

Příklad 1:

```

mod1 <- aov(loglym ~ infek, data=lymfo)
summary(mod1)

##              Df Sum Sq Mean Sq F value    Pr(>F)
## infek      4    54.85   13.712   10.65 9.88e-08 ***
## Residuals 171   220.10    1.287
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

with(lymfo, numSummary(loglym, groups=infekt, statistics=c("mean", "sd")))

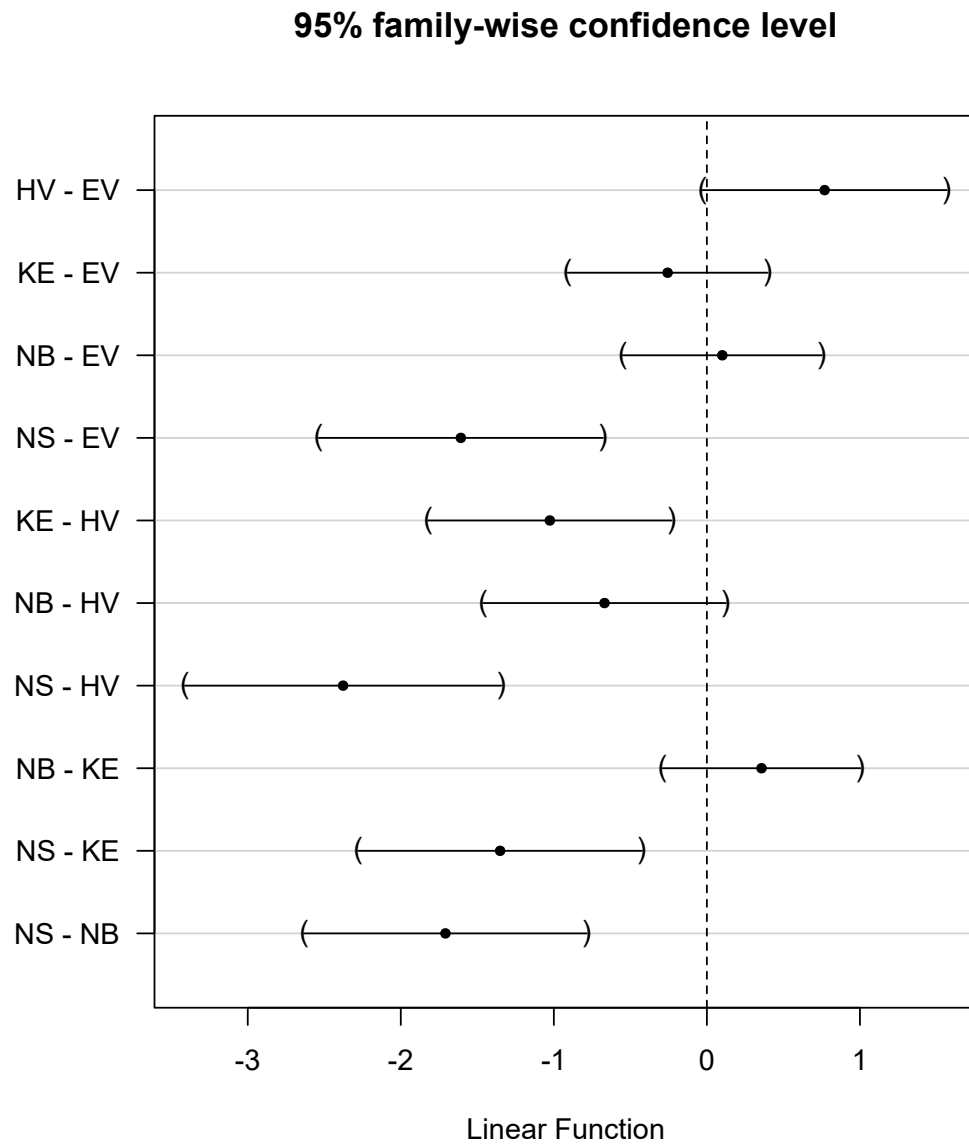
##          mean          sd data:n
## EV 4.398098 1.2333843      45
## HV 5.167492 1.3598121      23
## KE 4.141498 0.9084437      46
## NB 4.498643 1.1620989      47
## NS 2.790502 0.9721319      15

local({
  .Pairs <- glht(mod1, linfct = mcp(infekt = "Tukey"))
  print(summary(.Pairs)) # pairwise tests
  print(confint(.Pairs, level=0.95)) # confidence intervals
  print(cld(.Pairs, level=0.05)) # compact letter display
  old.oma <- par(oma=c(0, 5, 0, 0))
  plot(confint(.Pairs))
  par(old.oma)
})

##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: aov(formula = loglym ~ infek, data = lymfo)
##
## Linear Hypotheses:
##              Estimate Std. Error t value Pr(>|t|)
## HV - EV == 0    0.7694    0.2908   2.646  0.06420 .
## KE - EV == 0   -0.2566    0.2379  -1.079  0.81270
## NB - EV == 0    0.1005    0.2366   0.425  0.99290
## NS - EV == 0   -1.6076    0.3383  -4.753 < 0.001 ***
## KE - HV == 0   -1.0260    0.2897  -3.541  0.00438 **
## NB - HV == 0   -0.6688    0.2887  -2.317  0.14021
## NS - HV == 0   -2.3770    0.3765  -6.313 < 0.001 ***
## NB - KE == 0    0.3571    0.2353   1.518  0.54479
## NS - KE == 0   -1.3510    0.3373  -4.005 < 0.001 ***
## NS - NB == 0   -1.7081    0.3364  -5.077 < 0.001 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
##
##
## Simultaneous Confidence Intervals
##
## Multiple Comparisons of Means: Tukey Contrasts
##

