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Appendix S3: Model Selection and Wood's Test Statistic

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Contents

1 Procedures

Fit models predicting the demographic rate using body size, current environment, and the day by treatment. Fit models that contain all subsets of predictors. Find the best subset of predictors using AICc.

2 Preliminaries

```
library(reshape)
library(gamm4)
library(bbmle) #for AICtab
library(plyr)
```

Read in data that was already organized.

```
load("../Individual soil mite data.Rdata")
```

Set the maximum number of knots for the splines.

```
ke=10 #environment
kd=10 #days
kl=5 #length
```

3 Growth

```
temp=na.omit(subset(Indiv, stage!="egg")[
        ,c("l0.s", "l24", "density.s", "supply.s",
        "day", "trt", "l0", "pop.ID", "stage")])
temp=transform(temp, l24.s=scale(l24))
```

```
gm_full=gamm4(l24~s(l0.s, k=kl)+s(density.s, supply.s, k=ke)+trt+s(day, by=trt, k=kd)
        random=~(1|pop.ID), data=temp, REML=FALSE)
gm_eb=gamm4(l24~s(l0.s, k=kl)+s(density.s, supply.s, k=ke),
        random=~(1|pop.ID), data=temp, REML=FALSE)
gm_et=gamm4(l24~s(density.s, supply.s, k=ke)+trt+s(day, by=trt, k=kd),
        random=~(1|pop.ID), data=temp, REML=FALSE)
gm_bt=gamm4(l24~s(l0.s, k=kl)+trt+s(day, by=trt, k=kd),
        random=~(1|pop.ID), data=temp, REML=FALSE)
gm_b=gamm4(l24~s(l0.s, k=kl),
        random=~(1|pop.ID), data=temp, REML=FALSE)
gm_e=gamm4(l24~s(density.s, supply.s, k=ke),
        random=~(1|pop.ID), data=temp, REML=FALSE)
```

```
gm_t=gamm4(l24~trt+s(day, by=trt, k=kd),
        random=~(1|pop.ID), data=temp, REML=FALSE)
gm_0=gamm4(l24~1,
        random=~(1|pop.ID), data=temp, REML=FALSE)

gm_sfull=gamm4(l24~stage+s(l0.s, k=kl)+s(density.s, supply.s, k=ke)+
        trt+s(day, by=trt, k=kd), random=~(1|pop.ID), data=temp, REML=FALSE)

## Warning in optwrap(optimizer, devfun, getStart(start, rho$lower,
rho$pp), :  convergence code 1 from bobyqa:  bobyqa -- maximum number
of function evaluations exceeded

gm_seb=gamm4(l24~stage+s(l0.s, k=kl)+s(density.s, supply.s, k=ke),
        random=~(1|pop.ID), data=temp, REML=FALSE)
gm_set=gamm4(l24~stage+s(density.s, supply.s, k=ke)+trt+s(day, by=trt, k=kd),
        random=~(1|pop.ID), data=temp, REML=FALSE)
gm_sbt=gamm4(l24~stage+s(l0.s, k=kl)+trt+s(day, by=trt, k=kd),
        random=~(1|pop.ID), data=temp, REML=FALSE)
gm_sb=gamm4(l24~stage+s(l0.s, k=kl),
        random=~(1|pop.ID), data=temp, REML=FALSE)
gm_se=gamm4(l24~stage+s(density.s, supply.s, k=ke),
        random=~(1|pop.ID), data=temp, REML=FALSE)
gm_st=gamm4(l24~stage+trt+s(day, by=trt, k=kd),
        random=~(1|pop.ID), data=temp, REML=FALSE)
gm_s0=gamm4(l24~stage,
        random=~(1|pop.ID), data=temp, REML=FALSE)
```

