

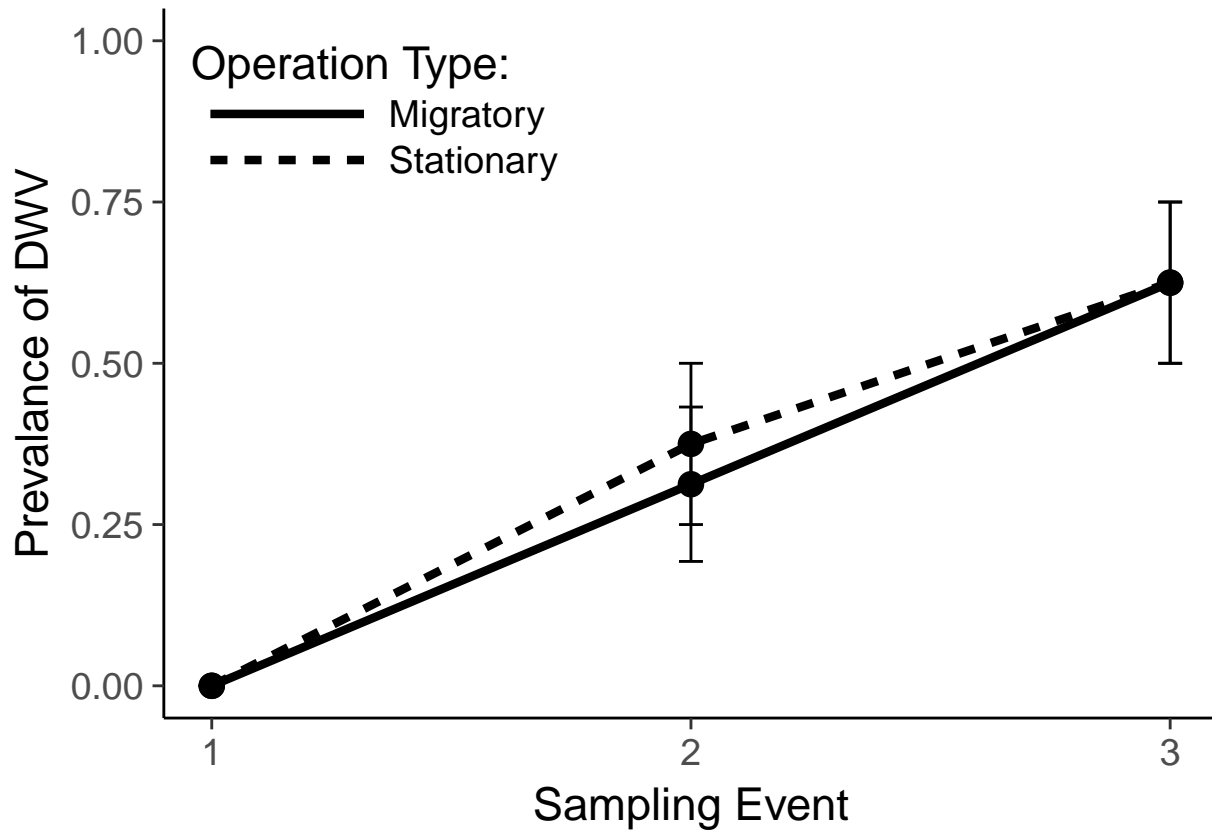
Migratory Stationary Technical Report

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EXPERIMENT I - (MIGRATORY vs STATIONARY)

Deformed Wing Virus Prevalence:



```
##      Treatment SamplingEvent  n  mean      sd      se
## 1  Migratory                1 16 0.0000 0.0000000 0.0000000
## 2  Migratory                2 16 0.3125 0.4787136 0.1196784
## 3  Migratory                3 16 0.6250 0.5000000 0.1250000
## 4  Stationary               1 16 0.0000 0.0000000 0.0000000
## 5  Stationary               2 16 0.3750 0.5000000 0.1250000
## 6  Stationary               3 16 0.6250 0.5000000 0.1250000
```

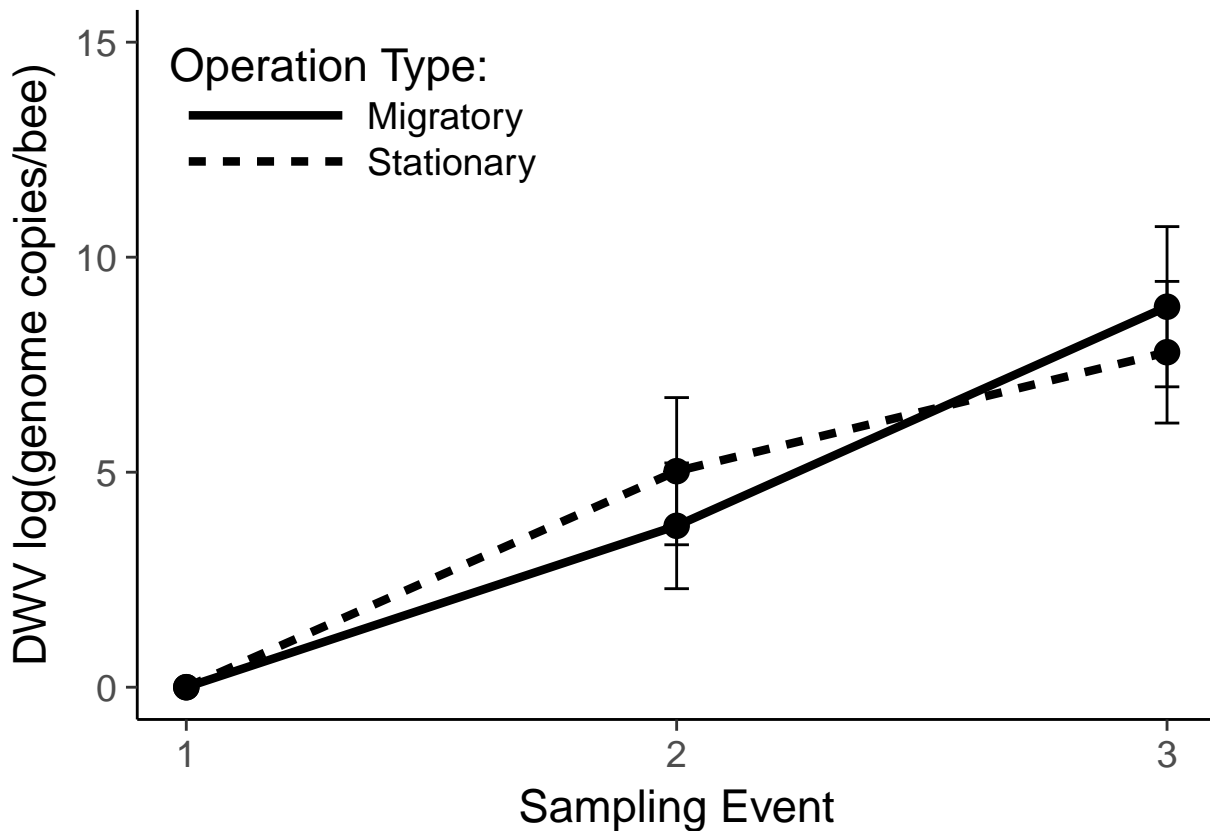
Initial Time Step One Analysis (Chi Square)

```
##
## Chi-squared test for given probabilities
##
## data:  x
## X-squared = 0, df = 1, p-value = 1
```

Full repeated measures Analysis (GLM)

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: DWVbinary
##               Chisq Df Pr(>Chisq)
## Treatment           0.0670  1    0.7958
## SamplingEvent       15.8045  1  7.023e-05 ***
## Treatment:SamplingEvent 0.0235  1    0.8781
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Deformed Wing Virus Load:



##	Treatment	SamplingEvent	n	mean	sd	se
## 1	Migratory	1	16	0.000000	0.000000	0.000000
## 2	Migratory	2	16	3.753490	5.849113	1.462278
## 3	Migratory	3	16	8.848642	7.451475	1.862869
## 4	Stationary	1	16	0.000000	0.000000	0.000000
## 5	Stationary	2	16	5.023841	6.845731	1.711433
## 6	Stationary	3	16	7.789912	6.587571	1.646893

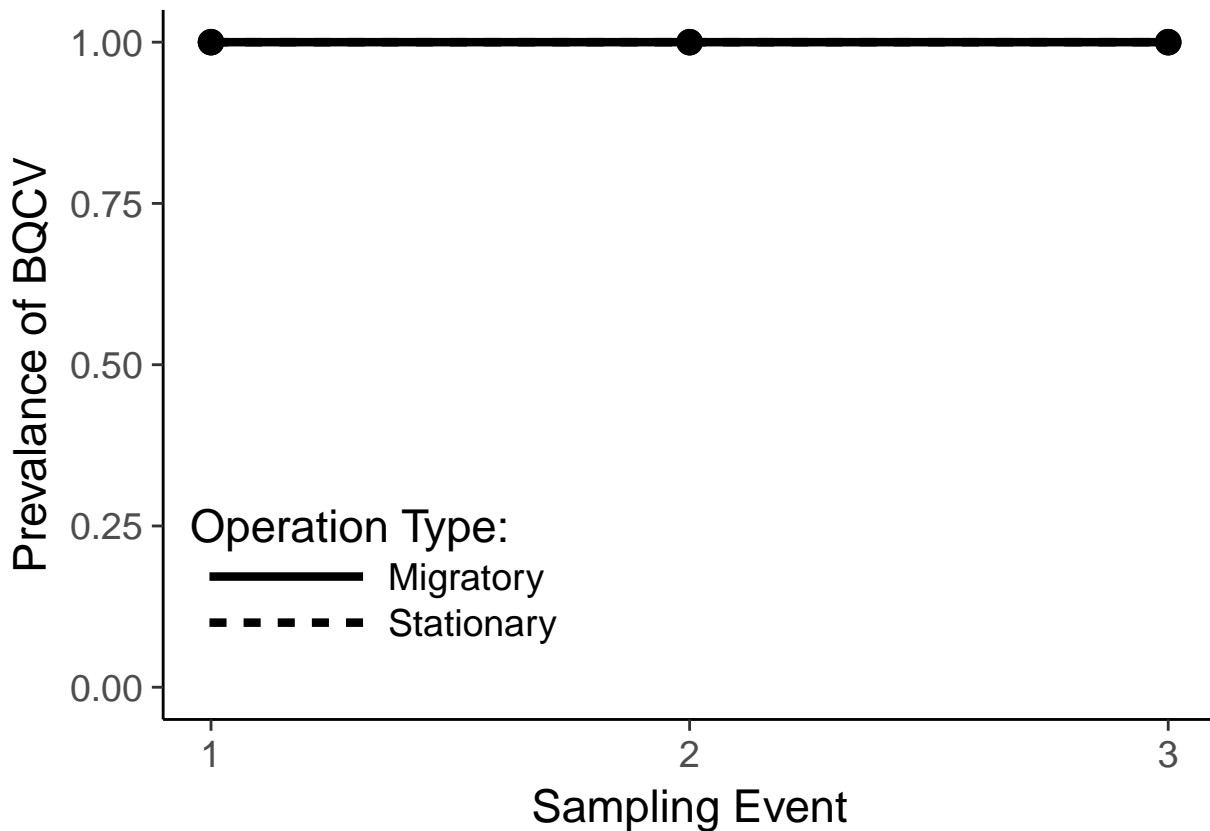
Initial Time Step One Analysis (ANOVA)

##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## MigStatExp_1_T1\$Treatment	1	0	0		
## Residuals	30	0	0		

Full repeated measures Analysis (Rep ANOVA)

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: logDWV
##               Chisq Df Pr(>Chisq)
## Treatment           0.0037  1    0.9516
## SamplingEvent       39.3276  1  3.583e-10 ***
## Treatment:SamplingEvent 0.1592  1    0.6899
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Black Queen Cell Virus Prevalence:



```
## Treatment SamplingEvent n mean sd se
## 1 Migratory           1 16    1 0 0
## 2 Migratory           2 16    1 0 0
## 3 Migratory           3 16    1 0 0
## 4 Stationary          1 16    1 0 0
## 5 Stationary          2 16    1 0 0
## 6 Stationary          3 16    1 0 0
```

Initial Time Step One Analysis (Chi Square)

