

## One-Way ANOVA for Fitness Response in *S.cerevisiae* against Mitochondrial Haplotype

Meghan Lenhardt

In eukaryotic cells, it is known that both the nucleus and the mitochondria possess genetic material crucial to proper cell function. In order to study the response effect on fitness of mitochondrial haplotype in yeast, we have switched out three different mitochondria into one nuclear background and measured any change in growth rates. Since yeast can ferment, it is the most appropriate model organism for this study as it is capable of surviving mitochondrial “swapping”.

One-Way ANOVA with Fixed Effects Model:

- ANOVA allows us to utilize a broad range of statistical methods that fall under the GLM group of analyses. Independent variables (here,  $V_{max}$  or growth rate) involve membership in classes. When more than two classes are present, this test allows extension of the simpler t-test strategy of mean comparison.

Data Structure:

- K groups with not necessarily the same number of observations and different means
- Let index (i,j) indicate the ith column and the jth row (object)

Assumptions:

Model:

- Hypotheses
  - Null=  $\alpha(i)=0$  for all i
  - Alternative= $\alpha(i) \neq 0$
  - Here  $\alpha(i)$  is NOT the same as type 1 error rate and is only a measure of how different any sample is from the grand mean.
- Grand mean (GM)= average ( $\mu$ ) of multiple sample  $\mu$ 's

Prototype in R:

```
> vmax=read.table("vmax.txt",header=TRUE)
> vmax
```

	Strain	Nuclear	Mito	Normalized.Vmax
1	F2e4	F2	e4	1.1788704
2	F2e4	F2	e4	1.1307913
3	F2e4	F2	e4	1.1456995
4	F2f1	F2	f1	1.0360538
5	F2f1	F2	f1	1.0017235
6	F2f1	F2	f1	1.0570134
7	F2f1	F2	f1	1.0052576
8	F2f1	F2	f1	0.9754644
9	F2f1	F2	f1	1.0427620
10	F2f2	F2	f2	1.0530383
11	F2f2	F2	f2	0.7393673
12	F2f2	F2	f2	1.0967643
13	F2f2	F2	f2	1.0241851
14	F2f2	F2	f2	1.0255871
15	F2f2	F2	f2	0.9723098

```

> attach(vmax)

> names(vmax)
[1] "Strain"          "Nuclear"          "Mito"             "Normalized.vmax"

> N<-factor(Nuclear)
> N
[1] F2 F2 F2 F2 F2 F2 F2 F2 F2 F2 F2 F2 F2 F2 F2
Levels: F2

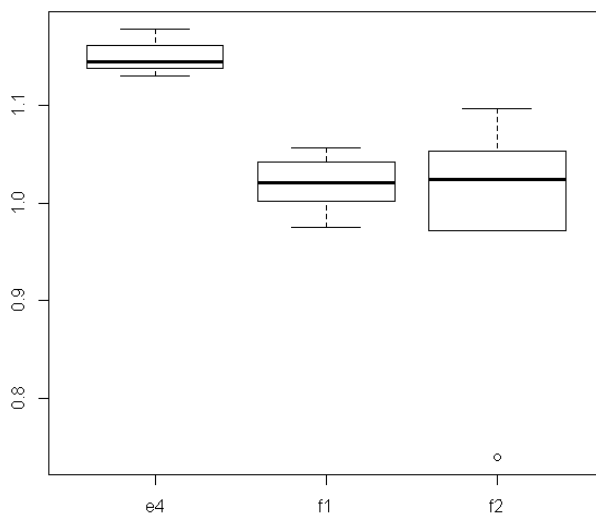
> M<-factor(Mito)
> M
[1] e4 e4 e4 f1 f1 f1 f1 f1 f1 f2 f2 f2 f2 f2 f2
Levels: e4 f1 f2

> NVM=Normalized.vmax
> NVM
[1] 1.1788704 1.1307913 1.1456995 1.0360538 1.0017235 1.0570134 1.0052576
0.9754644
[9] 1.0427620 1.0530383 0.7393673 1.0967643 1.0241851 1.0255871 0.9723098

> model=aov(NVM~M)
> summary(model)
          Df Sum Sq Mean Sq F value Pr(>F)
M           2  0.05709  0.028544   3.951  0.048 *
Residuals  12  0.08669  0.007224
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> interaction.plot(M,NVM)

```



- Test statistic

- Ratio of “between” versus “within” mean squares

$$F := \frac{MS_B}{MS_W}$$

- If Null is true, then  $F \sim F_{(k-1), (N-k)}$  where  $k = \#$  of classes,  $N =$  total observations

- Critical Value
  - Set type I error
  - $CV = qF[1-\alpha, (k-1), (N-k)]$
- Decision Rule: if  $F > CV$ , then reject null
- Probability value:  $1 - pF[F, (k-1), (N-k)]$
- Sum of Squares: square of difference of each class mean from the grand mean.
  - sample estimate of alpha squared

Results:

- $Pr(>F) = 0.048 < \alpha(0.05)$ ; reject the null.
- A significant difference in means exists between the three levels of M versus one level of N.
- In other words, an interactive relationship exists between mitochondrial haplotype and nuclear background with regards to fitness in yeast (although with this small data set, the test is not particularly convincing and is very close to the Type I error cutoff).