`gm_sfull` had a warning. It might be ok. So check out the components.

```
summary(gm_sfull$gam)

##
## Family: gaussian
## Link function: identity
##
## Formula:
## l24 ~ stage + s(l0.s, k = kl) + s(density.s, supply.s, k = ke) +
##     trt + s(day, by = trt, k = kd)
##
```

```
## Parametric coefficients:
##              Estimate Std. Error t value Pr(>|t|)    
## (Intercept)  0.541814   0.003953 137.072  < 2e-16 ***
## stageproto   0.002755   0.002544   1.083  0.27892    
## stagetrito  -0.003574   0.004140  -0.863  0.38814    
## stagemale   -0.020074   0.004847  -4.142 3.58e-05 ***
## stagefemale -0.016708   0.005102  -3.275  0.00107 ** 
## trtT2       -0.002651   0.003354  -0.790  0.42934    
## trtT3       -0.005223   0.002083  -2.508  0.01221 *  
## trtT4        0.001858   0.002069   0.898  0.36942    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                          edf Ref.df        F p-value    
## s(l0.s)                3.918  3.918 5504.201 < 2e-16 ***
## s(density.s,supply.s) 5.828  5.828    3.063 0.00618 ** 
## s(day):trtT1          1.000  1.000    0.031 0.85984    
## s(day):trtT2          1.000  1.000    2.863 0.09079 .  
## s(day):trtT3          1.000  1.000    7.842 0.00515 ** 
## s(day):trtT4          3.770  3.770    6.225 0.00010 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.993   
## lmer.REML = -11404  Scale est. = 0.00024229  n = 2087
```

```
summary(gm_sfull$mer)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
##
##      AIC      BIC   logLik deviance df.resid 
## -11357.9 -11228.1   5702.0 -11403.9     2064 
##
## Scaled residuals: 
##     Min      1Q  Median      3Q     Max 
## -3.6189 -0.5956 -0.0353  0.5737  3.5610 
##
## Random effects:
##  Groups   Name                  Variance  Std.Dev.
```

```
##  pop.ID   (Intercept)          1.532e-06 0.001238
##  Xr.4     s(day):trtT4         3.813e-02 0.195262
##  Xr.3     s(day):trtT3         0.000e+00 0.000000
##  Xr.2     s(day):trtT2         0.000e+00 0.000000
##  Xr.1     s(day):trtT1         0.000e+00 0.000000
##  Xr.0     s(density.s,supply.s) 7.814e-03 0.088398
##  Xr       s(l0.s)              1.134e+00 1.065099
##  Residual                      2.423e-04 0.015566
## Number of obs: 2087, groups:
## pop.ID, 8; Xr.4, 8; Xr.3, 8; Xr.2, 8; Xr.1, 8; Xr.0, 7; Xr, 3
##
## Fixed effects:
##                             Estimate Std. Error t value
## X(Intercept)               0.5418138  0.0039528  137.07
## Xstageproto                0.0027550  0.0025437    1.08
## Xstagetrito               -0.0035738  0.0041402   -0.86
## Xstagemale                -0.0200745  0.0048468   -4.14
## Xstagefemale              -0.0167082  0.0051020   -3.27
## XtrtT2                    -0.0026515  0.0033543   -0.79
## XtrtT3                    -0.0052233  0.0020825   -2.51
## XtrtT4                     0.0018579  0.0020695    0.90
## Xs(l0.s)Fx1                0.1918407  0.0030595   62.70
## Xs(density.s,supply.s)Fx1 -0.0029988  0.0011353   -2.64
## Xs(density.s,supply.s)Fx2  0.0019908  0.0009350    2.13
## Xs(day):trtT1Fx1          -0.0001325  0.0007501   -0.18
## Xs(day):trtT2Fx1          -0.0044768  0.0026458   -1.69
## Xs(day):trtT3Fx1          -0.0039615  0.0014146   -2.80
## Xs(day):trtT4Fx1          -0.0204536  0.0053623   -3.81
##
## Correlation of Fixed Effects:
##             X(Int) Xstgpr Xstgtr Xstgml Xstgfm XtrtT2 XtrtT3 XtrtT4 X(0.)F
## Xstageproto -0.724
## Xstagetrito -0.881  0.836
## Xstagemale  -0.909  0.712  0.923
## Xstagefemal -0.904  0.688  0.888  0.968
## XtrtT2      -0.324  0.018  0.024  0.019  0.014
## XtrtT3      -0.338  0.012  0.020  0.022  0.026  0.711
## XtrtT4      -0.360  0.031  0.050  0.062  0.075  0.560  0.580
## Xs(l0.s)Fx1  0.658 -0.674 -0.757 -0.645 -0.620 -0.076 -0.053 -0.105
```

```
## Xs(dn.,.)F1 -0.243  0.048  0.075  0.095  0.116  0.609  0.435  0.156 -0.089
## Xs(dn.,.)F2  0.092 -0.015 -0.025 -0.033 -0.048 -0.318 -0.253  0.083  0.047
## Xs(dy):T1F1 -0.020 -0.018 -0.009  0.006  0.021  0.060  0.039  0.022  0.008
## Xs(dy):T2F1 -0.211  0.008  0.014  0.018  0.017  0.809  0.513  0.299 -0.060
## Xs(dy):T3F1 -0.184 -0.025 -0.022 -0.016 -0.010  0.709  0.519  0.295 -0.034
## Xs(dy):T4F1 -0.109  0.033  0.037  0.033  0.034  0.259  0.196  0.120 -0.044
##             X(.,.)F1 X(.,.)F2 X():T1 X():T2 X():T3
## Xstageproto
## Xstagetrito
## Xstagemale
## Xstagefemal
## XtrtT2
## XtrtT3
## XtrtT4
## Xs(l0.s)Fx1
## Xs(dn.,.)F1
## Xs(dn.,.)F2 -0.406
## Xs(dy):T1F1  0.062   -0.010
## Xs(dy):T2F1  0.657   -0.401    0.117
## Xs(dy):T3F1  0.655   -0.431    0.132  0.767
## Xs(dy):T4F1  0.255   -0.064    0.027  0.263  0.265
## convergence code: 1
```

Some of the random effects variance components associated with treatment splines (past environment variable) are 0. The maximum correlation of fixed effects is 0.96. This is weak evidence that we should possibly stick to the simpler model `gm_full`. So to be safe we omit `gm_sfull`.

```
AICctab(gm_full$mer, gm_eb$mer, gm_et$mer, gm_bt$mer,
        gm_b$mer, gm_e$mer, gm_t$mer, gm_0$mer,
        gm_seb$mer, gm_set$mer, gm_sbt$mer, gm_sb$mer,
        gm_se$mer, gm_st$mer, gm_s0$mer, nobs=nrow(temp))

##             dAICc   df
## gm_sbt$mer      0.0 20
## gm_seb$mer      5.7 12
## gm_sb$mer      25.8 9
## gm_bt$mer      74.8 16
## gm_full$mer    80.6 19
## gm_eb$mer      81.5 8
```

```
## gm_b$mer      111.7 5
## gm_st$mer    4906.6 18
## gm_set$mer   4911.3 21
## gm_se$mer    5109.8 10
## gm_s0$mer    5397.9 7
## gm_e$mer    10217.0 6
## gm_et$mer   10217.3 17
## gm_t$mer    10219.8 14
## gm_0$mer    10245.1 3
```

