Grafiken

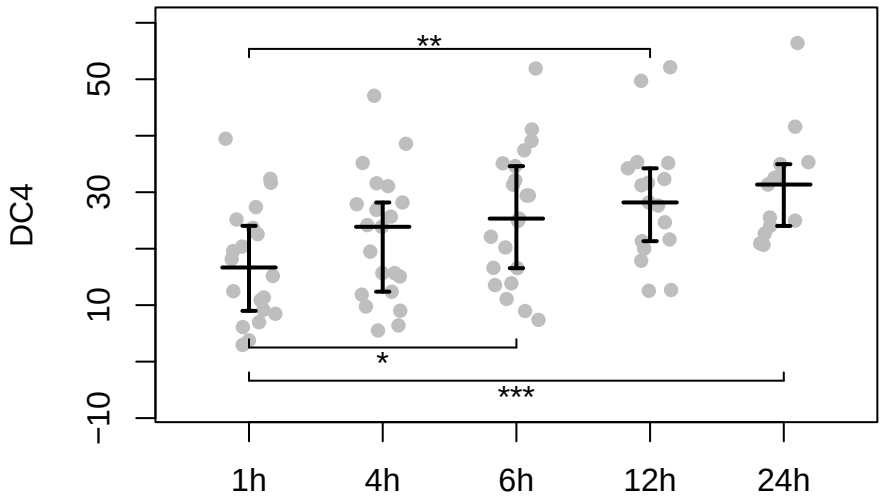
Funktionen

- Theme for lattice-plots set_lattice(), reset_lattice() und lattice::trellis.par.set(bw_theme(farbe()))
- auto_plot Einzelne lattice plots analog wie die Funktion Tabelle()
- Boxplot bwplot2()
- plot.bland_altman()
- Hilfsfunktionen wrap_sentence(), stp25plot:::plot.efflist()

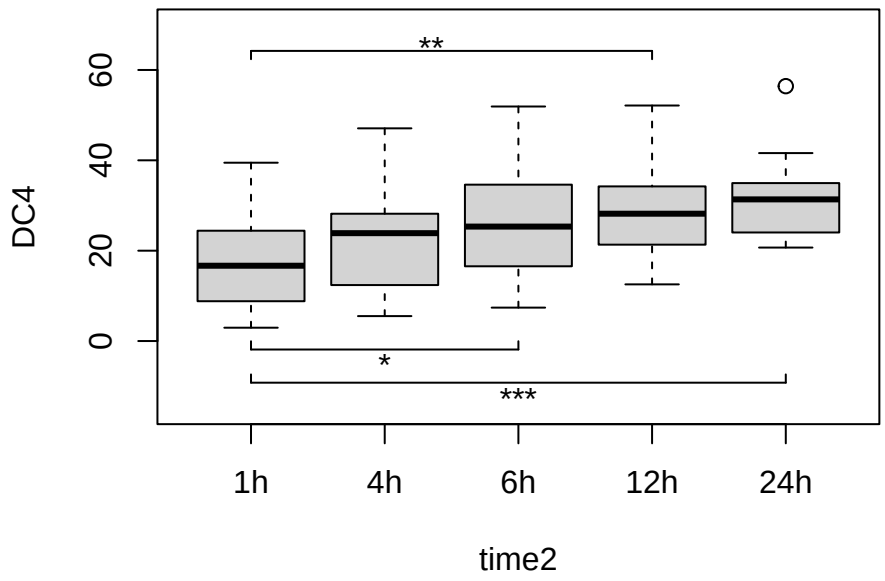
Signifikanz-Plot

Der Fliegen-Schiss-Plot mein absoluter lieblings Plot!!

```
#dat1 <- Long(dat, DC4 ~ nmp + time2, value = "DC4")
#fit2 <- lmer(DC4 ~ time2 + (1 | nmp), data = dat1)

fit1 <- lm(DC4 ~ time2, data = dat)
em1 <- emmeans(fit1, list(pairwise ~ time2), adjust = "tukey")
#em2 <- emmeans(fit2, list(pairwise ~ time2))
prism.plots(
  DC4 ~ time2,
  data = dat,
  #fun = mean,
  ylim = c(-8, 60)
)
plotSigBars(fit1)
```

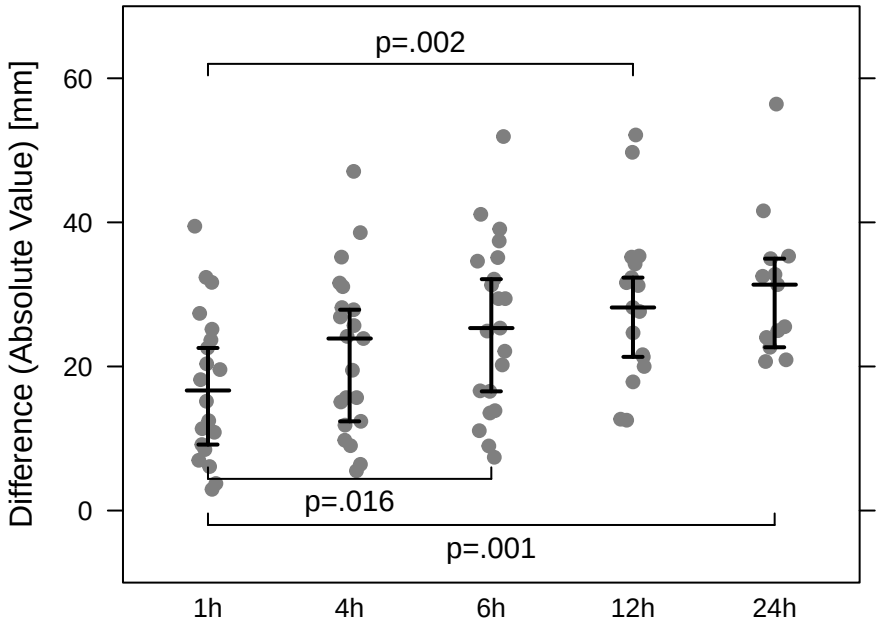



```
boxplot(  DC4 ~ time2,
          data = dat,
          ylim = c(-15, 70))

plotSigBars(fit1, stars=FALSE)
```

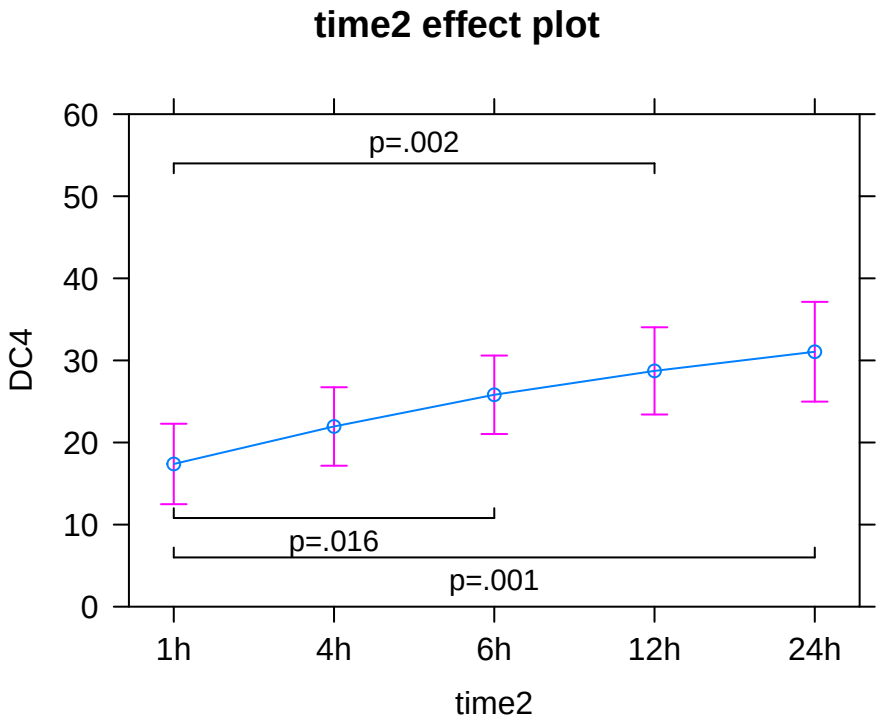



```
#plotSigBars(em1, stars=FALSE)
```

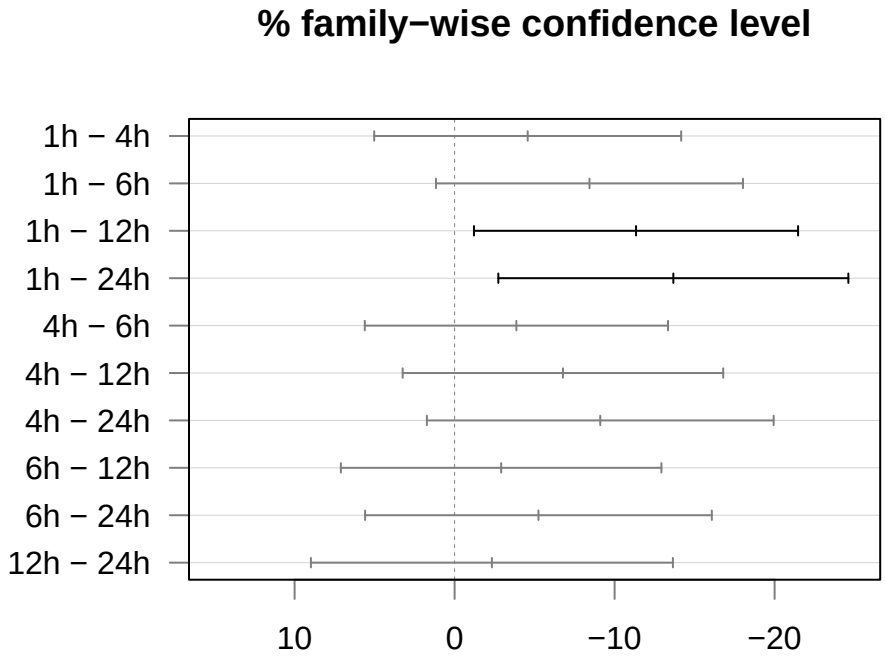
```
#stripplot(  DC4 ~ time2,  data = dat, jitter.data=TRUE,pch=20, col="gray50")

stripplot(
  DC4 ~ time2,
  data = dat, ylim=c(-10,70),
  ylab = "Difference (Absolute Value) [mm]", jitter.data=TRUE,
  panel = function(x, y, ...) {
    # panel.conf.int(x, y, ...)
    panel.stripplot(x,y, pch=19, col="gray50",...)
    #panel.points(x,y, pch=19,...)
    #panel.mean(x,y,  ...)
    panel.median(x,y, ...)
    panel.sig.bars(fit1, include.stars = FALSE, offset = .4)
  }
)
```




```
#require(latticeExtra)
#require(effects)
fit1 <- lm(DC4 ~ time2, data = dat)

p2<- plot(effect("time2", fit1), ylim=c(0,60))
p2 +  latticeExtra::layer( panel.sig.bars(fit1, include.stars = FALSE) )
```




```
require(emmeans)
plot_differenz <-
  function (x, ...)
  {
    cis <- as.data.frame(confint(x))
    x <- as.data.frame(x)
    xx <-
      cbind(
        diff = cis$estimate,
        lwr = cis$lower.CL,
        upr = cis$upper.CL,
        p.value = x$p.value
      )
    row.names(xx) <- cis$contrast
    psig <- ifelse( x$p.value<.1, "black", "gray50")
    stats:::plot.TukeyHSD(list(x = as.matrix(xx)), col=psig, ...)
    xx
  }
op=par(mar=c(4.2, 5, 3.8, 2))
fit1 %>%
  emmeans("time2") %>%
  pairs() %>%
  plot_differenz(las = 1, xlim =c(15, -25))
```

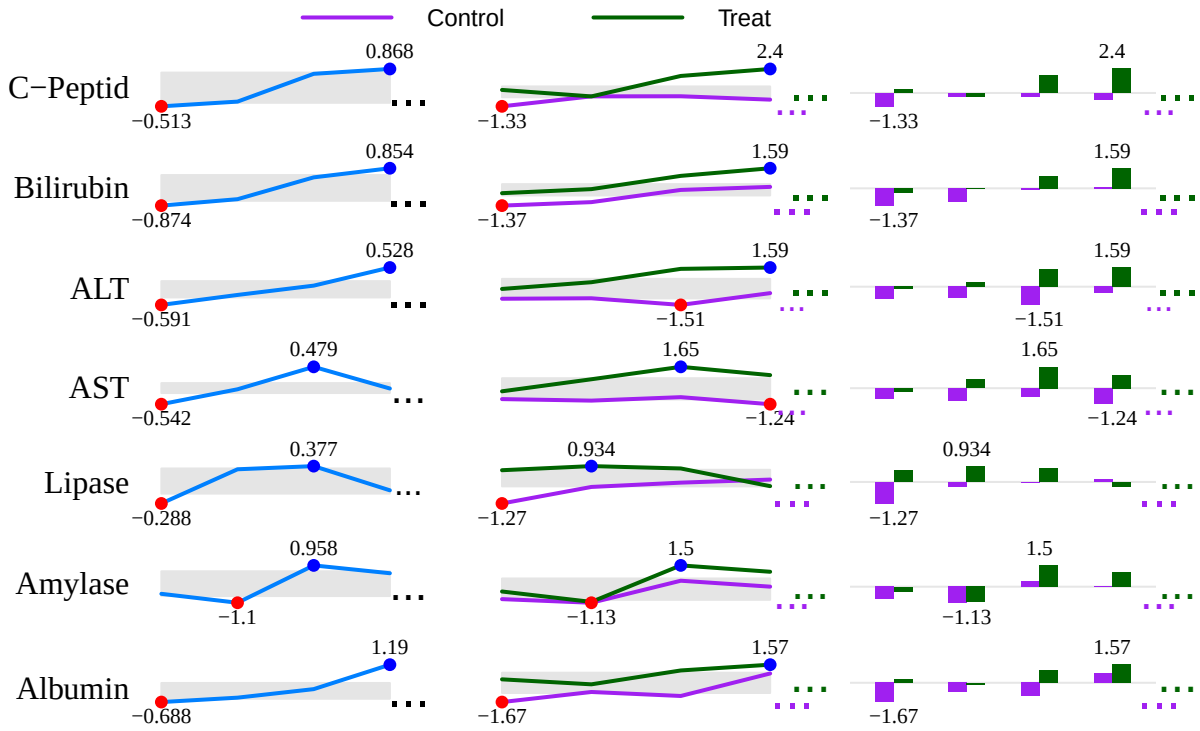



```
##                 diff       lwr       upr    p.value
## 1h - 4h    -4.567907 -14.16111  5.025301 0.67556397
## 1h - 6h    -8.430068 -18.02328  1.163140 0.11248355
## 1h - 12h  -11.339568 -21.46837 -1.210768 0.02027568
## 1h - 24h  -13.671896 -24.61063 -2.733167 0.00682780
## 4h - 6h    -3.862161 -13.33766  5.613334 0.78729677
## 4h - 12h   -6.771661 -16.78904  3.245721 0.33406688
## 4h - 24h   -9.103990 -19.93963  1.731654 0.14212665
## 6h - 12h   -2.909500 -12.92688  7.107883 0.92716613
## 6h - 24h   -5.241829 -16.07747  5.593815 0.66236834
## 12h - 24h  -2.332329 -13.64489  8.980236 0.97847868
```

```
par(op)
```

Sparkplot

Stolen from http://www.motioninsocial.com/tufte/#sparklines



Auto-Plot auto_plot()

Die Funktion klebt lattice- plots zu einer matrix zusammen.

Verwendung: auto_plot(formula, data) oder data %>% auto_plot(var_x, var_y, var_z) Die Funktion kann dabei Formel wie z.B. $a + b + c \sim g$

$a[box] + b[bar] + c[dot] \sim g$

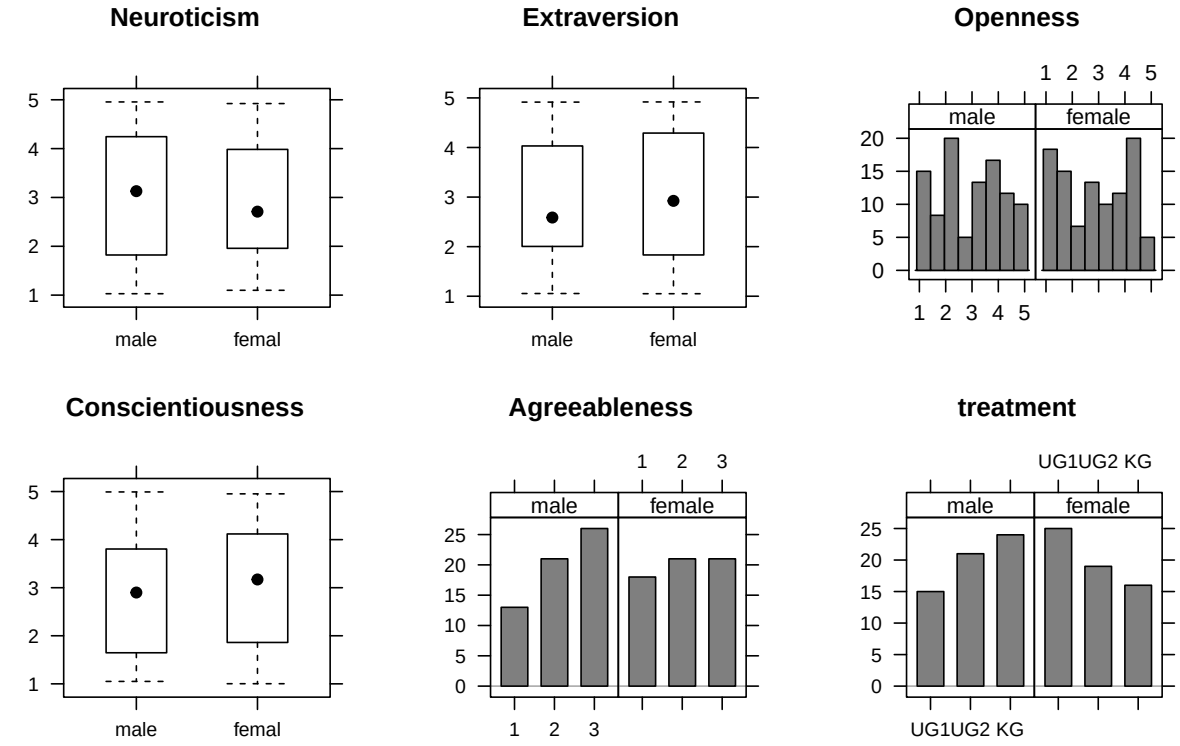
$log(a) + b + c \sim g$

$y \sim a + b + c$

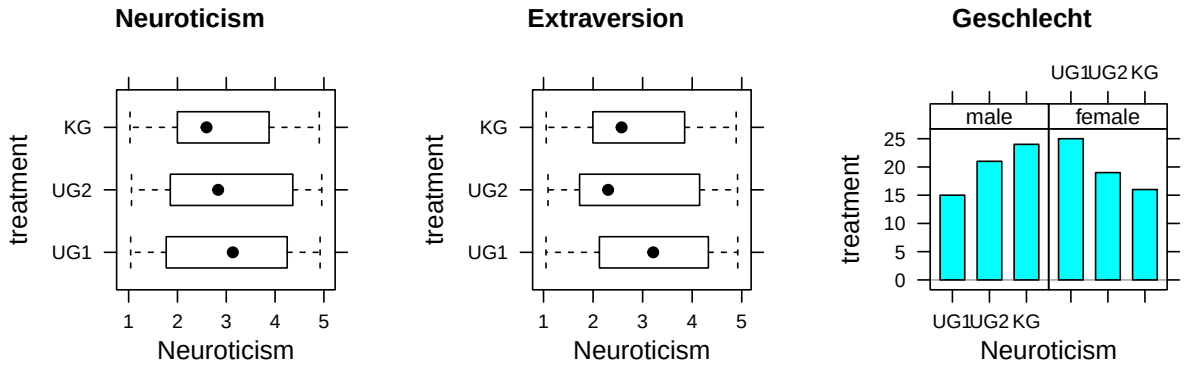
https://www.zahlen-kern.de/editor/

```
DF %>% auto_plot(
  n,
  e[box],
  o[hist],
  g,
  a,
  treatment,
  by =  ~ sex,
  par.settings = bw_theme()
)
```

```
##
##  in multi_av_plot
```



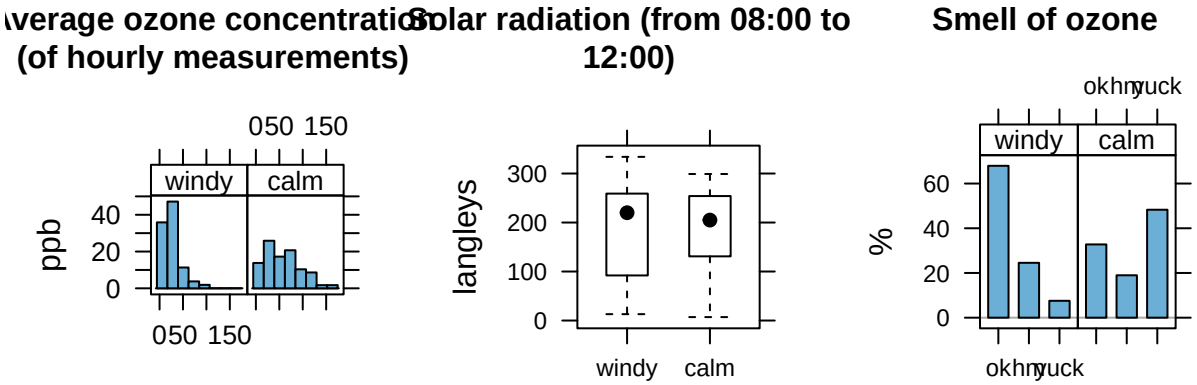

```
auto_plot(treatment ~ n + e + sex, DF)
```

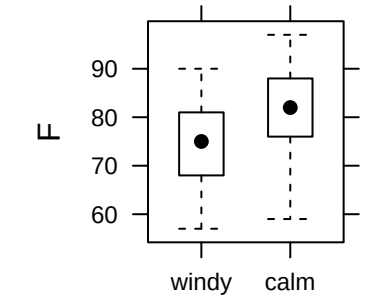



```
auto_plot(
  enviro2,
  ozone[hist],
  radiation,
  smell,
  temperature,
  by =  ~ is.windy,
  col.bar=  farbe("Blues")[3],
  ylab= c("ppb", "langleys",  "%",  "F"),
  include.percent=TRUE,
  wrap.main=30
 # levels.logical = c(TRUE, FALSE),
```

```
#  labels.logical = c("ja", "nein")
)
```

```
##
##  in multi_av_plot
```

