Analysis of *Xenorhabdus* transmission

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More indepth analysis of the different component of R_0 transmission mentionned in the paper which is calculated as follows:

$$R_0 = \frac{\beta f e^{-r}}{\nu}$$

where β is the proportion of insects injected with a given isolate that gave the emergence of new IJs, f is the number of IJs produced, r the average number of bacteria carried per IJ, and ν the IJ mortality rate (see Chapuis et al. (2012) P. Roy. Soc. B-Biol. Sci. for more details).

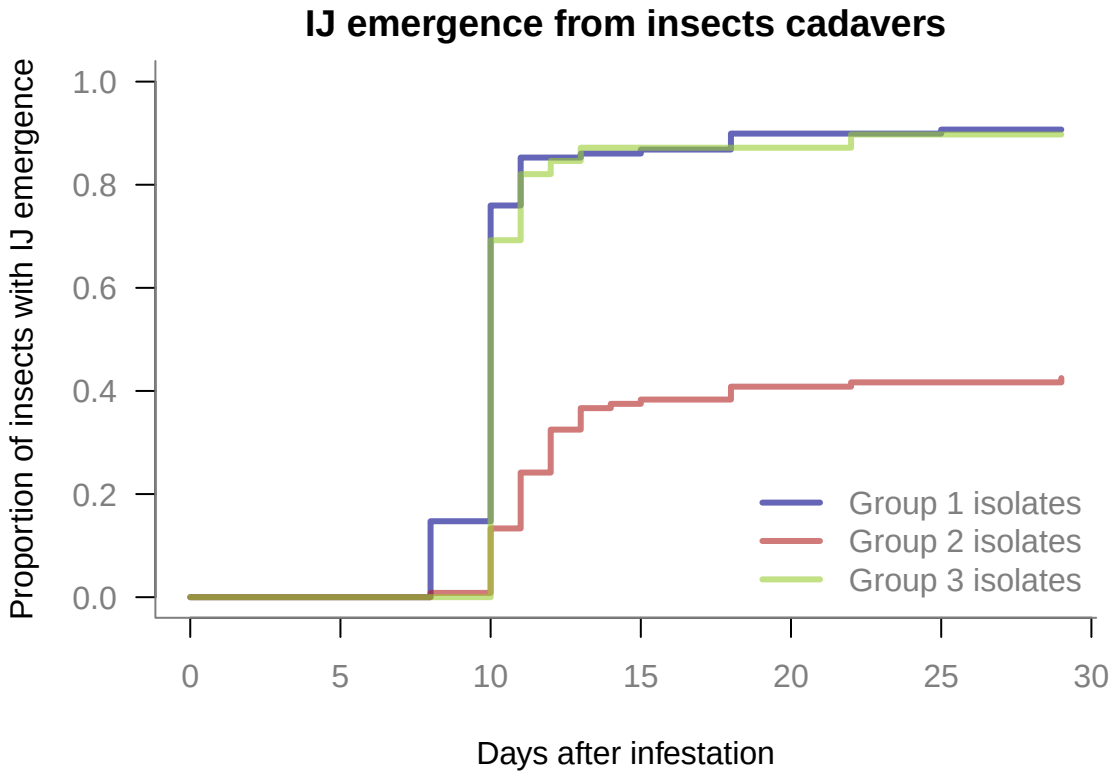
1 Data loading

```
rm(list=ls())
library(survival)
library(coxme)
library(beanplot)
library(spaMM)

d <- read.table("~/Documents/These/Papier_variants_JBF/data_R0_components_per_insect.csv", h=T)
d$isolate <- as.factor(d$isolate)
d$group <- as.factor(d$group)

colors <- c("1" = adjustcolor("blue4", alpha.f = 0.6),
            "2" = adjustcolor("firebrick", alpha.f = 0.6),
            "3" = adjustcolor("olivedrab3", alpha.f = 0.6))
```

2 Nematode emergence β

The proportion of emergence at the end of the experiment corresponds to the β parameter used in R_0 estimation, but we can also analyse more precisely the time before nematode emergence:

```
par(bty="l",las=1, mar=c(6,6,2,2), col.axis="grey50", col="grey50", col.lab="black", xpd=F)
plot(survfit(Surv(emergence_time,emergence)~group,data=d),
     lwd=3, fun="event", ylim=c(0,1),
     xlab="Days after infestation",
     main="IJ emergence from insects cadavers",
     ylab="Proportion of insects with IJ emergence",
     col=colors)#,xlim=c(7,21))
legend("bottomright", c("Group 1 isolates","Group 2 isolates","Group 3 isolates"),
       col=colors,
       lwd=3,
       bty="n",
       lty=c(1,1,1))
```



