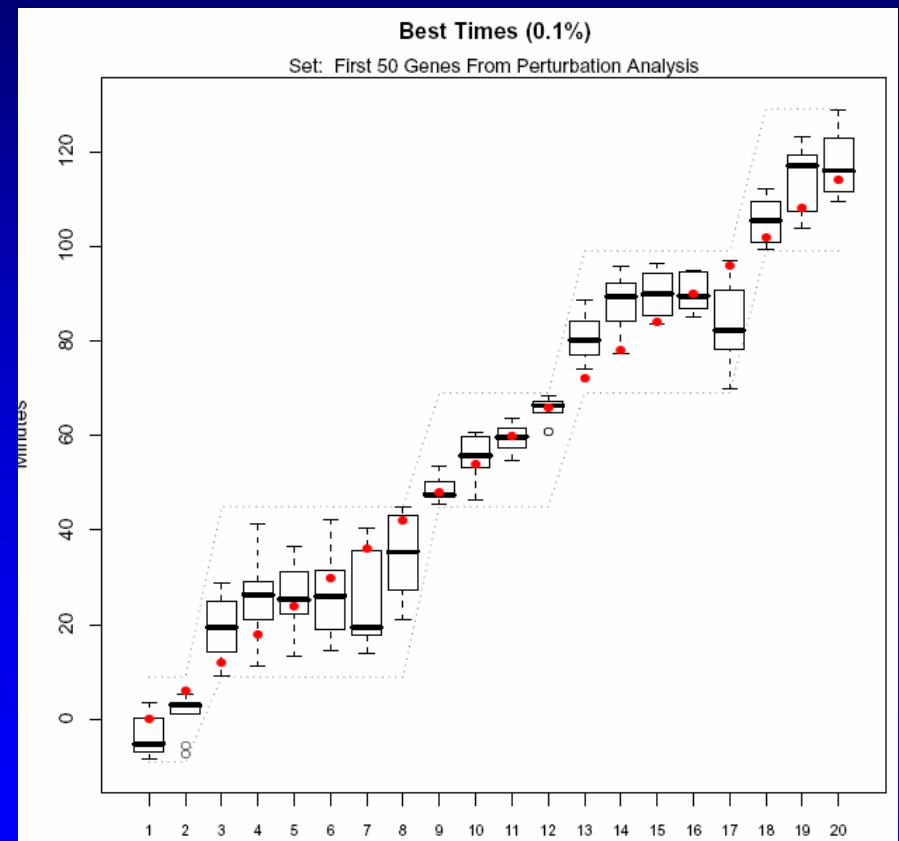
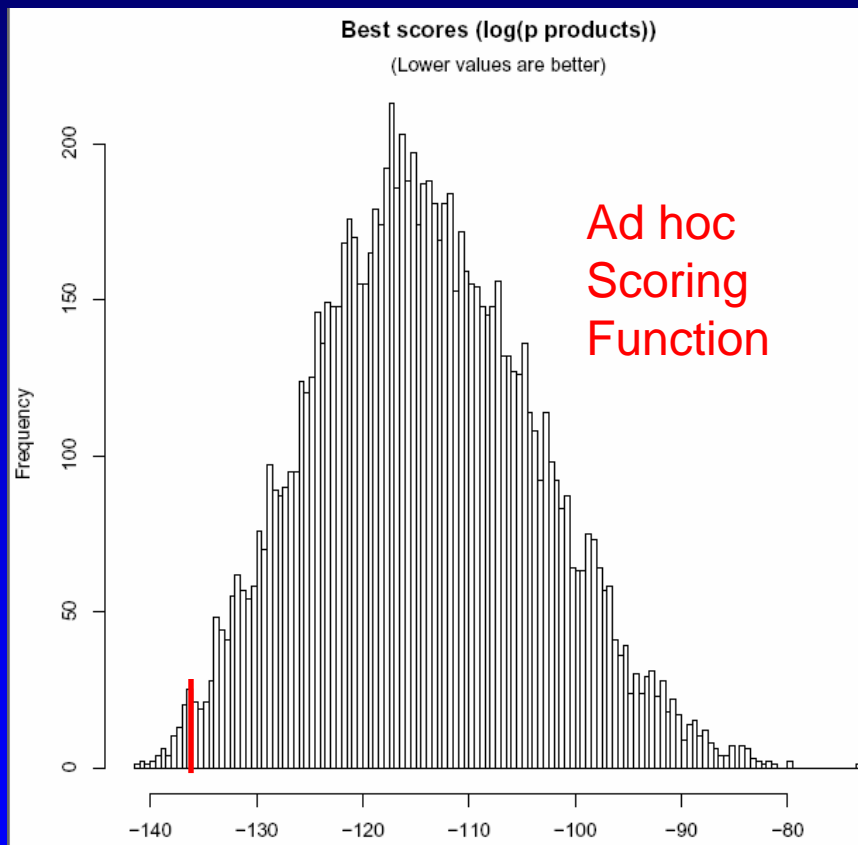
Are all time shifts "equal"?



## Numerical Experiment (mouse)

# 2.5% "perfect" periodic genes

Can time series time points be estimated?