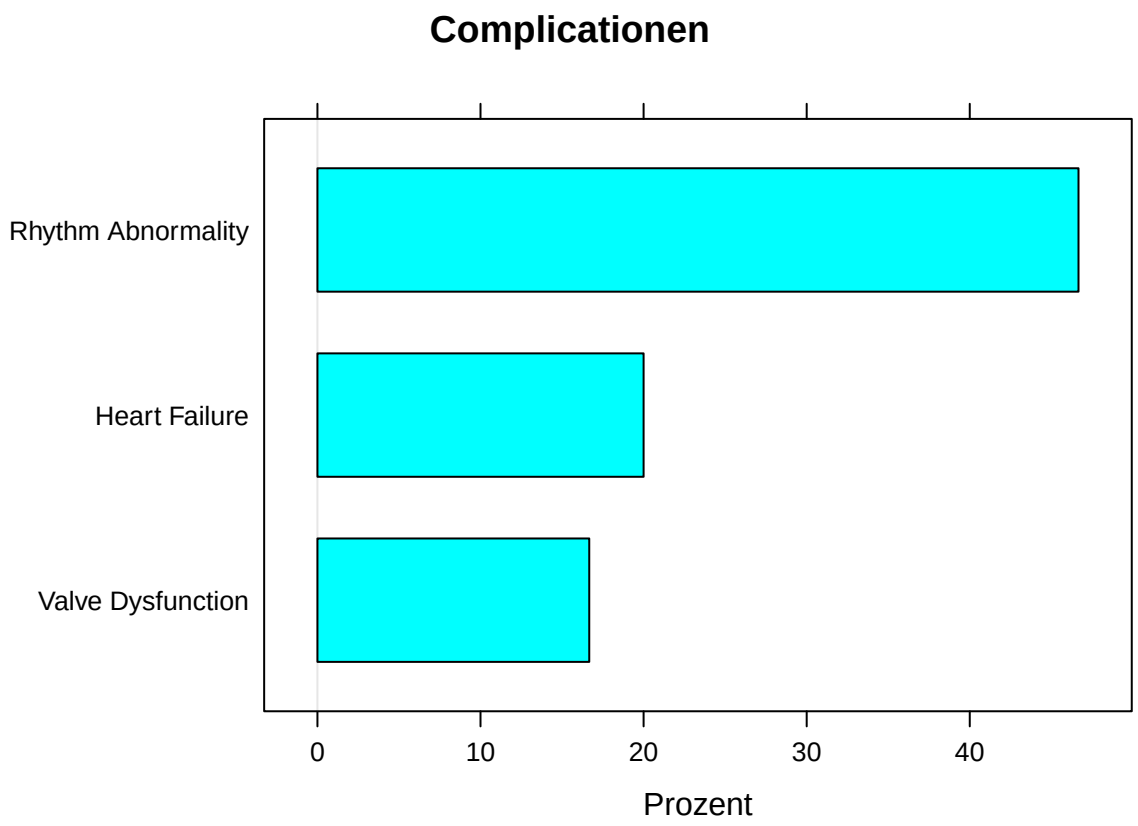




Mehrfachantworten mit multi_barplot().

```
# dat2[1:5] %>%
#   multi_barplot()
#
# dat2 %>%
#   multi_barplot(. ~ gender,
#                 reorder = TRUE,
#                 last = c("Others" ))
#
# dat2[1:5] %>%
#   auto_plot()
#
# dat2 %>%
#   auto_plot(. ~ gender)


dat2 %>%  auto_plot(comp_1, comp_2, comp_3 ,
                    include.percent=TRUE,
```

```
                    include.reorder=TRUE,
                    main ="Complicationen",
                    xlab= "Prozent")
```



set_lattice()

~Initialisieren der Lattice - Optionen mit set_lattice(). Im Hintergrund werden die latticeExtra::ggplot2like.opts() aufgerufen und die default Werte in opar und oopt gespeichert um sie mit reset_lattice() zurück seten zu können.~

```
reset_lattice()

p1<-barchart(xtabs(~treatment + sex + a,  DF),
             auto.key=list(space="top", columns=3,
                           cex=.7, between=.7 ),
             par.settings= standard_theme())
p2<-barchart(xtabs(~ treatment + sex + a,  DF),
             auto.key=list(space="top", columns=3,
                           cex=.7, between=.7 ),
             par.settings=bw_theme())
p3<-barchart(xtabs(~ treatment + sex + a,  DF),
             auto.key=list(space="top", columns=3,
```

```
                            cex=.7, between=.7 ),
              par.settings=ggplot_theme())

grid.arrange(p1, p2, p3, ncol=3)
```

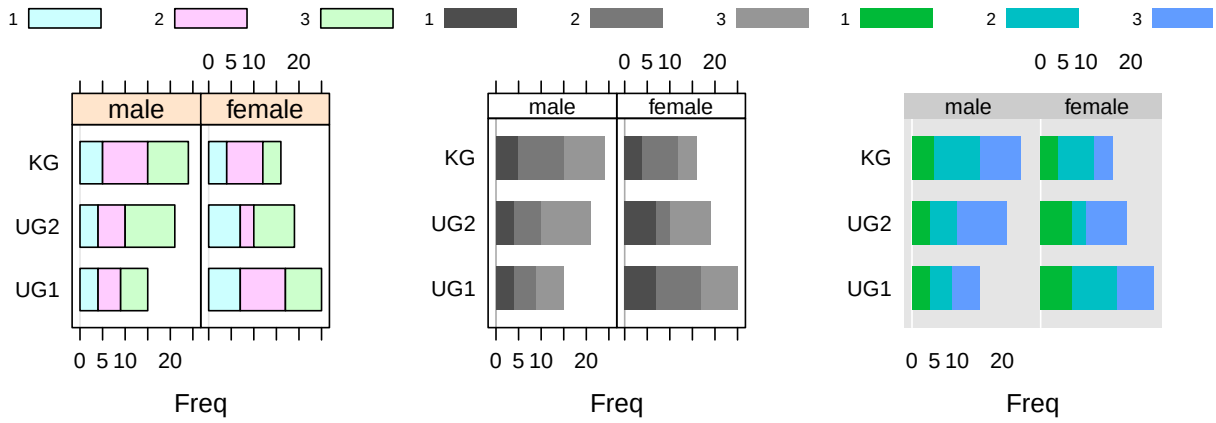


Figure 1: Plot mit grid.arrange - hier muss das Theme mit par.settings= set_lattice() uebergeben werden

Einbetten von set_lattice() über update()

```
obj <-
  xyplot(
    Sepal.Length + Sepal.Width ~ Petal.Length + Petal.Width,
    iris, type = c("p", "r"),
    jitter.x = TRUE, jitter.y = TRUE, factor = 5,
    auto.key = list(
      cex.title = 1.2,
      title = "Expected Tau",
      text = c("30 ms", "80 ms", "130 ms", "180 ms"),
      space = "top" # lines = TRUE, rectangles = TRUE
    ))

obj <- update(obj,
              legend = list(
                right =
                  list(fun = "draw.colorkey",
                       args = list(list(at = 0:100)))))

p1 <- update(obj, par.settings = custom.theme( ))
p2 <- update(obj, par.settings = ggplot_theme())
p3 <- update(obj, par.settings = bw_theme(), axis = axis.grid)

grid.arrange(p1, p2, p3, ncol = 3)
```

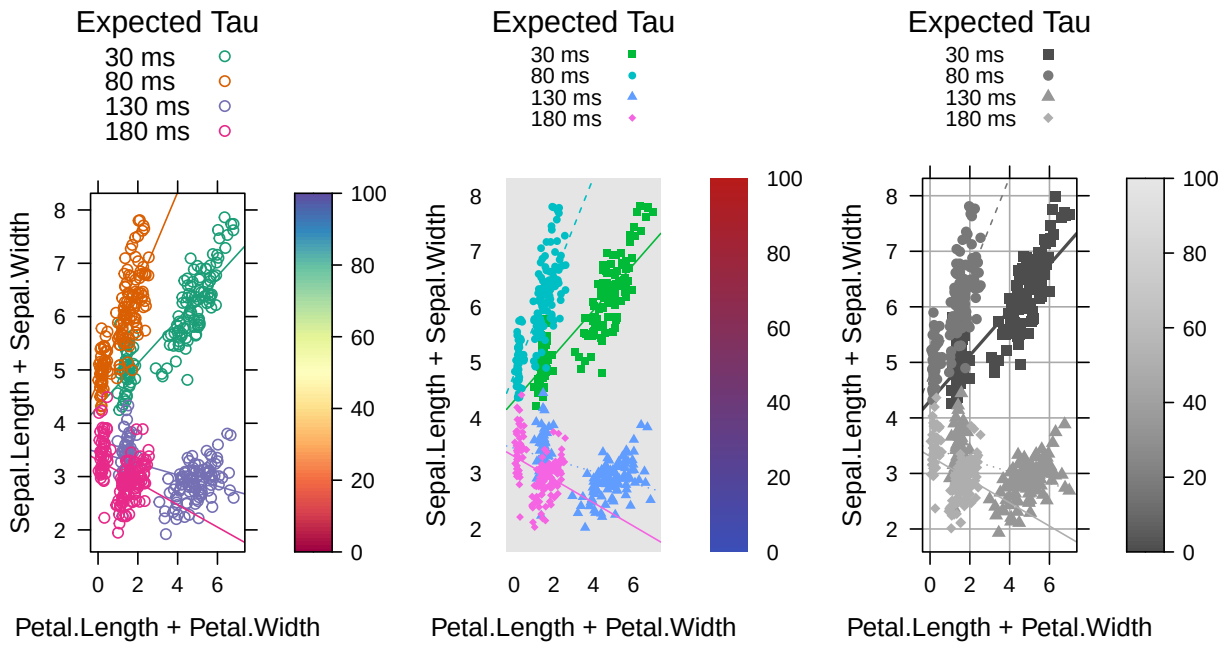
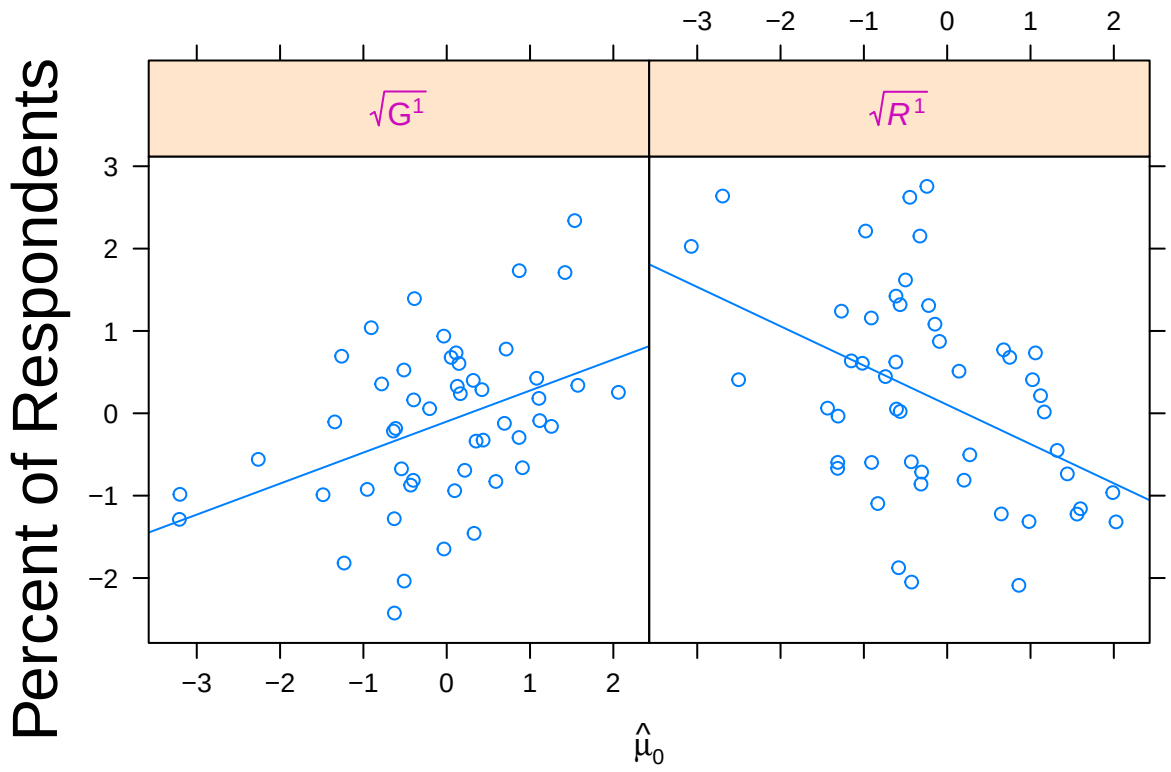


Figure 2: Plot mit grid.arrange und update

strip Sonderzeichen + Größe

```
 x1<-rnorm(100);  x2<-gl(2, 50, labels = c("Control", "Treat"))
 y<-(1.5-as.numeric(x2))*x1+rnorm(100)
#windows(7,4)
p1<- xyplot(y~x1|x2,
            xlab = expression(hat(mu)[0]),
            type=(c("p", "r")),
            # - auch mit fontsize=20
            ylab=list(label="Percent of Respondents", cex=2),
            par.strip.text=list(lines=2.5, col=6),
            strip=strip.custom(factor.levels=
                               expression(
                                 sqrt(G^{1}), sqrt(italic(R)^{1}))))
 print(p1)
```



bwplot2

Lattice bwplot mit groups. Ist eine erweiterung von lattice::bwplot. Die Funktion arbeitet mit panel.superpose.

```
p1 <- bwplot2(
  yield ~ site,
  data = barley, groups = year, main="bwplot2()", par.settings = bw_theme(),
  auto.key = list(points = FALSE, rectangles = TRUE, space = "right")

)

p2 <-
  bwplot(
    yield ~ site,
    barley,groups = year, main="panel.superpose", par.settings = bw_theme(),
    auto.key = list(points = FALSE, rectangles = TRUE, space = "right"),
    box.width = 1 / 4,
    panel = function(x, y, groups, subscripts, ...) {
      xx <-
        as.numeric(x) + scale(as.numeric(groups), scale = FALSE)/(nlevels(groups)+1)
      panel.superpose(
        xx,  y,  ...,
        panel.groups = panel.bwplot,
        groups = groups,
```

```
        subscripts = subscripts
      )
    }
  )


grid.arrange(p1, p2)
```

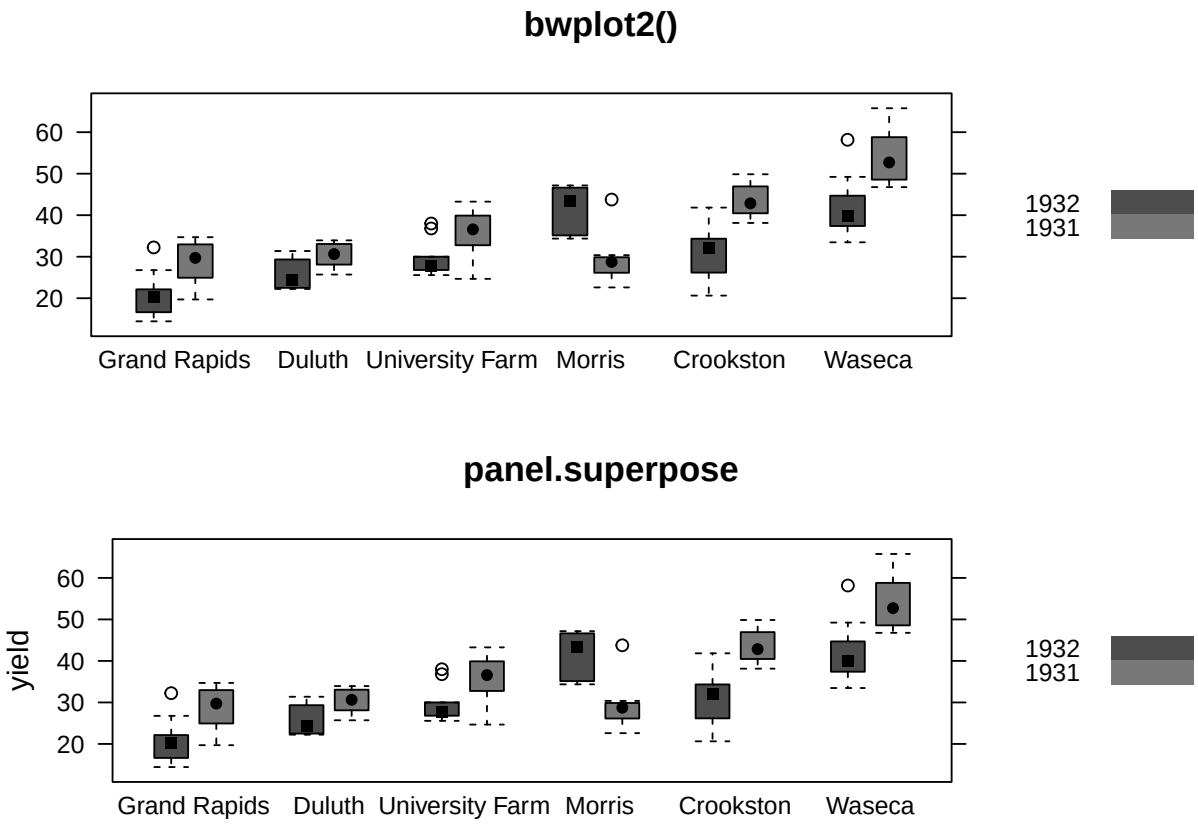


Figure 3: Boxplot mit bwplot2() und panel.superpose()

```
bwplot(yield ~ site, data = barley, groups=year,
       pch = "|", box.width = 1/3,
       auto.key = list(points = FALSE, rectangles = TRUE, space = "right"),
       panel = panel.superpose,
       panel.groups = function(x, y, ..., group.number) {
         panel.bwplot(x + (group.number-1.5)/3, y, ...)
         mean.values <- tapply(y, x, mean)
         panel.points(x + (group.number-1.5)/3, mean.values[x], pch=17)
}


)
```

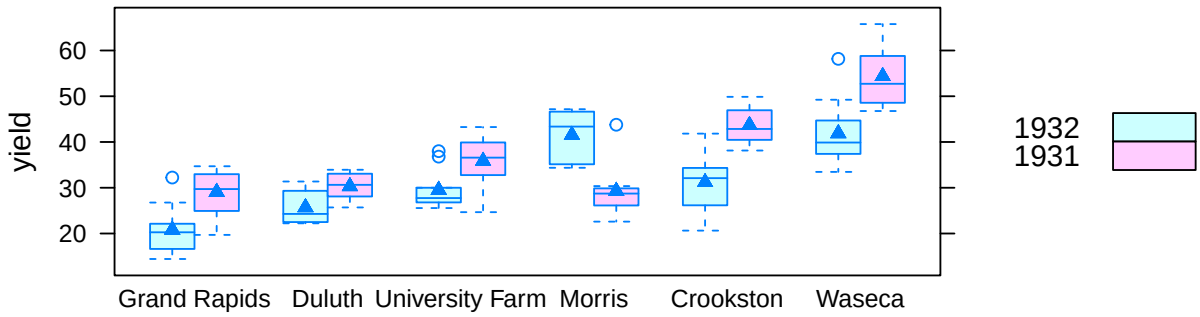


Figure 4: Boxplot mit panel.bwplot() und panel.superpose()

```
bwplot(
  yield ~ site,
  barley, groups = year, main="panel.superpose", par.settings = bw_theme(),
  auto.key = list( points = FALSE, rectangles = TRUE, space = "right"),
  box.width = 1 / 4,
  panel = function(x, y, groups, subscripts, ...) {
    xx <-
      as.numeric(x) + scale(as.numeric(groups), scale = FALSE) /
      (nlevels(groups)+1)
    panel.superpose(
      xx,  y,  ..., panel.groups = panel.mean,
      groups = groups, subscripts = subscripts
    )
   panel.grid(h = -1, v = 0)
    # panel.stripplot(x, y, ..., jitter.data = TRUE,
    #                 groups = groups, subscripts = subscripts)
    # panel.superpose(x, y, ..., panel.groups = panel.average,
    #                 groups = groups, subscripts = subscripts)
    # panel.points(x, y, ..., panel.groups = panel.average,
    #              groups = groups, subscripts = subscripts)
  }
)
```

Forest

forest_plot() Tabelle und Vertikaler-Plot gestohlen von survminer::ggforest()

ggplot_forest() Vertikaler-Plot ohne Tabelle aber dafuer sind Gruppen moeglich - stolen from https://github.com/NightingaleHealth/ggforestplot

```
model1 <- lm(mpg ~ wt, data = mtcars)
model2 <- lm(mpg ~ wt + cyl, data = mtcars)
prepare_forest(model1, model2)
```

```
##                       term         var level  N  estimate std.error  conf.low
```

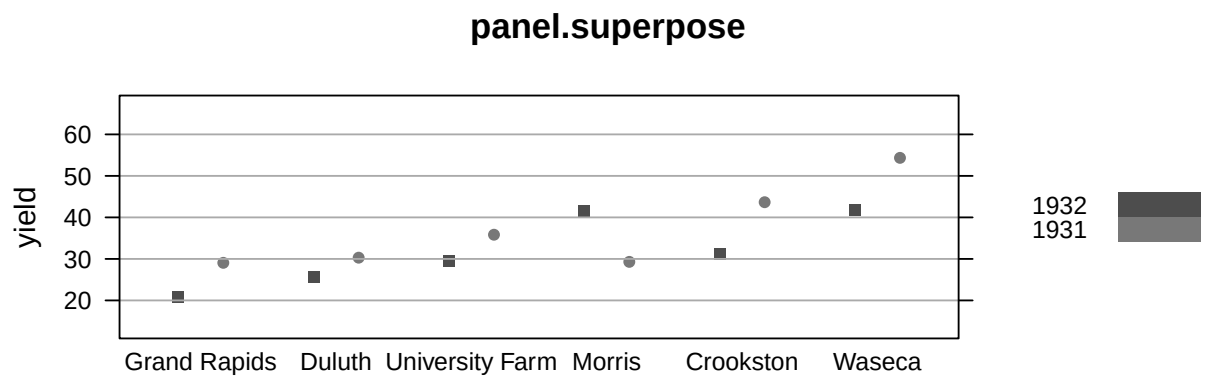
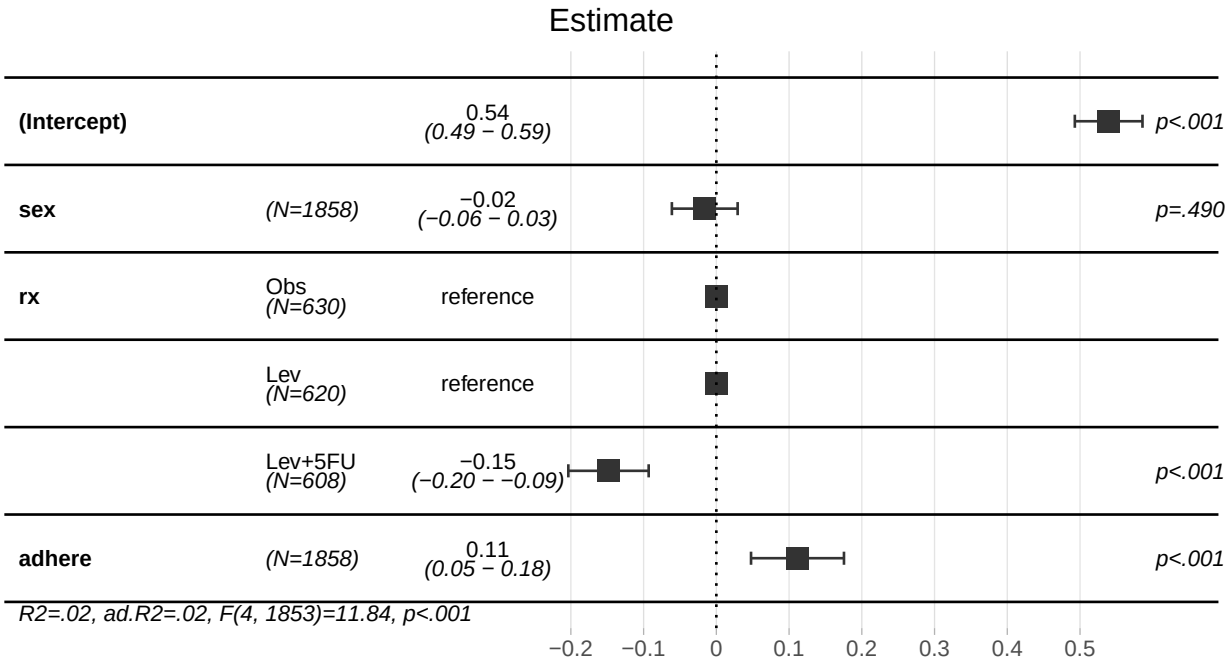