We analized the emergence time using a Cox proportional hazard model. In this model, differences among variants of the same group, and among cultures for any given variant, are modeled as random blocks. The three fixed effects considered here are the phase group of variants, the number of bacteria injected (log(CFU inoculum)) and the interaction between these two factors. Each simple effects is tested while controlling for the other simple effect (using the so called type II decomposition of deviance).

```
m1 <- coxme(Surv(emergence_time,emergence)~logCFU_inoculum*group+(1|isolate/well),data=d)
anova(m1)
```

```
## Analysis of Deviance Table
##  Cox model: response is Surv(emergence_time, emergence)
## Terms added sequentially (first to last)
##
##                        loglik   Chisq Df Pr(>|Chi|)
## NULL                  -1050.92
## logCFU_inoculum       -1015.87 70.0844  1  < 2.2e-16 ***
## group                  -994.37 43.0046  2  4.588e-10 ***
```

```
## logCFU_inoculum:group  -992.78  3.1817  2     0.2038
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
m1 <- coxme(Surv(emergence_time,emergence)~I(10^logCFU_inoculum)*group+(1|isolate/well),data=d)
anova(m1)
```

```
## Analysis of Deviance Table
##  Cox model: response is Surv(emergence_time, emergence)
## Terms added sequentially (first to last)
##
##                               loglik   Chisq Df Pr(>|Chi|)
## NULL                         -1050.92
## I(10^logCFU_inoculum)        -1015.56 70.7047  1  < 2.2e-16 ***
## group                         -994.50 42.1262  2  7.119e-10 ***
## I(10^logCFU_inoculum):group   -991.99  5.0153  2    0.08146 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

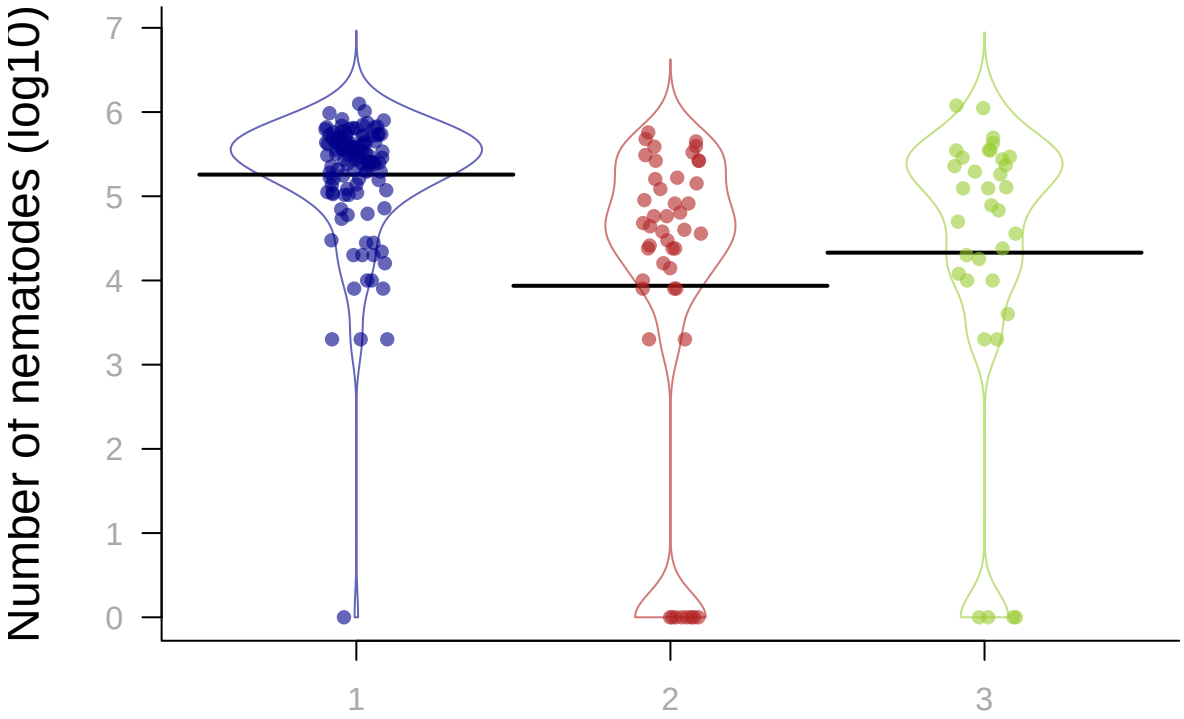
```
rm(list = ls(pattern = "m.*"))
```

3 Number of nematode per insect f

```
# pdf("~/Documents/These/Soutenance/presentation/fig_nb_nem.pdf",width=5,height=5)
par(bty="l",mar=c(4,4,2,2), las=1)
beanplot(log10(1+nb_ij)~as.factor(group),
         data = subset(d, emergence & !is.na(emergence_time)),
         what=c(0,1,1,0),
         border=c("1" = adjustcolor("blue4", alpha.f = 0.6),
                  "2" = adjustcolor("firebrick", alpha.f = 0.6),
                  "3" = adjustcolor("olivedrab3", alpha.f = 0.6)),
         col=as.list("white"),
         cex.axis=1,
         #names=NA,
         cutmin = 0,
         xlab="",
         cex.lab=1.5,
         col.axis="darkgray",
         #ylim=c(0,max(z)+15),
         ylab="Number of nematodes (log10)")
```

