# Appendix

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```
library(tibble)
library(dplyr)
library(purrr)
library(tidyr)
library(ggplot2)
library(stringr)
library(BAS)
library("R2jags")
library(knitr)
bioassay.read = read.table("http://stat.duke.edu/sites/stat.duke.edu/files/bioassay.txt",
                       header=T,stringsAsFactors = FALSE) %>% as.tibble()
bioassay=bind_cols(map_df(bioassay.read %>% select(uterus, weight, EE, ZM), ~.x %>% as.numeric(.)),
                   map_df(bioassay.read %>% select(protocol,lab,group),~.x %>% as.factor(.))
                   ) %>% as.tibble()
bioassay.fac=bioassay %>% mutate(EE=as.factor(EE),ZM=as.factor(ZM))
X.fac=model.matrix(data=bioassay.fac,object =~ EE+ZM+lab+protocol+weight+EE:protocol+ZM:protocol+EE:lab
```

## Containing Part I to Part IV

I use three different ways to settle down the problems. For part I(MLE), I mainly use t-test and F-test. For part II(BMA with hyper-g-n prior), I mainly use the posterior model probability, inclusive probability and the posterior pdf for each predictor. For part III(jags), I would just use visualization (CI) to illustrate. Actually, for each part, we can use boxplot to illustrate for convenience and directly. The long table and graph would be attached at the end of the document.

#### Part I

## summary

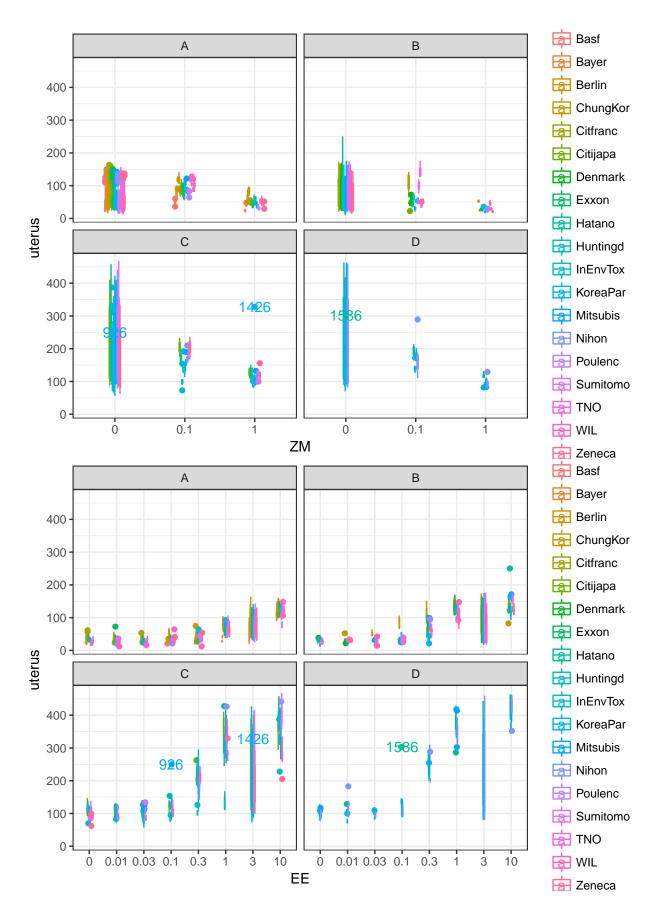
##1)We can consider `weight` and `uterus` as continuous variable. All other variables only have seperat summary(bioassay)

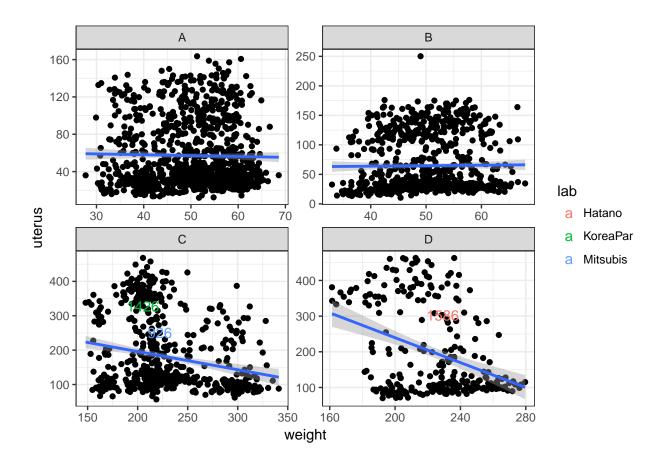
```
##
       uterus
                       weight
                                                           :0.0000
                                          : 0.000
  Min.
         : 10.4
                         : 27.7
                   Min.
                                   Min.
                                                    Min.
  1st Qu.: 32.8
                   1st Qu.: 48.4
                                   1st Qu.: 0.010
                                                    1st Qu.:0.0000
## Median: 80.0
                   Median: 56.1
                                   Median : 0.300
                                                    Median :0.0000
## Mean
          :100.8
                   Mean
                          :106.7
                                         : 1.875
                                                    Mean
                                                           :0.1009
                                   Mean
##
   3rd Qu.:124.4
                   3rd Qu.:200.2
                                   3rd Qu.: 3.000
                                                    3rd Qu.:0.0000
## Max.
           :468.3
                   Max.
                          :341.0
                                   Max.
                                          :10.000
                                                    Max.
                                                           :1.0000
## NA's
           :4
                   NA's
                          :2
## protocol
                  lab
                                group
## A:1032
           Hatano : 264
                            2
                                    : 246
## B: 792
           InEnvTox: 264
                            5
                                    : 246
## C: 594
            Nihon
                   : 264
                            6
                                    : 246
                            7
## D: 263
           Mitsubis: 263
                                   : 246
##
            Citijapa: 198
                                    : 246
```

```
##
             Sumitomo: 198
                              9 : 246
##
              (Other) :1230
                              (Other):1205
bioassay %>% select(EE) %>% table()
## .
##
      0 0.01 0.03 0.1 0.3
                                1
                                      3
                                          10
## 486 234 239 246 246
                              246 738 246
bioassay %>% select(ZM) %>% table()
## .
##
      0 0.1
                 1
## 2189 246 246
##2) There are significant interaction among variables. Because each labs adopted differet treatment.
table(bioassay$EE,bioassay.fac$lab)
##
##
          Basf Bayer Berlin ChungKor Citfranc Citijapa Denmark Exxon Hatano
##
     0
            12
                   12
                          12
                                    24
                                             12
                                                       36
                                                               12
                                                                       6
                                                                             48
##
     0.01
             0
                    0
                           6
                                    12
                                              6
                                                       18
                                                                6
                                                                       6
                                                                             24
##
     0.03
                    0
                           6
                                    12
                                              6
                                                       18
                                                                6
                                                                       6
                                                                             24
             6
##
     0.1
             6
                    6
                           6
                                    12
                                              6
                                                       18
                                                                 6
                                                                       6
                                                                             24
##
     0.3
             6
                    6
                           6
                                    12
                                              6
                                                       18
                                                                6
                                                                       6
                                                                             24
##
             6
                    6
                           6
                                    12
                                              6
                                                                6
                                                                       6
                                                                             24
     1
                                                       18
##
     3
            18
                   18
                          18
                                    36
                                             18
                                                       54
                                                               18
                                                                      18
                                                                             72
##
             6
                    6
                           6
                                    12
                                              6
                                                       18
                                                                6
                                                                       6
                                                                             24
     10
##
##
          Huntingd InEnvTox KoreaPar Mitsubis Nihon Poulenc Sumitomo TNO WIL
##
                                                                              24
     0
                 12
                          48
                                    24
                                             48
                                                    48
                                                            12
                                                                      36
                                                                          24
     0.01
##
                  6
                          24
                                    12
                                             24
                                                    24
                                                             6
                                                                      18
                                                                         12
                                                                              12
##
     0.03
                  6
                          24
                                             23
                                                    24
                                                             6
                                                                      18 12
                                    12
                                                                              12
##
     0.1
                  6
                          24
                                    12
                                             24
                                                    24
                                                             6
                                                                      18 12
                                                                              12
                                    12
                                                                      18 12
                                                                              12
##
     0.3
                  6
                          24
                                             24
                                                    24
                                                             6
##
                  6
                          24
                                    12
                                             24
                                                    24
                                                             6
                                                                      18 12
                                                                              12
     1
##
     3
                 18
                          72
                                    36
                                             72
                                                    72
                                                            18
                                                                      54 36
                                                                              36
##
     10
                  6
                          24
                                    12
                                             24
                                                    24
                                                             6
                                                                      18 12 12
##
##
          Zeneca
##
     0
              36
##
     0.01
              18
##
     0.03
              18
##
              18
     0.1
              18
##
     0.3
##
              18
     1
##
     3
              54
##
     10
              18
##visualization for points
\#ggplot(data=bioassay, mapping = aes(y = lab, x = protocol, color=as.factor(ZM))) +
# geom_jitter(alpha=0.5)
\#ggplot(data=bioassay.fac, mapping = aes(y = lab, x = ZM, color=protocol)) +
# geom_jitter(alpha=0.5)
\#qqplot(data=bioassay, mapping = aes(y = lab, x = protocol, color=as.factor(EE))) +
# geom_jitter(alpha=0.5)
\#gqplot(data=bioassay, mapping = aes(y = lab, x = protocol, color=as.factor(EE))) +
```

```
# geom_count(alpha=0.5,position = "jitter")
```

 $\mathbf{EDA}$ 





#### Model and Results

