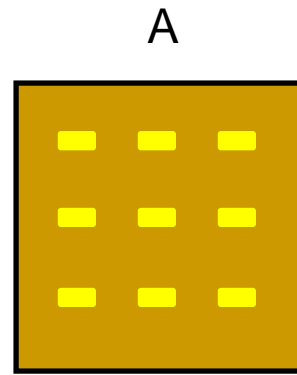
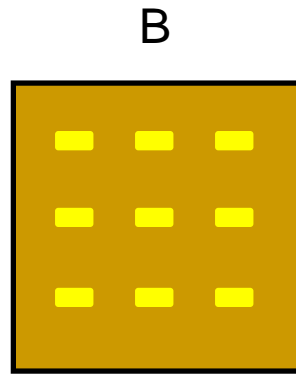
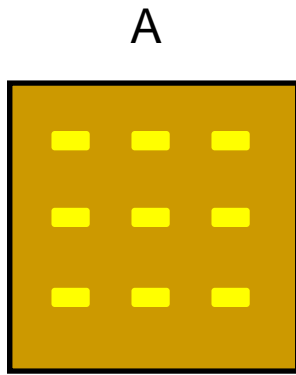
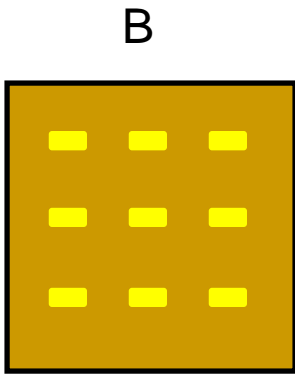
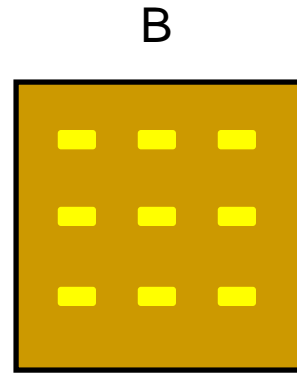
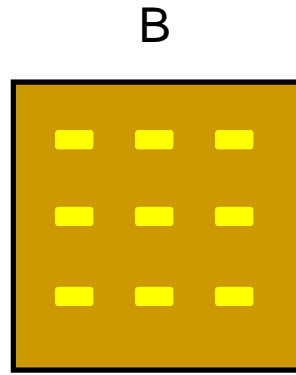
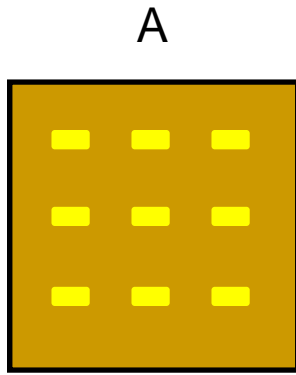
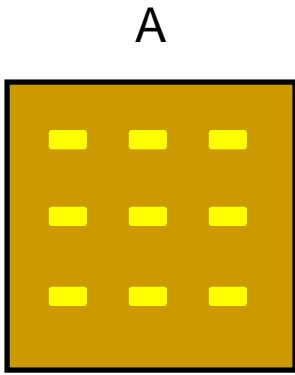


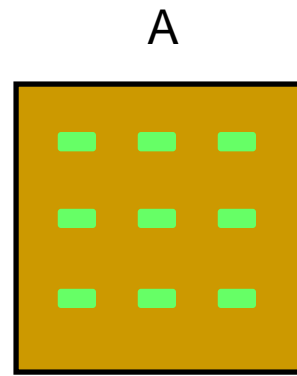
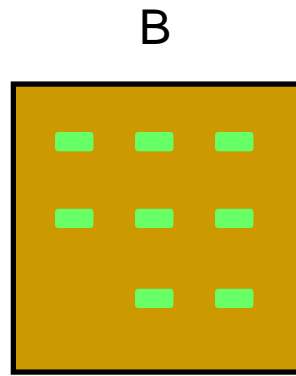
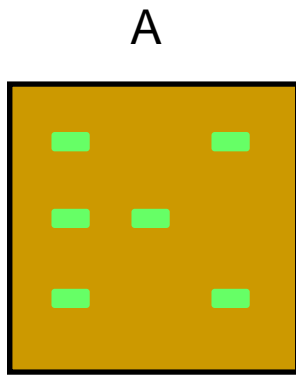
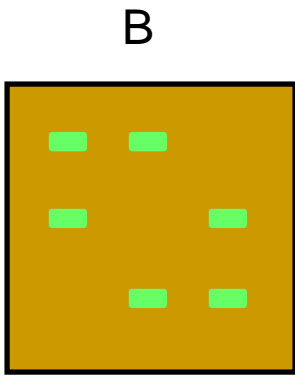
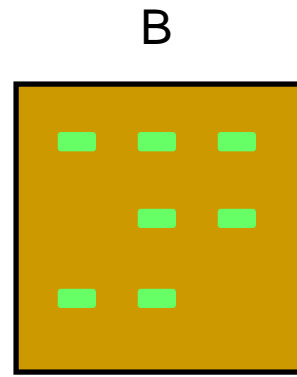
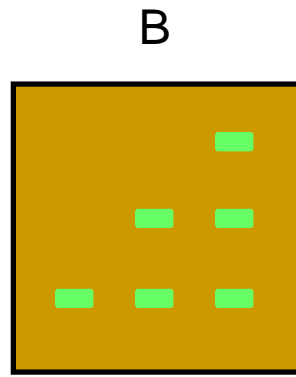
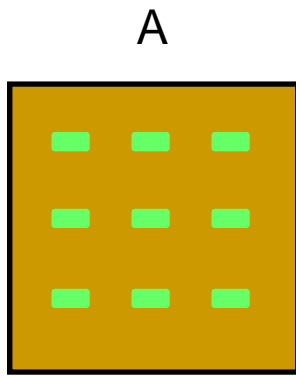
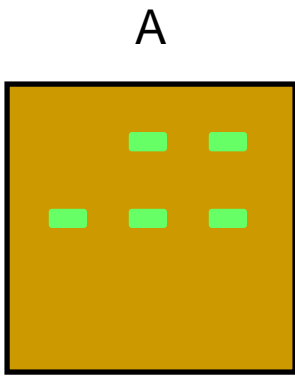
An Example Analysis Based on the Aitken Model