Maybe. Quite time consuming to explore alternatives.<sup>32</sup>

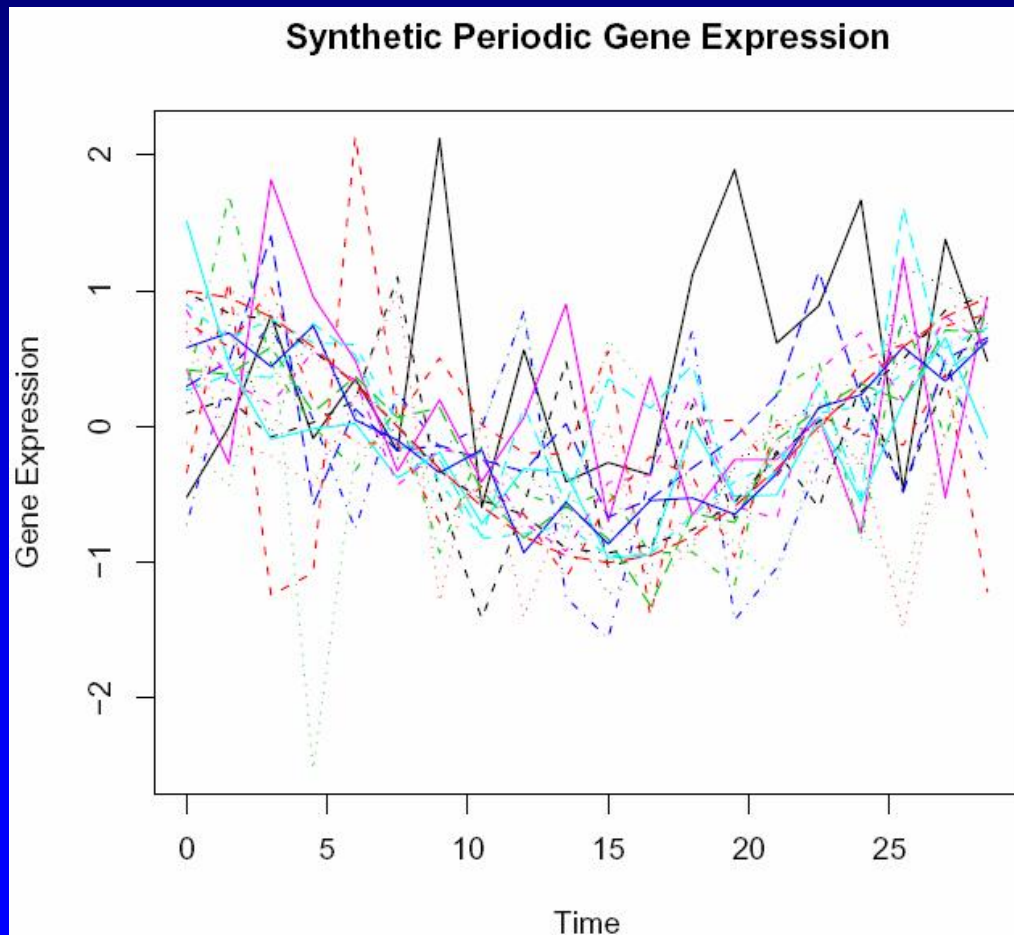


## Numerical Experiment (zebrafish)

# 20 genes with signal-to-noise gradient

$$\text{Expression} = w * \text{Cosine} + (1-w) * \text{Gaussian}$$

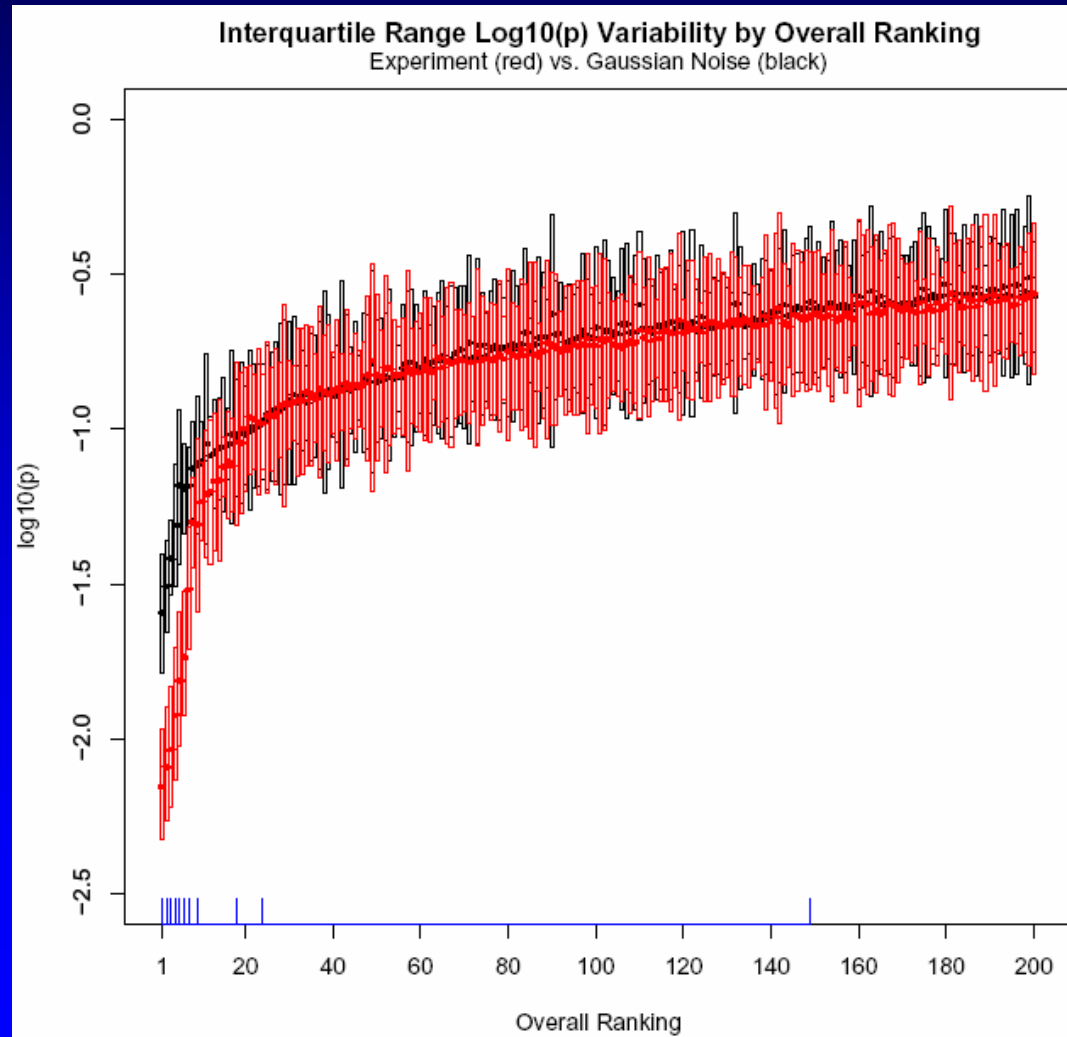
$w = 0.00$  to  $1.00$   
by  $0.05$



## Numerical Experiment (zebrafish)

# 20 genes with signal-to-noise gradient

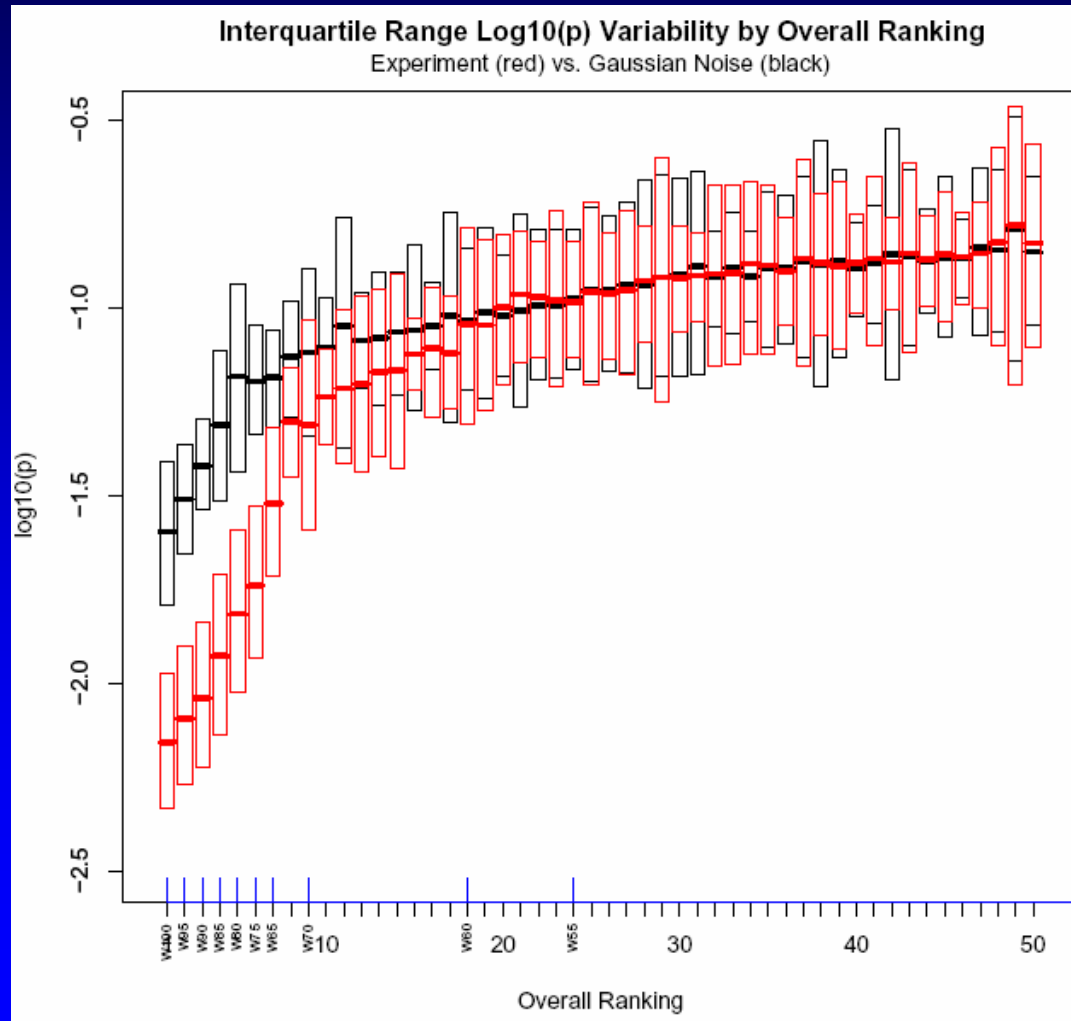
Rank	w
1	1.00
2	0.95
3	0.90
4	0.85
5	0.80
6	0.75
7	0.65
9	0.70
18	0.60
24	0.55
149	0.45