Now do Wood's test on the full model to see what's non-zero. Also check the best models's r^2 and population variance.

```
summary(gm_full$gam)

##
## Family: gaussian
## Link function: identity
##
## Formula:
## l24 ~ s(l0.s, k = kl) + s(density.s, supply.s, k = ke) + trt +
##     s(day, by = trt, k = kd)
##
## Parametric coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.529256   0.001393 379.995   <2e-16 ***
## trtT2        0.002335   0.004437   0.526   0.5988
## trtT3       -0.001518   0.001855  -0.819   0.4131
## trtT4        0.003652   0.001977   1.847   0.0649 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                          edf Ref.df         F  p-value
## s(l0.s)                3.880  3.880 69545.091  < 2e-16 ***
## s(density.s,supply.s) 5.773  5.773     4.372 0.000292 ***
## s(day):trtT1           1.000  1.000     0.052 0.820098
## s(day):trtT2           2.864  2.864     0.849 0.458313
## s(day):trtT3           1.000  1.000     0.068 0.793572
## s(day):trtT4           1.000  1.000     6.644 0.010014 *
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.993
## lmer.REML = -11311  Scale est. = 0.00025413  n = 2087
```

```
summary(gm_sbt$gam)[["r.sq"]]
```

```
## [1] 0.9928647
```

```
summary(gm_sbt$mer)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
##
##      AIC      BIC   logLik deviance df.resid
## -11353.6 -11240.7   5696.8 -11393.6     2067
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.6166 -0.5955 -0.0504  0.5619  3.6141
##
## Random effects:
##  Groups   Name          Variance  Std.Dev.
##  pop.ID   (Intercept)   1.477e-06 1.215e-03
##  Xr.3     s(day):trtT4 1.187e-01 3.445e-01
##  Xr.2     s(day):trtT3 0.000e+00 0.000e+00
##  Xr.1     s(day):trtT2 9.628e-16 3.103e-08
##  Xr.0     s(day):trtT1 0.000e+00 0.000e+00
##  Xr       s(l0.s)      1.384e+00 1.176e+00
##  Residual              2.440e-04 1.562e-02
## Number of obs: 2087, groups:
## pop.ID, 8; Xr.3, 8; Xr.2, 8; Xr.1, 8; Xr.0, 8; Xr, 3
##
## Fixed effects:
##                      Estimate Std. Error t value
## X(Intercept)        0.5386004  0.0036981  145.64
## Xstageproto         0.0032827  0.0025467    1.29
## Xstagetrito        -0.0023875  0.0041290   -0.58
## Xstagemale         -0.0185940  0.0048274   -3.85
## Xstagefemale       -0.0148305  0.0050769   -2.92
```

```
## XtrtT2            0.0034161  0.0018149    1.88
## XtrtT3           -0.0028136  0.0015385   -1.83
## XtrtT4            0.0039005  0.0015433    2.53
## Xs(l0.s)Fx1       0.1904810  0.0030569   62.31
## Xs(day):trtT1Fx1 -0.0001667  0.0007093   -0.24
## Xs(day):trtT2Fx1  0.0002169  0.0013468    0.16
## Xs(day):trtT3Fx1 -0.0016907  0.0006548   -2.58
## Xs(day):trtT4Fx1 -0.0250289  0.0068840   -3.64
##
## Correlation of Fixed Effects:
##             X(Int) Xstgpr Xstgtr Xstgml Xstgfm XtrtT2 XtrtT3 XtrtT4 X(0.)F
## Xstageproto -0.755
## Xstagetrito -0.915  0.834
## Xstagemale  -0.942  0.709  0.922
## Xstagefemal -0.933  0.685  0.886  0.967
## XtrtT2      -0.060 -0.049 -0.083 -0.120 -0.153
## XtrtT3      -0.167 -0.019 -0.032 -0.043 -0.050  0.438
## XtrtT4      -0.236  0.006  0.014  0.027  0.043  0.406  0.491
## Xs(l0.s)Fx1  0.667 -0.672 -0.756 -0.642 -0.617  0.033  0.020 -0.066
## Xs(dy):T1F1 -0.029 -0.005  0.011  0.028  0.043 -0.013  0.000  0.015 -0.006
## Xs(dy):T2F1  0.098 -0.047 -0.075 -0.099 -0.129  0.432  0.012 -0.012  0.034
## Xs(dy):T3F1  0.156 -0.107 -0.141 -0.159 -0.177  0.042 -0.025 -0.012  0.075
## Xs(dy):T4F1 -0.030  0.031  0.033  0.028  0.029 -0.002 -0.001 -0.013 -0.031
##             X():T1 X():T2 X():T3
## Xstageproto
## Xstagetrito
## Xstagemale
## Xstagefemal
## XtrtT2
## XtrtT3
## XtrtT4
## Xs(l0.s)Fx1
## Xs(dy):T1F1
## Xs(dy):T2F1 -0.015
## Xs(dy):T3F1 -0.015  0.034
## Xs(dy):T4F1  0.000 -0.002 -0.004
```

The estimate of the standard deviation among populations is small relative to other estimates.

4 Probability of Initiating Transition in 24 Hours

Subset data to only include the juvenile survivors.

```
tempT=transform(subset(Indiv, (!stage %in% c("male","female") & (s24==1))),
        t.init.24=as.numeric(t24 %in% c("next stage", "quiescent")),
        t.done.24=as.numeric(t24 == "next stage"),
        stage=stage[, drop=TRUE]
        )
temp=na.omit(tempT[
        ,c("t.init.24","l0.s","trt","day","density.s", "supply.s", "pop.ID", "stage")
```

```
t24m_full=gamm4(t.init.24~s(l0.s, k=kl)+s(density.s, supply.s, k=ke)+
        trt+s(day, by=trt, k=kd), family=binomial, random=~(1|pop.ID), data=temp)
t24m_eb=gamm4(t.init.24~s(l0.s, k=kl)+s(density.s, supply.s, k=ke),
        family=binomial, random=~(1|pop.ID), data=temp)
t24m_et=gamm4(t.init.24~s(density.s, supply.s, k=ke)+trt+s(day, by=trt, k=kd),
        family=binomial, random=~(1|pop.ID), data=temp)
t24m_bt=gamm4(t.init.24~s(l0.s, k=kl)+trt+s(day, by=trt, k=kd),
        family=binomial, random=~(1|pop.ID), data=temp)
t24m_b=gamm4(t.init.24~s(l0.s, k=kl),
        family=binomial, random=~(1|pop.ID), data=temp)
t24m_e=gamm4(t.init.24~s(density.s, supply.s, k=ke),
        family=binomial, random=~(1|pop.ID), data=temp)
t24m_t=gamm4(t.init.24~trt+s(day, by=trt, k=kd),
        family=binomial, random=~(1|pop.ID), data=temp)
t24m_0=gamm4(t.init.24~1,
        family=binomial, random=~(1|pop.ID), data=temp)

t24m_sfull=gamm4(t.init.24~stage+ s(l0.s, k=kl)+s(density.s, supply.s, k=ke)+
        trt+s(day, by=trt, k=kd), family=binomial, random=~(1|pop.ID), data=temp)
t24m_seb=gamm4(t.init.24~stage+ s(l0.s, k=kl)+s(density.s, supply.s, k=ke),
        family=binomial, random=~(1|pop.ID), data=temp)
t24m_set=gamm4(t.init.24~stage+ s(density.s, supply.s, k=ke)+trt+s(day, by=trt, k=kd)
        family=binomial, random=~(1|pop.ID), data=temp)
t24m_sbt=gamm4(t.init.24~stage+ s(l0.s, k=kl)+trt+s(day, by=trt, k=kd),
        family=binomial, random=~(1|pop.ID), data=temp)
t24m_sb=gamm4(t.init.24~stage+ s(l0.s, k=kl),
        family=binomial, random=~(1|pop.ID), data=temp)
```

```
t24m_se=gamm4(t.init.24~stage+ s(density.s, supply.s, k=ke),
        family=binomial, random=~(1|pop.ID), data=temp)
t24m_st=gamm4(t.init.24~stage+ trt+s(day, by=trt, k=kd),
        family=binomial, random=~(1|pop.ID), data=temp)

## Warning in (function (fn, par, lower = rep.int(-Inf, n), upper
= rep.int(Inf, :  failure to converge in 10000 evaluations

t24m_s0=gamm4(t.init.24~stage,
        family=binomial, random=~(1|pop.ID), data=temp)
```

