Rep_agree

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Settings

Used software: R

```
setwd("C:/pendrivok/oktatos/oktatas_2019tavasz/nemet_stat/2")
```

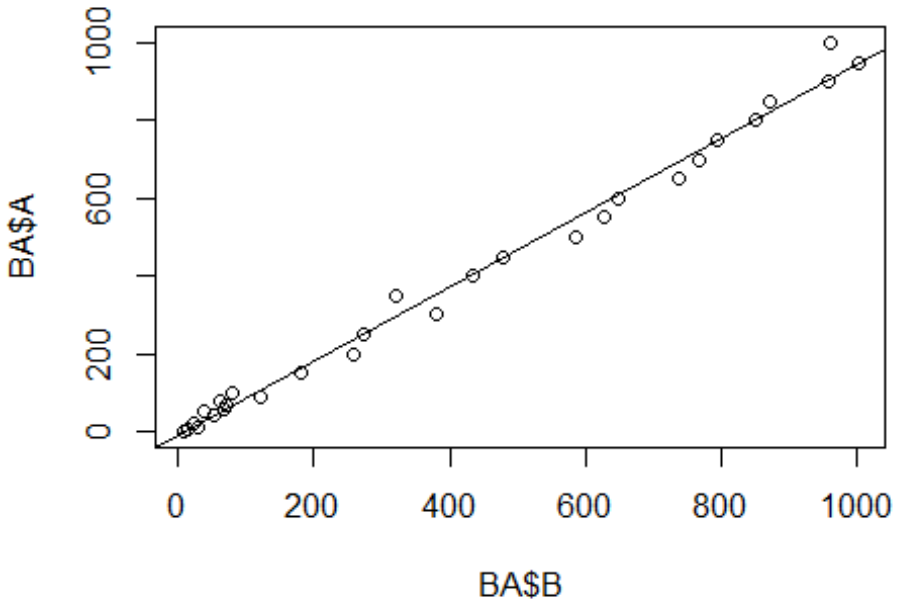
Bland-Altman plot

Comparing 2 measurement: eg. blood pressure measured with Arm and Finger Device

```
BA_original <- read.csv("BA_original.csv", sep=";")
BA <- read.csv("BA.csv", sep=";")
```

Create correlation

```
plot(BA$A~BA$B)
abline(lm(BA$A~BA$B))
```



Correlation coefficient

```r
cor.test(BA$A,BA$B)
```

```
##
##  Pearson's product-moment correlation
##
## data:  BA$A and BA$B
## t = 58, df = 28, p-value <2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0,9911 0,9980
## sample estimates:
##    cor
## 0,9958
```

Regression

```r
lm(BA$A~BA$B)
```

```
##
## Call:
## lm(formula = BA$A ~ BA$B)
##
## Coefficients:
## (Intercept)         BA$B
##      -8,388        0,952
```

Opinion?

```r
summary(BA)
```

```
##        A                B             X             X.1
##  Min.   :   1,0   Min.   :   8,0   Mode:logical   Mode:logical
##  1st Qu.:  62,5   1st Qu.:  63,5   NA's:30        NA's:30
##  Median : 275,0   Median : 297,5
##  Mean   : 364,2   Mean   : 391,4
##  3rd Qu.: 637,5   3rd Qu.: 715,5
##  Max.   :1000,0   Max.   :1001,0
##    X.2            X.3
##  Mode:logical   Mode:logical
##  NA's:30        NA's:30
##
##
##
##
```

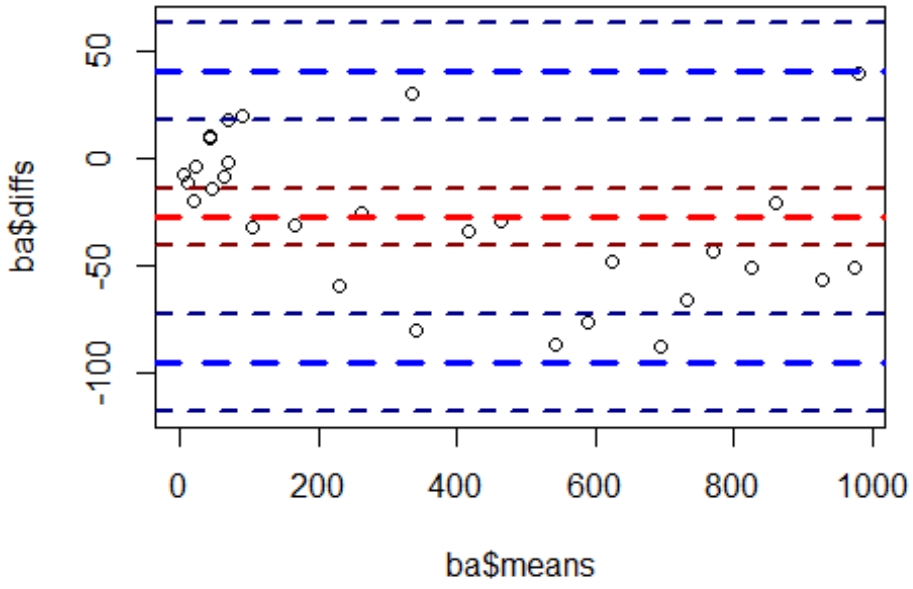
```r
t.test(BA$A,BA$B)
```

```
##
##  Welch Two Sample t-test
##
## data:  BA$A and BA$B
## t = -0,31, df = 58, p-value = 0,8
```

```
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -203,5  149,2
## sample estimates:
## mean of x mean of y
##     364,2     391,4
```