```
## new function
```

```
with(subset(d, emergence & !is.na(emergence_time)),
points(log10(1+nb_ij)~I(as.numeric(group)+runif(length(nb_ij),-0.1, 0.1)),
       bg=c("1" = adjustcolor("blue4", alpha.f = 0.6),
            "2" = adjustcolor("firebrick", alpha.f = 0.6),
            "3" = adjustcolor("olivedrab3", alpha.f = 0.6))[group],
       col=NA,
       pch=21)
)
```




```
# dev.off()
with(subset(d, emergence & !is.na(emergence_time)),
     kruskal.test(log10(1+nb_ij), as.factor(group))
)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  log10(1 + nb_ij) and as.factor(group)
## Kruskal-Wallis chi-squared = 37.892, df = 2, p-value = 5.914e-09
```

Analysis of the number of IJs produced for each emergence using a Generalized Linear Model with Mixed effects (GLMM). The response variable analyzed here is the number of IJs counted in a 20 μL drop taken from the 10mL flasks where IJs are stored after emergence. The model includes an offset parameter, corresponding to these volumes, so that it can predict the total number of IJs produced by an emergence. The number of IJs counted is assumed to be a Poisson distributed variable, and the model includes gamma distributed random blocks (which describe the variance among bacterial strains, among replicate cultures for each strain, and among insect lots). The mixture of these two distributions produces a negative binomial response, which allows to reduce potential over-dispersion (see text for further details). The fixed effects considered in this model are the group of the bacteria injected, the insect weight the number of bacteria injected into the insect (log(CFU inoculum)) and the number of days between the infection and the first emergence (emergence time). As before, we used a type II decomposition of deviance.

```
d$dil <- log(10000/20)
m1 <- HLfit(nb_ij~scale(insect_weight)+(emergence_time+group+scale(logCFU_inoculum))^2+(1|isolate/well)+
            data=subset(d, emergence & !is.na(emergence_time) & nb_ij>0),
            HLmethod="ML", family=poisson,
            control.HLfit=list(max.iter=1000),
            rand.family=Gamma(log))
m1
```

```
## formula: nb_ij ~ scale(insect_weight) + (emergence_time + group + scale(logCFU_inoculum))^2 +
##     (1 | isolate/well) + offset(dil)
```

```
## Estimation of lambda by Laplace ML approximation (p_v).
## Estimation of fixed effects by Laplace ML approximation (p_v).
## Family: poisson ( link = log )
##  ------------ Fixed effects (beta) ------------
##                                       Estimate  Cond. SE    t-value
## (Intercept)                           8.139167 0.1261694    64.5098
## scale(insect_weight)                  0.099914 0.0001756   569.1128
## emergence_time                       -0.171100 0.0001663 -1028.9781
## group2                                0.878739 0.2078369     4.2280
## group3                               -0.976350 0.3150214    -3.0993
## scale(logCFU_inoculum)                0.423541 0.1537329     2.7550
## emergence_time:group2                -0.133187 0.0007704  -172.8743
## emergence_time:group3                 0.007724 0.0006292    12.2761
## emergence_time:scale(logCFU_inoculum) -0.019700 0.0001970  -100.0236
## group2:scale(logCFU_inoculum)         -0.250820 0.3126787    -0.8022
## group3:scale(logCFU_inoculum)         -0.660392 0.2415702    -2.7337
##  --------------- Random effects ---------------
## Family: Gamma ( link = log )
##            --- Variance parameters ('lambda'):
## lambda = var(u) for u ~ Gamma(sh=1/lambda, sc=1/lambda);
##    well:isol.  :  0.6468
##    isolate  :  2.742e-06
##             --- Coefficients for log(lambda):
##       Group        Term Estimate Cond.SE
##  well:isol. (Intercept)  -0.4357  0.1496
##     isolate (Intercept)   -12.81   64.45
## # of obs: 183; # of groups: well:isol., 81; isolate, 32
##  ------------- Likelihood values  -------------
##                         logLik
## p_v(h) (marginal L): -7308098
## lambda leverages numerically 1 were replaced by 1- 1e-08 (as controlled by option 'regul_lev_lambda'
```

Testing the effect of the **interaction between the group of the injected isolate and the number of injected bacteria**:

```
m <- update(m1, .~.-group:scale(logCFU_inoculum))
anova(m1,m)
```

```
##      chi2_LR df    p_value
## p_v 6.788959  2 0.03355802
```

Testing the effect of the **interaction between the time of emergence and the number of injected bacteria**:

```
m <- update(m1, .~.-emergence_time:scale(logCFU_inoculum))
anova(m1, m)
```

```
##      chi2_LR df p_value
## p_v 9918.386  1       0
```

Testing the effect of the **interaction between the group of the injected isolate and the time of emergence**:

```
m <- update(m1, .~.-emergence_time:group)
anova(m1, m)
```

```
##      chi2_LR df p_value
## p_v 33075.29  2       0
```

Testing the effect of the **emergence time**:

```
m2 <- update(m1, .~.-emergence_time:group-emergence_time:scale(logCFU_inoculum))
m <- update(m2, .~.-emergence_time)
anova(m2,m)
```