```
lm.full.fac=lm(data = bioassay.fac[-c(1586,926),],formula = uterus~EE+ZM+lab+protocol+weight+EE:protoco
#plot(lm.full.fac) ##use the plot to check model assumption. (detect outliers, normality, influential p
\#bioassay.fac \%>\% \ select(EE,ZM) \%>\% \ table() -- there is imbalanced distribution
#summary(lm.full.fac)
#Adjusted R-squared: 0.9538
##if consider EE,ZM as numeric
\#lm.full.q=lm(data = bioassay,formula = \#uterus\sim poly(EE,2)+poly(ZM,2)+lab+protocol+weight+EE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protocol+ZE:protoc
#anova(lm.full.q)
#summary(lm.full.q) #0.8286 #p=69
eff.tbl=function(lm.obj){
      if (is.matrix(lm.obj)){
            ind.mat=matrix(0,nrow=ncol(lm.obj),ncol=7)
            colnames(ind.mat)=c("EE","ZM","lab","protocol","EEdose","ZMdose","interaction")
            ind.mat=cbind(coef=lm.obj%>%colnames(.),ind.mat)
      }else{
            ind.mat=matrix(0,nrow=nrow(summary(lm.obj)$coefficients),ncol=7)
            colnames(ind.mat)=c("EE","ZM","lab","protocol","EEdose","ZMdose","interaction")
            ind.mat=cbind(coef=summary(lm.obj)$coefficients%>%rownames(.),ind.mat)
      }
```

```
ind.mat[str_detect(ind.mat[,1],"EE"),"EE"]=1
    ind.mat[str_detect(ind.mat[,1],"ZM"),"ZM"]=1
    ind.mat[str_detect(ind.mat[,1],"EE.*protocol"),"interaction"]=1
    ind.mat[str detect(ind.mat[,1],"ZM.*protocol"),"interaction"]=1
    ind.mat[str_detect(ind.mat[,1],"EE.*lab"),"interaction"]=1
    ind.mat[str_detect(ind.mat[,1],"ZM.*lab"),"interaction"]=1
    for (dose in c(bioassay.fac$EE %>% levels())){
          ind.mat[str_detect(ind.mat[,1],paste0("EE",dose)),"EEdose"]=dose
    }
    for (dose in c(bioassay.fac$ZM %>% levels())){
          ind.mat[str_detect(ind.mat[,1],paste0("ZM",dose)),"ZMdose"]=dose
    for (lab in c(bioassay.fac$lab %>% levels())){
          ind.mat[str_detect(ind.mat[,1],paste0("lab",lab)),"lab"]=lab
    }
    for (protocol in c(bioassay.fac$protocol %>% levels())){
          ind.mat[str_detect(ind.mat[,1],paste0("protocol",protocol)), "protocol"]=protocol
    ind.tbl=ind.mat%>% as.tibble()
    return(ind.tbl)
}
t.test=function(lm.obj,str.ee,str.lab,str.ori){
ind.tbl=eff.tbl(lm.obj)
cov.coef=vcov(lm.obj)
p=nrow(ind.tbl)
i.levels=bioassay.fac %>% pull(str.ori) %>% levels() #original colnames in bioassay.fac
i.n=i.levels %>% length(.)
lambda=matrix(nrow=i.n,ncol=nrow(ind.tbl))
lab.ee=t.value=p.value=denominator=nominator=numeric(i.n)
for (i in 1:i.n){
    lambda[i,] = ((ind.tbl[str.lab] == i.levels[i]) & (ind.tbl[str.ee] == "1")) & ((ind.tbl[str.ee] == "1") & (ind.tbl[str.ee] == "
    lab.ee[i]=summary(lm.obj)$coefficients[lambda[i,],"Estimate"] %>% sum()
    denominator[i]=(cov.coef[lambda[i,],lambda[i,]]) %>% sum() %>% sqrt()
    nominator[i]=lab.ee[i] %>% abs()
    t.value[i]=(nominator[i])/(denominator[i])
   p.value[i]=pt(q = t.value[i],df = summary(lm.obj)$df[2],lower.tail = FALSE)
res=list(t.test=tibble(i.levels,p.value,estimator=lab.ee),value=tibble(i.levels,variance=denominator,es
return(res)
}
a.1
uterotrophic bioassay successful overal at identifying effects of EE and ZM. F-test for EE,ZM are significant.
For the significant coefficients, all EE are positive, ZM are negative.
#0 '*** 0.001 '** 0.01 '* 0.05 '. ' 0.1 ' 1
```

## Analysis of Variance Table

anova(lm.full.fac)

```
##
## Response: uterus
##
                     Sum Sq Mean Sq
                                       F value
## EE
                  7 6493181 927597 2437.9005 < 2.2e-16 ***
## ZM
                  2 2091034 1045517 2747.8158 < 2.2e-16 ***
## lab
                 18 2399373
                            133298
                                     350.3335 < 2.2e-16 ***
## protocol
                  3 7374975 2458325 6460.9417 < 2.2e-16 ***
## weight
                  1
                     116191
                              116191
                                      305.3720 < 2.2e-16 ***
## EE:protocol
                 21 2228787
                              106133
                                      278.9368 < 2.2e-16 ***
## ZM:protocol
                  6
                     964465
                              160744
                                      422.4660 < 2.2e-16 ***
## EE:lab
                123
                     307285
                                2498
                                        6.5659 < 2.2e-16 ***
                                        7.7190 < 2.2e-16 ***
## ZM:lab
                 36
                     105732
                                2937
## Residuals
               2457
                     934864
                                 380
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
coefs=rownames(summary(lm.full.fac)$coefficients)
res=summary(lm.full.fac)$coefficients %>%
  cbind(coef=coefs,.) %>%
  as.tibble() #qet the coefficients matrix
colnames(res)=c("coef","estimate","std_error","t_value","p_value")
res %>% filter(as.numeric(p_value)<0.05) %>% slice(1:10)
## # A tibble: 10 x 5
##
                            estimate
                                               std error
                                                                    t value
             coef
##
            <chr>>
                               <chr>>
                                                   <chr>>
                                                                      <chr>>
    1 (Intercept)
                   17.5174725602682
                                        6.0832664338643
                                                          2.87961619809253
##
##
    2
                   69.3169543543242
                                       9.89986651384673
                                                          7.00180696955581
              EE3
##
   3
             EE10 85.6474733135621
                                       9.90017366264282
                                                          8.65110817568213
##
   4
            ZMO.1 -44.2697077991087
                                       11.2619188955346
                                                          -3.9309204949666
              ZM1 -68.4662160221504
##
                                        11.261889153971 -6.07946101103372
##
    6 labChungKor
                  17.0236675479605
                                       7.21540009027292 2.35935184951284
##
    7 labCitfranc
                  19.9168751325116
                                        8.1423844433654
                                                          2.44607403040768
                                                          10.5443649367664
##
    8
        protocolC
                   56.9794121460095
                                       5.40377846249726
        protocolD 47.3180475238927
##
    9
                                       6.15630309938495
                                                          7.68611401355793
## 10
           weight 0.101351933549335 0.0269475706902319
                                                           3.7610786780893
## # ... with 1 more variables: p_value <chr>
a.2 do some labs fail to detect such effects
There are some labs fail to detect such effects, as follows: "Huntingd" "Bayer" "ChungKor" "TNO" "Zeneca". Or
just pick out the labs with significant p value at "EE:lab_i" but opposite t value. ("Huntingd" "Bayer" "Zeneca")
a.2.ee=t.test(lm.full.fac,"EE","lab","lab")$t.test
a.2.ee
## # A tibble: 19 x 3
##
      i.levels
                    p.value estimator
##
                       <dbl>
                                 <dbl>
##
   1
          Basf 2.937598e-05
                              164.2023
##
         Bayer 1.297653e-05
                              148.7924
##
        Berlin 8.081249e-10
                              270.6481
   4 ChungKor 9.973079e-14
                              244.7607
## 5 Citfranc 3.911202e-05 176.8314
```

```
6 Citijapa 2.504636e-12 197.9101
##
  7
      Denmark 1.725524e-06
                             227.4437
         Exxon 2.001695e-04
                            211.2410
##
       Hatano 2.850135e-17
##
  9
                             221.4205
## 10 Huntingd 1.178475e-05 -211.9685
## 11 InEnvTox 7.907738e-15
                             202.7865
## 12 KoreaPar 2.228704e-06 167.7607
## 13 Mitsubis 4.957299e-15
                             204.5481
## 14
         Nihon 1.228075e-14
                             201.2653
## 15
     Poulenc 1.477856e-04 161.9877
## 16 Sumitomo 3.479523e-21
                             269.7772
           TNO 1.605547e-11
## 17
                             224.8464
## 18
           WIL 1.125449e-07 171.9591
## 19
       Zeneca 1.077435e-08 160.2037
a.2.ee %>% filter(((p.value<0.05)&(estimator<0))|(p.value>0.05))# %>% pull(i.levels)
## # A tibble: 1 x 3
                  p.value estimator
     i.levels
##
        <chr>>
                     <dbl>
                               <dbl>
## 1 Huntingd 1.178475e-05 -211.9685
a.2.zm=t.test(lm.full.fac,"ZM","lab","lab")$t.test
a.2.zm
## # A tibble: 19 x 3
                    p.value
##
      i.levels
                             estimator
##
         <chr>>
                      <dbl>
                                 <dbl>
   1
         Basf 4.220254e-09 -112.73592
   2
##
        Bayer 6.804663e-02 -29.08390
##
       Berlin 4.049193e-06
                            -87.23322
##
  4 ChungKor 6.389885e-02 -22.01560
  5 Citfranc 1.763902e-04
                            -69.79584
##
   6 Citijapa 2.304572e-09
                             -73.19550
      Denmark 6.965919e-05
##
  7
                            -81.37726
## 8
         Exxon 6.126571e-07 -94.87320
## 9
       Hatano 1.954502e-19 -103.41602
## 10 Huntingd 3.707009e-04
                              73.75550
## 11 InEnvTox 2.959297e-12 -79.17206
## 12 KoreaPar 1.941093e-04 -56.54709
## 13 Mitsubis 3.288518e-20 -105.47859
## 14
         Nihon 7.278050e-20 -104.46423
## 15
      Poulenc 4.017327e-02 -34.12421
## 16 Sumitomo 4.094885e-13
                            -89.55271
           TNO 1.913899e-01 -12.61549
## 17
## 18
           WIL 9.920550e-04 -44.74128
## 19
        Zeneca 2.106639e-01
                              10.00848
a.2.zm %>% filter(((p.value<0.05)&(estimator>0))|(p.value>0.05))#%>% pull(i.levels)
## # A tibble: 5 x 3
##
     i.levels
                  p.value estimator
##
        <chr>>
                     <dbl>
                               <dbl>
        Bayer 0.0680466340 -29.08390
## 2 ChungKor 0.0638988547 -22.01560
## 3 Huntingd 0.0003707009 73.75550
```