`t24m_st` did not converge, indicating that it might be overparemeterized, so we omit it from AIC comparison.

```
AICctab(t24m_full$mer, t24m_eb$mer, t24m_et$mer, t24m_bt$mer,
        t24m_b$mer, t24m_e$mer, t24m_t$mer,t24m_0$mer,
        t24m_sfull$mer, t24m_seb$mer, t24m_set$mer, t24m_sbt$mer,
        t24m_sb$mer, t24m_se$mer, t24m_s0$mer, nobs=nrow(temp))

##                dAICc df
## t24m_seb$mer     0.0 9
## t24m_sb$mer      8.2 6
## t24m_sbt$mer    13.6 17
## t24m_sfull$mer  14.7 20
## t24m_eb$mer    165.1 7
## t24m_full$mer  177.9 18
## t24m_bt$mer    187.0 15
## t24m_b$mer     217.0 4
## t24m_se$mer    242.9 7
## t24m_set$mer   258.7 18
## t24m_e$mer     273.3 5
## t24m_et$mer    289.0 16
## t24m_t$mer     295.6 13
## t24m_s0$mer    328.9 4
## t24m_0$mer     353.7 2
```

Now do Wood's test on the full model to see what's non-zero. Also check the best models's r^2 and population variance.

```
summary(t24m_sfull$gam)

##
## Family: binomial
## Link function: logit
##
## Formula:
## t.init.24 ~ stage + s(l0.s, k = kl) + s(density.s, supply.s,
##     k = ke) + trt + s(day, by = trt, k = kd)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   4.6581     0.6320   7.370 1.70e-13 ***
## stageproto   -5.5702     0.6000  -9.284  < 2e-16 ***
## stagetrito  -13.9131     1.3623 -10.213  < 2e-16 ***
## trtT2        -1.1407     0.9877  -1.155    0.248
## trtT3         0.2351     0.3795   0.619    0.536
## trtT4        -1.8931     0.3789  -4.996 5.85e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                        edf Ref.df  Chi.sq p-value
## s(l0.s)                  1      1 126.004 < 2e-16 ***
## s(density.s,supply.s)    2      2   4.748 0.09309 .
## s(day):trtT1             1      1   0.096 0.75653
## s(day):trtT2             1      1   0.175 0.67605
## s(day):trtT3             1      1   2.512 0.11300
## s(day):trtT4             1      1  10.591 0.00114 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.415
## glmer.ML = 528.15  Scale est. = 1         n = 995

summary(t24m_seb$gam)[["r.sq"]]

## [1] 0.451062

summary(t24m_seb$mer)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
##
##      AIC      BIC   logLik deviance df.resid
##    554.1    598.2   -268.0    536.1      986
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -2.653 -0.271 -0.087 -0.016 36.953
##
## Random effects:
##  Groups Name                  Variance  Std.Dev.
##  pop.ID (Intercept)           6.536e-03  0.08084
##  Xr.0   s(density.s,supply.s) 1.212e+03 34.81968
##  Xr     s(l0.s)               9.167e+03 95.74623
## Number of obs: 995, groups:  pop.ID, 8; Xr.0, 7; Xr, 3
##
## Fixed effects:
##                            Estimate Std. Error z value Pr(>|z|)
## X(Intercept)                 6.3526     0.9639   6.590 4.39e-11 ***
## Xstageproto                 -8.7425     1.1986  -7.294 3.00e-13 ***
## Xstagetrito                -19.1178     2.2138  -8.636  < 2e-16 ***
## Xs(l0.s)Fx1                  5.1136     1.1491   4.450 8.58e-06 ***
## Xs(density.s,supply.s)Fx1  -0.5362     0.3048  -1.759   0.0785 .
## Xs(density.s,supply.s)Fx2   0.1934     0.2545   0.760   0.4474
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             X(Int) Xstgpr Xstgtr X(0.)F X(.,.)F1
## Xstageproto -0.882
## Xstagetrito -0.961  0.798
## Xs(l0.s)Fx1  0.084 -0.412 -0.011
## Xs(dn.,.)F1  0.124 -0.072 -0.064  0.129
## Xs(dn.,.)F2  0.046 -0.029 -0.067  0.019  0.073
```

The estimate of the standard deviation among populations is small relative to other estimates.