```
##     chi2_LR df p_value
## p_v 1619060  1       0
```

Testing the effect of the **group of the injected isolate**:

```
m2 <- update(m1, .~.-emergence_time:group-group:scale(logCFU_inoculum))
m2
```

```
## formula: nb_ij ~ 1 + scale(insect_weight) + emergence_time + group + scale(logCFU_inoculum) +
##     (1 | isolate/well) + emergence_time:scale(logCFU_inoculum) +
##     offset(dil)
## Estimation of lambda by Laplace ML approximation (p_v).
## Estimation of fixed effects by Laplace ML approximation (p_v).
## Family: poisson ( link = log )
##  ------------ Fixed effects (beta) ------------
##                                      Estimate  Cond. SE   t-value
## (Intercept)                           8.26647 0.1338980    61.737
## scale(insect_weight)                  0.09993 0.0001750   571.104
## emergence_time                       -0.17690 0.0001555 -1137.387
## group2                               -0.75017 0.2110522    -3.554
## group3                               -0.46076 0.3459554    -1.332
## scale(logCFU_inoculum)                0.16787 0.1224355     1.371
## emergence_time:scale(logCFU_inoculum) -0.01994 0.0001765  -113.022
##  --------------- Random effects ---------------
## Family: Gamma ( link = log )
##            --- Variance parameters ('lambda'):
## lambda = var(u) for u ~ Gamma(sh=1/lambda, sc=1/lambda);
##    well:isol.  :  0.692
##    isolate  :  6.741e-06
##              --- Coefficients for log(lambda):
##       Group        Term Estimate Cond.SE
##  well:isol. (Intercept)  -0.3681  0.1491
##     isolate (Intercept)   -11.91   45.07
## # of obs: 183; # of groups: well:isol., 81; isolate, 32
##  ------------- Likelihood values  -------------
##                         logLik
## p_v(h) (marginal L): -7324640
## lambda leverages numerically 1 were replaced by 1- 1e-08 (as controlled by option 'regul_lev_lambda'
```

```
m <- update(m2, .~.-group)
anova(m2,m)
```

```
##      chi2_LR df     p_value
## p_v 10.27135  2 0.005883067
```

Testing the effect of the **number of injected bacteria**:

```
m2 <- update(m1, .~.-emergence_time:scale(logCFU_inoculum)-group:scale(logCFU_inoculum))
m <- update(m2, .~.-scale(logCFU_inoculum))
anova(m2,m)
```

```
##        chi2_LR df   p_value
```

```
## p_v 0.09238965  1 0.7611609
```

Testing the effect of **insect weight**:

```
m <- update(m1, .~.-scale(insect_weight))
anova(m, m1)
```

```
##      chi2_LR df p_value
## p_v 324501.4  1       0
```

Standard deviation of the **random effects**:

```
sqrt(m1$lambda) # standard deviation of random effects
```

```
##  well:isol.     isolate
## 0.804228280 0.001656001
## attr(,"cum_n_u_h")
## [1]   0  81 113
```

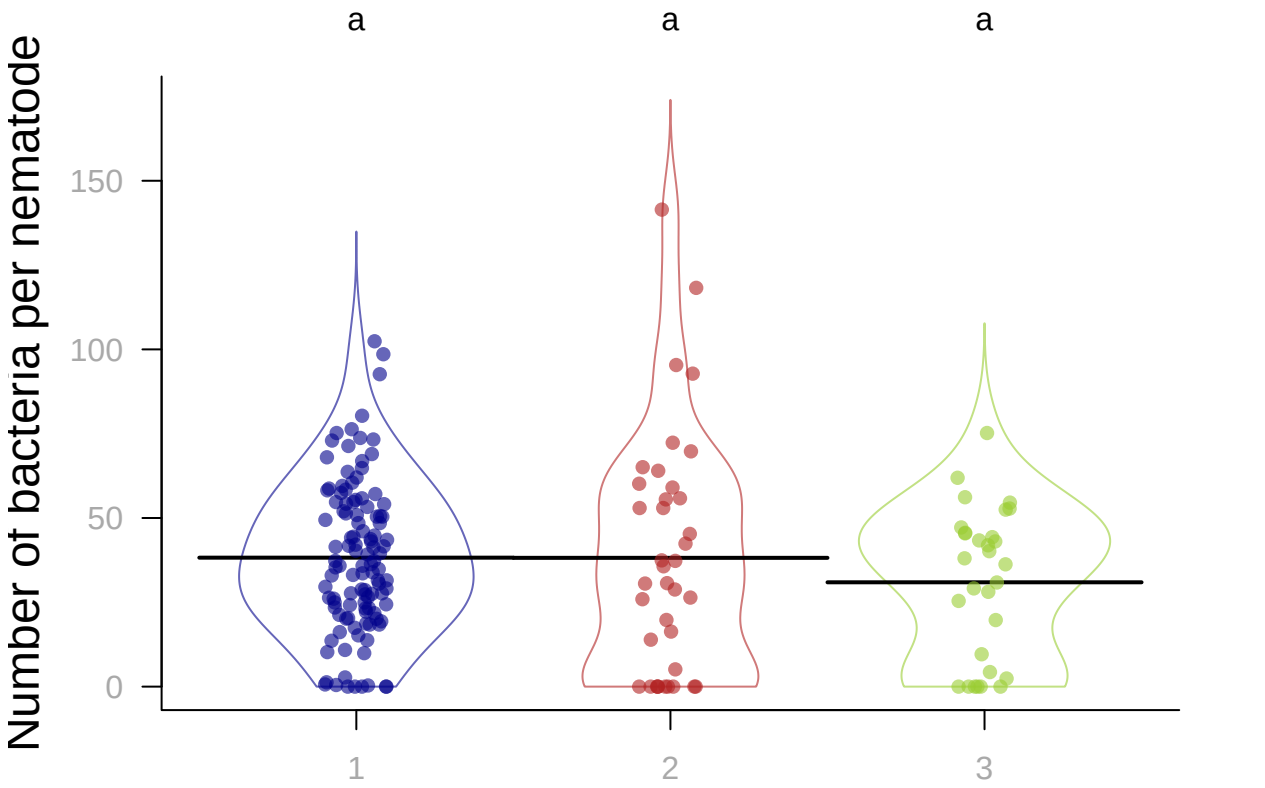
```
rm(list = ls(pattern = "m.*"))
```

4 Bacterial retention of newly emerged nematodes r