Figure 5: Mittelwerte mit einer Variante von panel.superpose()

```
## (Intercept)  (Intercept):  (Intercept)       NA 37.285126 1.8776273 33.450500
## wt                    wt:           wt       32 -5.344472 0.5591010 -6.486308
## (Intercept)1 (Intercept):  (Intercept)       NA 39.686261 1.7149840 36.178725
## wt1                   wt:           wt       32 -3.190972 0.7569065 -4.739020
## cyl                  cyl:          cyl       32 -1.507795 0.4146883 -2.355928
##                conf.high statistic      p.value  group
## (Intercept)  41.1197528 19.857575 8.241799e-19 model1
## wt           -4.2026349 -9.559044 1.293959e-10 model1
## (Intercept)1 43.1937976 23.140893 3.043182e-20 model2
## wt1          -1.6429245 -4.215808 2.220200e-04 model2
## cyl          -0.6596622 -3.635972 1.064282e-03 model2
```

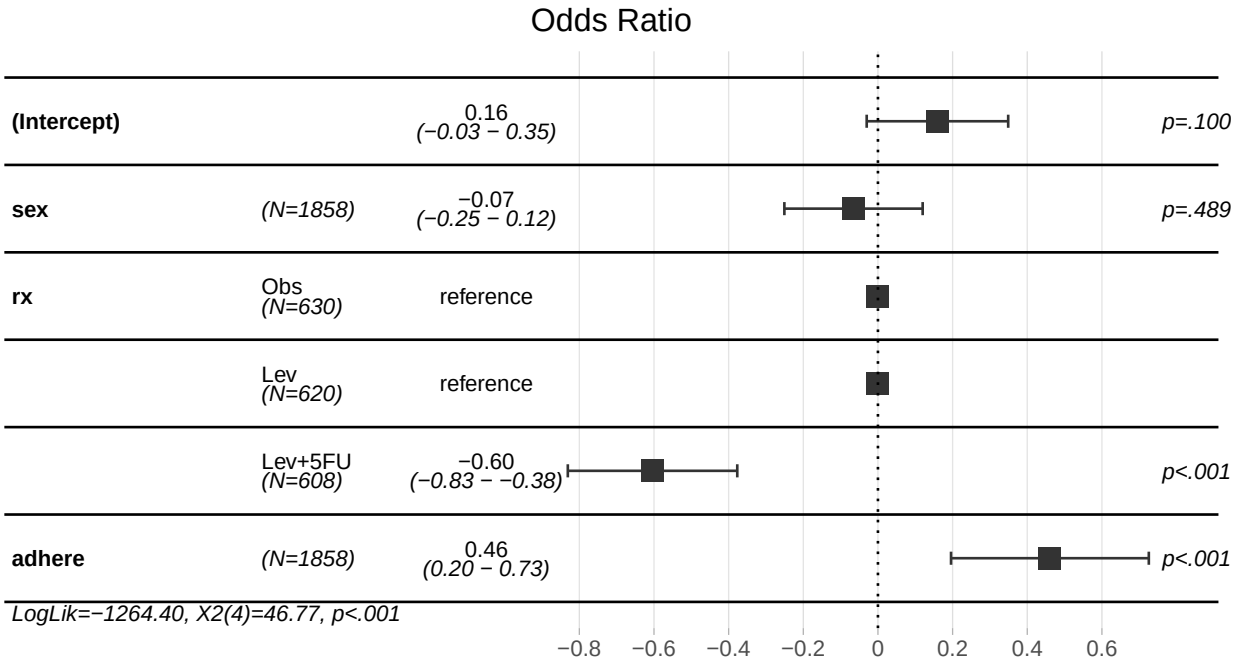
```
fit1 <- lm(status ~ sex + rx + adhere,
           data = colon)
forest_plot(fit1)
```

```
## Warning: Removed 2 rows containing missing values (‘geom_text()‘).
```



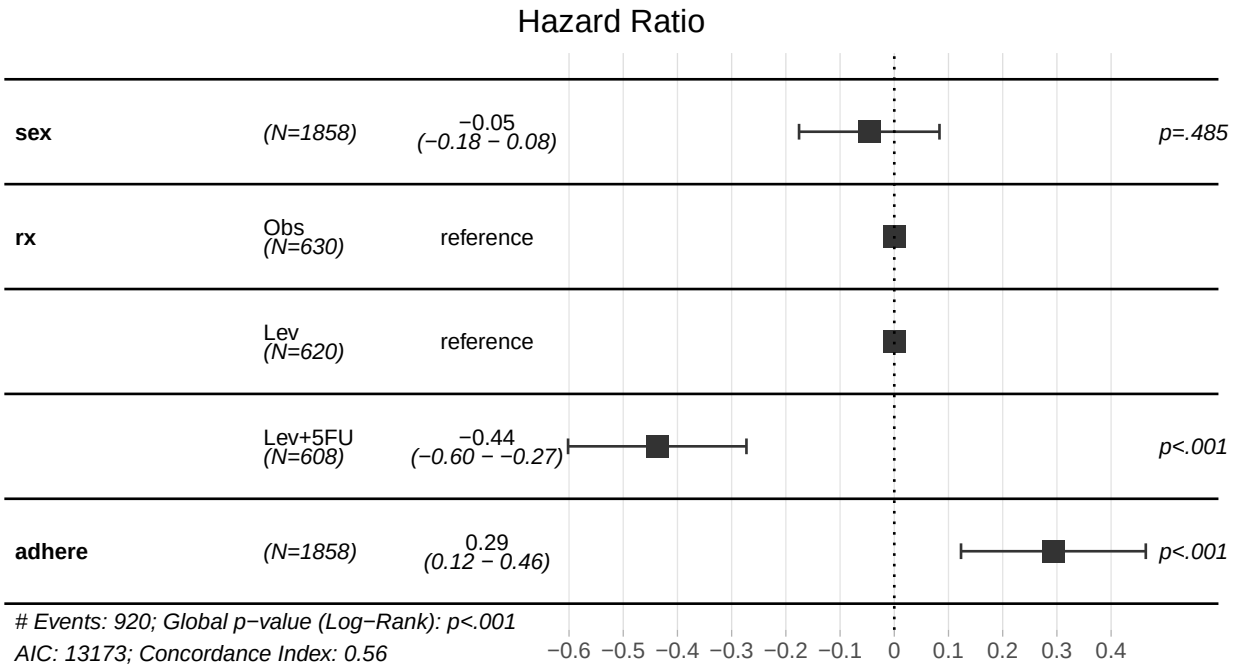

```
fit2 <- glm(status ~ sex + rx + adhere,
            data = colon, family = binomial())

forest_plot(fit2)
```

```
## Waiting for profiling to be done...

## Warning: Removed 2 rows containing missing values (‘geom_text()‘).
```




```
fit3 <- coxph(Surv(time, status) ~ sex + rx + adhere,
              data = colon)

forest_plot(fit3, colon)
```

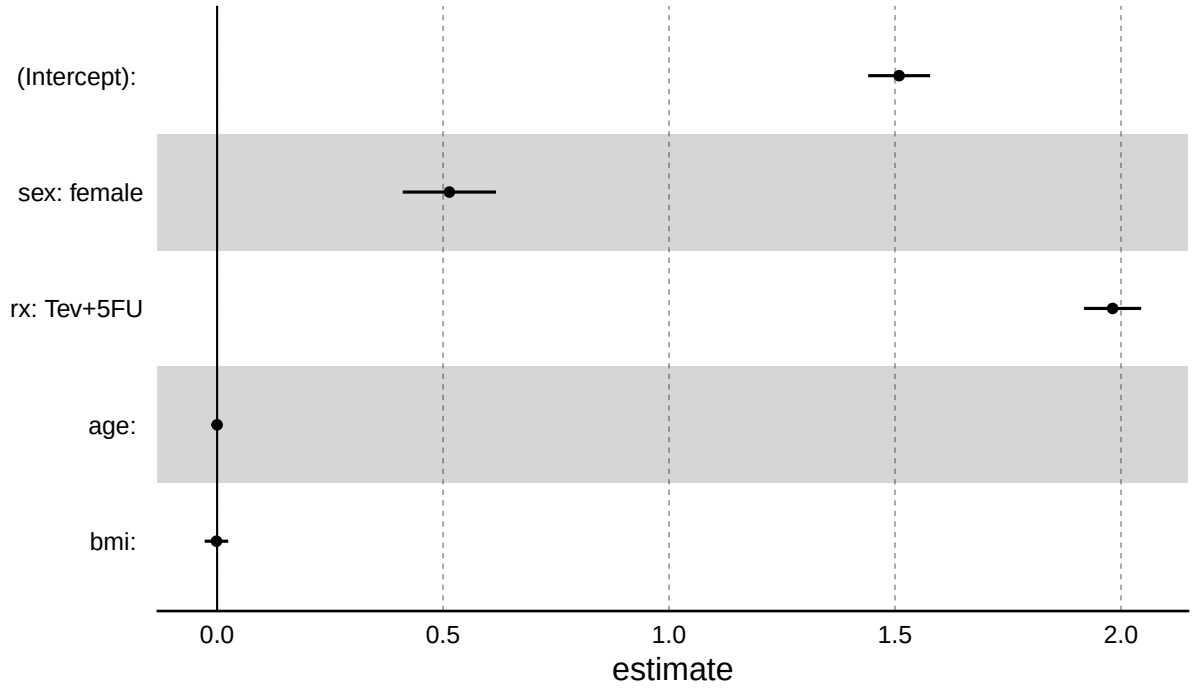
```
## Warning: Removed 2 rows containing missing values (‘geom_text()‘).
```



```
fit1 <- lm(y ~ sex + rx + age + bmi,  dat)
tab<-forest_plot(fit1, plot=FALSE)

tab
```

```
##                       term         var   level    N      estimate    std.error
## (Intercept) (Intercept):  (Intercept)           NA  1.509113e+00 3.496073e-02
## NA               sex: male         sex    male 3000            NA           NA
## sexfemale]     sex: female         sex  female 3000  5.138877e-01 5.263392e-02
## NA.1              rx: Obs          rx     Obs 2000            NA           NA
## NA.2              rx: Tev          rx     Tev 2000            NA           NA
## rxTev+5FU]     rx: Tev+5FU          rx Tev+5FU 2000  1.981428e+00 3.224119e-02
## age                 age:         age         6000 -4.975787e-06 1.519368e-05
## bmi                 bmi:         bmi         6000 -1.410221e-03 1.329780e-02
##                    conf.low    conf.high  statistic      p.value
## (Intercept)  1.440578e+00 1.5776488463 43.1659484 0.000000e+00
## NA                     NA           NA         NA           NA
## sexfemale]   4.107063e-01 0.6170691346  9.7634320 2.369740e-22
## NA.1                   NA           NA         NA           NA
## NA.2                   NA           NA         NA           NA
## rxTev+5FU]   1.918223e+00 2.0446319556 61.4564135 0.000000e+00
## age         -3.476088e-05 0.0000248093 -0.3274905 7.433084e-01
## bmi         -2.747870e-02 0.0246582586 -0.1060492 9.155469e-01
```

```
ggplot_forest(tab)
```

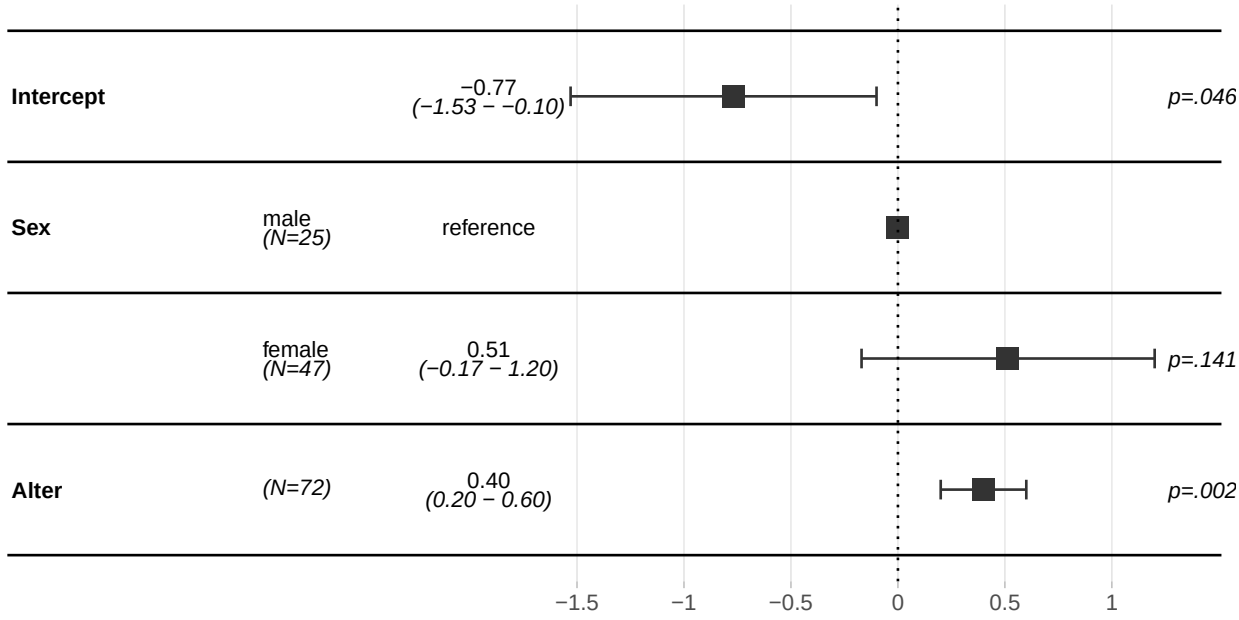



```
ggplot_table(
data.frame(
  var = c("Intercept", "Sex", "Sex", "Alter"),
```

```
  level = c(NA, "male", "female", NA),
  N = c(NA, 25, 47, 25+47),
  estimate = c(-.77, NA, .51 , .4),
  conf.low = c(-1.53, NA, -.17, .2),
  conf.high = c(-0.1, NA, 1.2, .6),
  p.value = c(0.046, NA, 0.1407, 0.0021)
)
)
```

```
## Warning: Removed 2 rows containing missing values (`geom_text()`).
```

```
## Warning: Removed 1 rows containing missing values (`geom_text()`).
```

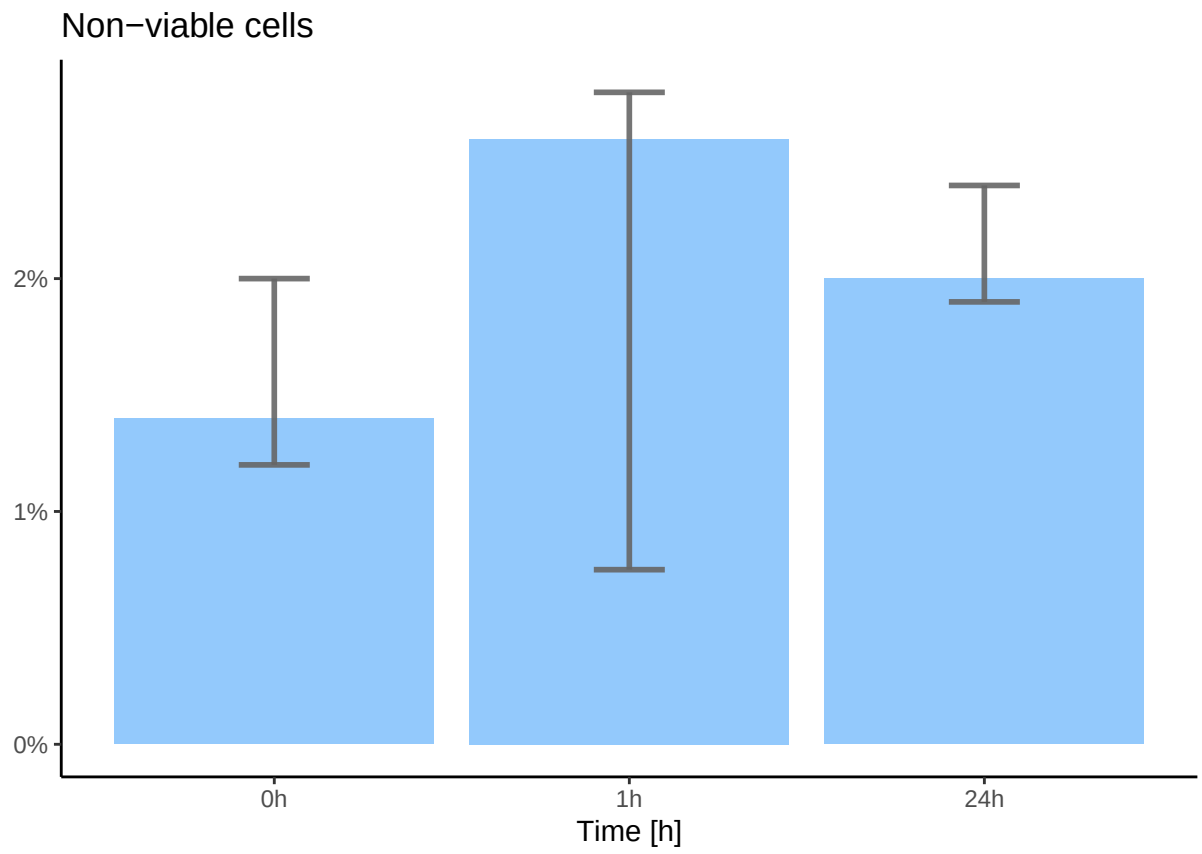


Balken mít Errorbars

```
mycol <- c("#0433FF",
                    "#00F801",
                    "#FF2600",
                    "#918E00",
                    "#FE9300")

data <- data.frame(
  name = c("0h", "1h", "24h"),
  value = c(1.4,    2.6,    2) / 100,
  sd1 =   c(1.2,    2.8,    1.9) / 100,
  sd2 =   c(2,      0.75,   2.4) / 100
)
```

```r
# Most basic error bar
  ggplot(data) +
  geom_bar(
    aes(x = name, y = value),
    stat = "identity",
    fill = "#64B2FC",
    alpha = 0.7
  ) +
  geom_errorbar(
    aes(x = name,
        ymin = sd1,
        ymax = sd2),
    width = 0.2,
    colour = "gray40",
    alpha = 0.9,
    size = 1
  ) + scale_y_continuous(labels = scales::percent) +
  labs(title = "Non-viable cells",
       # subtitle = "(1973-74)",
       # caption = "Data from the 1974 Motor Trend US magazine.",
     #   tag = "B",
       x = "Time [h]",
       y = "",) +
  theme_classic()
```

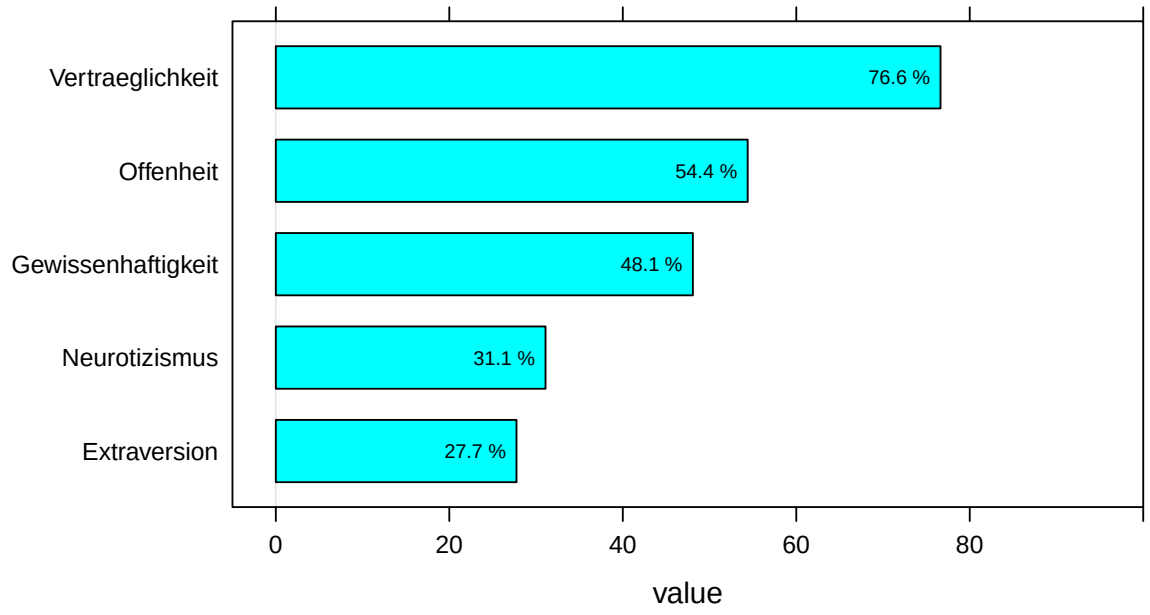
```
## Warning: Using ‘size‘ aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use ‘linewidth‘ instead.
```



Balken mit Zahlen

```
set.seed(2)

DF_balk <-
  data.frame(
    value = runif(2 * 5, min = 20, max = 80),
    sex = factor(rep(c("male", "female"), times = 5)),
    variable = factor(rep(
      c(
        n = "Neurotizismus",
        e = "Extraversion",
        o = "Offenheit",
        g = "Gewissenhaftigkeit",
        a = "Vertraeglichkeit"
      ),
      times = 2
    ))
  )


barchart(
  reorder(variable, value) ~ value,
  subset(DF_balk, sex == "male"),
```

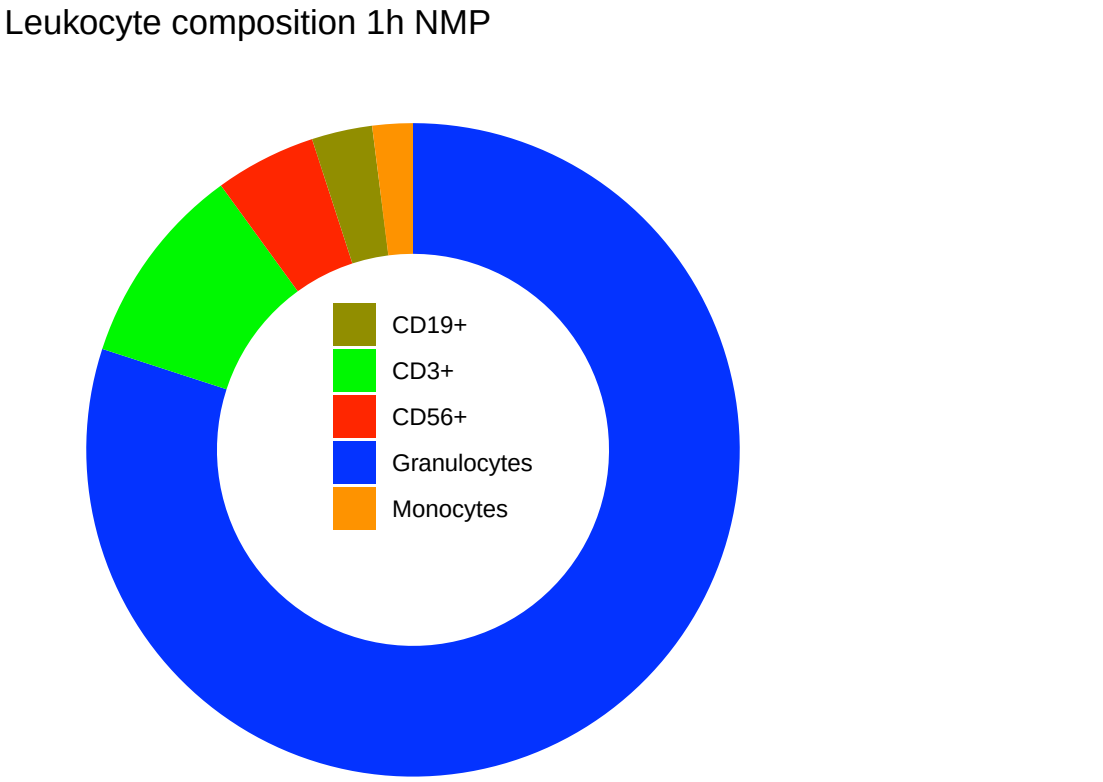
```
  box.ratio = 2,
  xlim = c(-5, 100),
  origin = 0,
  #' par.settings=colorset,
  panel = function(...)   {
    panel.barchart(...)
    panel.barchart.text(..., digits = 1, suffix = " %")
  }
)
```



