

MSU Center for Animal Functional Genomics and National Bovine Functional Genomics Consortium - NetScape

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MSU Center for Animal Functional Genomics and National Bovine Functional Genomics Consortium
EST and Microarray Database

Home Page Search Libraries Microarray Experiments BLAST Order Form About Libraries View Clusters Links Tools Contact Us

About Libraries

NBFGC	National Bovine Functional Genomics Consortium Library
BOTL	Bovine Total Leukocyte cDNA Library
POSM	Porcine Skeletal Muscle cDNA Library
MARC-Ovary	USDA Meat Animal Research Center Ovary cDNA Library
BEGG	Bovine Oocyte cDNA Library
BMAM	Bovine Mammary cDNA Library
TROUT	Rainbow Trout cDNA Library
PBL	Porcine Brain cDNA library
DSRL	Dog Subtracted Retinal cDNA Library

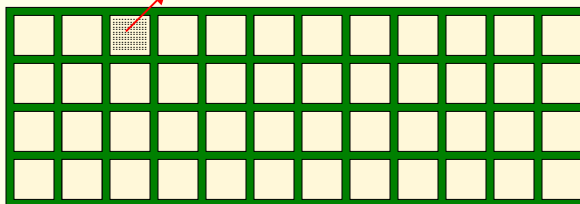
Web and Server System
developed by INCOGEN
<http://www.inco-gen.com>

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Center for Animal Functional Genomics Michigan State University

- cDNA microarray BOTL-3
- 709 bovine EST clone inserts
- 345 amplicons (known genes)

Slides: 4 x 12 patches
(9 x 9 spots /each)



Controls

β actin
RPL19
GAPDH
Lambda Q
DMSO
Blank
etc.

Different types of "replication" in microarray experiments

(Churchill, 2002)

1. Assessing measurement error

- ⇒ Multiple spots per gene on an array
- ⇒ Multiple arrays to study the same sample
- * Useful for quality control ...
But not too useful for inference on treatment effects!

2. Assessing biological variability

- ⇒ True replication

But... Should use appropriate error terms for testing treatments !

Example 1

- ⇒ Effect of diet on blood pressure



- ① Two individuals (one vegetarian; another non-vegetarian)
- ② Same gender, same age, nonsmoking, etc.
- ③ The diastolic pressure is measured 3 times
(consecutive days, for example)

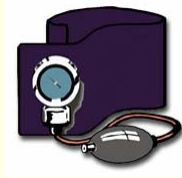
Vegan	Meat
80	80
95	100
110	90

Can we have a baseline and compare both groups?



Example 2

⇒ Multiple individuals per group



Vegan				Meat			
V_1	V_2	...	V_n	M_1	M_2	...	M_n
80	88	...	73	110	93	...	115

$$y_{ij} = \mu + G_i + \varepsilon_{ij}$$

$$\begin{cases} i = 1, 2 \\ j = 1, 2, \dots, n \end{cases}$$

ANOVA TABLE

SV	DF	E[MS]
Group	1	$\sigma_R^2 + n\phi_G$
Residual	$2(n - 1)$	σ_R^2
Total	$2n - 1$	

Example 3

⇒ Repeated measurements in each individual

Vegan				Meat			
V_1	V_2	...	V_n	M_1	M_2	...	M_n
80	88	...	73	110	93	...	115
105	89	...	79	106	105	...	90
90	100	...	75	105	89	...	97

$$y_{ij} = \mu + G_i + I_{ij} + \varepsilon_{ijk}$$

$$\begin{cases} i = 1, 2 \\ j = 1, 2, \dots, n \\ k = 1, 2, \dots, r \end{cases}$$

ANOVA TABLE

SV	DF	E[MS]
Group	1	$\sigma_S^2 + n\sigma_I^2 + nr\phi_G$
Indiv. Group	$2(n - 1)$	$\sigma_S^2 + r\sigma_I^2$
Residual	$2n(r - 1)$	σ_S^2
Total	$2nr - 1$	

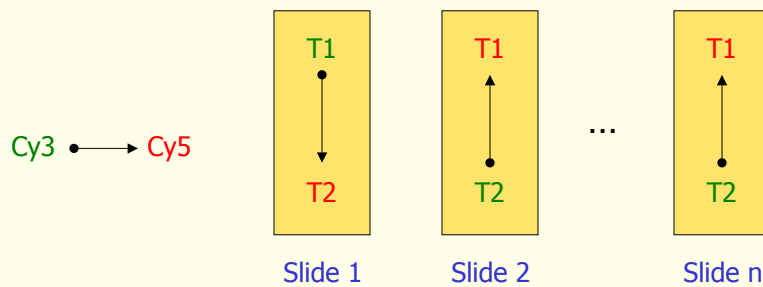


Back to microarray experiments ...