5 Probability of Reproducing

Remove ones that were dead at 24hrs. Use females only.

```
Indivtmp=subset(Indiv, stage=="female" & !is.na(s24))
```

```
temp=na.omit(subset(Indivtmp, !is.na(l0.s*as.numeric(trt)*f24) & (s24==1))[
        ,c("f24","l0.s","trt","day","density.s", "supply.s", "pop.ID")])
```

```
fbm_full=gamm4(as.numeric(f24>0)~s(l0.s, k=kl)+s(density.s, supply.s, k=ke)+
        trt+s(day, by=trt, k=kd), family=binomial, random=~(1|pop.ID), data=temp)
fbm_eb=gamm4(as.numeric(f24>0)~s(l0.s, k=kl)+s(density.s, supply.s, k=ke),
        family=binomial, random=~(1|pop.ID), data=temp)
fbm_et=gamm4(as.numeric(f24>0)~s(density.s, supply.s, k=ke)+trt+s(day, by=trt, k=kd),
        family=binomial, random=~(1|pop.ID), data=temp)

## Warning in (function (fn, par, lower = rep.int(-Inf, n), upper
= rep.int(Inf, :  failure to converge in 10000 evaluations

fbm_bt=gamm4(as.numeric(f24>0)~s(l0.s, k=kl)+trt+s(day, by=trt, k=kd),
        family=binomial, random=~(1|pop.ID), data=temp)
fbm_b=gamm4(as.numeric(f24>0)~s(l0.s, k=kl),
        family=binomial, random=~(1|pop.ID), data=temp)
fbm_e=gamm4(as.numeric(f24>0)~s(density.s, supply.s, k=ke),
        family=binomial, random=~(1|pop.ID), data=temp)
fbm_t=gamm4(as.numeric(f24>0)~trt+s(day, by=trt, k=kd),
        family=binomial, random=~(1|pop.ID), data=temp)
fbm_0=gamm4(as.numeric(f24>0)~1,
        family=binomial, random=~(1|pop.ID), data=temp)
```

`fbm_et` did not converge, indicating that it might be overparemeterized, so we omit it from AIC comparison.

```
AICctab(fbm_full$mer, fbm_eb$mer, fbm_bt$mer,
        fbm_b$mer, fbm_e$mer, fbm_t$mer, fbm_0$mer, nobs=nrow(temp))

##              dAICc df
## fbm_eb$mer     0.0 7
```

```
## fbm_full$mer   2.2 18
## fbm_bt$mer    18.0 15
## fbm_e$mer     20.5 5
## fbm_t$mer     28.8 13
## fbm_b$mer     82.0 4
## fbm_0$mer    169.2 2
```

```
summary(fbm_full$gam)
```

```
##
## Family: binomial
## Link function: logit
##
## Formula:
## as.numeric(f24 > 0) ~ s(l0.s, k = kl) + s(density.s, supply.s,
##     k = ke) + trt + s(day, by = trt, k = kd)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   2.1597     0.3729   5.792 6.96e-09 ***
## trtT2        -1.6526     0.7576  -2.181   0.0292 *
## trtT3         0.5145     0.5304   0.970   0.3320
## trtT4        -2.3255     0.4549  -5.112 3.19e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                          edf Ref.df Chi.sq  p-value
## s(l0.s)                1.000  1.000 23.763 1.09e-06 ***
## s(density.s,supply.s) 2.000  2.000 17.951 0.000126 ***
## s(day):trtT1          1.000  1.000  0.074 0.784928
## s(day):trtT2          1.000  1.000  0.149 0.699583
## s(day):trtT3          2.396  2.396 10.871 0.007447 **
## s(day):trtT4          1.000  1.000  0.001 0.976011
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.478
## glmer.ML = 395.08  Scale est. = 1         n = 568
```

```r
summary(fbm_eb$gam)[["r.sq"]]
```

```
## [1] 0.3839028
```

```r
summary(fbm_eb$mer)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
##
##      AIC      BIC   logLik deviance df.resid
##    442.0    472.4   -214.0    428.0      561
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -6.7025 -0.2539  0.2499  0.3691  4.8874
##
## Random effects:
##  Groups Name                  Variance Std.Dev.
##  pop.ID (Intercept)             0.877   0.9365
##  Xr.0   s(density.s,supply.s) 277.581  16.6608
##  Xr     s(l0.s)                 0.000   0.0000
## Number of obs: 568, groups:  pop.ID, 8; Xr.0, 7; Xr, 3
##
## Fixed effects:
##                            Estimate Std. Error z value Pr(>|z|)
## X(Intercept)                 1.4338     0.3613   3.968 7.24e-05 ***
## Xs(l0.s)Fx1                  0.8367     0.1760   4.755 1.99e-06 ***
## Xs(density.s,supply.s)Fx1  -0.9570     0.3438  -2.783  0.00538 **
## Xs(density.s,supply.s)Fx2   1.0313     0.3860   2.672  0.00754 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             X(Int) X(0.)F X(.,.)F1
## Xs(l0.s)Fx1  0.107
## Xs(dn.,.)F1 -0.044 -0.104
## Xs(dn.,.)F2  0.024 -0.213  0.231
```

The estimate of the standard deviation among populations is in the same range as other estimates. This could indicate that populations behaved differently. Figure S1 shows that the two populations within a treatment do not track each other perfectly, but fairly well.