```
## 4
          TNO 0.1913899445 -12.61549
       Zeneca 0.2106639006 10.00848
## 5
res %>% filter(str_detect(res$coef, "EE.*lab")) %>%
   filter(p_value<0.05,t_value<0)</pre>
## # A tibble: 3 x 5
##
                                                                       t_value
                  coef
                                 estimate
                                                  std_error
##
                  <chr>
                                    <chr>
                                                      <chr>
                                                                         <chr>
          EE3:labBayer -28.2023694053915 13.8970614794358 -2.02937645826235
## 1
## 2 EE0.1:labHuntingd -30.049402348541 14.7449822505579
                                                             -2.0379408966331
## 3
         EE3:labZeneca -23.5618392029676 11.6930187049281 -2.01503476540555
## # ... with 1 more variables: p_value <chr>
res %>% filter(str detect(res$coef, "ZM.*lab")) %>%
   filter(p_value<0.05,t_value<0)
## # A tibble: 0 x 5
## # ... with 5 variables: coef <chr>, estimate <chr>, std_error <chr>,
       t_value <chr>, p_value <chr>
a.3 the change dose for EE? vary across labs?
```

From the output of summary (See the end of part I). The change dose for EE is EE3. Dose larger than this is significant, less than this is not significant. The value varies across labs. Because for different labs, the dose changing points is different. For example, SUmitomo. EE0.3 may be the changing dose point. For Huntingd,

b. does the dose reponse vary across labs? are there certain labs stands out as being different? From the output of summary. There exist several significant interaction cofficients, meaning dose reponse vary across labs. The labs Berlin and Sumitomo stands out as being different. (with pvalue < 0.001 for EE:labs). The labs Bayer, Poulenc, Zeneca stands out as being different. (with pvalue < 0.005 for ZM:labs)

```
res %>% filter(str_detect(res$coef, "EE.*lab")) %>%
  filter(p_value<0.001)
## # A tibble: 2 x 5
##
                coef
                              estimate
                                              std_error
                                                                  t value
##
               <chr>
                                                   <chr>
                                                                     <chr>
                                 <chr>>
       EE1:labBerlin 49.4837223304949 13.8970357690877 3.56073936576932
## 1
## 2 EE1:labSumitomo 42.0319864090083 11.6927892205068 3.59469290144157
## # ... with 1 more variables: p_value <chr>
res %>% filter(str detect(res$coef, "ZM.*lab")) %>%
  filter(p_value<0.005)
## # A tibble: 3 x 5
##
                 coef
                               estimate
                                               std_error
                                                                   t_value
##
                <chr>>
                                  <chr>
                                                    <chr>
                                                                      <chr>
       ZMO.1:labBayer 50.8727460593738 15.9269030374418 3.19413924601535
## 2 ZM0.1:labPoulenc 49.0113737477311 15.9267123836315 3.07730638735599
## 3
        ZM1:labZeneca 44.7841287734452 13.358278781101 3.35253736707494
## # ... with 1 more variables: p_value <chr>
```

c.Do the protocols differ in sensitivity to detect? Which one recommend?

EE0.1 may be the changing dose point.

From the result from anova. The protocols differ. And the variance of protocol C,D is super large. Protocol A and B would be recommended.

```
anova(lm.full.fac)["EE:protocol", ]
## Analysis of Variance Table
##
## Response: uterus
##
              Df Sum Sq Mean Sq F value
## EE:protocol 21 2228787 106133 278.94 < 2.2e-16 ***
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
anova(lm.full.fac)["ZM:protocol", ]
## Analysis of Variance Table
##
## Response: uterus
##
              Df Sum Sq Mean Sq F value
## ZM:protocol 6 964465 160744 422.47 < 2.2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
res %>% filter(str_detect(res$coef, "^protocol"))
## # A tibble: 3 x 5
##
         coef
                       estimate
                                       std_error
                                                            t_value
        <chr>>
                          <chr>>
                                           <chr>>
                                                              <chr>
## 1 protocolB -2.16077131127482 2.4955877941489 -0.865836624277823
## 2 protocolC 56.9794121460095 5.40377846249726
                                                   10.5443649367664
## 3 protocolD 47.3180475238927 6.15630309938495
                                                   7.68611401355793
## # ... with 1 more variables: p_value <chr>
res %>% filter(str_detect(res$coef, "EE.*protocol"))
## # A tibble: 21 x 5
##
                 coef
                                estimate
                                                std_error
                                                                     t_value
##
                <chr>
                                   <chr>
                                                    <chr>>
                                                                       <chr>
##
                       1.19108136858824 4.31635717989136 0.275945969934356
   1 EE0.01:protocolB
## 2 EE0.03:protocolB
                         3.541307048283 4.31635426940738 0.820439386401249
  3 EE0.1:protocolB 7.45488173303661 4.31641616363892 1.72709985562463
## 4 EE0.3:protocolB 35.0983219034887 4.31635334591939 8.13147559772188
## 5
        EE1:protocolB 58.2145220892542 4.31639052433566
                                                            13.4868524432724
## 6
        EE3:protocolB
                        34.4029534792872 4.31637929244136
                                                            7.97032678280428
##
       EE10:protocolB
                        17.5749522283604 4.32796829285087
                                                            4.06078580968154
  8 EE0.01:protocolC -0.323072655511128 4.9003836743018 -0.065928032779425
## 9 EE0.03:protocolC
                        2.72255040119417 4.90038109624472 0.555579320816605
## 10 EE0.1:protocolC
                        14.0429742703248 4.92125955112887
                                                            2.85353254068942
## # ... with 11 more rows, and 1 more variables: p_value <chr>
res %>% filter(str_detect(res$coef,"ZM.*protocol"))
## # A tibble: 6 x 5
##
               coef
                             estimate
                                             std_error
                                                                 t_value
##
              <chr>>
                                <chr>>
                                                 <chr>
                                                                   <chr>>
## 1 ZMO.1:protocolB -61.037963794127 4.98061458836321 -12.255106816885
      ZM1:protocolB -53.8667551088683 4.98057530455602 -10.8153680679405
## 3 ZMO.1:protocolC -158.414580874021 5.67997807489639 -27.8899986558329
      ZM1:protocolC -171.324039321919 5.66139549748667 -30.261803719238
## 5 ZMO.1:protocolD -183.644764786495 7.20742931513241 -25.4799258871567
```

```
## 6 ZM1:protocolD -217.250601221133 7.20370581533531 -30.1581723060718
## # ... with 1 more variables: p_value <chr>
```

## Part II

With the same model, using Bayesian Average Model to estimate the parameter with hyper-g-n prior (mixture prior). To answer the questions, I mainly concentrate on inclusion probability, posterior model probability and the shape of posterior distribution for  $\beta_i$  (or confidence interval).

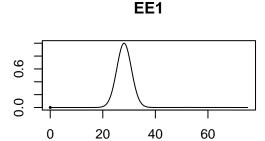
```
n=nrow(bioassay.fac)
bas.fac.2=bas.lm(formula =uterus~EE+ZM+lab+protocol+weight+EE:protocol+ZM:protocol+EE:lab+ZM:lab,
                  data=bioassay.fac,
                  prior="hyper-g-n",
                  alpha=n,
                  #n.models=20000,
                  method = "MCMC",
                  thin=10.
                  #initprobs = "eploqp",
                  MCMC.iterations = 500000)
## Warning in bas.lm(formula = uterus ~ EE + ZM + lab + protocol + weight + :
## dropping 4 rows due to missing data
##diagonose
diagnostics(bas.fac.2,"pip")
                                                                                    00
      0.8
                                                                               0
                                                                                     0
pip (MCMC)
                                              0
      Ö
                                                             0
                                      0
      0.4
                                                           0
                                                     0
                          0
                     0
                                                                  0
                                                    0
      0.0
            0.0
                           0.2
                                         0.4
                                                        0.6
                                                                      8.0
                                                                                    1.0
                                        pip (renormalized)
```

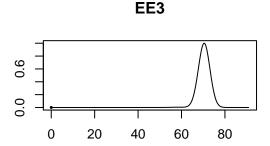
##More iteration would be better

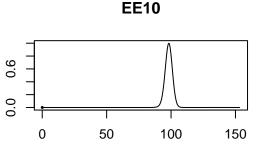
a.1 Similar to Part I, we want to test whether the coefficients before EE all equal to 0. Here I use sum posterior model probabiliters over all models that include EE, is 0.99982. Similar for ZM,is 0.99982. For the coefficients EE with high inclusion probability, all of them are larger than 0 with high probability. Simlar for ZM(negative). So the method successful overall at identifying effects.

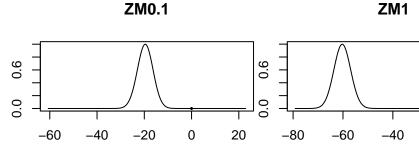
```
a_1=function(str_ee){
  which.mat=list2matrix.which(bas.fac.2,)
  ind.tbl.bas=eff.tbl(X.fac) #part II model assumption is the same to part I
  head(ind.tbl.bas)
  ind.var=((ind.tbl.bas[str_ee]=="1")&(ind.tbl.bas$interaction=="0"))
  n.ind=sum(ind.var)
  poll.in=(which.mat[,ind.var] %*% rep(1,n.ind))>0
  res=list(prob=sum(poll.in*bas.fac.2$postprobs),ind=ind.var)
  return(res)
}
a_1("EE")$prob
## [1] 0.9998599
a_1("ZM")$prob
## [1] 0.9992996
#image(bas.fac.2)--to much predictor, cannot visualization
#plot(bas.fac.2)
par(mfrow=c(2,2))
ind.ee=which(a_1("EE")$ind)
coef(bas.fac.2) %>% plot(.,ask=F,subset=ind.ee)
                EE0.01
                                                              EE0.03
                                              9.0
             0
                   5
                              15
                                                                0
                                                                        5
                                                                               10
       -5
                        10
                                                       -5
                EE0.1
                                                               EE0.3
                                              0.4
                                              0.0
0.0
          -5
                0
                                                -10
   -10
                            10
                                  15
                                                        0
                                                              10
                                                                    20
                                                                          30
                                                                                40
ind.zm=which(a_1("ZM")$ind)
```

coef(bas.fac.2) %>% plot(.,ask=F,subset=ind.zm)









a.2 Concerntrate on EE:lab\_i, ZM:lab\_i. Pick out the labs with high inclusive probability but opposite location compared to others. ("Huntingd""Zeneca""TNO""KoreaPar""ChungKor""Poulenc""EnvTox") Simply, the rule is for EE, if EE:lab\_i is at the left side of the verticle black line and the verticle black line is short, we may consider the lab fail to detect. Similar for ZM.