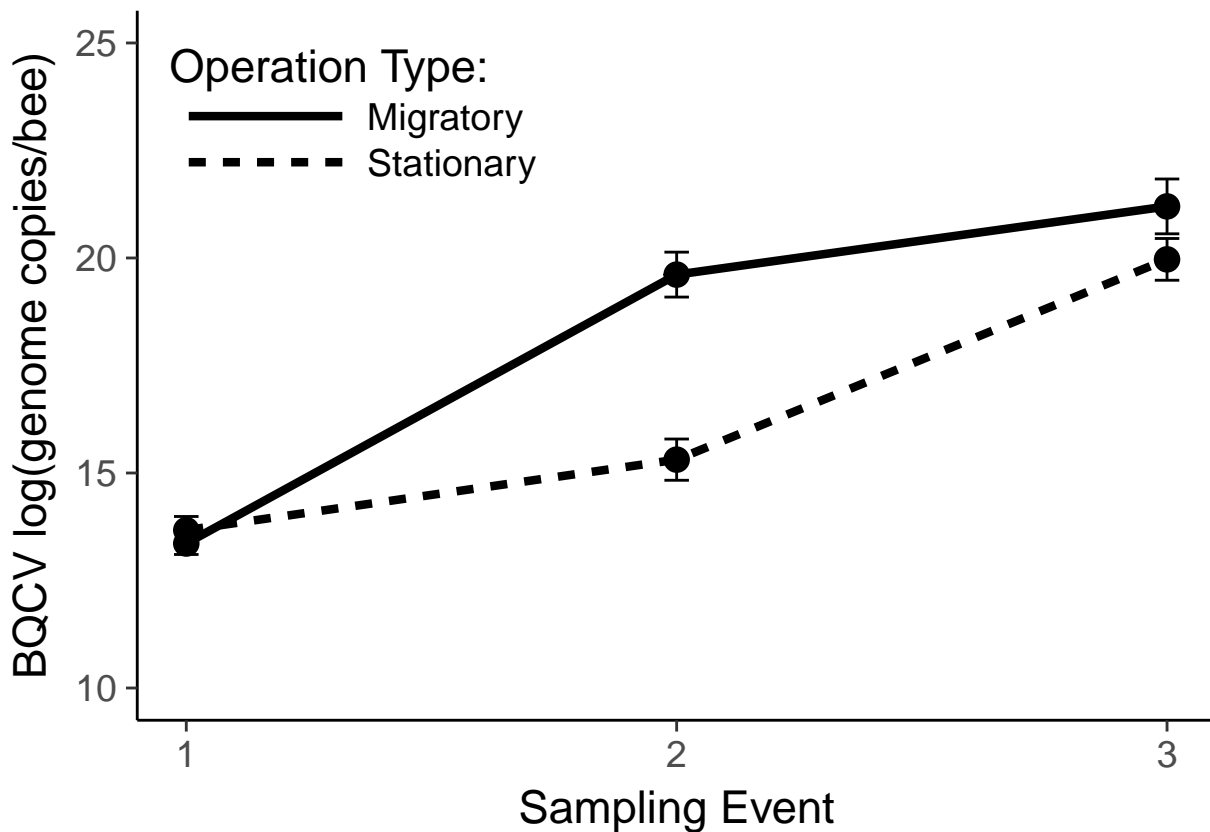
```
##
## Chi-squared test for given probabilities
##
```

```
## data: x
## X-squared = 0, df = 1, p-value = 1
```

Full repeated measures Analysis (GLM)

```
#BQCV prevalence using glmer
#Fullmod2 <- glmer(data=MigStatExp_1, formula = BQCVbinary~Treatment * SamplingEvent + (1|ID), family =
#Anova(Fullmod2)
```

Black Queen Cell Virus Load:



##	Treatment	SamplingEvent	n	mean	sd	se
## 1	Migratory	1	16	13.36015	1.021698	0.2554245
## 2	Migratory	2	16	19.61332	2.090001	0.5225002
## 3	Migratory	3	16	21.19942	2.549945	0.6374862
## 4	Stationary	1	16	13.67099	1.269596	0.3173990
## 5	Stationary	2	16	15.31059	1.918286	0.4795715
## 6	Stationary	3	16	19.96779	1.942679	0.4856697

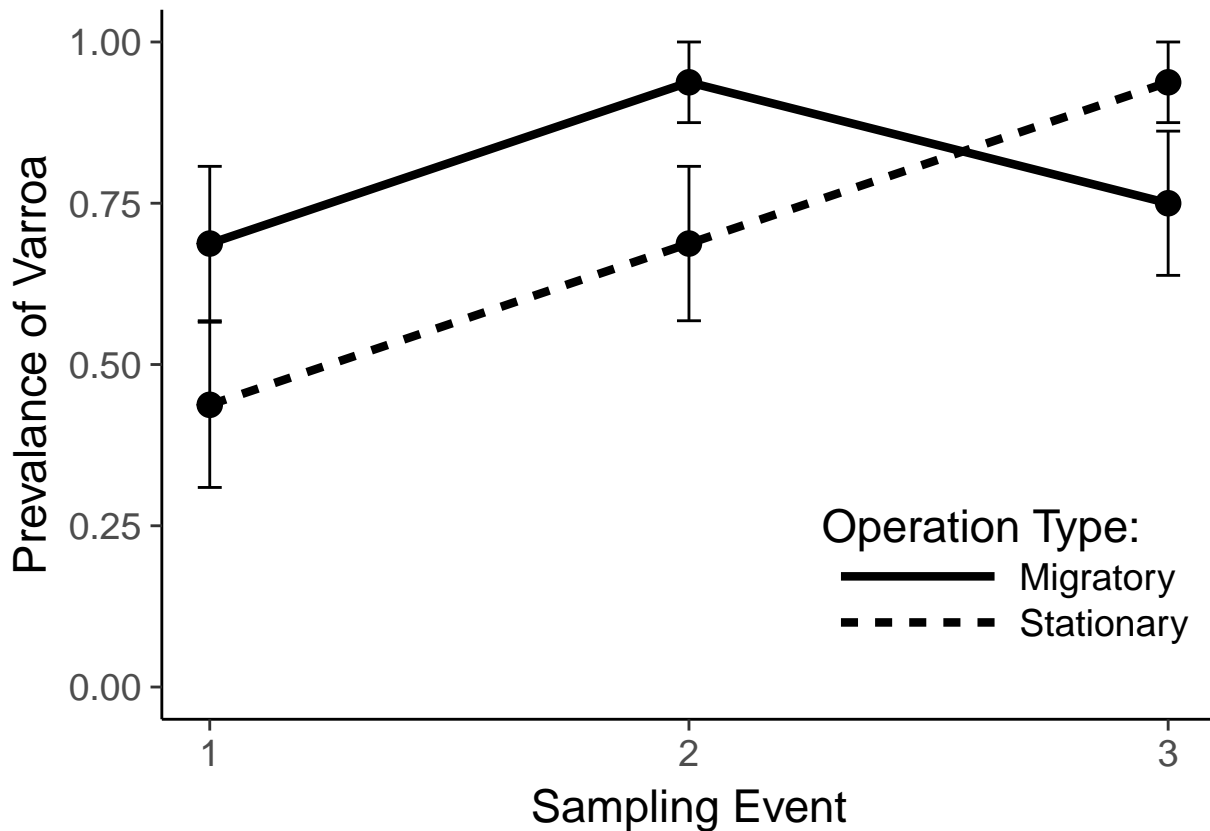
Initial Time Step One Analysis (ANOVA)

##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## MigStatExp_1_T1\$Treatment	1	0.77	0.773	0.582	0.451
## Residuals	30	39.84	1.328		

Full repeated measures Analysis (Rep ANOVA)

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: logBQCV
##               Chisq Df Pr(>Chisq)
## Treatment      16.4884  1  4.895e-05 ***
## SamplingEvent  187.2346  1 < 2.2e-16 ***
## Treatment:SamplingEvent  2.2293  1  0.1354
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Varroa Mite Prevalence:



##	Treatment	SamplingEvent	n	mean	sd	se
## 1	Migratory	1	16	0.6875	0.4787136	0.1196784
## 2	Migratory	2	16	0.9375	0.2500000	0.0625000
## 3	Migratory	3	16	0.7500	0.4472136	0.1118034
## 4	Stationary	1	16	0.4375	0.5123475	0.1280869
## 5	Stationary	2	16	0.6875	0.4787136	0.1196784
## 6	Stationary	3	16	0.9375	0.2500000	0.0625000

Initial Time Step One Analysis (Chi Square)

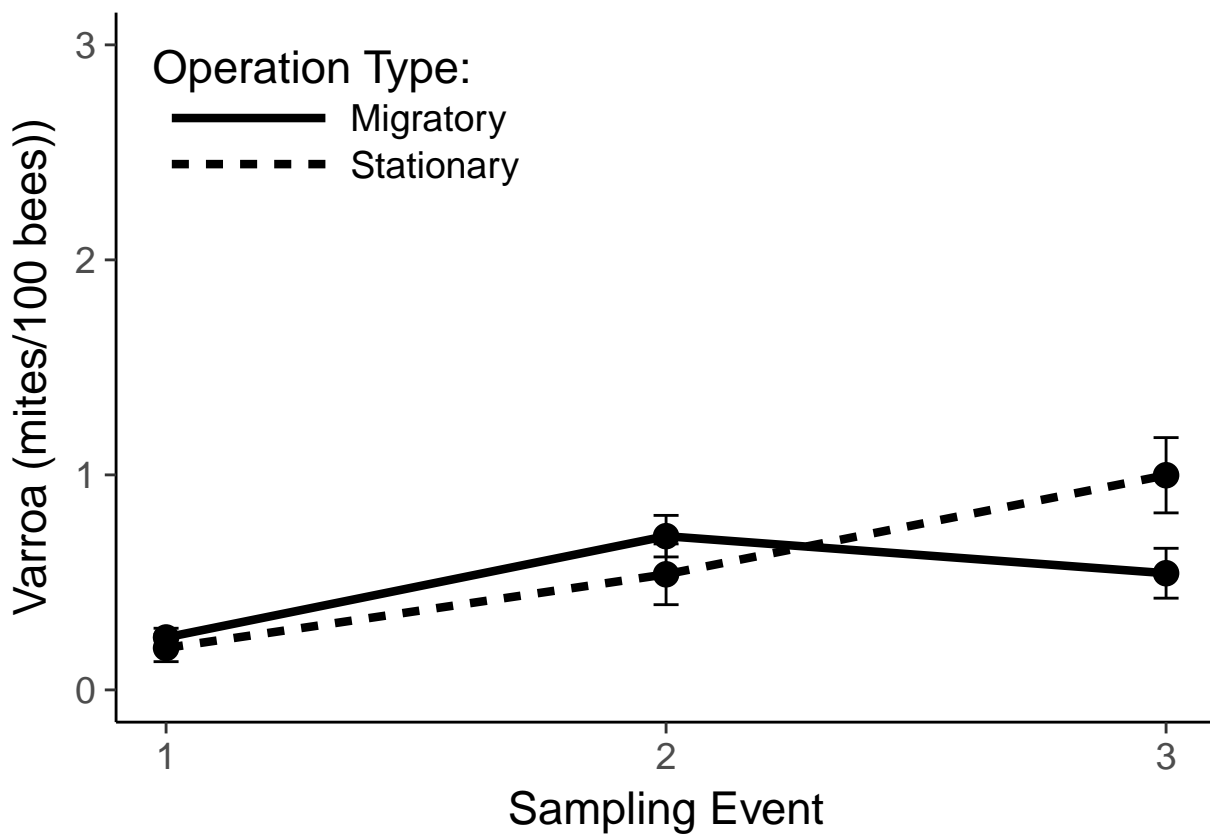
```
##
## Pearson's Chi-squared test with Yates' continuity correction
##
```

```
## data: x
## X-squared = 1.1429, df = 1, p-value = 0.285
```

Full repeated measures Analysis (GLM)

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: VarroaBinary
##               Chisq Df Pr(>Chisq)
## Treatment      1.2899  1    0.25607
## SamplingEvent   4.8963  1    0.02691 *
## Treatment:SamplingEvent 3.2100  1    0.07319 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Varroa Mite Load:



```
##   Treatment SamplingEvent  n    mean      sd      se
## 1 Migratory              1 16 0.2438021 0.1716146 0.04290364
## 2 Migratory              2 16 0.7150268 0.3865965 0.09664914
## 3 Migratory              3 16 0.5426076 0.4639379 0.11598447
## 4 Stationary             1 16 0.1948285 0.2539957 0.06349893
## 5 Stationary             2 16 0.5376645 0.5653539 0.14133847
## 6 Stationary             3 16 0.9983903 0.7002526 0.17506314
```