## Numerical Experiment (zebrafish)

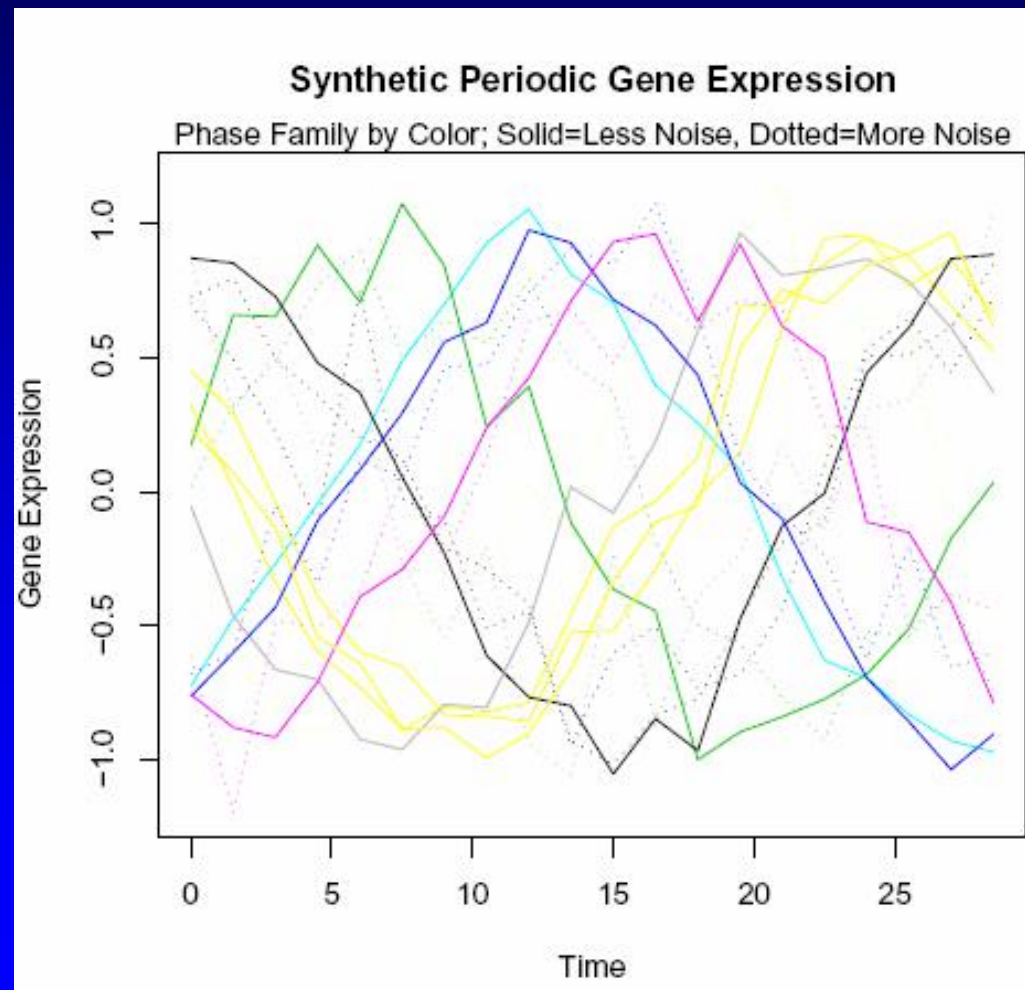
# 20 genes with signal-to-noise gradient

Rank	w
1	1.00
2	0.95
3	0.90
4	0.85
5	0.80
6	0.75
7	0.65
9	0.70
18	0.60
24	0.55
149	0.45



## Numerical Experiment (zebrafish)

16 genes, half good, half not so good

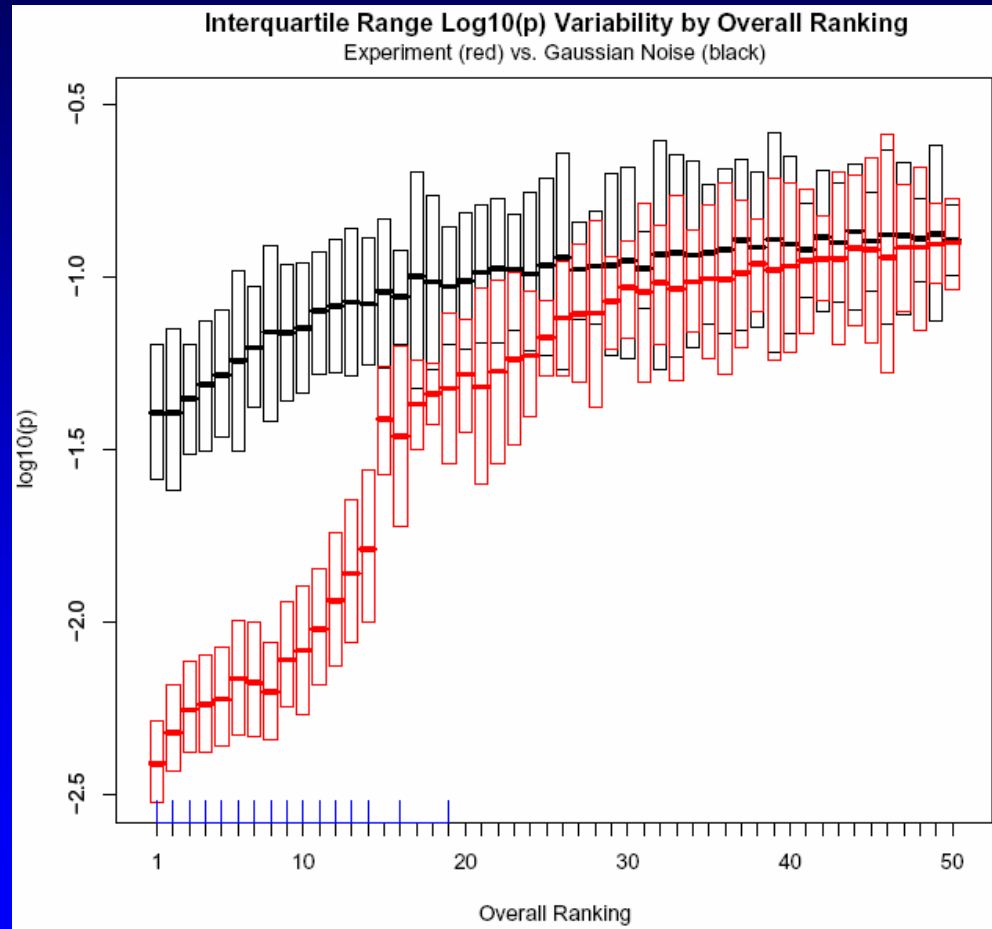


## Numerical Experiment (zebrafish)

# 16 genes, half good, half not so good

Rank	w	shift[min]
1	0.90	26.25
2	0.90	22.5
3	0.75	7.5
4	0.90	7.5
5	0.90	22.5
6	0.90	11.25
7	0.90	4
8	0.90	22.5
9	0.75	18.75
10	0.90	0
11	0.90	18.75
12	0.75	0
13	0.75	11.25
14	0.75	22.5
16	0.75	0
19	0.75	26.25

