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# BODY WEIGHT
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library(mgcv)
library(itsadug)
library(gratia)
library(dplyr)
library(tidyr)
library(stringi)
library(ggplot2)

xdata = read.table("clipboard", dec=".",header=T, na.strings=c("x","xxx"))
attach(xdata ,warn.conflicts = FALSE)
#hist(xdata)
xdata$zoo=tolower(xdata$zoo)
xdata$name=tolower(xdata$name)
xdata$rearing=tolower(xdata$rearing)
xdata$sexO=as.ordered(xdata$sexOrd)
contrasts(xdata$sexO) <- "contr.treatment"
xdata$sex=as.factor(xdata$sex)
xdata$sire=as.factor(xdata$sire)
xdata$dam=as.factor(xdata$dam)
xdata$wildparityrearing=as.factor(xdata$wildparityrearing)
xdata$wildparityrearingO=as.ordered(xdata$wildparityrearing)
contrasts(xdata$wildparityrearingO) <- "contr.treatment"
xdata$name=as.factor(xdata$name)
xdata$zoo=as.factor(xdata$zoo)
xdata$weight_kg=xdata$weight_kg
xdata$weight_kg25=xdata$weight_kg^(1/2.5)
attach(xdata ,warn.conflicts = FALSE)
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#Please be aware that some of these models may require 32Gb of RAM and may need several days to finish.
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#Body weight in kg:


# MODELS WERE RUN WITH k=11 SINCE k=10 YIELDS STRANGE RESULTS
#Full incl Wild without agemoth:

ndata= xdata %>% drop_na (sex,age)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
par(mfrow=c(1,1))

# sex-specific change of bodyweight over age (= growth curves):
res <- bam(weight_kg~  sex  + s(age,by= sex, bs = "cr",k=11)  + s(age,wildparityrearing,bs = "fs",k=11)  + s(date_of_weight, zoo,bs = "fs", k=11,m=1) +s(age,name, bs = "fs", k=11,m=1) + s(age,zoo, by=sex, bs = "fs", k=11,m=1),method="ML", nthreads=8, data = ndata,select = F , rho=0.3, AR.start = ARstart)
resstat <- bam(weight_kg~  sexO + s(age, bs = "cr", k=11)  + s(age,by= sexO, bs = "cr", k=11)  + s(age,wildparityrearingO,bs = "fs",k=11)  + s(date_of_weight, zoo,bs = "fs", k=11,m=1) +s(age,name, bs = "fs",k=11,m=1) + s(age,zoo, by=sex, bs = "fs",k=11,m=1),method="ML", nthreads=8, data = ndata,select = F , rho=0.3, AR.start = ARstart)
null <- bam(weight_kg ~ 1 + s(age,wildparityrearing,bs = "fs",k=11)  + s(date_of_weight, zoo,bs = "fs", k=11,m=1) +s(age,name, bs = "fs", k=11,m=1) + s(age,zoo, by=sex, bs = "fs", k=11,m=1),method="ML", nthreads=8, data = ndata,select = F , rho=0.3, AR.start = ARstart)
gam.check(res)
compareML(null, resstat)
summary(res, freq=TRUE)
summary(resstat, freq=TRUE)
#write.table(residuals(res,type="response"), file="clipboard-16384", sep="\t")
pp <- get_predictions(res,cond=list(sex=c("f","m"), age=seq(0,60,length=1000)))
#write.table(pp, file="clipboard-16384", sep="\t")
par(mar=c(7,7,4,3))
plot_diff(res, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE, col="gray70", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, ylab="",main="Sex difference in body weight (kg): Male minus female")
plot_diff(res, view="age", comp=list(sex=c("m","f")),xlim=c(max(min(fdata$age),min(mdata$age)),min(max(fdata$age),max(mdata$age))),shade=TRUE, mark.diff = TRUE, rm.ranef=TRUE, col="black",add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))
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plot_data(res, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, main=" Body weight (kg)", xlab="Age (years)", ylab="Body weight (kg)")
plot_data(res, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(res, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(res, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(res, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))


# 1.Ableitung= GrowthRate over age:
fd <- derivatives(res,c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age >= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
    geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
    theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40),
          legend.position="none") +
    xlab("Age (years)") + ylab("Growth rate (kg/year)") + scale_x_continuous(lim=c(0,60), expand=c(0,0.5),breaks = seq(0, 60, by = 5))


# 1.Ableitung= change of GrowthRate over age - DIFF:
fdd <- derivatives(resstat, c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
fdd= fdd %>% filter(smooth %in% c("s(age):sexO1", "s(age):sexO0"))
fdd$sexO=stri_sub(fdd$smooth, -1,-1)
attach(fdd ,warn.conflicts = FALSE)
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fdd= fdd %>% filter(!derivative==0 & sexO %in% c("0", "1")) %>% rename(age = data) %>% filter(age >= max(min(fdata$age),min(mdata$age)) & age <= min(max(fdata$age),max(mdata$age)))
attach(fdd ,warn.conflicts = FALSE)

ggplot(fdd, aes(x = age, y = derivative, colour = sexO, fill = sexO)) + scale_color_manual(values=c("black", "blue"))  + scale_fill_manual(values=c("black", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.3, colour = NA) +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
         axis.title.y = element_text(face = "bold", size = 50),
         axis.text.x = element_text(size = 40),
         axis.text.y = element_text(size = 40),
         legend.position="none") +
   xlab("Age (years)") + ylab("Growth rate (kg/year)") + scale_x_continuous(lim=c(0,60), expand=c(0,0.5),breaks = seq(0, 60, by = 5)) + scale_y_continuous(breaks=c(-3,0,3))



########################################################################################################################################################
#age <= 20yrs old

ndata= xdata %>% filter(age<=20 & age>=0) %>% drop_na (sex,age)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
par(mfrow=c(1,1))

# sex-specific change of bodyweight over age (= growth curves):
res20 <- bam(weight_kg~  sex  + s(age,by= sex, bs = "cr",k=11)  + s(age,wildparityrearing,bs = "fs",k=11)  + s(date_of_weight, zoo,bs = "fs", k=11, m=1) +s(age,name, bs = "fs", k=11,m=1) + s(age,zoo, by=sex, bs = "fs", k=11,m=1),method="ML", nthreads=8, data = ndata,select = F , rho=0.3, AR.start = ARstart)
res20stat <- bam(weight_kg~  sexO + s(age, bs = "cr", k=11)  + s(age,by= sexO, bs = "cr", k=11)  + s(age,wildparityrearingO,bs = "fs",k=11)  + s(date_of_weight, zoo,bs = "fs", k=11, m=1) +s(age,name, bs = "fs",k=11,m=1) + s(age,zoo, by=sex, bs = "fs",k=11,m=1),method="ML", nthreads=8, data = ndata,select = F , rho=0.3, AR.start = ARstart)
null20 <- bam(weight_kg~ 1 + s(age,wildparityrearing,bs = "fs",k=11)  + s(date_of_weight, zoo,bs = "fs", k=11, m=1) +s(age,name, bs = "fs", k=11,m=1) + s(age,zoo, by=sex, bs = "fs", k=11,m=1),method="ML", nthreads=8, data = ndata,select = F , rho=0.3, AR.start = ARstart)
gam.check(res20)
compareML(null20, res20stat)
summary(res20, freq=TRUE)
summary(res20stat, freq=TRUE)
#write.table(residuals(res20,type="response"), file="clipboard-16384", sep="\t")
pp <- get_predictions(res20,cond=list(sex=c("f","m"), age=seq(0,60,length=1000)))
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#write.table(pp, file="clipboard-16384", sep="\t")
par(mar=c(7,7,4,3))
plot_diff(res20, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE, col="gray70", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, ylab="",main="Sex difference in body weight (kg): Male minus female")
plot_diff(res20, view="age", comp=list(sex=c("m","f")),xlim=c(max(min(fdata$age),min(mdata$age)),min(max(fdata$age),max(mdata$age))),shade=TRUE, mark.diff = TRUE, rm.ranef=TRUE, col="black",add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))
plot_data(res20, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, main=" Body weight (kg)", xlab="Age (years)", ylab="Body weight (kg)")
plot_data(res20, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(res20, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(res20, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(res20, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))

# 1.Ableitung= GrowthRate over age:
fd <- derivatives(res20,c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age >= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
        legend.position="none") +
   xlab("Age (years)") + ylab("Growth rate (kg/year)") + scale_x_continuous(lim=c(0,20), expand=c(0,0.5),breaks = seq(0, 60, by = 5))
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#SingleLinePlots for comparison plot
fdm=fd %>% filter(sex=="m")
fdf=fd %>% filter(sex=="f")

ggplot(fdm, aes(x = age, y = derivative)) + geom_line(size = 3,linetype=5, color="black") +
    theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40),
          legend.position="none") +
    xlab("Age (years)") + ylab("Male growth rate (kg/year)") + scale_x_continuous(lim=c(0,20), expand=c(0,0.5),breaks = seq(0, 60, by = 5))

ggplot(fdf, aes(x = age, y = derivative)) + geom_line(size = 3,linetype=5, color="black") +
    theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40),
          legend.position="none") +
    xlab("Age (years)") + ylab("Female growth rate (kg/year)") + scale_x_continuous(lim=c(0,20), expand=c(0,0.5),breaks = seq(0, 60, by = 5))


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#Reduced dataset without wild-born individuals, additionally controlling for kinship (sire & dam) and maternal age at birth

ndata= xdata %>% filter(!rearing=="WC") %>% drop_na (sex,age)
ndata$agemoth=as.numeric(ndata$agemoth)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
par(mfrow=c(1,1))

# sex-specific change of bodyweight over age (= growth curves):
resagemoth <- bam(weight_kg~  sex  + s(age,by= sex, bs = "cr",k=10) + s(agemoth, bs="cr", k=3)+ ti(age,agemoth, bs="cr", k=c(10,3))  + s(age,wildparityrearing,bs = "fs",k=10)  + s(date_of_weight, zoo,bs = "fs", k=11, m=1) +s(age,name, bs = "fs", k=10,m=1) +s(age,sire, bs = "fs", k=10,m=1) +s(age,dam, bs = "fs", k=10,m=1) + s(age,zoo, by=sex, bs = "fs", k=10,m=1), method="ML", nthreads=8, data = ndata,select = F, rho=0.3, AR.start = ARstart)
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resstatagemoth <- bam(weight_kg~  sexO  + s(age, bs = "cr", k=10)  + s(age,by= sexO, bs = "cr", k=10)  + s(agemoth, bs="cr", k=3) + ti(age,agemoth, bs="cr", k=c(10,3))  +
s(age,wildparityrearing,bs = "fs",k=10)  + s(date_of_weight, zoo,bs = "fs", k=11, m=1) +s(age,name, bs = "fs", k=10,m=1) +s(age,sire, bs = "fs", k=10,m=1) +s(age,dam, bs =
"fs", k=10,m=1) + s(age,zoo, by=sex, bs = "fs", k=10,m=1), method="ML", nthreads=8, data = ndata,select = F, rho=0.3, AR.start = ARstart)
nullagemoth <- bam(weight_kg ~ 1 + te(age,agemoth, bs="cr", k=c(10,3))   + s(age,wildparityrearing,bs = "fs",k=10)  + s(date_of_weight, zoo,bs = "fs", k=11, m=1)
+s(age,name, bs = "fs", k=10,m=1) +s(age,sire, bs = "fs", k=10,m=1) +s(age,dam, bs = "fs", k=10,m=1) + s(age,zoo, by=sex, bs = "fs", k=10,m=1), method="ML", nthreads=8,
data = ndata,select = F, rho=0.3, AR.start = ARstart)
gam.check(resagemoth)
compareML(nullagemoth, resagemoth)
summary(resagemoth, freq=TRUE)
summary(resstatagemoth, freq=TRUE)
#write.table(residuals(resagemoth,type="response"), file="clipboard-16384", sep="\t")
par(mar=c(5,6,6,3) + 0.1)
fvisgam(resagemoth,view=c("age","agemoth"),  rm.ranef=TRUE, add.color.legend=TRUE,n.grid = 100,too.far = 0.1)
points(ndata$age, ndata$agemoth)
vis.gam(resagemoth,view=c("age","agemoth"),  rm.ranef=TRUE,too.far = 0.1,theta= -50,phi=30,alpha=0.2)


par(mar=c(7,7,4,3))
plot_diff(resagemoth, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE, col="gray70", cex.main=4, cex.lab=4,cex.axis=2.5,
hide.label=T, yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, ylab="",main="Sex difference in body weight (kg): Male minus female")
plot_diff(resagemoth, view="age", comp=list(sex=c("m","f")),xlim=c(max(min(fdata$age),min(mdata$age)),min(max(fdata$age),max(mdata$age))),shade=TRUE, mark.diff =
TRUE, rm.ranef=TRUE, col="black",add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))
plot_data(resagemoth, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n",
xaxt="n",mgp=c(5,2,0),las=2, main=" Body weight (kg)", xlab="Age (years)", ylab="Body weight (kg)")
plot_data(resagemoth, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(resagemoth, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(resagemoth, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(resagemoth, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))


# 1.Ableitung= GrowthRate over age:
fd <- derivatives(resagemoth,c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
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fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age >= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
  geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
  theme_classic() +
  theme(axis.title.x = element_text(face = "bold", size = 40),
        axis.title.y = element_text(face = "bold", size = 40),
        axis.text.x = element_text(size = 30),
        axis.text.y = element_text(size = 30),
        legend.text = element_text(size = 30), legend.title = element_blank()) +
  xlab("Age (years)") + ylab("Growth rate (Bodyweight, kg/year)") + scale_x_continuous(breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65))


# 1.Ableitung= change of GrowthRate over age - DIFF:
fdd <- derivatives(resstatagemoth, c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
fdd= fdd %>% filter(smooth %in% c("s(age):sexO1", "s(age):sexO0"))
fdd$sexO=stri_sub(fdd$smooth, -1,-1)
attach(fdd ,warn.conflicts = FALSE)
fdd= fdd %>% filter(!derivative==0 & sexO %in% c("0", "1")) %>% rename(age = data) %>% filter(age >= max(min(fdata$age),min(mdata$age)) & age <= min(max(fdata$age),max(mdata$age)))
attach(fdd ,warn.conflicts = FALSE)

ggplot(fdd, aes(x = age, y = derivative, colour = sexO, fill = sexO)) + scale_color_manual(values=c("black", "blue"))  + scale_fill_manual(values=c("black", "blue")) +
  geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.3, colour = NA) +
  theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
  theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
        legend.position="none") +
  scale_x_continuous(lim=c(0,70), expand=c(0,0.5),breaks = seq(0, 70, by = 5)) + scale_y_continuous(breaks=c(-1,0,1)) +
  xlab("Age (years)") + ylab("Growth rate (Bodyweight, kg/year)")
```

```
#####################################################################################################################################################################################
#Only individuals with data on arm length, body weight, testosterone AND DHEA

ndata= xdata %>% filter(AllVarFilter==1) %>% drop_na (sex,age)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
par(mfrow=c(1,1))

# sex-specific change of bodyweight over age (= growth curves):
resALL <- bam(weight_kg~  sex  + s(age,by= sex, bs = "cr",k=10)  + s(age,wildparityrearing,bs = "fs",k=10)  + s(date_of_weight, zoo,bs = "fs", k=11, m=1) +s(age,name, bs = "fs", k=6,m=1) + s(age,zoo, by=sex, bs = "fs", k=6,m=1),method="ML", nthreads=8, data = ndata,select = F , rho=0.3, AR.start = ARstart)
resALLstat <- bam(weight_kg~  sexO + s(age, bs = "cr", k=10)  + s(age,by= sexO, bs = "cr", k=10)  + s(age,wildparityrearingO,bs = "fs",k=10)  + s(date_of_weight, zoo,bs = "fs", k=11, m=1) +s(age,name, bs = "fs",k=6,m=1) + s(age,zoo, by=sex, bs = "fs",k=6,m=1),method="ML", nthreads=8, data = ndata,select = F , rho=0.3, AR.start = ARstart)
null <- bam(weight_kg~ 1 + s(age,wildparityrearing,bs = "fs",k=10)  + s(date_of_weight, zoo,bs = "fs", k=10, m=1) +s(age,name, bs = "fs", k=6,m=1) + s(age,zoo, by=sex, bs = "fs", k=6,m=1),method="ML", nthreads=8, data = ndata,select = F , rho=0.3, AR.start = ARstart)
gam.check(resALL)
compareML(null, resALLstat)
summary(resALL, freq=TRUE)
summary(resALLstat, freq=TRUE)
#write.table(residuals(resALL,type="response"), file="clipboard-16384", sep="\t")
pp <- get_predictions(resALL,cond=list(sex=c("f","m"), age=seq(0,60,length=1000)))
#write.table(pp, file="clipboard-16384", sep="\t")
par(mar=c(7,7,4,3))
plot_diff(resALL, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE, col="gray70", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, ylab="",main="Sex difference in body weight (kg): Male minus female")
plot_diff(resALL, view="age", comp=list(sex=c("m","f")),xlim=c(max(min(fdata$age),min(mdata$age)),min(max(fdata$age),max(mdata$age))),shade=TRUE, mark.diff = TRUE, rm.ranef=TRUE, col="black",add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))
plot_data(resALL, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, main=" Body weight (kg)", xlab="Age (years)", ylab="Body weight (kg)")
plot_data(resALL, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(resALL, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(resALL, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(resALL, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))
```

```
# 1.Ableitung= GrowthRate over age:
fd <- derivatives(resALL,c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age
>= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
         axis.title.y = element_text(face = "bold", size = 50),
         axis.text.x = element_text(size = 40),
         axis.text.y = element_text(size = 40),
         legend.position="none") +
   xlab("Age (years)") + ylab("Growth rate (kg/year)") + scale_x_continuous(lim=c(0,20), expand=c(0,0.5),breaks = seq(0, 60, by = 5))
```

```
#######################################################################################################
#######################################################################################################
#######################################################################################################
#Body weight in kg^(1/2.5):

# MODELS WERE RUN WITH k=11 SINCE k=10 YIELDS STRANGE RESULTS
#Full incl Wild without agemoth:

ndata= xdata %>% drop_na (sex,age)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
par(mfrow=c(1,1))