TWO-SAMPLE EXPERIMENTS

* Slides as blocks

- Two treatments (different experimental conditions)
- J 'biological' replications per treatment
- J slides total



TWO-SAMPLE EXPERIMENTS

★ One slide per experimental unity (individual or pooled mRNA)

★ Model:

$$\log(y_{gijkm}) = \mu_g + T_{gi} + B_{gj} + D_{gk} + TB_{gij} + \text{interactions} + S | B_{g(j)m} + \epsilon_{ijkm}$$

★ ANOVA:

Biological replication

SV	DF
Trt (T)	1
Animal (B)	J - 1
Dye (D)	1
T*B	J - 1
Others	ϕ_1
Spot (S B)	J(s - 1)
Residual	ϕ_2
Total	2sJ - 1

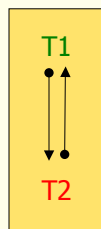
$$F_T = \frac{MS(T)}{MS(T * B)}$$

TWO-SAMPLE EXPERIMENTS

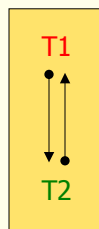
★ Slides as blocks

- Two treatments (different experimental conditions)
- J 'biological' replications per treatment
- 2J slides total (dye swap)

Cy3 → Cy5

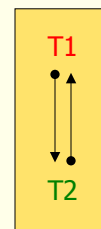


Slide 1



Slide 2

...



Slide n

TWO-SAMPLE EXPERIMENTS

★ Two slides (dye swap) per experimental unity

★ Model:

$$\log(y_{ijklm}) = \mu_g + T_{gi} + B_{gj} + D_{gk} + TB_{gij} + A | B_{g(j)l} + \text{interactions} + S | A_{g(l)m} + \varepsilon_{ijklm}$$

★ ANOVA:

Biological replication

SV	DF
Trt (T)	1
Animal (B)	J - 1
Dye (D)	1
T*B	J - 1
Array (A B)	J
Others	ϕ_1
Spot (S B)	2J(s - 1)
Residual	ϕ_2
Total	4sJ - 1

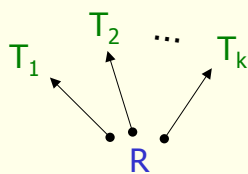
$$F_T = \frac{MS(T)}{MS(T * B)}$$

MULTIPLE SAMPLES (TREATMENTS)

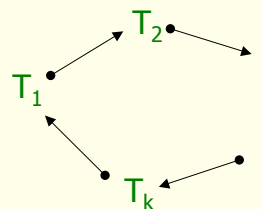
★ Incomplete block structure

- { k treatments (different experimental conditions)
- { n 'biological' replications per treatment
- { k × n slides total

Reference Design



Loop Design

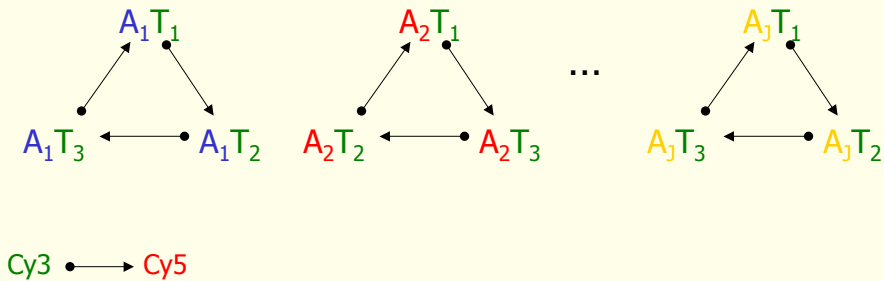


Cy3 → Cy5

LOOP EXPERIMENTS

- * Each animal under all trts (within a loop)

$\left\{ \begin{array}{l} I \text{ treatments} \\ J \text{ animals (or pools)} \\ I \times J \text{ slides total (} J \text{ loops of } I \text{ slides)} \end{array} \right.$
2 (I × J) if dye swap



LOOP EXPERIMENTS

- * Animal \Leftrightarrow Loop

- * Model:

$$\log(y_{ijklm}) = \mu_g + T_{gi} + B_{gj} + D_{gk} + TB_{gij} + A | B_{g(j)l} + \text{interactions} + S | A_{g(l)m} + \epsilon_{ijklm}$$

- * ANOVA:

SV	DF
Trt (T)	I - 1
Animal (B)	J - 1
Dye (D)	1
T*B	(I - 1)(J - 1)
Array (A B)	J(I - 1)
Others	ϕ_1
Spot (S B)	IJ(s - 1)
Residual	ϕ_2
Total	2sIJ - 1