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An Example Experiment

Researchers were interested in comparing the dry weight of maize seedlings from two different genotypes. For each genotype, nine seeds were planted in each of four trays. The eight trays in total were randomly positioned in a growth chamber. Three weeks after the emergence of the first seedling, emerged seedlings were harvested from each tray and weighed together after drying to obtain one weight for each tray. Although nine seeds were planted in each tray, fewer than nine seedlings emerged in many of the trays. Thus, weights were recorded on a per seedling basis, and the number of seedlings that emerged in each tray was also recorded.





```
d=read.delim(
"http://www.public.iastate.edu/~dnett/S511/SeedlingDryWeight.txt")
```

d

	Genotype	Tray	AverageWeight PerSeedling	NumberOf Seedlings
1	A	1	10	5
2	A	2	18	9
3	A	3	14	6
4	A	4	19	9
5	B	5	13	6
6	B	6	10	7
7	B	7	15	6
8	B	8	9	8

```
y=d[,3]
geno=d[,1]
count=d[,4]
```

```
X=matrix(model.matrix(~geno),nrow=8)
```

```
X
```

```
      [,1] [,2]
[1,]    1    0
[2,]    1    0
[3,]    1    0
[4,]    1    0
[5,]    1    1
[6,]    1    1
[7,]    1    1
[8,]    1    1
```

```
V=diag(1/count)
```

```
#Compute  $V^{-.5}$ 
```

```
A=diag(sqrt(count))
```

```
#In general, we could compute  $V^{-.5}$  as follows:
```

```
e=eigen(V)
```

```
A=e$vector%*%diag(1/sqrt(e$values))%*%t(e$vector)
```

#Now transform y and X to z and W.

$z = A \% * \% y$

$W = A \% * \% X$

$o = \text{lm}(z \sim W - 1)$

`summary(o)`

Call:

`lm(formula = z ~ W - 1)`

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
W1	16.103	1.650	9.763	6.64e-05	***
W2	-4.622	2.376	-1.946	0.0997	.

Residual standard error: 8.883 on 6 degrees of freedom

Multiple R-squared: 0.959, Adjusted R-squared: 0.9454

F-statistic: 70.21 on 2 and 6 DF, p-value: 6.882e-05

```
#Because V is diagonal in this case, we can
#alternatively analyze using lm and the weights
#argument.
```

```
o2=lm(y~geno,weights=count)
summary(o2)
```

Call:

```
lm(formula = y ~ geno, weights = count)
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	16.103	1.650	9.763	6.64e-05	***
genoB	-4.622	2.376	-1.946	0.0997	.

```
Residual standard error: 8.883 on 6 degrees of freedom
Multiple R-squared: 0.3868, Adjusted R-squared: 0.2847
F-statistic: 3.785 on 1 and 6 DF, p-value: 0.09966
```

```
#The unweighted (OLS) analysis is inferior in this
#case. The OLS estimator of beta is still unbiased,
#but it's variance is larger than that of the GLS
#estimator. OLS inferences regarding beta are not,
#in general, valid.
```

```
o3=lm(y~geno)
```

```
summary(o3)
```

```
Call:
```

```
lm(formula = y ~ geno)
```

```
Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	15.250	1.750	8.714	0.000126	***
genoB	-3.500	2.475	-1.414	0.207031	

```
Residual standard error: 3.5 on 6 degrees of freedom
```

```
Multiple R-squared: 0.25, Adjusted R-squared: 0.125
```

```
F-statistic: 2 on 1 and 6 DF, p-value: 0.2070 11
```