

EconomicalWeights

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Economical Weights

Economical weights are factors to produce an aggregate genotype from multiple traits. There is one economical weight per involved trait. The economical weight per trait is the change in profit (Sfr.) per additional unit of the trait. Here the aggregate genotype consists of the traits carcass fat, carcass conformation and carcass weight. Consequently the three traits need an economical weight each. Also aggregate genotypes have to be computed for each breed and animal group separately. As an example the economic values will appear for the most distinct breeds, Angus and Limousin and the group stirks.

Carcass fat

The trait carcass fat has the unit carcass fat class (see table??). Therefore the economical weight for carcass fat is the additional revenue per unit of carcass fat class. I choose the unit Swiss Francs (Sfr.) per 1 carcass fat class.

Initial Situation

To get the minus of Sfr. per 1 carcass fat class, I need to calculate the mean price difference in a population when I change the mean carcass fat score in the population. To do so I change the population slightly, but try to conserve the initial distribution shape. The change should predict the possible change when breeding.

I know the initial distribution of the population over the carcass fat scores from the data of Qualitas AG. The distribution is discrete, which means I know the share of the population within each carcass fat class.

```
#Vectors of animal numbers Carcass fat
#Angus with a=stirks and c=calves.
Ancfc <- c(189,706,935,125,2)
Ancfa <- c(802,3415,15673,6314,481)
#Limousin with a=stirks and c=calves.
Lmcfc <- c(735,1504,1419,72,0)
Lmcfa <- c(5102,21958,50705,7169,148)

#Shares Carcass fat
#Angus with a=stirks and c=calves.
Ancfc <- c(189,706,935,125,2)/sum(Ancfc)
Ancfa <- c(802,3415,15673,6314,481)/sum(Ancfa)
#Limousin with a=stirks and c=calves.
Lmcfc <- c(735,1504,1419,72,0)/sum(Lmcfc)
Lmcfa <- c(5102,21958,50705,7169,148)/sum(Lmcfa)

#Values Carcass fat classes
Vcf <- c(1:5)

#Means (M)
#Angus
AncfcM <- sum(Vcf*Ancfc)
AncfaM <- sum(Vcf*Ancfa)
```

```

#Limousin
LmcfcM <- sum(Vcf*Lmcfc)
LmcfaM <- sum(Vcf*Lmcfa)

#Standard deviations (S)
#Angus
AncfcS <- 0.76
AncfaS <- 0.74
#Limousin
LmcfcS <- 0.78
LmcfaS <- 0.71

#New means (M2)
#Angus
ac<- 0.01
aa<- 0.01
AncfcM2 <- AncfcM+ac
AncfaM2 <- AncfaM+aa
#Limousin
lc <- 0.01
la <- 0.01
LmcfcM2 <- LmcfcM+lc
LmcfaM2 <- LmcfaM+la

```

Changing the mean is difficult without changing the distribution shape for a discrete distribution. Therefore I will use the assumption that the data is normally distributed. The initial normal distribution is defined by the mean and the standard deviation. I will change then the mean of the normal distribution to get the normal distribution after selection. I leave the standard deviation as it is, because it ensures that the shape of the normal distribution stays the same. Afterwards I need to transform the normal distribution back to a discrete distribution.

Borders in the normal distribution to get shares in classes of second scenario.

I get the borders of the discrete distribution by the R-command `qnorm()`. This command gives me the quantil of the area under the normal distribution, when I know the area. The area is the share of animals which belong to specific carcass fat classes.

```

#Borders normal distribution carcass fat
#Angus with a=stirks and c=calves.
AncfcB<- qnorm(cumsum(Ancfc),sd=AncfcS,mean=AncfcM, lower.tail = T)
AncfaB<- qnorm(cumsum(Ancfa),sd=AncfaS,mean=AncfaM, lower.tail = T)
#Limousin with a=stirks and c=calves.
LmcfcB<- qnorm(cumsum(Lmcfc),sd=LmcfcS,mean=LmcfcM, lower.tail = T)
LmcfaB<- qnorm(cumsum(Lmcfa),sd=LmcfaS,mean=LmcfaM, lower.tail = T)

```

Then I take the normal distribution and divide it into different parts according to the computed borders. Each part represents a fat score, the result is again a discrete distribution. I get the shares per fat score for the population of the second scenario, when I use the R-command `pnorm()`.

```

#Shares second mean carcass fat
#Angus with a=stirks and c=calves.
Ancfc2<- diff(c(0,pnorm(AncfcB,sd=AncfcS,mean=AncfcM2, lower.tail = T)))
Ancfa2<- diff(c(0,pnorm(AncfaB,sd=AncfaS,mean=AncfaM2, lower.tail = T)))
#Limousin with a=stirks and c=calves.
Lmcfc2<- diff(c(0,pnorm(LmcfcB,sd=LmcfcS,mean=LmcfcM2, lower.tail = T)))

```

```
Lmcfa2<- diff(c(0,pnorm(LmcfaB,sd=LmcfaS,mean=LmcfaM2, lower.tail = T)))
```

Then I just need to subtract the mean revenue from the initial scenario from the mean revenue of the second scenario. The mean revenue is determined by the price plus or minus of a carcass fat class and by how many animals are classified in the specific class.