Tortendiagramme

```
# Create test data.
data <- data.frame(
  category=c("Granulocytes", "CD3+", "CD56+",  "CD19+", "Monocytes"),
  count=c(80,10,5,3,2)
)

# Compute percentages
data$fraction <- data$count / sum(data$count)
# Compute the cumulative percentages (top of each rectangle)
data$ymax <- cumsum(data$fraction)
# Compute the bottom of each rectangle
data$ymin <- c(0, head(data$ymax, n=-1))
# Compute label position
data$labelPosition <- (data$ymax + data$ymin) / 2
# Compute a good label
#data$label <- paste0(data$category, "\n value: ", data$count)
```

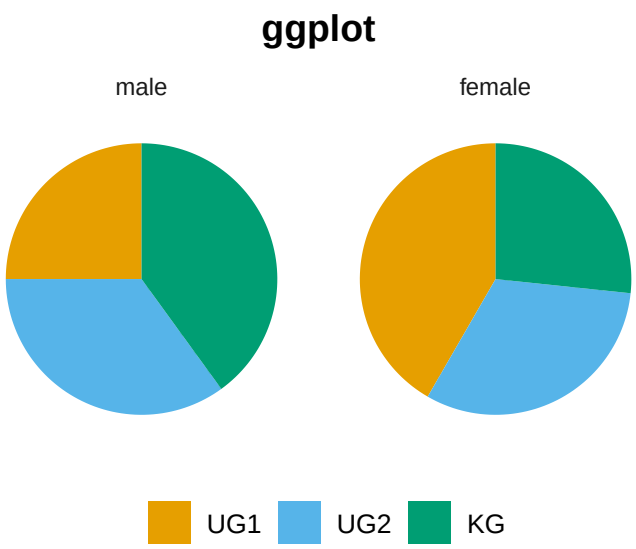
```r
# Make the plot
ggplot(data,
           aes(ymax=ymax, ymin=ymin, xmax=4, xmin=2,
               fill=category)) +
  geom_rect() +
  # geom_text( x=2,
  #            aes(y=labelPosition,
  #                label=label,
  #                color=1), size=6) + # x here controls label position (inner / outer)
  scale_fill_manual(
    values =
      c("#918E00","#00F801","#FF2600","#0433FF","#FE9300")) +
 coord_polar(theta="y") +
  xlim(c(-1, 4)) +
 theme_void() +
  theme(legend.position = "top") +
  labs(title = "Leukocyte composition 1h NMP") +
  theme(legend.title = element_blank(),# element_text(size=12, color = "salmon", face="bold"),
        legend.justification=c(0,1),
        legend.position=c(0.4, 0.7),
        legend.background = element_blank(),
        legend.key = element_blank()
        )
```




```r
#  Geht nicht problemlos in Markdown
```

```
print(torte(~treatment+sex, DF, init.angle=45, main="lattice"))
```

```
gtorte(~treatment+sex, DF, init.angle=45, main="ggplot")
```




```
#  Geht nicht problemlos in Markdown
tab <- as.data.frame(xtabs( ~ treatment + sex, DF))
# par(new = TRUE)

  stp25plot::piechart(~Freq|sex,
  tab, groups= treatment,
  auto.key=list(columns=3))
```

MetComp_BAP

Tukey Mean Difference oder auch Bland Altman Metode

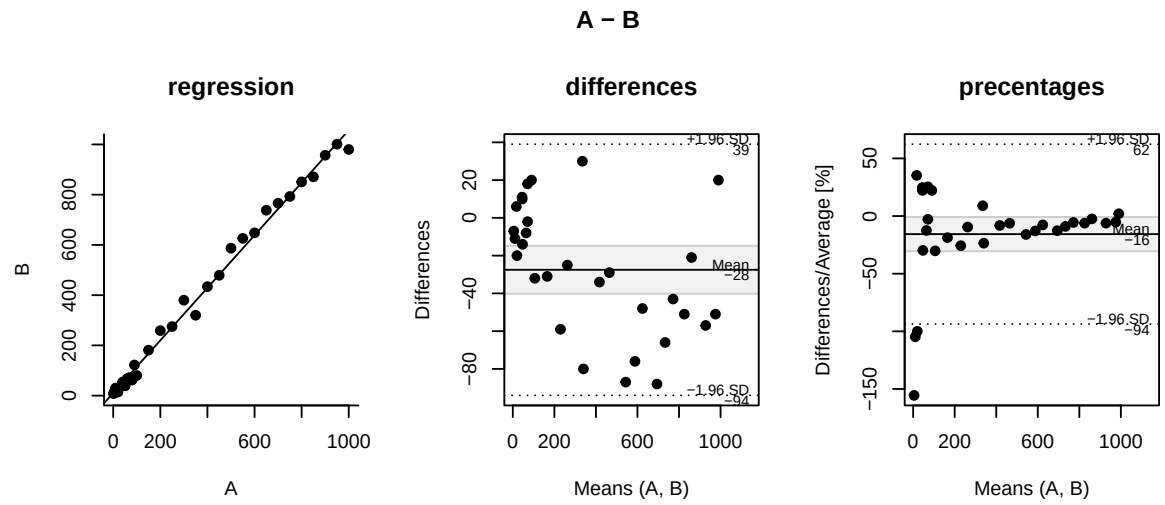
```
require(stp25metcomp)
```

```
## Loading required package: stp25metcomp
```

```
##
## Attaching package: 'stp25metcomp'
```

```
## The following object is masked from 'package:stp25stat2':
##
##     Tbll_icc
```

```
x<- MetComp_BAP(~A+B, DF2)
plot(x)
```




```
x
```

```
##
##
##                Parameter   Unit                 CI    SE   Percent
## 1               df (n-1)     29               <NA>
## 2    difference mean (d) -27.50  [-40.17,  -14.83]  6.20  <0.1% ()
## 3 standard deviation (s)  33.94               <NA>        39.8% ()
## 4  critical.diff (1.96s)  66.52               <NA>        78.0% ()
## 5               d-1.96s -94.02 [-115.97,  -72.07] 10.73  <0.1% ()
## 6               d+1.96s  39.02    [17.07,  60.97] 10.73 117.8% ()
```

cowplot

gridExtra::grid.arrange( )

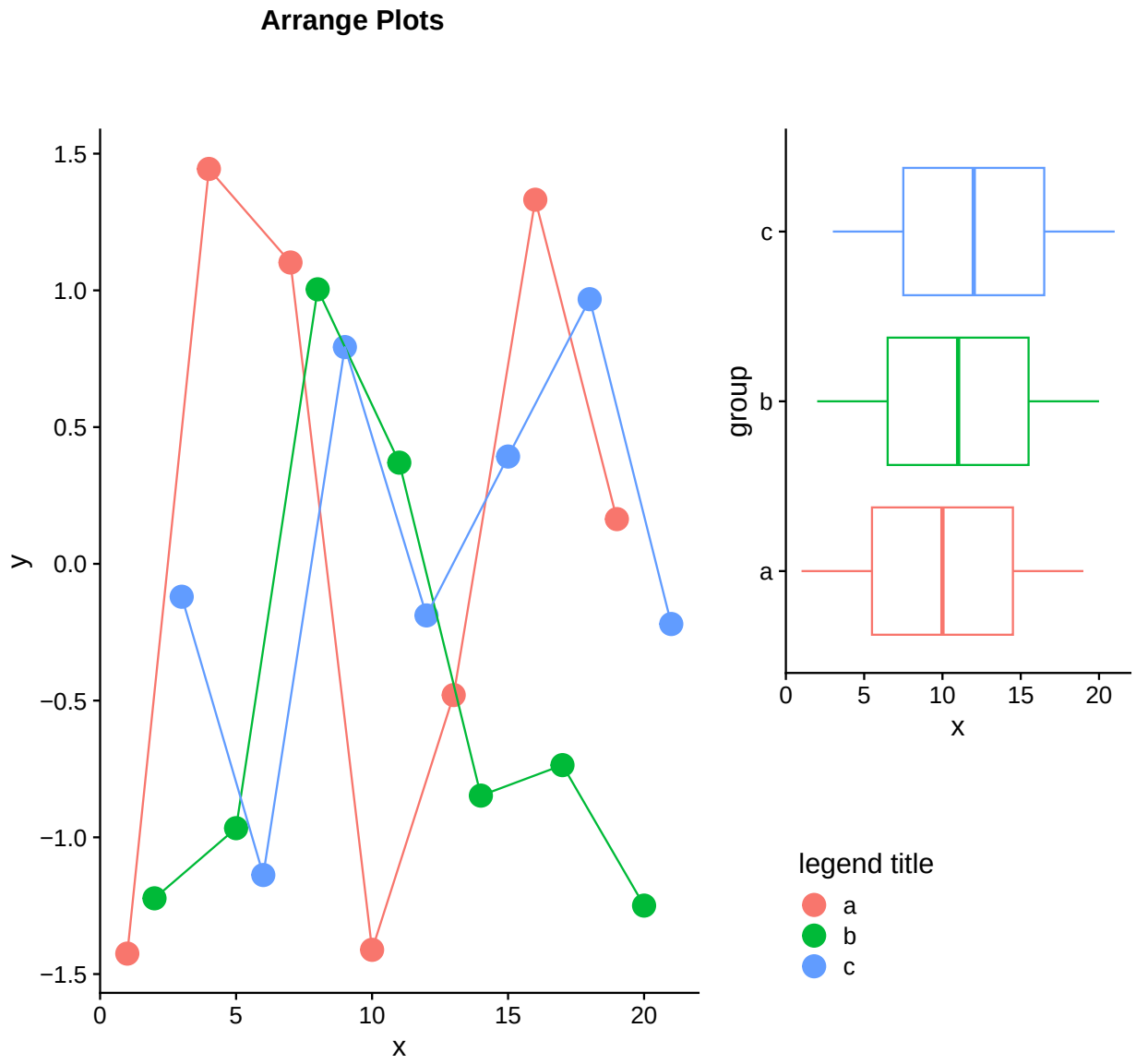
Zusammen mixen von unterschiedlichen Grafik-Typen.

The cowplot package is a simple add-on to ggplot. https://wilkelab.org/cowplot/articles/index.html

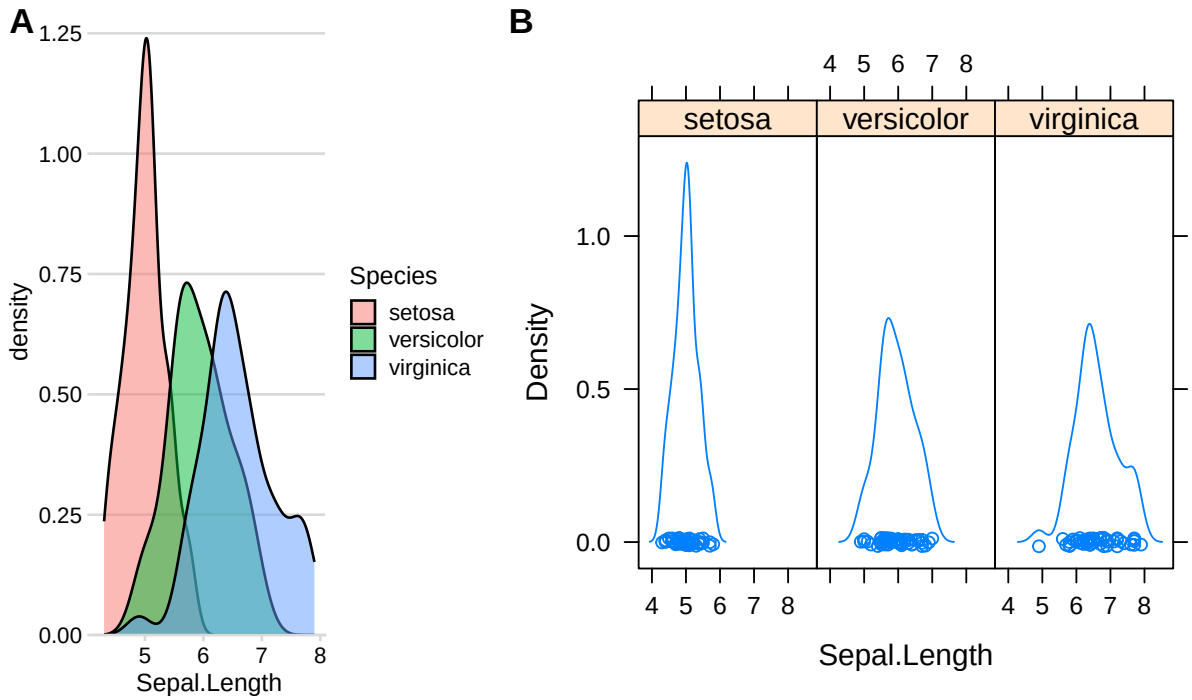
```
library(ggplot2)

library(grid)
library(gridExtra)
library(cowplot)


theme_set(theme_half_open())
set.seed(0815)                                  # Create example data

data <-
  data.frame(x = 1:21,
             # Create example data
             y = rnorm(21),
             group = rep(letters[1:3], 7))
```

```r
p1 <-
  ggplot(data, aes(x, y, color = group)) +    # Create ggplot2 plot
  geom_point(size = 5) +
  geom_line() # Draw default ggplot2 plot


p2 <- ggplot(data, aes(x, group , color = group)) + geom_boxplot()



title <-
  ggdraw() +
  draw_label("Arrange Plots", fontface = 'bold')


p1 <- p1 +
  guides(colour = guide_legend(
    title = "legend title",
    override.aes =
      list(
        size =  5,
        fill = NA,
        linetype = 0
      )
  )) +
  theme(legend.position  = c(.2, .5))


legend <- get_legend(p1)


p1 <- p1 +
  theme(legend.position = "none")

p2 <- p2 +
  theme(legend.position = "none")

p2 <-
  plot_grid(p2,
            legend,
            ncol = 1,
            rel_heights = c(1, .5))


plot_grid(
  title,
  NULL,
  p1,
  p2,
  nrow = 2,

  rel_widths =  c(1, .6),
  rel_heights = c(0.2, 1)
```

```
)
```




```
#require(ggplot2)
#require(cowplot)
#require(lattice)
p1<- ggplot(iris, aes(Sepal.Length, fill = Species)) +
  geom_density(alpha = 0.5) +
  scale_y_continuous(expand = expansion(mult = c(0, 0.05))) +
  theme_minimal_hgrid(10)
p2<- densityplot(~Sepal.Length|Species , iris)

plot_grid(p1, p2,  rel_widths = c(1, 1.5)
          , labels = c('A', 'B'))
```

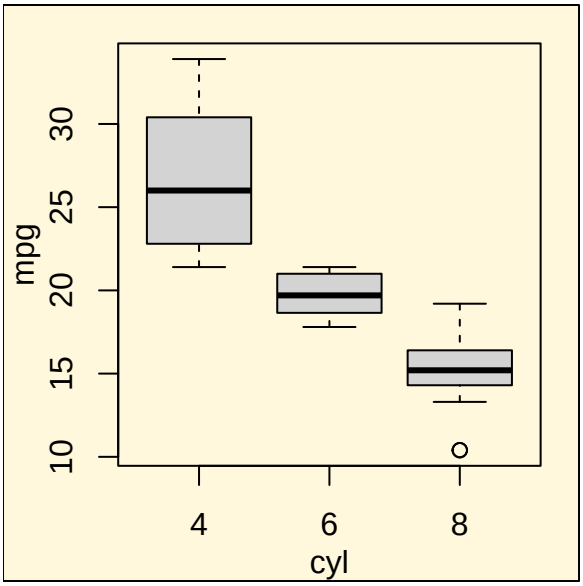


Mixing different plotting frameworks

```
# require(ggplot2)
# require(cowplot)
# require(lattice)
 require(gridGraphics)
```

```
## Loading required package: gridGraphics
```

```
p1 <- function() {
  par(
    mar = c(3, 3, 1, 1),
    mgp = c(2, 1, 0)
  )
  boxplot(mpg ~ cyl, xlab = "cyl", ylab = "mpg", data = mtcars)
}

ggdraw(p1) +
  theme(plot.background = element_rect(fill = "cornsilk"))
```



ggformula

Quelle https://rpruim.github.io/Statistical-Rethinking/Examples/ggformula.html

gf_point() for scatter plots

gf_line() for line plots (connecting dots in a scatter plot)

gf_density() or *gf_dens()* or *gf_histogram()* or *gf_freqpoly()* to display distributions of a quantitative variable

gf_boxplot() or *gf_violin()* for comparing distributions side-by-side

gf_counts() for bar-graph style depictions of counts.

gf_bar() for more general bar-graph style graphics

```
#require(ggplot2)
require(ggformula)
```

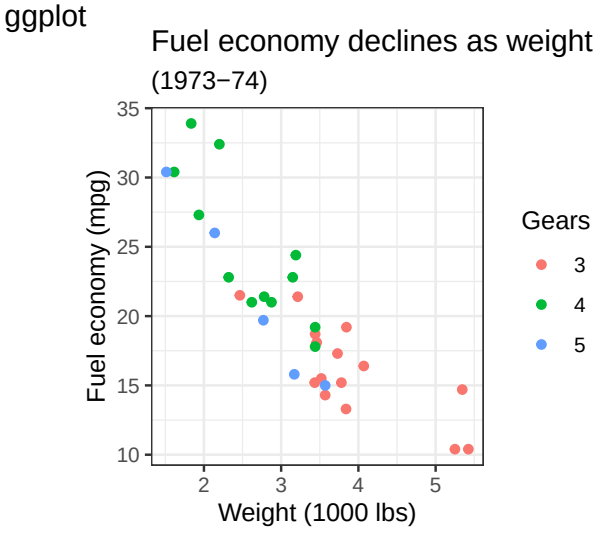
```
## Loading required package: ggformula

## Loading required package: ggstance

##
## Attaching package: 'ggstance'

## The following objects are masked from 'package:ggplot2':
##
##     geom_errorbarh, GeomErrorbarh

## Loading required package: scales

## Loading required package: ggridges
```

```
##
## New to ggformula?  Try the tutorials:
##  learnr::run_tutorial("introduction", package = "ggformula")
##  learnr::run_tutorial("refining", package = "ggformula")
```

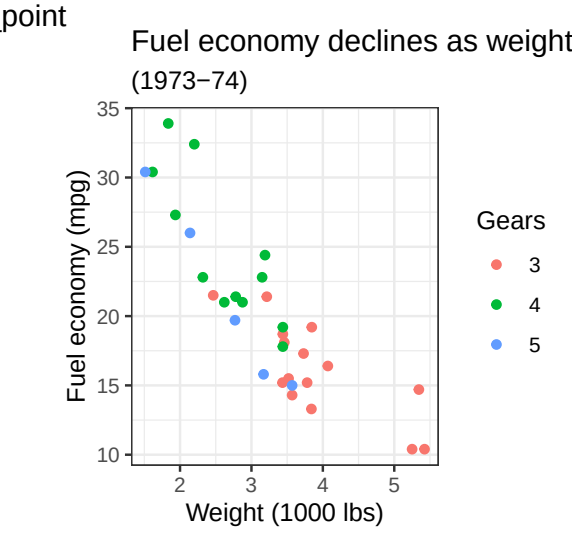
```
#require(lattice)


theme_set(theme_bw())

mtcars2 <- within(mtcars, {
  vs <- factor(vs, labels = c("V-shaped", "Straight"))
  am <- factor(am, labels = c("Automatic", "Manual"))
  cyl  <- factor(cyl)
  gear <- factor(gear)
})
#' ggplot
p1 <-
  ggplot(mtcars2) +
  geom_point(aes(x = wt, y = mpg, colour = gear)) +
  labs(
    title = "Fuel economy declines as weight increases",
    subtitle = "(1973-74)",
    caption = "Data from the 1974 Motor Trend US magazine.",
    tag = "ggplot",
    x = "Weight (1000 lbs)",
    y = "Fuel economy (mpg)",
    colour = "Gears"
  )
#' ggformula
p2 <-
  gf_point(mpg ~ wt , data = mtcars2, color = ~ gear) +
  labs(
    title = "Fuel economy declines as weight increases",
    subtitle = "(1973-74)",
    caption = "Data from the 1974 Motor Trend US magazine.",
    tag = "gf_point",
    x = "Weight (1000 lbs)",
    y = "Fuel economy (mpg)",
    colour = "Gears"
  )
#' lattice
p3 <-
  xyplot(
    mpg ~ wt,
    mtcars2,
    groups = gear,
    par.settings = bw_theme(farbe(), cex.main = .8, cex.add = .8),
    grid=TRUE,
    main = "Fuel economy declines as weight increases\n(1973-74)",
    sub =  "Data from the 1974 Motor Trend US magazine.",
    xlab = "Weight (1000 lbs)",
    ylab = "Fuel economy (mpg)",
    auto.key = list(space = "right", title = "Gears")
```

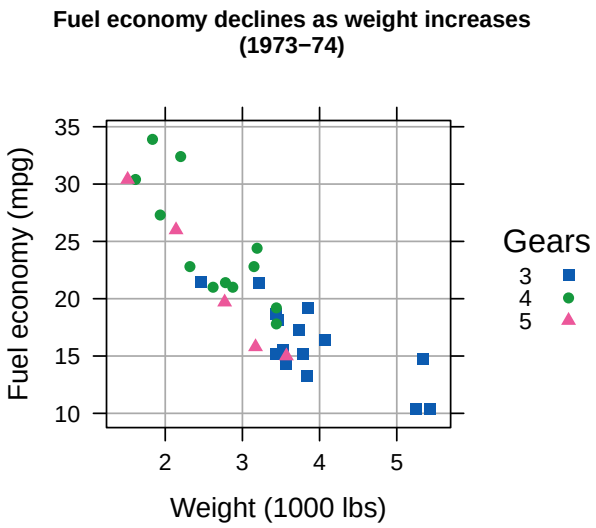
```
  )

cowplot::plot_grid(p1, p2, p3, ncol=2)
```

ggplot



gf_point



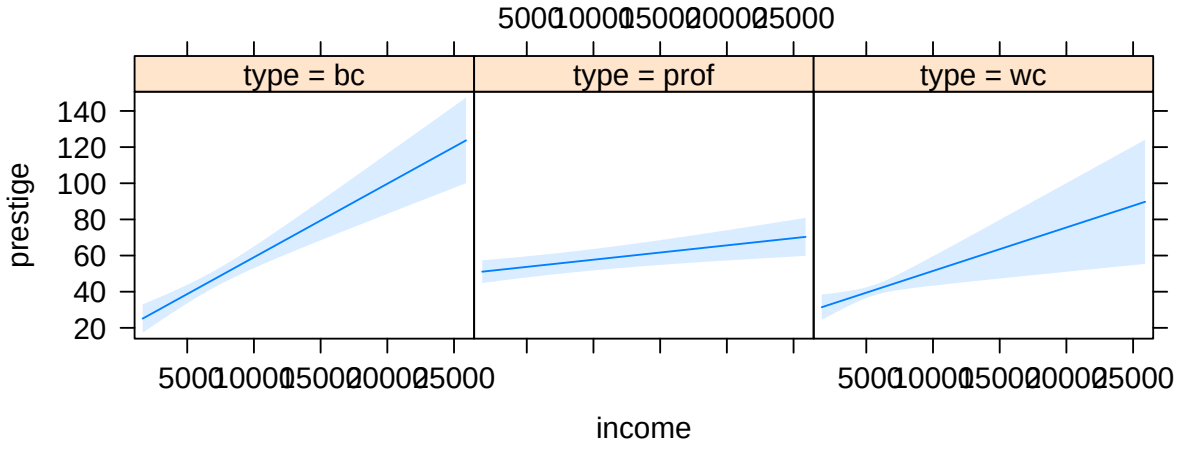


Effectplot mit effect

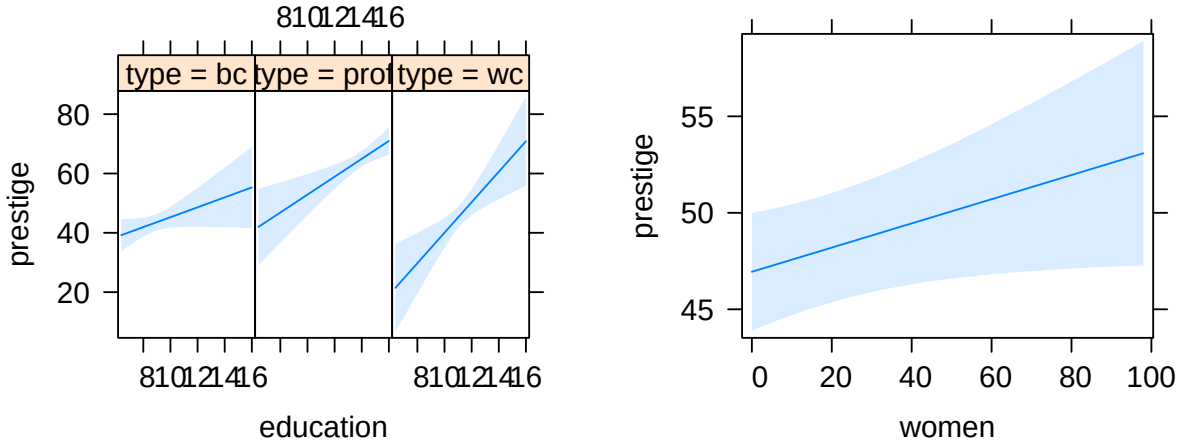
predictorEffect()

Von mir lang ignorierte Variante von Effect mit Formeln!