```
coef(bas.fac.2) %>% plot(.,ask=F)
#bas.a_2=function(lm.obj,int.tbl,str.ee,str.lab,str.ori){
#p=nrow(ind.tbl)
#i.levels=bioassay.fac %>% pull(str.ori) %>% levels() #original colnames in bioassay.fac
#i.n=i.levels %>% length(.)
\#lambda=matrix(nrow=i.n,ncol=nrow(ind.tbl))
\#lab.ee=prob=numeric(i.n)
#for (i in 1:i.n){
\# \quad lambda[i,] = ((ind.\,tbl[str.\,lab] == i.\,levels[i]) \\ @(ind.\,tbl[str.\,ee] == "1")) \\ / ((ind.\,tbl[str.\,ee] == "1") \\ @(ind.\,tbl[str.\,ee] == "1") \\ @(in
        n.ind=sum(lambda[i,])
# poll.in=(which.mat[,lambda[i,]] %*% rep(1,n.ind))>0
# prob[i]=sum(poll.in*lm.obj$postprobs)
\#res=list(prob.res=tibble(i.levels,probability=prob),ind=lambda)
#return(res)
#}
#ind.tbl.bas=eff.tbl(X.fac)
#a_21=bas.a_2(bas.fac.2, ind.tbl.bas, "EE", "lab", "lab")
#a 21$prob.res
#a_22=bas.a_2(bas.fac.2,ind.tbl.bas,"ZM","lab","lab")
#a_22$prob.res
#ind.ee=which(a 21$ind[2,])
#coef(bas.fac.2) %>% plot(.,ask=F,subset=ind.ee)
\#ind.zm=which(a_22\$ind)
```

```
#coef(bas.fac.2) %>% plot(.,ask=F,subset=ind.zm)
```

- a.3 Concerntrate on EE,ZM, see which dose level the inclusive probability significantly change. EE1. And concerntrate on EE:lab\_i,ZM:lab\_i to see which dose level the inclusive probability significantly change. They vary.
  - b. The dose response vary across labs, because there exist EE:lab\_i,ZM:lab\_i with high inclusive probability. There are certain labs ("Huntingd""Zeneca""TNO""KoreaPar""ChungKor""Poulenc""EnvTox") stand out as being different.

c.Protocols differ in the sensitivity to detect effects. Protocol B would be recommended because the length of CI for protocolB:EE and protocolB:ZM are small compared to others.

```
coefs=rownames(confint(coef(bas.fac.2)))
ci.length=apply(confint(coef(bas.fac.2)),1,function(x) as.numeric(x[2])-as.numeric(x[1]))
bas.coef=confint(coef(bas.fac.2)) %>%
  cbind(coef=coefs,.) %>%
  as.tibble() %>% #get the coefficients matrix
  mutate(ci.length=ci.length)
bas.coef %>% filter(str_detect(coef, "EE.*protocol")) %>% arrange(sort(ci.length)) %>% slice(1:10)
## # A tibble: 10 x 5
                                     `2.5%`
                                                      97.5%
##
                  coef
##
                 <chr>
                                      <chr>>
                                                       <chr>>
##
    1 EE0.01:protocolB
                                                            0
    2 EE0.03:protocolB
                                          0
                                                            0
##
       EE0.1:protocolB -0.0135462322313029 5.64948028016795
##
    3
##
       EE0.3:protocolB
                          27.1876433269464 40.7757236066607
##
   5
         EE1:protocolB
                          55.1128254216363 68.7955186902028
         EE3:protocolB
                          30.3833572486354 43.5304473427211
##
    6
##
    7
        EE10:protocolB
                          8.57468296506471 21.9287038946634
    8 EE0.01:protocolC
##
                                          0
                                                            0
    9 EE0.03:protocolC
                                          0
                                                            0
## 10 EE0.1:protocolC
                          5.36070599999337 23.0620517038165
## # ... with 2 more variables: beta <chr>, ci.length <dbl>
bas.coef %>% filter(str_detect(coef, "ZM.*protocol")) %>% arrange(sort(ci.length)) %>% slice(1:10)
## # A tibble: 6 x 5
##
                coef
                                 `2.5%`
                                                   `97.5%`
                                                                        beta
##
               <chr>
                                  <chr>
                                                    <chr>
                                                                       <chr>
  1 ZMO.1:protocolB -73.2279748564225 -55.3020377469021 -64.0385722880611
       ZM1:protocolB -64.1068020530248 -46.0849425311256 -55.2392164362778
## 3 ZM0.1:protocolC -173.181109596846 -152.127342750239 -162.622779253208
## 4
       ZM1:protocolC -186.166307290317 -164.891951856785 -174.862333405958
## 5 ZMO.1:protocolD -204.150300772104 -177.680407633948 -190.718322637718
       ZM1:protocolD -235.972031892832 -209.305899281633 -222.251824403968
## # ... with 1 more variables: ci.length <dbl>
```

### Part III

Because I set iteration=30000, and include many predictors. So the jags would be slow. So I load the data I got. An improvement for this is to adjust the distribution for  $\sigma_L^2/\lambda_l$  behave like double exponential

distribution. The hyperparameter a here is important for adjusting whether we want our model more robust. I chose a=2 for I want to let my model get less sensitive to labs "outliers".

Prepare the data

```
# Create a data list with inputs for JAGS
X.fac=model.matrix(data=bioassay,object =~EE+ZM+lab+protocol+weight+EE:protocol+ZM:protocol+EE:lab+ZM:1
n=nrow(bioassay)
## scale X such that X^TX has ones on the diagonal;
## scale divides by the standard deviation so we need
## to divide by the sqrt(n-1)
scaled.X = scale(X.fac)/sqrt(n-1)
# are diagonal elements 1?
# check
#t(scaled.X) %*% scaled.X
data = list(Y = bioassay$uterus,
            X=scaled.X,
            p=ncol(scaled.X),
            n = n
#extract the scales from the scaled object and fix--add to attr
data$scales = attr(scaled.X, "scaled:scale")*sqrt(n-1) # fix scale
data$Xbar = attr(scaled.X, "scaled:center")
Jags code
##For jags: need to use <-; use precision instead of sigma_sq
rr.model = function() {
  a <- 2
  shape < -a/2
  for (i in 1:n) {
    mu[i] <- alpha0 + inprod(X[i,], alpha)</pre>
    prec[i] <- phi</pre>
    Y[i] ~ dnorm(mu[i], prec[i])
  phi ~ dgamma(1.0E-6, 1.0E-6) ##jags do not allow improper prior
  alpha0 ~ dnorm(0, 1.0E-6)
  for (j in 1:p) {
    phi.1[j] <- pow(i.phi.1[j], -2)</pre>
    prec.beta[j] <- lambda.l[j]*phi*phi.l[j]</pre>
    alpha[j] ~ dnorm(0, prec.beta[j])
    # transform back to original coefficients
    beta[j] <- alpha[j]/scales[j]</pre>
    lambda.l[j] ~ dgamma(shape, shape)
    i.phi.l[j] \sim dt(0,1,1)%_{-}%T(0,)
  }
  # transform intercept to usual parameterization
  beta0 <- alpha0 - inprod(beta[1:p], Xbar)</pre>
  sigma <- pow(phi, -.5)
}
```

Load the data I stored.

```
stack.sim=readRDS("stack.sim.rds")
```

Analysis on simulation result.

```
# create an MCMC object with the results for the MCMC draws
stack.mcmc = as.mcmc(stack.sim$BUGSoutput$sims.matrix) #get the simulation points

mcmc.df=stack.mcmc %>% as.tibble()
lambda.plot=mcmc.df %>% select(`lambda[1]`:`lambda[21]`) %>% gather(.)
lamda.levels=paste0("lambda[",1:21,"]")
ggplot(data = lambda.plot,mapping = aes(x = key,y = value,fill=key))+geom_boxplot()+
    theme(axis.text.x = element_text(angle = 45, hjust = 1))+scale_x_discrete(limits=lamda.levels)+ guide

apply(stack.mcmc[,c("beta0","beta[1]","beta[2]","beta[3]")],2,quantile,c(.025, .975))
#plot(stack.sim)
#summary(stack.sim) # names of objects in bf.sim
#stack.sim # print gives summary
#quantile(stack.mcmc[,"beta0"], c(.025, .5, .975))
#HPDinterval(stack.mcmc)
```

## Table for the whole model