```

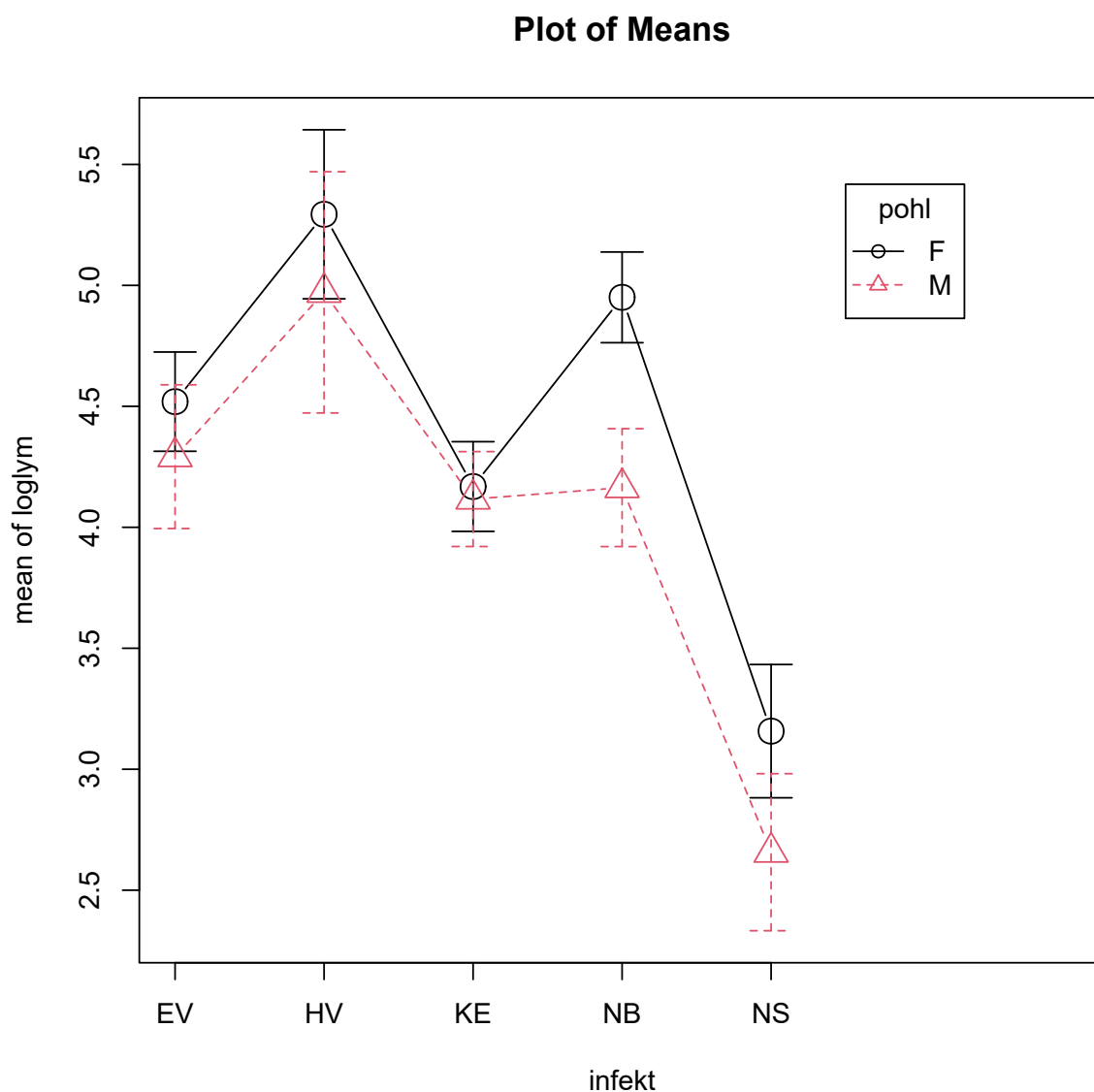
```
##
## Fit: aov(formula = loglym ~ infek, data = lymfo)
##
## Quantile = 2.743
## 95% family-wise confidence level
##
##
## Linear Hypotheses:
##           Estimate lwr      upr
## HV - EV == 0  0.76939 -0.02829  1.56707
## KE - EV == 0 -0.25660 -0.90910  0.39590
## NB - EV == 0  0.10054 -0.54851  0.74960
## NS - EV == 0 -1.60760 -2.53542 -0.67977
## KE - HV == 0 -1.02599 -1.82073 -0.23125
## NB - HV == 0 -0.66885 -1.46077  0.12307
## NS - HV == 0 -2.37699 -3.40981 -1.34417
## NB - KE == 0  0.35714 -0.28830  1.00259
## NS - KE == 0 -1.35100 -2.27630 -0.42569
## NS - NB == 0 -1.70814 -2.63102 -0.78526
##
##      EV      HV      KE      NB      NS
## "bc"   "c"   "b"  "bc"   "a"
```