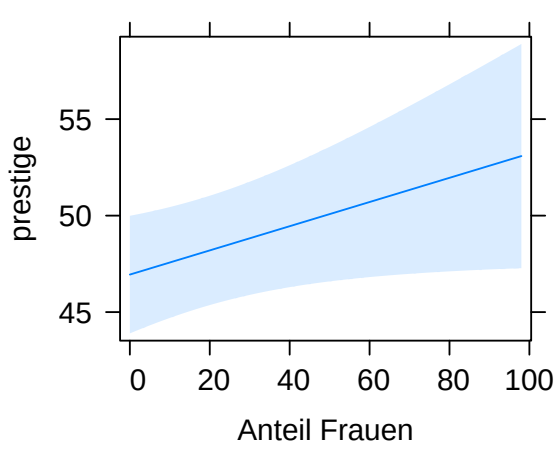
```
mod <- lm(prestige ~ type*(education + income) + women, Prestige)
plot(predictorEffect("income", mod), main="", rug=FALSE)
```

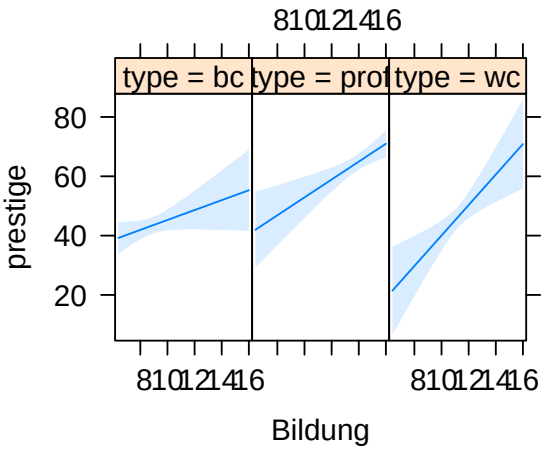



```
plot(predictorEffects(mod, ~ education + women), main="", rug=FALSE)
```




```
plot(predictorEffects(mod, ~ women+ education),
     axes= list(x=list( women=list(lab="Anteil Frauen"),
                        education=list(lab="Bildung"))), main="", rug=FALSE)
```

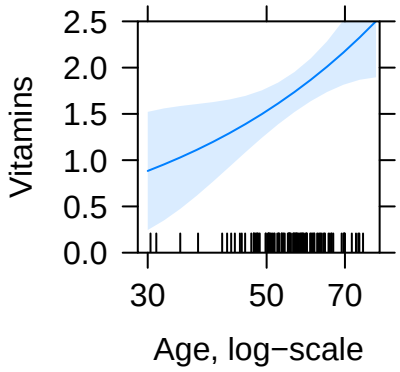


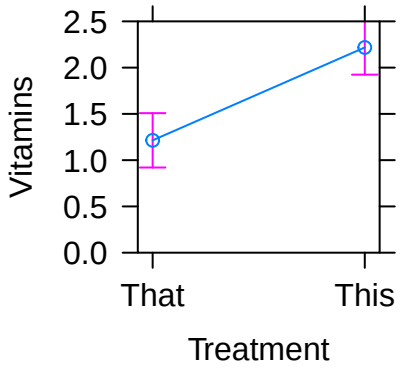


Modifizier plot.efflist

allEffects

```
ef <- allEffects(lm(A ~ B + C))
plot(ef,
     axes = list(
       x = list(
        B = list(
         transform = list(trans = log, inverse = exp),
         ticks = list(at = c(30, 50, 70)),
         lab = "Age, log-scale"),
       C = list(lab = "Treatment")
      ),
     y = list(lim= c(.0, 2.5),
              lab = "Vitamins"
              #  transform = list(link = Logit, inverse = invLogit),
              #  transform=list(trans=log, inverse=exp),
              #  type="rescale",
              #  ticks = list(at = c(.05, .25, .50, .75)),
              #
       )),
     main = "")
```





Das ist hingegen obsolet!

```
plot.efflist <- stp25plot:::plot.efflist
ef <- allEffects(lm(A ~ B + C))
plot(ef, xlab = c("Foo", "Bar"), main="Modifiziert")
```

ggeffects

Quelle: https://strengejacke.github.io/ggeffects/

```
require(ggeffects)
```

```
## Loading required package: ggeffects
```

```
##
## Attaching package: 'ggeffects'
```

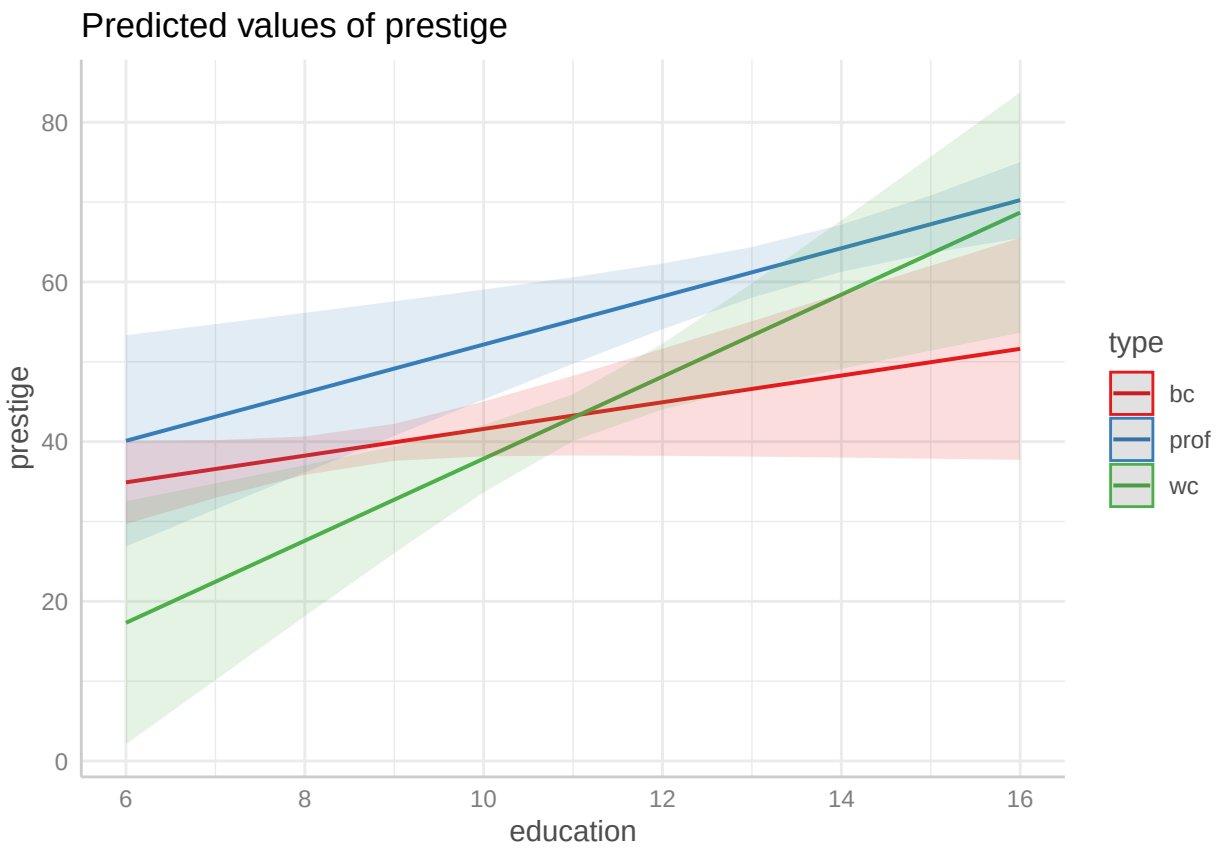
```
## The following object is masked from 'package:cowplot':
##
##     get_title
```

```
mod <- lm(prestige ~ type*(education + income) + women, Prestige)
mydf<-ggpredict(mod, terms =c( "education", "type"))
mydf
```

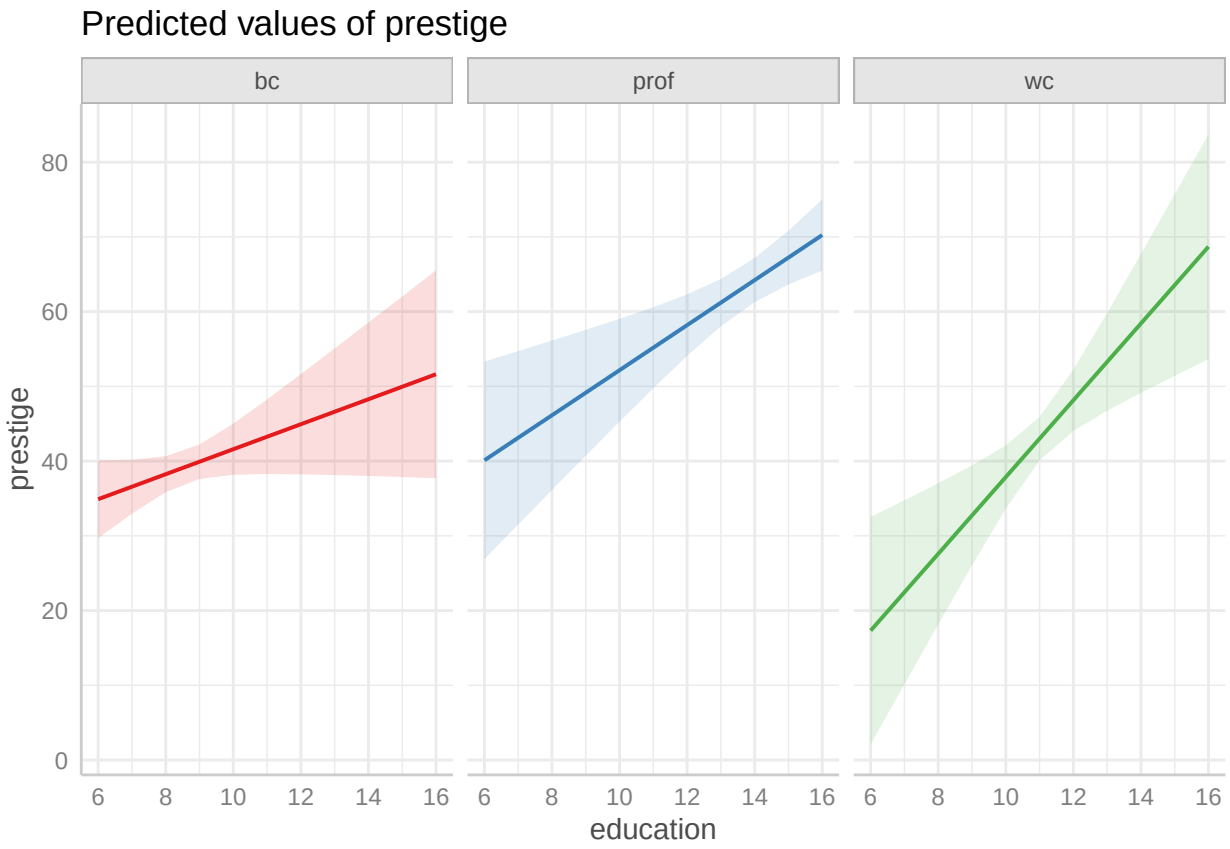
```
## # Predicted values of prestige
##
## # type = bc
##
## education | Predicted |         95% CI
## --------------------------------------
##         6 |     34.90 | [29.69, 40.11]
##         8 |     38.24 | [35.84, 40.65]
##         9 |     39.92 | [37.60, 42.23]
##        11 |     43.26 | [38.27, 48.26]
```

```
##        13 |     46.61 | [38.13, 55.08]
##        16 |     51.62 | [37.72, 65.53]
##
## # type = prof
##
## education | Predicted |         95% CI
## ------------------------------------
##         6 |     40.10 | [26.88, 53.33]
##         8 |     46.13 | [36.13, 56.13]
##         9 |     49.15 | [40.73, 57.57]
##        11 |     55.18 | [49.76, 60.59]
##        13 |     61.21 | [58.04, 64.37]
##        16 |     70.25 | [65.48, 75.02]
##
## # type = wc
##
## education | Predicted |         95% CI
## ------------------------------------
##         6 |     17.31 | [ 2.09, 32.53]
##         8 |     27.59 | [18.13, 37.05]
##         9 |     32.73 | [26.03, 39.42]
##        11 |     43.00 | [40.08, 45.92]
##        13 |     53.28 | [46.73, 59.83]
##        16 |     68.69 | [53.64, 83.75]
##
## Adjusted for:
## * income = 6035.50
## *  women =   28.99
```

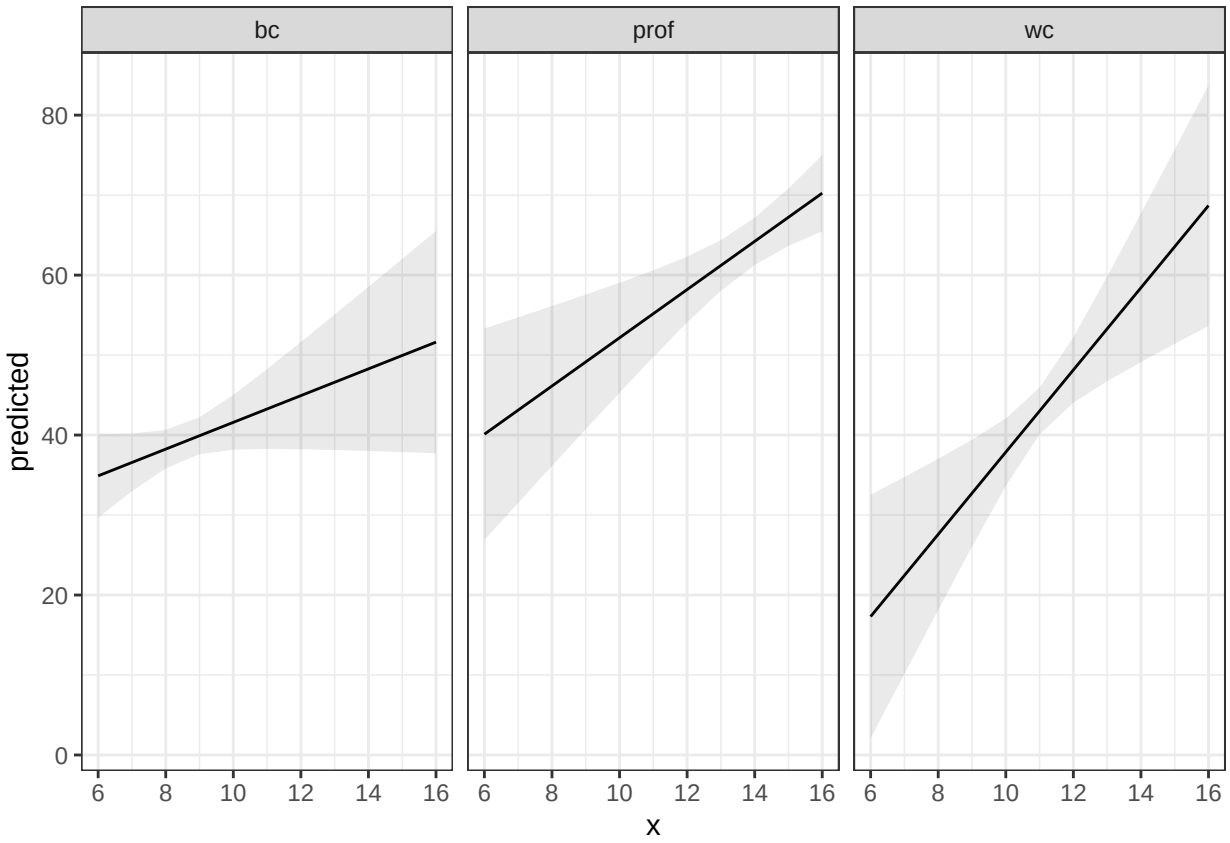
```
# ggplot(mydf, aes(x, predicted)) +
#   geom_line() +
#   geom_ribbon(aes(ymin = conf.low, ymax = conf.high), alpha = .1)

p1 <-plot(mydf)
p1
```




```
p1 +
  facet_wrap(~group)  +

  theme(legend.position = "none")
```




```
#plot(allEffects(mod))

ggplot(mydf, aes(x = x, y = predicted, group =group)) +
  geom_line() +
  geom_ribbon(aes(ymin = conf.low, ymax = conf.high), alpha = .1) +
  facet_wrap(~group)
```



grid.arrange(plot(eff), g, xyplot(y~education, dat), plot(mydf), ncol = 2)

Effectplot mit emmeans

```
require(emmeans)
head(pigs)
```

```
##   source percent conc
## 1   fish       9 27.8
## 2   fish       9 23.7
## 3   fish      12 31.5
## 4   fish      12 28.5
## 5   fish      12 32.8
## 6   fish      15 34.0
```

```
pigs.lm1 <- lm(log(conc) ~ source + factor(percent), data = pigs)
ref_grid(pigs.lm1)
```

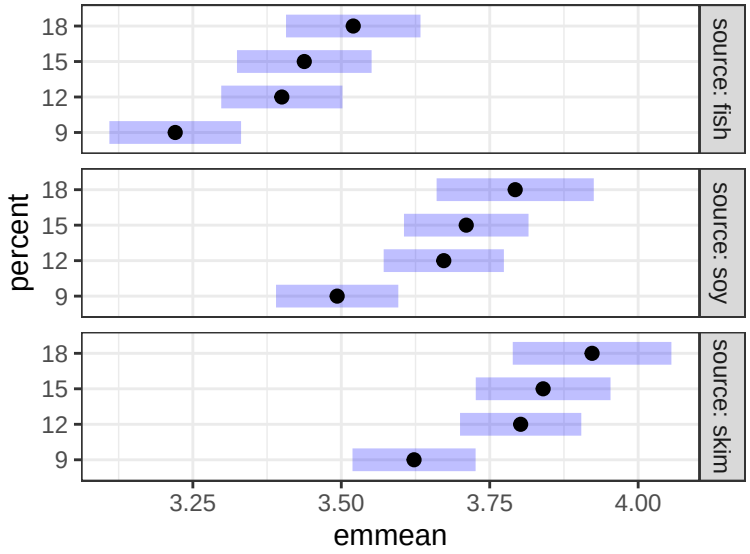
```
## 'emmGrid' object with variables:
##     source = fish, soy, skim
##     percent =  9, 12, 15, 18
## Transformation: "log"
```

```
pigs.lm2 <- lm(log(conc) ~ source + percent, data = pigs)
ref_grid(pigs.lm2)
```

```
## 'emmGrid' object with variables:
##     source = fish, soy, skim
##     percent = 12.931
## Transformation: "log"
```

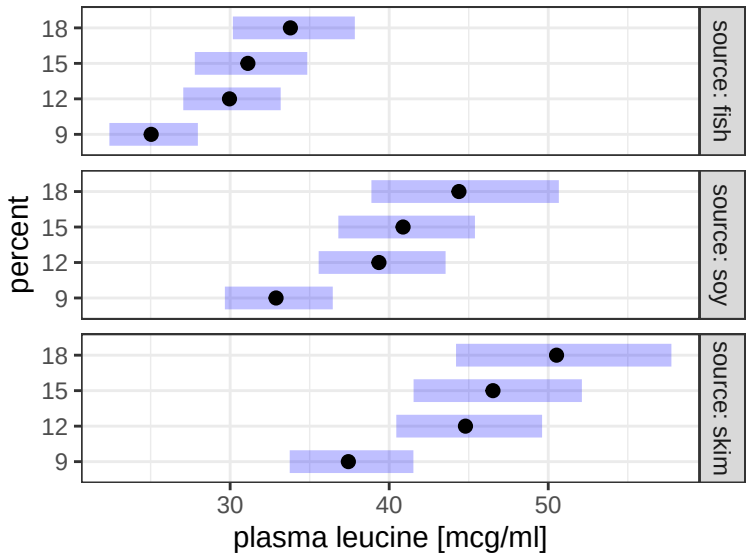
emmeans default

```
plot(emmeans(pigs.lm1,
             ~ percent | source))
```

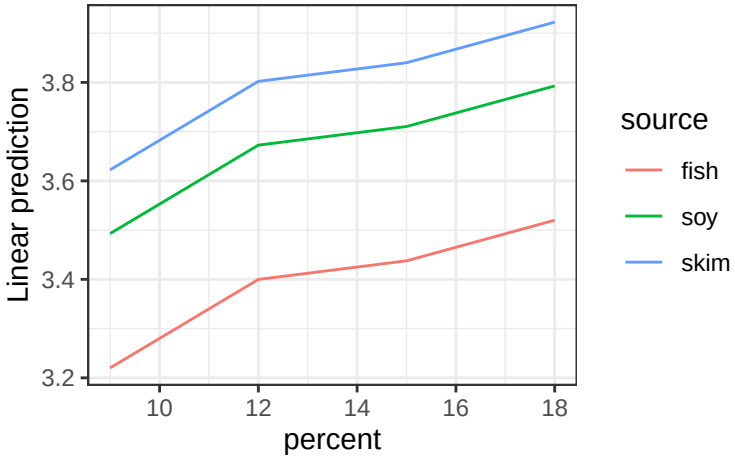


emmeans ruecktransformiert

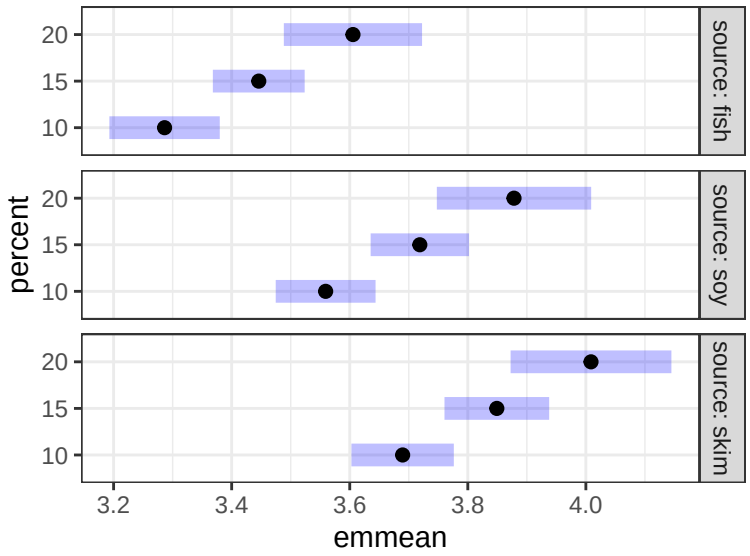
```
plot(emmeans(pigs.lm1,
             ~ percent | source),
             xlab= "plasma leucine [mcg/ml]" ,
             type = "response")
```