```
kable(summary(lm.full.fac)$coefficients, format = "markdown")
```

	Estimate	Std. Error	t value	$\Pr(> t )$
(Intercept)	17.5174726	6.0832664	2.8796162	0.0040160
EE0.01	1.7634590	6.2225208	0.2833995	0.7768945
EE0.03	1.0348581	9.8997869	0.1045334	0.9167546
EE0.1	2.7516396	9.9000339	0.2779424	0.7810799
EE0.3	-1.2258396	9.8997530	-0.1238253	0.9014637
EE1	4.9137998	9.8997612	0.4963554	0.6196881
EE3	69.3169544	9.8998665	7.0018070	0.0000000
EE10	85.6474733	9.9001737	8.6511082	0.0000000
ZM0.1	-44.2697078	11.2619189	-3.9309205	0.0000870
ZM1	-68.4662160	11.2618892	-6.0794610	0.0000000
labBayer	13.6089109	8.1539860	1.6689888	0.0952470
labBerlin	5.2019905	8.1706700	0.6366663	0.5244015
labChungKor	17.0236675	7.2154001	2.3593518	0.0183847
labCitfranc	19.9168751	8.1423844	2.4460740	0.0145118

	Estimate	Std. Error	t value	Pr(> t )
labCitijapa	13.4596775	6.8936320	1.9524798	0.0509947
labDenmark	9.6122452	8.5189868	1.1283320	0.2592899
labExxon	15.6678556	9.8999699	1.5826165	0.1136376
labHatano	11.9391885	6.7473960	1.7694513	0.0769426
labHuntingd	-8.3391169	8.8013746	-0.9474789	0.3434880
labInEnvTox	4.8104074	6.7951943	0.7079131	0.4790663
labKoreaPar	-2.3948281	7.4778542	-0.3202561	0.7488015
labMitsubis	11.9407498	6.7484149	1.7694155	0.0769486
labNihon	5.9191632	6.7487889	0.8770704	0.3805341
labPoulenc	-3.8337704	8.1513040	-0.4703260	0.6381639
labSumitomo	10.7213694	6.8927463	1.5554568	0.1199661
labTNO	5.1741985	7.2817950	0.7105663	0.4774204
labWIL	6.7631678	7.2179124	0.9369978	0.3488518
labZeneca	-4.0680776	6.9129760	-0.5884698	0.5562711
protocolB	-2.1607713	2.4955878	-0.8658366	0.3866643
protocolC	56.9794121	5.4037785	10.5443649	0.0000000
protocolD	47.3180475	6.1563031	7.6861140	0.0000000
weight	0.1013519	0.0269476	3.7610787	0.0000000
EE0.01:protocolB	1.1910814	4.3163572	0.2759460	0.7826128
EE0.03:protocolB	3.5413070	4.3163543	0.8204394	0.4120453
EE0.1:protocolB	7.4548817	4.3164162	1.7270999	0.4120455 $0.0842754$
EE0.3:protocolB	35.0983219	4.3163533	8.1314756	0.00042104
EE1:protocolB	58.2145221	4.3163905	13.4868524	0.0000000
EE3:protocolB	34.4029535	4.3163793	7.9703268	0.0000000
EE10:protocolB	17.5749522	4.3279683	4.0607858	0.0000504
EE0.01:protocolC	-0.3230727	4.9003837	-0.0659280	0.9474405
EE0.03:protocolC	2.7225504	4.9003811	0.5555793	0.5785491
EE0.1:protocolC	14.0429743	4.9212596	2.8535325	0.0763431 $0.0043598$
EE0.3:protocolC	100.2001531	4.9010674	20.4445572	0.0000000
EE1:protocolC	186.2957590	4.9056058	37.9760965	0.0000000
EE3:protocolC	170.0100300	4.9148171	34.5913240	0.0000000
EE10:protocolC	157.5564078	4.9217713	32.0121353	0.0000000
EE0.01:protocolD	6.4547359	6.2222407	1.0373652	0.2996678
EE0.03:protocolD	4.8409616	6.2794259	0.7709242	0.4408260
EE0.1:protocolD	24.4881903	6.2874449	3.8947761	0.0001009
EE0.3:protocolD	140.9911182	6.2315658	22.6253118	0.0001003
EE1:protocolD	230.5357409	6.2588387	36.8336284	0.0000000
EE3:protocolD	208.1653132	6.2771622	33.1623280	0.0000000
EE10:protocolD	216.9748633	6.2947772	34.4690300	0.0000000
ZM0.1:protocolB	-61.0379638	4.9806146	-12.2551068	0.0000000
ZM1:protocolB	-53.8667551	4.9805753	-10.8153681	0.0000000
ZM0.1:protocolC	-158.4145809	5.6799781	-27.8899987	0.0000000
ZM1:protocolC	-171.3240393	5.6613955	-30.2618037	0.0000000
ZM0.1:protocolD	-183.6447648	7.2074293	-25.4799259	0.0000000
ZM1:protocolD	-217.2506012	7.2037058	-30.1581723	0.0000000
EE0.1:labBayer	-1.9456140	13.8970874	-0.1400016	0.8886702
EE0.1.labBayer EE0.3:labBayer	-1.0689227	13.8971751	-0.1400010	0.9386962
EE0.3.labBayer EE1:labBayer	2.4451549	13.8974734	0.1759424	0.9580902 $0.8603537$
EE1:labBayer EE3:labBayer	-28.2023694	13.8970615	-2.0293765	0.0425276
EE3.labBayer EE10:labBayer	13.3618173	13.8973214	0.9614671	0.0423270 $0.3364120$
EE10.labBayer EE0.01:labBerlin	-0.8711178	11.5688730	-0.0752984	0.9399834
EE0.01.labBerlin	2.9075964	13.8970389	0.2092242	0.9399834
EE0.05.1a0DeHIII	4.9070904	19.0910909	0.409444	0.0042900

	_			
	Estimate	Std. Error	t value	$\frac{\Pr(> \mathbf{t} )}{}$
EE0.1:labBerlin	-2.8133528	13.8977646	-0.2024320	0.8395957
EE0.3:labBerlin	15.6240363	13.8971717	1.1242601	0.2610125
EE1:labBerlin	49.4837223	13.8970358	3.5607394	0.0003768
EE3:labBerlin	36.1854101	13.8971988	2.6037916	0.0092754
EE10:labBerlin	5.9294383	13.8987704	0.4266160	0.6696964
EE0.01:labChungKor	-4.4112228	9.0183089	-0.4891408	0.6247857
EE0.03:labChungKor	3.6572980	12.2566224	0.2983936	0.7654280
EE0.1:labChungKor	25.1157672	12.2569386	2.0491061	0.0405577
EE0.3:labChungKor	29.9697260	12.2567299	2.4451649	0.0145484
EE1:labChungKor	33.4910175	12.2566535	2.7324765	0.0063310
EE3:labChungKor	5.8710111	12.2568226	0.4789994	0.6319817
EE10:labChungKor	-13.1352580	12.2576968	-1.0715927	0.2840083
EE0.01:labCitfranc	-5.4581770	11.5691596	-0.4717868	0.6371209
EE0.03:labCitfranc	2.1032608	13.8970370	0.1513460	0.8797152
EE0.1:labCitfranc	-4.7742861	13.8972539	-0.3435417	0.7312204
EE0.3:labCitfranc	4.4922701	13.8970495	0.3232535	0.7465308
EE1:labCitfranc	15.3991170	13.8970550	1.1080849	0.2679336
EE3:labCitfranc	-11.4493741	13.8970501	-0.8238708	0.4100929
EE10:labCitfranc	12.3162322	13.8971999	0.8862384	0.3755758
EE0.01:labCitijapa	-3.0151260	7.9637089	-0.3786083	0.7050115
EE0.03:labCitijapa	-4.5806369	11.6928831	-0.3917457	0.6952801
EE0.1:labCitijapa	-6.1052594	11.6939503	-0.5220870	0.6016568
EE0.3:labCitijapa	-3.2741206	11.6927905	-0.2800119	0.7794919
EE1:labCitijapa	35.0675543	11.6929228	2.9990410	0.0027355
EE3:labCitijapa	5.0502495	11.6927877	0.4319115	0.6658436
EE10:labCitijapa	10.5650698	11.6931765	0.9035244	0.3663362
EE0.01:labDenmark	-2.1078621	11.5430753	-0.1826084	0.8551204
EE0.03:labDenmark	-3.8631575	14.5521183	-0.2654705	0.7906693
EE0.1:labDenmark	-5.2945269	14.5519685	-0.3638358	0.7160119
EE0.3:labDenmark	27.6921013	14.5519290	1.9029849	0.0571593
EE1:labDenmark	40.2593492	14.5522648	2.7665350	0.0057080
EE3:labDenmark	8.8664099	14.5520236	0.6092905	0.5423882
EE10:labDenmark	-2.3109937	14.5553893	-0.1587724	0.8738613
EE0.01:labExxon	5.2457749	12.8665555	0.4077062	0.6835249
EE0.03:labExxon	0.6607488	14.9945279	0.0440660	0.9648554
EE0.1:labExxon	-0.3802441	14.9949332	-0.0253582	0.9797713
EE0.3:labExxon	9.4611994	14.9945142	0.6309774	0.5281140
EE1:labExxon	11.9059065	14.9945225	0.7940171	0.4272622
EE3:labExxon	5.4743729	14.9949929	0.3650801	0.7150831
EE10:labExxon	14.6708826	14.9947799	0.9783993	0.3279732
EE0.01:labHatano	-3.1285617	7.5814767	-0.4126586	0.6798928
EE0.03:labHatano	-3.6387506	11.4378435	-0.3181326	0.7504114
EE0.1:labHatano	-3.0319622	11.4536376	-0.2647161	0.7912504
EE0.3:labHatano	2.9262057	11.4357534	0.2558822	0.7980632
EE1:labHatano	25.9831604	11.4358435	2.2720808	0.0231677
EE3:labHatano	14.2633513	11.4358590	1.2472479	0.2124255
EE10:labHatano	23.8446654	11.4651242	2.0797564	0.0376513
EE0.01:labHuntingd	7.8757716	11.6203523	0.6777567	0.4979898
EE0.03:labHuntingd	-5.1484581	14.7358705	-0.3493827	0.7268320
EE0.1:labHuntingd	-30.0494023	14.7449823	-2.0379409	0.0416627
EE0.3:labHuntingd	-91.0483605	14.7382196	-6.1777042	0.0000000