```
# pdf("~/Documents/These/Soutenance/presentation/fig_retention.pdf",width=5,height=5)
par(bty="l",mar=c(4,4,2,2), las=1)
beanplot(retention_CFU_per_ij~group,
         data = subset(d, nb_ij!=0
                       & !is.na(nb_ij)
                       & emergence),
         what=c(0,1,1,0),
         border=colors,
         cutmin = 0,
         col=as.list("white"),
         cex.axis=1,
         #names=NA,
         xlab="",
         cex.lab=1.5,
         col.axis="darkgray",
         #ylim=c(0,max(z)+15),
         ylab="Number of bacteria per nematode")
```

```
## new function
```

```
with(subset(d, nb_ij!=0 &
               !is.na(nb_ij) &
               emergence),
          points(retention_CFU_per_ij~I(as.numeric(group)+runif(length(retention_CFU_per_ij),-0.1, 0.1)),
                 bg=colors[group],
                 col=NA,
                 pch=21)
)

mtext(c("a", "a", "a"),side = 3, 1, at=c(1,2,3))
```




```
# dev.off()
```

Analysis of the number of bacteria carried by the IJs using a Generalized Linear Model with Mixed effects (GLMM). The response variable analyzed here is the number of bacteria counted for 20 grounded IJs. The model includes an offset parameter, corresponding to this number of IJs, so that it can predict the number of bacteria per nematode. The number of bacteria counted is assumed to be a Poisson distributed variable, and the model includes gamma distributed random blocks (which describe the variance among bacterial strains, among replicate cultures for each strain, and among insect lots). The mixture of these two distributions produces a negative binomial response, which allows to reduce potential over-dispersion (see text for further details). Fixed effects in this model are the phase group of the bacteria injected (Phase group), the number of days between the infection and the first emergence (emergence time) and the number of IJs produced for each emergence (log(Number of IJs produced)). As before, we used a type II decomposition of deviance.

```
m <- HLfit(retention_nb_CFU~insect_weight+
             logCFU_inoculum+logCFU_inoculum:group+
             (emergence_time+group+log(1+nb_ij))^2+
             offset(-log(300)+log(100)+log(retention_nb_ij))+
             (1|isolate/well)+(1|insect_batch),
           data=subset(d, nb_ij!=0 &
                         !is.na(nb_ij) &
                         emergence),
           HLmethod="ML", family=poisson,
           rand.family=Gamma(log))
m
```

```
## formula: retention_nb_CFU ~ insect_weight + logCFU_inoculum + logCFU_inoculum:group +
##     (emergence_time + group + log(1 + nb_ij))^2 + offset(-log(300) +
##     log(100) + log(retention_nb_ij)) + (1 | isolate/well) + (1 |
##     insect_batch)
## Estimation of lambda by Laplace ML approximation (p_v).
```