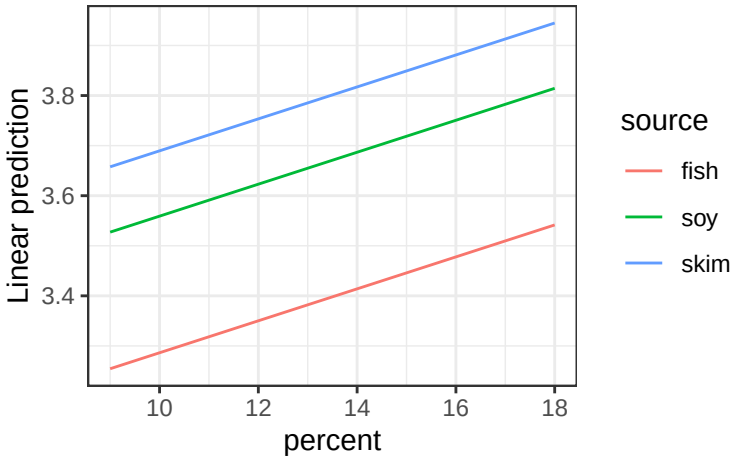

```
emmip(pigs.lm1,
      source ~ percent)
```



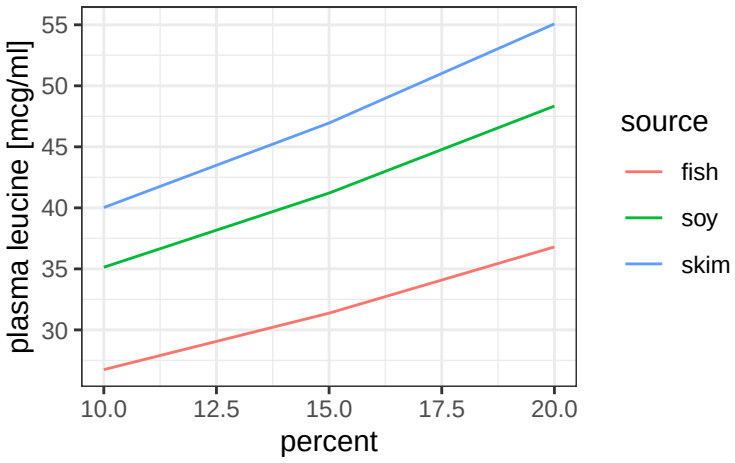

```
plot(emmeans(pigs.lm2,
             ~ percent | source,
             at = list(percent = c(10, 15, 20))
             )
     )
```




```
emmip(
  ref_grid(pigs.lm2, cov.reduce = FALSE),
  source ~ percent)
```

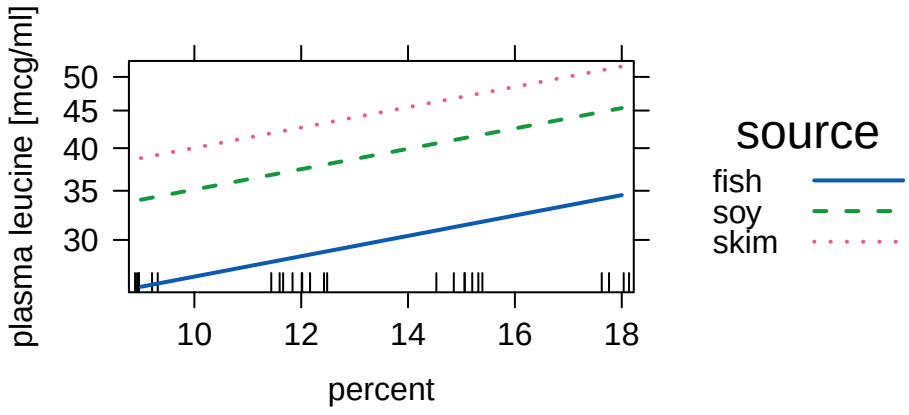



```
emmip(ref_grid(pigs.lm2,
               at= list(percent = c(10, 15, 20))),
      source ~ percent,
      ylab= "plasma leucine [mcg/ml]" ,
      type = "response"
      )
```



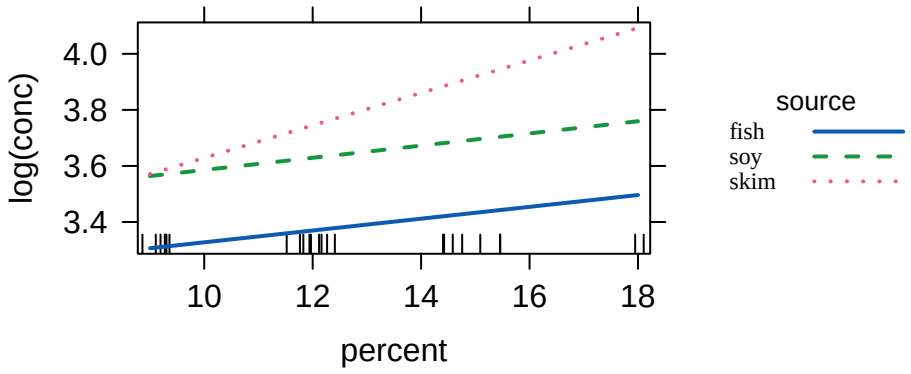
Klassiker mit Effect()

```
 lattice::trellis.par.set(bw_theme(farbe()))
plot(Effect(c("source", "percent"),
            pigs.lm2,
            transformation=list(link=log, inverse=exp)),
     multiline=TRUE,
     key.args = list(space="right" ),
     main="",
     ylab="plasma leucine [mcg/ml]")
```



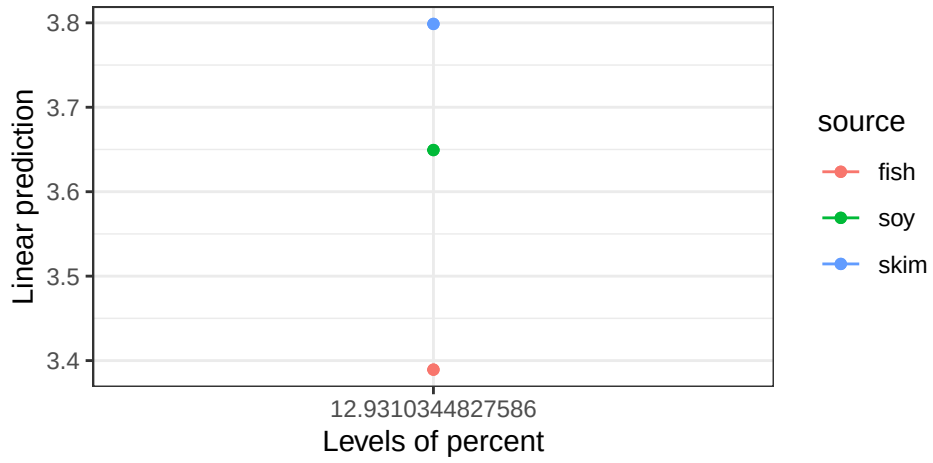

```
pigs.lm3 <- lm(log(conc) ~ source * percent, data = pigs)

plot(
  allEffects(pigs.lm3),
  main = "",
  multiline = TRUE,
  key.args = list(
    space = "right", columns = 1,
```

```
    border = FALSE,
    fontfamily = "serif",
    cex.title = .80,  cex = 0.75
  )
)
```

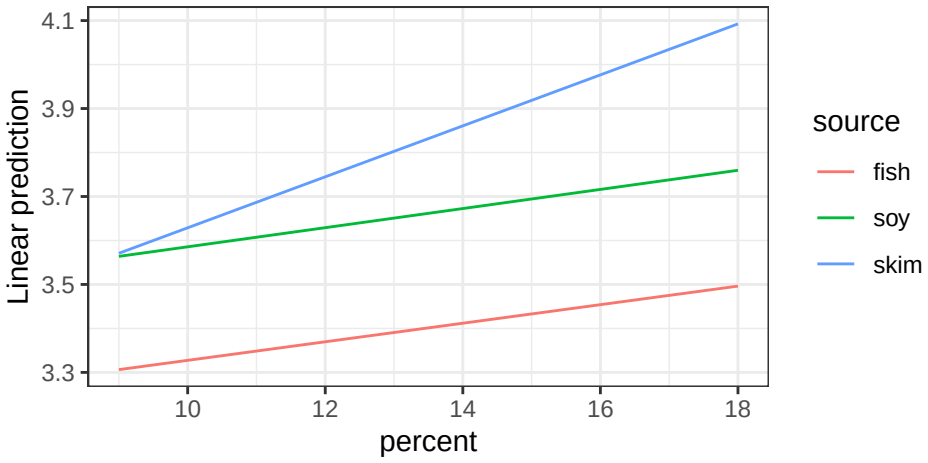



```
emmip(
  ref_grid(pigs.lm3, cov.reduce = TRUE),
  source ~ percent)
```

```
## Suggestion: Add 'at = list(percent = ...)' to call to see > 1 value per group.

## `geom_line()`: Each group consists of only one observation.
## i Do you need to adjust the group aesthetic?
```




```
emmip(
  ref_grid(pigs.lm3, cov.reduce = FALSE),
  source ~ percent)
```

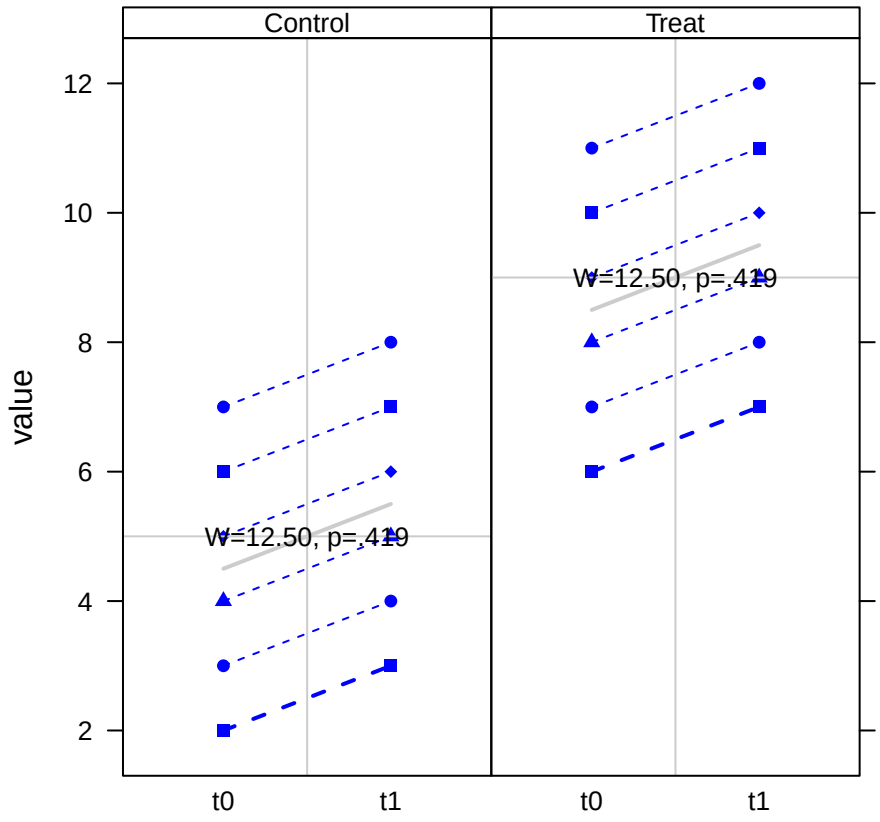



```
raw_data <-
  data.frame(
    subject_id = rep(1:6, 4),
    time = as.factor(rep(c("t0", "t1"), each = 12)),
    group = rep(rep(c("Control", "Treat"), each = 6), 2),
    value = c(2:7, 6:11, 3:8, 7:12)
  )


head(raw_data)
```

```
##   subject_id time   group value
## 1          1   t0 Control     2
## 2          2   t0 Control     3
## 3          3   t0 Control     4
## 4          4   t0 Control     5
## 5          5   t0 Control     6
## 6          6   t0 Control     7
```

```
stripplot(
  value ~ time | group,
  groups = subject_id,
  data = raw_data,
  panel = function(x, y, ...) {
    panel.stripplot(x, y,
                    type =  "b",
                    col="blue",
                    lty = 2, ...)
      panel.average(x, y, fun = mean, lwd = 2, col = "gray80", ...)     # plot line connecting means
      mm<-mean(y)
      panel.abline(h=mm, v=1.5, col="gray80")
      panel.text(x=1.5,y=mm, APA(wilcox.test(y~x)) )



  }
)
```

```
## Warning in wilcox.test.default(x = DATA[[1L]], y = DATA[[2L]], ...): cannot
## compute exact p-value with ties

## Warning in wilcox.test.default(x = DATA[[1L]], y = DATA[[2L]], ...): cannot
## compute exact p-value with ties
```

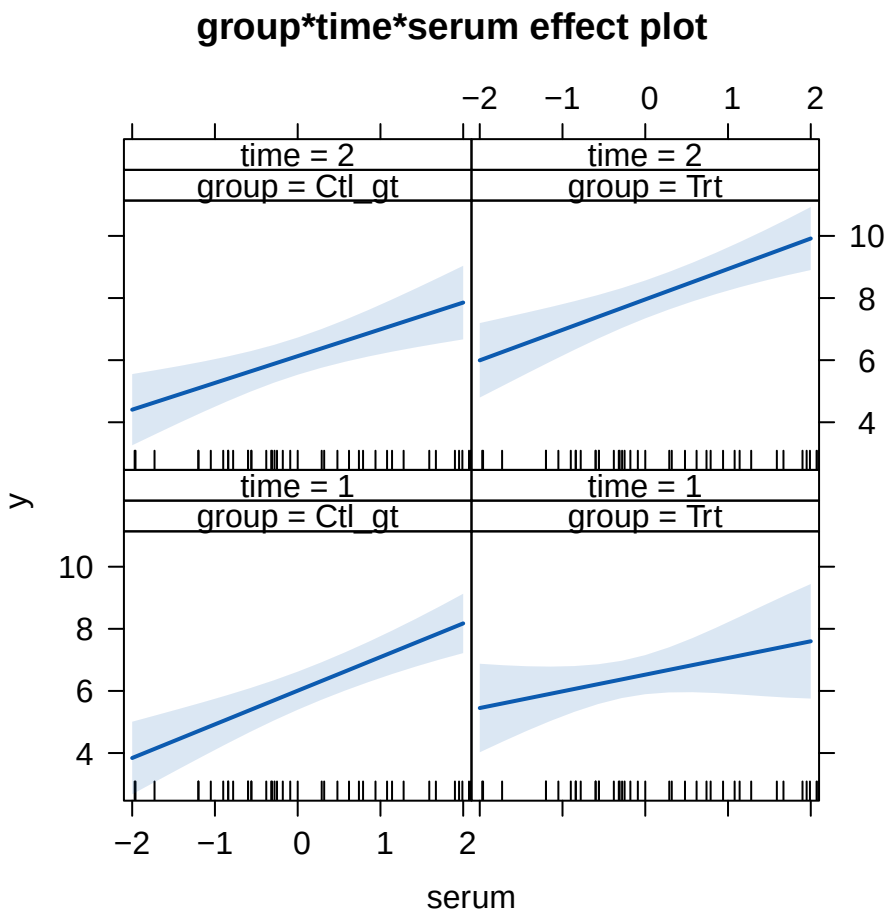


transformation

require(effects) John Fox URL http://www.jstatsoft.org/v32/i01/

```
fit <- lm(y ~ group * time * serum, DF)
```

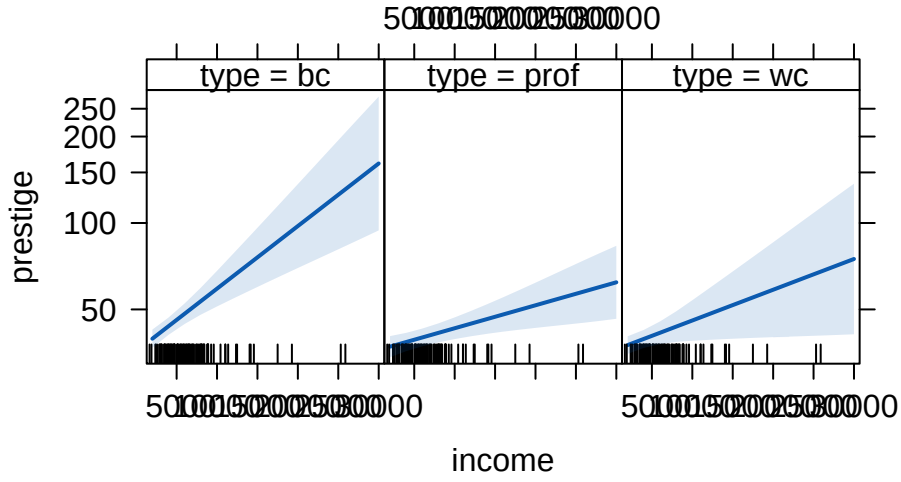
```
plot(effects::allEffects(fit))
```




```
Tbll_desc( ~ log(prestige) + income + type + education,
      data = Prestige)
```

```
## # A tibble: 7 x 3
##   Item               n     m
## * <chr>              <chr> <chr>
## 1 "prestige (mean)"  "102" "3.77 (0.39)"
## 2 "income (mean)"    "102" "6798 (4246)"
## 3 "type "            "98"  ""
## 4 "    bc"           ""    "45% (44)"
## 5 "    prof"         ""    "32% (31)"
## 6 "    wc"           ""    "23% (23)"
## 7 "education (mean)" "102" "10.74 (2.73)"
```

```
mod <- lm(log(prestige) ~ income:type + education, data = Prestige)

# does not work: effect("income:type", mod, transformation=list(link=log, inverse=exp))

plot(Effect(c("income", "type"), mod,
            transformation=list(link=log, inverse=exp)),
     main="", ylab="prestige")
```



Effectplot mit ggplot

Konfidenz-Band mit *geom_ribbon()*

```
ef1 <-
  as.data.frame(
    effects::effect(term = "hp", fit,
                    xlevels = list(
                      hp = seq(50, 350, by =10))))
```

```
## NOTE: hp is not a high-order term in the model
```

```
p1 <- ggplot(ef1, aes(hp, fit)) +
  geom_line() +
  geom_ribbon(aes(ymin = lower, ymax = upper), alpha = 0.3) +
  labs(y = 'Miles/(US) gallon',
       x = 'Gross horsepower',
       title = 'Main-Effect-Plot') +
  theme_classic()
```

Interaction mit *geom_line()*

```
ef2 <- as.data.frame(effects::effect("hp:wt", fit))

ef2$Weight <- factor(ef2$wt)

p2 <- ggplot(ef2, aes(hp, fit, col = Weight)) +
  geom_line() +
  labs(y = 'Miles/(US) gallon',
       x = 'Gross horsepower',
       title = 'Interaction-Plot') +
  theme_classic()
```

Fehlerbalken mit **

```
#ef3<-  as.data.frame(effects::effect("am", fit))

ef4 <-  as.data.frame(effects::effect("cyl_ord", fit2))
p3 <- ggplot(ef4, aes(cyl_ord, fit, group=1 )) +
  geom_point()+
  geom_line()+
  geom_errorbar(
    aes(x = cyl_ord,
        ymin = lower,
        ymax = upper),
    width = 0.2,
    colour = "gray40",
    alpha = 0.9,
    linewidth = .75
  ) +   labs(y = 'Miles/(US) gallon',
             x = 'Number of cylinders',
             title = 'Cylinder Ordinal (nicht linear)')  +
  theme_classic()

ef4 <-  as.data.frame(effects::effect("cyl", fit))
p4 <- ggplot(ef4, aes(cyl, fit, group=1 )) +
  geom_point()+
  geom_line()+
  geom_errorbar(
    aes(x = cyl,
        ymin = lower,
        ymax = upper),
    width = 0.2,
    colour = "gray40",
    alpha = 0.9,
    linewidth = .75
  ) +   labs(y = 'Miles/(US) gallon',
             x = 'Number of cylinders ',
             title = 'Cylinder Metrisch (linear)')  +
  ylim(c(8,23))+
 # xlim(c(4, 8))+
  annotate("text", x = 6, y=9, label =  stp25stat2::APA(fit)) +
  theme_classic()
```

```
library(patchwork)
```

```
##
## Attaching package: 'patchwork'

## The following object is masked from 'package:cowplot':
##
##     align_plots
```

```
p1 + p2 + p3 + p4 +
  plot_layout(ncol=2)
```

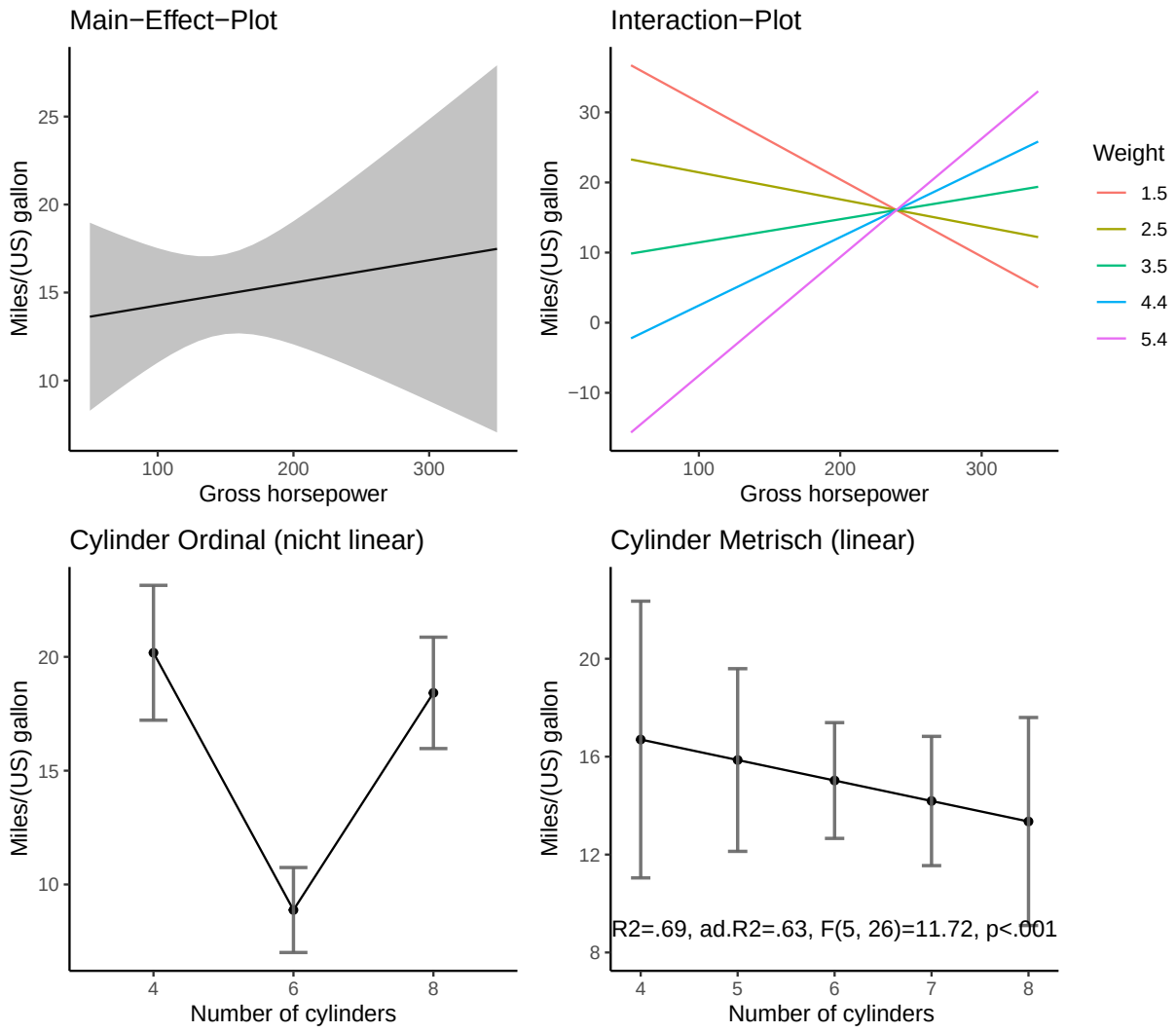


Figure 6: Effect ggplot

GOF-Plots

```
require(car)
```

```
## Loading required package: car
```

```
car::residualPlots(fit)
```