EE1:labHuntingd	-151.3072461	14.7357224	-10.2680576	0.0000000
	101.0012101	11.1001221	10.200010	3.000000

	Estimate	Std. Error	t value	$\Pr(> t )$
EE3:labHuntingd	-101.1729866	14.7419254	-6.8629425	0.0000000
EE10:labHuntingd	-5.3201467	14.7374840	-0.3609942	0.7181348
EE0.01:labInEnvTox	-5.5008881	7.5810410	-0.7256112	0.4681463
EE0.03:labInEnvTox	-2.4986614	11.4377038	-0.2184583	0.8270902
EE0.1:labInEnvTox	2.0522573	11.4391119	0.1794070	0.8576329
EE0.3:labInEnvTox	8.1025280	11.4357597	0.7085256	0.4786862
EE1:labInEnvTox	35.7901398	11.4359495	3.1296168	0.0017709
EE3:labInEnvTox	5.7978376	11.4362920	0.5069683	0.6122226
EE10:labInEnvTox	-5.1590307	11.4364117	-0.4511057	0.6519532
EE0.01:labKoreaPar	-4.5600764	9.0012641	-0.5066040	0.6124782
EE0.03:labKoreaPar	-9.0474745	12.7018088	-0.7122981	0.4763478
EE0.1:labKoreaPar	-12.0801279	12.7043258	-0.9508673	0.3417653
EE0.3:labKoreaPar	-8.2114601	12.7018086	-0.6464796	0.5180292
EE1:labKoreaPar	32.4911955	12.7020103	2.5579569	0.0105884
EE3:labKoreaPar	-5.7024976	12.7024277	-0.4489297	0.6535219
EE10:labKoreaPar	10.6688331	12.7031098	0.8398599	0.4010686
EE0.01:labMitsubis	-6.9589534	7.5812514	-0.9179162	0.3587528
EE0.03:labMitsubis	-3.6469335	11.4534126	-0.3184146	0.7501975
EE0.1:labMitsubis	-5.4309427	11.4626114	-0.4737963	0.6356873
EE0.3:labMitsubis	10.1528255	11.4359123	0.8878020	0.3747342
EE1:labMitsubis	24.0054736	11.4365053	2.0990218	0.0359168
EE3:labMitsubis	12.0242638	11.4361293	1.0514278	0.2931656
EE10:labMitsubis	10.1999962	11.4358854	0.8919289	0.3725184
EE0.01:labNihon	1.1443408	7.5814228	0.1509401	0.8800353
EE0.03:labNihon	-6.8516033	11.4377109	-0.5990362	0.5492039
EE0.1:labNihon	-8.6410539	11.4380866	-0.7554632	0.4500435
EE0.3:labNihon	-4.3106596	11.4359951	-0.3769379	0.7062523
EE1:labNihon	22.3213216	11.4357866	1.9518834	0.0510655
EE3:labNihon	16.6933209	11.4357639	1.4597469	0.1444875
EE10:labNihon	16.7073132	11.4360027	1.4609399	0.1441598
EE0.01:labPoulenc	-2.6746648	11.5688865	-0.2311947	0.8171828
EE0.03:labPoulenc	-1.0820997	13.8970357	-0.0778655	0.9379414
EE0.1:labPoulenc	-2.1316505	13.8971591	-0.1533875	0.8781053
EE0.3:labPoulenc	15.6353563	13.8971182	1.1250790	0.2606654
EE1:labPoulenc	31.5495444	13.8970358	2.2702355	0.0232795
EE3:labPoulenc	-17.8699366	13.8970993	-1.2858753	0.1986078
EE10:labPoulenc	-25.6412231	13.8972852	-1.8450527	0.0651501
EE0.01:labSumitomo	-0.7738165	7.9635207	-0.0971701	0.9225992
EE0.03:labSumitomo	-1.5638764	11.6928688	-0.1337462	0.8936142
EE0.1:labSumitomo	-5.9424405	11.6939738	-0.5081626	0.6113849
EE0.3:labSumitomo	11.7129107	11.6928318	1.0017172	0.3165788
EE1:labSumitomo	42.0319864	11.6927892	3.5946929	0.0003312
EE3:labSumitomo	24.4487282	11.6928765	2.0909079	0.0366388
EE10:labSumitomo	35.6613733	11.6931561	3.0497646	0.0023147
EE0.01:labTNO	0.1459632	9.0558909	0.0161180	0.9871415
EE0.03:labTNO	-0.9345580	12.2903092	-0.0760402	0.9393933
EE0.1:labTNO	-5.5301417	12.2904691	-0.4499537	0.6527835
EE0.3:labTNO	2.7554038	12.2903618	0.2241922	0.8226264
EE1:labTNO	32.7429120	12.2903774	2.6641096	0.0077697
EE3:labTNO	10.9566903	12.2903462	0.8914875	0.3727550
EE10:labTNO	20.5077951	12.2903402 $12.2917541$	1.6684189	0.0953600
EE0.01:labWIL	2.3868885	9.0177255	0.2646885	0.7912716
	2.5500000	0.0111200	0.2010000	5.1012110

	Estimate	Std. Error	t value	Pr(> t )
EE0.03:labWIL	-0.9974044	12.2565949	-0.0813770	0.9351488
EE0.1:labWIL	1.6262677	12.2572149	0.1326784	0.8944586
EE0.3:labWIL	-0.5899327	12.2566676	-0.0481316	0.9616153
EE1:labWIL	13.0420573	12.2566878	1.0640768	0.2873985
EE3:labWIL	-12.0139275	12.2569909	-0.9801694	0.3270990
EE10:labWIL	4.3028315	12.2582459	0.3510153	0.7256070
EE0.03:labZeneca	0.2504818	11.6928837	0.0214217	0.9829110
EE0.1:labZeneca	1.1680882	11.6941543	0.0998865	0.9204426
EE0.3:labZeneca	13.2661190	11.6928050	1.1345540	0.2566729
EE1:labZeneca	21.7877479	11.6928006	1.8633473	0.0625326
EE3:labZeneca	-23.5618392	11.6930187	-2.0150348	0.0440097
EE10:labZeneca	-16.9092188	11.6936855	-1.4460128	0.1483012
ZM0.1:labBayer	50.8727461	15.9269030	3.1941392	0.0014202
ZM1:labBayer	32.7792790	15.9267178	2.0581315	0.0396828
ZM0.1:labBerlin	27.7253380	15.9267127	1.7408073	0.0818425
ZM1:labBerlin	-2.2226356	15.9267230	-0.1395539	0.8890239
ZM0.1:labChungKor	57.6940393	14.0160636	4.1162798	0.0000398
ZM1:labChungKor	33.0262842	14.0160945	2.3563115	0.0185356
ZM0.1:labCitfranc	30.2045937	15.9267649	1.8964676	0.0580154
ZM1:labCitfranc	12.7354950	15.9267284	0.7996303	0.4240023
ZM0.1:labCitijapa	31.8017854	13.3591547	2.3805238	0.0173639
ZM1:labCitijapa	7.7386338	13.3582359	0.5793155	0.5624294
ZM0.1:labDenmark	23.1410049	16.6873655	1.3867381	0.1656474
ZM1:labDenmark	8.2176564	16.6873351	0.4924487	0.6224462
ZM0.1:labExxon	23.0663308	15.9269827	1.4482549	0.1476734
ZM1:labExxon	-5.2036023	15.9268284	-0.3267193	0.7439080
ZM0.1:labHatano	9.0102103	13.0802294	0.6888419	0.4909878
ZM1:labHatano	0.3096981	13.0582014	0.0237167	0.9810805
ZM0.1:labHuntingd	72.4342844	16.9076766	4.2841063	0.0000191
ZM1:labHuntingd	114.0571430	16.9017085	6.7482612	0.0000000
ZM0.1:labInEnvTox	23.3265752	13.0584338	1.7863226	0.0741703
ZM1:labInEnvTox	10.2372871	13.0581623	0.7839761	0.4331297
ZM0.1:labKoreaPar	16.1498041	14.5364690	1.1109854	0.2666834
ZM1:labKoreaPar	40.0390337	14.5346073	2.7547379	0.0059172
ZM0.1:labMitsubis	13.2492104	13.0584341	1.0146094	0.3103919
ZM1:labMitsubis	-5.9918796	13.0581623	-0.4588609	0.6463747
ZM0.1:labNihon	12.5949318	13.0584778	0.9645023	0.3348891
ZM1:labNihon	-4.3232424	13.0581774	-0.3310755	0.7406157
ZM0.1:labPoulenc	49.0113737	15.9267124	3.0773064	0.0021118
ZM1:labPoulenc	29.6003373	15.9267334	1.8585316	0.0632131
ZM0.1:labSumitomo	30.8781749	13.3592364	2.3113727	0.0208946
ZM1:labSumitomo	-7.6949612	13.3582819	-0.5760442	0.5646380
ZM0.1:labTNO	77.4798497	14.0160034	5.5279560	0.0000000
ZM1:labTNO	22.6405850	14.0159523	1.6153440	0.1063646
ZM0.1:labWIL	38.1873945	14.0159664	2.7245638	0.0064843
ZM1:labWIL	29.8072517	14.0159523	2.1266662	0.0335472
ZM0.1:labZeneca	77.9602706	13.3595517	5.8355454	0.0000000
ZM1:labZeneca	44.7841288	13.3582788	3.3525374	0.0008129

kable((bas.coef), format = "markdown")

coef	2.5%	97.5%	beta	ci.length
Intercept	100.036820937202	101.583563597679	100.828516996638	1.5409907
EE0.01	0	0	- 0.0135641574206643	0.0000000
EE0.03	0	0	-	0.0000000
LL0.03	O	O	0.0174033110726117	0.0000000
EE0.1	0	3.27683821604305	0.241144916762948	2.9584409
EE0.3	0	7.38889239771093	1.30107451842365	7.2782803
EE1	22.799259767423	33.6948190576837	28.1641105139007	10.8563622
EE3	65.2905764105867	75.7674761997246	70.3230646667041	10.5729944
EE10	92.6715715913264	103.772082142886	98.1600672143778	11.0331730
ZM0.1	-26.2071304995685	-13.1362320406623	-19.6262208946546	13.0782959
ZM1	-66.7048201737219	-53.6882053510567	-60.1751375023389	13.2176995
labBayer	0	13.5515895508666	1.64426581938186	13.7001928
labBerlin	0	14.7575452581015	1.54983791919021	14.7695631
labChungKor	8.78197423464812	25.4477966304742	16.0188073748791	16.6218299
labCitfranc	7.80226296385238	23.4480358878725	14.674070051507	15.7200626