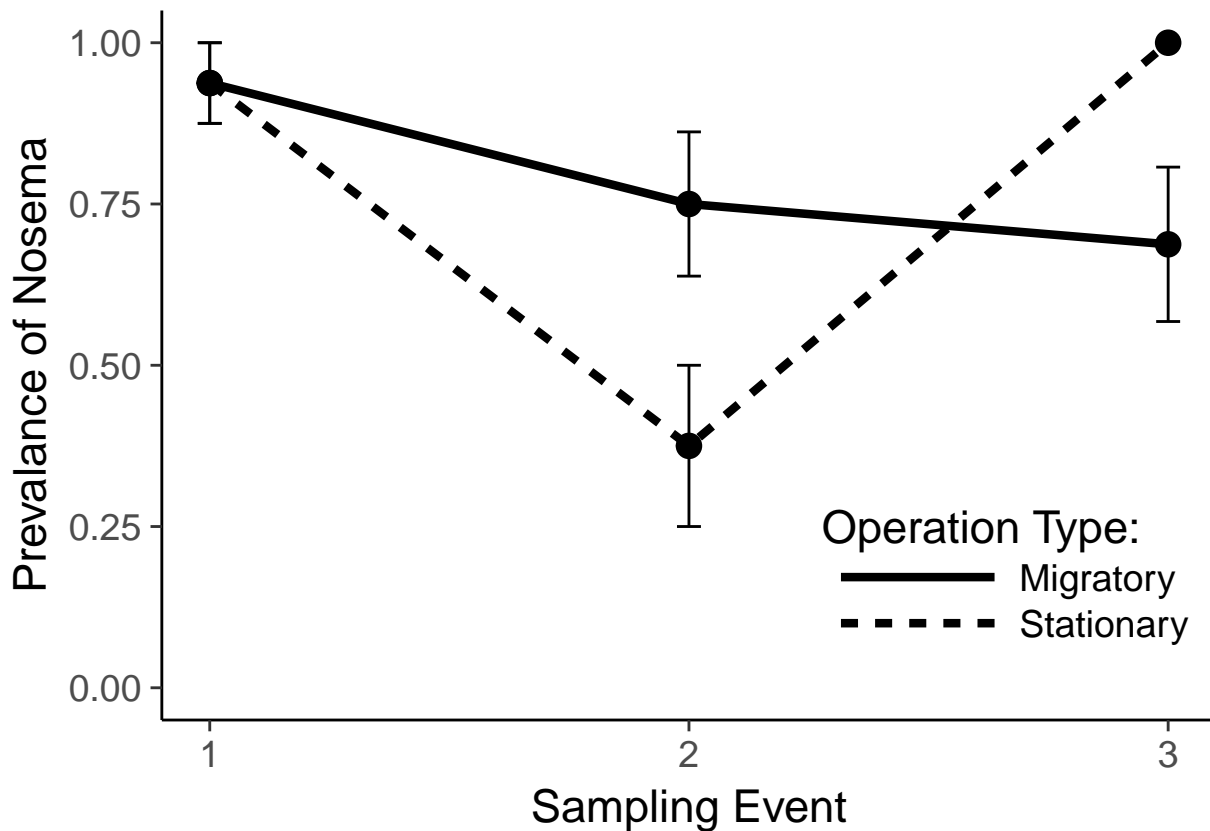
Initial Time Step One Analysis (ANOVA)

```
##               Df Sum Sq Mean Sq F value Pr(>F)
## MigStatExp_1_T1$Treatment  1 0.0192 0.01919    0.408  0.528
## Residuals                30 1.4095 0.04698
```

Full repeated measures Analysis (Rep ANOVA)

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: Varroa
##               Chisq Df Pr(>Chisq)
## Treatment          0.4134  1    0.52024
## SamplingEvent      30.1850  1   3.927e-08 ***
## Treatment:SamplingEvent  6.3285  1    0.01188 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Nosema Prevalence:



```
## Treatment SamplingEvent n mean sd se
## 1 Migratory          1 16 0.9375 0.2500000 0.0625000
## 2 Migratory          2 16 0.7500 0.4472136 0.1118034
## 3 Migratory          3 16 0.6875 0.4787136 0.1196784
## 4 Stationary         1 16 0.9375 0.2500000 0.0625000
## 5 Stationary         2 16 0.3750 0.5000000 0.1250000
## 6 Stationary         3 16 1.0000 0.0000000 0.0000000
```

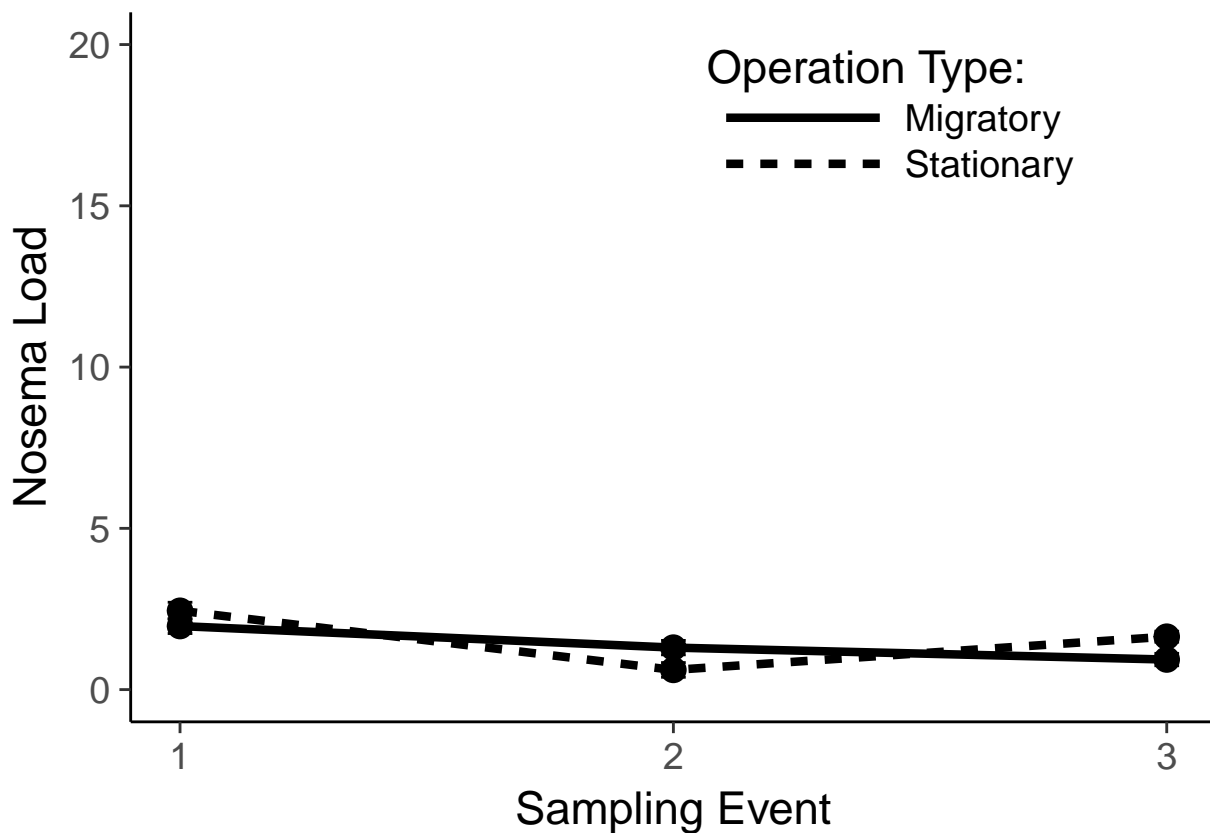
Initial Time Step One Analysis (Chi Square)

```
##  
## Pearson's Chi-squared test  
##  
## data: x  
## X-squared = 0, df = 1, p-value = 1
```

Full repeated measures Analysis (GLM)

```
## Analysis of Deviance Table (Type II Wald chisquare tests)  
##  
## Response: NosemaBinary  
##  
##           Chisq Df Pr(>Chisq)  
## Treatment      0.0367 1      0.8481  
## SamplingEvent    0.6236 1      0.4297  
## Treatment:SamplingEvent 2.3758 1      0.1232
```

Nosema Load:



```
## Treatment SamplingEvent n mean sd se  
## 1 Migratory 1 16 1.9698865 0.9254476 0.2313619  
## 2 Migratory 2 16 1.3018461 0.8902946 0.2225737  
## 3 Migratory 3 16 0.9318390 0.7672246 0.1918061  
## 4 Stationary 1 16 2.4448214 1.0472956 0.2618239  
## 5 Stationary 2 16 0.6102725 0.9093340 0.2273335  
## 6 Stationary 3 16 1.6414654 0.6815193 0.1703798
```

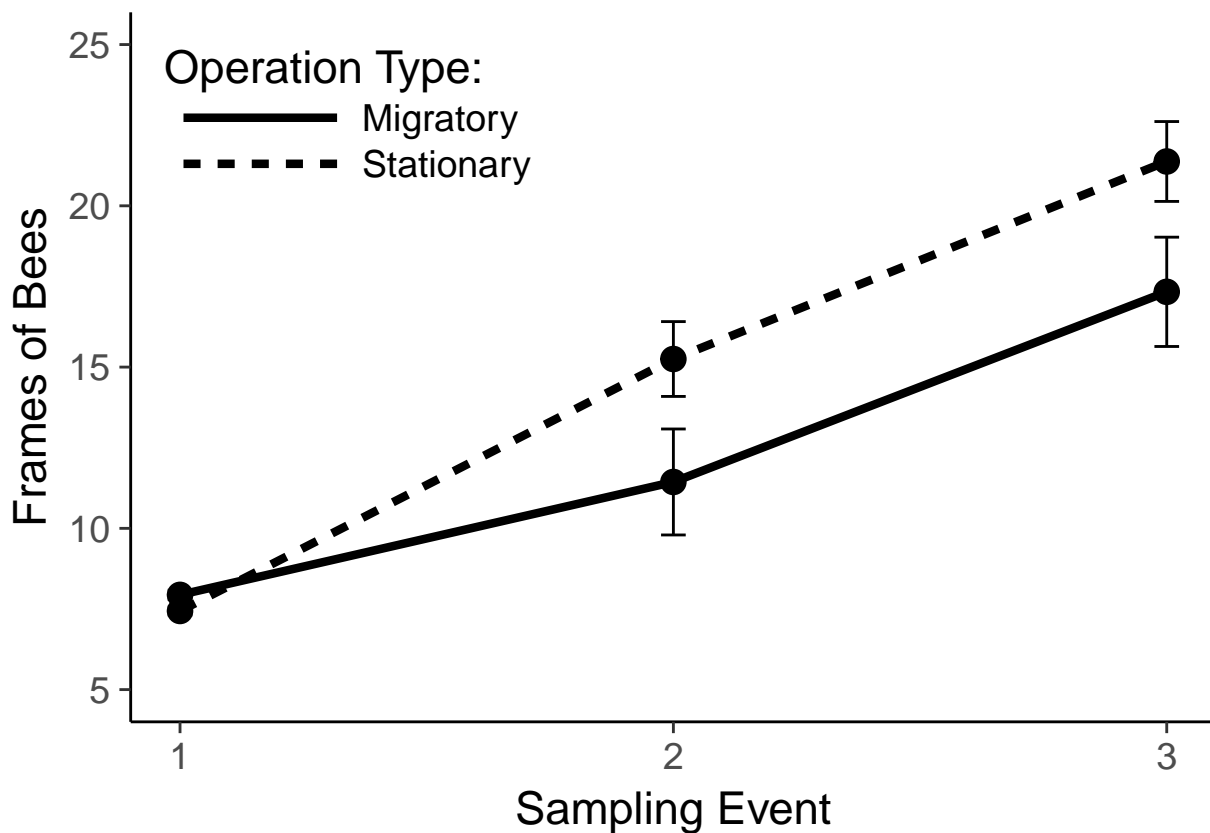

Initial Time Step One Analysis (ANOVA)

```
##                               Df Sum Sq Mean Sq F value Pr(>F)
## MigStatExp_1_T1$Treatment    1  1.805   1.8045   1.848  0.184
## Residuals                    30 29.299   0.9766
```

Full repeated measures Analysis (Rep ANOVA)

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: NosemaLoadRecount
##                               Chisq Df Pr(>Chisq)
## Treatment                     0.6448  1  0.4219688
## SamplingEvent                 13.7016  1  0.0002143 ***
## Treatment:SamplingEvent       0.2226  1  0.6370876
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Frames of Bees:



```
## Treatment SamplingEvent n mean sd se
## 1 Migratory 1 16 7.93750 0.5737305 0.1434326
## 2 Migratory 2 16 11.43750 6.5723537 1.6430884
## 3 Migratory 3 16 17.33333 6.7788186 1.6947046
## 4 Stationary 1 16 7.43750 0.5123475 0.1280869
## 5 Stationary 2 16 15.25000 4.6404023 1.1601006
## 6 Stationary 3 16 21.37500 4.9514308 1.2378577
```

