LASERI-trajectories

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## R Markdown

This analysis produces a model for trajectories of human body burdens of persistent organic pollutants (POPs).

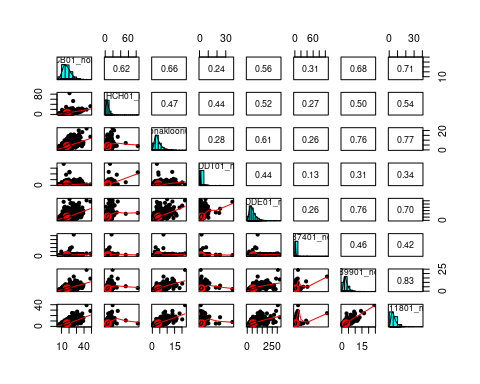
library(foreign)  
library(psych)  
  
df <- read.spss("~/Documents/priv/VS \_Henkilökohtaiset\_POP-trajektorit\_LASERI-aineistossa/updated\_korjattu\_LASERI\_data\_2020\_05\_WORKCOPY.sav", to.data.frame = TRUE)

## Warning in read.spss("~/Documents/priv/VS  
## \_Henkilökohtaiset\_POP-trajektorit\_LASERI-aineistossa/  
## updated\_korjattu\_LASERI\_data\_2020\_05\_WORKCOPY.sav", : ~/Documents/  
## priv/VS \_Henkilökohtaiset\_POP-trajektorit\_LASERI-aineistossa/  
## updated\_korjattu\_LASERI\_data\_2020\_05\_WORKCOPY.sav: Compression bias (0) is not  
## the usual value of 100

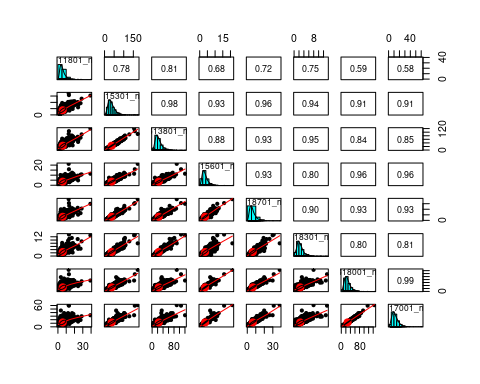
## Warning in read.spss("~/Documents/priv/VS  
## \_Henkilökohtaiset\_POP-trajektorit\_LASERI-aineistossa/  
## updated\_korjattu\_LASERI\_data\_2020\_05\_WORKCOPY.sav", : Undeclared level(s) 0  
## added in variable: bintup80

## Warning in read.spss("~/Documents/priv/VS  
## \_Henkilökohtaiset\_POP-trajektorit\_LASERI-aineistossa/  
## updated\_korjattu\_LASERI\_data\_2020\_05\_WORKCOPY.sav", : Undeclared level(s) 0  
## added in variable: bintup01

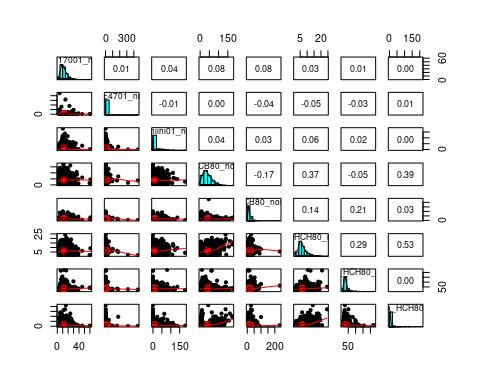
#colnames(df)[grep("PI",toupper(colnames(df)))]  
  
units <- read.csv("POP\_units.csv")  
  
tmp <- df[grepl("\_norm",colnames(df))][-2] # remove alfa\_HCH01\_norm, which contains no data  
pairs.panels(tmp[1:8])



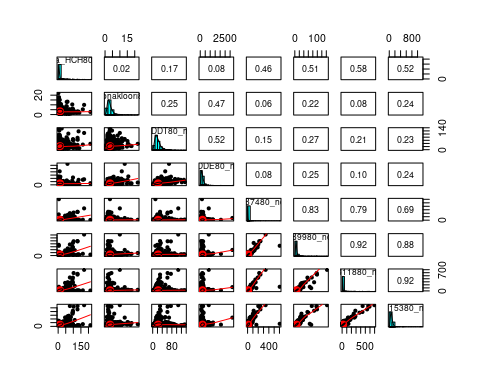
pairs.panels(tmp[8:15])



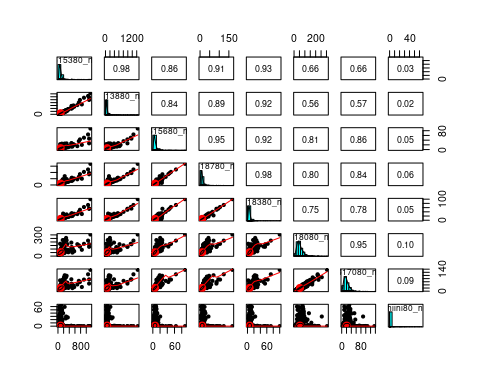
pairs.panels(tmp[15:22])



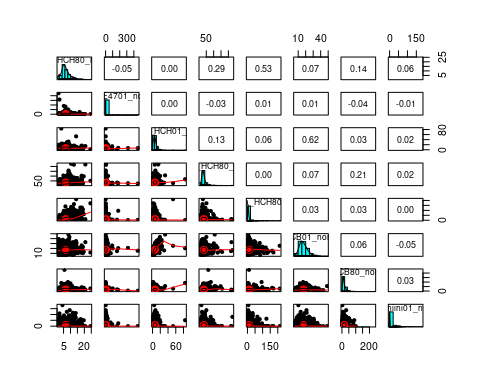
pairs.panels(tmp[22:29])