6 Egg Counts, Given Reproduction

```
temp=na.omit(subset(Indivtmp, (f24>0) & (s24==1))[
        ,c("f24","l0.s","trt","day","density.s", "supply.s", "pop.ID")])
```

```
fcm_full=gamm4(f24-1~s(l0.s,k=kl)+s(density.s, supply.s, k=ke)+trt+s(day, by=trt, k=k
        family=poisson, random=~(1|pop.ID), data=temp)
fcm_eb=gamm4(f24-1~s(l0.s, k=kl)+s(density.s, supply.s, k=ke),
        family=poisson, random=~(1|pop.ID), data=temp)
fcm_et=gamm4(f24-1~s(density.s, supply.s, k=ke)+trt+s(day, by=trt, k=kd),
        family=poisson, random=~(1|pop.ID), data=temp)
fcm_bt=gamm4(f24-1~s(l0.s, k=kl)+trt+s(day, by=trt, k=kd),
        family=poisson, random=~(1|pop.ID), data=temp)
fcm_b=gamm4(f24-1~s(l0.s, k=kl),
        family=poisson, random=~(1|pop.ID), data=temp)
fcm_e=gamm4(f24-1~s(density.s, supply.s, k=ke),
        family=poisson, random=~(1|pop.ID), data=temp)
fcm_t=gamm4(f24-1~trt+s(day, by=trt, k=kd),
        family=poisson, random=~(1|pop.ID), data=temp)
fcm_0=gamm4(f24-1~1,
        family=poisson, random=~(1|pop.ID), data=temp)

AICctab(fcm_full$mer, fcm_eb$mer, fcm_et$mer, fcm_bt$mer,
        fcm_b$mer, fcm_e$mer, fcm_t$mer, fcm_0$mer, nobs=nrow(temp))

##              dAICc df
## fcm_eb$mer     0.0 7
## fcm_full$mer   8.5 18
## fcm_bt$mer    13.9 15
## fcm_t$mer    129.7 13
## fcm_et$mer   133.6 16
## fcm_e$mer    188.2 5
## fcm_b$mer    410.4 4
## fcm_0$mer    909.3 2
```

```
summary(fcm_full$gam)
```

```
##
## Family: poisson
## Link function: log
##
## Formula:
## f24 - 1 ~ s(l0.s, k = kl) + s(density.s, supply.s, k = ke) +
##     trt + s(day, by = trt, k = kd)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   1.0088     0.1085   9.300  < 2e-16 ***
## trtT2        -0.3792     0.4363  -0.869  0.38470
## trtT3         0.5504     0.1778   3.096  0.00196 **
## trtT4        -0.3533     0.1942  -1.819  0.06889 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                         edf Ref.df  Chi.sq p-value
## s(l0.s)               3.182  3.182 149.766 < 2e-16 ***
## s(density.s,supply.s) 7.327  7.327 349.382 < 2e-16 ***
## s(day):trtT1          1.000  1.000   0.013 0.91027
## s(day):trtT2          1.000  1.000   0.361 0.54810
## s(day):trtT3          1.000  1.000   6.673 0.00979 **
## s(day):trtT4          1.000  1.000   1.210 0.27129
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.763
## glmer.ML = 677.08  Scale est. = 1         n = 409
```

```
summary(fcm_eb$gam)[["r.sq"]]
```

```
## [1] 0.7393331
```

```
summary(fcm_eb$mer)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
```

```
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
##
##      AIC      BIC   logLik deviance df.resid
##   1810.9   1839.0   -898.5   1796.9      402
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.3432 -0.9055 -0.1298  0.6910  7.8782
##
## Random effects:
##  Groups Name                  Variance  Std.Dev.
##  pop.ID (Intercept)             0.02758  0.1661
##  Xr.0   s(density.s,supply.s) 122.76138 11.0798
##  Xr     s(l0.s)                 0.00000  0.0000
## Number of obs: 409, groups:  pop.ID, 8; Xr.0, 7; Xr, 3
##
## Fixed effects:
##                           Estimate Std. Error z value Pr(>|z|)
## X(Intercept)               1.05810    0.07075  14.955   <2e-16 ***
## Xs(l0.s)Fx1                0.39709    0.02835  14.007   <2e-16 ***
## Xs(density.s,supply.s)Fx1  0.73155    0.08451   8.657   <2e-16 ***
## Xs(density.s,supply.s)Fx2 -0.19052    0.08249  -2.310   0.0209 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              X(Int) X(0.)F X(.,.)F1
## Xs(l0.s)Fx1 -0.109
## Xs(dn.,.)F1 -0.167 -0.043
## Xs(dn.,.)F2  0.145  0.083 -0.569
```

The estimate of the standard deviation among populations is smaller than the other estimates.