labCitijapa	5.67715398734195	20.6464515447827	10.8812000493123	15.0380258
labDenmark	0	17.2346356707779	4.84894301697913	17.4496404
labExxon	6.92765052382146	23.4889496041168	14.2866178068743	16.6477113
labHatano	6.89516060648219	20.2057491575301	11.8691101080254	13.2280497
labHuntingd	-14.6268612027184	0	-1.64906974646117	15.0274342
labInEnvTox	0	12.839176322115	1.54563289914755	12.7387276
labKoreaPar	-15.5800557075945	0	-10.0764288648397	15.4772293
labMitsubis	4.78057298070868	18.0856683512415	9.80233091722985	13.2953453
labNihon	-	11.7398724216264	1.33119278937294	11.7848066
1.15. 1	0.0255452009226396		0 5005400550050	10 00000
labPoulenc	-11.1402883901806	0	-2.5835108579873	10.9922956
labSumitomo	3.74087527405247	22.1949888381437	11.3529929370615	17.9502096
labTNO	0	13.3518006890406	1.84284237589857	13.4286300
labWIL	-	10.8868623074881	1.13110743539557	11.0082054
labZeneca	0.0674805559409845	0	-0.556288534141927	7 600/170
	-7.60456846170738	0.056803461504894	-0.000200004141927	7.6804178 $0.4321453$
protocolB	-0.170237161065909	0.000005401004694	0.0580651046352453	0.4521455
protocolC	54.1211314095767	77.7108648539803	70.3847036300859	23.4684518
protocolD	45.6050639796799	72.593283976141	64.0382170310725	26.8936726
weight	0	0.109064442801529	0.0178747234530543	0.1089744
EE0.01:protocolB	0	0.103004442001323	0.0110141204000040	0.0000000
LL0.01.protocoid	O	O	0.0579375379948751	0.0000000
EE0.03:protocolB	0	0	-	0.0000000
EE0.00.protocolB	O .	V	0.00720933809662991	0.0000000
EE0.1:protocolB	_	5.64948028016795	0.593667961085243	5.6233514
EE0.1.protocolB	0.0135462322313029	0.01010020010100	0.000001001000210	0.0200011
EE0.3:protocolB	27.1876433269464	40.7757236066607	34.1174581733035	13.9350629
EE1:protocolB	55.1128254216363	68.7955186902028	61.4719947751982	13.5864555
EE3:protocolB	30.3833572486354	43.5304473427211	36.8155376709099	13.2982703
EE10:protocolB	8.57468296506471	21.9287038946634	15.3993237476973	13.3420177
EE0.01:protocolC	0	0	-	0.0000000
r			0.0664143500766211	
EE0.03:protocolC	0	0	-	0.0000000
•			0.0535631700799431	
EE0.1:protocolC	5.36070599999337	23.0620517038165	13.7494842772417	17.4151493
•				

coef	2.5%	97.5%	beta	ci.length
EE0.3:protocolC	92.5521807720085	108.996972532077	100.806821850728	16.4671191
EE1:protocolC	182.327895134534	198.921866657694	190.269932036467	16.6205913
EE3:protocolC	166.687013150633	183.468070618334	174.983781796972	17.0111687
EE10:protocolC	147.361455186168	164.530231843865	155.877141286351	17.2709431
EE0.01:protocolD	0	0	0.142295178535078	0.0000000
EE0.03:protocolD	0	0	0.00607080141150072	0.0000000
EE0.1:protocolD	18.3273108446186	37.4811813718871	27.9278414594051	19.1259762
EE0.3:protocolD	128.356832497812	149.732270205173	139.10571224148	21.3247642
EE1:protocolD	218.51155453568	239.849197456098	228.901615050531	21.4456243
EE3:protocolD	201.82905107417	223.282742909793	212.328084872981	21.5436547
EE10:protocolD	202.75203728476	224.945636640941	213.569556525163	22.2983032
ZM0.1:protocolB	-73.2279748564225	-55.3020377469021	-64.0385722880611	17.7849516
ZM1:protocolB	-64.1068020530248	-46.0849425311256	-55.2392164362778	18.0976754
ZM0.1:protocolC	-173.181109596846	-152.127342750239	-162.622779253208	20.9590240
ZM1:protocolC	-186.166307290317	-164.891951856785	-174.862333405958	21.1955111
ZM0.1:protocolD	-204.150300772104	-177.680407633948	-190.718322637718	26.7960533
ZM1:protocolD	-235.972031892832	-209.305899281633	-222.251824403968	26.8546668
EE0.01:labBayer	0	0	0	0.0000000
EE0.03:labBayer	0	0	0	0.0000000
EE0.1:labBayer	0	6.75029759680471	0.654593218229763	8.2707249
EE0.3:labBayer	0	0	0.233468050309372	0.0000000
EE1:labBayer	-18.5073523117852	0	-1.69169087148743	17.9512362
EE3:labBayer	-6.964035236597	0.125884724017705	-0.610492987004873	6.4745385
EE10:labBayer	0	4.51992952091361	0.585790120542057	3.1240580
EE0.01:labBerlin	0	0	0.0296405041992463	0.0000000
EE0.03:labBerlin	0	0	0.12905812757024	0.0000000
EE0.1:labBerlin	0	0	-	0.0000000
			0.0108211875467356	
EE0.3:labBerlin	0	17.7772906613976	1.85632507396288	17.8263392
EE1:labBerlin	0	39.7587737320982	19.3599266556044	40.0700914
EE3:labBerlin	20.4227543447451	43.8043647816643	32.2720974247051	23.5060349
EE10:labBerlin	-5.65426200436079	0	-0.468311728064526	4.3903183
EE0.01:labChungKor	0	0	-0.308164459022454	0.0000000
EE0.03:labChungKor	0	0	0.165451408663825	0.0000000
EE0.1:labChungKor	14.7063066175657	41.4775915687459	28.0497754919486	26.5875761
EE0.3:labChungKor	7.42036216312981	43.1027397341555	24.0056373248844	35.8492005
EE1:labChungKor	-0.753961425296961	1.99991465560127	0.431897805534246	1.2399860
EE3:labChungKor	-2.5522660466886	5.25407167191048	0.494616691856925	8.4148322
EE10:labChungKor	-42.2212420424942	-13.0997619014617	-27.5589443448086	28.9072876
EE0.01:labCitfranc	0	0	-	0.0000000
			0.0114519495691639	
EE0.03:labCitfranc	-0.814686879329034	0	0.412672271657143	1.4828208
EE0.1:labCitfranc	0	0	0.0351644365891377	0.0000000
EE0.3:labCitfranc	0	0	0.273622983329916	0.0211455
EE1:labCitfranc	0	0	-0.241075661000662	0.0000000
EE3:labCitfranc	-10.9787537958895	0	-0.95366892992701	9.9475589
EE10:labCitfranc	0	0	0.0923921098411862	0.0000000
EE0.01:labCitijapa	0	0	-	0.0000000
-0.0 0.101Japa	-	-	0.0528044992869181	2.2200000
EE0 00 1 1 Cmm				
EE0.03:labCitijapa	0	0	-	0.0000000

coef	2.5%	97.5%	beta	ci.length
EE0.1:labCitijapa	0	0	-	0.0000000
			0.0520824876629108	
EE0.3:labCitijapa	-8.86517709765021	0	-0.763765962130375	8.4188179
EE1:labCitijapa	0	13.836615811736	1.74241441654019	14.2694970
EE3:labCitijapa	0	7.04584703012385	0.706788469774731	7.4176012
EE10:labCitijapa	-	2.45267784072859	-0.168770205011758	1.1401873
	0.0648119957747237			
EE0.01:labDenmark	0	0	0.0463801005972885	0.0000000
EE0.03:labDenmark	0	0	0.0309670965790302	0.0000000
EE0.1:labDenmark	-0.125420119173116	0.712939917182219	0.244649019513296	0.0000000
EE0.3:labDenmark	0	41.8302446684514	20.208692314452	41.9215795
EE1:labDenmark	-	21.0099792731574	2.3345781699027	21.2220341
	0.0391427329555771			
EE3:labDenmark	0	12.8361905895903	1.26498456648356	12.5876443
EE10:labDenmark	-24.3748372033106	0	-2.93568323805003	24.9957719
EE0.01:labExxon	0	0	0.352986384370801	0.0000000
EE0.03:labExxon	0	0	0.0630011357667294	0.0000000
EE0.1:labExxon	0	0	0.0623567452652723	0.0000000
EE0.3:labExxon	-0.984864514262695	1.80874213442985	0.385400152743111	1.0222435
EE1:labExxon	-16.0738195602091	0	-1.50133693698061	15.6529364
EE3:labExxon	0	0	-	0.0000000
			0.0485958594231877	
EE10:labExxon	0	0	0.0658989142944608	0.0000000
EE0.01:labHatano	0	0	-0.107479039923413	0.0000000
EE0.03:labHatano	-0.748407892377969	0.181678441892199	-0.132448233428601	0.5169082
EE0.1:labHatano	-	5.39907975838858	0.506007885482095	5.9167675
	0.0160332262245326			
EE0.3:labHatano	-0.169223233475746	0.0145171869603349	-0.132486507689674	0.0000000
EE1:labHatano	0	0	-0.146545311886994	0.0000000
EE3:labHatano	-0.155108915441997	0.199036003878343	0.267773797894886	1.0789600
EE10:labHatano	-	16.1640568058374	2.9768031167196	15.8581472