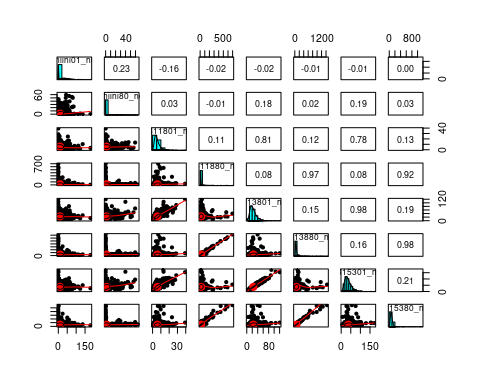
pairs.panels(tmp[29:36])



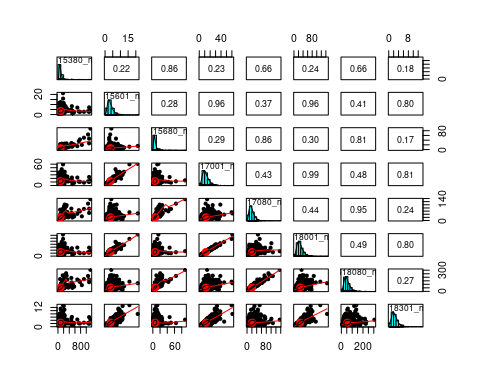
# Compare 1980 and 2001 in pairwise correlations  
tmp <- tmp[sort(colnames(tmp))]  
pairs.panels(tmp[1:8])



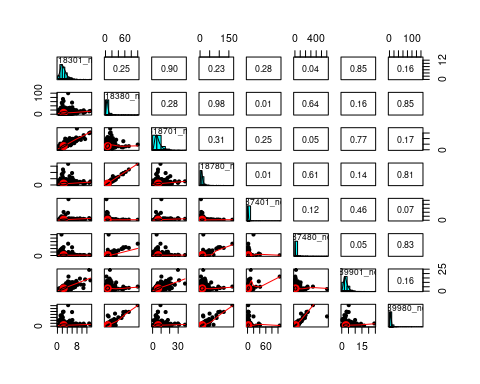
pairs.panels(tmp[8:15])



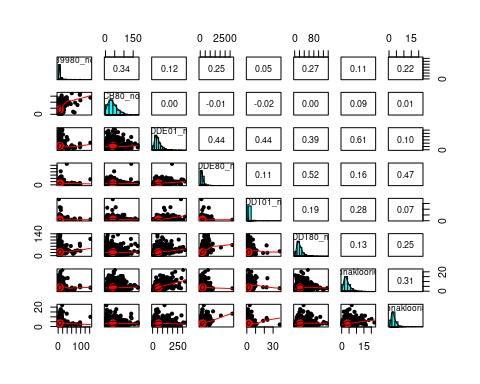
pairs.panels(tmp[15:22])



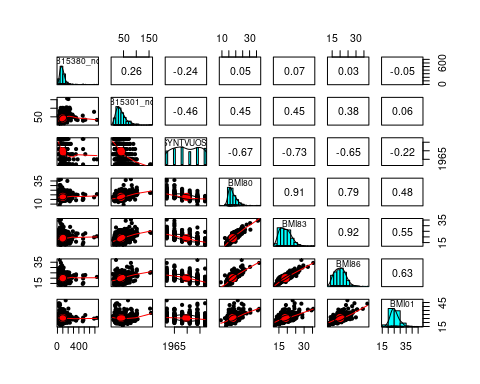
pairs.panels(tmp[22:29])



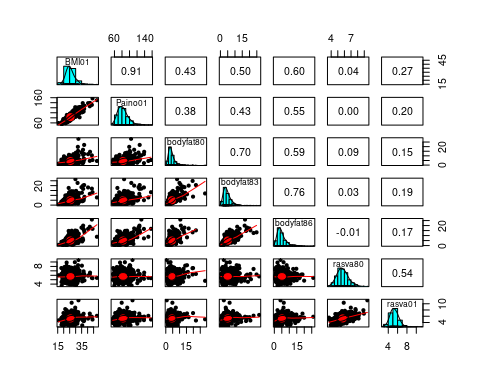
pairs.panels(tmp[29:36])



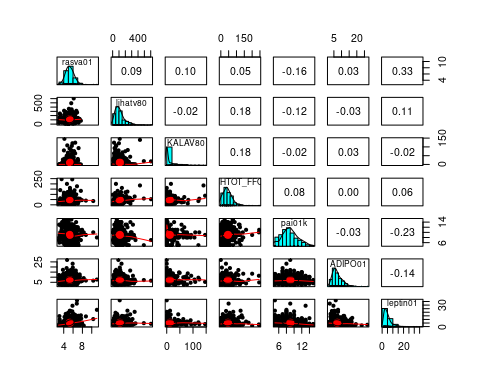
#colnames(tmp)  
# [1] "HCB01\_norm" "beta\_HCH01\_norm" "Trans\_nonakloori01\_norm"  
# [4] "pp\_DDT01\_norm" "pp\_DDE01\_norm" "PCB7401\_norm"   
# [7] "PCB9901\_norm" "PCB11801\_norm" "PCB15301\_norm"   
#[10] "PCB13801\_norm" "PCB15601\_norm" "PCB18701\_norm"   
#[13] "PCB18301\_norm" "PCB18001\_norm" "PCB17001\_norm"   
#[16] "BDE4701\_norm" "kotiniini01\_norm" "PeCB80\_norm"   
#[19] "HCB80\_norm" "alfa\_HCH80\_norm" "beta\_HCH80\_norm"   
#[22] "gamma\_HCH80\_norm" "Trans\_nonakloori80\_norm" "pp\_DDT80\_norm"   
#[25] "pp\_DDE80\_norm" "PCB7480\_norm" "PCB9980\_norm"   
#[28] "PCB11880\_norm" "PCB15380\_norm" "PCB13880\_norm"   
#[31] "PCB15680\_norm" "PCB18780\_norm" "PCB18380\_norm"   
#[34] "PCB18080\_norm" "PCB17080\_norm" "kotiniini80\_norm"   
  