7 Egg Size

Take the average within female as the response.

```
load("../Egg size from sampling MB.Rdata")
eggdat$day=as.numeric(eggdat$date.samp-min(eggdat$date.samp)+1)
temp=na.omit(ddply(eggdat, .(fem.ID), summarize,
                esize=mean(esize, na.omit=TRUE),
                l0.s=l0.s[1],
                pop.ID=pop.ID[1],
                density.s= density.s[1],
                supply.s= supply.s[1],
                day=day[1],
                trt=trt[1]))

esm_full=gamm4(esize~s(l0.s, k=kl)+s(density.s, supply.s, k=ke)+trt+s(day, by=trt, k=
        REML=FALSE, random=~(1|pop.ID), data=temp)
esm_eb=gamm4(esize~s(l0.s, k=kl)+s(density.s, supply.s, k=ke),
        REML=FALSE, random=~(1|pop.ID), data=temp)
esm_et=gamm4(esize~s(density.s, supply.s, k=ke)+trt+s(day, by=trt, k=kd),
        REML=FALSE, random=~(1|pop.ID), data=temp)
esm_bt=gamm4(esize~s(l0.s, k=kl)+trt+s(day, by=trt, k=kd),
        REML=FALSE, random=~(1|pop.ID), data=temp)
esm_b=gamm4(esize~s(l0.s, k=kl),
        REML=FALSE, random=~(1|pop.ID), data=temp)
esm_e=gamm4(esize~s(density.s, supply.s, k=ke),
        REML=FALSE, random=~(1|pop.ID), data=temp)
esm_t=gamm4(esize~trt+s(day, by=trt, k=kd),
        REML=FALSE, random=~(1|pop.ID), data=temp)
esm_0=gamm4(esize~1,
        REML=FALSE, random=~(1|pop.ID), data=temp)

AICctab(esm_full$mer, esm_eb$mer, esm_et$mer, esm_bt$mer,
        esm_b$mer, esm_e$mer, esm_t$mer, esm_0$mer, nobs=nrow(temp))
```

```
##              dAICc df
## esm_e$mer     0.0  6
## esm_eb$mer    1.6  8
## esm_t$mer     8.0  14
## esm_bt$mer   12.2  16
## esm_et$mer   12.5  17
## esm_b$mer    13.6  5
## esm_0$mer    14.9  3
```

```
## esm_full$mer 16.9  19

summary(esm_full$gam)

##
## Family: gaussian
## Link function: identity
##
## Formula:
## esize ~ s(l0.s, k = kl) + s(density.s, supply.s, k = ke) + trt +
##     s(day, by = trt, k = kd)
##
## Parametric coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.1772784  0.0006767 261.993   <2e-16 ***
## trtT2       -0.0048530  0.0027293  -1.778   0.0762 .
## trtT3       -0.0015562  0.0011223  -1.387   0.1663
## trtT4       -0.0008934  0.0011663  -0.766   0.4441
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                         edf Ref.df     F p-value
## s(l0.s)               1.000  1.000 0.002 0.96070
## s(density.s,supply.s) 2.000  2.000 0.925 0.39723
## s(day):trtT1          1.000  1.000 0.032 0.85724
## s(day):trtT2          1.000  1.000 2.730 0.09925 .
## s(day):trtT3          2.331  2.331 5.867 0.00205 **
## s(day):trtT4          1.000  1.000 7.355 0.00697 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.0647
## lmer.REML = -2827.5  Scale est. = 5.8515e-05  n = 410

summary(esm_e$gam)[["r.sq"]]

## [1] 0.06183376

summary(esm_e$mer)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
##
##      AIC      BIC   logLik deviance df.resid
##  -2804.7  -2780.6   1408.3  -2816.7      404
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.4629 -0.6682  0.0804  0.5928  2.7496
##
## Random effects:
##  Groups   Name                  Variance  Std.Dev.
##  pop.ID   (Intercept)           0.000e+00 0.000000
##  Xr       s(density.s,supply.s) 7.827e-04 0.027977
##  Residual                       5.987e-05 0.007737
## Number of obs: 410, groups:  pop.ID, 8; Xr, 7
##
## Fixed effects:
##                             Estimate Std. Error t value
## X(Intercept)               0.1764325  0.0003821   461.7
## Xs(density.s,supply.s)Fx1 -0.0013077  0.0005515    -2.4
## Xs(density.s,supply.s)Fx2  0.0013731  0.0006216     2.2
##
## Correlation of Fixed Effects:
##             X(Int) X(.,.)F1
## Xs(dn.,.)F1  0.000
## Xs(dn.,.)F2  0.000 -0.141
```

The estimate of the standard deviation among populations is 0.