Zebrafish somite period is assumed to be 30 minutes

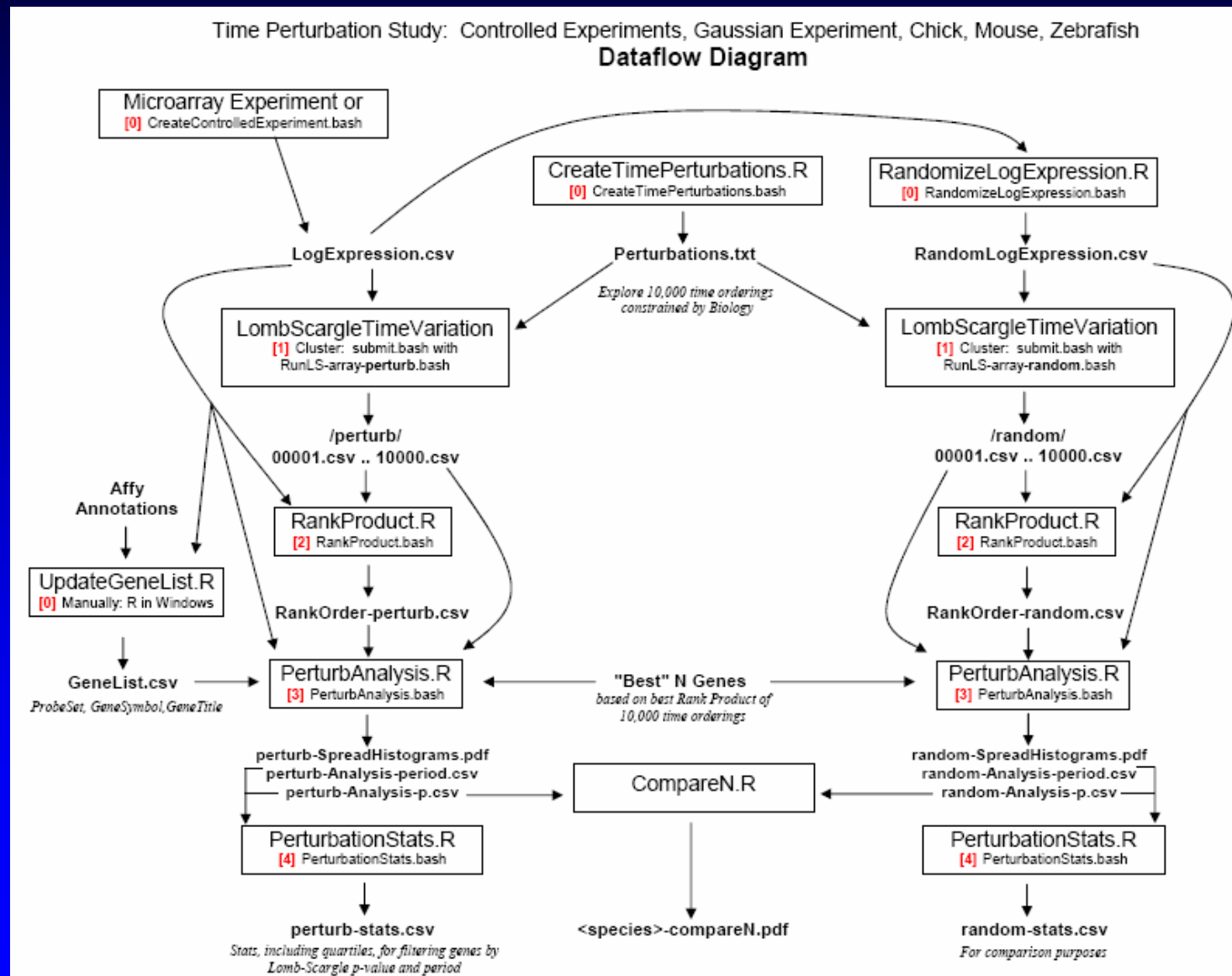


*But is Gaussian noise the appropriate comparison for real experiments?*

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# Time Perturbation Somitogenesis Studies



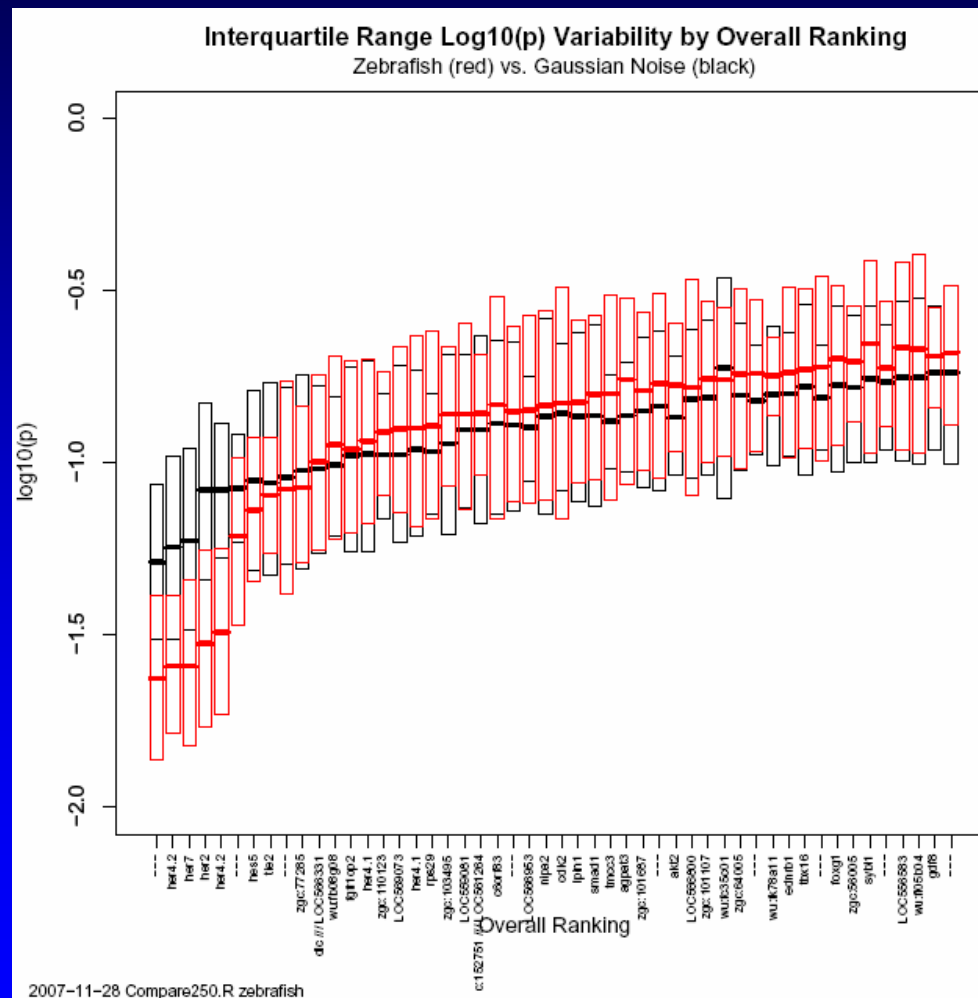
# Time Perturbation Somitogenesis Studies

- Zebrafish
- Mouse
- Chick



# Somitogenesis Experiment

## Zebrfish

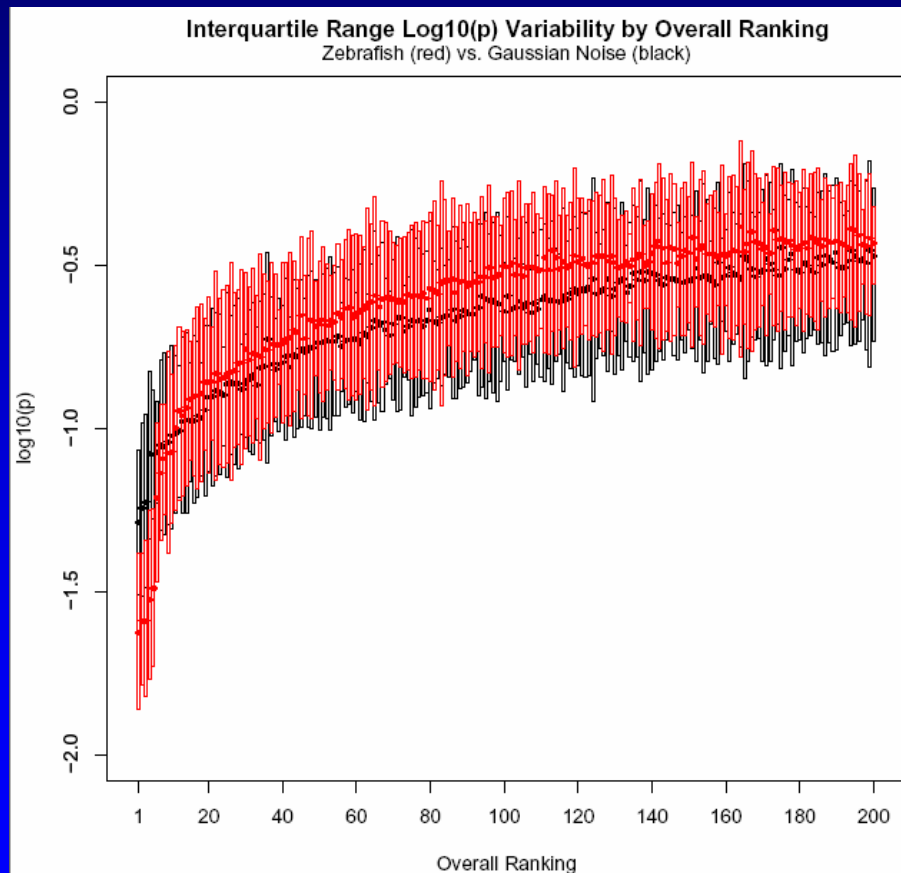


Is Gaussian assumption valid? Is Gaussian "too" random?