# sex-specific change of bodyweight over age (= growth curves):
res <- bam(weight_kg25~  sex  + s(age,by= sex, bs = "cr",k=11)  + s(age,wildparityrearing,bs = "fs",k=11)  + s(date_of_weight, zoo,bs = "fs", k=11, m=1) +s(age,name, bs = "fs", k=11,m=1) + s(age,zoo, by=sex, bs = "fs", k=11,m=1),method="ML", nthreads=8, data = ndata,select = F , rho=0.3, AR.start = ARstart)
resstat <- bam(weight_kg25~  sexO + s(age, bs = "cr", k=11)  + s(age,by= sexO, bs = "cr", k=11)  + s(age,wildparityrearingO,bs = "fs",k=11)  + s(date_of_weight, zoo,bs = "fs", k=11, m=1) +s(age,name, bs = "fs",k=11,m=1) + s(age,zoo, by=sex, bs = "fs",k=11,m=1),method="ML", nthreads=8, data = ndata,select = F , rho=0.3, AR.start = ARstart)
null <- bam(weight_kg25 ~ 1 + s(age,wildparityrearing,bs = "fs",k=11)  + s(date_of_weight, zoo,bs = "fs", k=11, m=1) +s(age,name, bs = "fs", k=11,m=1) + s(age,zoo, by=sex, bs = "fs", k=11,m=1),method="ML", nthreads=8, data = ndata,select = F , rho=0.3, AR.start = ARstart)
gam.check(res)
compareML(null, resstat)
summary(res, freq=TRUE)
summary(resstat, freq=TRUE)
#write.table(residuals(res,type="response"), file="clipboard-16384", sep="\t")
pp <- get_predictions(res,cond=list(sex=c("f","m"), age=seq(0,60,length=1000)))
#write.table(pp, file="clipboard-16384", sep="\t")
par(mar=c(7,7,4,3))

resplot <- bam(weight_kg25~  sex  + s(age,by= sex, bs = "cr",k=11)  + s(age, by=wildparityrearing,bs = "cr",k=11)  + s(date_of_weight, zoo,bs = "fs", k=11, m=1) +s(age,name, bs = "fs", k=11,m=1) + s(age,zoo, by=sex, bs = "fs", k=11,m=1),method="ML", nthreads=8, data = ndata,select = F , rho=0.3, AR.start = ARstart) # for plotting, wildparityrearing as factor-smooth yielded unrealistic confidence intervals, which was not the case if it was entered as factor-by-variable

plot_diff(resplot, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE, col="gray70", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, ylab="",main="Sex difference in body weight (kg): Male minus female")
plot_diff(resplot, view="age", comp=list(sex=c("m","f")),xlim=c(max(min(fdata$age),min(mdata$age)),min(max(fdata$age),max(mdata$age))),shade=TRUE, mark.diff = TRUE, rm.ranef=TRUE, col="black",add=TRUE)
```

```
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))
plot_data(resplot, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, main=" Body weight (kg)", xlab="Age (years)", ylab="Body weight (kg)")
plot_data(resplot, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(resplot, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(resplot, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(resplot, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))


# 1.Ableitung= GrowthRate over age:
fd <- derivatives(resplot,c(1,2), n=1000, ncores=8)
write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age >= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
        legend.position="none") +
   xlab("Age (years)") + ylab("Growth rate (kg/year)") + scale_x_continuous(lim=c(0,60), expand=c(0,0.5),breaks = seq(0, 60, by = 5))


# 1.Ableitung= change of GrowthRate over age - DIFF:
fdd <- derivatives(resstat, c(1,2), n=1000, ncores=8)
fdd= fdd %>% filter(smooth %in% c("s(age):sexO1", "s(age):sexO0"))
fdd$sexO=stri_sub(fdd$smooth, -1,-1)
```

```
attach(fdd ,warn.conflicts = FALSE)
fdd= fdd %>% filter(!derivative==0 & sexO %in% c("0", "1")) %>% rename(age = data) %>% filter(age >= max(min(fdata$age),min(mdata$age)) & age <= min(max(fdata$age),max(mdata$age)))
attach(fdd ,warn.conflicts = FALSE)

ggplot(fdd, aes(x = age, y = derivative, colour = sexO, fill = sexO)) + scale_color_manual(values=c("black", "blue"))  + scale_fill_manual(values=c("black", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.3, colour = NA) +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
        legend.position="none") +
   xlab("Age (years)") + ylab("Growth rate (kg/year)") + scale_x_continuous(lim=c(0,60), expand=c(0,0.5),breaks = seq(0, 60, by = 5)) #+ scale_y_continuous(breaks=c(-3,0,3))


###################################################################################################################
#age <= 20yrs old

ndata= xdata %>% filter(age<=20 & age>=0) %>% drop_na (sex,age)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
par(mfrow=c(1,1))

# sex-specific change of bodyweight over age (= growth curves):
res20 <- bam(weight_kg25~  sex  + s(age,by= sex, bs = "cr",k=20)  + s(age,by=wildparityrearing,bs = "cr",k=11)  + s(date_of_weight, zoo,bs = "fs", k=11, m=1) +s(age,name, bs = "fs", k=6,m=1) +  s(age,zoo, by=sex, bs = "fs", k=6,m=1),method="ML", nthreads=8, data = ndata,select = F , rho=0.3, AR.start = ARstart) # for plotting, wildparityrearing as factor-smooth yielded unrealistic confidence intervals, which was not the case if it was entered as factor-by-variable
res20stat <- bam(weight_kg25~  sexO + s(age, bs = "cr", k=20)  + s(age,by= sexO, bs = "cr", k=20)  + s(age,wildparityrearingO,bs = "fs",k=11)  + s(date_of_weight, zoo,bs = "fs", k=11, m=1) +s(age,name, bs = "fs",k=6,m=1) + s(age,zoo, by=sex, bs = "fs",k=6,m=1),method="ML", nthreads=8, data = ndata,select = F , rho=0.3, AR.start = ARstart)
null <- bam(weight_kg25~ 1 + s(age,wildparityrearing,bs = "fs",k=11)  + s(date_of_weight, zoo,bs = "fs", k=11, m=1) +s(age,name, bs = "fs", k=11,m=1) + s(age,zoo, by=sex, bs = "fs", k=11,m=1),method="ML", nthreads=8, data = ndata,select = F , rho=0.3, AR.start = ARstart)
gam.check(res20)
compareML(null, res20stat)
summary(res20, freq=TRUE)
summary(res20stat, freq=TRUE)
#write.table(residuals(res20,type="response"), file="clipboard-16384", sep="\t")
```

```
pp <- get_predictions(res20,cond=list(sex=c("f","m"), age=seq(0,60,length=1000)))
#write.table(pp, file="clipboard-16384", sep="\t")
par(mar=c(7,7,4,3))
plot_diff(res20, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE, col="gray70", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T,
yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, ylab="",main="Sex difference in body weight (kg): Male minus female")
plot_diff(res20, view="age", comp=list(sex=c("m","f")),xlim=c(max(min(fdata$age),min(mdata$age)),min(max(fdata$age),max(mdata$age))),shade=TRUE, mark.diff = TRUE,
rm.ranef=TRUE, col="black",add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))
plot_data(res20, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n",
xaxt="n",mgp=c(5,2,0),las=2, main=" Body weight (kg)", xlab="Age (years)", ylab="Body weight (kg)")
plot_data(res20, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(res20, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(res20, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(res20, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))

# 1.Ableitung= GrowthRate over age:
fd <- derivatives(res20,c(1,2), n=1000, ncores=8)
write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age
>= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
         axis.title.y = element_text(face = "bold", size = 50),
         axis.text.x = element_text(size = 40),
         axis.text.y = element_text(size = 40),
         legend.position="none") +
   xlab("Age (years)") + ylab("Growth rate (kg/year)") + scale_x_continuous(lim=c(0,20), expand=c(0,0.5),breaks = seq(0, 60, by = 5))
```

```
##############################################################################################################################################################################
#Reduced dataset without wild-born individuals, additionally controlling for kinship (sire & dam) and maternal age at birth

ndata= xdata %>% filter(!rearing=="WC") %>% drop_na (sex,age)
ndata$agemoth=as.numeric(ndata$agemoth)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
par(mfrow=c(1,1))

# sex-specific change of bodyweight over age (= growth curves):
# sex-specific change of bodyweight over age (= growth curves):
resagemoth <- bam(weight_kg25~  sex  + s(age,by= sex, bs = "cr",k=10)  + s(agemoth, bs="cr", k=3)+ ti(age,agemoth, bs="cr", k=c(10,3)) + s(age, wildparityrearing,bs = "fs", k=10)  + s(date_of_weight, zoo,bs = "fs", k=11, m=1) +s(age,name, bs = "fs", k=10,m=1) +s(age,sire, bs = "fs", k=10,m=1) +s(age,dam, bs = "fs", k=10,m=1) + s(age,zoo, bs = "fs", k=10,m=1),method="ML", nthreads=8, data = ndata,select = F, rho=0.3, AR.start = ARstart)
resstatagemoth <- bam(weight_kg25~  sexO  + s(age, bs = "cr", k=11)  + s(age,by= sexO, bs = "cr", k=11) + s(agemoth, bs="cr", k=3) + ti(age,agemoth, bs="cr", k=c(11,3)) + s(age, wildparityrearing,bs = "fs", k=10) + s(date_of_weight, zoo,bs = "fs", k=11, m=1) +s(age,name, bs = "fs",k=10,m=1) +s(age,sire, bs = "fs", k=10,m=1) +s(age,dam, bs = "fs", k=10,m=1) + s(age,zoo, bs = "fs",k=10,m=1),method="ML", nthreads=8, data = ndata,select = F, rho=0.3, AR.start = ARstart)
nullagemoth <- bam(weight_kg25 ~ 1 + s(age, wildparityrearing,bs = "fs", k=10) + s(date_of_weight, zoo,bs = "fs", k=11, m=1) +s(age,name, bs = "fs",k=10,m=1) +s(age,sire, bs = "fs", k=10,m=1) +s(age,dam, bs = "fs", k=10,m=1) + s(age,zoo, bs = "fs",k=10,m=1),method="ML", nthreads=8, data = ndata,select = F, rho=0.3, AR.start = ARstart)
gam.check(resagemoth)
compareML(nullagemoth, resagemoth)
summary(resagemoth, freq=TRUE)
summary(resstatagemoth, freq=TRUE)
#write.table(residuals(resagemoth,type="response"), file="clipboard-16384", sep="\t")
par(mar=c(5,6,6,3) + 0.1)
fvisgam(resagemoth,view=c("age","agemoth"),  rm.ranef=TRUE, add.color.legend=TRUE,n.grid = 100,too.far = 0.1)
points(ndata$age,ndata$agemoth)
vis.gam(resagemoth,view=c("age","agemoth"),  rm.ranef=TRUE,too.far = 0.1,theta= -50,phi=30,alpha=0.2)


par(mar=c(7,7,4,3))
plot_diff(resagemoth, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE, col="gray70", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, ylab="",main="Sex difference in body weight (kg): Male minus female")
plot_diff(resagemoth, view="age", comp=list(sex=c("m","f")),xlim=c(max(min(fdata$age),min(mdata$age)),min(max(fdata$age),max(mdata$age))),shade=TRUE, mark.diff = TRUE, rm.ranef=TRUE, col="black",add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))
```

```r
plot_data(resagemoth, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, main=" Body weight (kg)", xlab="Age (years)", ylab="Body weight (kg)")
plot_data(resagemoth, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(resagemoth, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(resagemoth, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(resagemoth, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))


# 1.Ableitung= GrowthRate over age:
fd <- derivatives(resagemoth,c(1,2), n=1000, ncores=8)
write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age >= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
    geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
    theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40),
          legend.position="none") +
    xlab("Age (years)") + ylab("Growth rate (Bodyweight, kg/year)") + scale_x_continuous(breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65))


# 1.Ableitung= change of GrowthRate over age - DIFF:
fdd <- derivatives(resstatagemoth, c(1,2), n=1000, ncores=8)
fdd= fdd %>% filter(smooth %in% c("s(age):sexO1", "s(age):sexO0"))
fdd$sexO=stri_sub(fdd$smooth, -1,-1)
attach(fdd ,warn.conflicts = FALSE)
```

```
fdd= fdd %>% filter(!derivative==0 & sexO %in% c("0", "1")) %>% rename(age = data) %>% filter(age >= max(min(fdata$age),min(mdata$age)) & age <=
min(max(fdata$age),max(mdata$age)))
attach(fdd ,warn.conflicts = FALSE)

ggplot(fdd, aes(x = age, y = derivative, colour = sexO, fill = sexO)) + scale_color_manual(values=c("black", "blue"))  + scale_fill_manual(values=c("black", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.3, colour = NA) +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
        legend.position="none") +
   scale_x_continuous(lim=c(0,70), expand=c(0,0.5),breaks = seq(0, 70, by = 5)) + scale_y_continuous(breaks=c(-1,0,1)) +
   xlab("Age (years)") + ylab("Growth rate (Bodyweight, kg/year)")


######################################################################################################################################################
#Only individuals with data on arm length, body weight, testosterone AND DHEA

ndata= xdata %>% filter(AllVarFilter==1) %>% drop_na (sex,age)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
par(mfrow=c(1,1))

# sex-specific change of bodyweight over age (= growth curves):
resALL <- bam(weight_kg25~  sex  + s(age,by= sex, bs = "cr",k=10)  + s(age,wildparityrearing,bs = "fs",k=10)  + s(date_of_weight, zoo,bs = "fs", k=11, m=1) +s(age,name, bs =
"fs", k=6,m=1) + s(age,zoo, by=sex, bs = "fs", k=6,m=1),method="ML", nthreads=8, data = ndata,select = F , rho=0.3, AR.start = ARstart)
resALLstat <- bam(weight_kg25~  sexO + s(age, bs = "cr", k=10)  + s(age,by= sexO, bs = "cr", k=10)  + s(age,wildparityrearingO,bs = "fs",k=10)  + s(date_of_weight, zoo,bs =
"fs", k=11, m=1) +s(age,name, bs = "fs",k=6,m=1) +s(age,sire, bs = "fs", k=6,m=1) +s(age,dam, bs = "fs", k=6,m=1) + s(age,zoo, by=sex, bs = "fs",k=6,m=1),method="ML",
nthreads=8, data = ndata,select = F , rho=0.3, AR.start = ARstart)
null <- bam(weight_kg25 ~ 1 + s(age,wildparityrearing,bs = "fs",k=10)  + s(date_of_weight, zoo,bs = "fs", k=10, m=1) +s(age,name, bs = "fs", k=6,m=1) + s(age,zoo, by=sex, bs
= "fs", k=6,m=1),method="ML", nthreads=8, data = ndata,select = F , rho=0.3, AR.start = ARstart)
gam.check(resALL)
compareML(null, resALLstat)
summary(resALL, freq=TRUE)
summary(resALLstat, freq=TRUE)
#write.table(residuals(resALL,type="response"), file="clipboard-16384", sep="\t")
pp <- get_predictions(resALL,cond=list(sex=c("f","m"), age=seq(0,60,length=1000)))
```

```
#write.table(pp, file="clipboard-16384", sep="\t")
par(mar=c(7,7,4,3))
plot_diff(resALL, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE, col="gray70", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T,
yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, ylab="",main="Sex difference in body weight (kg): Male minus female")
plot_diff(resALL, view="age", comp=list(sex=c("m","f")),xlim=c(max(min(fdata$age),min(mdata$age)),min(max(fdata$age),max(mdata$age))),shade=TRUE, mark.diff =
TRUE, rm.ranef=TRUE, col="black",add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))
plot_data(resALL, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n",
xaxt="n",mgp=c(5,2,0),las=2, main=" Body weight (kg)", xlab="Age (years)", ylab="Body weight (kg)")
plot_data(resALL, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(resALL, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(resALL, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(resALL, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))

# 1.Ableitung= GrowthRate over age:
fd <- derivatives(resALL,c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age
>= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
         axis.title.y = element_text(face = "bold", size = 50),
         axis.text.x = element_text(size = 40),
         axis.text.y = element_text(size = 40),
         legend.position="none") +

   xlab("Age (years)") + ylab("Growth rate (Bodyweight, kg/year)") + scale_x_continuous(breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65))
```

```
################################################################################################
################################################################################################
################################################################################################
# LOWER ARM LENGTH
################################################################################################
################################################################################################
################################################################################################

#R-CODE
library(mgcv)
library(itsadug)
library(gratia)
library(dplyr)
library(tidyr)
library(stringi)
library(ggplot2)

xdata = read.table("clipboard", dec=".",header=T, na.strings=c("x","xxx"))
attach(xdata ,warn.conflicts = FALSE)
#hist(xdata)
xdata$zoo=tolower(xdata$zoo)
xdata$name=tolower(xdata$name)
xdata$sire=as.factor(xdata$sire)
xdata$dam=as.factor(xdata$dam)
xdata$wildparityrearing=as.factor(xdata$wildparityrearing)
xdata$wildparityrearingO=as.ordered(xdata$wildparityrearing)
contrasts(xdata$wildparityrearingO) <- "contr.treatment"
xdata$sex=as.factor(xdata$sex)
xdata$sexO=as.ordered(xdata$sexOrd)
contrasts(xdata$sexO) <- "contr.treatment"
xdata$name=as.factor(xdata$name)
xdata$zoo=as.factor(xdata$zoo)
xdata$Length_cm=xdata$arm_Length_cm
xdata$Length_cm25=xdata$Length_cm^2.5
attach(xdata ,warn.conflicts = FALSE)
```

```
#################################################################################################################
#################################################################################################################
#################################################################################################################
#Length in cm:

#par(omi=c(1,1,1,1))
ndata= xdata %>% drop_na (sex,age, wildparityrearing)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
attach(fdata ,warn.conflicts = FALSE)
attach(mdata ,warn.conflicts = FALSE)
par(mfrow=c(1,1))