```
## Estimation of fixed effects by Laplace ML approximation (p_v).
## Family: poisson ( link = log )
##  ------------ Fixed effects (beta) ------------
##                                 Estimate  Cond. SE   t-value
## (Intercept)                   -1.184e+00 0.8326691  -1.42161
## insect_weight                  4.121e-06 0.0001976   0.02085
## logCFU_inoculum                4.343e-02 0.2970838   0.14619
## emergence_time                 2.680e-01 0.0290463   9.22503
## group2                        -6.455e+00 1.4016618  -4.60555
## group3                        -6.902e-01 1.1078828  -0.62303
## log(1 + nb_ij)                 4.691e-01 0.0308543  15.20232
## logCFU_inoculum:group2         1.363e+00 0.5348513   2.54781
## logCFU_inoculum:group3        -4.445e-01 0.4799687  -0.92604
## group2:emergence_time         -1.789e-01 0.0167555 -10.67490
## group3:emergence_time          5.232e-02 0.0120436   4.34460
## emergence_time:log(1 + nb_ij) -3.127e-02 0.0027659 -11.30360
## group2:log(1 + nb_ij)          4.734e-01 0.0207987  22.76090
## group3:log(1 + nb_ij)          6.728e-02 0.0189076   3.55851
##  --------------- Random effects ---------------
## Family: Gamma ( link = log )
##            --- Variance parameters ('lambda'):
## lambda = var(u) for u ~ Gamma(sh=1/lambda, sc=1/lambda);
##    well:isol.  :  0.7689
##    isolate  :  7.745e-07
##    insect_ba.  :  0.00561
##             --- Coefficients for log(lambda):
##       Group        Term Estimate Cond.SE
##  well:isol. (Intercept)  -0.2628  0.1551
##     isolate (Intercept)   -14.07     104
##  insect_ba. (Intercept)   -5.183  0.9682
## # of obs: 182; # of groups: well:isol., 81; isolate, 32; insect_ba., 3
##  ------------- Likelihood values  -------------
##                         logLik
## p_v(h) (marginal L): -5006.063
## lambda leverages numerically 1 were replaced by 1- 1e-08 (as controlled by option 'regul_lev_lambda'
```

Testing the effect of the **interaction between the group of the injected isolate and the number of IJs produced**:

```
m1 <- update(m, .~.-log(1+nb_ij):group)
anova(m1,m)
```

```
##      chi2_LR df p_value
## p_v 592.7429  2       0
```

Testing the effect of the **interaction between the group of the injected isolate and the emergence time**:

```
m2 <- update(m1, .~.-emergence_time:group)
anova(m2,m)
```

```
##      chi2_LR df p_value
## p_v 935.8197  4       0
```

Testing the effect of the **interaction between the number of IJs produced and the emergence time**:

```
m3 <- update(m1, .~.-log(1+nb_ij):emergence_time)
anova(m3,m)
```

```
##      chi2_LR df p_value
## p_v 669.8323  3       0
```

Testing the effect of the **interaction between the group of the injected isolate and the number of injected bacteria**:

```
m4 <- update(m1, .~.-logCFU_inoculum:group)
anova(m,m4)
```

```
##     chi2_LR df p_value
## p_v 596.771  4       0
```

Testing the effect of **insect weight**:

```
anova(m,update(m, .~.-insect_weight))
```

```
##          chi2_LR df   p_value
## p_v 0.0004283719  1 0.9834872
```

Testing the effect of the **number of injected cells**:

```
anova(m4,update(m4, .~.-logCFU_inoculum))
```

```
##        chi2_LR df   p_value
## p_v 0.09189866  1 0.7617771
```

Testing the effect of the **group of the injected isolate**

```
m12 <- update(m1, .~.-emergence_time:group)
mgroup <-update(m12, .~.-group)
anova(m12, mgroup)
```

```
##      chi2_LR df   p_value
## p_v 3.303296  2 0.1917336
```

Testing the effect of the **time of emergence**:

```
m23 <- update(m2, .~.-log(1+nb_ij):emergence_time)
mT <- update(m23, .~.-emergence_time, control.HLfit=list(max.iter=1000))
anova(m23, mT)
```

```
##      chi2_LR df      p_value
## p_v 31.86136  1 1.655786e-08
```

Testing the effect of the **number of IJs produced**:

```
m13 <- update(m1, .~.-log(1+nb_ij):emergence_time)
mviv <- update(m13, .~.-log(1+nb_ij))
anova(m13, mviv)
```

```
##      chi2_LR df p_value
## p_v 1147.996  1       0
```

Standard deviation of the **random effects**:

```
sqrt(m$lambda) # écarts type effets aléatoires
```

```
##   well:isol.      isolate   insect_ba.
## 0.8768712889 0.0008800635 0.0748988363
## attr(,"cum_n_u_h")
```