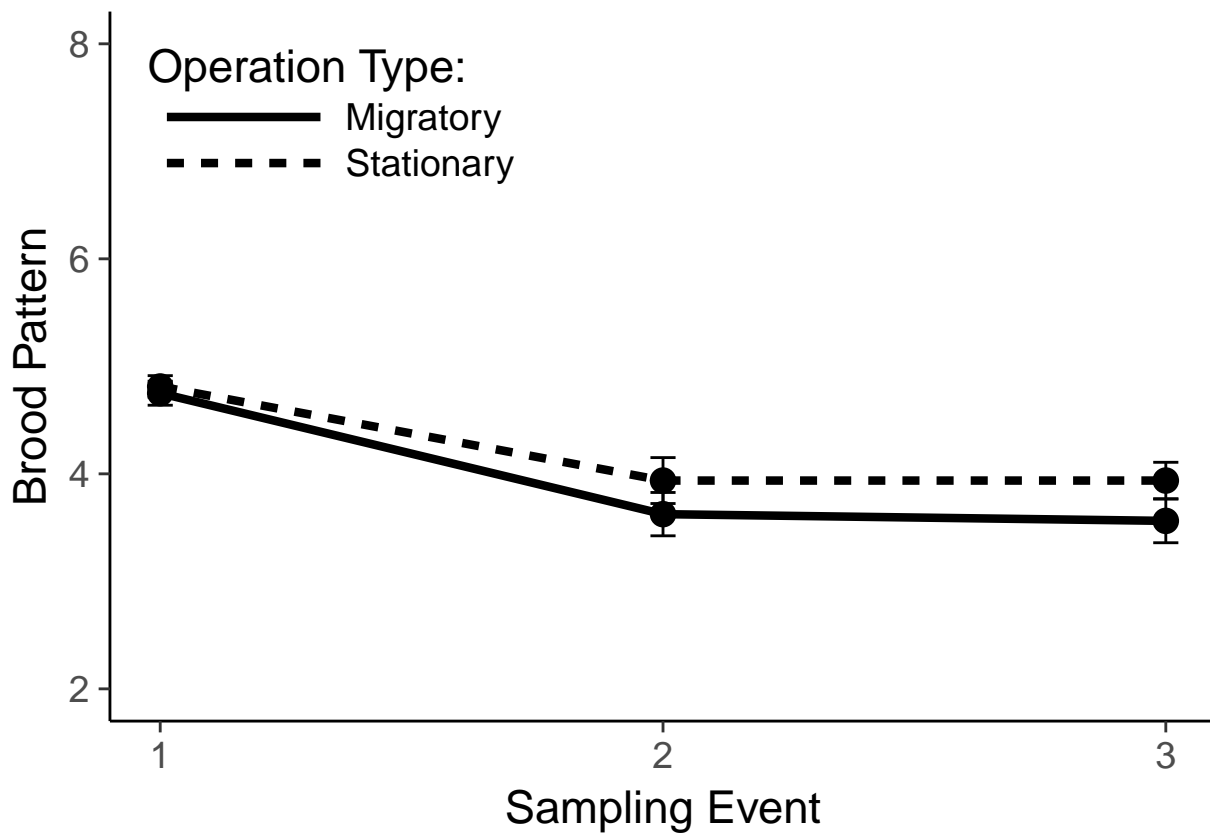
Initial Time Step One Analysis (ANOVA)

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## MigStatExp_1_T1$Treatment  1  2.000  2.0000   6.761 0.0143 *
## Residuals                 30  8.875  0.2958
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Warning in chisq.test(x): Chi-squared approximation may be incorrect
##
## Pearson's Chi-squared test
##
## data:  x
## X-squared = 5.8889, df = 2, p-value = 0.05263
```

Full repeated measures Analysis (Rep ANOVA)

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: FOB
##              Chisq Df Pr(>Chisq)
## Treatment          3.5968  1    0.05789 .
## SamplingEvent      152.8381  1    < 2e-16 ***
## Treatment:SamplingEvent  5.6507  1    0.01745 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Brood Pattern:



```
##      Treatment SamplingEvent  n   mean      sd      se
## 1  Migratory                1 16 4.7500 0.4472136 0.1118034
## 2  Migratory                2 16 3.6250 0.8062258 0.2015564
## 3  Migratory                3 16 3.5625 0.8139410 0.2034853
## 4  Stationary               1 16 4.8125 0.4031129 0.1007782
## 5  Stationary               2 16 3.9375 0.8539126 0.2134781
## 6  Stationary               3 16 3.9375 0.6800735 0.1700184
```

Initial Time Step One Analysis (ANOVA)

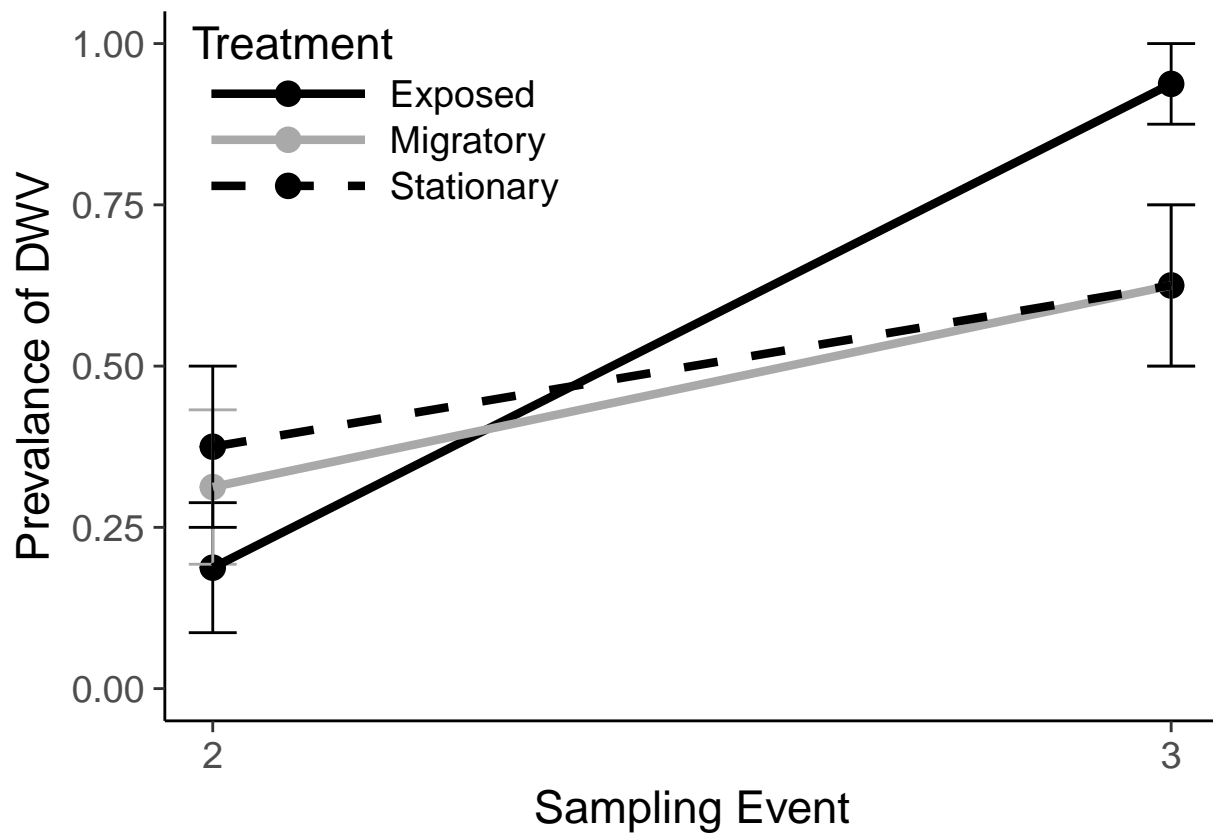
```
##              Df Sum Sq Mean Sq F value Pr(>F)
## MigStatExp_1_T1$Treatment  1  0.031 0.03125  0.172  0.681
## Residuals                 30  5.437 0.18125
```

Full repeated measures Analysis (Rep ANOVA)

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: BroodPattern
##              Chisq Df Pr(>Chisq)
## Treatment      1.7225  1    0.1894
## SamplingEvent 48.1126  1 4.024e-12 ***
## Treatment:SamplingEvent 1.1045  1    0.2933
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

EXPERIMENT II - (EXPOSED vs STATIONARY)

Deformed Wing Virus Prevalence:



##	Treatment	SamplingEvent	n	mean	sd	se
## 1	Exposed	2	16	0.1875	0.4031129	0.1007782
## 2	Exposed	3	16	0.9375	0.2500000	0.0625000
## 3	Migratory	2	16	0.3125	0.4787136	0.1196784
## 4	Migratory	3	16	0.6250	0.5000000	0.1250000
## 5	Stationary	2	16	0.3750	0.5000000	0.1250000
## 6	Stationary	3	16	0.6250	0.5000000	0.1250000

Initial Time Step One Analysis (Chi Square)

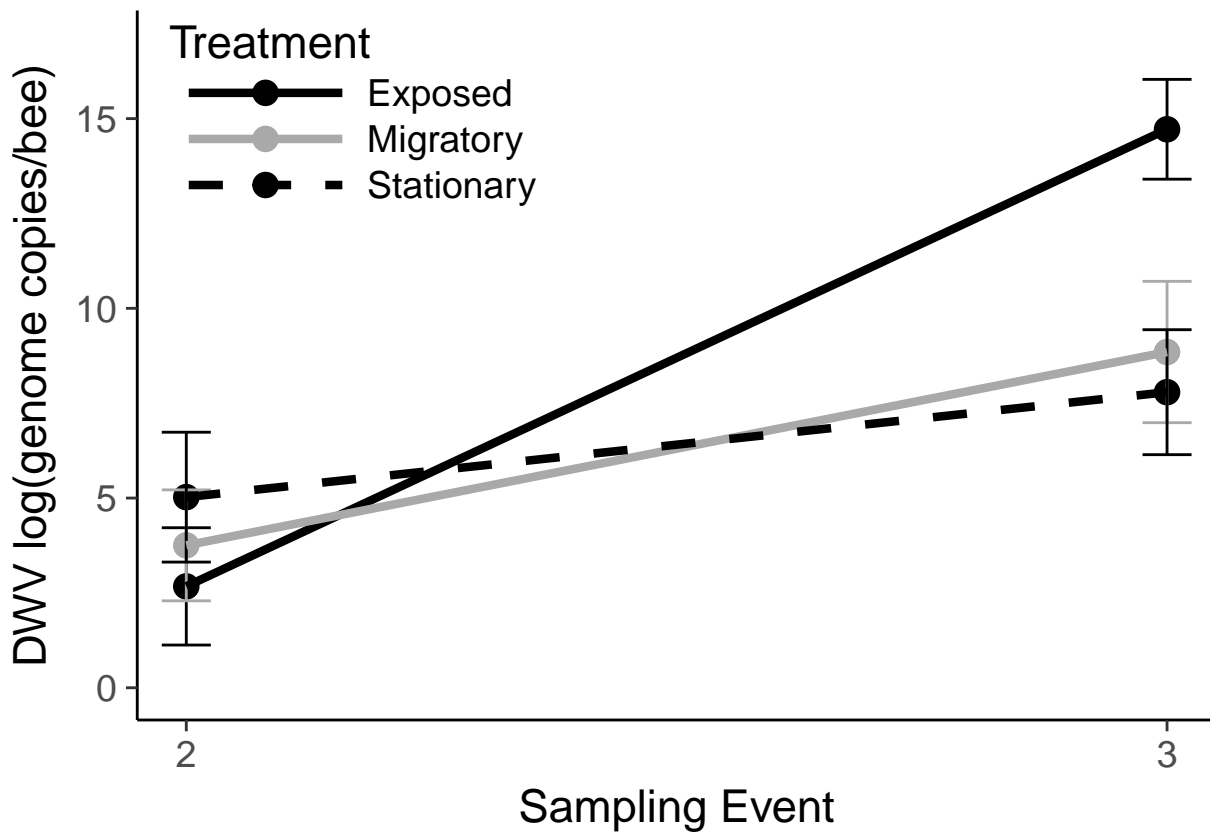
```
## Warning in chisq.test(x): Chi-squared approximation may be incorrect
##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: x
## X-squared = 0.61836, df = 1, p-value = 0.4317
```

Full repeated measures Analaysis (GLM)

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: DWVbinary
```

```
##                               Chisq Df Pr(>Chisq)
## Treatment                    0.0251  1    0.874164
## SamplingEvent                8.8112  1    0.002994 **
## Treatment:SamplingEvent      4.9447  1    0.026171 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Deformed Wing Virus Load:



```
##      Treatment SamplingEvent  n      mean      sd      se
## 1      Exposed                2 16  2.671716 6.184479 1.546120
## 2      Exposed                3 16 14.718737 5.260002 1.315001
## 3      Migratory               2 16  3.753490 5.849113 1.462278
## 4      Migratory               3 16  8.848642 7.451475 1.862869
## 5      Stationary              2 16  5.023841 6.845731 1.711433
## 6      Stationary              3 16  7.789912 6.587571 1.646893
```

Initial Time Step One Analysis (ANOVA)

```
##                               Df Sum Sq Mean Sq F value Pr(>F)
## MigStatExp_2_analysis_T2$Treatment  1   44.3   44.26    1.04  0.316
## Residuals                        30 1276.7   42.56
```

Full repeated measures Analysis (Rep ANOVA)