POP <- c(  
 "HCB", # https://en.wikipedia.org/wiki/Hexachlorobenzene  
 "alfa\_HCH", # https://en.wikipedia.org/wiki/Alpha-Hexachlorocyclohexane  
 "beta\_HCH",  
 "gamma\_HCH", # also known as lindane  
 "Trans\_nonakloori", # https://en.wikipedia.org/wiki/Chlordane  
 "pp\_DDT", # para,para'-DDT https://en.wikipedia.org/wiki/DDT  
 "pp\_DDE",   
 "PCB74", # https://en.wikipedia.org/wiki/Polychlorinated\_biphenyl  
 "PCB99",  
 "PCB118",  
 "PCB153",  
 "PCB138",  
 "PCB156",  
 "PCB187",  
 "PCB183",  
 "PCB180",  
 "PCB170",  
 "BDE47", # https://en.wikipedia.org/wiki/Pentabromodiphenyl\_ether  
 "kotiniini80\_norm" # https://en.wikipedia.org/wiki/Cotinine  
)  
  
# Take all-male panel of interesting variables  
df <- df[df$SP=="Poika", c(  
 "PCB15380\_norm", # PCB 153 ug/kg fat in 1980  
 "PCB15301\_norm", # PCB 153 ug/kg fat in 2001  
 "SYNTVUOSI", # birth year  
 "BMI80", # body mass index in 1980  
 "BMI83", # body mass index in 1983  
 "BMI86", # body mass index in 1986  
 "BMI01", # body mass index in 2001  
 "Paino01", # body weight kg in 2001  
 "bodyfat80", # body fat % in 1980  
 "bodyfat83", # body fat % in 1983  
 "bodyfat86", # body fat % in 1986  
 "rasva80", # serum fat content mg/ml in 1980  
 "rasva01", # serum fat content mg/ml in 2001  
 "lihatv80", # consumption of meat and meat products g/d in 1980  
 "KALAV80", # consumption of fish and fish products g/d in 1980  
 "FISHTOT\_FFQ07", # total fish consumption, g/d in 2007 food frequency questionnaire  
 "pai01k", # physical activity index in 2001  
 "ADIPO01", # adiponectin hormone in serum, ug/ml in 2001  
 "leptin01" # leptin hormone concentration ng/ml in 2001  
)] # Very few observations in bodyfat92, Paino80, leptin80 --> omit  
# It would be good to obtain these variables:  
# ENERC07 energy consumption kJ/d from 2007 FFQ  
# FAT07 fat consumption g/d from 2007 FFQ  
  
pairs.panels(df[1:7])



pairs.panels(df[7:13])



pairs.panels(df[13:19])



### Select the population for analysis  
  
dfs <- na.omit(df[c(1:4,7:8,16)])  
  
## Indices used  
  
AGE <- 0:40  
H <- length(AGE)  
YEAR <- 1960:2020  
I <- nrow(dfs)  
SYNT <- dfs$SYNTVUOSI  
  
## Data used  
  
U <- 365 # unit conversion factor: 1/d --> 1/a  
A <- 0.9 # fraction, absorption fraction  
N <- params$N  
b <- 0.07 # 1/a, rate of decrease of the POP in the environment and intake  
c <- params$c # year of peak exposure  
P <- rep(1,H) # age-specific intake relative to lifetime average  
# Estimated from the Bayesian model:  
## k <- 0.35 # 1/a, elimination constant of the POP  
## a <- 1.1 # ug/kg/d, average intake at the peak exposure  
  
conc <- dfs[1:I,c("PCB15380\_norm","PCB15301\_norm")]  
fish <- dfs$FISHTOT\_FFQ07[1:I]  
  
# https://www.kasvuseula.fi/  
W <- t(matrix(rep(c(5,10,13,15,17,20,22,26,28,31,35,38,44,48,55,60,65,68,70,71,72,  
 rep(75,10),rep(80,10)),I),  
 nrow=H, dimnames=list(Age=AGE, Individual = 1:I)))  
  
# A simplistic model uses the population average as default until the weight reaches the  
# observed value of that individual. Then, actual value is used to replace 80 kg (the max default),  
# if larger. This leads to situation where people suddenly gain weight when at 31 or at 2001.  
W <- pmin(W, dfs$Paino01, na.rm = TRUE)  
W <- ifelse(W==80, pmax(W, dfs$Paino01, na.rm=TRUE), W)  
tmp <- dfs$SYNTVUOSI + matrix(rep(AGE,each=I),nrow=I)>=2001  
W <- ifelse(!is.na(dfs$Paino01) & tmp, dfs$Paino01, W)  
  
# A simplistic model that assumes that average BMI is equal to lifetime fat percentage.  
M <- W \* ifelse(is.na(dfs$BMI01), dfs$BMI80, (dfs$BMI80 + dfs$BMI01)/2) / 100  
  
#aggregate(df$Paino01, by=df[c("Age80")], FUN=function(x) mean(x, na.rm=TRUE))

The following conclusions can be made from the graphs above

* 1. PCBs correlate very well with each other.
  2. PCB correlation is much stronger between congeners at the same year (R>0.8) than the same congener 21 years apart (R = 0.2 - 0.4).
  3. DDT and DDE congeners correlate moderately with each other and across years (R ca. 0.4)
  4. Trans-nonachlor correlates well with DDE of the same year (R 0.45-0.6) and moderately across years (R ).
  5. HCH congeners correlate only with alpha-HCH in 1980 (R 0.3 - 0.5) but not across years nor beta vs gamma.
  6. HCB correlates well with alpha-HCH in 1980 but poorly across other congeners or years.
  7. Cotinine correlates poorly across years (R = 0.2) and not at all with POPs.

library(ggplot2)

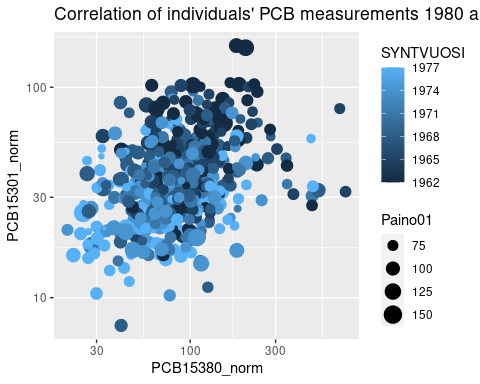
##   
## Attaching package: 'ggplot2'