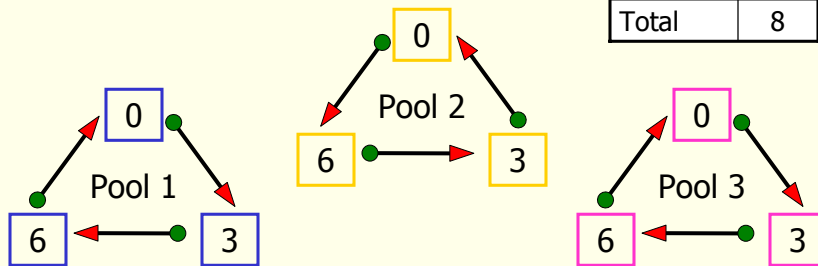
$$F_T = \frac{MS(T)}{MS(T*B)}$$

Cartilage Impact

Pooi-See Chang and Dr. Mike Orth

- Time after impact (0, 3 and 6 h)
- Three pools of three animals each
- Multiple Loop Design

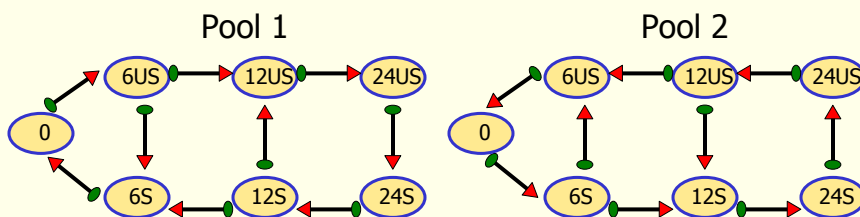
S.V.	d.f.
Pool	2
Time	2
Residual	4
Total	8



In Vitro Bovine Immune Response to *Trypanosoma brucei* Infection

Dr. Emmeline Hill and Dr. Paul Coussens

- Time course (0, 6, 12 and 24 h)
- Stimulated (S) and Non Stimulated (NS)
- Two pools of two animals

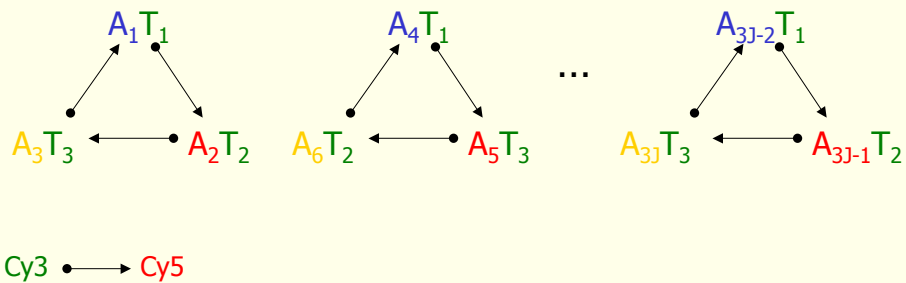


Error Term for testing Trt: Pool*Treatment (6 d.f.)

LOOP EXPERIMENTS

★ Each animal under one trt

- I treatments
- J animals per treatment (I × J animals in total)
- I × J slides total (J loops of I slides)



LOOP EXPERIMENTS

★ Model:

$$y_{gijklmn} = \mu_g + T_{gi} + B | T_{g(i)j} + D_{gk} + L_l + A | L_{g(l)m} + \text{interactions} + S | A_{g(m)n} + \epsilon_{ijklmn}$$

★ ANOVA:

SV	DF
Trt (T)	I - 1
Dye (D)	1
Animal (B T)	I(J - 1)
Loop (L)	J - 1
Array (A L)	J(I - 1)
Others	ϕ_1
Spot (S B)	IJ(s - 1)
Residual	ϕ_2
Total	2sIJ - 1

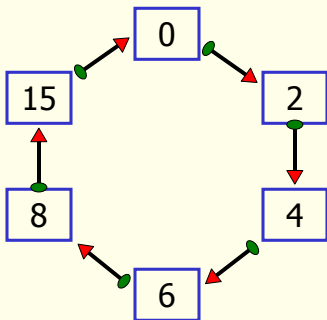
$$F_T = \frac{MS(T)}{MS(B|T)}$$

mRNA Profiles Post Infection

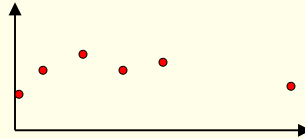
Dr. Line Morgills and Dr. Jeanne Burton

- Time after infection (0, 2, 4, 6, 8, 15 days)
- A different animal per time point
- Loop Design

