Laseri fat trajectories

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## Overview and tasks

This project aims to create individual trajectories of fat mass change in individuals in the Laseri study.

### To be done:

library(reshape2)  
library(tidyverse)

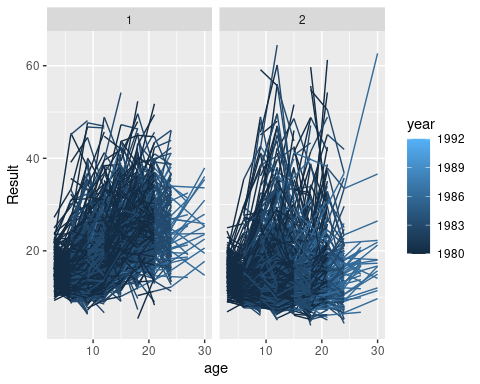
## ── Attaching packages ─────────────────────────────────────── tidyverse 1.3.0 ──

## ✓ ggplot2 3.3.2 ✓ purrr 0.3.4  
## ✓ tibble 3.0.4 ✓ dplyr 1.0.2  
## ✓ tidyr 1.1.2 ✓ stringr 1.4.0  
## ✓ readr 1.4.0 ✓ forcats 0.5.0

## ── Conflicts ────────────────────────────────────────── tidyverse\_conflicts() ──  
## x dplyr::filter() masks stats::filter()  
## x dplyr::lag() masks stats::lag()

df <- read.csv("data/priv/rasvapopperus.csv")[-(11:85)] # Remove POP variables  
# Each row is an individual  
dfl <- melt(df, id.vars = c("tutkno80","SP","IKA80"), variable.name = "Parameter", value.name = "Result")  
dfl$year[grepl("80",dfl$Parameter)] <- 1980  
dfl$year[grepl("83",dfl$Parameter)] <- 1983  
dfl$year[grepl("86",dfl$Parameter)] <- 1986  
dfl$year[grepl("92",dfl$Parameter)] <- 1992  
dfl$year[grepl("01",dfl$Parameter)] <- 2001  
dfl$Parameter <- gsub("(80|83|86|92|01)","",dfl$Parameter)   
dfl$age <- dfl$year - 1980 + dfl$IKA80  
  
ggplot(dfl[dfl$Parameter=="PFDWB",], aes(x=age, y=Result, colour=year, group=tutkno80))+geom\_line()+facet\_wrap(~SP)

## Warning: Removed 4910 row(s) containing missing values (geom\_path).



tmp <- dfl[dfl$Parameter=="PFDWB",]  
tmp <- aggregate(tmp["Result"], by = tmp[c("age","SP","year")], FUN=function(x) mean(x, na.rm = TRUE))  
ggplot(tmp, aes(x=age, y=Result, colour=year, group=year))+geom\_line()+facet\_wrap(~SP)



## Hierarchical Bayes

library(rjags) # JAGS

## Loading required package: coda

## Linked to JAGS 4.3.0

## Loaded modules: basemod,bugs

library(MASS) # mvrnorm

##   
## Attaching package: 'MASS'

## The following object is masked from 'package:dplyr':  
##   
## select

library(car) # scatterplotMatrix

## Loading required package: carData

##   
## Attaching package: 'car'

## The following object is masked from 'package:dplyr':  
##   
## recode

## The following object is masked from 'package:purrr':  
##   
## some

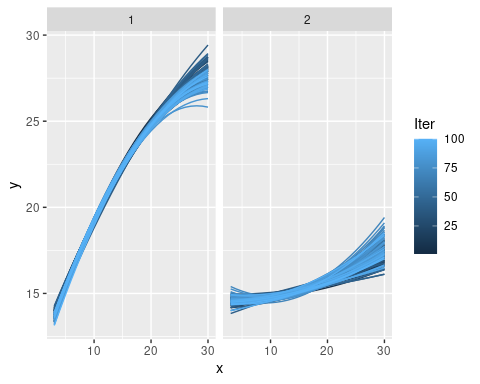
library(mcmcr) # as.mcarray

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

N <- 100 # params$N # defined as render parameter  
   
 # Hierarchical Bayes model.  
   
 mod <- textConnection(  
 "  
 var a[2], b[2], c[2], fat[I,4], s[I], age[I];  
 model{  
 a[1] ~ dnorm(0, 0.01)  
 a[2] ~ dnorm(0, 0.01)  
 b[1] ~ dnorm(0, 0.01)  
 b[2] ~ dnorm(0, 0.01)  
 c[1] ~ dnorm(0, 0.01)  
 c[2] ~ dnorm(0, 0.01)  
 tau[1] ~ dgamma(1.0,1.0)   
 tau[2] ~ dgamma(1.0,1.0)   
  
 for(i in 1:I) {   
 for(y in 1:length(YEAR)) {  
 fat[i,y] ~ dnorm(a[s[i]] + b[s[i]]\*(YEAR[y]+age[i]) + c[s[i]]\*(YEAR[y]+age[i])^2 , tau[s[i]])  
 pred[i,y] ~ dnorm(a[s[i]] + b[s[i]]\*(YEAR[y]+age[i]) + c[s[i]]\*(YEAR[y]+age[i])^2 , tau[s[i]])  
 }  
 }  
 }  
 ")  
  
 jags <- jags.model(  
 mod,  
 data = list(  
 YEAR = c(0,3,6,12), # Year since 1980  
 age = df$IKA80, # Age at 1980  
 fat = df[c("PFDWB80","PFDWB83","PFDWB86","PFDWB92")], # Fat percentage  
 s = df$SP,  
 I = nrow(df)  
 ),  
 n.chains = 4,  
 n.adapt = 300  
 )

## Compiling model graph  
## Declaring variables  
## Resolving undeclared variables  
## Allocating nodes  
## Graph information:  
## Observed stochastic nodes: 9246  
## Unobserved stochastic nodes: 19530  
## Total graph size: 36071  
##   
## Initializing model

samps.c <- coda.samples(  
 jags,   
 variable.names=c("a","b","c","tau"), # "pred"  
 n.iter=N\*10,  
 thin=10  
 )  
   
 samps.j <- jags.samples(  
 jags,   
 variable.names=c("a","b","c","tau"), # "pred"  
 n.iter=N\*10,  
 thin=10  
 )  
  
 #scatterplotMatrix(samps.j$k, main="Elimination constant k")  
   
# plot(samps.c)  
  
 age <- 3:30  
 out <- data.frame()  
 for(i in 1:100) {  
 for(j in 1:2) {  
 out <- rbind(out, data.frame(  
 Iter = i,  
 sex = j,  
 x = age,  
 y = samps.j$a[j,i,1] + samps.j$b[j,i,1]\*age + samps.j$c[j,i,1]\*age^2  
 ))  
 }  
 }  
  
ggplot(out, aes(x=x,y=y,colour=Iter,group=Iter))+geom\_line()+facet\_wrap(~sex)



Note that the echo = FALSE parameter was added to the code chunk to prevent printing of the R code that generated the plot.