Střední hodnoty se liší, zamítám stejnost pairwise comparison, popsát rozdíly, vyšly significantní

Příklad 2:

```
plotMeans(loglym, infek, pohl, error.bars="se", connect=TRUE, legend.pos="farright")
```



```
mod2 <- lm(loglym ~ infektt+pohl, data=lymfo, contrasts=list(infektt="contr.Sum", pohl="contr.Sum"))
Anova(mod2)

## Anova Table (Type II tests)
##
## Response: loglym
##          Sum Sq Df F value    Pr(>F)
## infektt  49.023  4  9.7121 4.247e-07 ***
## pohl       5.580  1  4.4218  0.03695 *
## Residuals 214.524 170
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Tapply(loglym ~ infektt + pohl, mean, na.action=na.omit, data=lymfo) # means

##          pohl
## infektt      F      M
##      EV 4.519428 4.291934
##      HV 5.293726 4.971128
##      KE 4.168507 4.116740
```

```
##      NB 4.950482 4.163947
##      NS 3.157443 2.657069

Tapply(loglym ~ infek + pohl, sd, na.action=na.omit, data=lymfo)

##      pohl
## infek  F      M
##      EV 0.9400891 1.4548185
##      HV 1.3070840 1.4958171
##      KE 0.8694006 0.9608281
##      NB 0.8383912 1.2658070
##      NS 0.5508724 1.0763715

# std. deviations
xtabs(~ infek + pohl, data=lymfo) # counts

##      pohl
## infek  F  M
##      EV 21 24
##      HV 14  9
##      KE 22 24
##      NB 20 27
##      NS  4 11
```

dobrý si udělat plot of means, interakce tam nejsou