# sex-specific change of bodyweight over age (= growth curves):
res <- gam(Length_cm ~  sex  + s(age,by= sex,bs = "cr",k=10)  + s(age, wildparityrearing,bs = "fs", k=10)  + s(measure_date , zoo,bs = "fs", k=6,m=1) +s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
resstat <- gam(Length_cm ~  sexO  + s(age,bs = "cr",k=10)  + s(age,by= sexO,bs = "cr",k=10)  + s(age, wildparityrearing,bs = "fs",k=10)  + s(measure_date , zoo,bs = "fs",k=6,m=1) +s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
null <- gam(Length_cm ~  1 + s(age, wildparityrearing,bs = "fs", k=10) + s(measure_date , zoo,bs = "fs",k=6,m=1) +s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex,bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
acf_resid(res)
#gam.check(res)
summary(res, freq=TRUE)
summary(resstat, freq=TRUE)
compareML(null, resstat)
pp <- get_predictions(res,cond=list(sex=c("f","m"), age=seq(0,60,length=1000)))
#write.table(pp, file="clipboard-16384", sep="\t")

par(mar=c(7,7,4,3))

plot_diff(res, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE, col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, ylim=c(-5,5), ylab="", main="Sex difference in lower arm length (cm): Male minus female")
plot_diff(res, view="age", comp=list(sex=c("m","f")), xlim=c(max(min(fdata$age),min(mdata$age)), min(max(fdata$age),max(mdata$age))), shade=TRUE, mark.diff = TRUE, rm.ranef=TRUE, col="black",add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65,70),,mgp=c(5,2,0))
axis(2,pos=-0.5, at=c(-4,0,4),cex.axis=3,mgp=c(2,1,0))
```

```r
plot_data(res, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n",
xaxt="n",mgp=c(5,2,0),las=2, main="Lower arm length (cm)" , xlab="Age (years)", ylab=" Lower arm length (cm)")
plot_data(res, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(res, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(res, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(res, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65,70),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))


# 1.Ableitung= GrowthRate over age:
fd <- derivatives(res,c(1,2), n=1000, ncores=8, frequentist=F)
#write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age
>= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
        legend.position="none") +
   scale_x_continuous(lim=c(0,70), expand=c(0,0.5),breaks = seq(0, 70, by = 5)) + scale_y_continuous(breaks= c(0,1, 2,3, 4,5,6)) +
   xlab("Age (years)") + ylab("Growth rate (Armlength, cm/year)")


# 1.Ableitung= change of GrowthRate over age - DIFF:
fdd <- derivatives(resstat, c(1,2), n=1000, ncores=8, frequentist=F)
fdd= fdd %>% filter(smooth %in% c("s(age):sexO1", "s(age):sexO0"))
fdd$sexO=stri_sub(fdd$smooth, -1,-1)
attach(fdd ,warn.conflicts = FALSE)
```

```
fdd= fdd %>% filter(!derivative==0 & sexO %in% c("0", "1")) %>% rename(age = data) %>% filter(age >= max(min(fdata$age),min(mdata$age)) & age <=
min(max(fdata$age),max(mdata$age)))
attach(fdd ,warn.conflicts = FALSE)

ggplot(fdd, aes(x = age, y = derivative, colour = sexO, fill = sexO)) + scale_color_manual(values=c("black", "blue"))  + scale_fill_manual(values=c("black", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.3, colour = NA) +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
        legend.position="none") +
   scale_x_continuous(lim=c(0,70), expand=c(0,0.5),breaks = seq(0, 70, by = 5)) + scale_y_continuous(breaks=c(-1,0,1)) +
   xlab("Age (years)") + ylab("Growth rate (Armlength, cm/year)")

###########################################################################################################
#age <= 20yrs old

ndata= xdata %>% filter(age<=20 & age>=0) %>% drop_na (sex,age, wildparityrearing) %>% group_by(name) %>% filter(n() >= 0)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
attach(fdata ,warn.conflicts = FALSE)
attach(mdata ,warn.conflicts = FALSE)
par(mfrow=c(1,1))

# sex-specific change of bodyweight over age (= growth curves):
res <- gam(Length_cm ~  sex  + s(age,by= sex,bs = "cr",k=10)  + s(age, wildparityrearing,bs = "fs", k=10)  + s(measure_date , zoo,bs = "fs", k=5,m=1) +s(age,name, bs = "fs",
k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
par(mar=c(7,7,4,3))

plot_diff(res, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE, col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T,
yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, ylim=c(-5,6), ylab="", main="Sex difference in lower arm length (cm): Male minus female")
plot_diff(res, view="age", comp=list(sex=c("m","f")), xlim=c(max(min(fdata$age),min(mdata$age)), min(max(fdata$age),max(mdata$age))), shade=TRUE, mark.diff = TRUE,
rm.ranef=TRUE, col="black",add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65,70),,mgp=c(5,2,0))
axis(2,pos=-0.5, at=c(-4,0,4),cex.axis=3,mgp=c(2,1,0))
plot_data(res, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n",
xaxt="n",mgp=c(5,2,0),las=2, main="Lower arm length (cm)" , xlab="Age (years)", ylab=" Lower arm length (cm)")
```

```
plot_data(res, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(res, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(res, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(res, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65,70),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))


# 1.Ableitung= GrowthRate over age:
fd <- derivatives(res,c(1,2), n=1000, ncores=8, frequentist=F)
#write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age
>= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
        legend.position="none") +
   scale_x_continuous(lim=c(0,20), expand=c(0,0.5),breaks = seq(0, 20, by = 5)) + scale_y_continuous(breaks= c(0,1, 2,3, 4,5,6)) +
   xlab("Age (years)") + ylab("Growth rate (Armlength, cm/year)")



###########################################################################################################################################
#############
#AGEMOTH (=reduced dataset, no wild-born):
#par(omi=c(1,1,1,1))
xdata$damparity=as.factor(xdata$damparity)
xdata$damparityO=ordered(xdata$damparity, levels=c("p","m","w"))
```

```
xdata$damparityO=as.ordered(xdata$damparityO)
ndata= xdata %>% filter(!agemoth=="WC") %>% drop_na (sex,age, wildparityrearing)
ndata$agemoth=as.numeric(ndata$agemoth)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
attach(fdata ,warn.conflicts = FALSE)
attach(mdata ,warn.conflicts = FALSE)
par(mfrow=c(1,1))


# sex-specific change of bodyweight over age (= growth curves) - AGEMOTH:
resagemoth <- gam(Length_cm ~  sex  + s(age,by= sex,bs = "cr",k=10)  + s(age, wildparityrearing,bs = "fs", k=5)  + te(age, agemoth, bs = "cr", k = c(5, 3)) + s(measure_date , zoo,bs = "fs", k=4,m=1) + s(age, sire, bs = "fs", k = 3, m = 1) + s(age,dam, bs = "fs", k = 3, m = 1) +s(name, bs="re") + s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
resstatagemoth <- gam(Length_cm ~  sexO  + s(age,bs = "cr",k=10)  + s(age,by= sexO,bs = "cr",k=10)  + s(age, wildparityrearing,bs = "fs", k=5) + s(agemoth, bs = "cr", k = 3) + ti(age, agemoth, bs = "cr", k = c(5, 3))  + s(measure_date , zoo,bs = "fs", k=4,m=1) + s(age, sire, bs = "fs", k = 3, m = 1) + s(age,dam, bs = "fs", k = 3, m = 1) +s(name, bs="re") + s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
#nullagemoth <- gam(Length_cm ~  1 + s(age, wildparityrearing,bs = "fs", k=10) + s(measure_date , zoo,bs = "fs", k=4,m=1) + s(age, sire, bs = "fs", k = 3, m = 1) + s(age,dam, bs = "fs", k = 3, m = 1) +s(name, bs="re") + s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
acf_resid(resagemoth)
gam.check(resagemoth)
summary(resagemoth, freq=TRUE)
summary(resstatagemoth, freq=TRUE)


pp <- get_predictions(resagemoth,cond=list(sex=c("f","m"), age=seq(0,60,length=1000)))
#write.table(pp, file="clipboard-16384", sep="\t")

par(mar=c(7,7,4,3))

plot_diff(resagemoth, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE, col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, ylim=c(-5,5),  ylab="", main="Sex difference in lower arm length (cm): Male minus female")
plot_diff(resagemoth, view="age", comp=list(sex=c("m","f")), xlim=c(max(min(fdata$age),min(mdata$age)), min(max(fdata$age),max(mdata$age))), shade=TRUE, mark.diff = TRUE, rm.ranef=TRUE, col="black",add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65,70),,mgp=c(5,2,0))
axis(2,pos=-0.5, at=c(-4,0,4),cex.axis=3,mgp=c(2,1,0))
plot_data(resagemoth, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, main="Lower arm length (cm)" , xlab="Age (years)", ylab=" Lower arm length (cm)")
```

```
plot_data(resagemoth, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(resagemoth, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(resagemoth, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(resagemoth, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65,70),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))

# 1.Ableitung= GrowthRate over age:
fd <- derivatives(resagemoth,c(1,2), n=1000, ncores=8, frequentist=F)
#write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age
>= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
    geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
    theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40),
          legend.position="none") +
    scale_x_continuous(lim=c(0,70), expand=c(0,0.5),breaks = seq(0, 70, by = 5)) + scale_y_continuous(breaks= c(0,1, 2,3, 4,5,6)) +
    xlab("Age (years)") + ylab("Growth rate (Armlength, cm/year)")

# 1.Ableitung= change of GrowthRate over age - DIFF:
fdd <- derivatives(resstatagemoth, c(1,2), n=1000, ncores=8, frequentist=F)
fdd= fdd %>% filter(smooth %in% c("s(age):sexO1", "s(age):sexO0"))
fdd$sexO=stri_sub(fdd$smooth, -1,-1)
attach(fdd ,warn.conflicts = FALSE)
fdd= fdd %>% filter(!derivative==0 & sexO %in% c("0", "1")) %>% rename(age = data) %>% filter(age >= max(min(fdata$age),min(mdata$age)) & age <=
min(max(fdata$age),max(mdata$age)))
attach(fdd ,warn.conflicts = FALSE)
```

```
ggplot(fdd, aes(x = age, y = derivative, colour = sexO, fill = sexO)) + scale_color_manual(values=c("black", "blue"))  + scale_fill_manual(values=c("black", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.3, colour = NA) +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
        legend.position="none") +
   scale_x_continuous(lim=c(0,70), expand=c(0,0.5),breaks = seq(0, 70, by = 5)) + scale_y_continuous(breaks=c(-1,0,1)) +
   xlab("Age (years)") + ylab("Growth rate (Armlength, cm/year)")
```

```
#########################################################################################################################################
```

#Only individuals with data on arm length, body weight, testosterone AND DHEA

```
#par(omi=c(1,1,1,1))
ndata= xdata %>% filter(AllVarFilter==1) %>%  drop_na (sex,age, wildparityrearing)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
attach(fdata ,warn.conflicts = FALSE)
attach(mdata ,warn.conflicts = FALSE)
par(mfrow=c(1,1))


# sex-specific change of bodyweight over age (= growth curves):
res <- gam(Length_cm ~  sex  + s(age,by= sex,bs = "cr",k=10)  + s(age, wildparityrearing,bs = "fs", k=10)  + s(measure_date , zoo,bs = "fs", k=5,m=1) +s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
resstat <- gam(Length_cm ~  sexO  + s(age,bs = "cr",k=10)  + s(age,by= sexO,bs = "cr",k=10)  + s(age, wildparityrearing,bs = "fs",k=10)  + s(measure_date , zoo,bs = "fs",k=5,m=1) +s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
null <- gam(Length_cm ~  1 + s(age, wildparityrearing,bs = "fs", k=10) + s(measure_date , zoo,bs = "fs",k=5,m=1) +s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex,bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
acf_resid(res)
#gam.check(res)
summary(res, freq=TRUE)
summary(resstat, freq=TRUE)
compareML(null, resstat)
pp <- get_predictions(res,cond=list(sex=c("f","m"), age=seq(0,60,length=1000)))
#write.table(pp, file="clipboard-16384", sep="\t")
```

```
par(mar=c(7,7,4,3))

plot_diff(res, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE, col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T,
yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, ylim=c(-5,5), ylab="", main="Sex difference in lower arm length (cm): Male minus female")
plot_diff(res, view="age", comp=list(sex=c("m","f")), xlim=c(max(min(fdata$age),min(mdata$age)), min(max(fdata$age),max(mdata$age))), shade=TRUE, mark.diff = TRUE,
rm.ranef=TRUE, col="black",add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65,70),,mgp=c(5,2,0))
axis(2,pos=-0.5, at=c(-4,0,4),cex.axis=3,mgp=c(2,1,0))
plot_data(res, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n",
xaxt="n",mgp=c(5,2,0),las=2, main="Lower arm length (cm)" , xlab="Age (years)", ylab=" Lower arm length (cm)")
plot_data(res, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(res, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(res, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(res, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65,70),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))


# 1.Ableitung= GrowthRate over age:
fd <- derivatives(res,c(1,2), n=1000, ncores=8, frequentist=F)
#write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age
>= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
        legend.position="none") +
```

```
    scale_x_continuous(lim=c(0,70), expand=c(0,0.5),breaks = seq(0, 70, by = 5)) + scale_y_continuous(breaks= c(0,1, 2,3, 4,5,6)) +
    xlab("Age (years)") + ylab("Growth rate (Armlength, cm/year)")


# 1.Ableitung= change of GrowthRate over age - DIFF:
fdd <- derivatives(resstat, c(1,2), n=1000, ncores=8, frequentist=F)
fdd= fdd %>% filter(smooth %in% c("s(age):sexO1", "s(age):sexO0"))
fdd$sexO=stri_sub(fdd$smooth, -1,-1)
attach(fdd ,warn.conflicts = FALSE)
fdd= fdd %>% filter(!derivative==0 & sexO %in% c("0", "1")) %>% rename(age = data) %>% filter(age >= max(min(fdata$age),min(mdata$age)) & age <=
min(max(fdata$age),max(mdata$age)))
attach(fdd ,warn.conflicts = FALSE)

ggplot(fdd, aes(x = age, y = derivative, colour = sexO, fill = sexO)) + scale_color_manual(values=c("black", "blue"))  + scale_fill_manual(values=c("black", "blue")) +
    geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.3, colour = NA) +
    theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40),
          legend.position="none") +
    scale_x_continuous(lim=c(0,70), expand=c(0,0.5),breaks = seq(0, 70, by = 5)) + scale_y_continuous(breaks=c(-1,0,1)) +
    xlab("Age (years)") + ylab("Growth rate (Armlength, cm/year)")
```

```
###############################################################################################################
###############################################################################################################
###############################################################################################################
#Length in cm^2.5:

#par(omi=c(1,1,1,1))
ndata= xdata %>% drop_na (sex,age,rearing)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
attach(fdata ,warn.conflicts = FALSE)
attach(mdata ,warn.conflicts = FALSE)
par(mfrow=c(1,1))


# sex-specific change of bodyweight over age (= growth curves):
res <- gam(Length_cm25 ~  sex  + s(age,by= sex,bs = "cr",k=10)  + s(age, wildparityrearing,bs = "fs", k=10)  + s(measure_date , zoo,bs = "fs", k=5,m=1) +s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
resstat <- gam(Length_cm25 ~  sexO  + s(age,bs = "cr",k=10)  + s(age,by= sexO,bs = "cr",k=10)  + s(age, wildparityrearing,bs = "fs",k=10)  + s(measure_date , zoo,bs = "fs",k=5,m=1) +s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
null <- gam(Length_cm25 ~  1 + s(age, wildparityrearing,bs = "fs", k=10) + s(measure_date , zoo,bs = "fs",k=5,m=1) +s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex,bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
acf_resid(res)
#gam.check(res)
summary(res, freq=TRUE)
summary(resstat, freq=TRUE)
compareML(null, resstat)
pp <- get_predictions(res,cond=list(sex=c("f","m"), age=seq(0,60,length=1000)))
#write.table(pp, file="clipboard-16384", sep="\t")

par(mar=c(7,7,4,3))

plot_diff(res, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE, col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, ylim=c(-1000,2000), ylab="", main="Sex difference in lower arm length (cm): Male minus female")
plot_diff(res, view="age", comp=list(sex=c("m","f")), xlim=c(max(min(fdata$age),min(mdata$age)), min(max(fdata$age),max(mdata$age))), shade=TRUE, mark.diff = TRUE, rm.ranef=TRUE, col="black",add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65,70),,mgp=c(5,2,0))
axis(2,pos=-0.5, at=c(-1000,0,1000,2000,3000),cex.axis=3,mgp=c(2,1,0))
```

```
plot_data(res, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, main="Lower arm length (cm)" , xlab="Age (years)", ylab=" Lower arm length (cm)")
plot_data(res, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(res, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(res, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(res, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65,70),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))


# 1.Ableitung= GrowthRate over age:
fd <- derivatives(res,c(1,2), n=1000, ncores=8, frequentist=F)
#write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age >= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
        legend.position="none") +
   scale_x_continuous(lim=c(0,70), expand=c(0,0.5),breaks = seq(0, 70, by = 5)) + scale_y_continuous(breaks= c(0,200,400,600,800)) +
   xlab("Age (years)") + ylab("Growth rate (Armlength, cm^2.5/year)")


# 1.Ableitung= change of GrowthRate over age - DIFF:
fdd <- derivatives(resstat, c(1,2), n=1000, ncores=8, frequentist=F)
fdd= fdd %>% filter(smooth %in% c("s(age):sexO1", "s(age):sexO0"))
fdd$sexO=stri_sub(fdd$smooth, -1,-1)
attach(fdd ,warn.conflicts = FALSE)
```

```
fdd= fdd %>% filter(!derivative==0 & sexO %in% c("0", "1")) %>% rename(age = data) %>% filter(age >= max(min(fdata$age),min(mdata$age)) & age <=
min(max(fdata$age),max(mdata$age)))
attach(fdd ,warn.conflicts = FALSE)

ggplot(fdd, aes(x = age, y = derivative, colour = sexO, fill = sexO)) + scale_color_manual(values=c("black", "blue"))  + scale_fill_manual(values=c("black", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.3, colour = NA) +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
        legend.position="none") +
   scale_x_continuous(lim=c(0,70), expand=c(0,0.5),breaks = seq(0, 70, by = 5)) + scale_y_continuous(breaks=c(-200,0,200,400)) +
   xlab("Age (years)") + ylab("Growth rate (Armlength, cm^2.5/year)")



################################################################################################################################################################
#age <= 20yrs old
ndata= xdata %>% filter(age<=20 & age>=0) %>% drop_na (sex,age,rearing) %>% group_by(name) %>% filter(n() >= 0)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
attach(fdata ,warn.conflicts = FALSE)
attach(mdata ,warn.conflicts = FALSE)
par(mfrow=c(1,1))