8 Survival

```
temp=na.omit(Indiv[
        ,c("s24","l0.s","trt","day","density.s", "supply.s", "pop.ID", "stage")])
```

```
sm_full=gamm4(s24~s(l0.s, k=kl)+s(density.s, supply.s, k=ke)+
        trt+s(day, by=trt, k=kd), family=binomial, random=~(1|pop.ID), data=temp)
sm_eb=gamm4(s24~s(l0.s, k=kl)+s(density.s, supply.s, k=ke),
```

```
        family=binomial, random=~(1|pop.ID), data=temp)
sm_et=gamm4(s24~s(density.s, supply.s, k=ke)+trt+s(day, by=trt, k=kd),
        family=binomial, random=~(1|pop.ID), data=temp)
sm_bt=gamm4(s24~s(l0.s, k=kl)+trt+s(day, by=trt, k=kd),
        family=binomial, random=~(1|pop.ID), data=temp)
sm_b=gamm4(s24~s(l0.s, k=kl),
        family=binomial, random=~(1|pop.ID), data=temp)
sm_e=gamm4(s24~s(density.s, supply.s, k=ke),
        family=binomial, random=~(1|pop.ID), data=temp)
sm_t=gamm4(s24~trt+s(day, by=trt, k=kd),
        family=binomial, random=~(1|pop.ID), data=temp)
sm_0=gamm4(s24~1,
        family=binomial, random=~(1|pop.ID), data=temp)
sm_sfull=gamm4(s24~stage+ s(l0.s, k=kl)+s(density.s, supply.s, k=ke)+
        trt+s(day, by=trt, k=kd), family=binomial, random=~(1|pop.ID), data=temp)
sm_seb=gamm4(s24~stage+ s(l0.s, k=kl)+s(density.s, supply.s, k=ke),
        family=binomial, random=~(1|pop.ID), data=temp)
sm_set=gamm4(s24~stage+ s(density.s, supply.s, k=ke)+trt+s(day, by=trt, k=kd),
        family=binomial, random=~(1|pop.ID), data=temp)
sm_sbt=gamm4(s24~stage+ s(l0.s, k=kl)+trt+s(day, by=trt, k=kd),
        family=binomial, random=~(1|pop.ID), data=temp)
sm_sb=gamm4(s24~stage+ s(l0.s, k=kl),
        family=binomial, random=~(1|pop.ID), data=temp)
sm_se=gamm4(s24~stage+ s(density.s, supply.s, k=ke),
        family=binomial, random=~(1|pop.ID), data=temp)
sm_st=gamm4(s24~stage+ trt+s(day, by=trt, k=kd),
        family=binomial, random=~(1|pop.ID), data=temp)
sm_s0=gamm4(s24~stage,
        family=binomial, random=~(1|pop.ID), data=temp)

AICctab(sm_full$mer, sm_eb$mer, sm_et$mer, sm_bt$mer,
        sm_b$mer, sm_e$mer, sm_t$mer, sm_0$mer,
        sm_sfull$mer, sm_seb$mer, sm_set$mer,
        sm_sbt$mer, sm_sb$mer, sm_se$mer, sm_st$mer, sm_s0$mer, nobs=nrow(temp))
```

```
##              dAICc df
## sm_se$mer     0.0  9
## sm_seb$mer    3.8  11
## sm_s0$mer     8.4  6
```

```
## sm_e$mer      9.7  5
## sm_eb$mer    11.3  7
## sm_sb$mer    11.5  8
## sm_0$mer     16.9  2
## sm_st$mer    17.5  17
## sm_set$mer   19.6  20
## sm_b$mer     19.9  4
## sm_sbt$mer   21.5  19
## sm_sfull$mer 23.4  22
## sm_t$mer     27.0  13
## sm_et$mer    29.0  16
## sm_bt$mer    29.3  15
## sm_full$mer  30.7  18
```

```
summary(sm_sfull$gam)
```

```
##
## Family: binomial
## Link function: logit
##
## Formula:
## s24 ~ stage + s(l0.s, k = kl) + s(density.s, supply.s, k = ke) +
##     trt + s(day, by = trt, k = kd)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.66176    0.61444   4.332 1.48e-05 ***
## stageproto   0.18406    0.38759   0.475    0.635
## stagetrito   1.51998    0.62466   2.433    0.015 *
## stagemale    0.15889    0.71979   0.221    0.825
## stagefemale  0.31692    0.90874   0.349    0.727
## trtT2        0.28508    0.53668   0.531    0.595
## trtT3       -0.04604    0.33689  -0.137    0.891
## trtT4        0.06820    0.31447   0.217    0.828
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                       edf Ref.df Chi.sq p-value
## s(l0.s)                 1      1  0.290   0.590
```

```
## s(density.s,supply.s)   2      2  4.056   0.132
## s(day):trtT1            1      1  1.141   0.285
## s(day):trtT2            1      1  1.041   0.308
## s(day):trtT3            1      1  0.264   0.608
## s(day):trtT4            1      1  0.000   0.988
##
## R-sq.(adj) =  0.0109
## glmer.ML = 877.19  Scale est. = 1         n = 2241
```

```
summary(sm_se$gam)[["r.sq"]]
```

```
## [1] 0.01224263
```

```
summary(sm_se$mer)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
##
##      AIC      BIC   logLik deviance df.resid
##    898.9    950.3   -440.4    880.9     2232
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -10.2986   0.1811   0.2215   0.2556   0.3666
##
## Random effects:
##  Groups Name                   Variance  Std.Dev.
##  pop.ID (Intercept)           5.856e-03 0.0765270
##  Xr     s(density.s,supply.s) 1.032e-08 0.0001016
## Number of obs: 2241, groups:  pop.ID, 8; Xr, 7
##
## Fixed effects:
##                           Estimate Std. Error z value Pr(>|z|)
## X(Intercept)               2.92729    0.24776  11.815  < 2e-16 ***
## Xstageproto                0.10703    0.35420   0.302 0.762510
## Xstagetrito                1.29929    0.47865   2.714 0.006638 **
## Xstagemale                -0.20930    0.29623  -0.707 0.479848
## Xstagefemale              -0.14494    0.29592  -0.490 0.624274
## Xs(density.s,supply.s)Fx1  0.11831    0.12259   0.965 0.334499
```

```
## Xs(density.s,supply.s)Fx2 -0.33729    0.09433  -3.576 0.000349 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             X(Int) Xstgpr Xstgtr Xstgml Xstgfm X(.,.)F1
## Xstageproto -0.675                                    
## Xstagetrito -0.497  0.349                             
## Xstagemale  -0.813  0.565  0.417                      
## Xstagefemal -0.809  0.565  0.418  0.676               
## Xs(dn.,.)F1  0.034  0.010  0.001  0.000  0.009        
## Xs(dn.,.)F2 -0.119  0.006 -0.020  0.042  0.005  0.156
```

```
summary(sm_sfull$gam)
```

```
##
## Family: binomial
## Link function: logit
##
## Formula:
## s24 ~ stage + s(l0.s, k = kl) + s(density.s, supply.s, k = ke) +
##     trt + s(day, by = trt, k = kd)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.66176    0.61444   4.332 1.48e-05 ***
## stageproto   0.18406    0.38759   0.475    0.635
## stagetrito   1.51998    0.62466   2.433    0.015 *
## stagemale    0.15889    0.71979   0.221    0.825
## stagefemale  0.31692    0.90874   0.349    0.727
## trtT2        0.28508    0.53668   0.531    0.595
## trtT3       -0.04604    0.33689  -0.137    0.891
## trtT4        0.06820    0.31447   0.217    0.828
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                         edf Ref.df Chi.sq p-value
## s(l0.s)                   1      1  0.290   0.590
## s(density.s,supply.s)     2      2  4.056   0.132
```

```
## s(day):trtT1           1      1  1.141   0.285
## s(day):trtT2           1      1  1.041   0.308
## s(day):trtT3           1      1  0.264   0.608
## s(day):trtT4           1      1  0.000   0.988
##
## R-sq.(adj) =  0.0109
## glmer.ML = 877.19  Scale est. = 1         n = 2241
```

The estimate of the standard deviation among populations is smaller than the other estimates.

9 Version Info

```
sessionInfo()
```

```
## R version 3.2.1 (2015-06-18)
## Platform: x86_64-apple-darwin13.4.0 (64-bit)
## Running under: OS X 10.10.4 (Yosemite)
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats4    stats     graphics  grDevices utils     datasets  methods
## [8] base
##
## other attached packages:
##  [1] gamm4_0.2-3   lme4_1.1-9    Matrix_1.2-1  plyr_1.8.3    bbmle_1.0.17
##  [6] mgcv_1.8-6    nlme_3.1-120  ggplot2_1.0.1 reshape_0.8.5 knitr_1.11
##
## loaded via a namespace (and not attached):
##  [1] Rcpp_0.12.0      magrittr_1.5     splines_3.2.1
##  [4] MASS_7.3-40      munsell_0.4.2    colorspace_1.2-6
##  [7] lattice_0.20-31  minqa_1.2.4      stringr_1.0.0
## [10] highr_0.5        tools_3.2.1      grid_3.2.1
## [13] gtable_0.1.2     digest_0.6.8     numDeriv_2014.2-1
## [16] nloptr_1.0.4     reshape2_1.4.1   formatR_1.2
## [19] codetools_0.2-11 evaluate_0.7.2   labeling_0.3
## [22] stringi_0.5-5    scales_0.2.5     proto_0.3-10
```