|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Sectors | Gene | System | Mean (SD) | P-value |
| Surma | N | Isolation Center Drain Effluent | 35.99 (3.87) | 0.184 |
| Market Place | 38.27 (2.00) |
| ORF | Isolation Center Drain Effluent | 38.14 (3.64) | 0.807 |
| Market Place | 37.69 (3.03) |
| Jamuna | N | Isolation Center Drain Effluent | 36.48 (4.15) | 0.966 |
| Market Place | 36.55 (3.57) |
| ORF | Isolation Center Drain Effluent | 37.67 (2.46) | 0.509 |
| Market Place | 36.04 (3.86) |
| Padma | N | Isolation Center Drain Effluent | 39.34 (3.33) | 0.791 |
| Market Place | 39.9 (2.76) |
| ORF | Isolation Center Drain Effluent | 36.91 (3.33) | 0.595 |
| Market Place | 38.88 (2.43) |
| Meghna | N | Isolation Center Drain Effluent | 35.92 (5.04) | 0.371 |
| Market Place | 38.29 (3.60) |
| ORF | Isolation Center Drain Effluent | 33.42 (3.35) | **0.006** |
| Market Place | 38.15 (3.97) |
| Overall | N | Isolation Center Drain Effluent | 36.96 (4.19) | 0.268 |
| Market Place | 38.26 (3.07) |
| ORF | Isolation Center Drain Effluent | 36.46 (3.65) | 0.217 |
| Market Place | 37.72 (3.36) |

Using the Wilcoxon-Mann-Whitney (WMW) test, Table x shows that most of the sectors’s Isolation Center Drain and Effluent Market Place has no significant difference in mean values except the Megna. In Meghna the p-value of Isolation Center Drain and Effluent Market Place of ORF gene is 0.289. So, according to ORF gene this two place has different mean and they are statistically significant. This difference also showed in boxplot and the variation between two places is also seen to be significant compare to others.

E:\ResearchProject\Aminul\Sweage\Rplot44.tiff

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Sectors | Gene | System | Mean (SD) | P-value |
| Surma | N | Drainage | 37.16 (3.21) | 0.172 |
| Without Drainage | 38.73 (2.55) |
| ORF | Drainage | 37.85 (3.52) | 0.821 |
| Without Drainage | 37.86 (2.44) |
| Jamuna | N | Drainage | 38.61 (3.25) | 0.360 |
| Without Drainage | 37.77 (3.37) |
| ORF | Drainage | 36.99 (3.43) | 0.463 |
| Without Drainage | 37.92 (3.47) |
| Padma | N | Drainage | 37.42 (3.21) | **0.035** |
| Without Drainage | 38.84 (3.31) |
| ORF | Drainage | 38.28 (2.86) | 0.910 |
| Without Drainage | 38.20 (2.96) |
| Meghna | N | Drainage | 36.6 (3.63) | 0.402 |
| Without Drainage | 37.59 (3.54) |
| ORF | Drainage | 36.25 (3.91) | 0.009 |
| Without Drainage | 38.68 (3.37) |
| Overall | N | Drainage | 37.37 (3.33) | 0.106 |
| Without Drainage | 38.21 (3.17) |
| ORF | Drainage | 37.52 (3.41) | 0.129 |
| Without Drainage | 38.15 (3.03) |

(Similar just change in Padma and N) Using the Wilcoxon-Mann-Whitney (WMW) test, Table x shows that most of the sectors’s Isolation Center Drain and Effluent Market Place has no significant difference in mean values except the Megna. In Meghna the p-value of Isolation Center Drain and Effluent Market Place of ORF gene is 0.289. So, according to ORF gene this two place has different mean and they are statistically significant. This difference also showed in boxplot and the variation between two places is also seen to be significant compare to others.

***Model With ORF ct value***

Family: gaussian ( identity )

Formula: Ct.Value ~ Site + Region + nPH + nTemp + (1 | Month)

Data: data

AIC BIC logLik deviance df.resid

931.1 959.7 -456.6 913.1 168

Random effects:

Conditional model:

Groups Name Variance Std.Dev.

Month (Intercept) 1.155e-08 0.0001075

Residual 1.019e+01 3.1914061

Number of obs: 177, groups: Month, 2

Dispersion estimate for gaussian family (sigma^2): 10.2

Conditional model:

Estimate Std. Error z value Pr(>|z|)

(Intercept) 36.237096 0.774541 46.79 <2e-16 \*\*\*

SiteWithout drainage 0.948385 0.502340 1.89 0.059 .

RegionMeghna 0.018415 0.732128 0.03 0.980

RegionPadma 1.024562 0.703746 1.46 0.145

RegionSurma 0.394168 0.722953 0.55 0.586

nPH 0.052211 0.046314 1.13 0.260

nTemp 0.009235 0.011530 0.80 0.423

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Table X. Models for Ct value. Site and region are included as covariates in the models

Table X gives the Ct value results of models fitted to the data presented as 2 response values, with the site and region as a subject level covariate. Adding the covariates in the model as a subject, reduced substantially the variability. Thus, this low variability shows that the treatment effect was not significant as p-value greater than 0.05. After adjusting time intercept a different linear trend in time among the treatments (observation level) was also non-significant.

***Model with N ct value***

Family: gaussian ( identity )

Formula: Ct.Value ~ Site + Region + nPH + nTemp + (1 | Month)

Data: data

AIC BIC logLik deviance df.resid

930.6 959.2 -456.3 912.6 168

Random effects:

Conditional model:

Groups Name Variance Std.Dev.