# sex-specific change of bodyweight over age (= growth curves):
res <- gam(Length_cm25 ~  sex  + s(age,by= sex,bs = "cr",k=10)  + s(age, wildparityrearing,bs = "fs", k=10)  + s(measure_date , zoo,bs = "fs", k=5,m=1) +s(age,name, bs = "fs",
k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
par(mar=c(7,7,4,3))

plot_diff(res, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE, col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T,
yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, ylim=c(-1000,2500), ylab="", main="Sex difference in lower arm length (cm): Male minus female")
plot_diff(res, view="age", comp=list(sex=c("m","f")), xlim=c(max(min(fdata$age),min(mdata$age)), min(max(fdata$age),max(mdata$age))), shade=TRUE, mark.diff = TRUE,
rm.ranef=TRUE, col="black",add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65,70),,mgp=c(5,2,0))
axis(2,pos=-0.5, at=c(-1000,0,1000,2000,3000),cex.axis=3,mgp=c(2,1,0))
```

```
plot_data(res, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n",
xaxt="n",mgp=c(5,2,0),las=2, main="Lower arm length (cm)" , xlab="Age (years)", ylab=" Lower arm length (cm)")
plot_data(res, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(res, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(res, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(res, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65,70),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))


# 1.Ableitung= GrowthRate over age:
fd <- derivatives(res,c(1,2), n=1000, ncores=8, frequentist=F)
#write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age
>= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
         axis.title.y = element_text(face = "bold", size = 50),
         axis.text.x = element_text(size = 40),
         axis.text.y = element_text(size = 40),
         legend.position="none") +
   scale_x_continuous(lim=c(0,20), expand=c(0,0.5),breaks = seq(0, 20, by = 5)) + scale_y_continuous(breaks= c(0,200,400,600,800)) +

  xlab("Age (years)") + ylab("Growth rate (Armlength, cm^2.5/year)")



##################################################################################################################
#no WC (=reduced dataset):
#par(omi=c(1,1,1,1))
ndata= xdata %>% filter(!agemoth=="WC") %>% drop_na (sex,age,rearing)
```

```
ndata$agemoth=as.numeric(ndata$agemoth)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
attach(fdata ,warn.conflicts = FALSE)
attach(mdata ,warn.conflicts = FALSE)
par(mfrow=c(1,1))


# sex-specific change of bodyweight over age (= growth curves) - AGEMOTH:
resagemoth <- gam(Length_cm25 ~  sex  + s(age,by= sex,bs = "cr",k=10)  + s(age, wildparityrearing,bs = "fs", k=5)  + te(age, agemoth, bs = "cr", k = c(5, 3)) + s(measure_date
, zoo,bs = "fs", k=4,m=1) + s(age, sire, bs = "fs", k = 3, m = 1) + s(age,dam, bs = "fs", k = 3, m = 1) +s(name, bs="re") + s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML",
nthreads=8,data = ndata,select = F)
resstatagemoth <- gam(Length_cm25 ~  sexO  + s(age,bs = "cr",k=10)  + s(age,by= sexO,bs = "cr",k=10)  + s(age, wildparityrearing,bs = "fs", k=5) + s(agemoth, bs = "cr", k = 3)
+ ti(age, agemoth, bs = "cr", k = c(5, 3))  + s(measure_date , zoo,bs = "fs", k=4,m=1) + s(age, sire, bs = "fs", k = 3, m = 1) + s(age,dam, bs = "fs", k = 3, m = 1) +s(name, bs="re")
+ s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
#nullagemoth <- gam(Length_cm25 ~  1 + s(age, wildparityrearing,bs = "fs", k=10) + s(measure_date , zoo,bs = "fs", k=4,m=1) + s(age, sire, bs = "fs", k = 3, m = 1) +
s(age,dam, bs = "fs", k = 3, m = 1) +s(name, bs="re") + s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
acf_resid(resagemoth)
gam.check(resagemoth)
summary(resagemoth, freq=TRUE)
summary(resstatagemoth, freq=TRUE)

pp <- get_predictions(resagemoth,cond=list(sex=c("f","m"), age=seq(0,60,length=1000)))
#write.table(pp, file="clipboard-16384", sep="\t")

par(mar=c(7,7,4,3))

plot_diff(resagemoth, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE, col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T,
yaxt="n", xaxt="n",mgp=c(5,2,0),las=2,  ylim=c(-1000,2000), ylab="", main="Sex difference in lower arm length (cm): Male minus female")
plot_diff(resagemoth, view="age", comp=list(sex=c("m","f")), xlim=c(max(min(fdata$age),min(mdata$age)), min(max(fdata$age),max(mdata$age))), shade=TRUE, mark.diff
= TRUE, rm.ranef=TRUE, col="black",add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65,70),,mgp=c(5,2,0))
axis(2,pos=-0.5, at=c(-1000,0,1000,2000,3000),cex.axis=3,mgp=c(2,1,0))
plot_data(resagemoth, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n",
xaxt="n",mgp=c(5,2,0),las=2, main="Lower arm length (cm)" , xlab="Age (years)", ylab=" Lower arm length (cm)")
plot_data(resagemoth, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(resagemoth, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(resagemoth, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
```

```
plot_smooth(resagemoth, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65,70),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))


# 1.Ableitung= GrowthRate over age:
fd <- derivatives(resagemoth,c(1,2), n=1000, ncores=8, frequentist=F)
#write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age
>= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
    geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
    theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40),
          legend.position="none") +
    scale_x_continuous(lim=c(0,70), expand=c(0,0.5),breaks = seq(0, 70, by = 5)) + scale_y_continuous(breaks= c(0,200,400,600,800)) +
    xlab("Age (years)") + ylab("Growth rate (Armlength, cm^2.5/year)")


# 1.Ableitung= change of GrowthRate over age - DIFF:
fdd <- derivatives(resstatagemoth, c(1,2), n=1000, ncores=8, frequentist=F)
fdd= fdd %>% filter(smooth %in% c("s(age):sexO1", "s(age):sexO0"))
fdd$sexO=stri_sub(fdd$smooth, -1,-1)
attach(fdd ,warn.conflicts = FALSE)
fdd= fdd %>% filter(!derivative==0 & sexO %in% c("0", "1")) %>% rename(age = data) %>% filter(age >= max(min(fdata$age),min(mdata$age)) & age <=
min(max(fdata$age),max(mdata$age)))
attach(fdd ,warn.conflicts = FALSE)
```

```
ggplot(fdd, aes(x = age, y = derivative, colour = sexO, fill = sexO)) + scale_color_manual(values=c("black", "blue"))  + scale_fill_manual(values=c("black", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.3, colour = NA) +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
        legend.position="none") +
   scale_x_continuous(lim=c(0,70), expand=c(0,0.5),breaks = seq(0, 70, by = 5)) + scale_y_continuous(breaks= c(-200,0,200,400)) +

   xlab("Age (years)") + ylab("Growth rate (Armlength, cm^2.5/year)")


#########################################################################################################
#Only individuals with data on arm length, body weight, testosterone AND DHEA

#par(omi=c(1,1,1,1))
ndata= xdata %>% filter(AllVarFilter==1) %>%  drop_na (sex,age, wildparityrearing)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
attach(fdata ,warn.conflicts = FALSE)
attach(mdata ,warn.conflicts = FALSE)
par(mfrow=c(1,1))


# sex-specific change of bodyweight over age (= growth curves):
res <- gam(Length_cm25 ~  sex  + s(age,by= sex,bs = "cr",k=10)  + s(age, wildparityrearing,bs = "fs", k=10)  + s(measure_date , zoo,bs = "fs", k=5,m=1) +s(age,name, bs = "fs",
k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
resstat <- gam(Length_cm25 ~  sexO  + s(age,bs = "cr",k=10)  + s(age,by= sexO,bs = "cr",k=10)  + s(age, wildparityrearing,bs = "fs",k=10)  + s(measure_date , zoo,bs =
"fs",k=5,m=1) +s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
null <- gam(Length_cm25 ~  1 + s(age, wildparityrearing,bs = "fs", k=10) + s(measure_date , zoo,bs = "fs",k=5,m=1) +s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex,bs =
"fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
acf_resid(res)
#gam.check(res)
summary(res, freq=TRUE)
summary(resstat, freq=TRUE)
compareML(null, resstat)
pp <- get_predictions(res,cond=list(sex=c("f","m"), age=seq(0,60,length=1000)))
#write.table(pp, file="clipboard-16384", sep="\t")
```

```
par(mar=c(7,7,4,3))

plot_diff(res, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE, col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T,
yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, ylim=c(-1000,2000), ylab="", main="Sex difference in lower arm length (cm): Male minus female")
plot_diff(res, view="age", comp=list(sex=c("m","f")), xlim=c(max(min(fdata$age),min(mdata$age)), min(max(fdata$age),max(mdata$age))), shade=TRUE, mark.diff = TRUE,
rm.ranef=TRUE, col="black",add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65,70),,mgp=c(5,2,0))
axis(2,pos=-0.5, at=c(-1000,0,1000,2000,3000),cex.axis=3,mgp=c(2,1,0))
plot_data(res, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n",
xaxt="n",mgp=c(5,2,0),las=2, main="Lower arm length (cm)" , xlab="Age (years)", ylab=" Lower arm length (cm)")
plot_data(res, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(res, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(res, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(res, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65,70),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))


# 1.Ableitung= GrowthRate over age:
fd <- derivatives(res,c(1,2), n=1000, ncores=8, frequentist=F)
#write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age
>= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
```

```
      legend.position="none") +
   scale_x_continuous(lim=c(0,70), expand=c(0,0.5),breaks = seq(0, 70, by = 5)) + scale_y_continuous(breaks= c(0,200,400,600,800)) +
   xlab("Age (years)") + ylab("Growth rate (Armlength, cm^2.5/year)")


# 1.Ableitung= change of GrowthRate over age - DIFF:
fdd <- derivatives(resstat, c(1,2), n=1000, ncores=8, frequentist=F)
fdd= fdd %>% filter(smooth %in% c("s(age):sexO1", "s(age):sexO0"))
fdd$sexO=stri_sub(fdd$smooth, -1,-1)
attach(fdd ,warn.conflicts = FALSE)
fdd= fdd %>% filter(!derivative==0 & sexO %in% c("0", "1")) %>% rename(age = data) %>% filter(age >= max(min(fdata$age),min(mdata$age)) & age <=
min(max(fdata$age),max(mdata$age)))
attach(fdd ,warn.conflicts = FALSE)

ggplot(fdd, aes(x = age, y = derivative, colour = sexO, fill = sexO)) + scale_color_manual(values=c("black", "blue"))  + scale_fill_manual(values=c("black", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.3, colour = NA) +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
      axis.title.y = element_text(face = "bold", size = 50),
      axis.text.x = element_text(size = 40),
      axis.text.y = element_text(size = 40),
      legend.position="none") +
   scale_x_continuous(lim=c(0,70), expand=c(0,0.5),breaks = seq(0, 70, by = 5)) + scale_y_continuous(breaks=c(-200,0,200,400)) +
   xlab("Age (years)") + ylab("Growth rate (Armlength, cm^2.5/year)")
```

```
##############################################################################################################
##############################################################################################################
##############################################################################################################
# Creatinine
##############################################################################################################
##############################################################################################################
##############################################################################################################
#R-CODE Creatinine


#-------------------------------------------------

#COPY VALUES FROM TABLE INTO R:

library(mgcv)
library(itsadug)
library(gratia)
library(dplyr)
library(tidyr)
library(stringi)
library(ggplot2)

xdata = read.table("clipboard", dec=".",header=T, na.strings=c("x","xxx"))
attach(xdata ,warn.conflicts = FALSE)
#hist(xdata)
xdata$zoo=tolower(xdata$zoo)
xdata$name=tolower(xdata$name)
xdata$sire=as.factor(xdata$sire)
xdata$dam=as.factor(xdata$dam)
xdata$sex=as.factor(xdata$sex)
xdata$sexO=as.ordered(xdata$sex)
contrasts(xdata$sexO) <- "contr.treatment"
xdata$name=as.factor(xdata$name)
xdata$zoo=as.factor(xdata$zoo)
xdata$wildparityrearing=as.factor(xdata$wildparityrearing)
```

```
xdata$wildparityrearingO=ordered(xdata$wildparityrearing, levels=c("w","p.mr","p.hr","m.mr","m.hr"))
xdata$wildparityrearingO=as.ordered(xdata$wildparityrearingO)
contrasts(xdata$wildparityrearingO) <- "contr.treatment"
xdata$SGq=log(xdata$SG0)
xdata$CRq=log(xdata$Crea_mg_ml)
attach(xdata ,warn.conflicts = FALSE)
xdata$CRqR=residuals(gam(CRq~s(SGq,bs="cr",k=5),method="ML"))
attach(xdata ,warn.conflicts = FALSE)


#R-CODE statistics:

#par(omi=c(1,1,1,1))
ndata= xdata %>% drop_na (sex,age,rearing)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
par(mfrow=c(1,1))

# sex-specific change of bodyweight over age (= growth curves):
res <- gam(CRqR~  sex  + s(age,by= sex,bs = "cr",k=6)  + s(age, wildparityrearing,bs = "fs", k=6)  + s(samplingdate, zoo,bs = "fs", k=5, m=1)+s(age,name, bs = "fs", k=3,m=1) +
s(age,zoo, by=sex, bs = "fs", k=3,m=1) + s(daytime,bs = "cr", k=3),method="ML", nthreads=8,data = ndata,select = F)
resstat <- gam(CRqR~  sexO  + s(age,bs = "cr",k=6)  + s(age,by= sexO,bs = "cr",k=6)  + s(age, wildparityrearing, bs = "fs",k=6)  + s(samplingdate, zoo,bs = "fs", k=5, m=1)
+s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=3,m=1) + s(daytime,bs = "cr", k=3),method="ML", nthreads=8,data = ndata,select = F)
null <- gam(CRqR~  1  + s(age, wildparityrearing, bs = "fs",k=6)  + s(samplingdate, zoo,bs = "fs", k=5, m=1) +s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs",
k=3,m=1) + s(daytime,bs = "cr", k=5), method="ML", nthreads=8,data = ndata,select = F)
acf_resid(res)
#gam.check(res)
compareML(null, resstat)
summary(res, freq=TRUE)
summary(resstat, freq=TRUE)
pp <- get_predictions(res,cond=list(sex=c("f","m"), age=seq(0,60,length=1000)))
#write.table(pp, file="clipboard-16384", sep="\t")

par(mar=c(7,7,4,3))

plot_diff(res, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE, col="gray70", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T,
yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, ylim=c(-0.4,0.7), ylab="", main="Sex difference in Ln(Creatinine): Male minus female")
```

```r
plot_diff(res, view="age", comp=list(sex=c("m","f")), xlim=c(max(min(fdata$age),min(mdata$age)), min(max(fdata$age),max(mdata$age))), shade=TRUE, mark.diff = TRUE, rm.ranef=TRUE, col="black",add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65,70),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))
plot_data(res, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, main="Ln(Creatinine) - corrected for specific gravity" , xlab="Age (years)", ylab=" Ln(Creatinine)")
plot_data(res, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(res, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(res, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(res, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65,70),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))



# 1.Ableitung= GrowthRate over age:
fd <- derivatives(res,c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = T)
#write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age >= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
        legend.position="none") +
   scale_x_continuous(lim=c(0,65), expand=c(0,0.5),breaks = seq(0, 65, by = 5)) +
   xlab("Age (years)") + ylab("Growth rate (Creatinine)")

# 1.Ableitung= change of GrowthRate over age - DIFF:
```

```
fdd <- derivatives(resstat, c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = T)
fdd= fdd %>% filter(smooth %in% c("s(age):sexOm", "s(age):sexOf"))
fdd$sexO=stri_sub(fdd$smooth, -1,-1)
attach(fdd ,warn.conflicts = FALSE)
fdd= fdd %>% filter(!derivative==0 & sexO %in% c("f", "m")) %>% rename(age = data) %>% filter(age >= max(min(fdata$age),min(mdata$age)) & age <=
min(max(fdata$age),max(mdata$age)))
attach(fdd ,warn.conflicts = FALSE)

ggplot(fdd, aes(x = age, y = derivative, colour = sexO, fill = sexO)) + scale_color_manual(values=c("black", "blue"))  + scale_fill_manual(values=c("black", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.3, colour = NA) +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
        legend.position="none") +
   scale_x_continuous(lim=c(0,65), expand=c(0,0.5),breaks = seq(0, 65, by = 5)) + scale_y_continuous(breaks=c(-0.1,0,0.1)) +
   xlab("Age (years)") + ylab("Growth rate (Creatinine)")


#########################################################################################################
###########################################
#AGEMOTH:
#par(omi=c(1,1,1,1))
ndata= xdata %>% filter(!wildparityrearing=="w") %>% drop_na (sex,age,rearing)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
par(mfrow=c(1,1))

# sex-specific change of bodyweight over age (= growth curves):
resagemoth <- gam(CRqR~  sex  + s(age,by= sex,bs = "cr",k=6)   + s(age, wildparityrearing,bs = "fs", k=5)  + te(age, agemoth, bs = "cr", k = c(5, 3)) + s(daytime,bs = "cr",k=3) +
s(samplingdate , zoo,bs = "fs", k=4,m=1) + s(age, sire, bs = "fs", k = 3, m = 1) + s(age,dam, bs = "fs", k = 3, m = 1) +s(name, bs="re") + s(age,zoo, by=sex, bs = "fs",
k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
resstatagemoth <- gam(CRqR~  sexO  + s(age,bs = "cr",k=6)  + s(age,by= sexO,bs = "cr",k=6) + s(age, wildparityrearing,bs = "fs", k=5) + s(agemoth,bs = "cr",k=5) + ti(age,
agemoth,bs = "cr", k=c(5,3)) + s(daytime,bs = "cr",k=3) + s(samplingdate , zoo,bs = "fs", k=4,m=1) + s(age, sire, bs = "fs", k = 3, m = 1) + s(age,dam, bs = "fs", k = 3, m = 1)
+s(name, bs="re") + s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
nullagemoth <- gam(CRqR~  1  + s(age, wildparityrearing, bs = "fs",k=5)  + s(daytime,bs = "cr",k=3) + s(samplingdate , zoo,bs = "fs", k=4,m=1) + s(age, sire, bs = "fs", k = 3, m
= 1) + s(age,dam, bs = "fs", k = 3, m = 1) +s(name, bs="re") + s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
```

