SAS Data Analysis for Response to Different Bacteria

data migrate;

input ddgeno $ bacteria $ agnst $ block numcells gram $;

datalines;

QS39 Bs Kp 1 100 P

QS39 Kp Bs 1 26 N

QS39 Kp Ef 1 18 N

QS39 Ef Kp 1 36 P

QS39 Ef Bu 1 10 P

QS39 Bu Ef 1 100 N

QS39 Bu Sa 1 41 N

QS39 Sa Bu 1 37 P

QS39 Sa Pf 1 49 P

QS39 Pf Sa 1 109 N

QS39 Pf Ml 1 71 N

QS39 Ml Pf 1 127 P

QS39 Ml Ec 1 30 P

QS39 Ec Ml 1 125 N

QS39 Bs Kp 2 135 P

QS39 Kp Bs 2 104 N

QS39 Kp Ef 2 117 N

QS39 Ef Kp 2 8 P

QS39 Ef Bu 2 1 P

QS39 Bu Ef 2 211 N

QS39 Bu Sa 2 96 N

QS39 Sa Bu 2 18 P

QS39 Sa Pf 2 15 P

QS39 Pf Sa 2 120 N

QS39 Pf Ml 2 132 N

QS39 Ml Pf 2 12 P

QS39 Ml Ec 2 16 P

QS39 Ec Ml 2 54 N

QS39 Bs Kp 3 170 P

QS39 Kp Bs 3 102 N

QS39 Ef Bu 3 9 P

QS39 Bu Ef 3 85 N

QS39 Bu Sa 3 63 N

QS39 Sa Bu 3 24 P

QS39 Sa Pf 3 11 P

QS39 Pf Sa 3 149 N

QS39 Pf Ml 3 89 N

QS39 Ml Pf 3 33 P

QS39 Ml Ec 3 33 P

QS39 Ec Ml 3 99 N

QS39 Ec Bs 3 95 N

QS39 Bs Ec 3 197 P

QS39 Bs Kp 4 156 P

QS39 Kp Bs 4 200 N

QS39 Kp Ef 4 221 N

QS39 Ef Kp 4 25 P

QS39 Bu Sa 4 155 N

QS39 Sa Bu 4 49 P

QS39 Sa Pf 4 65 P

QS39 Pf Sa 4 416 N

QS39 Pf Ml 4 240 N

QS39 Ml Pf 4 89 P

QS39 Ml Ec 4 37 P

QS39 Ec Ml 4 213 N

QS39 Ec Bs 4 181 N

QS39 Bs Ec 4 162 P

QS32 Bs Kp 1 131 P

QS32 Kp Bs 1 59 N

QS32 Kp Ef 1 163 N

QS32 Ef Kp 1 29 P

QS32 Ef Bu 1 14 P

QS32 Bu Ef 1 83 N

QS32 Bu Sa 1 45 N

QS32 Sa Bu 1 28 P

QS32 Sa Pf 1 43 P

QS32 Pf Sa 1 74 N

QS32 Pf Ml 1 91 N

QS32 Ml Pf 1 37 P

QS32 Ml Ec 1 38 P

QS32 Ec Ml 1 69 N

QS32 Bs Kp 2 66 P

QS32 Kp Bs 2 105 N

QS32 Kp Ef 2 106 N

QS32 Ef Kp 2 50 P

QS32 Ef Bu 2 34 P

QS32 Bu Ef 2 59 N

QS32 Bu Sa 2 92 N

QS32 Sa Bu 2 49 P

QS32 Sa Pf 2 56 P

QS32 Pf Sa 2 49 N

QS32 Pf Ml 2 67 N

QS32 Ml Pf 2 28 P

QS32 Ml Ec 2 16 P

QS32 Ec Ml 2 75 N

QS32 Bs Kp 3 143 P

QS32 Kp Bs 3 166 N

QS32 Ef Bu 3 46 P

QS32 Bu Ef 3 85 N

QS32 Bu Sa 3 94 N

QS32 Sa Bu 3 59 P

QS32 Sa Pf 3 54 P

QS32 Pf Sa 3 119 N

QS32 Pf Ml 3 118 N

QS32 Ml Pf 3 33 P

QS32 Ml Ec 3 39 P

QS32 Ec Ml 3 118 N

QS32 Ec Bs 3 105 N

QS32 Bs Ec 3 167 P

QS32 Bs Kp 4 53 P

QS32 Kp Bs 4 287 N

QS32 Kp Ef 4 154 N

QS32 Ef Kp 4 0 P

QS32 Bu Sa 4 160 N

QS32 Sa Bu 4 57 P

QS32 Sa Pf 4 18 P

QS32 Pf Sa 4 437 N

QS32 Pf Ml 4 350 N

QS32 Ml Pf 4 33 P

QS32 Ml Ec 4 17 P

QS32 Ec Ml 4 271 N

QS32 Ec Bs 4 157 N

QS32 Bs Ec 4 63 P

QS40 Bs Kp 1 116 P

QS40 Kp Bs 1 64 N

QS40 Kp Ef 1 139 N

QS40 Ef Kp 1 31 P

QS40 Ef Bu 1 34 P

QS40 Bu Ef 1 147 N

QS40 Bu Sa 1 104 N

QS40 Sa Bu 1 61 P

QS40 Sa Pf 1 63 P

QS40 Pf Sa 1 116 N

QS40 Pf Ml 1 186 N

QS40 Ml Pf 1 153 P

QS40 Ml Ec 1 85 P

QS40 Ec Ml 1 77 N

QS40 Bs Kp 2 92 P

QS40 Kp Bs 2 50 N

QS40 Kp Ef 2 81 N

QS40 Ef Kp 2 6 P

QS40 Ef Bu 2 0 P

QS40 Bu Ef 2 31 N

QS40 Bu Sa 2 92 N

QS40 Sa Bu 2 28 P

QS40 Sa Pf 2 26 P

QS40 Pf Sa 2 65 N

QS40 Pf Ml 2 38 N

QS40 Ml Pf 2 13 P

QS40 Ml Ec 2 26 P

QS40 Ec Ml 2 33 N

QS40 Bs Kp 3 152 P

QS40 Kp Bs 3 53 N

QS40 Ef Bu 3 26 P

QS40 Bu Ef 3 161 N

QS40 Bu Sa 3 65 N

QS40 Sa Bu 3 22 P