```
##
```

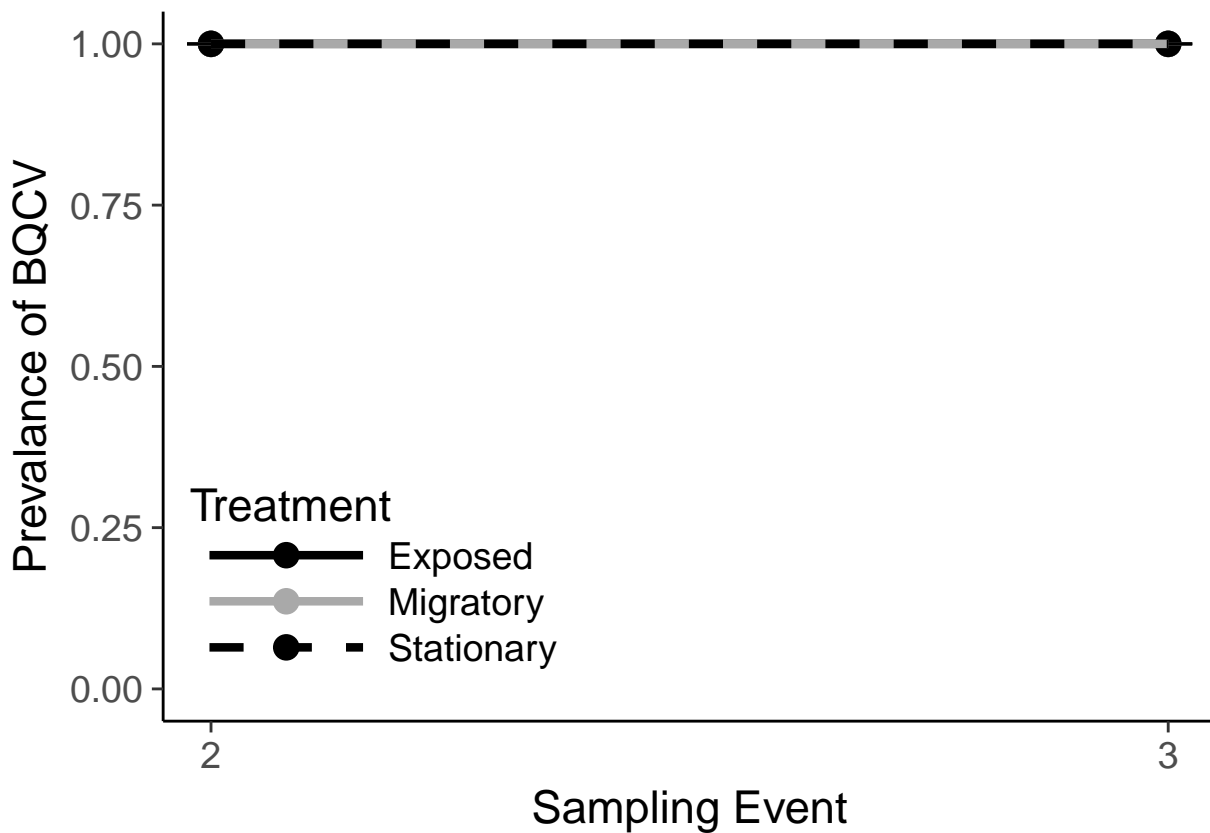
```

## Error: ID
##           Df Sum Sq Mean Sq F value Pr(>F)
## Treatment  1   83.8   83.78    2.056   0.162
## Residuals 30 1222.6   40.75
##
## Error: Within
##           Df Sum Sq Mean Sq F value    Pr(>F)
## SamplingEvent      1  877.7   877.7   23.510 3.57e-05 ***
## Treatment:SamplingEvent 1  344.5   344.5    9.229  0.0049 **
## Residuals          30 1120.0    37.3
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: logDWV
##           Chisq Df Pr(>Chisq)
## Treatment      2.0559  1  0.151622
## SamplingEvent  23.5099  1  1.243e-06 ***
## Treatment:SamplingEvent 9.2288  1  0.002382 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Black Queen Cell Virus Prevalence:



```

##   Treatment SamplingEvent  n mean sd se
## 1   Exposed              2  16   1  0  0

```

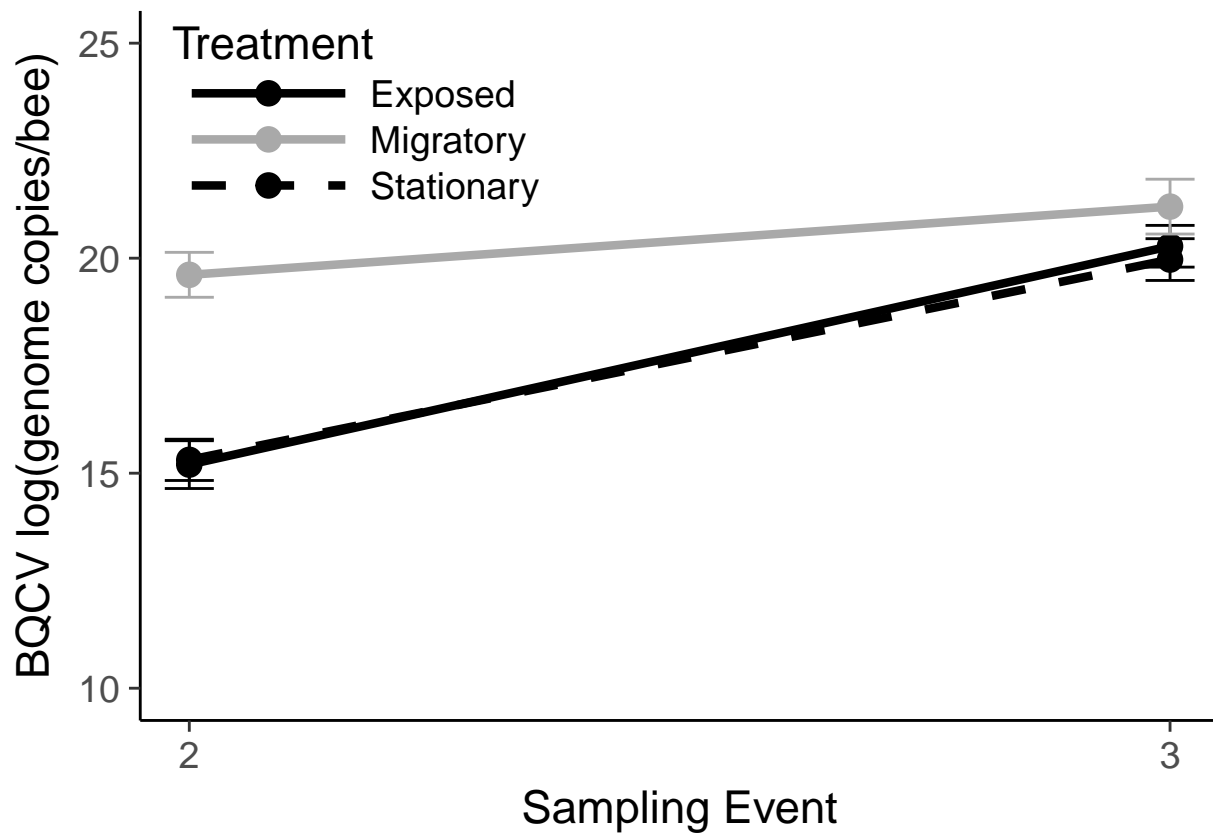
```
## 2    Exposed          3 16    1 0 0
## 3    Migratory        2 16    1 0 0
## 4    Migratory        3 16    1 0 0
## 5    Stationary       2 16    1 0 0
## 6    Stationary       3 16    1 0 0
```

Initial Time Step One Analysis (Chi Square)

```
##
## Chi-squared test for given probabilities
##
## data:  x
## X-squared = 0, df = 1, p-value = 1
```

Full repeated measures Analysis (GLM)

Black Queen Cell Virus Load:



```
##   Treatment SamplingEvent  n   mean    sd    se
## 1    Exposed              2 16 15.19960 2.222482 0.5556204
## 2    Exposed              3 16 20.27747 1.940819 0.4852047
## 3    Migratory           2 16 19.61332 2.090001 0.5225002
## 4    Migratory           3 16 21.19942 2.549945 0.6374862
## 5    Stationary          2 16 15.31059 1.918286 0.4795715
## 6    Stationary          3 16 19.96779 1.942679 0.4856697
```

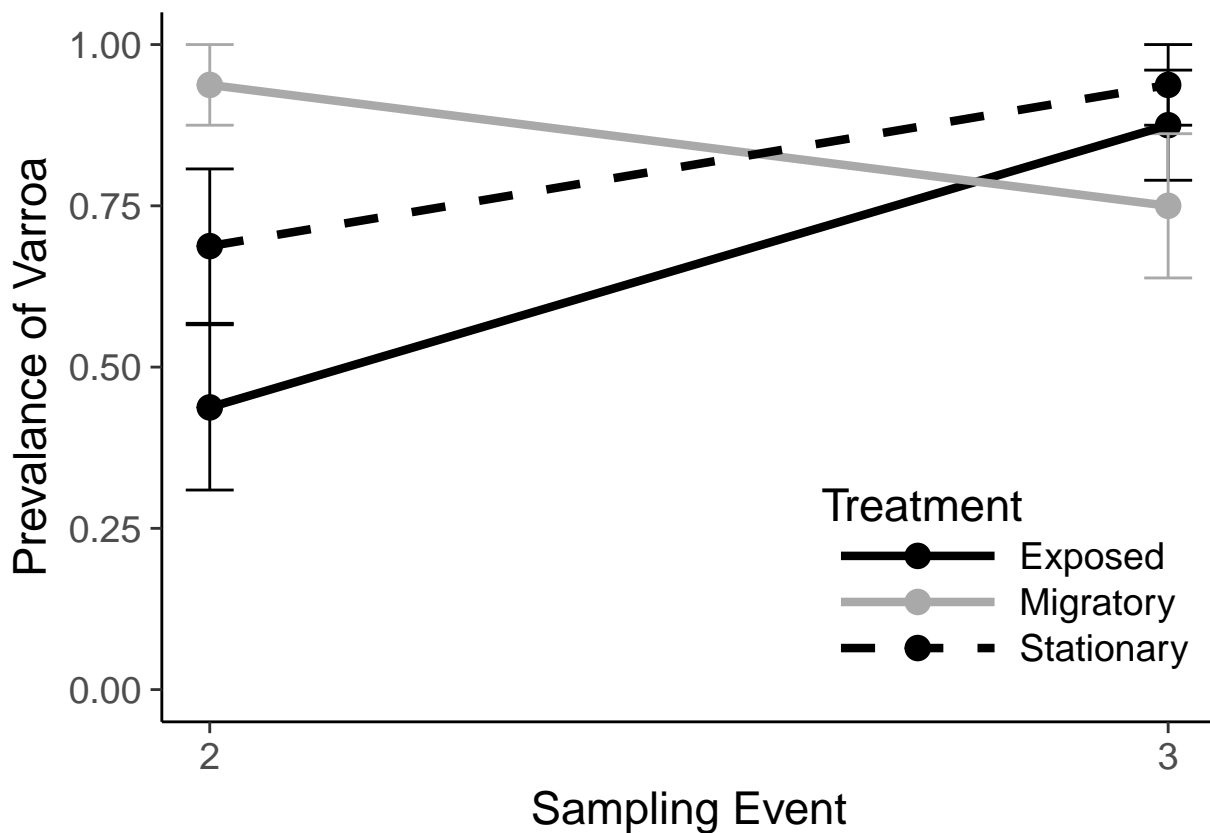
Initial Time Step One Analysis (ANOVA)

```
##                               Df Sum Sq Mean Sq F value Pr(>F)
## MigStatExp_2_analysis_T2$Treatment  1    0.1    0.099    0.023  0.881
## Residuals                        30  129.3    4.310
```

Full repeated measures Analysis (Rep ANOVA)

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: logBQCV
##                               Chisq Df Pr(>Chisq)
## Treatment                    0.0391  1    0.8433
## SamplingEvent                93.8332  1    <2e-16 ***
## Treatment:SamplingEvent      0.1752  1    0.6755
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Varroa Mite Prevalence:



```
## Treatment SamplingEvent n mean sd se
## 1 Exposed 2 16 0.4375 0.5123475 0.12808688
## 2 Exposed 3 16 0.8750 0.3415650 0.08539126
## 3 Migratory 2 16 0.9375 0.2500000 0.06250000
## 4 Migratory 3 16 0.7500 0.4472136 0.11180340
## 5 Stationary 2 16 0.6875 0.4787136 0.11967839
## 6 Stationary 3 16 0.9375 0.2500000 0.06250000
```