## The following objects are masked from 'package:psych':  
##   
## %+%, alpha

mimax <- c(min(df[c("PCB15380\_norm","PCB15301\_norm")]),max(df[c("PCB15380\_norm","PCB15301\_norm")]))  
ggplot()+  
 geom\_point(data=df, aes(x=PCB15380\_norm, y=PCB15301\_norm, size=Paino01, colour=SYNTVUOSI))+  
 geom\_line(data=data.frame(x=mimax, y=mimax), aes(x=x, y=y),color="red")+  
 scale\_x\_log10()+scale\_y\_log10()+  
 labs(title="Correlation of individuals' PCB measurements 1980 and 2001")

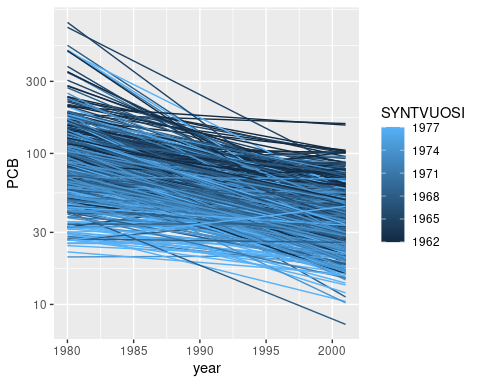
## Warning: Removed 27 rows containing missing values (geom\_point).

## Warning: Removed 2 row(s) containing missing values (geom\_path).

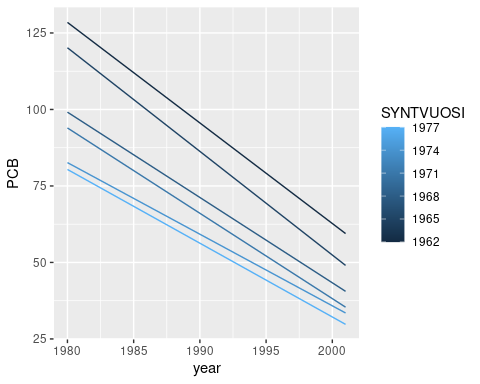


df$id <- 1:nrow(df)  
df$Paino80 <- NA  
df$bodyfat01 <- NA  
long <- reshape(df[-c(5,6,10:19)],  
 idvar=c("SYNTVUOSI","id"),  
 varying=list(  
 PCB=c("PCB15380\_norm","PCB15301\_norm"),  
 BMI= c("BMI80","BMI01"),  
 weight=c("Paino80","Paino01"),  
 fat=c("bodyfat80","bodyfat01")  
 ),  
 v.names =c("PCB","BMI","weight","fat"),  
 timevar="year",  
 times=c(1980,2001),  
 direction="long")  
  
ggplot(long, aes(x=year, y=PCB, colour=SYNTVUOSI, group=id))+geom\_line()+  
 scale\_y\_log10()

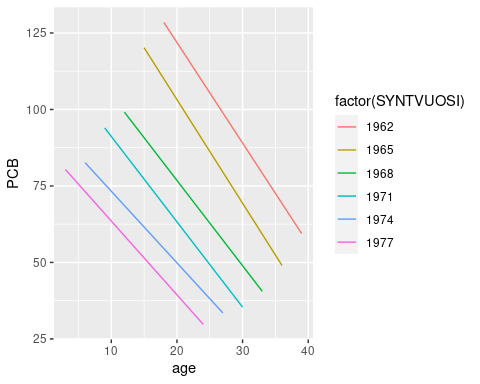
## Warning: Removed 27 row(s) containing missing values (geom\_path).



ggplot(aggregate(long["PCB"], by=long[c("SYNTVUOSI","year")], FUN=function(x) mean(x, na.rm=TRUE)),  
 aes(x=year, y=PCB, colour=SYNTVUOSI, group=SYNTVUOSI))+geom\_line()



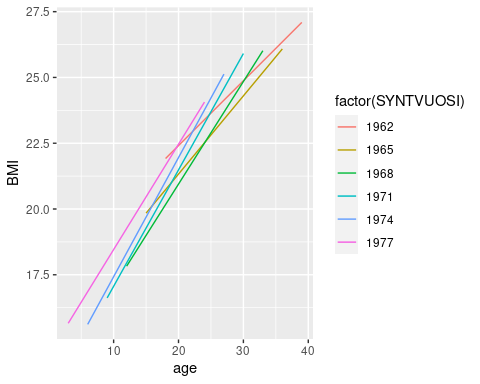
long$age <- long$year - long$SYNTVUOSI  
ggplot(aggregate(long["PCB"], by=long[c("SYNTVUOSI","age")], FUN=function(x) mean(x, na.rm=TRUE)),  
 aes(x=age, y=PCB, colour=factor(SYNTVUOSI), group=SYNTVUOSI))+geom\_line()



cat("Concentrations in 20-year-old people decrease", signif((1-(40/120)^(1/(1977-1962)))\*100,2), " % per year\n")

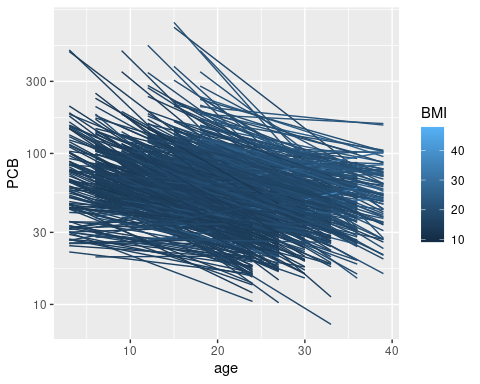
## Concentrations in 20-year-old people decrease 7.1 % per year

ggplot(aggregate(long["BMI"], by=long[c("SYNTVUOSI","age")], FUN=function(x) mean(x, na.rm=TRUE)),  
 aes(x=age, y=BMI, colour=factor(SYNTVUOSI), group=SYNTVUOSI))+geom\_line()



tmp <- aggregate(long["PCB"], by=long[c("age","year")], FUN=mean)  
ggplot(long,  
 aes(x=age, y=PCB, colour=BMI, group=id))+geom\_line()+  
 scale\_y\_log10()