Month (Intercept) 6.198e-09 7.872e-05

Residual 1.016e+01 3.187e+00

Number of obs: 177, groups: Month, 2

Dispersion estimate for gaussian family (sigma^2): 10.2

Conditional model:

Estimate Std. Error z value Pr(>|z|)

(Intercept) 3.710e+01 7.734e-01 47.97 <2e-16 \*\*\*

SiteWithout drainage 1.031e+00 5.016e-01 2.06 0.0399 \*

RegionMeghna -9.599e-01 7.311e-01 -1.31 0.1892

RegionPadma -1.162e-01 7.027e-01 -0.17 0.8687

RegionSurma -3.462e-01 7.219e-01 -0.48 0.6316

nPH 6.082e-02 4.625e-02 1.32 0.1885

nTemp -2.038e-05 1.151e-02 0.00 0.9986

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

***Model With ORF viral load***

*Family: gaussian ( identity )*

*Formula: VLLog ~ Site + Region + nPH + nTemp + (1 | Month)*

*Data: data*

*AIC BIC logLik deviance df.resid*

*363.7 392.3 -172.9 345.7 168*

*Random effects:*

*Conditional model:*

*Groups Name Variance Std.Dev.*

*Month (Intercept) 9.302e-11 9.645e-06*

*Residual 4.129e-01 6.425e-01*

*Number of obs: 177, groups: Month, 2*

*Dispersion estimate for gaussian family (sigma^2): 0.413*

*Conditional model:*

*Estimate Std. Error z value Pr(>|z|)*

*(Intercept) 5.8858605 0.1559435 37.74 <2e-16 \*\*\**

*SiteWithout drainage -0.1659265 0.1011395 -1.64 0.101*

*RegionMeghna 0.1049935 0.1474042 0.71 0.476*

*RegionPadma -0.0022140 0.1416899 -0.02 0.988*

*RegionSurma 0.0263322 0.1455570 0.18 0.856*

*nPH -0.0122257 0.0093247 -1.31 0.190*

*nTemp -0.0002468 0.0023214 -0.11 0.915*

*---*

*Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1*

***Model With N viral load***

*Family: gaussian ( identity )*

*Formula: VLLog ~ Site + Region + nPH + nTemp + (1 | Month)*

*Data: data*

*AIC BIC logLik deviance df.resid*

*363.7 392.3 -172.9 345.7 168*

*Random effects:*

*Conditional model:*

*Groups Name Variance Std.Dev.*

*Month (Intercept) 9.302e-11 9.645e-06*

*Residual 4.129e-01 6.425e-01*

*Number of obs: 177, groups: Month, 2*

*Dispersion estimate for gaussian family (sigma^2): 0.413*

*Conditional model:*

*Estimate Std. Error z value Pr(>|z|)*

*(Intercept) 5.8858605 0.1559435 37.74 <2e-16 \*\*\**

*SiteWithout drainage -0.1659265 0.1011395 -1.64 0.101*

*RegionMeghna 0.1049935 0.1474042 0.71 0.476*

*RegionPadma -0.0022140 0.1416899 -0.02 0.988*

*RegionSurma 0.0263322 0.1455570 0.18 0.856*

*nPH -0.0122257 0.0093247 -1.31 0.190*

*nTemp -0.0002468 0.0023214 -0.11 0.915*

*---*

*Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1*

***Model With ORF copy number***

*Family: gaussian ( identity )*

*Formula: CNLog ~ Site + Region + nPH + nTemp + (1 | Month)*

*Data: data*

*AIC BIC logLik deviance df.resid*

*380.8 409.4 -181.4 362.8 168*

*Random effects:*

*Conditional model:*

*Groups Name Variance Std.Dev.*

*Month (Intercept) 1.442e-09 3.797e-05*

*Residual 4.547e-01 6.743e-01*

*Number of obs: 177, groups: Month, 2*

*Dispersion estimate for gaussian family (sigma^2): 0.455*

*Conditional model:*

*Estimate Std. Error z value Pr(>|z|)*

*(Intercept) 3.209251 0.163654 19.610 <2e-16 \*\*\**

*SiteWithout drainage -0.100155 0.106140 -0.944 0.345*

*RegionMeghna 0.011990 0.154692 0.078 0.938*

*RegionPadma -0.205048 0.148695 -1.379 0.168*

*RegionSurma -0.188194 0.152754 -1.232 0.218*

*nPH -0.009511 0.009786 -0.972 0.331*

*nTemp -0.001666 0.002436 -0.684 0.494*

*---*

*Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1*

***Model With N copy number***

*Family: gaussian ( identity )*

*Formula: CNLog ~ Site + Region + nPH + nTemp + (1 | Month)*

*Data: data*

*AIC BIC logLik deviance df.resid*

*394.7 423.2 -188.3 376.7 168*

*Random effects:*

*Conditional model:*

*Groups Name Variance Std.Dev.*

*Month (Intercept) 8.521e-11 9.231e-06*

*Residual 4.917e-01 7.012e-01*

*Number of obs: 177, groups: Month, 2*

*Dispersion estimate for gaussian family (sigma^2): 0.492*

*Conditional model:*

*Estimate Std. Error z value Pr(>|z|)*

*(Intercept) 3.064e+00 1.702e-01 18.004 <2e-16 \*\*\**

*SiteWithout drainage -1.831e-01 1.104e-01 -1.659 0.0971 .*

*RegionMeghna 8.349e-02 1.609e-01 0.519 0.6037*

*RegionPadma -1.326e-02 1.546e-01 -0.086 0.9316*

*RegionSurma -6.350e-03 1.588e-01 -0.040 0.9681*

*nPH -1.123e-02 1.018e-02 -1.104 0.2697*

*nTemp -4.813e-05 2.533e-03 -0.019 0.9848*

*---*

*Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1*