QS40 Sa Pf 3 16 P

QS40 Pf Sa 3 161 N

QS40 Pf Ml 3 189 N

QS40 Ml Pf 3 21 P

QS40 Ml Ec 3 47 P

QS40 Ec Ml 3 119 N

QS40 Ec Bs 3 134 N

QS40 Bs Ec 3 193 P

QS40 Bs Kp 4 84 P

QS40 Kp Bs 4 171 N

QS40 Kp Ef 4 244 N

QS40 Ef Kp 4 1 P

QS40 Bu Sa 4 56 N

QS40 Sa Bu 4 54 P

QS40 Sa Pf 4 37 P

QS40 Pf Sa 4 268 N

QS40 Pf Ml 4 190 N

QS40 Ml Pf 4 60 P

QS40 Ml Ec 4 33 P

QS40 Ec Ml 4 234 N

QS40 Ec Bs 4 172 N

QS40 Bs Ec 4 46 P

;

proc print;

run;

/\* FULL MODEL \*/

proc mixed data=migrate;

class ddgeno bacteria agnst gram block;

model numcells=gram/ddfm=SATTERTHWAITE;

random ddgeno bacteria(gram) agnst(gram) block ddgeno\*gram ddgeno\*block ddgeno\*bacteria(gram);

run;

/\* REDUCED MODEL REMOVING N.S. TERMS\*/

proc mixed data=migrate;

class ddgeno bacteria agnst gram block;

model numcells=gram/ddfm=satterthwaite;

random ddgeno bacteria(gram) block;

run;

|  |  |
| --- | --- |
| **Model Information** | |
| **Data Set** | WORK.MIGRATE |
| **Dependent Variable** | numcells |
| **Covariance Structure** | Variance Components |
| **Estimation Method** | REML |
| **Residual Variance Method** | Profile |
| **Fixed Effects SE Method** | Model-Based |
| **Degrees of Freedom Method** | Satterthwaite |

|  |  |  |
| --- | --- | --- |
| **Class Level Information** | | |
| **Class** | **Levels** | **Values** |
| **ddgeno** | 3 | QS32 QS39 QS40 |
| **bacteria** | 8 | Bs Bu Ec Ef Kp Ml Pf Sa |
| **agnst** | 8 | Bs Bu Ec Ef Kp Ml Pf Sa |
| **gram** | 2 | N P |
| **block** | 4 | 1 2 3 4 |

|  |  |
| --- | --- |
| **Dimensions** | |
| **Covariance Parameters** | 8 |
| **Columns in X** | 3 |
| **Columns in Z** | 65 |
| **Subjects** | 1 |
| **Max Obs per Subject** | 168 |

|  |  |
| --- | --- |
| **Number of Observations** | |
| **Number of Observations Read** | 168 |
| **Number of Observations Used** | 168 |
| **Number of Observations Not Used** | 0 |

|  |  |  |  |
| --- | --- | --- | --- |
| **Iteration History** | | | |
| **Iteration** | **Evaluations** | **-2 Res Log Like** | **Criterion** |
| **0** | 1 | 1874.80673670 |  |
| **1** | 3 | 1822.87711632 | 0.00001241 |
| **2** | 1 | 1822.86721503 | 0.00000009 |
| **3** | 1 | 1822.86714843 | 0.00000000 |

|  |
| --- |
| Convergence criteria met. |

|  |  |
| --- | --- |
| **Covariance Parameter Estimates** | |
| **Cov Parm** | **Estimate** |
| **ddgeno** | 0 |
| **bacteria(gram)** | 965.38 |
| **agnst(gram)** | 0 |
| **block** | 948.56 |
| **ddgeno\*gram** | 0 |
| **ddgeno\*block** | 88.1235 |
| **ddgeno\*bacteri(gram)** | 0 |
| **Residual** | 2828.54 |

|  |  |
| --- | --- |
| **Fit Statistics** | |
| **-2 Res Log Likelihood** | 1822.9 |
| **AIC (Smaller is Better)** | 1830.9 |
| **AICC (Smaller is Better)** | 1831.1 |
| **BIC (Smaller is Better)** | 1827.3 |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Type 3 Tests of Fixed Effects** | | | | |
| **Effect** | **Num DF** | **Den DF** | **F Value** | **Pr > F** |
| **gram** | 1 | 5.87 | 9.23 | 0.0235 |