## Warning: Removed 27 row(s) containing missing values (geom\_path).



# Remove the least important variables from the model  
#reg <- lm(PCB15380\_norm ~ SYNTVUOSI + BMI80 + bodyfat80 + KALAV80 + lihatv80, data=df)  
#reg <- lm(PCB15380\_norm ~ SYNTVUOSI + BMI80 + bodyfat80 + KALAV80, data=df)  
reg <- lm(PCB15380\_norm ~ SYNTVUOSI + BMI80 + bodyfat80, data=df)  
summary(reg)

##   
## Call:  
## lm(formula = PCB15380\_norm ~ SYNTVUOSI + BMI80 + bodyfat80, data = df)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -79.72 -32.89 -14.55 12.24 593.65   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 7552.2648 1534.7089 4.921 1.12e-06 \*\*\*  
## SYNTVUOSI -3.7926 0.7697 -4.927 1.09e-06 \*\*\*  
## BMI80 3.1155 1.7621 1.768 0.0776 .   
## bodyfat80 -8.4619 1.5169 -5.579 3.70e-08 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 66.86 on 587 degrees of freedom  
## (1 observation deleted due to missingness)  
## Multiple R-squared: 0.1261, Adjusted R-squared: 0.1217   
## F-statistic: 28.24 on 3 and 587 DF, p-value: < 2.2e-16

#reg <- lm(PCB15301\_norm ~ SYNTVUOSI + BMI80 + BMI01 + Paino01 + PCB15380\_norm + bodyfat80 + KALAV80 + lihatv80 + FISHTOT\_FFQ07, data=df)   
#reg <- lm(PCB15301\_norm ~ SYNTVUOSI + BMI80 + BMI01 + Paino01 + PCB15380\_norm + bodyfat80 + KALAV80 + FISHTOT\_FFQ07, data=df)   
#reg <- lm(PCB15301\_norm ~ SYNTVUOSI + BMI80 + BMI01 + Paino01 + PCB15380\_norm + bodyfat80 + FISHTOT\_FFQ07, data=df)   
#reg <- lm(PCB15301\_norm ~ SYNTVUOSI + BMI80 + BMI01 + Paino01 + PCB15380\_norm + FISHTOT\_FFQ07, data=df)   
reg <- lm(PCB15301\_norm ~ SYNTVUOSI + BMI80 + BMI01 + PCB15380\_norm + FISHTOT\_FFQ07, data=df)   
reg <- step(reg, direction = "both")

## Start: AIC=2142.71  
## PCB15301\_norm ~ SYNTVUOSI + BMI80 + BMI01 + PCB15380\_norm + FISHTOT\_FFQ07  
##   
## Df Sum of Sq RSS AIC  
## <none> 112865 2142.7  
## - FISHTOT\_FFQ07 1 1582.1 114447 2145.9  
## - BMI01 1 2232.2 115097 2148.0  
## - SYNTVUOSI 1 3231.0 116096 2151.2  
## - PCB15380\_norm 1 4062.6 116928 2153.9  
## - BMI80 1 11122.9 123988 2175.8

summary(reg)

##   
## Call:  
## lm(formula = PCB15301\_norm ~ SYNTVUOSI + BMI80 + BMI01 + PCB15380\_norm +   
## FISHTOT\_FFQ07, data = df)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -51.865 -10.461 -3.021 8.375 100.639   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 1631.40537 505.96243 3.224 0.001376 \*\*   
## SYNTVUOSI -0.82494 0.25451 -3.241 0.001299 \*\*   
## BMI80 2.66412 0.44299 6.014 4.38e-09 \*\*\*  
## BMI01 -0.74422 0.27623 -2.694 0.007381 \*\*   
## PCB15380\_norm 0.04359 0.01199 3.635 0.000318 \*\*\*  
## FISHTOT\_FFQ07 0.06032 0.02660 2.268 0.023902 \*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 17.54 on 367 degrees of freedom  
## (219 observations deleted due to missingness)  
## Multiple R-squared: 0.3243, Adjusted R-squared: 0.3151   
## F-statistic: 35.22 on 5 and 367 DF, p-value: < 2.2e-16

For PCB15380, we can see that

1. KALAV80 and lihatv80 bring little if any predictive power to the regression model
2. FISHTOT\_FFQ07 seems to have some predictive power

## Bayesian hierachical model

# This was forked from Dioxdistboys\_individual\_rows.Rmd and  
# originally from code Op\_en3104/bayes on page [[EU-kalat]]  
  
## This code builds an iterative model with varying intake  
## https://github.com/jtuomist/dioxdisthuman/wiki#iterative-model-with-varying-intake-primary-choice  
  
#if(params$run\_bayes) {  
 library(OpasnetUtils)  
 library(reshape2)  
 library(rjags) # JAGS

## Loading required package: coda

## Linked to JAGS 4.3.0

## Loaded modules: basemod,bugs

library(MASS) # mvrnorm  
 library(car) # scatterplotMatrix

## Loading required package: carData

##   
## Attaching package: 'car'

## The following object is masked from 'package:psych':  
##   
## logit

library(mcmcr) # as.mcarray

## Registered S3 method overwritten by 'mcmcr':  
## method from   
## as.mcmc.list.mcarray rjags

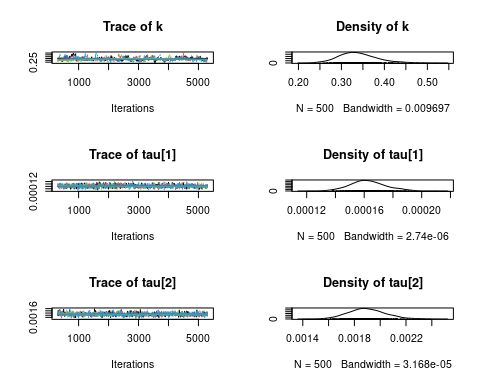
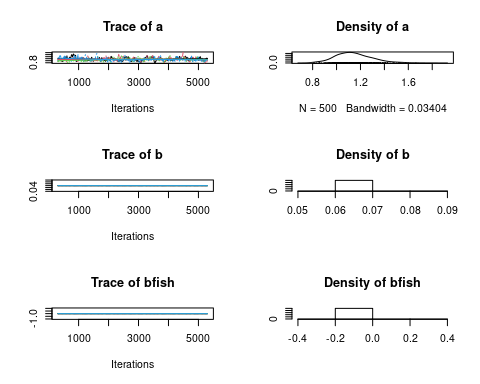
##   
## Attaching package: 'mcmcr'