	0.00232267920382512			
EE0.01:labHuntingd	-0.777330917660822	4.78980571341747	0.668899727926247	7.2589098
EE0.03:labHuntingd	0	0	-0.164357002905122	0.0000000
EE0.1:labHuntingd	-45.2631361619849	0	-26.1878509400334	45.0981515
EE0.3:labHuntingd	-115.407555555259	-77.2727795470411	-96.1001537044823	37.9228203
EE1:labHuntingd	-200.899438042908	-162.228971159235	-181.78131917499	38.8899466
EE3:labHuntingd	-130.257436839841	-90.2928235586133	-110.171488954809	39.5727850
EE10:labHuntingd	-36.1829691532915	0	-11.5329713209157	36.1594216
${\bf EE0.01: lab In Env Tox}$		0.0669958147672842	-0.269814143197872	2.1638643
EE0.03:labInEnvTox	0	0	-	0.0000000
			0.0198596944725898	
EE0.1:labInEnvTox	0	0	0.198113211623869	0.4331374
EE0.3:labInEnvTox	0	0.0565261307985327	0.244942632758154	0.5531915
EE1:labInEnvTox	-0.016483888782604	13.889576892932	2.18362410952765	13.7817782
EE3:labInEnvTox	-	1.85232441159161	0.216967732558436	2.0926008
	0.0642112589391362			
EE10:labInEnvTox	-29.9167516154172	-9.26446837684033	-19.4484420783779	20.8944719
EE0.01:labKoreaPar	0	0	0.0541288911749422	0.0000000
EE0.03:labKoreaPar	0	0	-	0.0000000
			0.0587900713505704	
EE0.1:labKoreaPar	0	0	-0.133503345139568	0.0000000

coef	2.5%	97.5%	beta	ci.length
EE0.3:labKoreaPar	-10.4430404557932	0	-0.95331327656264	11.4631529
EE1:labKoreaPar	0	13.1951682783445	1.19674538908997	12.6593315
EE3:labKoreaPar	-18.35991335626	0	-3.9560545097737	18.4341906
EE10:labKoreaPar	0	0	0.154131051846838	0.0000000
EE0.01:labMitsubis	-1.25841256867784	0.00891111396308819	-0.212997101363976	0.0000000
EE0.03:labMitsubis	0	0	-	0.0000000
			0.00466552881689559	
EE0.1:labMitsubis	0	0	0.16177864272756	0.0000000
EE0.3:labMitsubis	0	11.9793534799371	1.538006357876	12.1701088
EE1:labMitsubis	-0.132920637798541	0.0205239999297708	-0.179533696283202	0.3357814
EE3:labMitsubis	0	0	0.128647793551087	0.0000000
EE10:labMitsubis	-0.370456149869834	0.394256991669286	-0.205412937115234	0.6226706
EE0.01:labNihon	-	6.70679403004006	0.602706167725066	6.3911419
	0.0926150938620802			
EE0.03:labNihon	0	0	-0.073946130778594	0.0000000
EE0.1:labNihon	-3.61583167964788	0.488547980495747	-0.357615663580601	3.9025329
EE0.3:labNihon	-8.51849128610648	0.0173936908297421	-0.801441564086679	8.9331253
EE1:labNihon	0	0	-0.18225553201103	0.0000000
EE3:labNihon	0	12.8537156647034	4.93065066295152	12.7164589
EE10:labNihon	0	9.64835135172112	0.918938435073705	9.7587250
EE0.01:labPoulenc	0	0	-0.260309966680061	0.0000000
EE0.03:labPoulenc	0	0	-0.196420483141612	0.0000000
EE0.1:labPoulenc	0	0	-0.190278954748983	0.0000000
EE0.3:labPoulenc	- 0.0407831197220165	11.4799175865129	1.00000641308105	12.6709729
EE1:labPoulenc	0.0407031137220103	0	0.265184576053756	0.0000000
EE3:labPoulenc	-18.3063887149329	0	-3.10967144358129	18.0676240
EE10:labPoulenc	-60.8998448207124	-22.6552314616183	-42.6520230172029	37.9680143
EE0.01:labSumitomo		0	-0.113850688729352	0.0000000
EE0.03:labSumitomo		0.892832926520797	-	1.0934133
220.00.1000.0111101110	0.2000001,2000100	0.002002020101	0.0914926251715059	1.0001100
EE0.1:labSumitomo	-5.69461833112859	0	-0.473935888840207	6.0200956
EE0.3:labSumitomo	0	9.56093556860904	0.833409457697126	9.6106600
EE1:labSumitomo	0	22.1808820240674	6.66022646131383	22.3160401
EE3:labSumitomo	0	28.0998426838003	13.1848788212295	28.2072140
EE10:labSumitomo	0	29.6493047273644	17.8505385437028	29.8367812
EE0.01:labTNO	0	0	0.0583185097447064	0.0000000
EE0.03:labTNO	0	0	0.0290312359336136	0.0000000
EE0.1:labTNO	0	0	-	0.0000000
			0.0301542291118373	
EE0.3:labTNO	0	0	-	0.0000000
			0.0187680775294185	
EE1:labTNO	0	6.25365261728723	0.536106932167458	4.9654459
EE3:labTNO	0	21.0064483447876	5.54932157987083	21.0618166
EE10:labTNO	-	9.39552044614434	0.823336918415435	8.9530414
	0.0158741321175224			
EE0.01:labWIL	-0.402583046575016	5.23127843565326	0.482896878870143	5.4988501
${\rm EE}0.03:{\rm labWIL}$	0	0	0.163051623135706	0.0000000
${\rm EE}0.1:{\rm labWIL}$	0	11.2914957056626	1.05141572100714	11.0832606
${\rm EE}0.3:{\rm labWIL}$	0	0	-	0.0000000
			0.0407128391130763	
EE1:labWIL	-15.6864420677208	0	-1.90333299397989	15.7085350

coef	2.5%	97.5%	beta	ci.length
EE3:labWIL	0	0	-0.105797286121864	0.0000000
EE10:labWIL	-3.44769155505026	0.132270737156848	-0.434871908156067	4.3818000
EE0.01:labZeneca	0	0	-	0.0000000
			0.0635353318985676	
EE0.03:labZeneca	0	0	-0.051128689237527	0.0000000
EE0.1:labZeneca	0	0	0.114617000586065	0.0000000
EE0.3:labZeneca	0	10.7628740588517	0.98310458550964	10.6285152
EE1:labZeneca	-15.1385520227373	0	-2.19340028739806	15.1358157
EE3:labZeneca	-43.6031809821232	-20.858585287215	-32.1036995780036	22.9706407
EE10:labZeneca	-45.1788369591492	-22.0059892206899	-33.4070103818475	23.3895945
ZM0.1:labBayer	-0.841589991889759	1.64514517374371	0.459433857562753	3.9438825
ZM1:labBayer	0	0	0.251404736435241	0.0000000
ZM0.1:labBerlin	0	0	0.415742123470327	0.0000000
ZM1:labBerlin	-10.6458382895187	0.0138227169372254	-0.974775161194298	11.2779102
ZM0.1:labChungKor	20.7724614479803	50.3388965660111	34.4139956920773	30.0705749
ZM1:labChungKor	0	37.5701367338519	24.932380668404	37.4281558
ZM0.1:labCitfranc	0	0	-0.116962121545106	0.0000000
ZM1:labCitfranc	0	0	-0.224343692317283	0.0000000
ZM0.1:labCitijapa	0	17.0948206956576	3.08578825933271	17.4544260
ZM1:labCitijapa	0	0	0.0323571307697211	0.0000000
ZM0.1:labDenmark	0	7.89644303918105	0.569735770640364	6.1468796
ZM1:labDenmark	0	0	0.349980829219699	0.0000000
ZM0.1:labExxon	0	0	0.0937890132436849	0.0000000
ZM1:labExxon	-9.01069869564251	0.17863961036802	-0.831770040747281	9.1245293
ZM0.1:labHatano	-6.90018460073409	0	-0.650122216500344	7.7061615
ZM1:labHatano	0	0	0.083558665334959	0.0000000
ZM0.1:labHuntingd	29.0006474380612	79.3147111215844	53.0864537662125	50.9075286
ZM1:labHuntingd	85.3923304914508	135.567334788346	110.349893126842	50.6811957
ZM0.1:labInEnvTox	0	0	0.10061975962431	0.0000000
ZM1:labInEnvTox	0	5.46730509319931	0.382345769088357	4.8077967
ZM0.1:labKoreaPar	-15.5853290517046	0.0272076653920763	-1.53573058427409	15.3748148
ZM1:labKoreaPar	15.2864643040364	48.7093316185739	30.9805791773632	33.7229680
ZM0.1:labMitsubis	0	0	-	0.0000000
			0.0467294615046819	
ZM1:labMitsubis	-6.74380049414242	0	-0.601834969216268	6.1167465
ZM0.1:labNihon	0	0	-0.061429763120017	0.0000000
ZM1:labNihon	0	0.139036451698536	-0.256945835765046	0.0000000
ZM0.1:labPoulenc	0	0	0.460054480631033	0.0000000
ZM1:labPoulenc	0	0	0.146988291849367	0.0000000
ZM0.1:labSumitomo	0	29.0597995511206	9.36042064153042	28.7630775
ZM1:labSumitomo	-26.5321588451397	0	-7.53984793445858	26.4303645
ZM0.1:labTNO	35.6075212237099	73.0179067000997	55.9480555317764	37.5787001
ZM1:labTNO	0	32.2839067079326	14.0238034194365	31.9966840
ZM0.1:labWIL	0	0	0.156282703571003	0.0000000
ZM1:labWIL	-	16.5912273012854	1.94676530983727	16.3935953
	0.00428714994181867			
ZM0.1:labZeneca	41.2939513990152	70.1751463584581	55.8876627390035	29.1231196
ZM1:labZeneca	23.8539152795503	52.8427099814592	38.925698725295	29.0951460