```
library(ggplot2) install.packages(c("glmtoolbox","ssym","sf"))
data(richness,package="glmtoolbox") ggplot(richness, aes(x=Biomass,y=Species,color=pH,shape=pH)) +
geom smooth(method="lm",formula=y ~ x,se=FALSE,size=1,linetype="solid") + geom point(size=2.75) +
scale_y_continuous(breaks=seq(from=0,to=45,by=5)) + scale_x_continuous(breaks=seq(from=0,to=10,by=1)) +
labs(title="Species richness",x="Biomass",y="Number of plant species", color="Soil pH\n level",shape="Soil pH\n level")
+ scale color manual(values=c("red","black","blue")) + scale shape manual(values=c(15,16,17)) + mitema
data(Ovocytes,package="ssym") ggplot(Ovocytes, aes(x=time,y=fraction,color=type,shape=type)) +
geom smooth(method="gam",formula=y ~ s(x,bs="cr",sp=40),se=FALSE,linetype="solid") + geom point(size=2.75) +
scale_x_continuous(breaks=seq(from=0,to=20,by=2.5)) + scale_y_continuous(breaks=seq(from=0.2,to=1.0,by=0.1)) +
labs(title="Hyper-osmotic test on goat ovocytes", x="Time since exposition to propanediol", y="Fraction of initial cell
volume", color="Stage of \nthe ovocytes", shape="Stage of \nthe ovocytes") +
scale_color_manual(values=c("red","black")) + scale_shape_manual(values=c(15,16)) + mitema
data(depression,package="glmtoolbox") ggplot(depression,aes(x=factor(visit),y=dep,fill=group)) + geom_boxplot() +
scale y continuous(breaks=seg(from=0.to=30.by=5)) + labs(title="Treatment for severe postnatal depression",
x="Months since the treatment began", y="Postnatal Depression Scale", fill="Type of patches") + scale_fill_manual(values=c("salmon2", "green2")) + mitema
data(cellular,package="glmtoolbox") ggplot(cellular,aes(factor(tnf))) +
geom bar(aes(fill=factor(ifn),weight=0.5*cells),position=position dodge(),color="black") +
scale y continuous(breaks=seg(from=0,to=100,by=20)) + labs(title="Agents to stimulate cellular differentiation".
x="Dose of TNF, in U/ml", y="% of differentiated cells", fill="Dose of IFN,\n in U/ml") + scale fill brewer(palette="Reds")
library(readxl) library(dplyr) mundoshp <- sf::st_read("admin00.shp",quiet=TRUE) usashp <- mundoshp %>%
filter(CNTRY_NAME=="United States" & ADMIN_NAME!="Alaska" & ADMIN_NAME!="Hawaii") counties <-
read_excel("counties.xlsx") elections <- read_excel("elections.xlsx") usa <- elections %>%
inner_join(counties,by=c("codecounty"="codecounty")) %>% mutate(codestate2=paste0("US",codestate)) %>%
group by(year,codestate2) %>% summarise(y=100*sum(democrat)/sum(democrat+republic+other)) usa2 <- usashp
%>% inner_join(usa,by=c("FIPS_ADMIN"="codestate2")) %>% filter(year > 2000) ggplot(usa2) +
geom sf(aes(fill=y),col="darkgray",linetype="solid") +
geom_sf text(aes(label=ADMIN_NAME),col="black",fontface="bold",size=1.75,
check overlap=TRUE,fun.geometry=function(x) sf::st centroid(x)) + labs(x="Longitud",y="Latitud",title="Elecciones
Presidenciales USA", fill="% de votos\npor el partido\ndemócrata") +
scale_fill_gradient(low="white",high="red",n.breaks=5) +
facet wrap(vars(year),ncol=2,nrow=2,strip.position="top",dir="h",scales="fixed") + mitema
```