## The following object is masked from 'package:OpasnetUtils':  
##   
## tidy

N <- params$N # defined as render parameter  
   
 # Hierarchical Bayes model.  
   
 mod <- textConnection(  
 "  
 var k, a, b, U, E[61], C[I,H], B[I,H], M[I,H], C1, C2, conc[I,2], SYNT[I], Efish[I],  
 B1[I], B2[I], B3[I], B4[I], B5[I], B6[I], B7[I], B8[I], B9[I], B10[I], B11[I],  
 B12[I], B13[I], B14[I], B15[I], B16[I], B17[I], B18[I], B19[I], B20[I], B21[I], B22[I],  
 B23[I], B24[I], B25[I], B26[I], B27[I], B28[I], B29[I], B30[I], B31[I], B32[I], B33[I],  
 B34[I], B35[I], B36[I], B37[I], B38[I], B39[I], B40[I], B41[I];  
 model{  
 # below.LOQ[i,j] ~ dinterval(-conc[i,j], -LOQ[j])  
 k ~ dnorm(0.3, 0.1)  
 a ~ dnorm(1, 0.1)  
# b ~ dnorm(0.1, 0.001)  
 tau[1] ~ dgamma(1.0,1.0)   
 tau[2] ~ dgamma(1.0,1.0)   
# bfish ~ dnorm(1.0,0.001)   
 bfish <- 0  
 Efish[] <- fish[] \* bfish  
 for(year in YEAR) {  
 E[year-1959] <- max(0,a\*b\*exp(1)\*(year-c+1/b)\*exp(-b\*(year-c+1/b)))  
 }  
 B2[] <- B1[] \* (1 - k) + U \* A \* W[,1] \* (E[SYNT[]-1960+1] + Efish[]) \* P[1]  
 B3[] <- B2[] \* (1 - k) + U \* A \* W[,2] \* (E[SYNT[]-1960+2] + Efish[]) \* P[2]  
 B4[] <- B3[] \* (1 - k) + U \* A \* W[,3] \* (E[SYNT[]-1960+3] + Efish[]) \* P[3]  
 B5[] <- B4[] \* (1 - k) + U \* A \* W[,4] \* (E[SYNT[]-1960+4] + Efish[]) \* P[4]  
 B6[] <- B5[] \* (1 - k) + U \* A \* W[,5] \* (E[SYNT[]-1960+5] + Efish[]) \* P[5]  
 B7[] <- B6[] \* (1 - k) + U \* A \* W[,6] \* (E[SYNT[]-1960+6] + Efish[]) \* P[6]  
 B8[] <- B7[] \* (1 - k) + U \* A \* W[,7] \* (E[SYNT[]-1960+7] + Efish[]) \* P[7]  
 B9[] <- B8[] \* (1 - k) + U \* A \* W[,8] \* (E[SYNT[]-1960+8] + Efish[]) \* P[8]  
 B10[] <- B9[] \* (1 - k) + U \* A \* W[,9] \* (E[SYNT[]-1960+9] + Efish[]) \* P[9]  
 B11[] <- B10[] \* (1 - k) + U \* A \* W[,10] \* (E[SYNT[]-1960+10] + Efish[]) \* P[10]  
 B12[] <- B11[] \* (1 - k) + U \* A \* W[,11] \* (E[SYNT[]-1960+11] + Efish[]) \* P[11]  
 B13[] <- B12[] \* (1 - k) + U \* A \* W[,12] \* (E[SYNT[]-1960+12] + Efish[]) \* P[12]  
 B14[] <- B13[] \* (1 - k) + U \* A \* W[,13] \* (E[SYNT[]-1960+13] + Efish[]) \* P[13]  
 B15[] <- B14[] \* (1 - k) + U \* A \* W[,14] \* (E[SYNT[]-1960+14] + Efish[]) \* P[14]  
 B16[] <- B15[] \* (1 - k) + U \* A \* W[,15] \* (E[SYNT[]-1960+15] + Efish[]) \* P[15]  
 B17[] <- B16[] \* (1 - k) + U \* A \* W[,16] \* (E[SYNT[]-1960+16] + Efish[]) \* P[16]  
 B18[] <- B17[] \* (1 - k) + U \* A \* W[,17] \* (E[SYNT[]-1960+17] + Efish[]) \* P[17]  
 B19[] <- B18[] \* (1 - k) + U \* A \* W[,18] \* (E[SYNT[]-1960+18] + Efish[]) \* P[18]  
 B20[] <- B19[] \* (1 - k) + U \* A \* W[,19] \* (E[SYNT[]-1960+19] + Efish[]) \* P[19]  
 B21[] <- B20[] \* (1 - k) + U \* A \* W[,20] \* (E[SYNT[]-1960+20] + Efish[]) \* P[20]  
 B22[] <- B21[] \* (1 - k) + U \* A \* W[,21] \* (E[SYNT[]-1960+21] + Efish[]) \* P[21]  
 B23[] <- B22[] \* (1 - k) + U \* A \* W[,22] \* (E[SYNT[]-1960+22] + Efish[]) \* P[22]  
 B24[] <- B23[] \* (1 - k) + U \* A \* W[,23] \* (E[SYNT[]-1960+23] + Efish[]) \* P[23]  
 B25[] <- B24[] \* (1 - k) + U \* A \* W[,24] \* (E[SYNT[]-1960+24] + Efish[]) \* P[24]  
 B26[] <- B25[] \* (1 - k) + U \* A \* W[,25] \* (E[SYNT[]-1960+25] + Efish[]) \* P[25]  
 B27[] <- B26[] \* (1 - k) + U \* A \* W[,26] \* (E[SYNT[]-1960+26] + Efish[]) \* P[26]  
 B28[] <- B27[] \* (1 - k) + U \* A \* W[,27] \* (E[SYNT[]-1960+27] + Efish[]) \* P[27]  
 B29[] <- B28[] \* (1 - k) + U \* A \* W[,28] \* (E[SYNT[]-1960+28] + Efish[]) \* P[28]  
 B30[] <- B29[] \* (1 - k) + U \* A \* W[,29] \* (E[SYNT[]-1960+29] + Efish[]) \* P[29]  
 B31[] <- B30[] \* (1 - k) + U \* A \* W[,30] \* (E[SYNT[]-1960+30] + Efish[]) \* P[30]  
 B32[] <- B31[] \* (1 - k) + U \* A \* W[,31] \* (E[SYNT[]-1960+31] + Efish[]) \* P[31]  
 B33[] <- B32[] \* (1 - k) + U \* A \* W[,32] \* (E[SYNT[]-1960+32] + Efish[]) \* P[32]  
 B34[] <- B33[] \* (1 - k) + U \* A \* W[,33] \* (E[SYNT[]-1960+33] + Efish[]) \* P[33]  
 B35[] <- B34[] \* (1 - k) + U \* A \* W[,34] \* (E[SYNT[]-1960+34] + Efish[]) \* P[34]  
 B36[] <- B35[] \* (1 - k) + U \* A \* W[,35] \* (E[SYNT[]-1960+35] + Efish[]) \* P[35]  
 B37[] <- B36[] \* (1 - k) + U \* A \* W[,36] \* (E[SYNT[]-1960+36] + Efish[]) \* P[36]  
 B38[] <- B37[] \* (1 - k) + U \* A \* W[,37] \* (E[SYNT[]-1960+37] + Efish[]) \* P[37]  
 B39[] <- B38[] \* (1 - k) + U \* A \* W[,38] \* (E[SYNT[]-1960+38] + Efish[]) \* P[38]  
 B40[] <- B39[] \* (1 - k) + U \* A \* W[,39] \* (E[SYNT[]-1960+39] + Efish[]) \* P[39]  
 B41[] <- B40[] \* (1 - k) + U \* A \* W[,40] \* (E[SYNT[]-1960+40] + Efish[]) \* P[40]  
   