```
## [1]   0  81 113 116
```

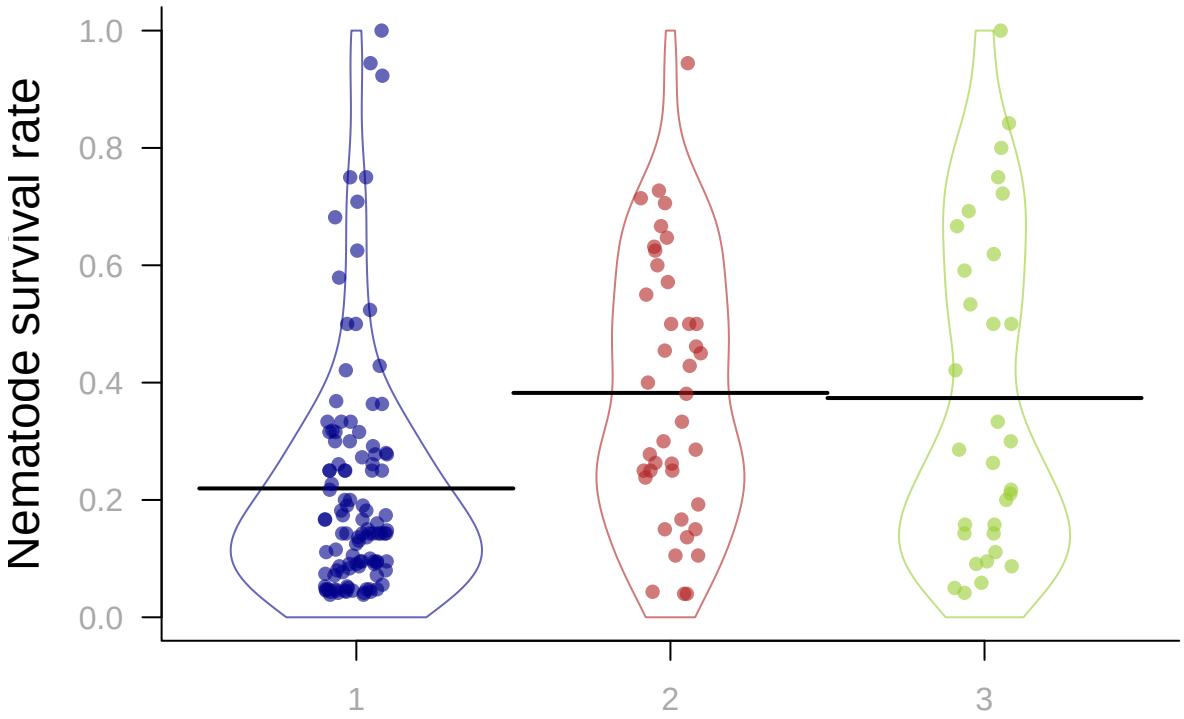
```
rm(list = ls(pattern = "m.*"))
```

5 Survival of newly emerged nematodes ν

```
# pdf("~/Documents/These/Soutenance/presentation/fig_survie.pdf",width=5,height=5)
par(bty="l",mar=c(4,4,2,2), las=1)
beanplot(nem_survival_rate~group,
         data = subset(d,nem_survival_nb_s5<=nem_survival_nb_s1 & nem_survival_nb_s1>0),
         what=c(0,1,1,0),
         border=colors,
         cutmin = 0,
         cutmax=1,
         log="",
         col=as.list("white"),
         cex.axis=1,
         #names=NA,
         xlab="",
         cex.lab=1.5,
         col.axis="darkgray",
         #ylim=c(0,max(z)+15),
         ylab="Nematode survival rate")
```

```
## new function
```

```
with(subset(d,nem_survival_nb_s5<=nem_survival_nb_s1 & nem_survival_nb_s1>0),
          points(nem_survival_rate~I(as.numeric(group)+runif(length(nem_survival_rate),-0.1, 0.1)),
                 bg=colors[group],
                 col=NA,
                 pch=21)
)
```




```
# dev.off()
```

Analysis of the survival rate of newly emerged IJs using a Generalized Linear Model with Mixed effects (GLMM). The response variable analyzed here are the number of dead and alive IJs after 5 weeks of experiment. Insect death is assumed to be a binomial variable, and the model includes beta distributed random blocks (which describe the variance among bacterial isolates of each group, among replicate cultures for each isolate, and among insect lots). Fixed effects in this model are the phase group of the injected isolate, the number of days between the infection and the first emergence (emergence time), the number of IJs produced for each emergence, and the mean number of bacteria carried by nematodes. As before, we used a type II decomposition of deviance.

```
m <- HLfit(cbind(nem_survival_nb_s1-nem_survival_nb_s5,nem_survival_nb_s5)~insect_weight+
             (group+emergence_time+nb_ij+retention_CFU_per_ij)^2+
             (1|isolate/well)+(1|insect_batch),
           HLmethod="ML",
           control.HLfit=list(max.iter=1000),
           data=subset(d, nem_survival_nb_s1>0 &
                         nem_survival_nb_s5<=nem_survival_nb_s1),
           family=binomial, rand.family=Beta(logit))
m
```

```
## formula: cbind(nem_survival_nb_s1 - nem_survival_nb_s5, nem_survival_nb_s5) ~
##     insect_weight + (group + emergence_time + nb_ij + retention_CFU_per_ij)^2 +
##         (1 | isolate/well) + (1 | insect_batch)
## Estimation of lambda by Laplace ML approximation (p_v).
## Estimation of fixed effects by Laplace ML approximation (p_v).
## Family: binomial ( link = logit )
##  ------------ Fixed effects (beta) ------------
##                                      Estimate  Cond. SE t-value
## (Intercept)                        -8.264e-01 6.430e-01 -1.2853
## insect_weight                      -3.650e-03 1.544e-03 -2.3647
## group2                              1.094e+00 8.415e-01  1.2996
```