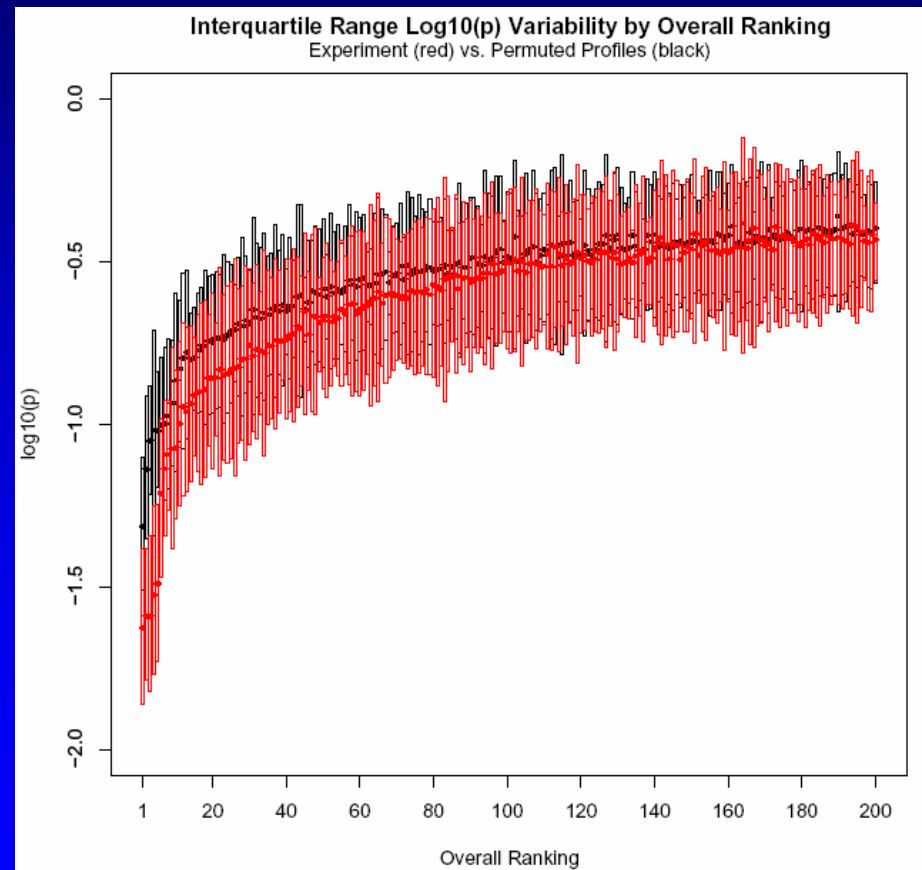
## Somitogenesis Experiment

# Zebrafish

### Gaussian Noise



### Permuted GeneChip Noise

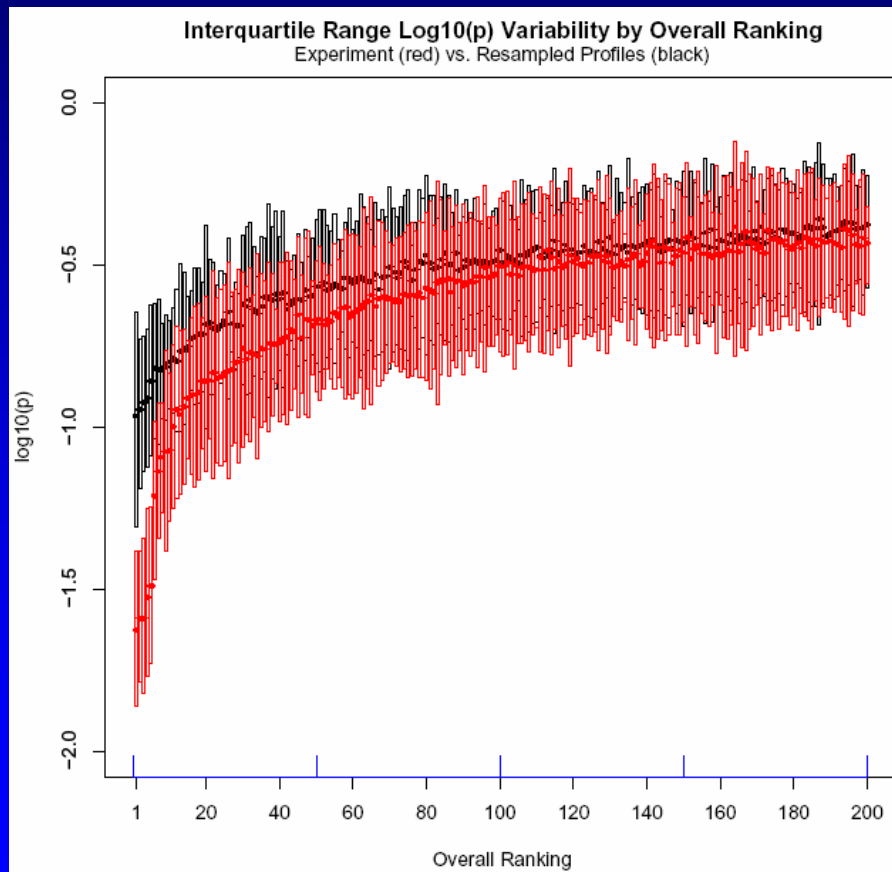


Is Gaussian assumption valid? Is Gaussian "too" random?