 C[,1] <- B1 / M[,1]  
 C[,2] <- B2 / M[,2]  
 C[,3] <- B3 / M[,3]  
 C[,4] <- B4 / M[,4]  
 C[,5] <- B5 / M[,5]  
 C[,6] <- B6 / M[,6]  
 C[,7] <- B7 / M[,7]  
 C[,8] <- B8 / M[,8]  
 C[,9] <- B9 / M[,9]  
 C[,10] <- B10 / M[,10]  
 C[,11] <- B11 / M[,11]  
 C[,12] <- B12 / M[,12]  
 C[,13] <- B13 / M[,13]  
 C[,14] <- B14 / M[,14]  
 C[,15] <- B15 / M[,15]  
 C[,16] <- B16 / M[,16]  
 C[,17] <- B17 / M[,17]  
 C[,18] <- B18 / M[,18]  
 C[,19] <- B19 / M[,19]  
 C[,20] <- B20 / M[,20]  
 C[,21] <- B21 / M[,21]  
 C[,22] <- B22 / M[,22]  
 C[,23] <- B23 / M[,23]  
 C[,24] <- B24 / M[,24]  
 C[,25] <- B25 / M[,25]  
 C[,26] <- B26 / M[,26]  
 C[,27] <- B27 / M[,27]  
 C[,28] <- B28 / M[,28]  
 C[,29] <- B29 / M[,29]  
 C[,30] <- B30 / M[,30]  
 C[,31] <- B31 / M[,31]  
 C[,32] <- B32 / M[,32]  
 C[,33] <- B33 / M[,33]  
 C[,34] <- B34 / M[,34]  
 C[,35] <- B35 / M[,35]  
 C[,36] <- B36 / M[,36]  
 C[,37] <- B37 / M[,37]  
 C[,38] <- B38 / M[,38]  
 C[,39] <- B39 / M[,39]  
 C[,40] <- B40 / M[,40]  
 C[,41] <- B41 / M[,41]  
   
 for(i in 1:I) {   
 conc[i,1] ~ dnorm(C[i,1980 - SYNT[i]+1], tau[1]) # Age 0 is at position 1  
 conc[i,2] ~ dnorm(C[i,2001 - SYNT[i]+1], tau[2])  
 pred[i,1] ~ dnorm(C[i,1980 - SYNT[i]+1], tau[1])  
 pred[i,2] ~ dnorm(C[i,2001 - SYNT[i]+1], tau[2])  
 }  
 }  
 ")  
  
 jags <- jags.model(  
 mod,  
 data = list(  
 YEAR = YEAR,  
 W = W[1:I,1:H],  
 M = M[1:I,1:H],  
 H = H,  
 I = I,  
 U = U,  
 A = A,  
 b = b,  
 c = c,  
 P = P[1:H],  
 SYNT = SYNT,  
 conc = conc,  
 fish = fish,  
 B1 = rep(0,I)  
 ),  
 n.chains = 4,  
 n.adapt = 300  
 )

## Compiling model graph  
## Declaring variables  
## Resolving undeclared variables  
## Allocating nodes  
## Graph information:  
## Observed stochastic nodes: 746  
## Unobserved stochastic nodes: 750  
## Total graph size: 34815  
##   
## Initializing model

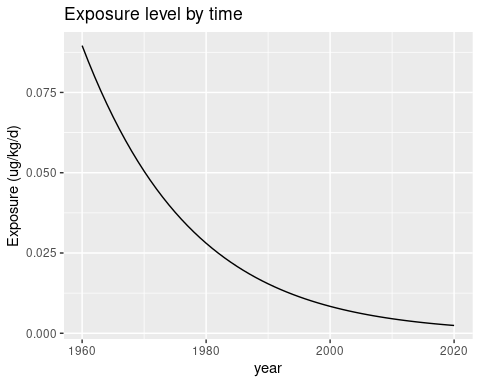
samps.c <- coda.samples(  
 jags,   
 variable.names=c("k","a","b","tau","bfish"),   
 n.iter=N\*10,  
 thin=10  
 )  
   
 samps.j <- jags.samples(  
 jags,   
 variable.names=c("k","a","b","tau","E","pred","bfish"),   
 n.iter=N\*10,  
 thin=10  
 )  
  