```
acf_resid(resagemoth)
#gam.check(resagemoth)
compareML(nullagemoth, resstatagemoth)
summary(resagemoth, freq=TRUE)
summary(resstatagemoth, freq=TRUE)
par(mar=c(7,7,4,3))

plot_diff(resagemoth, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE, col="gray70", cex.main=4, cex.lab=4,cex.axis=2.5,
hide.label=T, yaxt="n", xaxt="n",mgp=c(5,2,0),las=2, ylim=c(-0.4,0.7), ylab="", main="Sex difference in Ln(Creatinine): Male minus female")
plot_diff(resagemoth, view="age", comp=list(sex=c("m","f")), xlim=c(max(min(fdata$age),min(mdata$age)), min(max(fdata$age),max(mdata$age))), shade=TRUE, mark.diff
= TRUE, rm.ranef=TRUE, col="black",add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65,70),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))
plot_data(resagemoth, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5, hide.label=T, yaxt="n",
xaxt="n",mgp=c(5,2,0),las=2, main="Ln(Creatinine) - corrected for specific gravity" , xlab="Age (years)", ylab=" Ln(Creatinine)")
plot_data(resagemoth, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(resagemoth, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(resagemoth, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(resagemoth, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1,cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65,70),,mgp=c(5,2,0))
axis(2,pos=-0.5, cex.axis=3,mgp=c(2,1,0))



# 1.Ableitung= GrowthRate over age:
fd <- derivatives(resagemoth,c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = T)
#write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age
>= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
```

```
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40),
          legend.position="none") +
    scale_x_continuous(lim=c(0,65), expand=c(0,0.5),breaks = seq(0, 65, by = 5)) +
    xlab("Age (years)") + ylab("Growth rate (Creatinine)")

# 1.Ableitung= change of GrowthRate over age - DIFF:
fdd <- derivatives(resstatagemoth, c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = T)
fdd= fdd %>% filter(smooth %in% c("s(age):sexOm", "s(age):sexOf"))
fdd$sexO=stri_sub(fdd$smooth, -1,-1)
attach(fdd ,warn.conflicts = FALSE)
fdd= fdd %>% filter(!derivative==0 & sexO %in% c("f", "m")) %>% rename(age = data) %>% filter(age >= max(min(fdata$age),min(mdata$age)) & age <=
min(max(fdata$age),max(mdata$age)))
attach(fdd ,warn.conflicts = FALSE)

ggplot(fdd, aes(x = age, y = derivative, colour = sexO, fill = sexO)) + scale_color_manual(values=c("black", "blue"))  + scale_fill_manual(values=c("black", "blue")) +
    geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.3, colour = NA) +
    theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40),
          legend.position="none") +
    scale_x_continuous(lim=c(0,65), expand=c(0,0.5),breaks = seq(0, 65, by = 5)) + scale_y_continuous(breaks=c(-0.1,0,0.1)) +
    xlab("Age (years)") + ylab("Growth rate (Creatinine)")
```

```
################################################################################################
################################################################################################
################################################################################################
# Physiology
################################################################################################
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################################################################################################
#R-CODE DHEA

#COPY VALUES FROM TABLE INTO R:
library(mgcv)
library(itsadug)
library(gratia)
library(dplyr)
library(tidyr)
library(stringi)
library(ggplot2)

xdata = read.table("clipboard", dec=".",header=T, na.strings=c("x","xxx"))
attach(xdata ,warn.conflicts = FALSE)
#hist(xdata)
xdata$sexO=as.ordered(xdata$sex)
contrasts(xdata$sexO) <- "contr.treatment"
xdata$sex=as.factor(xdata$sex)
xdata$name=as.factor(xdata$name)
xdata$sire=as.factor(xdata$sire)
xdata$dam=as.factor(xdata$dam)
xdata$zoo=as.factor(xdata$zoo)
xdata$wildparityrearing=as.factor(xdata$wildparityrearing)
xdata$wildparityrearingO=ordered(xdata$wildparityrearing, levels=c("w","p.mr","p.hr","m.mr","m.hr"))
xdata$wildparityrearingO=as.ordered(xdata$wildparityrearingO)
contrasts(xdata$wildparityrearingO) <- "contr.treatment"
xdata$DHEAsq=log(xdata$DHEA_SG)
attach(xdata ,warn.conflicts = FALSE)
hist(DHEAsq)
```

#R-CODE statistics:

```
#par(omi=c(1,1,1,1))
ndata= xdata %>% drop_na (sex,age,wildparityrearing)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
attach(fdata ,warn.conflicts = FALSE)
attach(mdata ,warn.conflicts = FALSE)
par(mfrow=c(1,1))

# sex-specific change over age (= growth curves):
res <- gam(DHEAsq ~  sex  + s(age,by= sex,bs = "cr",k=10)  + s(age, wildparityrearing, bs = "fs", k=6) + s(daytime,bs = "cr",k=3)  + s(sampledate , zoo,bs = "fs", k=5, m=1) +s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=6,m=1),method="ML", nthreads=8,data = ndata,select = F)
resstat <- gam(DHEAsq ~  sexO + s(age,bs = "cr",k=20)  + s(age,by= sexO,bs = "cr",k=20)  + s(age, wildparityrearing, bs = "fs", k=6) + s(daytime,bs = "cr",k=3)  + s(sampledate , zoo,bs = "fs", k=5, m=1) +s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=6,m=1),method="ML", nthreads=8,data = ndata,select = F) # k=20 is needed, due to the different methods used for ordered factor variables
null <- gam(DHEAsq ~  1 + s(age, wildparityrearing, bs = "fs", k=6) + s(daytime,bs = "cr",k=3)  + s(sampledate , zoo,bs = "fs", k=5, m=1) +s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=6,m=1),method="ML", nthreads=8,data = ndata,select = F)
resNoSex <- gam(DHEAsq ~  s(age,bs = "cr",k=10)  + s(age, wildparityrearing, bs = "fs", k=6) + s(daytime,bs = "cr",k=3)  + s(sampledate , zoo,bs = "fs", k=5, m=1) +s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=6,m=1),method="ML", nthreads=8,data = ndata,select = F)
acf_resid(res)
#gam.check(res)
summary(res, freq=TRUE)
summary(resstat, freq=TRUE)
summary(resNoSex, freq=TRUE)
compareML(null, resstat)

par(mar=c(7,7,4,3)) #mar = c(bottom, left, top, right)
plot_diff(res, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE,  col="gray70", cex.main=4, cex.lab=4,cex.axis=2.5, ylim=c(-1,2.5), hide.label=T, yaxt="n",xaxt="n",mgp=c(5,2,0), las=2, main="Sex difference in Ln(DHEA): Male minus female", xlab="Age (years)",  ylab="")
plot_diff(res, view="age", comp=list(sex=c("m","f")),xlim=c(max(min(fdata$age),min(mdata$age)),min(max(fdata$age),max(mdata$age))),shade=TRUE, mark.diff = TRUE, rm.ranef=TRUE, col="black",add=TRUE)
axis(1, cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65), mgp=c(5,2,0)) #mgp=c(axis.title.position, axis.label.position, axis.line.position)
axis(2, pos=-0.5,cex.axis=3, mgp=c(2,1,0))
plot_data(res, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5,  hide.label=T, yaxt="n",xaxt="n",mgp=c(5,2,0), las=2, main="Ln(DHEA)", xlab="Age (years)",  ylab="Ln(DHEA)")
plot_data(res, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(res, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(res, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
```

```
plot_smooth(res, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1, cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65), mgp=c(5,2,0)) #mgp=c(axis.title.position, axis.label.position, axis.line.position)
axis(2, pos=-0.5,cex.axis=3, mgp=c(2,1,0))


# 1.Ableitung= GrowthRate over age:
fd <- derivatives(res,c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
#write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age >= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
   theme_classic() + theme(axis.text.y = element_text(angle = 90, hjust = 0.5)) + theme(plot.margin = unit(c(40,36,10,59), "pt")) + #margin(t,r,b,l)
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40), legend.position = "none") +
   xlab("Age (years)") + ylab("") + scale_x_continuous(lim=c(0,65),expand=c(0,0.5),breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65))    #+ scale_y_continuous(breaks=c(-0.3,0,0.3))


# 1.Ableitung= change of GrowthRate over age - DIFF:
fdd <- derivatives(resstat, c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
fdd= fdd %>% filter(smooth %in% c("s(age):sexOm", "s(age):sexOf"))
fdd$sexO=stri_sub(fdd$smooth, -1,-1)
attach(fdd ,warn.conflicts = FALSE)
fdd= fdd %>% filter(!derivative==0 & sexO %in% c("m", "f")) %>% rename(age = data) %>% filter(age >= max(min(fdata$age),min(mdata$age)) & age <= min(max(fdata$age),max(mdata$age)))
attach(fdd ,warn.conflicts = FALSE)

ggplot(fdd, aes(x = age, y = derivative, colour = sexO, fill = sexO)) + scale_color_manual(values=c("black", "blue"))  + scale_fill_manual(values=c("black", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
```

```
    theme_classic() + theme(axis.text.y = element_text(angle = 90, hjust = 0.5)) + theme(plot.margin = unit(c(40,36,10,59), "pt")) + #margin(t,r,b,l)
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40), legend.position = "none") +
    xlab("Age (years)") + ylab("") + scale_x_continuous(lim=c(0,65),expand=c(0,0.5),breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65)) + scale_y_continuous(breaks=c(-0.3,0,0.3))


#Plot without Sex
plot_data(res, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5,  hide.label=T, yaxt="n",xaxt="n",mgp=c(5,2,0), las=2, main="Ln(DHEA)", xlab="Age (years)",  ylab="Ln(DHEA)")
plot_data(res, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(res, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(resNoSex, view="age", rm.ranef=TRUE, rug= FALSE, col="black", add=TRUE)
axis(1, cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65), mgp=c(5,2,0)) #mgp=c(axis.title.position, axis.label.position, axis.line.position)
axis(2, pos=-0.5,cex.axis=3, mgp=c(2,1,0))

# 1.Ableitung= GrowthRate over age - NoSex:
fdNS <- derivatives(resNoSex,c(1), n=1000, ncores=8, interval = "confidence", frequentist = F)
#write.table(fdNS, file="clipboard-16384", sep="\t")
fdNS= fdNS %>% filter(smooth %in% c("s(age)"))
#fdNS$sex=stri_sub(fdNS$smooth, -1,-1)
attach(fdNS ,warn.conflicts = FALSE)
fdNS= fdNS %>% filter(!derivative==0) %>% rename(age = data) %>% filter(age >= min(ndata$age) & age <= max(ndata$age))
attach(fdNS ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fdNS, aes(x = age, y = derivative)) + scale_color_manual(values="black")  + scale_fill_manual(values= "black") +
    geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.5, colour="black", fill = "mediumorchid") +
    theme_classic() + theme(axis.text.y = element_text(angle = 90, hjust = 0.5)) + theme(plot.margin = unit(c(40,36,10,59), "pt")) + #margin(t,r,b,l)
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40), legend.position = "none") +
    xlab("Age (years)") + ylab("") + scale_x_continuous(lim=c(0,65),expand=c(0,0.5),breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65))    #+ scale_y_continuous(breaks=c(-0.3,0,0.3))
```

```
#SingleLinePlots for comparison plot
#fdm=fd %>% filter(sex=="m")
#fdf=fd %>% filter(sex=="f")

ggplot(fdNS, aes(x = age, y = derivative)) + geom_line(size = 3,linetype=3, color="black") +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
        legend.position="none") +
   xlab("Age (years)") + ylab("Male growth rate (DHEA/year)") + scale_x_continuous(lim=c(0,20), expand=c(0,0.5),breaks = seq(0, 60, by = 5))

pp <- get_predictions(resNoSex, cond=list(age=seq(0,60,length=1000)))
#fdm=pp %>% filter(sex=="m")
#fdf=pp %>% filter(sex=="f")

ggplot(pp, aes(x = age, y = fit)) + geom_line(size = 3,linetype=3, color="black") +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
        legend.position="none") +
   xlab("Age (years)") + ylab("Male level (DHEA)") + scale_x_continuous(lim=c(0,20), expand=c(0,0.5),breaks = seq(0, 60, by = 5))


#SingleLinePlots for comparison plot – Per SEX
fdm=fd %>% filter(sex=="m")
fdf=fd %>% filter(sex=="f")

ggplot(fdm, aes(x = age, y = derivative)) + geom_line(size = 3,linetype=3, color="black") +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
        legend.position="none") +
```

```
    xlab("Age (years)") + ylab("Male growth rate (DHEA/year)") + scale_x_continuous(lim=c(0,20), expand=c(0,0.5),breaks = seq(0, 60, by = 5))

ggplot(fdf, aes(x = age, y = derivative)) + geom_line(size = 3,linetype=3, color="black") +
    theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40),
          legend.position="none") +
    xlab("Age (years)") + ylab("Female growth rate (DHEA/year)") + scale_x_continuous(lim=c(0,20), expand=c(0,0.5),breaks = seq(0, 60, by = 5))


pp <- get_predictions(res,cond=list(sex=c("f","m"), age=seq(0,60,length=1000)))
fdm=pp %>% filter(sex=="m")
fdf=pp %>% filter(sex=="f")

ggplot(fdm, aes(x = age, y = fit)) + geom_line(size = 3,linetype=3, color="black") +
    theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40),
          legend.position="none") +
    xlab("Age (years)") + ylab("Male level (DHEA)") + scale_x_continuous(lim=c(0,20), expand=c(0,0.5),breaks = seq(0, 60, by = 5))

ggplot(fdf, aes(x = age, y = fit)) + geom_line(size = 3,linetype=3, color="black") +
    theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40),
          legend.position="none") +
    xlab("Age (years)") + ylab("Female level (DHEA)") + scale_x_continuous(lim=c(0,20), expand=c(0,0.5),breaks = seq(0, 60, by = 5)) #+ scale_y_continuous(lim=c(-2.5,1))

###############################################################################################################################
#AGEMOTH:
#par(omi=c(1,1,1,1))
ndata= xdata %>% filter(!wildparityrearing=="w") %>% drop_na (sex,age,wildparityrearing)
```

```
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
par(mfrow=c(1,1))

# sex-specific change over age (= growth curves):
resagemoth <- gam(DHEAsq ~  sex  + s(age,by= sex,bs = "cr",k=10)  + s(age, wildparityrearing,bs = "fs", k=5)  + te(age, agemoth, bs = "cr", k = c(5, 3)) + s(daytime,bs =
"cr",k=3) + s(sampledate , zoo,bs = "fs", k=4,m=1) + s(age, sire, bs = "fs", k = 3, m = 1) + s(age,dam, bs = "fs", k = 3, m = 1) +s(name, bs="re") + s(age,zoo, by=sex, bs = "fs",
k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
resstatagemoth <- gam(DHEAsq ~  sexO  + s(age,bs = "cr",k=10)  + s(age,by= sexO,bs = "cr",k=10) + s(age, wildparityrearing, bs = "fs", k=5) + s(agemoth,bs = "cr",k=5) +
ti(age, agemoth, bs = "cr", k = c(5, 3)) + s(daytime,bs = "cr",k=3) + s(sampledate , zoo,bs = "fs", k=4,m=1) + s(age, sire, bs = "fs", k = 3, m = 1) + s(age,dam, bs = "fs", k = 3, m =
1) +s(name, bs="re") + s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
resagemothNoSex <- gam(DHEAsq ~  s(age,bs = "cr",k=10)  + s(age, wildparityrearing,bs = "fs", k=5)  + te(age, agemoth, bs = "cr", k = c(5, 3)) + s(daytime,bs = "cr",k=3) +
s(sampledate , zoo,bs = "fs", k=4,m=1) + s(age, sire, bs = "fs", k = 3, m = 1) + s(age,dam, bs = "fs", k = 3, m = 1) +s(name, bs="re") + s(age,zoo, by=sex, bs = "fs",
k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)

#null <- gam(DHEAsq ~  1  + s(age, wildparityrearing, bs = "fs", k=5) + s(daytime,bs = "cr",k=3)  + s(sampledate , zoo,bs = "fs", k=4,m=1) + s(age, sire, bs = "fs", k = 3, m = 1) +
s(age,dam, bs = "fs", k = 3, m = 1) +s(name, bs="re") + s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
acf_resid(resagemoth)
#gam.check(resagemoth)
#compareML(null, resstatagemoth)
summary(resagemoth, freq=TRUE)
summary(resstatagemoth, freq=TRUE)

par(mar=c(7,7,4,3)) #mar = c(bottom, left, top, right)
plot_diff(resagemoth, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE,  col="gray70", cex.main=4, cex.lab=4,cex.axis=2.5, ylim=c(-
1,2.5), hide.label=T, yaxt="n",xaxt="n",mgp=c(5,2,0), las=2, main="Sex difference in Ln(DHEA): Male minus female", xlab="Age (years)",  ylab="")
plot_diff(resagemoth, view="age", comp=list(sex=c("m","f")),xlim=c(max(min(fdata$age),min(mdata$age)),min(max(fdata$age),max(mdata$age))),shade=TRUE, mark.diff =
TRUE, rm.ranef=TRUE, col="black",add=TRUE)
axis(1, cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65), mgp=c(5,2,0)) #mgp=c(axis.title.position, axis.label.position, axis.line.position)
axis(2, pos=-0.5,cex.axis=3, mgp=c(2,1,0))
plot_data(resagemoth, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5,  hide.label=T,
yaxt="n",xaxt="n",mgp=c(5,2,0), las=2, main="Ln(DHEA)", xlab="Age (years)",  ylab="Ln(DHEA)")
plot_data(resagemoth, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(resagemoth, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(resagemoth, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(resagemoth, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1, cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65), mgp=c(5,2,0)) #mgp=c(axis.title.position, axis.label.position, axis.line.position)
axis(2, pos=-0.5,cex.axis=3, mgp=c(2,1,0))
```

```
# 1.Ableitung= GrowthRate over age:
fd <- derivatives(resagemoth,c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
#write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age >= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
    geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
    theme_classic() + theme(axis.text.y = element_text(angle = 90, hjust = 0.5)) + theme(plot.margin = unit(c(40,36,10,59), "pt")) + #margin(t,r,b,l)
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40), legend.position = "none") +
    xlab("Age (years)") + ylab("") + scale_x_continuous(lim=c(0,65),expand=c(0,0.5),breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65))    #+ scale_y_continuous(breaks=c(-0.3,0,0.3))