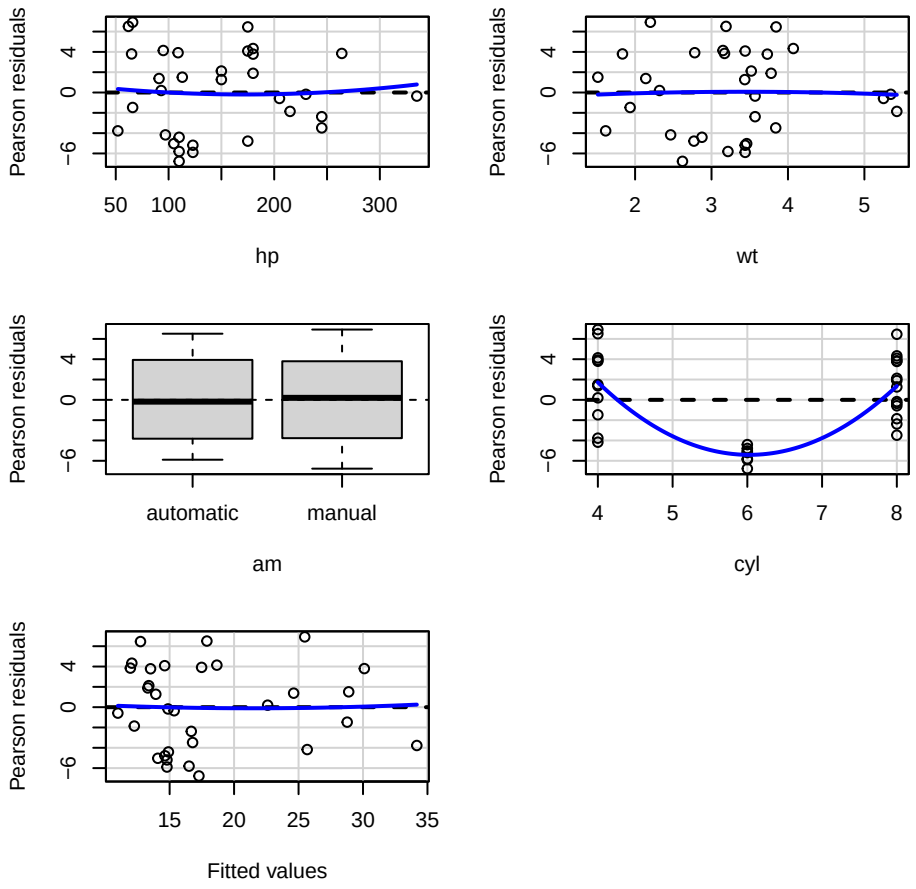


Figure 7: residualPlots

```
##             Test stat Pr(>|Test stat|)
## hp             0.3656           0.7177
## wt            -0.2858           0.7774
## am
## cyl            8.8179        3.809e-09 ***
## Tukey test     0.1215           0.9033
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
car::marginalModelPlots(fit)
```

```
## Warning in mmps(...): Interactions and/or factors skipped
```

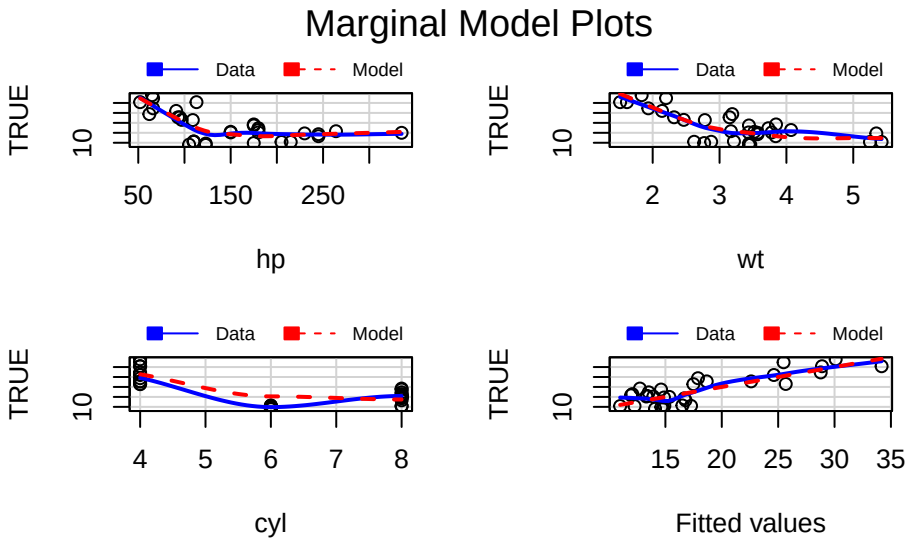


Figure 8: marginalModelPlots

```
car::avPlots(fit)
```

library(visreg)

Patrick Breheny and Woodrow Burchett URL: https://cran.r-project.org/web/packages/visreg/vignettes/quick-start.html

Limitation: plot kann nicht einfach in cowplot::plot_grid integriert werdrn.

```
par(mfrow=c(1,3))
visreg::visreg(fit)
```

```
## Conditions used in construction of plot
## wt: 3.325
## am: automatic
## cyl: 6

## Conditions used in construction of plot
## hp: 123
## am: automatic
## cyl: 6

## Conditions used in construction of plot
## hp: 123
## wt: 3.325
## cyl: 6
```

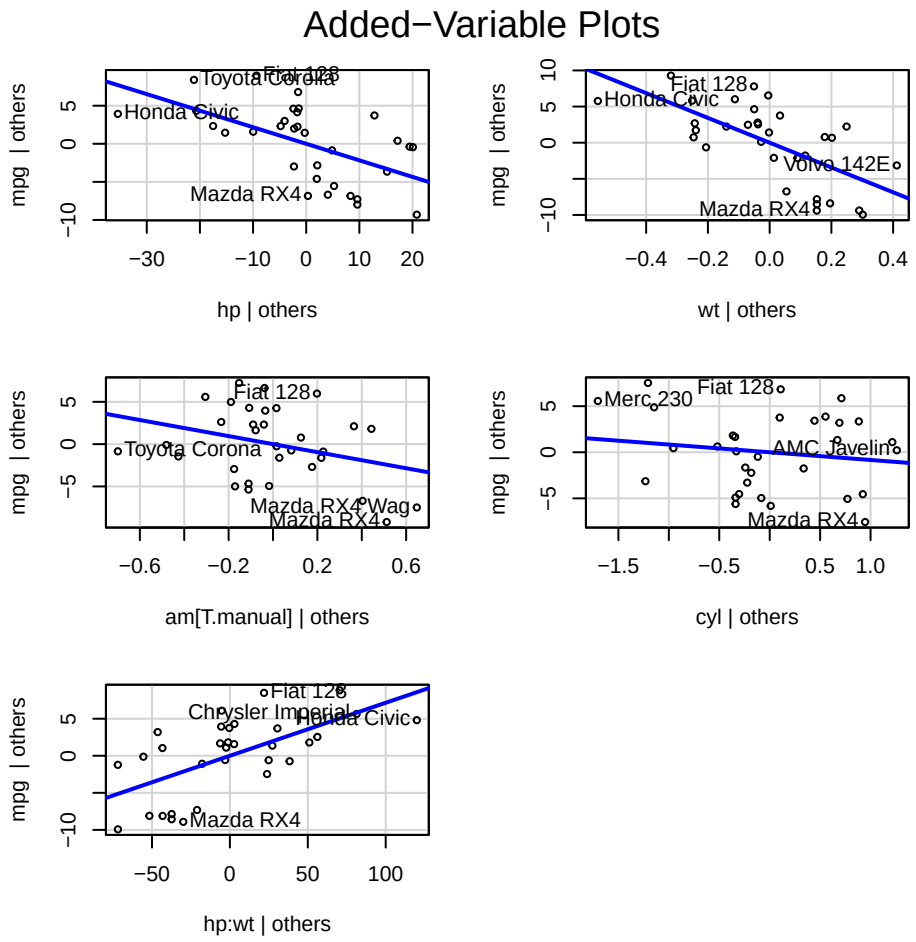


Figure 9: avPlots

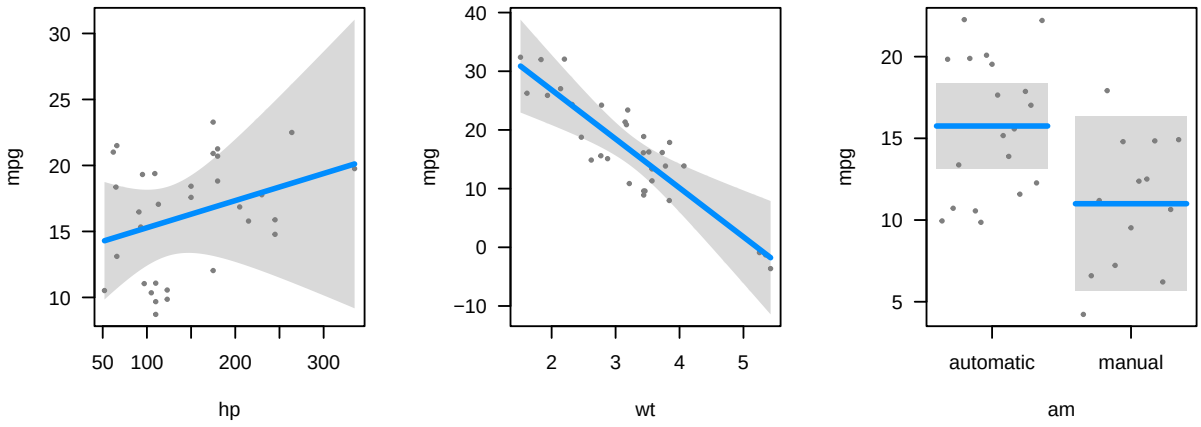


Figure 10: visreg

```
## Conditions used in construction of plot
## hp: 123
## wt: 3.325
## am: automatic
```

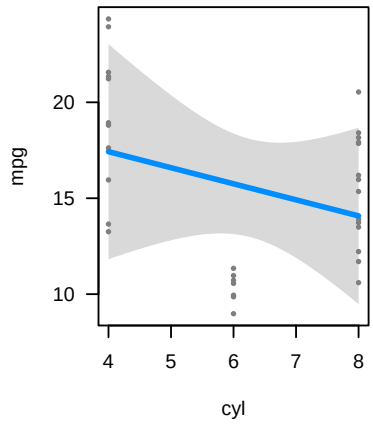
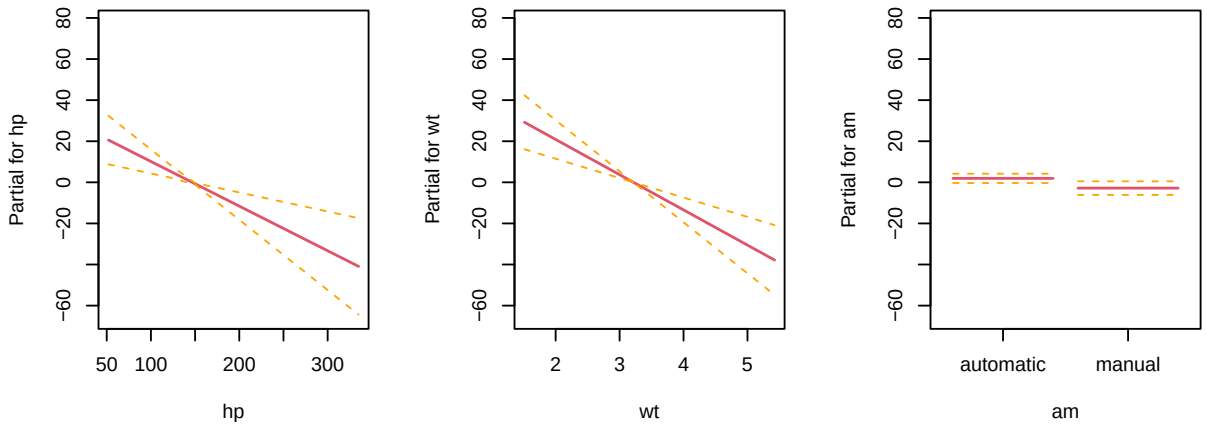
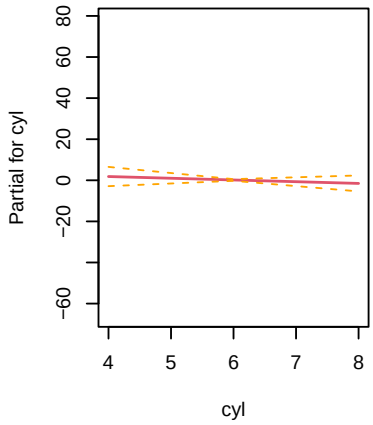


Figure 11: visreg

library(stats) termplot

```
par(mfrow=c(1,3))
stats::termplot(fit,
                se = TRUE,
                resid = TRUE,
                plot=TRUE, ask=FALSE)
```





library(rockchalk) Paul E. Johnson URL https://github.com/pauljohn32/rockchalk

Hier gibt es keine Updates mehr???

```
rockchalk::plotSlopes(fit,
                      plotx = "group",
                      interval = "confidence")

rockchalk::plotSlopes(fit,
                      plotx = "group",
                      modx = "time",
                      interval = "confidence")
```

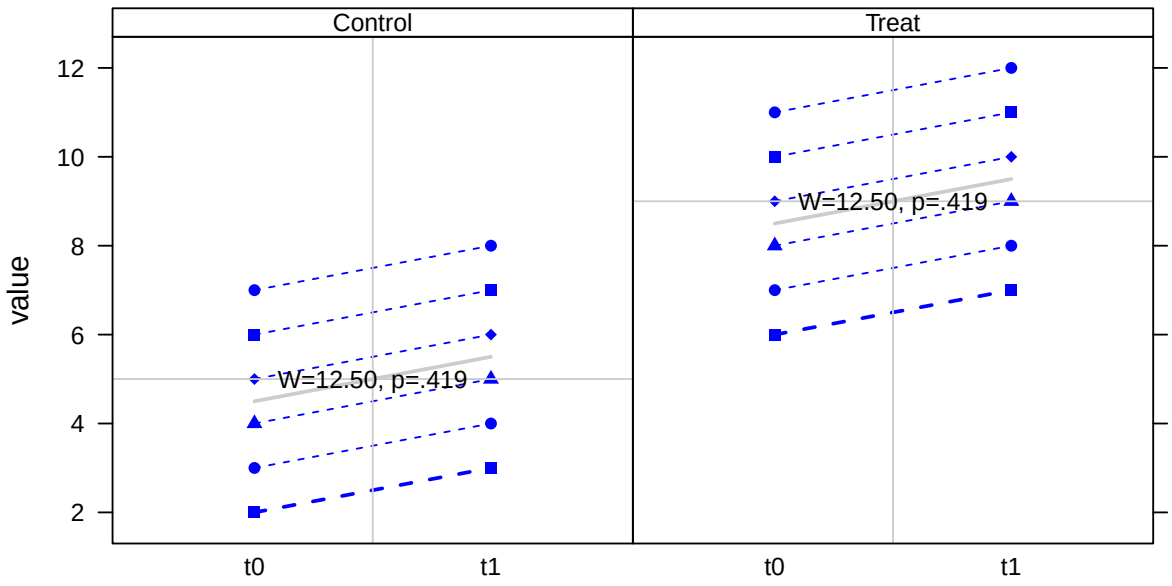
```
raw_data <-
  data.frame(
    subject_id = rep(1:6, 4),
    time = as.factor(rep(c("t0", "t1"), each = 12)),
    group = rep(rep(c("Control", "Treat"), each = 6), 2),
    value = c(2:7, 6:11, 3:8, 7:12)
  )
head(raw_data)
```

```
##   subject_id time   group value
## 1          1   t0 Control     2
## 2          2   t0 Control     3
## 3          3   t0 Control     4
## 4          4   t0 Control     5
## 5          5   t0 Control     6
## 6          6   t0 Control     7
```

```
stripplot(
  value ~ time | group,
  groups = subject_id,
  data = raw_data,
  panel = function(x, y, ...) {
    panel.stripplot(x,
```

```
                    y,
                    type =  "b",
                    col = "blue",
                    lty = 2,
                    ...)
    panel.average(x,
                  y,
                  fun = mean,
                  lwd = 2,
                  col = "gray80",
                  ...)    # plot line connecting means
    mm <- mean(y)
    panel.abline(h = mm, v = 1.5, col = "gray80")
    panel.text(x = 1.5, y = mm, APA(wilcox.test(y ~ x)))

  }
)
```

```
## Warning in wilcox.test.default(x = DATA[[1L]], y = DATA[[2L]], ...): cannot
## compute exact p-value with ties

## Warning in wilcox.test.default(x = DATA[[1L]], y = DATA[[2L]], ...): cannot
## compute exact p-value with ties
```



Altman and Bland (Tukey Mean-Difference Plot)

```
# A - Goldstandart
```

```
x <- MetComp_BAP(~A+B, Giavarina)
#> Warning: Warning in bland.altman.stats:Mehr als 2 Methoden.
# x %>% Output("BA-Analyse der Messwertreihe")
plot(x)
```

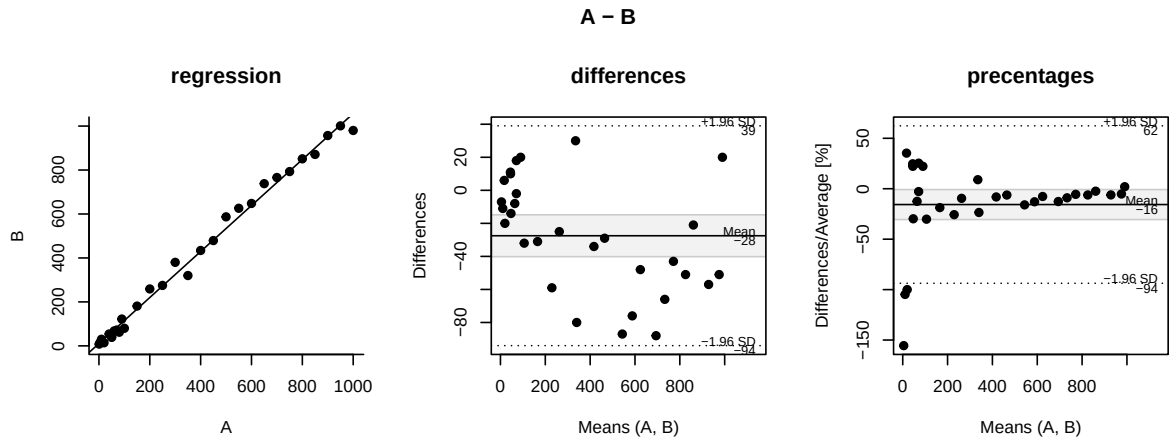


Figure 12: Bland Altman

```
lattice::tmd( A ~ B, Giavarina)
```

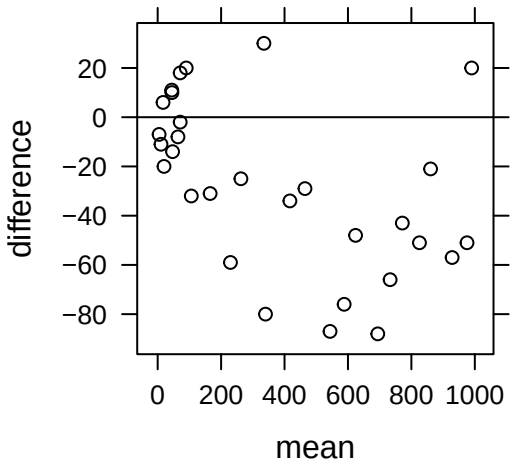
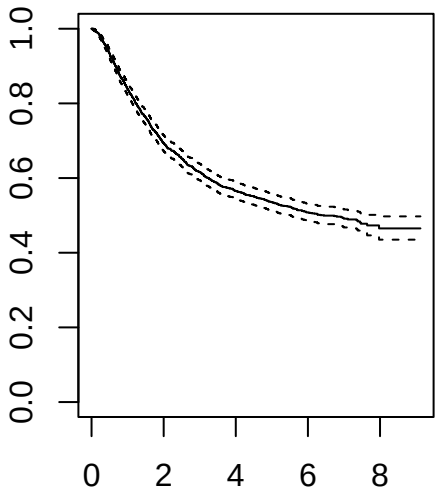


Figure 13: Bland Altman

Survival Analysis

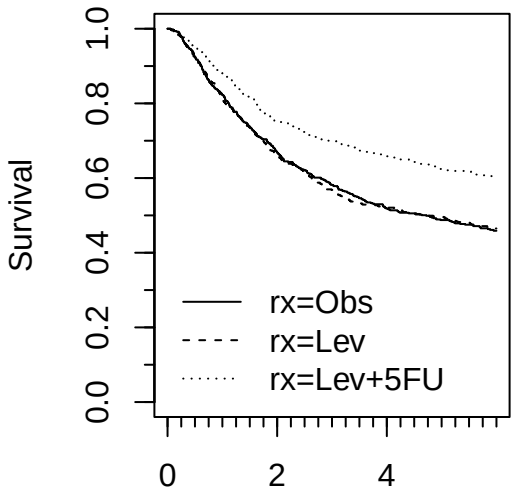
Add number-at-risk annotations to a plot

```r
require("survival")

s <- Surv(colon$time / 365, colon$status)

## Need to increase margins a bit
par(mar = c(10, 6, 2, 1),mfrow = c(1,2))

## no stratification
fit1 <- survfit(s ~ 1)
plot(fit1)
addNrisk(fit1)

## with stratification
at <- c(0, 2, 4)
lty <- 1:3
xlim <- c(0, 6)
fit2 <- survfit(s ~ rx, data = colon)
plot(fit2,
     xlab = 'Time (years)',
     ylab = 'Survival',
     xaxt = "n",
     xlim=xlim,
     lty = lty)

addNrisk(fit2, at)
axis(1, at = at, gap.axis = 1 / 4)
legend(
  'bottomleft',
  legend = names(fit2$strata),
  lty = lty,
  bty = 'n'
)
Hmisc::minor.tick(nx = 4, tick.ratio = 1 / 2)
```



Number at risk

1858 1028 50



Time (years)

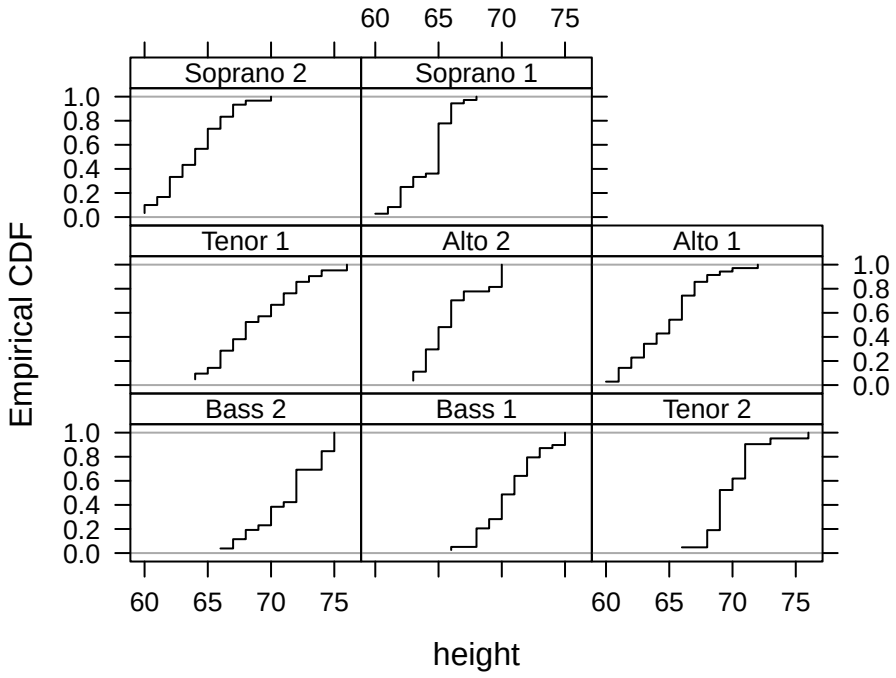
Number at risk

Obs	630	417	318
Lev	620	406	319
Lev+5FU	608	453	391

ECDF-Plot

ecdfplot {latticeExtra}

```
# data(Chem97, package = "mlmRev")
#
# ecdfplot(~gcsescore | factor(score), data = Chem97,
#     groups = gender,
#     auto.key = list(columns = 2),
#     subset = gcsescore > 0,
#     xlab = "Average GCSE Score")

data(singer, package = "lattice")
ecdfplot(~height | voice.part, data = singer)
```



data(singer, package = "lattice")