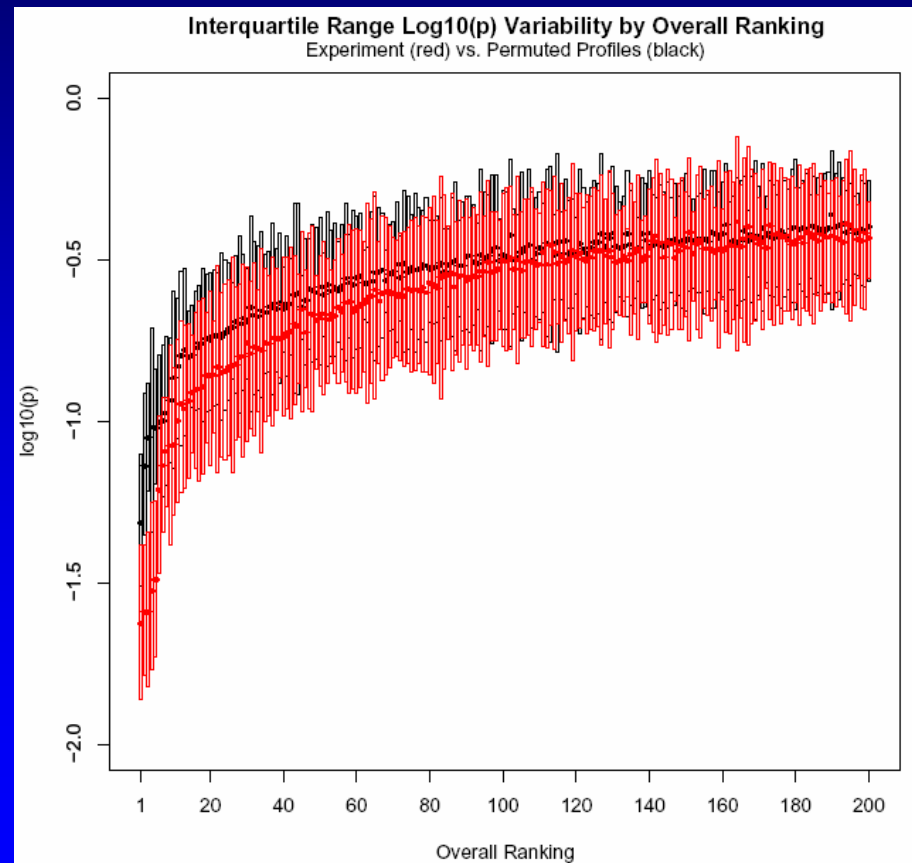
## Somitogenesis Experiment

# Zebrafish

## Resampled GeneChip Noise



## Permuted GeneChip Noise

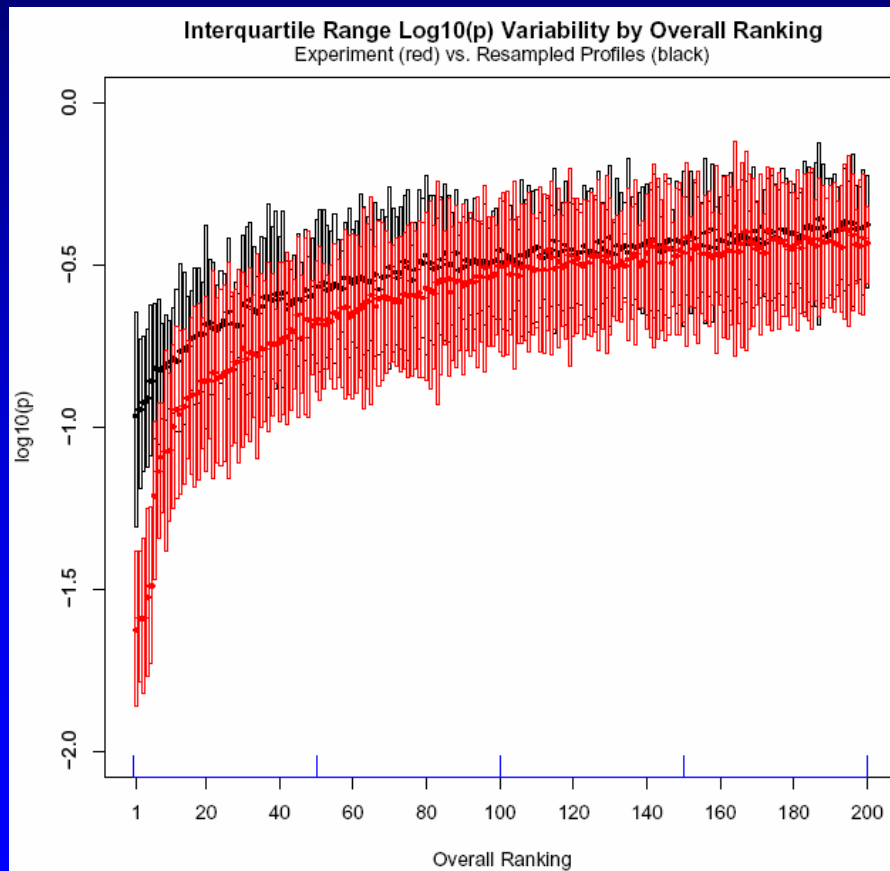


Resampled GeneChips seem to be best "noise" reference

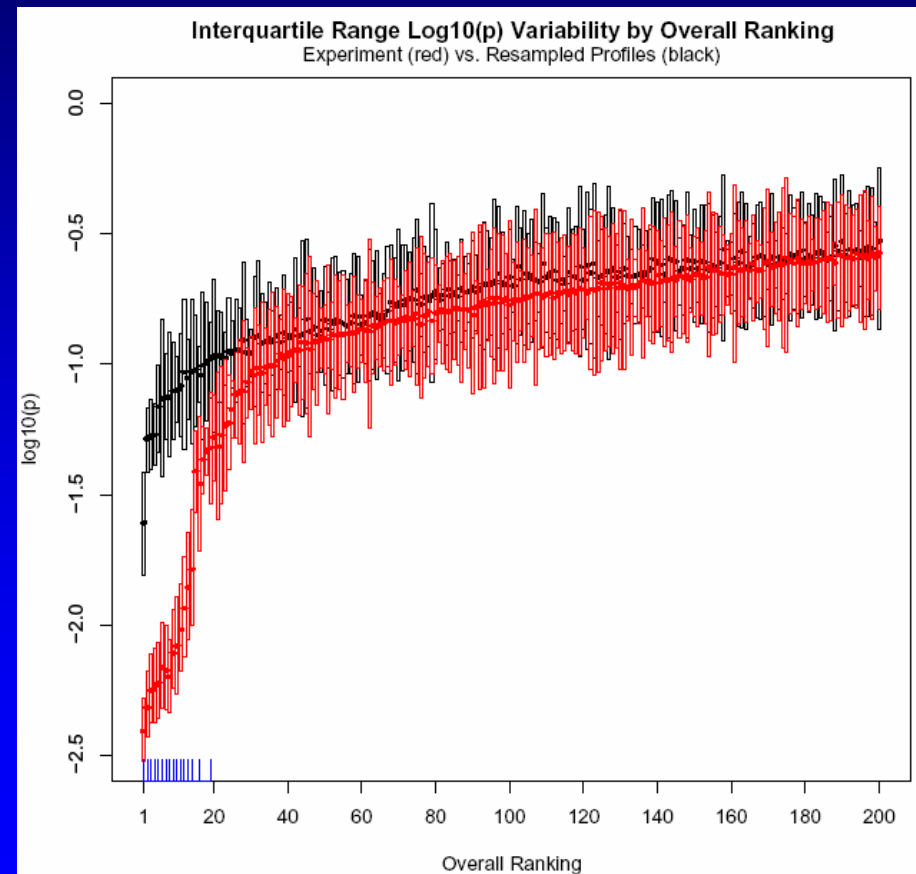
# Somitogenesis Experiment

## Zebrafish

### Actual Experiment

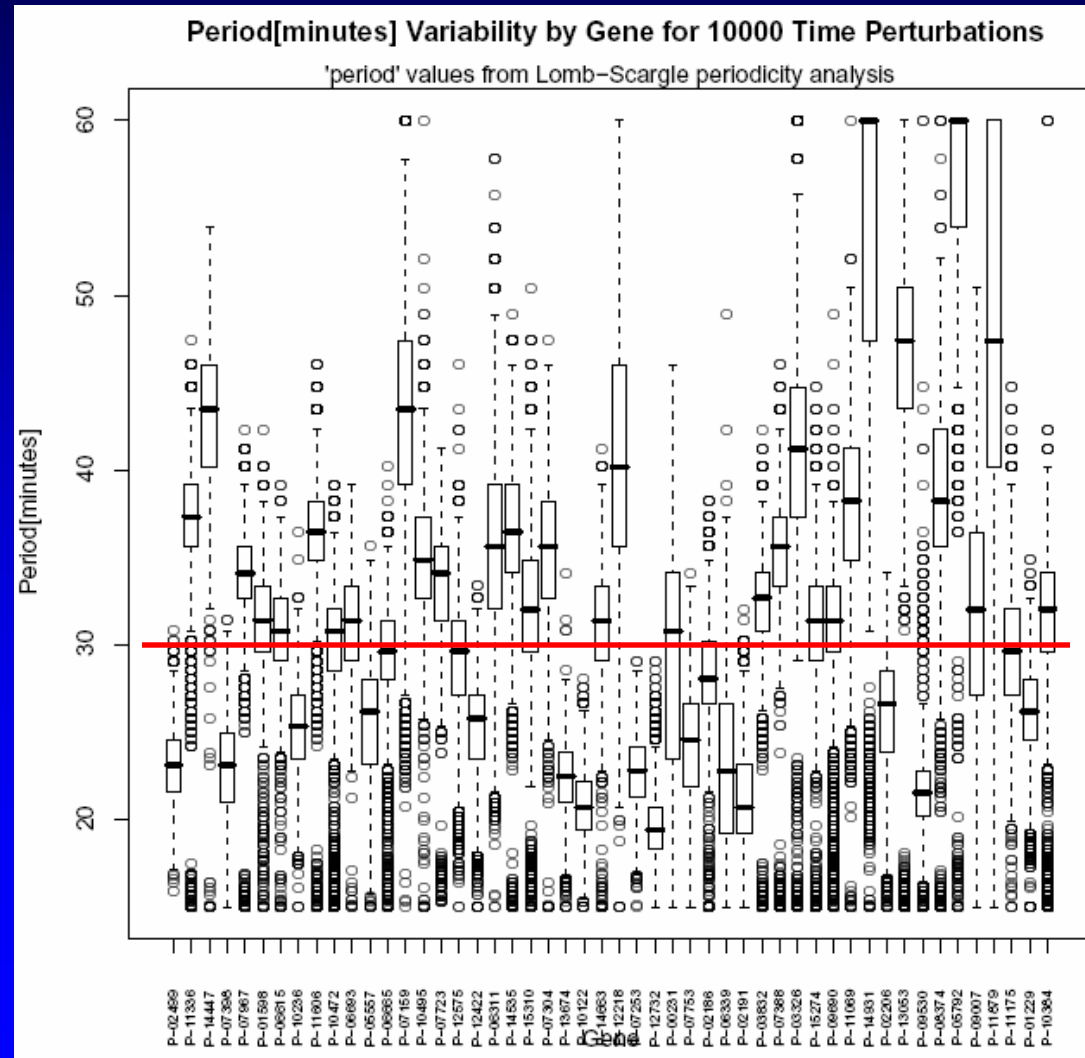


### Simulated Experiment (16)



# Somitogenesis Experiment

## Zebrafish

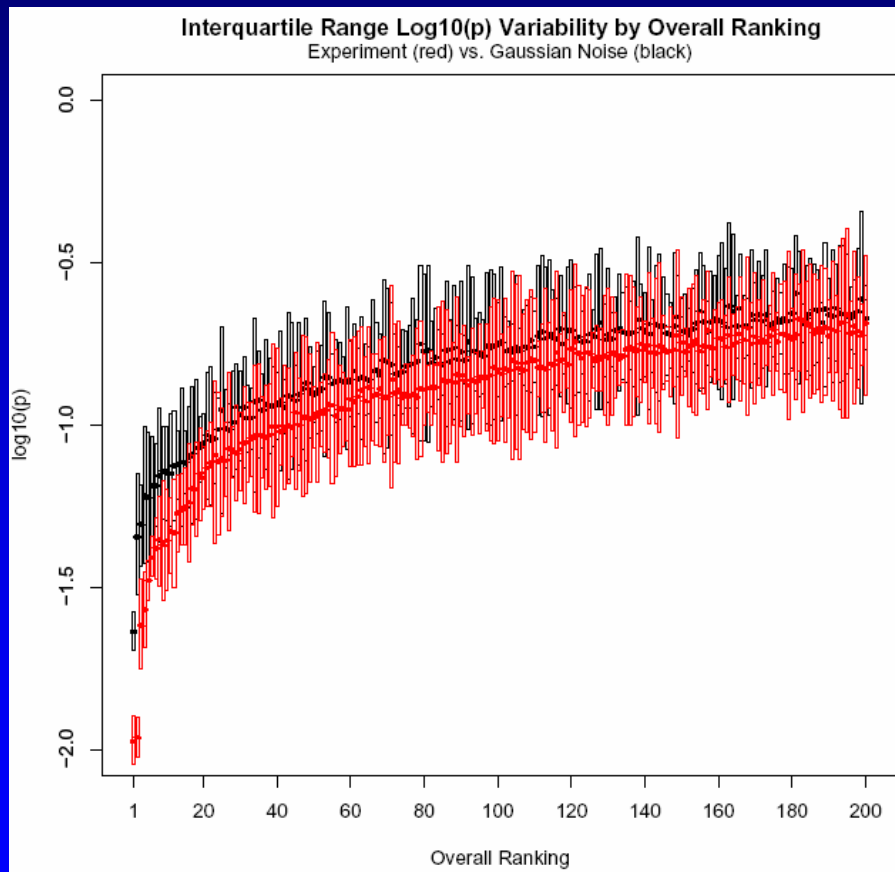