# 1.Ableitung= change of GrowthRate over age - DIFF:
fdd <- derivatives(resstatagemoth, c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
fdd= fdd %>% filter(smooth %in% c("s(age):sexOm", "s(age):sexOf"))
fdd$sexO=stri_sub(fdd$smooth, -1,-1)
attach(fdd ,warn.conflicts = FALSE)
fdd= fdd %>% filter(!derivative==0 & sexO %in% c("m", "f")) %>% rename(age = data) %>% filter(age >= max(min(fdata$age),min(mdata$age)) & age <= min(max(fdata$age),max(mdata$age)))
attach(fdd ,warn.conflicts = FALSE)

ggplot(fdd, aes(x = age, y = derivative, colour = sexO, fill = sexO)) + scale_color_manual(values=c("black", "blue"))  + scale_fill_manual(values=c("black", "blue")) +
    geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
    theme_classic() + theme(axis.text.y = element_text(angle = 90, hjust = 0.5)) + theme(plot.margin = unit(c(40,36,10,59), "pt")) + #margin(t,r,b,l)
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
```

```
        axis.text.y = element_text(size = 40), legend.position = "none") +
    xlab("Age (years)") + ylab("") + scale_x_continuous(lim=c(0,65),expand=c(0,0.5),breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65)) + scale_y_continuous(breaks=c(-
0.3,0,0.3))



#Plot without Sex
plot_data(resagemoth, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5,  hide.label=T,
yaxt="n",xaxt="n",mgp=c(5,2,0), las=2, main="Ln(DHEA)", xlab="Age (years)",  ylab="Ln(DHEA)")
plot_data(resagemoth, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(resagemoth, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(resagemothNoSex, view="age", rm.ranef=TRUE, rug= FALSE, col="black", add=TRUE)
axis(1, cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65), mgp=c(5,2,0)) #mgp=c(axis.title.position, axis.label.position, axis.line.position)
axis(2, pos=-0.5,cex.axis=3, mgp=c(2,1,0))

# 1.Ableitung= GrowthRate over age - NoSex:
fdNS <- derivatives(resagemothNoSex,c(1), n=1000, ncores=8, interval = "confidence", frequentist = F)
#write.table(fdNS, file="clipboard-16384", sep="\t")
fdNS= fdNS %>% filter(smooth %in% c("s(age)"))
#fdNS$sex=stri_sub(fdNS$smooth, -1,-1)
attach(fdNS ,warn.conflicts = FALSE)
fdNS= fdNS %>% filter(!derivative==0) %>% rename(age = data) %>% filter(age >= min(ndata$age) & age <= max(ndata$age))
attach(fdNS ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fdNS, aes(x = age, y = derivative)) + scale_color_manual(values="black")  + scale_fill_manual(values= "black") +
    geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.5, colour="black", fill = "mediumorchid") +
    theme_classic() + theme(axis.text.y = element_text(angle = 90, hjust = 0.5)) + theme(plot.margin = unit(c(40,36,10,59), "pt")) + #margin(t,r,b,l)
    theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40), legend.position = "none") +
    xlab("Age (years)") + ylab("") + scale_x_continuous(lim=c(0,65),expand=c(0,0.5),breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65))    #+ scale_y_continuous(breaks=c(-
0.3,0,0.3))
```

```
#########################################################################################################################################################################
#Only individuals with data on arm length, body weight, testosterone AND DHEA

#par(omi=c(1,1,1,1))
ndata= xdata  %>% filter(AllVarFilter==1) %>% drop_na (sex,age, wildparityrearing)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
attach(fdata ,warn.conflicts = FALSE)
attach(mdata ,warn.conflicts = FALSE)
par(mfrow=c(1,1))

# sex-specific change over age (= growth curves):
res <- gam(DHEAsq ~  sex  + s(age,by= sex,bs = "cr",k=10)  + s(age, wildparityrearing, bs = "fs", k=6) + s(daytime,bs = "cr",k=3)  + s(sampledate , zoo,bs = "fs", k=5, m=1) +s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=6,m=1),method="ML", nthreads=8,data = ndata,select = F)
resstat <- gam(DHEAsq ~  sexO + s(age,bs = "cr",k=20)  + s(age,by= sexO,bs = "cr",k=20)  + s(age, wildparityrearing, bs = "fs", k=6) + s(daytime,bs = "cr",k=3)  + s(sampledate , zoo,bs = "fs", k=5, m=1) +s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=6,m=1),method="ML", nthreads=8,data = ndata,select = F) # k=20 is needed, due to the different methods used for ordered factor variables
null <- gam(DHEAsq ~  1 + s(age, wildparityrearing, bs = "fs", k=6) + s(daytime,bs = "cr",k=3)  + s(sampledate , zoo,bs = "fs", k=5, m=1) +s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=6,m=1),method="ML", nthreads=8,data = ndata,select = F)
resNoSex <- gam(DHEAsq ~  s(age,bs = "cr",k=10)  + s(age, wildparityrearing, bs = "fs", k=6) + s(daytime,bs = "cr",k=3)  + s(sampledate , zoo,bs = "fs", k=5, m=1) +s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=6,m=1),method="ML", nthreads=8,data = ndata,select = F)
resAgeOnly <- gam(DHEAsq ~  s(age,bs = "cr",k=10) + s(daytime,bs = "cr",k=3)  + s(sampledate , zoo,bs = "fs", k=5, m=1) +s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=6,m=1),method="ML", nthreads=8,data = ndata,select = F)
acf_resid(res)
#gam.check(res)
summary(res, freq=TRUE)
summary(resstat, freq=TRUE)
summary(resNoSex, freq=TRUE)
summary(resAgeOnly, freq=TRUE)
compareML(null, resstat)

par(mar=c(7,7,4,3)) #mar = c(bottom, left, top, right)
plot_diff(res, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE,  col="gray70", cex.main=4, cex.lab=4,cex.axis=2.5, ylim=c(-1,2.5), hide.label=T, yaxt="n",xaxt="n",mgp=c(5,2,0), las=2, main="Sex difference in Ln(DHEA): Male minus female", xlab="Age (years)",  ylab="")
plot_diff(res, view="age", comp=list(sex=c("m","f")),xlim=c(max(min(fdata$age),min(mdata$age)),min(max(fdata$age),max(mdata$age))),shade=TRUE, mark.diff = TRUE, rm.ranef=TRUE, col="black",add=TRUE)
axis(1, cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65), mgp=c(5,2,0)) #mgp=c(axis.title.position, axis.label.position, axis.line.position)
axis(2, pos=-0.5,cex.axis=3, mgp=c(2,1,0))
```

```
plot_data(res, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5,  hide.label=T,
yaxt="n",xaxt="n",mgp=c(5,2,0), las=2, main="Ln(DHEA)", xlab="Age (years)",  ylab="Ln(DHEA)")
plot_data(res, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(res, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(res, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(res, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1, cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65), mgp=c(5,2,0)) #mgp=c(axis.title.position, axis.label.position, axis.line.position)
axis(2, pos=-0.5,cex.axis=3, mgp=c(2,1,0))


# 1.Ableitung= GrowthRate over age:
fd <- derivatives(res,c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
#write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age
>= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
   theme_classic() + theme(axis.text.y = element_text(angle = 90, hjust = 0.5)) + theme(plot.margin = unit(c(40,36,10,59), "pt")) + #margin(t,r,b,l)
   theme(axis.title.x = element_text(face = "bold", size = 50),
         axis.title.y = element_text(face = "bold", size = 50),
         axis.text.x = element_text(size = 40),
         axis.text.y = element_text(size = 40), legend.position = "none") +
   xlab("Age (years)") + ylab("") + scale_x_continuous(lim=c(0,65),expand=c(0,0.5),breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65))    #+ scale_y_continuous(breaks=c(-
0.3,0,0.3))


# 1.Ableitung= change of GrowthRate over age - DIFF:
fdd <- derivatives(resstat, c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
fdd= fdd %>% filter(smooth %in% c("s(age):sexOm", "s(age):sexOf"))
fdd$sexO=stri_sub(fdd$smooth, -1,-1)
attach(fdd ,warn.conflicts = FALSE)
```

```
fdd= fdd %>% filter(!derivative==0 & sexO %in% c("m", "f")) %>% rename(age = data) %>% filter(age >= max(min(fdata$age),min(mdata$age)) & age <=
min(max(fdata$age),max(mdata$age)))
attach(fdd ,warn.conflicts = FALSE)

ggplot(fdd, aes(x = age, y = derivative, colour = sexO, fill = sexO)) + scale_color_manual(values=c("black", "blue"))  + scale_fill_manual(values=c("black", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
   theme_classic() + theme(axis.text.y = element_text(angle = 90, hjust = 0.5)) + theme(plot.margin = unit(c(40,36,10,59), "pt")) + #margin(t,r,b,l)
   theme(axis.title.x = element_text(face = "bold", size = 50),
         axis.title.y = element_text(face = "bold", size = 50),
         axis.text.x = element_text(size = 40),
         axis.text.y = element_text(size = 40), legend.position = "none") +
   xlab("Age (years)") + ylab("") + scale_x_continuous(lim=c(0,65),expand=c(0,0.5),breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65)) + scale_y_continuous(breaks=c(-
0.3,0,0.3))


#Plot without Sex
plot_data(res, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5,  hide.label=T,
yaxt="n",xaxt="n",mgp=c(5,2,0), las=2, main="Ln(DHEA)", xlab="Age (years)",  ylab="Ln(DHEA)")
plot_data(res, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(res, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(resNoSex, view="age", rm.ranef=TRUE, rug= FALSE, col="black", add=TRUE)
axis(1, cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65), mgp=c(5,2,0)) #mgp=c(axis.title.position, axis.label.position, axis.line.position)
axis(2, pos=-0.5,cex.axis=3, mgp=c(2,1,0))

plot_data(res, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5,  hide.label=T,
yaxt="n",xaxt="n",mgp=c(5,2,0), las=2, main="Ln(DHEA)", xlab="Age (years)",  ylab="Ln(DHEA)")
plot_data(res, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(res, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(resAgeOnly, view="age", rm.ranef=TRUE, rug= FALSE, col="black", add=TRUE)
axis(1, cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65), mgp=c(5,2,0)) #mgp=c(axis.title.position, axis.label.position, axis.line.position)
axis(2, pos=-0.5,cex.axis=3, mgp=c(2,1,0))

# 1.Ableitung= GrowthRate over age - NoSex:
fdNS <- derivatives(resNoSex,c(1), n=1000, ncores=8, interval = "confidence", frequentist = F)
#write.table(fdNS, file="clipboard-16384", sep="\t")
fdNS= fdNS %>% filter(smooth %in% c("s(age)"))
#fdNS$sex=stri_sub(fdNS$smooth, -1,-1)
attach(fdNS ,warn.conflicts = FALSE)
```

```r
fdNS= fdNS %>% filter(!derivative==0) %>% rename(age = data) %>% filter(age >= min(ndata$age) & age <= max(ndata$age))
attach(fdNS ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fdNS, aes(x = age, y = derivative)) + scale_color_manual(values="black")  + scale_fill_manual(values= "black") +
    geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.5, colour="black", fill = "mediumorchid") +
    theme_classic() + theme(axis.text.y = element_text(angle = 90, hjust = 0.5)) + theme(plot.margin = unit(c(40,36,10,59), "pt")) + #margin(t,r,b,l)
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40), legend.position = "none") +
    xlab("Age (years)") + ylab("") + scale_x_continuous(lim=c(0,65),expand=c(0,0.5),breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65))    #+ scale_y_continuous(breaks=c(-0.3,0,0.3))


# 1.Ableitung= GrowthRate over age - AgeOnly:
fdAO <- derivatives(resAgeOnly,c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
write.table(fdAO, file="clipboard-16384", sep="\t")
fdAO= fdAO %>% filter(smooth %in% c("s(age)"))
#fdAO$sex=stri_sub(fdAO$smooth, -1,-1)
attach(fdAO ,warn.conflicts = FALSE)
fdAO= fdAO %>% filter(!derivative==0) %>% rename(age = data) %>% filter(age >= min(ndata$age) & age <= max(ndata$age))
attach(fdAO ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fdAO, aes(x = age, y = derivative)) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.5, colour="black", fill = "mediumorchid") +    geom_line(size = 1.2,colour="black") +
    theme_classic() + theme(axis.text.y = element_text(angle = 90, hjust = 0.5)) + theme(plot.margin = unit(c(40,36,10,59), "pt")) + #margin(t,r,b,l)
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40), legend.position = "none") +
    xlab("Age (years)") + ylab("") + scale_x_continuous(lim=c(0,65),expand=c(0,0.5),breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65))    #+ scale_y_continuous(breaks=c(-0.3,0,0.3))
```

#R-CODE Testosterone

```r
#--------------------------------------------
#COPY VALUES FROM TABLE INTO R:
library(mgcv)
library(itsadug)
library(gratia)
library(dplyr)
library(tidyr)
library(stringi)
library(ggplot2)
xdata = read.table("clipboard", dec=".",header=T, na.strings=c("x","xxx"))
attach(xdata ,warn.conflicts = FALSE)
#hist(xdata)
#xdata$sexO=ordered(xdata$sexO, levels=c("0","1"))
xdata$sexO=as.ordered(xdata$sex)
contrasts(xdata$sexO) <- "contr.treatment"
xdata$sex=as.factor(xdata$sex)
xdata$name=as.factor(xdata$name)
xdata$sire=as.factor(xdata$sire)
xdata$dam=as.factor(xdata$dam)
xdata$zoo=as.factor(xdata$zoo)
xdata$wildparityrearing=as.factor(xdata$wildparityrearing)
xdata$wildparityrearing=ordered(xdata$wildparityrearing, levels=c("w","p.mr","p.hr","m.mr","m.hr"))
xdata$wildparityrearing=as.ordered(xdata$wildparityrearing)
contrasts(xdata$wildparityrearing) <- "contr.treatment"
xdata$testosq=log(xdata$test_ng_ml_corr_sg)
attach(xdata ,warn.conflicts = FALSE)
#----------------------------------------------------
```

#R-CODE statistics - automatic smoothing parameter estimation, leading to oversmoothing:

```r
#par(omi=c(1,1,1,1))
ndata= xdata %>% filter(age<=150 & age>=0) %>% drop_na (sex,age,wildparityrearing) %>% group_by(name) %>% filter(n() >= 0)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
attach(fdata ,warn.conflicts = FALSE)
attach(mdata ,warn.conflicts = FALSE)
```

```r
par(mfrow=c(1,1)) # the first argument specifies the number of rows and the second the number of columns of plots.

ggplot(data = fdata, aes(x = age, y = testosq, color = name)) +  geom_line(aes(group = name)) + geom_point()
ggplot(data = mdata, aes(x = age, y = testosq, color = name)) +  geom_line(aes(group = name)) + geom_point()

#GeneralData plot - LOESS
ggplot(data = ndata, aes(x = age, y = testosq, color = sex, group=sex),show.legend = FALSE) + scale_color_manual(values=c("red3", "blue"))  +
scale_fill_manual(values=c("red3", "blue"))   + geom_point(size=2)  +  geom_smooth(alpha=0.3, size=0.5, se=T) +
    theme_classic() + theme(legend.position = "none") +
    theme(axis.title.x = element_text(face = "bold", size = 37),
          axis.title.y = element_text(face = "bold", size = 37),
          axis.text.x = element_text(size = 30),
          axis.text.y = element_text(size = 30),
          legend.text = element_text(size = 30), legend.title = element_blank()) +
    xlab("Age (years)") + ylab("log(Testosterone)") + scale_x_continuous(breaks = seq(-20, 60, by = 5))


# sex-specific change over age (= growth curves):
res <- gam(testosq ~  sex  + s(age,by= sex,bs = "cr",k=10)  + s(age, wildparityrearing, bs = "fs", k=6) + s(daytime,bs = "cr",k=3)  + s(sampledate , zoo,bs = "fs", k=5, m=1)
+s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=6,m=1),method="ML", nthreads=8,data = ndata,select = F)
summary(res, freq=TRUE)

par(mar=c(7,7,4,3)) #mar = c(bottom, left, top, right)
plot_data(res, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5,  hide.label=T,
yaxt="n",xaxt="n",mgp=c(5,2,0), las=2, main="Ln(Testosterone)", xlab="Age (years)",  ylab="Ln(Testosterone)")
plot_data(res, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(res, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(res, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(res, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1, cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65), mgp=c(5,2,0)) #mgp=c(axis.title.position, axis.label.position, axis.line.position)
axis(2, pos=-0.5,cex.axis=3, mgp=c(2,1,0))

# 1.Ableitung= GrowthRate over age:
fd <- derivatives(res,c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
#write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
```

```
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age >= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
   theme_classic() + theme(axis.text.y = element_text(angle = 90, hjust = 0.5)) + theme(plot.margin = unit(c(40,36,10,59), "pt")) + #margin(t,r,b,l)
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40), legend.position = "none") +
   xlab("Age (years)") + ylab("") + scale_x_continuous(lim=c(0,65),expand=c(0,0.5),breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65))    #+ scale_y_continuous(breaks=c(-0.3,0,0.3))
```

```
################################################################################################################################################################### ########
#age 20, automatic smoothing parameter estimation, leading to oversmoothing:

#par(omi=c(1,1,1,1))
ndata= xdata %>% filter(age<=20 & age>=0 & !rearing=="wc") %>% drop_na (sex,age,wildparityrearing) # only 3 wc-individuals with only 1 value each (wc=wild-caught), model with these values requires much lower k-values)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
attach(fdata ,warn.conflicts = FALSE)
attach(mdata ,warn.conflicts = FALSE)
par(mfrow=c(1,1)) # the first argument specifies the number of rows and the second the number of columns of plots.
res <- gam(testosq ~  sex  + s(age,by= sex,bs = "cr",k=8)  + s(age, wildparityrearing, bs = "fs", k=5) + s(daytime,bs = "cr",k=3)  + s(sampledate , zoo,bs = "fs", k=3, m=1) +s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
#acf_resid(res)
#gam.check(res)
summary(res, freq=TRUE)

par(mar=c(7,7,4,3)) #mar = c(bottom, left, top, right)
```

```
plot_data(res, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5,  hide.label=T,
yaxt="n",xaxt="n",mgp=c(5,2,0), las=2, main="Ln(Testosterone)", xlab="Age (years)",  ylab="Ln(Testosterone)")
plot_data(res, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(res, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(res, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(res, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1, cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65), mgp=c(5,2,0)) #mgp=c(axis.title.position, axis.label.position, axis.line.position)
axis(2, pos=-0.5,cex.axis=3, mgp=c(2,1,0))