Cy3 ● → Cy5



S.V.	d.f.
Linear	1
Quadratic	1
Lack of Fit	3
Total	5



OTHER EXPERIMENTAL DESIGNS

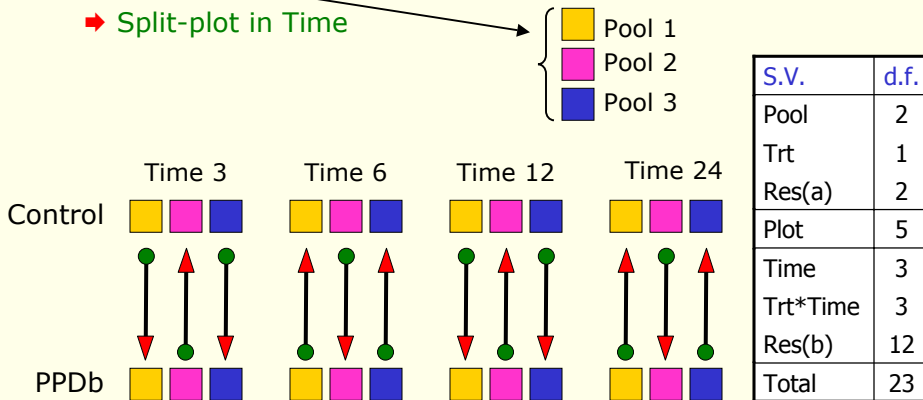
* SPLIT-PLOT

- ⇒ Within a CRD or RBD (on plots)
- ⇒ Split-Plot on Time

Bovine TB Experiment

Kieran Meade and Dr. Paul Coussens

- PPDb stimulation over time (3, 6 12, and 24 h)
- Three pools with two infected animals each
- Split-plot in Time

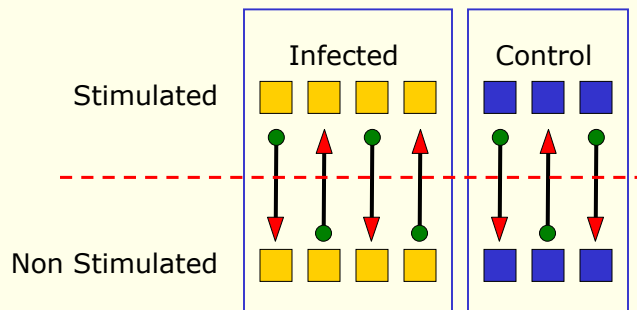


Peripheral Blood Mononuclear Cells from MPTb Infected Cows

Dr. Paul Coussens

- Infected ($n_1 = 4$) and Control ($n_2 = 3$) Cows
- Two treatments: Stimulation or not
- Split-plot Design

S.V.	d.f.
Group	1
Res(a)	5
Plot	6
Trt	1
Group*Trt	1
Res(b)	5
Total	13



Leptnin and IGF-I Intramammary Infusion

Brett Etchebarne and Dr. Mike VandeHaar

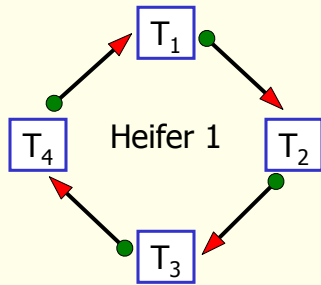
➔ Four (2 × 2) treatments, one in each quarter

➔ Six Heifers, Loop Design

➔ Treatments:

Trt	IGF	Lept
1	N	N
2	N	Y
3	Y	N
4	Y	Y

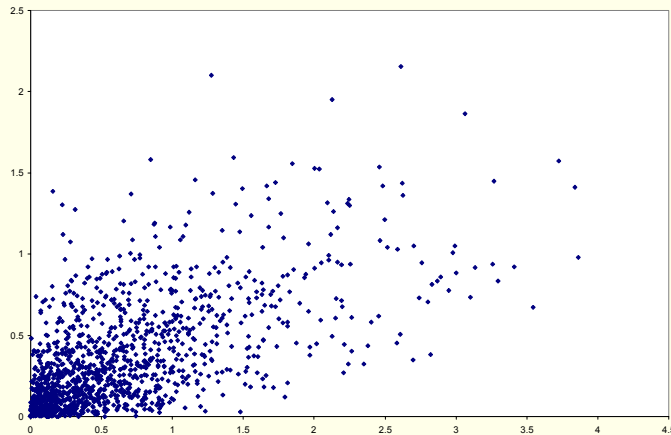
S.V.	d.f.
Dye	1
Trt	3
Heifer	5
Trt*Heifer	15
Array Heifer	18
Spot Array	48
Residual	53
Total	133



Leptnin and IGF-I Intramammary Infusion

Brett Etchebarne and Dr. Mike VandeHaar

➔ P-values (log scale) from fixed and mixed effects models



FINAL REMARKS

- ⇒ Experimental Design
- ⇒ Technical Replication:
 - Measurement error assessment
 - Future allocation of sampling efforts
- ⇒ Biological replication & Error variance
- ⇒ Borrowing information across genes (variance)

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