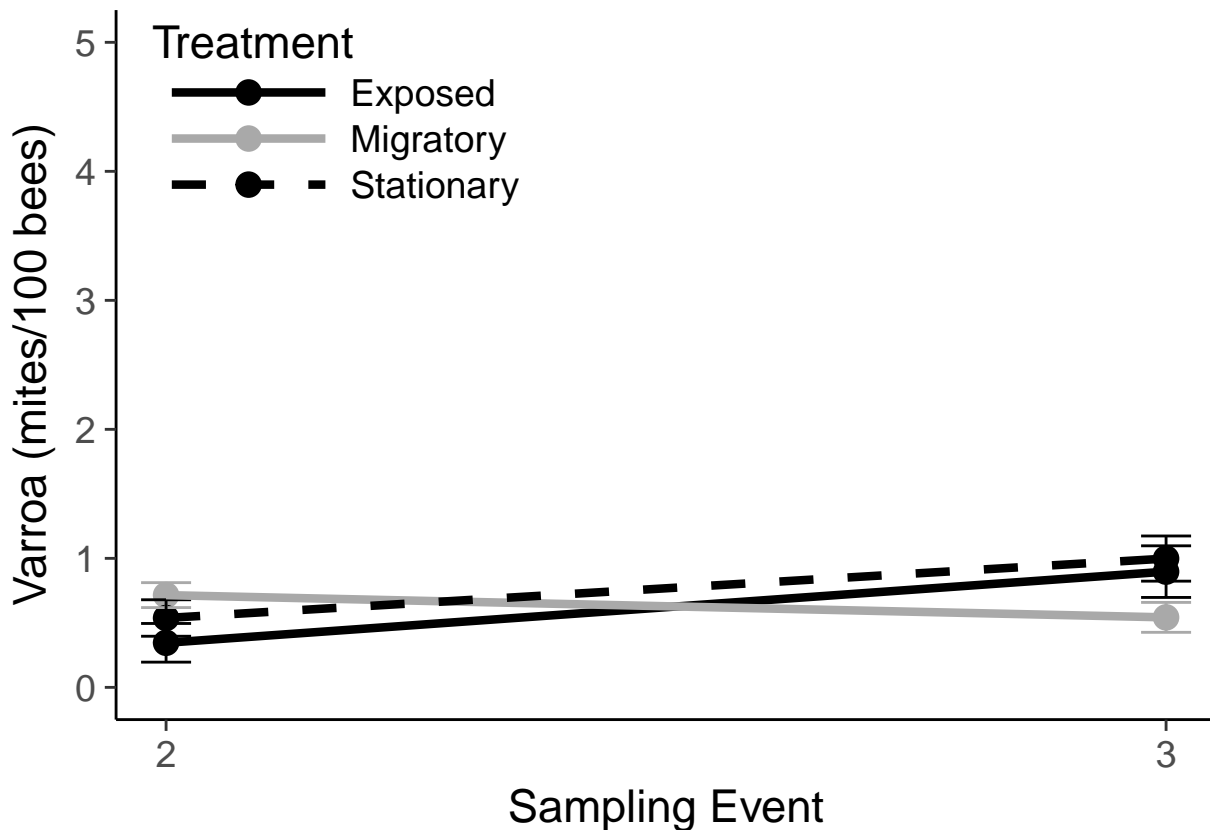

Initial Time Step One Analysis (Chi Square)

```
##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: x
## X-squared = 1.1429, df = 1, p-value = 0.285
```

Full repeated measures Analysis (GLM)

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: VarroaBinary
##
##               Chisq Df Pr(>Chisq)
## Treatment      1.3902  1  0.238369
## SamplingEvent  10.1291  1  0.001459 **
## Treatment:SamplingEvent 0.0603  1  0.806036
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Varroa Mite Load:



```
## Treatment SamplingEvent n mean sd se
## 1 Exposed 2 16 0.3453856 0.5997884 0.14994711
## 2 Exposed 3 16 0.8970989 0.8002553 0.20006382
## 3 Migratory 2 16 0.7150268 0.3865965 0.09664914
## 4 Migratory 3 16 0.5426076 0.4639379 0.11598447
```

```
## 5 Stationary          2 16 0.5376645 0.5653539 0.14133847
## 6 Stationary          3 16 0.9983903 0.7002526 0.17506314
```

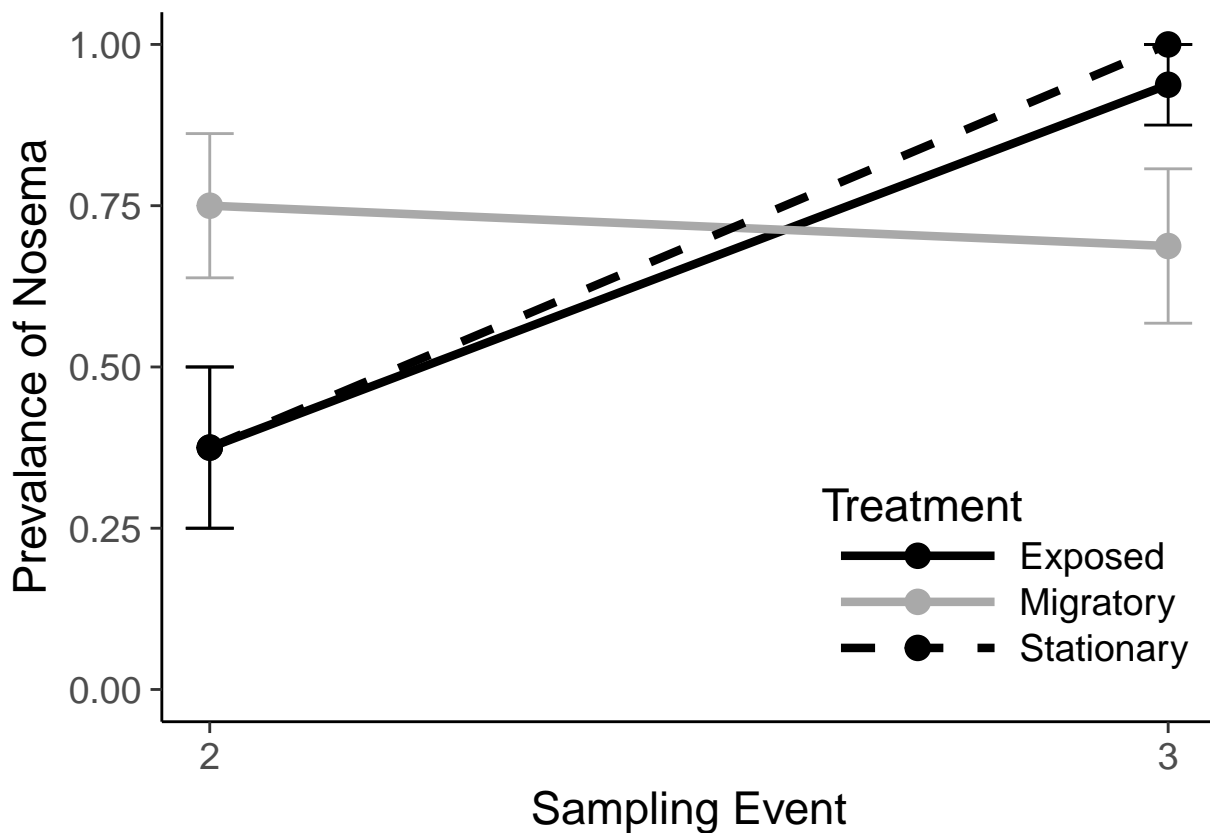
Initial Time Step One Analysis (ANOVA)

```
##                               Df Sum Sq Mean Sq F value Pr(>F)
## MigStatExp_2_analysis_T2$Treatment  1  0.296  0.2958    0.871  0.358
## Residuals                        30 10.191  0.3397
```

Full repeated measures Analysis (Rep ANOVA)

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: Varroa
##                               Chisq Df Pr(>Chisq)
## Treatment                   0.4711  1    0.4925
## SamplingEvent                23.6575  1  1.151e-06 ***
## Treatment:SamplingEvent      0.1911  1    0.6620
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Nosema Prevalence:



```
## Treatment SamplingEvent n mean sd se
## 1 Exposed 2 16 0.3750 0.5000000 0.1250000
## 2 Exposed 3 16 0.9375 0.2500000 0.0625000
```

```
## 3 Migratory      2 16 0.7500 0.4472136 0.1118034
## 4 Migratory      3 16 0.6875 0.4787136 0.1196784
## 5 Stationary     2 16 0.3750 0.5000000 0.1250000
## 6 Stationary     3 16 1.0000 0.0000000 0.0000000
```

Initial Time Step One Analysis (Chi Square)

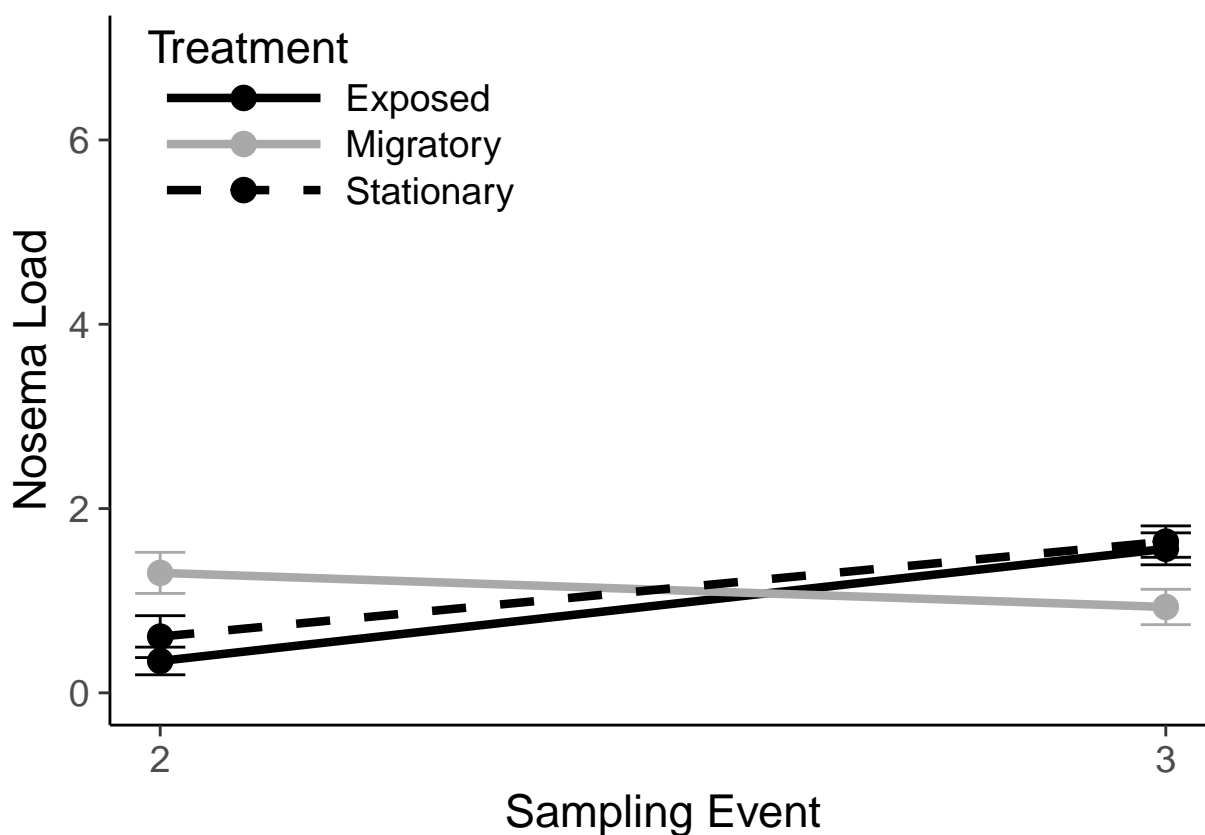
```
##
## Pearson's Chi-squared test
##
## data: x
## X-squared = 0, df = 1, p-value = 1
```

Full repeated measures Analysis (GLM)

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, : Model is nearly unidentifiable:
## - Rescale variables?

## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: NosemaBinary
##              Chisq Df Pr(>Chisq)
## Treatment      0.0000  1  0.999946
## SamplingEvent   7.7711  1  0.005309 **
## Treatment:SamplingEvent 0.0040  1  0.949451
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Nosema Load:



##	Treatment	SamplingEvent	n	mean	sd	se
## 1	Exposed	2	16	0.3458677	0.6001244	0.1500311
## 2	Exposed	3	16	1.5630667	0.6936680	0.1734170
## 3	Migratory	2	16	1.3018461	0.8902946	0.2225737
## 4	Migratory	3	16	0.9318390	0.7672246	0.1918061
## 5	Stationary	2	16	0.6102725	0.9093340	0.2273335
## 6	Stationary	3	16	1.6414654	0.6815193	0.1703798

Initial Time Step One Analysis (ANOVA)

##		Df	Sum Sq	Mean Sq	F value	Pr(>F)
##	MigStatExp_2_analysis_T2\$Treatment	1	0.559	0.5593	0.942	0.339
##	Residuals	30	17.806	0.5935		