 #scatterplotMatrix(samps.j$k, main="Elimination constant k")  
   
 plot(samps.c)



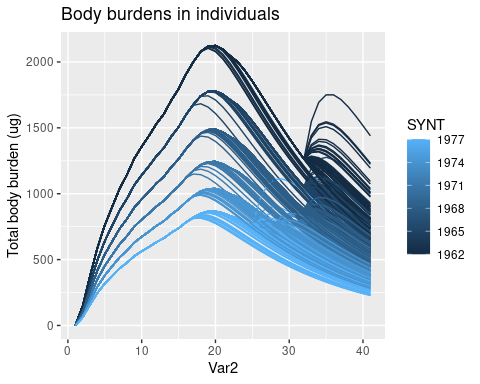
#}

* k: elimination constant (1/a)
* a: maximum exposure at the year of peak production (ug/kg/d)
* b: nominal rate of environmental concentration decrease (1/a)
* tau: precision for individual concentration estimate at year x (1980 or 2001)
* E: exposure at a calendar year y (between 1960 and 2020)
* pred: predicted individual concentration (ug/kg fat)

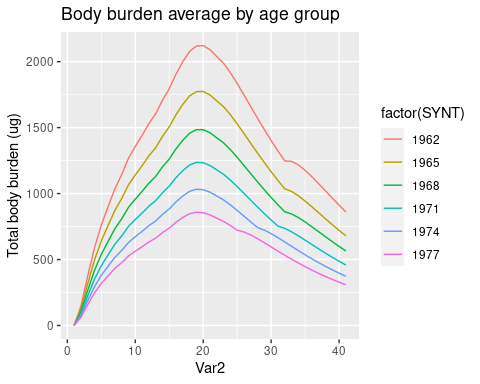
k <- mean(samps.j$k)  
a <- mean(samps.j$a)  
b <- mean(samps.j$b)  
  
E <- pmax(0,a\*b\*exp(1)\*(YEAR-c+1/b)\*exp(-b\*(YEAR-c+1/b)))  
B <- matrix(0, nrow=I, ncol=H)  
for(age in 2:H) {  
 B[,age] <- B[,age-1] \* (1 - k) + U \* A \* W[,age-1] \* E[SYNT-1963+age] \* P[age]  
}  
C <- B / M  
  
ggplot(data.frame(year=YEAR,exposure=E), aes(x=year, y=E))+geom\_line()+  
 labs(title="Exposure level by time",  
 y="Exposure (ug/kg/d)")



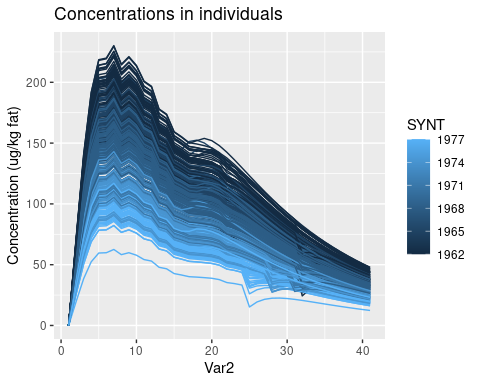
dat <- melt(B)#[seq(1,550, 10),])  
dat <- merge(dat, cbind(Var1= 1:I, SYNT=SYNT))  
  
ggplot(dat, aes(x=Var2, y=value, colour=SYNT, group=Var1))+geom\_line()+  
 labs(title="Body burdens in individuals",  
 y="Total body burden (ug)")



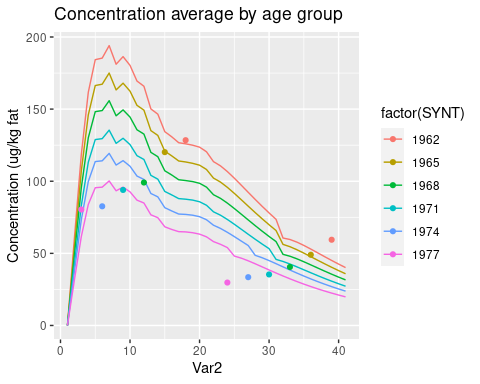
ggplot(aggregate(dat["value"], by=dat[c("Var2","SYNT")], FUN=function(x) mean(x, na.rm=TRUE)),   
 aes(x=Var2, y=value, colour=factor(SYNT), group=SYNT))+geom\_line()+  
 labs(title="Body burden average by age group",  
 y="Total body burden (ug)")



dat <- melt(C)#[seq(1,550, 10),])  
dat <- merge(dat, cbind(Var1= 1:I, SYNT=SYNT))  
  
ggplot(dat, aes(x=Var2, y=value, colour=SYNT, group=Var1))+geom\_line()+  
 labs(title="Concentrations in individuals",  
 y="Concentration (ug/kg fat)")



ggplot()+  
 geom\_line(data=aggregate(dat["value"], by=dat[c("Var2","SYNT")], FUN=function(x) mean(x, na.rm=TRUE)),   
 aes(x=Var2, y=value, colour=factor(SYNT), group=SYNT))+  
 geom\_point(data=aggregate(long["PCB"],by=long[c("SYNTVUOSI","age")],FUN=function(x) mean(x, na.rm=TRUE)),  
 aes(x=age, y=PCB,colour=factor(SYNTVUOSI)))+geom\_point()+  
 labs(title="Concentration average by age group",  
 y="Concentration (ug/kg fat")



tst <- rowMeans(samps.j$pred[,,,], dims=2)  
tst <- data.frame(PCB15380\_pred = tst[,1],PCB15301\_pred = tst[,2],  
 dfs[c("PCB15380\_norm","PCB15301\_norm")])  
pairs.panels(tst)