# 1.Ableitung= GrowthRate over age:
fd <- derivatives(res,c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
#write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age
>= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
    geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
    theme_classic() + theme(axis.text.y = element_text(angle = 90, hjust = 0.5)) + theme(plot.margin = unit(c(40,36,10,59), "pt")) + #margin(t,r,b,l)
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40), legend.position = "none") +
    xlab("Age (years)") + ylab("") + scale_x_continuous(lim=c(0,20),expand=c(0,0.5),breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65))    #+ scale_y_continuous(breaks=c(-
0.3,0,0.3))
```

***#R-CODE statistics* - smoothing penalty set to sp=1:**

```
#par(omi=c(1,1,1,1))
ndata= xdata %>% filter(age<=150 & age>=0) %>% drop_na (sex,age,wildparityrearing) %>% group_by(name) %>% filter(n() >= 0)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
attach(fdata ,warn.conflicts = FALSE)
attach(mdata ,warn.conflicts = FALSE)
par(mfrow=c(1,1)) # the first argument specifies the number of rows and the second the number of columns of plots.
```

```
#ggplot(data = fdata, aes(x = age, y = testosq, color = name)) +  geom_line(aes(group = name)) + geom_point()
#ggplot(data = mdata, aes(x = age, y = testosq, color = name)) +  geom_line(aes(group = name)) + geom_point()

#GeneralData plots - LOESS
ggplot(data = ndata, aes(x = age, y = testosq, color = sex, group=sex),show.legend = FALSE) + scale_color_manual(values=c("red3", "blue"))  +
scale_fill_manual(values=c("red3", "blue"))   + geom_point(size=2)  +  geom_smooth(alpha=0.3, size=0.5, se=T) +
   theme_classic() + theme(legend.position = "none") +
   theme(axis.title.x = element_text(face = "bold", size = 37),
        axis.title.y = element_text(face = "bold", size = 37),
        axis.text.x = element_text(size = 30),
        axis.text.y = element_text(size = 30),
        legend.text = element_text(size = 30), legend.title = element_blank()) +
   xlab("Age (years)") + ylab("log(Testosterone)") + scale_x_continuous(breaks = seq(-20, 60, by = 5))


# sex-specific change over age (= growth curves):
res <- gam(testosq ~  sex  + s(age,by= sex,bs = "cr",k=10, sp=1)  + s(age, wildparityrearing, bs = "fs", k=6) + s(daytime,bs = "cr",k=3)  + s(sampledate , zoo,bs = "fs", k=5, m=1)
+s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=6,m=1),method="ML", nthreads=8,data = ndata,select = F)
resstat <- gam(testosq ~  sexO  + s(age,bs = "cr",k=10, sp=1)  + s(age,by= sexO,bs = "cr",k=10, sp=1)  + s(age, wildparityrearing, bs = "fs", k=6) + s(daytime,bs = "cr",k=3)  +
s(sampledate , zoo,bs = "fs", k=5, m=1) +s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=6,m=1),method="ML", nthreads=8,data = ndata,select = F)
null <- gam(testosq ~  1 + s(age, wildparityrearing, bs = "fs", k=6) + s(daytime,bs = "cr",k=3)  + s(sampledate , zoo,bs = "fs", k=5, m=1) +s(age,name, bs = "fs", k=3,m=1) +
s(age,zoo, by=sex, bs = "fs", k=6,m=1),method="ML", nthreads=8,data = ndata,select = F)
acf_resid(res)
gam.check(res)
summary(res, freq=TRUE)
summary(resstat, freq=TRUE)
compareML(null, resstat)

par(mar=c(7,7,4,3)) #mar = c(bottom, left, top, right)
plot_diff(res, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE,  col="gray70", cex.main=4, cex.lab=4,cex.axis=2.5, ylim=c(-1,2.5),
hide.label=T, yaxt="n",xaxt="n",mgp=c(5,2,0), las=2, main="Sex difference in Ln(Testosterone): Male minus female", xlab="Age (years)",  ylab="")
plot_diff(res, view="age", comp=list(sex=c("m","f")),xlim=c(max(min(fdata$age),min(mdata$age)),min(max(fdata$age),max(mdata$age))),shade=TRUE, mark.diff = TRUE,
rm.ranef=TRUE, col="black",add=TRUE)
axis(1, cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65), mgp=c(5,2,0)) #mgp=c(axis.title.position, axis.label.position, axis.line.position)
axis(2, pos=-0.5,cex.axis=3, mgp=c(2,1,0))
plot_data(res, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5,  hide.label=T,
yaxt="n",xaxt="n",mgp=c(5,2,0), las=2, main="Ln(Testosterone)", xlab="Age (years)",  ylab="Ln(Testosterone)")
```

```
plot_data(res, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(res, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(res, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(res, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1, cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65), mgp=c(5,2,0)) #mgp=c(axis.title.position, axis.label.position, axis.line.position)
axis(2, pos=-0.5,cex.axis=3, mgp=c(2,1,0))


# 1.Ableitung= GrowthRate over age:
fd <- derivatives(res,c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
#write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age
>= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
    geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
    theme_classic() + theme(axis.text.y = element_text(angle = 90, hjust = 0.5)) + theme(plot.margin = unit(c(40,36,10,59), "pt")) + #margin(t,r,b,l)
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40), legend.position = "none") +
    xlab("Age (years)") + ylab("") + scale_x_continuous(lim=c(0,65),expand=c(0,0.5),breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65))    #+ scale_y_continuous(breaks=c(-
0.3,0,0.3))


# 1.Ableitung= change of GrowthRate over age - DIFF:
fdd <- derivatives(resstat, c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
fdd= fdd %>% filter(smooth %in% c("s(age):sexOm", "s(age):sexOf"))
fdd$sexO=stri_sub(fdd$smooth, -1,-1)
attach(fdd ,warn.conflicts = FALSE)
fdd= fdd %>% filter(!derivative==0 & sexO %in% c("m", "f")) %>% rename(age = data) %>% filter(age >= max(min(fdata$age),min(mdata$age)) & age <=
min(max(fdata$age),max(mdata$age)))
attach(fdd ,warn.conflicts = FALSE)
```

```
ggplot(fdd, aes(x = age, y = derivative, colour = sexO, fill = sexO)) + scale_color_manual(values=c("black", "blue"))  + scale_fill_manual(values=c("black", "blue")) +
    geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
    theme_classic() + theme(axis.text.y = element_text(angle = 90, hjust = 0.5)) + theme(plot.margin = unit(c(40,36,10,59), "pt")) + #margin(t,r,b,l)
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40), legend.position = "none") +
    xlab("Age (years)") + ylab("") + scale_x_continuous(lim=c(0,65),expand=c(0,0.5),breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65)) + scale_y_continuous(breaks=c(-
0.3,0,0.3))




##############################################################################################################
#age 20
#par(omi=c(1,1,1,1))
mean(testosq)+2*sd(testosq)
ndata= xdata %>% filter(age<=20 & age>=0 & !rearing=="wc" ) %>% drop_na (sex,age,wildparityrearing) # only 3 wc-individuals with only 1 value each (wc=wild-caught),
model with these values requires much lower k-values)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
attach(fdata ,warn.conflicts = FALSE)
attach(mdata ,warn.conflicts = FALSE)
par(mfrow=c(1,1)) # the first argument specifies the number of rows and the second the number of columns of plots.

res <- gam(testosq ~  sex  + s(age,by= sex,bs = "cr",k=10, sp=1)  + s(age, wildparityrearing, bs = "fs", k=3) + s(daytime,bs = "cr",k=3)  + s(sampledate , zoo,bs = "fs", k=3, m=1)
+s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
#acf_resid(res)
#gam.check(res)
summary(res, freq=TRUE)

par(mar=c(7,7,4,3)) #mar = c(bottom, left, top, right)
plot_diff(res, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE,  col="gray70", cex.main=4, cex.lab=4,cex.axis=2.5, ylim=c(-1,2.5),
hide.label=T, yaxt="n",xaxt="n",mgp=c(5,2,0), las=2, main="Sex difference in Ln(Testosterone): Male minus female", xlab="Age (years)",  ylab="")
plot_diff(res, view="age", comp=list(sex=c("m","f")),xlim=c(max(min(fdata$age),min(mdata$age)),min(max(fdata$age),max(mdata$age))),shade=TRUE, mark.diff = TRUE,
rm.ranef=TRUE, col="black",add=TRUE)
axis(1, cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65), mgp=c(5,2,0)) #mgp=c(axis.title.position, axis.label.position, axis.line.position)
```

```
axis(2, pos=-0.5,cex.axis=3, mgp=c(2,1,0))
plot_data(res, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5,  hide.label=T,
yaxt="n",xaxt="n",mgp=c(5,2,0), las=2, main="Ln(Testosterone)", xlab="Age (years)",  ylab="Ln(Testosterone)")
plot_data(res, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(res, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(res, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(res, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1, cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65), mgp=c(5,2,0)) #mgp=c(axis.title.position, axis.label.position, axis.line.position)
axis(2, pos=-0.5,cex.axis=3, mgp=c(2,1,0))


# 1.Ableitung= GrowthRate over age:
fd <- derivatives(res,c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
#write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age
>= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
    geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
    theme_classic() + theme(axis.text.y = element_text(angle = 90, hjust = 0.5)) + theme(plot.margin = unit(c(40,36,10,59), "pt")) + #margin(t,r,b,l)
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40), legend.position = "none") +
    xlab("Age (years)") + ylab("") + scale_x_continuous(lim=c(0,20),expand=c(0,0.5),breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65))    #+ scale_y_continuous(breaks=c(-
0.3,0,0.3))

#SingleLinePlots for comparison plot
fdm=fd %>% filter(sex=="m")
fdf=fd %>% filter(sex=="f")

ggplot(fdm, aes(x = age, y = derivative)) + geom_line(size = 3,linetype=1, color="black") +
    theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
```

```
  theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
        legend.position="none") +
  xlab("Age (years)") + ylab("Male growth rate (testo/year)") + scale_x_continuous(lim=c(0,20), expand=c(0,0.5),breaks = seq(0, 60, by = 5))

ggplot(fdf, aes(x = age, y = derivative)) + geom_line(size = 3,linetype=1, color="black") +
  theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
  theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
        legend.position="none") +
  xlab("Age (years)") + ylab("Female growth rate (testo/year)") + scale_x_continuous(lim=c(0,20), expand=c(0,0.5),breaks = seq(0, 60, by = 5))


pp <- get_predictions(res,cond=list(sex=c("f","m"), age=seq(0,60,length=1000)))
fdm=pp %>% filter(sex=="m")
fdf=pp %>% filter(sex=="f")

ggplot(fdm, aes(x = age, y = fit)) + geom_line(size = 3,linetype=1, color="black") +
  theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
  theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
        legend.position="none") +
  xlab("Age (years)") + ylab("Male level (Testos)") + scale_x_continuous(lim=c(0,20), expand=c(0,0.5),breaks = seq(0, 60, by = 5))

ggplot(fdf, aes(x = age, y = fit)) + geom_line(size = 3,linetype=1, color="black") +
  theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
  theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
        legend.position="none") +
  xlab("Age (years)") + ylab("Female level (Testos)") + scale_x_continuous(lim=c(0,20), expand=c(0,0.5),breaks = seq(0, 60, by = 5)) + scale_y_continuous(lim=c(-2.5,1))
```

```
############################################################################################################################################
#AGEMOTH:
#par(omi=c(1,1,1,1))
ndata= xdata %>% filter(!wildparityrearing=="w") %>% drop_na (sex,age,wildparityrearing)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
par(mfrow=c(1,1))

# sex-specific change over age (= growth curves):
resagemoth <- gam(testosq ~  sex  + s(age,by= sex,bs = "cr",k=10, sp=1)   + s(age, wildparityrearing,bs = "fs", k=5)  + te(age, agemoth, bs = "cr", k = c(5, 3)) + s(daytime,bs = "cr",k=3) + s(sampledate , zoo,bs = "fs", k=4,m=1) + s(age, sire, bs = "fs", k = 3, m = 1) + s(age,dam, bs = "fs", k = 3, m = 1) +s(name, bs="re") + s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
resstatagemoth <- gam(testosq ~  sexO  + s(age,bs = "cr",k=10, sp=1)  + s(age,by= sexO,bs = "cr",k=10, sp=1) + s(age, wildparityrearing, bs = "fs", k=5) + s(agemoth,bs = "cr",k=5) + ti(age, agemoth, bs = "cr", k = c(5, 3))+ s(daytime,bs = "cr",k=3) + s(sampledate , zoo,bs = "fs", k=4,m=1) + s(age, sire, bs = "fs", k = 3, m = 1) + s(age,dam, bs = "fs", k = 3, m = 1) +s(name, bs="re") + s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
null <- gam(testosq ~  1  + s(age, wildparityrearing, bs = "fs", k=5) + s(daytime,bs = "cr",k=3) + s(sampledate , zoo,bs = "fs", k=4,m=1) + s(age, sire, bs = "fs", k = 3, m = 1) + s(age,dam, bs = "fs", k = 3, m = 1) +s(name, bs="re") + s(age,zoo, by=sex, bs = "fs", k=3,m=1),method="ML", nthreads=8,data = ndata,select = F)
#gam.check(resagemoth)
compareML(null, resstatagemoth)
summary(resagemoth, freq=TRUE)
summary(resstatagemoth, freq=TRUE)

par(mar=c(7,7,4,3)) #mar = c(bottom, left, top, right)
fvisgam(resagemoth,view=c("age","agemoth"),  rm.ranef=TRUE, add.color.legend=TRUE,n.grid = 100,too.far = 0.1)
points(ndata$age, ndata$agemoth)
vis.gam(resagemoth,view=c("age","agemoth"),  rm.ranef=TRUE,too.far = 0.1,theta= -25,phi=30,alpha=0.2)

plot_diff(resagemoth, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE,  col="gray70", cex.main=4, cex.lab=4,cex.axis=2.5, ylim=c(-1,2.5), hide.label=T, yaxt="n",xaxt="n",mgp=c(5,2,0), las=2, main="Sex difference in Ln(Testosterone): Male minus female", xlab="Age (years)",  ylab="")
plot_diff(resagemoth, view="age", comp=list(sex=c("m","f")),xlim=c(max(min(fdata$age),min(mdata$age)),min(max(fdata$age),max(mdata$age))),shade=TRUE, mark.diff = TRUE, rm.ranef=TRUE, col="black",add=TRUE)
axis(1, cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65), mgp=c(5,2,0)) #mgp=c(axis.title.position, axis.label.position, axis.line.position)
axis(2, pos=-0.5,cex.axis=3, mgp=c(2,1,0))
plot_data(resagemoth, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5,  hide.label=T, yaxt="n",xaxt="n",mgp=c(5,2,0), las=2, main="Ln(Testosterone)", xlab="Age (years)",  ylab="Ln(Testosterone)")
plot_data(resagemoth, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(resagemoth, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(resagemoth, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
```

```r
plot_smooth(resagemoth, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1, cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65), mgp=c(5,2,0)) #mgp=c(axis.title.position, axis.label.position, axis.line.position)
axis(2, pos=-0.5,cex.axis=3, mgp=c(2,1,0))

# 1.Ableitung= GrowthRate over age:
fd <- derivatives(resagemoth,c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
#write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age >= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
    geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
    theme_classic() + theme(axis.text.y = element_text(angle = 90, hjust = 0.5)) + theme(plot.margin = unit(c(40,36,10,59), "pt")) + #margin(t,r,b,l)
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40), legend.position = "none") +
    xlab("Age (years)") + ylab("") + scale_x_continuous(lim=c(0,65),expand=c(0,0.5),breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65))    #+ scale_y_continuous(breaks=c(-0.3,0,0.3))

# 1.Ableitung= change of GrowthRate over age - DIFF:
fdd <- derivatives(resstatagemoth, c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
fdd= fdd %>% filter(smooth %in% c("s(age):sexOm", "s(age):sexOf"))
fdd$sexO=stri_sub(fdd$smooth, -1,-1)
attach(fdd ,warn.conflicts = FALSE)
fdd= fdd %>% filter(!derivative==0 & sexO %in% c("m", "f")) %>% rename(age = data) %>% filter(age >= max(min(fdata$age),min(mdata$age)) & age <= min(max(fdata$age),max(mdata$age)))
attach(fdd ,warn.conflicts = FALSE)

ggplot(fdd, aes(x = age, y = derivative, colour = sexO, fill = sexO)) + scale_color_manual(values=c("black", "blue"))  + scale_fill_manual(values=c("black", "blue")) +
    geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
    theme_classic() + theme(axis.text.y = element_text(angle = 90, hjust = 0.5)) + theme(plot.margin = unit(c(40,36,10,59), "pt")) + #margin(t,r,b,l)
    theme(axis.title.x = element_text(face = "bold", size = 50),
```

```
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40), legend.position = "none") +
   xlab("Age (years)") + ylab("") + scale_x_continuous(lim=c(0,65),expand=c(0,0.5),breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65)) + scale_y_continuous(breaks=c(-
0.3,0,0.3))


###################################################################################################################################################
#Only individuals with data on arm length, body weight, testosterone AND DHEA

ndata= xdata %>% filter(age<=150 & age>=0 & AllVarFilter==1) %>% drop_na (sex,age,wildparityrearing) %>% group_by(name) %>% filter(n() >= 0)
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
attach(fdata ,warn.conflicts = FALSE)
attach(mdata ,warn.conflicts = FALSE)
par(mfrow=c(1,1)) # the first argument specifies the number of rows and the second the number of columns of plots.