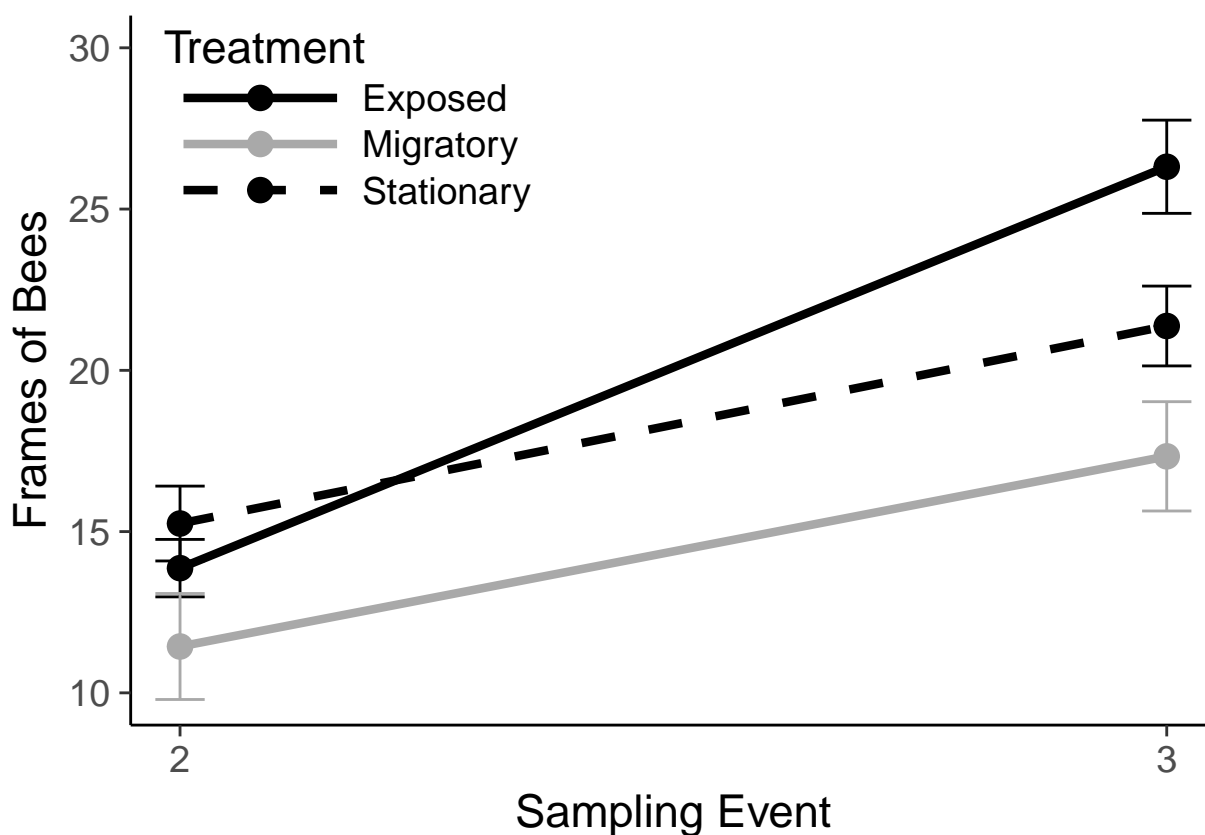
Full repeated measures Analysis (Rep ANOVA)

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: NosemaLoadRecount
##
```

##		Chisq	Df	Pr(>Chisq)
##	Treatment	0.8816	1	0.3478
##	SamplingEvent	37.9261	1	7.348e-10 ***
##	Treatment:SamplingEvent	0.2596	1	0.6104

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Frames of Bees:



```
##      Treatment SamplingEvent  n    mean      sd      se
## 1    Exposed                2 16 13.86667 3.563038 0.8907594
## 2    Exposed                3 16 26.31250 5.781796 1.4454490
## 3    Migratory              2 16 11.43750 6.572354 1.6430884
## 4    Migratory              3 16 17.33333 6.778819 1.6947046
## 5    Stationary             2 16 15.25000 4.640402 1.1601006
## 6    Stationary             3 16 21.37500 4.951431 1.2378577
```

Initial Time Step One Analysis (ANOVA)

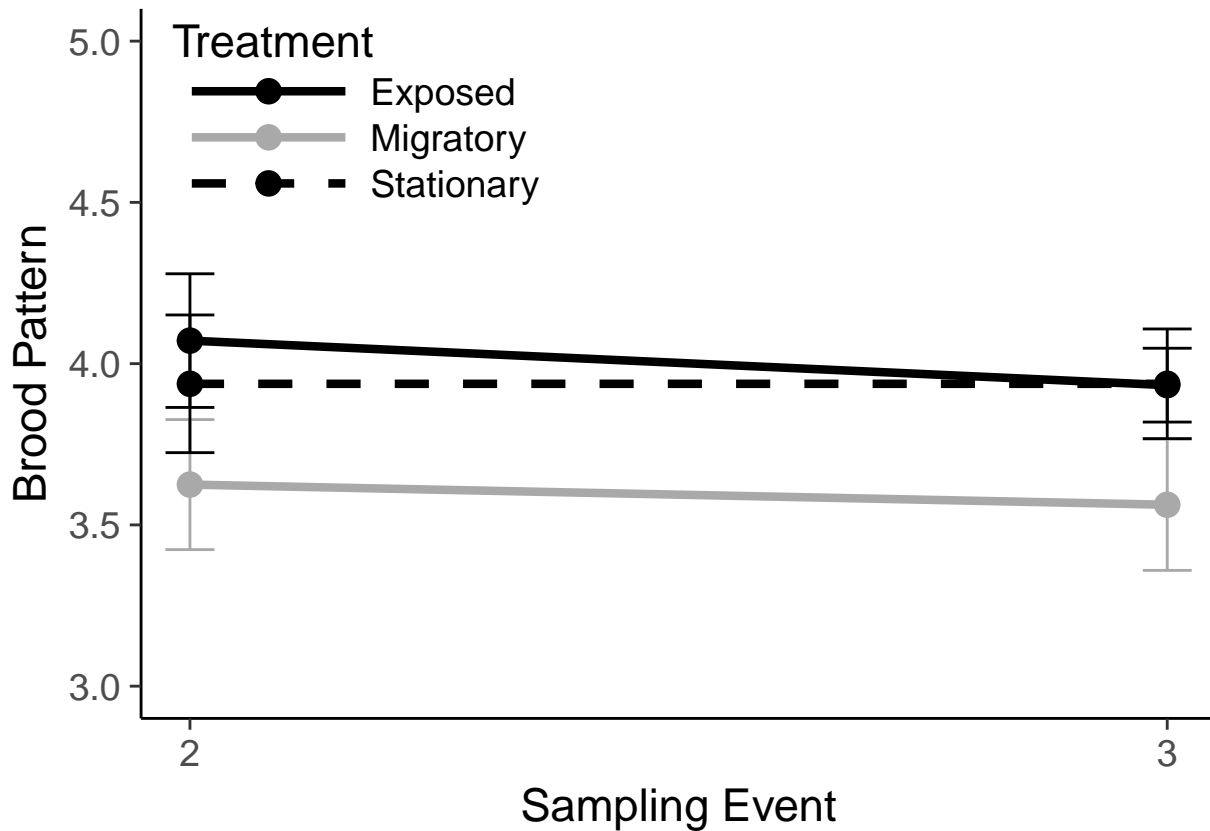
```
##                                     Df Sum Sq Mean Sq F value Pr(>F)
## MigStatExp_2_analysis_T2$Treatment 1   14.8   14.81    0.858  0.362
## Residuals                          29  500.7   17.27
## 1 observation deleted due to missingness
```

Full repeated measures Analysis (Rep ANOVA)

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: FOB
##               Chisq Df Pr(>Chisq)
## Treatment      1.8994 1  0.168146
## SamplingEvent 89.1906 1 < 2.2e-16 ***
## Treatment:SamplingEvent 9.9458 1  0.001612 **
## ---
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Brood Pattern:



##	Treatment	SamplingEvent	n	mean	sd	se
## 1	Exposed	2	16	4.071429	0.8287419	0.2071855
## 2	Exposed	3	16	3.933333	0.4577377	0.1144344
## 3	Migratory	2	16	3.625000	0.8062258	0.2015564
## 4	Migratory	3	16	3.562500	0.8139410	0.2034853
## 5	Stationary	2	16	3.937500	0.8539126	0.2134781
## 6	Stationary	3	16	3.937500	0.6800735	0.1700184

Initial Time Step One Analysis (ANOVA)

##		Df	Sum Sq	Mean Sq	F value	Pr(>F)
##	MigStatExp_2_analysis_T2\$Treatment	1	0.134	0.1339	0.189	0.667
##	Residuals	28	19.866	0.7095		

2 observations deleted due to missingness

Full repeated measures Analysis (Rep ANOVA)

Analysis of Deviance Table (Type II Wald chisquare tests)

##

Response: BroodPattern

##		Chisq	Df	Pr(>Chisq)
##	Treatment	0.1331	1	0.7152

```
## SamplingEvent      0.1815  1      0.6701
## Treatment:SamplingEvent 0.2156  1      0.6424
```

OVER-ARCHING STUDY-WIDE ANALYSES

Tempurature and Rainfall Date between CA and NC

Avg Temp. between NC and CA

```
##           Df Sum Sq Mean Sq F value Pr(>F)
## State      1    2.7    2.67    0.059  0.809
## Residuals  52 2350.7   45.21
```

Avg Windspeed between NC and CA

```
##           Df Sum Sq Mean Sq F value Pr(>F)
## State      1    32.2   32.20    3.106 0.0839 .
## Residuals  52   539.1   10.37
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

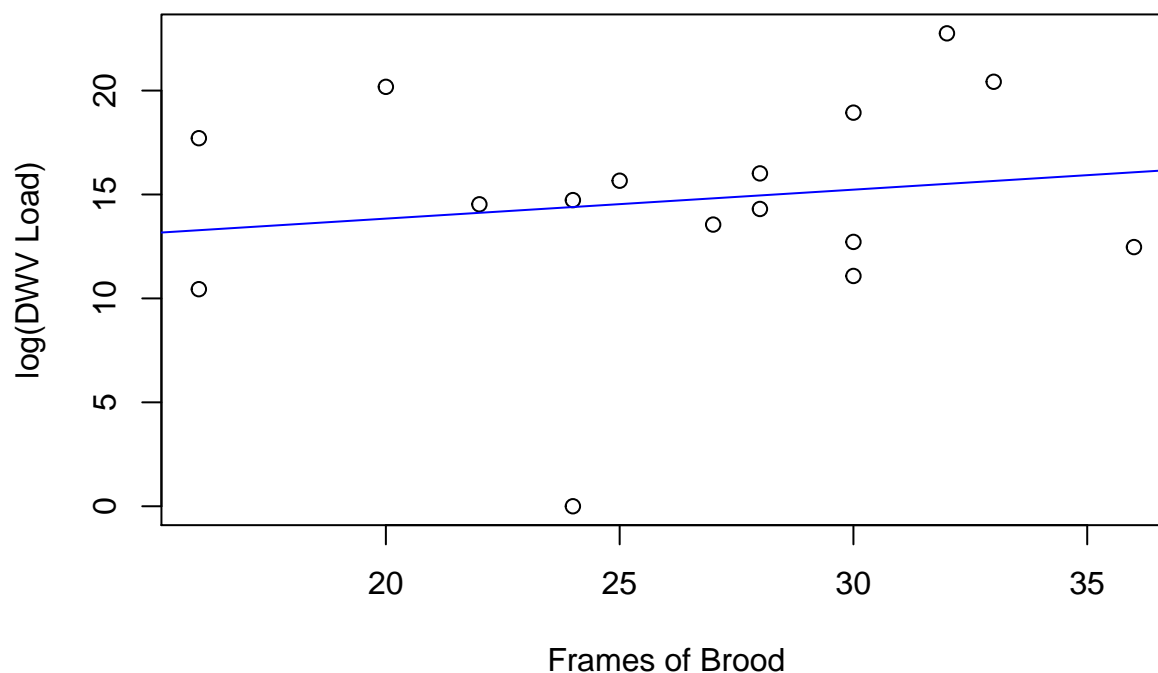
Rainfall between NC and CA

```
##           Df Sum Sq Mean Sq F value Pr(>F)
## State      1   0.040  0.04000    1.323  0.256
## Residuals  49   1.482  0.03024
## 3 observations deleted due to missingness
```

Linear regression between DWV load and Frames of bees

Regression between DWV and FOB

T3 Exposed



```
##
## Call:
## lm(formula = MigStat_3_Exp$logDWV ~ MigStat_3_Exp$FOB)
##
## Residuals:
```

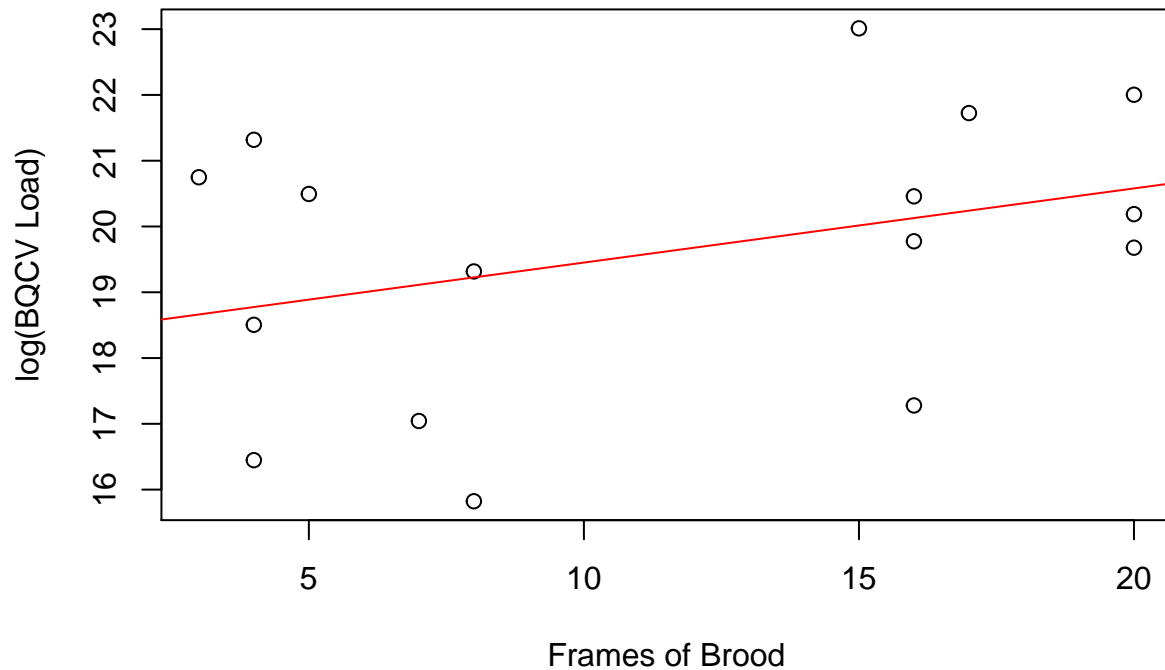
	Min	1Q	Median	3Q	Max
	-14.3965	-2.5956	0.3709	3.8857	7.2414