Interessante Grafik Beispiele

Lattice xyplot mit Pfeilen und verlaufende Farben.

```
dat <- stp25tools::get_data("
  variable        value change leverage
     happiness   4.62  -0.42    0.01
    motivation   3.6   -0.41    0.05
      training   3.4   -0.33    0.14
   performance   3.2    0.30    0.82
           lmx   2.96   0.21    0.33
 communication   2.9   -0.11    0.43
      autonomy   2.7    0.11    0.22
    insecurity   2.5    0.12    0.21
        stress   1.6    0.14    0.12")

#Create a function to generate a continuous color palette
rbPal <- colorRampPalette(c('gray','blue'))

xyplot(
  reorder(variable, value) ~ value ,
  xlab = "",  ylab = "",
  data = dat,
  xlim = c(0.85, 5.15),# drop.unused.levels = FALSE,
  scales = list(x = list(
     at = 1:5,
```

```
    labels = c( "low",  "moderate", "considerable", "hig","very high")
  )),
  panel = function(x, y, ...) {

    col <- rbPal(8)[as.numeric(cut(dat$leverage,breaks = 8))]

    panel.dotplot(
      x = x,  y = y,
      col = col,
      cex = 1.1 + 1 * dat$leverage,
      pch = 19
    )

    panel.arrows(
      x0 = x, y0 = y,
      x1 = x + x * dat$change, y1 = y,
      col=col, lwd = 2,
      angle = 30, code = 2, length = 0.1
    )
  }
)
```

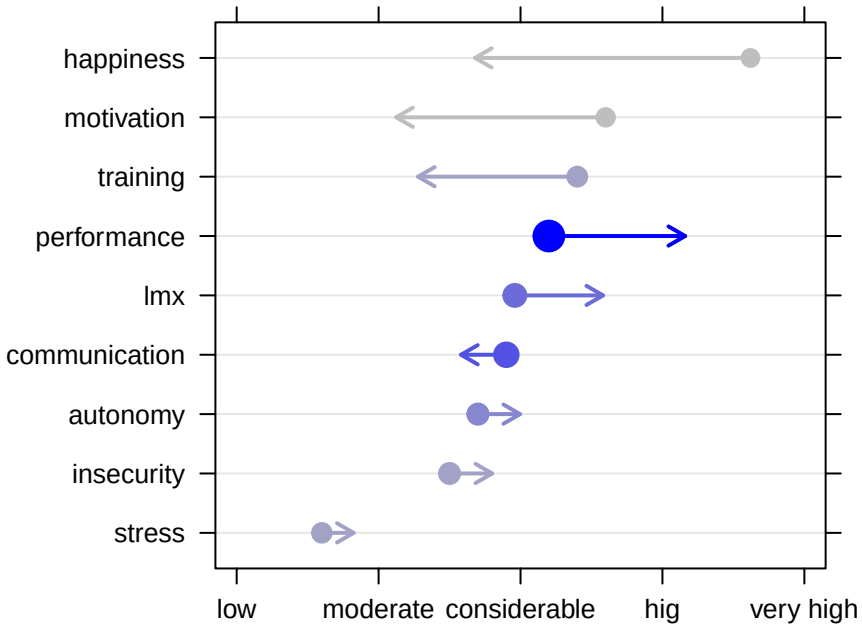
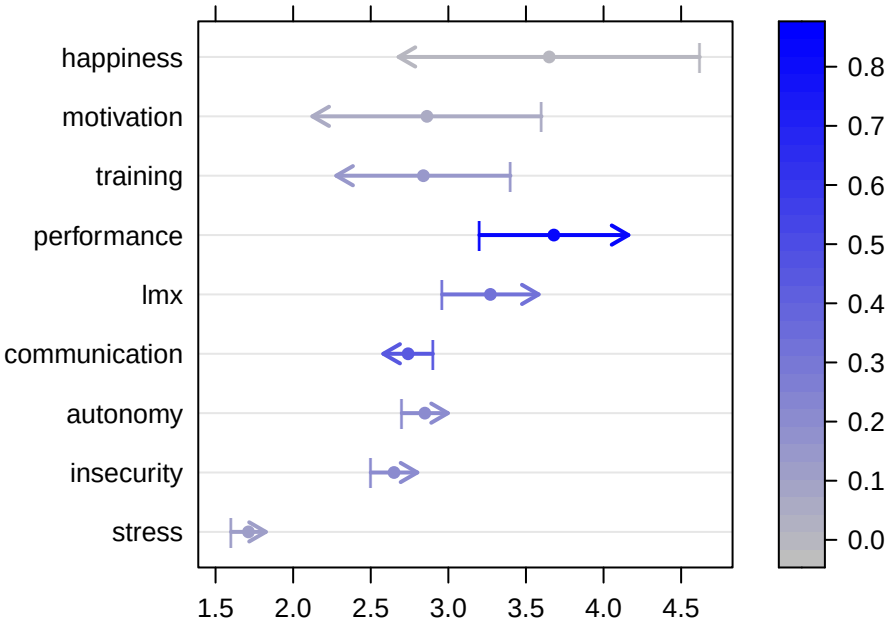


Figure 14: Lattice xyplot mit Pfeilen und verlaufende Farben.

```
# siehe panel.segplot
panel.arrows2 <- function(x0, y0 , x1, y1,
                          col, alpha, lty, lwd, ...) {
```

```
  panel.dotplot(
    x = x0,   y = y0,
    col = col,
    cex = 1.5,
    pch = "|"
  )
  panel.arrows(
    x0, y0, x1, y1,
    col = col ,
    alpha = alpha,
    lty = lty,
    lwd = lwd,
    ...
  )



}

dat$change <- dat$value + dat$change * dat$value
dat$centers <- (dat$value + dat$change) / 2
#require(latticeExtra)
segplot(
  reorder(variable, value) ~ value + change,
  level = leverage,
  data = dat,
  draw.bands = FALSE,
  centers = centers,
  segments.fun = panel.arrows2,
  lwd = 2,
  angle = 30,
  code = 2,
  length = 0.1,
  colorkey = TRUE,
  col.regions = rbPal# hcl.colors #terrain.colors

)
```

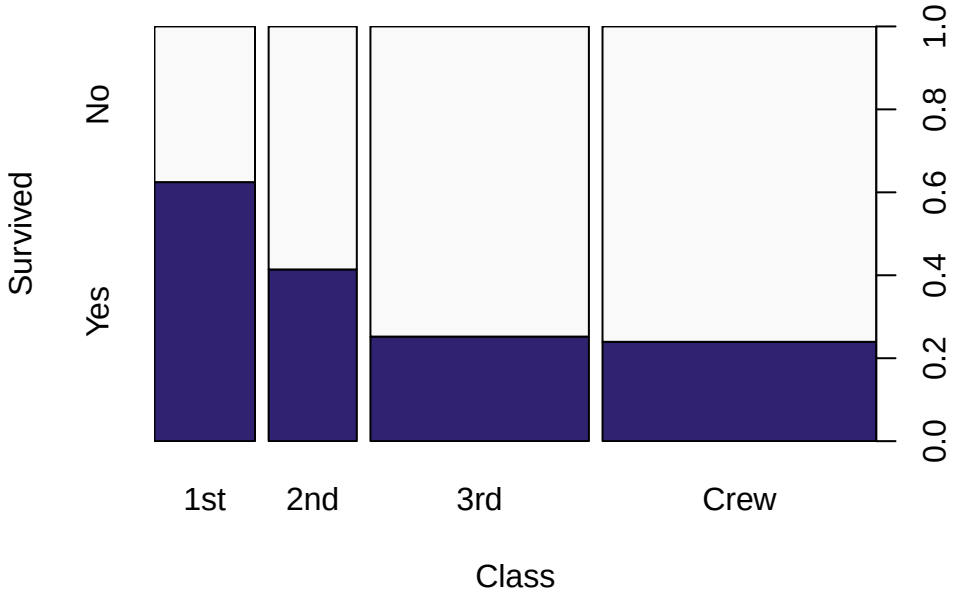


Spine Plots and Spinograms

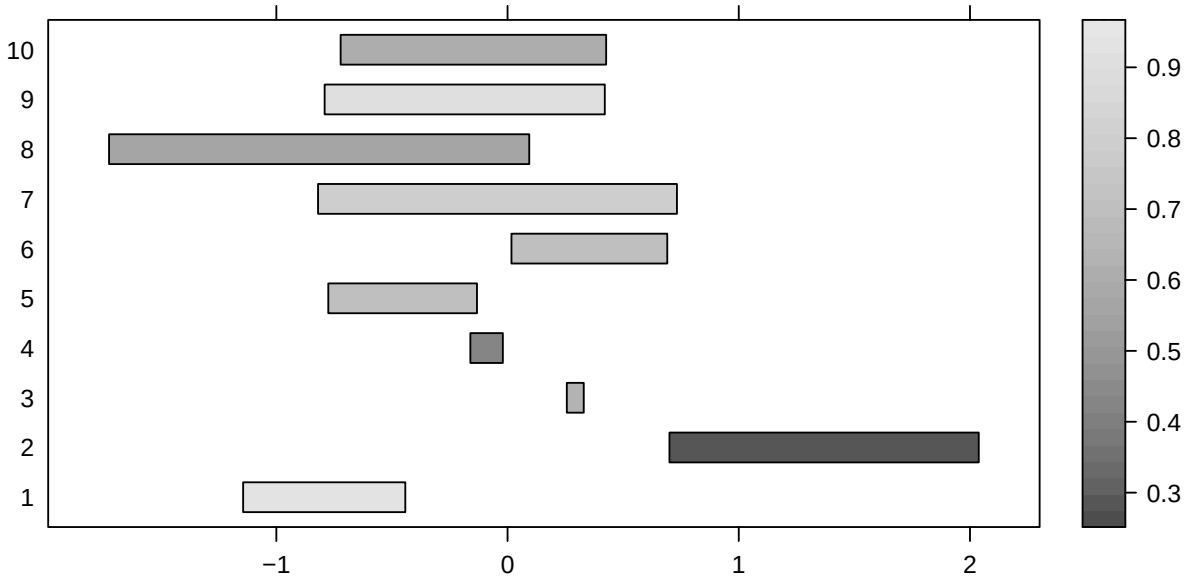
```
require("colorspace")
```

```
## Loading required package: colorspace
```

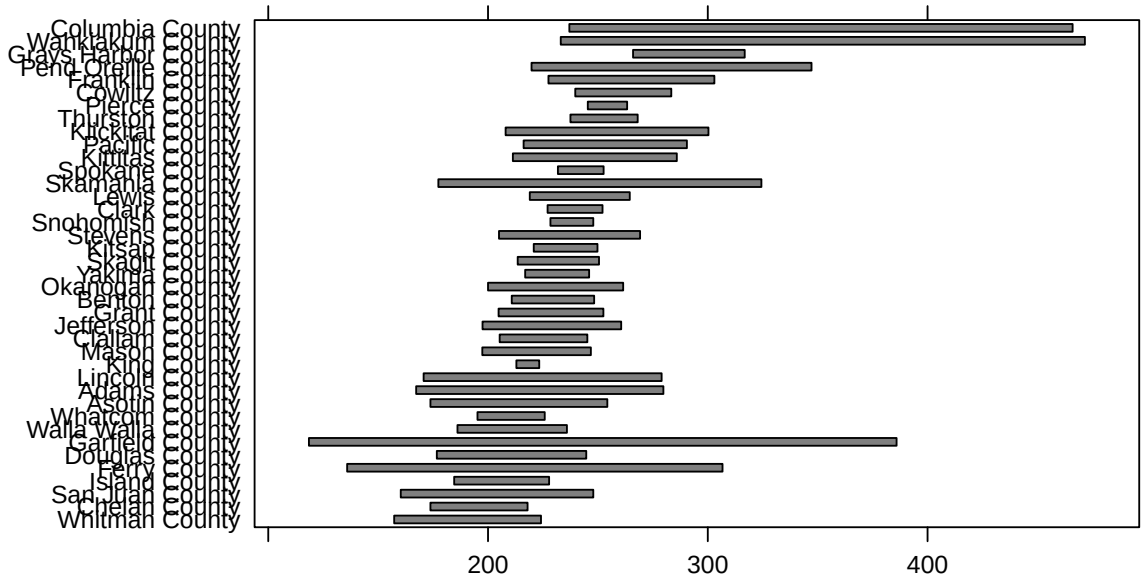
```
ttnc <- margin.table(Titanic, c(1, 4))

spineplot(ttnc, col = sequential_hcl(2, palette = "Purples 3"))
```



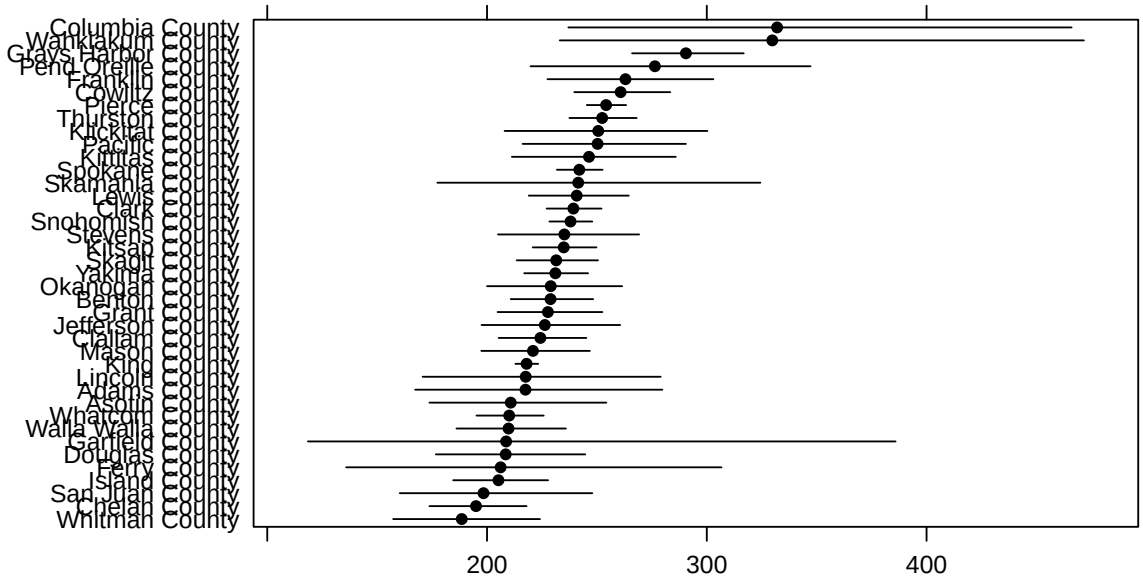

```
# require(latticeExtra)
 segplot(factor(1:10) ~ rnorm(10) + rnorm(10), level = runif(10))
```



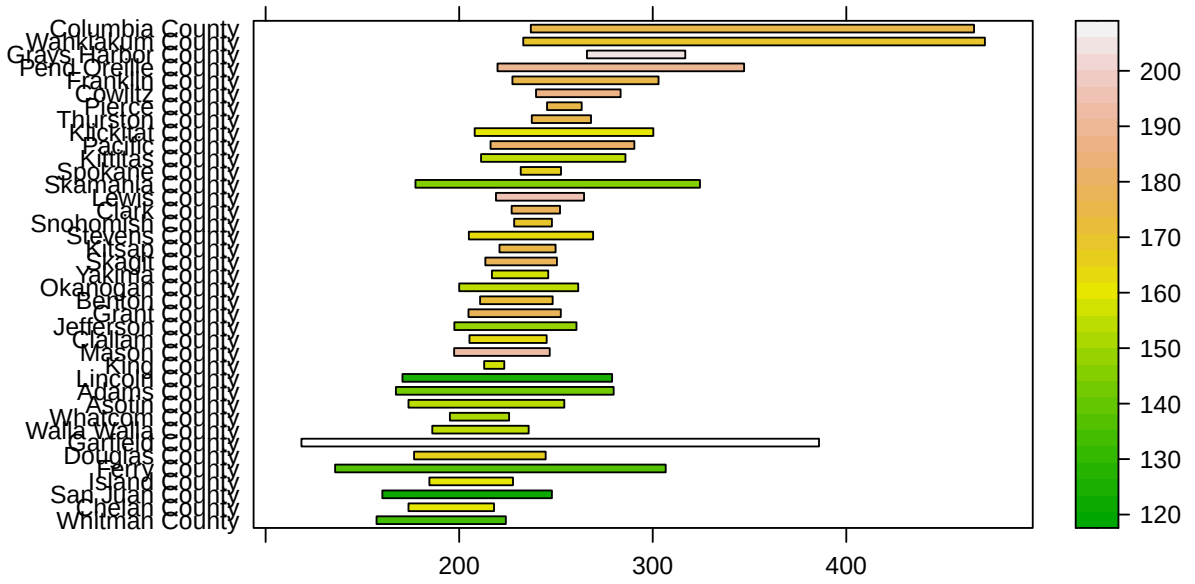
```
data(USCancerRates)

segplot(reorder(factor(county), rate.male) ~ LCL95.male + UCL95.male,
        data = subset(USCancerRates, state == "Washington"))
```



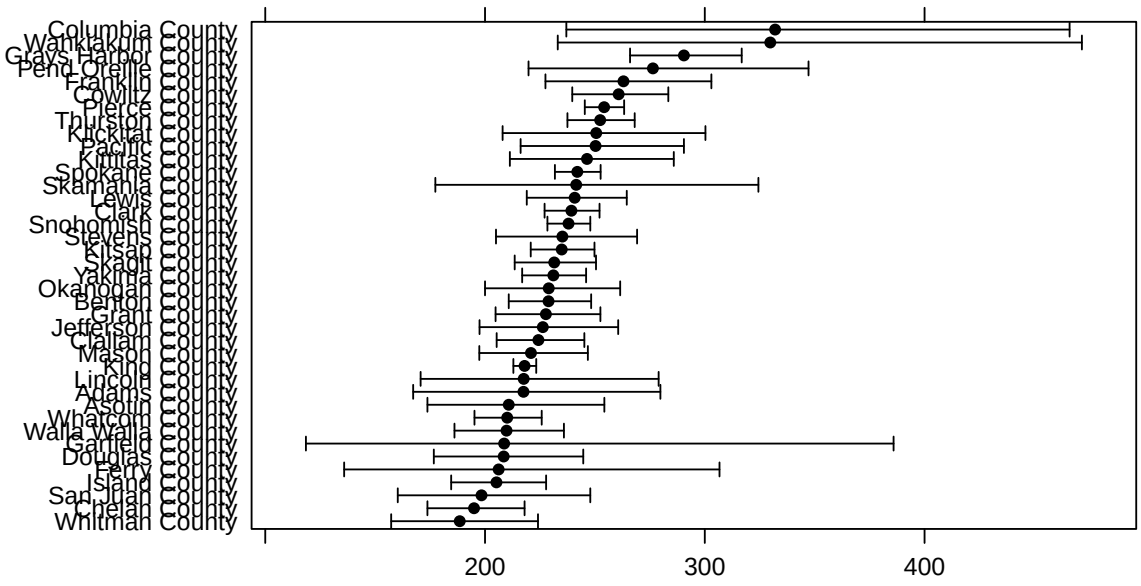

```
segplot(reorder(factor(county), rate.male) ~ LCL95.male + UCL95.male,
        data = subset(USCancerRates, state == "Washington"),
        draw.bands = FALSE,
        centers = rate.male)
```



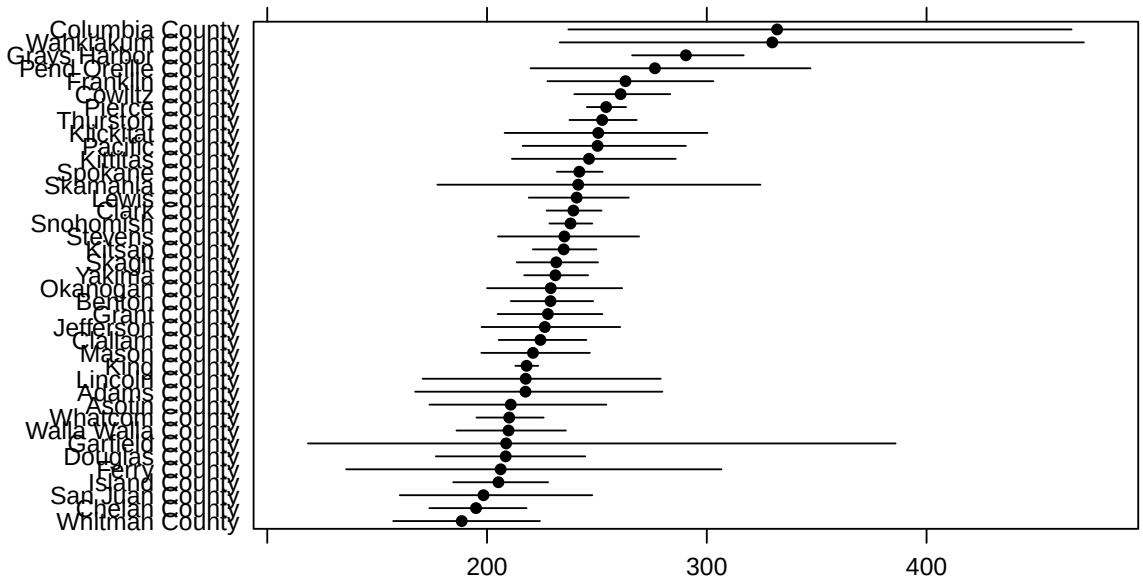

```
segplot(reorder(factor(county), rate.male) ~ LCL95.male + UCL95.male,
        data = subset(USCancerRates, state == "Washington"),
        level = rate.female,
        col.regions = terrain.colors)
```



```
segplot(reorder(factor(county), rate.male) ~ LCL95.male + UCL95.male,
        data = subset(USCancerRates, state == "Washington"),
        draw.bands = FALSE,
        centers = rate.male,
        segments.fun = panel.arrows,
        ends = "both",
        angle = 90,
        length = 1,
        unit = "mm")
```




```
segplot(reorder(factor(county), rate.male) ~ LCL95.male + UCL95.male,
        data = subset(USCancerRates, state ==  "Washington"),
        draw.bands = FALSE, centers = rate.male)
```



Misc

Speichern von Grafiken als PDF scheitert wen Unicode verwendet wird abhilfe bietet CairoPDF.

```
require(Cairo)

CairoPDF( paste0(Abb()[3],"-cell-count.pdf"),  width = 7, height =  0.66*8 +.4)
  plot_grid(p_all, p_cit, p_trns, p_dbd)

  invisible(dev.off())
```

Links

https://ggobi.github.io/ggally/index.html

http://www.sthda.com/english/articles/24-ggpubr-publication-ready-plots/78-perfect-scatter-plots-with-correlation-and-marginal-histograms/

ggpubr

http://www.sthda.com/english/articles/24-ggpubr-publication-ready-plots/78-perfect-scatter-plots-with-correlation-and-marginal-histograms/