```
## group3                                -1.113e-01 1.059e+00 -0.1051
## emergence_time                         1.187e-01 4.254e-02  2.7914
## nb_ij                                  2.125e-06 3.033e-06  0.7004
## retention_CFU_per_ij                  -1.239e-02 1.768e-02 -0.7006
## group2:emergence_time                 -4.213e-02 6.567e-02 -0.6416
## group3:emergence_time                  4.697e-02 9.267e-02  0.5069
## group2:nb_ij                          -3.373e-06 1.437e-06 -2.3476
## group3:nb_ij                          -1.084e-06 8.493e-07 -1.2768
## group2:retention_CFU_per_ij            1.266e-02 7.612e-03  1.6632
## group3:retention_CFU_per_ij            1.448e-02 7.560e-03  1.9154
## emergence_time:nb_ij                  -5.882e-07 2.996e-07 -1.9631
## emergence_time:retention_CFU_per_ij -2.134e-03 1.623e-03 -1.3148
## nb_ij:retention_CFU_per_ij             5.749e-08 1.436e-08  4.0036
##  --------------- Random effects ---------------
## Family: Beta ( link = logit )
##            --- Variance parameters ('lambda'):
## lambda = 4 var(u)/(1 - 4 var(u)) for u ~ Beta[1/(2*lambda),1/(2*lambda)];
##    well:isol.  :  0.07751
##    isolate  :  0.01159
##    insect_ba.  :  0.001228
##              --- Coefficients for log(lambda):
##       Group        Term Estimate Cond.SE
##  well:isol. (Intercept)   -2.557  0.2056
##     isolate (Intercept)   -4.458  0.5804
##  insect_ba. (Intercept)   -6.702   1.463
## # of obs: 181; # of groups: well:isol., 82; isolate, 32; insect_ba., 3
##  ------------- Likelihood values  -------------
##                          logLik
## p_v(h) (marginal L): -454.5244
```

Testing the effect of the **interaction between the group of the injected isolate and the emergence time:**

```
m1 <- update(m,.~.-group:emergence_time)
anova(m,m1)
```

```
##      chi2_LR df   p_value
## p_v 1.921025  2 0.3826967
```

Testing the effect of the **interaction between the group of the injected isolate and the number of IJs produced:**

```
m2 <- update(m,.~.-group:nb_ij)
anova(m,m2)
```

```
##      chi2_LR df    p_value
## p_v 6.348706  2 0.04182116
```

Testing the effect of the **interaction between the group of the injected isolate and the number of bacteria carried by IJs:**

```
m3 <- update(m,.~.-group:retention_CFU_per_ij)
anova(m,m3)
```

```
##      chi2_LR df   p_value
## p_v 4.478898  2 0.1065172
```

Testing the effect of the **interaction between the time of IJ emergence and the number of IJs**

produced:

```
m4 <- update(m, .~.-emergence_time:nb_ij)
anova(m,m4)
```

```
##      chi2_LR df  p_value
## p_v 3.270898  1 0.070519
```

Testing the effect of the **interaction between the time of IJ emergence and the number of bacteria carried by IJs:**

```
m5 <- update(m,.~.-emergence_time:retention_CFU_per_ij)
anova(m,m5)
```

```
##      chi2_LR df   p_value
## p_v 1.922025  1 0.1656336
```

Testing the effect of the **interaction between the number of IJs produced and the number of bacteria carried by IJs:**

```
m6 <- update(m,.~.-nb_ij:retention_CFU_per_ij)
anova(m,m6)
```

```
##      chi2_LR df      p_value
## p_v 14.28287  1 0.0001572895
```

Testing the effect of the **group of the injected isolate:**

```
m7 <- update(m1,.~.-group:nb_ij-group:retention_CFU_per_ij)
m8 <- update(m7, .~.-group)
anova(m7,m8)
```

```
##      chi2_LR df    p_value
## p_v 7.766805  2 0.02058069
```

Testing the effect of the **time of emergence:**

```
m9 <- update(m1,.~.-emergence_time:retention_CFU_per_ij-emergence_time:nb_ij)
m10 <- update(m9,.~.-emergence_time)
anova(m10,m9)
```

```
##      chi2_LR df    p_value
## p_v 3.009561  1 0.08277472
```

Testing the effect of the **number of IJ produced:**

```
m11 <- update(m,.~.-group:nb_ij-nb_ij:retention_CFU_per_ij-nb_ij:emergence_time)
m12 <- update(m11,.~.-nb_ij)
anova(m11,m12)
```

```
##     chi2_LR df      p_value
## p_v 37.5756  1 8.793757e-10
```

Testing the effect of the **number of bacteria carried by IJs:**

```
m13 <- update(m,.~.-emergence_time:retention_CFU_per_ij-nb_ij:retention_CFU_per_ij-group:retention_CFU_
m14 <- update(m13, .~.-retention_CFU_per_ij)
#anova(m13,m14)
cat("PROBLEME")
```

```
## PROBLEME
```

Testing the effect of **insect weight:**

```
m15 <- update(m,.~.-insect_weight)
anova(m,m15)
```

```
##      chi2_LR df    p_value
## p_v 4.025857  1 0.04480786
```

Standard deviation of **the random effects:**

```
pchisq(m$APHLs$p_v-m1$APHLs$p_v,1,lower.tail=F)
```

```
## [1] 0.3270578
```

```
rm(list = ls(pattern = "m.*"))
```