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	11.0517	6.4637	1.71	0.109
MigStat_3_Exp\$FOB	0.1394	0.2403	0.58	0.571

```
##
## Residual standard error: 5.38 on 14 degrees of freedom
## Multiple R-squared: 0.02347, Adjusted R-squared: -0.04628
## F-statistic: 0.3364 on 1 and 14 DF, p-value: 0.5711
```

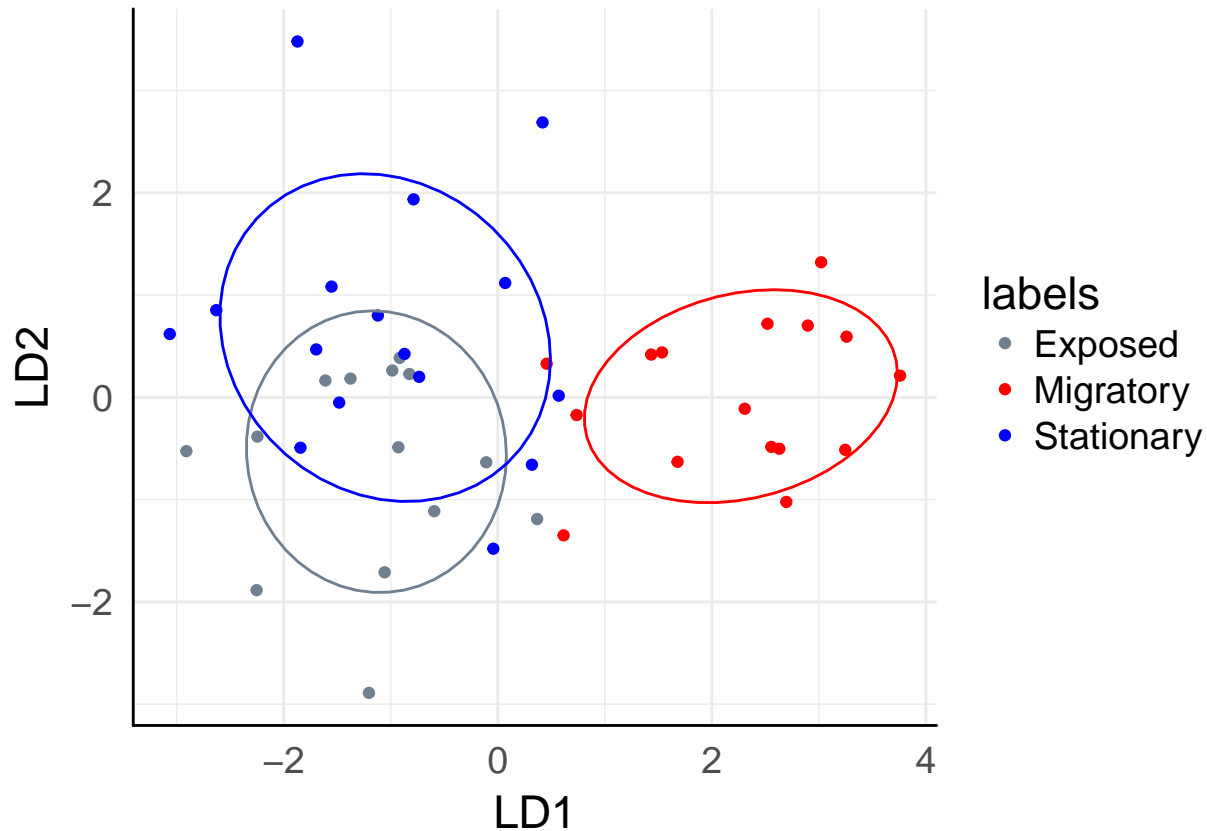

T2 Migratory



```
##
## Call:
## lm(formula = MigStat_1_Mig$logBQCV ~ MigStat_1_Mig$FOB)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.4030 -1.1930 -0.0894  1.5144  2.9973
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   18.32414    1.04016   17.617 5.96e-11 ***
## MigStat_1_Mig$FOB  0.11272    0.07947    1.418  0.178
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.023 on 14 degrees of freedom
## Multiple R-squared:  0.1256, Adjusted R-squared:  0.06318
## F-statistic: 2.012 on 1 and 14 DF,  p-value: 0.178
```

Linear Classification Analysis for all Vars on Grouping into Treatments (3 time points):

LDA for Time Point 2:



```
## Call:
## lda(Treatment ~ Varroa + NosemaLoadRecount + logBQCV + logDWV +
##     DWVbinary + FOB + BroodPattern + NosemaBinary + VarroaBinary,
##     data = Mig2, na.action = "na.omit")
##
## Prior probabilities of groups:
##   Exposed  Migratory  Stationary
## 0.3043478 0.3478261 0.3478261
##
## Group means:
##           Varroa NosemaLoadRecount logBQCV logDWV DWVbinary   FOB
## Exposed    0.2587094         0.3952774 15.06026 1.518077 0.1428571 14.5000
## Migratory  0.7150268         1.3018461 19.61332 3.753490 0.3125000 11.4375
## Stationary 0.5376645         0.6102725 15.31059 5.023841 0.3750000 15.2500
##           BroodPattern NosemaBinary VarroaBinary
## Exposed      4.071429      0.4285714      0.4285714
## Migratory     3.625000      0.7500000      0.9375000
## Stationary    3.937500      0.3750000      0.6875000
##
## Coefficients of linear discriminants:
##           LD1      LD2
## Varroa      -0.6270931236 0.6730349
## NosemaLoadRecount 0.0003142373 1.2911443
## logBQCV      0.5333840980 -0.1168643
## logDWV      -0.1401897367 0.4626860
## DWVbinary    1.5923705910 -5.0601769
## FOB         -0.1200868076 0.1489922
```

```

## BroodPattern      0.4217606041 -0.8709568
## NosemaBinary      0.4180525000 -2.0757503
## VarroaBinary      1.9351534667  0.5807554
##
## Proportion of trace:
##   LD1   LD2
## 0.8902 0.1098

## Warning in cbind(Mig2$Treatment, CA1$class): number of rows of result is
## not a multiple of vector length (arg 2)

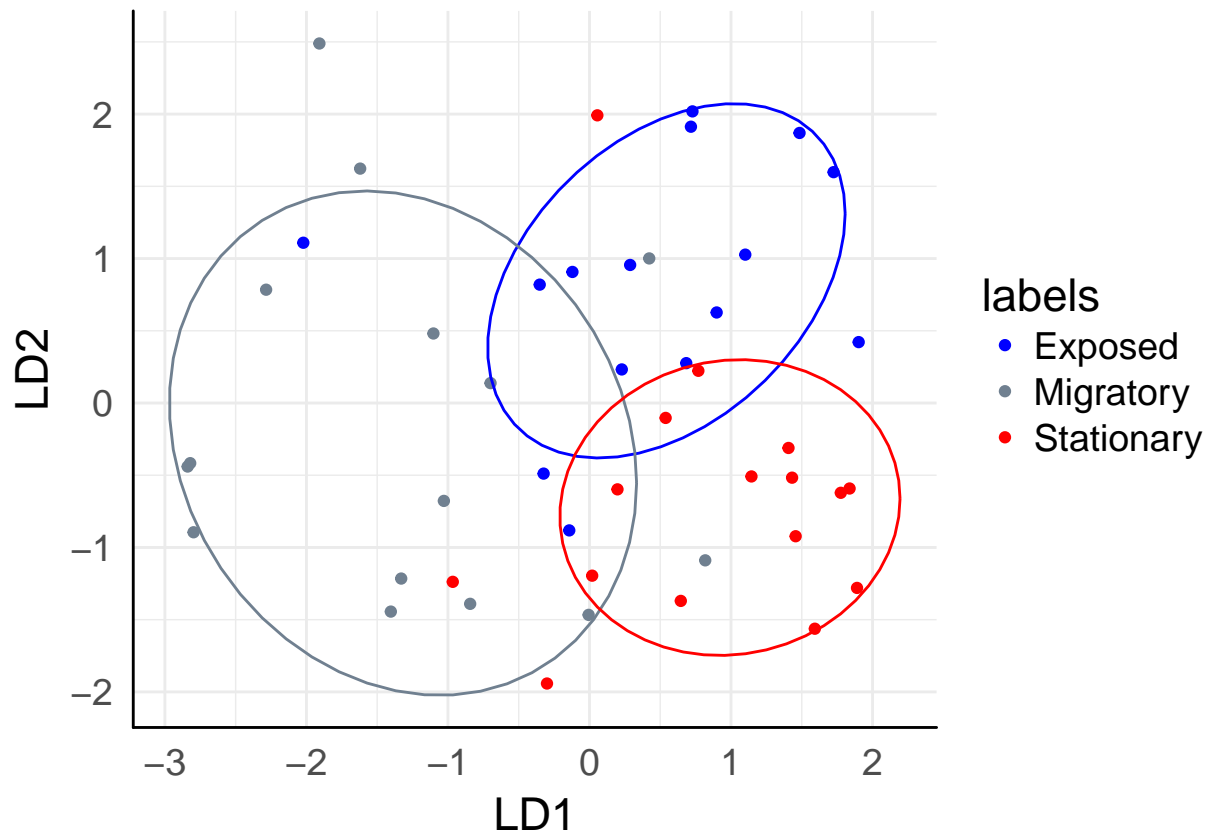
##           predicted
## actual      Exposed Migratory Stationary
##   Exposed         7         3         6
##   Migratory        3        11         2
##   Stationary        6         3         7

##           predicted
## actual      Exposed Migratory Stationary
##   Exposed    0.4375    0.1875    0.3750
##   Migratory  0.1875    0.6875    0.1250
##   Stationary 0.3750    0.1875    0.4375

##
## Call:
## adonis(formula = envdist1 ~ Treatment, data = Mig2x)
##
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## Treatment  2    0.6175 0.308772  5.1171 0.19225 0.001 ***
## Residuals 43    2.5947 0.060341          0.80775
## Total     45    3.2122          1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

LDA for Time Point 3:



```
## Call:
## lda(Treatment ~ Varroa + NosemaLoadRecount + logBQCV + logDWV +
##     DWVbinary + FOB + BroodPattern + NosemaBinary + VarroaBinary,
##     data = Mig3, na.action = "na.omit")
##
## Prior probabilities of groups:
##   Exposed  Migratory  Stationary
## 0.3260870 0.3260870 0.3478261
##
## Group means:
##           Varroa NosemaLoadRecount logBQCV logDWV DWVbinary
## Exposed    0.8967539         1.5246000 20.38791 14.354700 0.9333333
## Migratory  0.5359596         0.9104441 21.24670  9.438552 0.6666667
## Stationary 0.9983903         1.6414654 19.96779  7.789912 0.6250000
##           FOB BroodPattern NosemaBinary VarroaBinary
## Exposed    26.73333      3.933333 0.9333333 0.8666667
## Migratory  17.33333      3.666667 0.6666667 0.7333333
## Stationary 21.37500      3.937500 1.0000000 0.9375000
##
## Coefficients of linear discriminants:
##           LD1      LD2
## Varroa      0.7243155 -0.62808240
## NosemaLoadRecount 0.5627595 -0.35456078
## logBQCV      -0.1487690 0.04173594
## logDWV      -0.2009820 0.22050061
## DWVbinary    2.0889308 -1.94656235
## FOB          0.1139772 0.09907287
```

```

## BroodPattern      0.1074030 -0.23640435
## NosemaBinary      0.7996924  0.08542202
## VarroaBinary      0.9912785  0.14342108
##
## Proportion of trace:
##   LD1   LD2
## 0.6923 0.3077

## Warning in cbind(Mig3$Treatment, CA2$class): number of rows of result is
## not a multiple of vector length (arg 2)

##           predicted
## actual      Exposed Migratory Stationary
##   Exposed         9         3         4
##   Migratory        5         7         4
##   Stationary       4         2        10

##           predicted
## actual      Exposed Migratory Stationary
##   Exposed    0.5625   0.1875   0.2500
##   Migratory  0.3125   0.4375   0.2500
##   Stationary 0.2500   0.1250   0.6250

##
## Call:
## adonis(formula = envdist ~ Treatment, data = Mig3x)
##
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## Treatment  2    0.4067 0.203352  4.6287 0.17715 0.001 ***
## Residuals 43    1.8891 0.043933           0.82285
## Total     45    2.2958           1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```