Zebrafish  
somite period  
is assumed to  
be 30 minutes

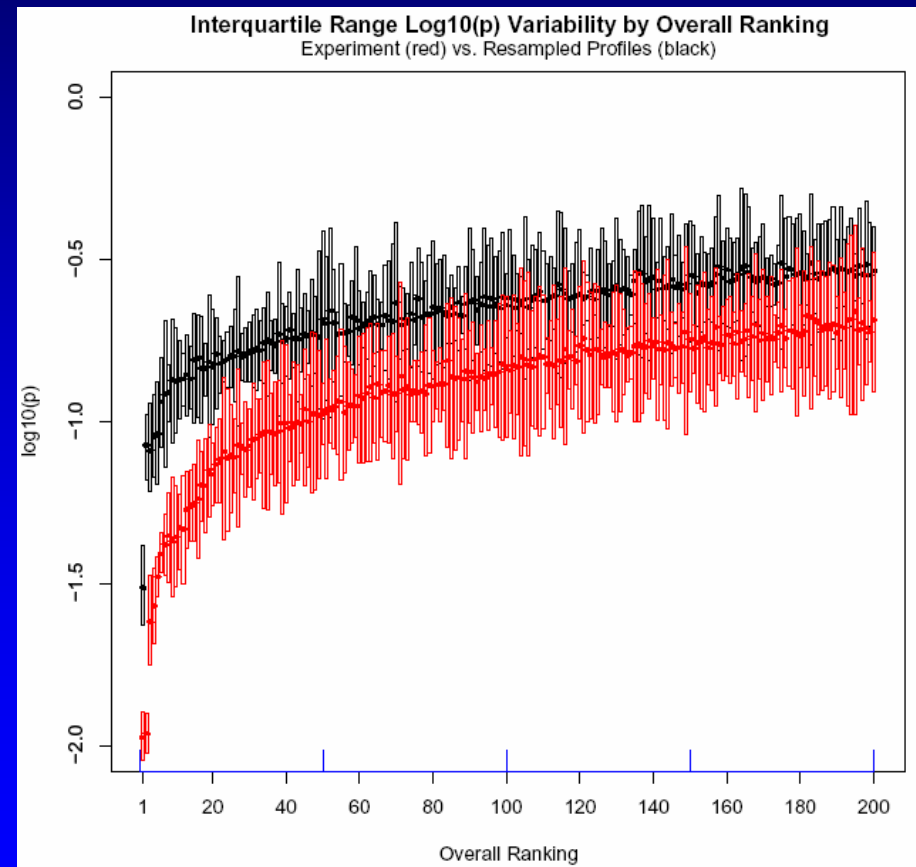
# Somitogenesis Experiment

## Mouse (17 points)

Gaussian Noise

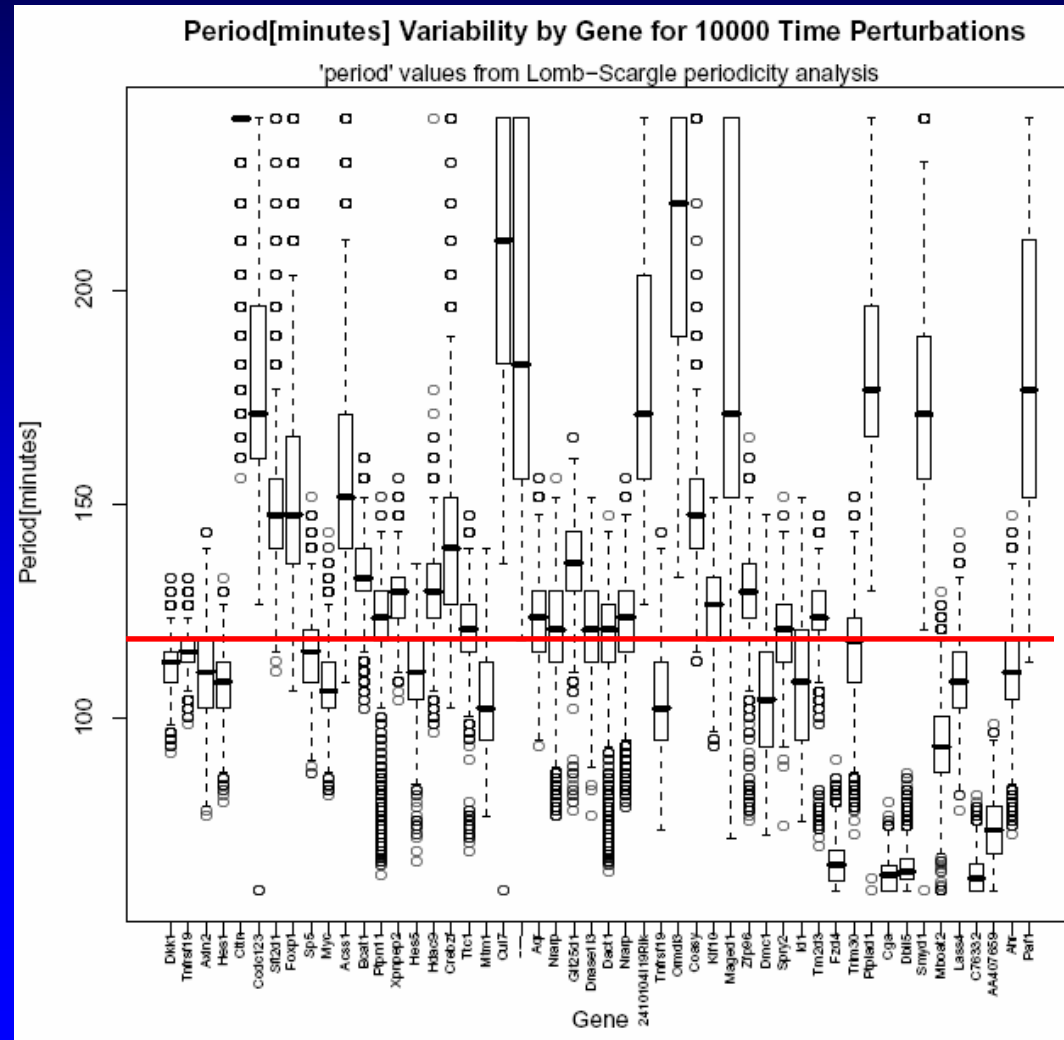


Resampled GeneChip Noise



# Somitogenesis Experiment

# Mouse (17 points)

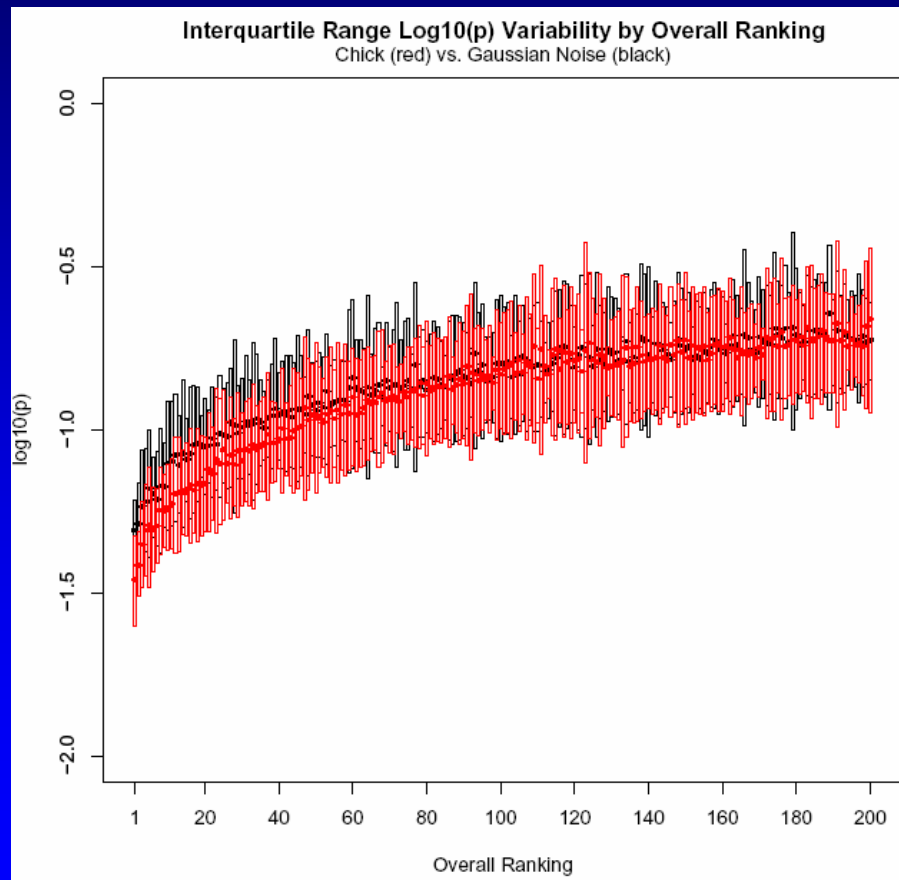


Mouse  
somite period  
is assumed to  
be 120 minutes

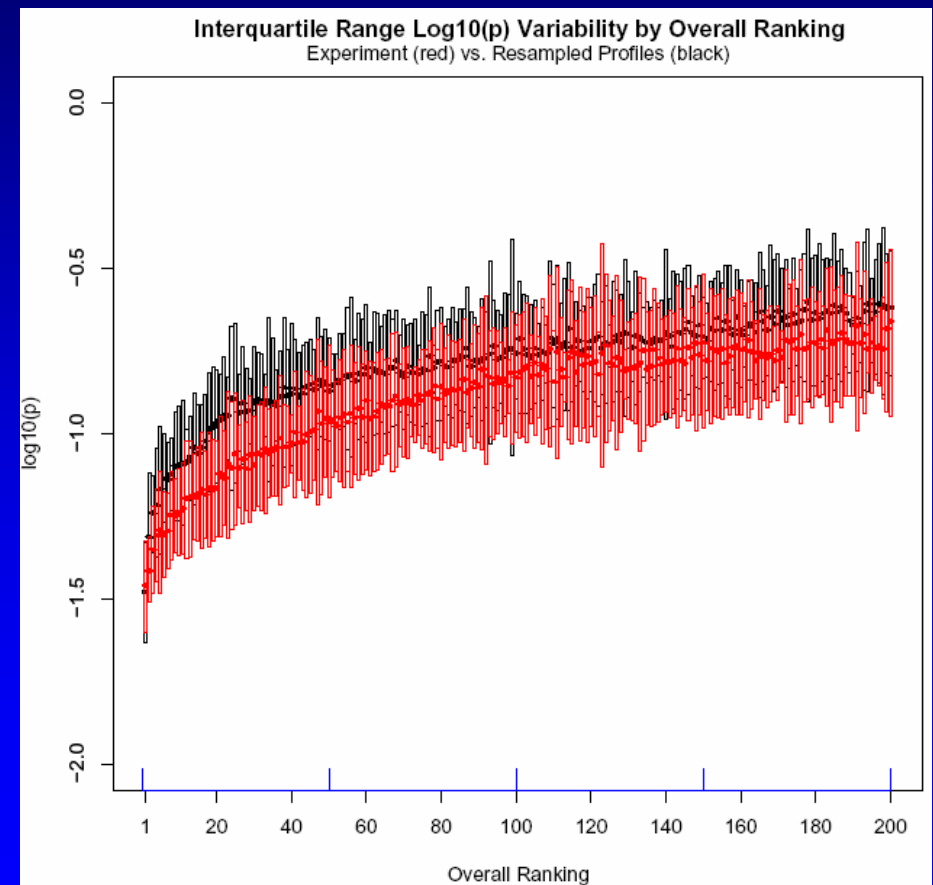
# Somitogenesis Experiment

## Chick

### Gaussian Noise



### Resampled GeneChip Noise





# Summary

- Common "time perturbation" methodology seems to be working for all species
- Simulated experiments can give insight into actual experiments
- Additional simulated experiments needed to understand mouse and chick results

# Acknowledgements

## Pourquoié Lab

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Mary-Lee Dequéant (Mouse)

Aurelie Krol (Chick)

Daniela Röllig (Zebrafish)

[Max Planck Institute]

## Bioinformatics

Arcady Mushegian

Jie Chen

[University of Missouri, Kansas City]