BA plot (req. BlandAltmanLeh)

```
bland.altman.plot(BA$A,BA$B, conf.int = 0.95)
```




```
## NULL
```

Kendall W, Kendall-Babington Smith test

Repeatability (agreement, concordance) in ordinal scale

```
KW_agree <- read.csv("KW_agree.csv", sep=";")

kendall.global(KW_agree)

## $Concordance_analysis
##           Group.1
## W           1e+00
## F             Inf
## Prob.F      0e+00
## Chi2        2e+01
## Prob.perm   1e-03
```

```
##
## attr(,"class")
## [1] "kendall.global"
```

```
kendall.post(KW_agree)
```

```
## $A_posteriori_tests
##                   J1    J2    J3    J4
## Spearman.mean  1,000 1,000 1,000 1,000
## W.per.species  1,000 1,000 1,000 1,000
## Prob           0,002 0,004 0,003 0,004
## Corrected prob 0,008 0,009 0,009 0,009
##
## $Correction.type
## [1] "holm"
##
## attr(,"class")
## [1] "kendall.post"
```

```
KW_rand <- read.csv("KW_rand1.csv", sep=";")
```

```
kendall.global(KW_rand)
```

```
## $Concordance_analysis
##            Group.1
## W          0,36737
## F          1,74214
## Prob.F     0,09402
## Chi2      19,10347
## Prob.perm  0,09200
##
## attr(,"class")
## [1] "kendall.global"
```

```
kendall.post(KW_rand)
```

```
## $A_posteriori_tests
##                    J1       J2     J3     J4
## Spearman.mean  0,1209 -0,02438 0,2258 0,3051
## W.per.species  0,3407  0,23171 0,4194 0,4788
## Prob           0,2510  0,55000 0,1080 0,0330
## Corrected prob 0,5020  0,55000 0,3240 0,1320
##
## $Correction.type
## [1] "holm"
##
## attr(,"class")
## [1] "kendall.post"
```

```
KW_real <- read.csv("KW_real.csv", sep=";")
```

```
kendall.global(KW_real)
```

```
## $Concordance_analysis
##             Group.1
## W         5,172e-01
## F         4,285e+00
## Prob.F    4,491e-26
## Chi2      2,664e+02
## Prob.perm 1,000e-03
##
## attr(,"class")
## [1] "kendall.global"
```

```
kendall.post(KW_real)
```

```
## $A_posteriori_tests
##                    J1     J2     J3     J4     J5
## Spearman.mean  0,4324 0,4497 0,3634 0,3595 0,3768
## W.per.species  0,5459 0,5598 0,4907 0,4876 0,5014
## Prob           0,0010 0,0010 0,0010 0,0010 0,0010
## Corrected prob 0,0050 0,0050 0,0050 0,0050 0,0050
##
## $Correction.type
## [1] "holm"
##
## attr(,"class")
## [1] "kendall.post"
```

Fleiss' kappa

Repeatability in nominal scale

```
fleiss_real <- read.csv("fleiss.csv", sep=",")
```

Reshape

```
fleiss_wide <- reshape(data = fleiss_real,direction = "wide", idvar = "ID",
timevar = "nameid")
```

% agreement?

```
fleiss_wide$pos <-rowSums(fleiss_wide[,2:7])
fleiss_wide$neg <-6-rowSums(fleiss_wide[,2:7])
fleiss_wide$perc <- apply(fleiss_wide[,8:9],1, max)/6
summary(fleiss_wide$perc)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   0,500   0,833   0,833   0,816   0,833   1,000
```

```
t.test(fleiss_wide$perc)
```

```
##
##  One Sample t-test
##
```

```
## data:  fleiss_wide$perc
## t = 24, df = 18, p-value = 3e-15
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  0,7455 0,8861
## sample estimates:
## mean of x
##    0,8158
```

```
kappam.fleiss(fleiss_wide[,2:7])
```

```
##  Fleiss' Kappa for m Raters
##
##  Subjects = 19
##    Raters = 6
##     Kappa = 0,346
##
##         z = 5,85
##   p-value = 4,94e-09
```