# sex-specific change over age (= growth curves):
res <- gam(testosq ~  sex  + s(age,by= sex,bs = "cr",k=10, sp=1)  + s(age, wildparityrearing, bs = "fs", k=6) + s(daytime,bs = "cr",k=3)  + s(sampledate , zoo,bs = "fs", k=5, m=1)
+s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=6,m=1),method="ML", nthreads=8,data = ndata,select = F)
resstat <- gam(testosq ~  sexO  + s(age,bs = "cr",k=10, sp=1)  + s(age,by= sexO,bs = "cr",k=10, sp=1)  + s(age, wildparityrearing, bs = "fs", k=6) + s(daytime,bs = "cr",k=3)  +
s(sampledate , zoo,bs = "fs", k=5, m=1) +s(age,name, bs = "fs", k=3,m=1) + s(age,zoo, by=sex, bs = "fs", k=6,m=1),method="ML", nthreads=8,data = ndata,select = F)
null <- gam(testosq ~  1 + s(age, wildparityrearing, bs = "fs", k=6) + s(daytime,bs = "cr",k=3)  + s(sampledate , zoo,bs = "fs", k=5, m=1) +s(age,name, bs = "fs", k=3,m=1) +
s(age,zoo, by=sex, bs = "fs", k=6,m=1),method="ML", nthreads=8,data = ndata,select = F)
#acf_resid(res)
#gam.check(res)
summary(res, freq=TRUE)
summary(resstat, freq=TRUE)
compareML(null, resstat)

par(mar=c(7,7,4,3)) #mar = c(bottom, left, top, right)
plot_diff(res, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE,  col="gray70", cex.main=4, cex.lab=4,cex.axis=2.5, ylim=c(-1,2.5),
hide.label=T, yaxt="n",xaxt="n",mgp=c(5,2,0), las=2, main="Sex difference in Ln(Testosterone): Male minus female", xlab="Age (years)",  ylab="")
plot_diff(res, view="age", comp=list(sex=c("m","f")),xlim=c(max(min(fdata$age),min(mdata$age)),min(max(fdata$age),max(mdata$age))),shade=TRUE, mark.diff = TRUE,
rm.ranef=TRUE, col="black",add=TRUE)
axis(1, cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65), mgp=c(5,2,0)) #mgp=c(axis.title.position, axis.label.position, axis.line.position)
axis(2, pos=-0.5,cex.axis=3, mgp=c(2,1,0))
```

```
plot_data(res, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5,  hide.label=T, yaxt="n",xaxt="n",mgp=c(5,2,0), las=2, main="Ln(Testosterone)", xlab="Age (years)",  ylab="Ln(Testosterone)")
plot_data(res, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(res, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(res, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(res, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1, cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65), mgp=c(5,2,0)) #mgp=c(axis.title.position, axis.label.position, axis.line.position)
axis(2, pos=-0.5,cex.axis=3, mgp=c(2,1,0))


# 1.Ableitung= GrowthRate over age:
fd <- derivatives(res,c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
#write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age >= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
   theme_classic() + theme(axis.text.y = element_text(angle = 90, hjust = 0.5)) + theme(plot.margin = unit(c(40,36,10,59), "pt")) + #margin(t,r,b,l)
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40), legend.position = "none") +
   xlab("Age (years)") + ylab("") + scale_x_continuous(lim=c(0,65),expand=c(0,0.5),breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65))    #+ scale_y_continuous(breaks=c(-0.3,0,0.3))


# 1.Ableitung= change of GrowthRate over age - DIFF:
fdd <- derivatives(resstat, c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
fdd= fdd %>% filter(smooth %in% c("s(age):sexOm", "s(age):sexOf"))
fdd$sexO=stri_sub(fdd$smooth, -1,-1)
attach(fdd ,warn.conflicts = FALSE)
```

```r
fdd= fdd %>% filter(!derivative==0 & sexO %in% c("m", "f")) %>% rename(age = data) %>% filter(age >= max(min(fdata$age),min(mdata$age)) & age <= min(max(fdata$age),max(mdata$age)))
attach(fdd ,warn.conflicts = FALSE)

ggplot(fdd, aes(x = age, y = derivative, colour = sexO, fill = sexO)) + scale_color_manual(values=c("black", "blue"))  + scale_fill_manual(values=c("black", "blue")) +
    geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
    theme_classic() + theme(axis.text.y = element_text(angle = 90, hjust = 0.5)) + theme(plot.margin = unit(c(40,36,10,59), "pt")) + #margin(t,r,b,l)
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40), legend.position = "none") +
    xlab("Age (years)") + ylab("") + scale_x_continuous(lim=c(0,65),expand=c(0,0.5),breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65)) + scale_y_continuous(breaks=c(-0.3,0,0.3))
```

#R-CODE IGFBP3

```
#--------------------------------------------
```

#COPY VALUES FROM TABLE INTO R:

```
library(mgcv)
library(itsadug)
library(gratia)
library(dplyr)
library(tidyr)
library(stringi)
library(ggplot2)

xdata = read.table("clipboard", dec=".",header=T, na.strings=c("x","xxx"))
attach(xdata ,warn.conflicts = FALSE)
#hist(xdata)
xdata$sex=as.factor(xdata$sex)
xdata$sexO=ordered(xdata$sex, levels=c("f","m"))
xdata$sexO=as.ordered(xdata$sexO)
contrasts(xdata$sexO) <- "contr.treatment"
xdata$name=as.factor(xdata$name)
xdata$sire=as.factor(xdata$sire)
xdata$dam=as.factor(xdata$dam)
xdata$zoo=as.factor(xdata$zoo)
xdata$wildparityrearing=as.factor(xdata$wildparityrearing)
xdata$wildparityrearing=ordered(xdata$wildparityrearing, levels=c("w","p.mr","p.hr","m.mr","m.hr"))
xdata$wildparityrearing=as.ordered(xdata$wildparityrearing)
contrasts(xdata$wildparityrearing) <- "contr.treatment"
xdata$IGFBPsq=log(xdata$IGFBP_SG)
attach(xdata ,warn.conflicts = FALSE)
```

#R-CODE statistics:

```
ndata= xdata %>% drop_na (sex,age) #Same model but without gestation values: no difference
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
par(mfrow=c(1,1))
```

```
# sex-specific change over age (= growth curves):
res <- gam(IGFBPsq~  sex  +  s(age,by= sex,bs = "cr",k=5) + s(daytime, bs="cr", k=3) + s(age,zoo, bs = "fs",k=3,m=1)  +s(name, bs = "re"),method="ML", data = ndata,select = F)
resstat <- gam(IGFBPsq  ~  sexO  +  s(age,bs = "cr",k=5)  + s(age,by= sexO,bs = "cr",k=5) + s(daytime, bs="cr", k=3) + s(age,zoo,bs = "fs",k=3,m=1)  +s(name, bs = "re"),method="ML", data = ndata,select = F)
null <- gam(IGFBPsq  ~  1 +  daytime + s(age,zoo,bs = "fs",k=3,m=1)  +s(name, bs = "re"),method="ML", data = ndata,select = F)
#acf_resid(res)
#gam.check(res)
compareML(null, res)
summary(res, freq=TRUE)
summary(resstat, freq=TRUE)
#write.table(residuals(res,type="response"), file="clipboard-16384", sep="\t")

par(mar=c(7,7,4,3)) #mar = c(bottom, left, top, right)
plot_diff(res, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE,  col="white", cex.main=4, cex.lab=4,cex.axis=2.5, ylim=c(-1.5,2),xlim=c(0,65), hide.label=T, yaxt="n",xaxt="n",mgp=c(5,2,0), las=2, main="Sex difference in Ln(IGFBP-3): Male minus female", xlab="Age (years)",  ylab="")
#plot_diff(res, view="age", comp=list(sex=c("m","f")),xlim=c(min(min(fdata$age),min(mdata$age)),max(max(fdata$age),max(mdata$age))),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE, col="grey70",add=TRUE)
plot_diff(res, view="age", comp=list(sex=c("m","f")),xlim=c(max(min(fdata$age),min(mdata$age)),min(max(fdata$age),max(mdata$age))),shade=TRUE, mark.diff = TRUE, rm.ranef=TRUE, col="black",add=TRUE)
axis(1, cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65), mgp=c(5,2,0)) #mgp=c(axis.title.position, axis.label.position, axis.line.position)
axis(2, pos=-0.5,cex.axis=3, mgp=c(2,1,0))
plot_data(res, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5,  hide.label=T, yaxt="n",xaxt="n",mgp=c(5,2,0), las=2, main="Ln(IGFBP-3)", xlab="Age (years)",  ylab="Ln(IGFBP-3)")
plot_data(res, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(res, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(res, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(res, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1, cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65), mgp=c(5,2,0)) #mgp=c(axis.title.position, axis.label.position, axis.line.position)
axis(2, pos=-0.5,cex.axis=3, mgp=c(2,1,0))


# 1.Ableitung= GrowthRate over age:
fd <- derivatives(res,c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
#write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
```

```
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age >= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
    geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
    theme_classic() + theme(axis.text.y = element_text(angle = 90, hjust = 0.5)) + theme(plot.margin = unit(c(40,36,10,59), "pt")) + #margin(t,r,b,l)
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40), legend.position = "none") +
    xlab("Age (years)") + ylab("") + scale_x_continuous(lim=c(0,65),expand=c(0,0.5),breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65))    #+ scale_y_continuous(breaks=c(-0.3,0,0.3))

# 1.Ableitung= change of GrowthRate over age - DIFF:
fdd <- derivatives(resstat, c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
fdd= fdd %>% filter(smooth %in% c("s(age):sexOm", "s(age):sexOf"))
fdd$sexO=stri_sub(fdd$smooth, -1,-1)
attach(fdd ,warn.conflicts = FALSE)
fdd= fdd %>% filter(!derivative==0 & sexO %in% c("m", "f")) %>% rename(age = data) %>% filter(age >= max(min(fdata$age),min(mdata$age)) & age <= min(max(fdata$age),max(mdata$age)))
attach(fdd ,warn.conflicts = FALSE)

ggplot(fdd, aes(x = age, y = derivative, colour = sexO, fill = sexO)) + scale_color_manual(values=c("black", "blue"))  + scale_fill_manual(values=c("black", "blue")) +
    geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
    theme_classic() + theme(axis.text.y = element_text(angle = 90, hjust = 0.5)) + theme(plot.margin = unit(c(40,36,10,59), "pt")) + #margin(t,r,b,l)
    theme(axis.title.x = element_text(face = "bold", size = 50),
          axis.title.y = element_text(face = "bold", size = 50),
          axis.text.x = element_text(size = 40),
          axis.text.y = element_text(size = 40), legend.position = "none") +
    xlab("Age (years)") + ylab("") + scale_x_continuous(lim=c(0,65),expand=c(0,0.5),breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65)) + scale_y_continuous(breaks=c(-0.5,0,0.5))


#SingleLinePlots for comparison plot
#fdm=fd %>% filter(sex=="m")
#fdf=fd %>% filter(sex=="f")
```

```
ggplot(fdNS, aes(x = age, y = derivative)) + geom_line(size = 3,linetype=5, color="black") +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
        legend.position="none") +
   xlab("Age (years)") + ylab("Male growth rate (IGFBP3/year)") + scale_x_continuous(lim=c(0,20), expand=c(0,0.5),breaks = seq(0, 60, by = 5))

pp <- get_predictions(resNoSex, cond=list(age=seq(0,60,length=1000)))
#fdm=pp %>% filter(sex=="m")
#fdf=pp %>% filter(sex=="f")

ggplot(pp, aes(x = age, y = fit)) + geom_line(size = 3,linetype=5, color="black") +
   theme_classic() + theme(axis.text.y=element_text(angle=90, hjust=0.5)) + theme(plot.margin=unit(c(40,36,10,59), "pt")) +
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40),
        legend.position="none") +
   xlab("Age (years)") + ylab("Male level (IGFBP3)") + scale_x_continuous(lim=c(0,20), expand=c(0,0.5),breaks = seq(0, 60, by = 5))


######################################################################################
#AGEMOTH
# sex-specific change over age (= growth curves): daytime could only be implemented as linear control variable, due to sample size constraints!
ndata= xdata %>% filter(age<=150 & age>=0 & !wildparityrearing=="w") %>% drop_na (sex,age) %>% group_by(name) %>% filter(n() >= 0) #Same model but without gestation values: no difference
fdata=ndata %>% filter(sex=="f")
mdata=ndata %>% filter(sex=="m")
resagemoth <- gam(IGFBPsq~  sex + wildparityrearing + s(age,by= sex,bs = "cr",k=5)  + te(age,agemoth,bs = "cr",k=c(3,3)) + daytime + s(age,zoo, bs = "fs",k=3,m=1) +s(sire, bs = "re")+s(dam, bs = "re"),method="ML", data = ndata,select = F)
resstatagemoth <- gam(IGFBPsq  ~  sexO  + wildparityrearing + s(age ,bs = "cr",k=5) + s(age,by= sexO,bs = "cr",k=5) + s(agemoth ,bs = "cr",k=3)+ ti(age,agemoth,bs = "cr",k=c(3,3)) + daytime + s(age,zoo, bs = "fs",k=3,m=1) +s(sire, bs = "re")+s(dam, bs = "re"),method="ML", data = ndata,select = F)
nullagemoth <- gam(IGFBPsq  ~  1 + wildparityrearing + daytime + s(age,zoo, bs = "fs",k=3,m=1) +s(sire, bs = "re")+s(dam, bs = "re"),method="ML", data = ndata,select = F)
#acf_resid(resagemoth)
#gam.check(resagemoth)
```

```
compareML(nullagemoth, resagemoth)
summary(resagemoth, freq=TRUE)
summary(resstatagemoth, freq=TRUE)


par(mar=c(7,7,4,3)) #mar = c(bottom, left, top, right)
plot_diff(resagemoth, view="age", comp=list(sex=c("m","f")),shade=TRUE, mark.diff = FALSE, rm.ranef=TRUE,  col="gray70", cex.main=4, cex.lab=4,cex.axis=2.5, ylim=c(-3,3), hide.label=T, yaxt="n",xaxt="n",mgp=c(5,2,0), las=2, main="Sex difference in Ln(IGFBP3): Male minus female", xlab="Age (years)",  ylab="")
plot_diff(resagemoth, view="age", comp=list(sex=c("m","f")),xlim=c(max(min(fdata$age),min(mdata$age)),min(max(fdata$age),max(mdata$age))),shade=TRUE, mark.diff = TRUE, rm.ranef=TRUE, col="black",add=TRUE)
axis(1, cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65), mgp=c(5,2,0)) #mgp=c(axis.title.position, axis.label.position, axis.line.position)
axis(2, pos=-0.5,cex.axis=3, mgp=c(2,1,0))
plot_data(resagemoth, view="age", cond=list(sex=c("f","m")), rm.ranef=TRUE, input="data", col="white", cex.main=4, cex.lab=4,cex.axis=2.5,  hide.label=T, yaxt="n",xaxt="n",mgp=c(5,2,0), las=2, main="Ln(IGFBP3)", xlab="Age (years)",  ylab="Ln(IGFBP3)", ylim=c(0,5))
plot_data(resagemoth, view="age", cond=list(sex="f"), rm.ranef=TRUE, input="data", col="red3",alpha = 0.5, cex=1.2,add=TRUE)
plot_data(resagemoth, view= "age", cond=list(sex="m"), rm.ranef=TRUE, input="data", col="blue",alpha = 0.5, cex=1.2,add=TRUE)
plot_smooth(resagemoth, view="age", cond=list(sex="f") ,xlim=c(min(fdata$age),max(fdata$age)), rm.ranef=TRUE, rug= FALSE, col="red3", add=TRUE)
plot_smooth(resagemoth, view="age", cond=list(sex="m"),xlim=c(min(mdata$age),max(mdata$age)), rm.ranef=TRUE, rug= FALSE, col="blue", add=TRUE)
axis(1, cex.axis=3,at=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65), mgp=c(5,2,0)) #mgp=c(axis.title.position, axis.label.position, axis.line.position)
axis(2, pos=-0.5,cex.axis=3, mgp=c(2,1,0))


# 1.Ableitung= GrowthRate over age:
fd <- derivatives(resagemoth,c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
#write.table(fd, file="clipboard-16384", sep="\t")
fd= fd %>% filter(smooth %in% c("s(age):sexf", "s(age):sexm"))
fd$sex=stri_sub(fd$smooth, -1,-1)
attach(fd ,warn.conflicts = FALSE)
fd= fd %>% filter(!derivative==0 & sex %in% c("f", "m")) %>% rename(age = data) %>% filter((sex=="f" & age >= min(fdata$age) & age <= max(fdata$age)) | (sex=="m" & age >= min(mdata$age) & age <= max(mdata$age)))
attach(fd ,warn.conflicts = FALSE)
#write.table(pp, file="clipboard-16384", sep="\t")

ggplot(fd, aes(x = age, y = derivative, colour = sex, fill = sex)) + scale_color_manual(values=c("red3", "blue"))  + scale_fill_manual(values=c("red3", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
   theme_classic() + theme(axis.text.y = element_text(angle = 90, hjust = 0.5)) + theme(plot.margin = unit(c(40,36,10,59), "pt")) + #margin(t,r,b,l)
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
```

```
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40), legend.position = "none") +
   xlab("Age (years)") + ylab("") + scale_x_continuous(lim=c(0,65),expand=c(0,0.5),breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65))    #+ scale_y_continuous(breaks=c(-0.3,0,0.3))

# 1.Ableitung= change of GrowthRate over age - DIFF:
fdd <- derivatives(resstatagemoth, c(1,2), n=1000, ncores=8, interval = "confidence", frequentist = F)
fdd= fdd %>% filter(smooth %in% c("s(age):sexOm", "s(age):sexOf"))
fdd$sexO=stri_sub(fdd$smooth, -1,-1)
attach(fdd ,warn.conflicts = FALSE)
fdd= fdd %>% filter(!derivative==0 & sexO %in% c("m", "f")) %>% rename(age = data) %>% filter(age >= max(min(fdata$age),min(mdata$age)) & age <= min(max(fdata$age),max(mdata$age)))
attach(fdd ,warn.conflicts = FALSE)

ggplot(fdd, aes(x = age, y = derivative, colour = sexO, fill = sexO)) + scale_color_manual(values=c("black", "blue"))  + scale_fill_manual(values=c("black", "blue")) +
   geom_line(size = 1.2) +  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.2, colour = NA) +
   theme_classic() + theme(axis.text.y = element_text(angle = 90, hjust = 0.5)) + theme(plot.margin = unit(c(40,36,10,59), "pt")) + #margin(t,r,b,l)
   theme(axis.title.x = element_text(face = "bold", size = 50),
        axis.title.y = element_text(face = "bold", size = 50),
        axis.text.x = element_text(size = 40),
        axis.text.y = element_text(size = 40), legend.position = "none") +
   xlab("Age (years)") + ylab("") + scale_x_continuous(lim=c(0,65),expand=c(0,0.5),breaks=c(0,5,10,15,20,25,30,35,40,45,50,55,60,65)) + scale_y_continuous(breaks=c(-0.3,0,0.3))
```