Mean price minus per carcass fat class

I know the share of animals in the different carcass fat classes, but I do not know the mean price plus or minus for the different carcass fat classes. The group “stirks” consists of the carcass categories MT, OB and RG. Therefore I will take the mean for the price plus or minus of the three carcass categories. At the moment it will be sufficient to use the price of the week 33 in 2018 (13.8.18).

```
# Mean price minus stirks / kg carcass weight
# mean price plus or minus for different carcass fat classes from Proviande 2018, week 33.
library(knitr)
```

```
## Warning: package 'knitr' was built under R version 3.4.3
```

```
z<-data.frame(class=c("1","2","3","4","5"))
x<-data.frame(MT=c(-0.9,-0.3,0,-0.3,-0.7),
              OB=c(-0.9,-0.3,0,-0.4,-0.9), RG=c(-0.9,-0.3,0,-0.5,-1))
y<-as.matrix(x)
#compute mean over categories
x$mean<-rowMeans(y)
x<-cbind(z,x)
#defintion of variable
cfap <- x$mean

#Mean price minus calves / kg carcass weight
cfcp <- c(-1.5,-0.6,0,-0.4,1)
```

Economical weight

First I multiply each part share of the discrete distribution with the attributing price minus. Then I can do the same with the second discrete distribution with the different mean. The difference of the two scenarios corrected by the difference of means will result in the economical weight per carcass fat score.

```
#Economic weights
#Angus with a=stirks and c=calves.
AncfcEW<- t(cfcp)%*%Ancfc2-t(cfcp)%*%Ancfc
AncfaEW<- t(cfap)%*%Ancfa2-t(cfap)%*%Ancfa
#Limousin with a=stirks and c=calves.
LmcfcEW<- t(cfcp)%*%Lmcfc2-t(cfcp)%*%Lmcfc
LmcfaEW<- t(cfap)%*%Lmcfa2-t(cfap)%*%Lmcfa
AncfcEW
```

```
##           [,1]
## [1,] 0.004529231
```

```
AncfaEW
```

```
##           [,1]
## [1,] -0.0005082929
```

```
LmcfcEW
```

```
##           [,1]
## [1,] 0.005915957
```

```
LmcfaEW
```

```
##           [,1]
## [1,] 0.001566957
```

Carcass Conformation

The method is about the same to compute economical weights for carcass conformation and carcass fat. However there are different shares and different price differences in the carcass conformation classes. Also, it is not possible to get a negative value for the economical value for carcass conformation.

First I will define the initial situation, with data from Sophie. Again I have different economic weights for the groups stirks and calves and for the breeds Angus and Limousin.

Initial Situation

```
#Vectors of animal numbers Carcass conformation (cc)
#Angus (An) with a=stirks and c=calves.
Anccc <- c(2,2,35,278,634,708,298)
Ancca <- c(0,17,247,3459,8308,8857,5797)
#Limousin (Lm) with a=stirks and c=calves.
Lmccc <- c(3,2,17,88,300,838,2482)
Lmcca <- c(2,11,57,1041,6652,21092,56227)

#Shares Carcass conformation
#Angus with a=stirks and c=calves.
Anccc <- Anccc/sum(Anccc)
Ancca <- Ancca/sum(Ancca)
#Limousin with a=stirks and c=calves.
Lmccc <- Lmccc/sum(Lmccc)
Lmcca <- Lmcca/sum(Lmcca)

#Values Carcass conformation classes
Vcc <- c(1:7)

#Means (M)
#Angus
AncccM <- sum(Vcc*Anccc)
AnccaM <- sum(Vcc*Ancca)
#Limousin
LmcccM <- sum(Vcc*Lmccc)
LmccaM <- sum(Vcc*Lmcca)

#Standard deviations (S)
#Angus
AncccS <- 0.99
AnccaS <- 1
#Limousin
LmcccS <- 0.8
LmccaS <- 0.7
```

```

#New means (M2)
#Angus
ac<- 0.01
aa<- 0.01
AncccM2 <- AncccM+ac
AnccaM2 <- AnccaM+aa
#Limousin
lc <- 0.01
la <- 0.01
LmcccM2 <- LmcccM+lc
LmccaM2 <- LmccaM+la

```

Then I define the situation after predicted change in mean (shift of the distribution).

Second scenario

First I define the borders of the normal distribution which I will shift.

```

#Borders normal distribution carcass conformation
#Angus with a=stirks and c=calves.
AncccB<- qnorm(cumsum(Anccc),sd=AncccS,mean=AncccM, lower.tail = T)
AnccaB<- qnorm(cumsum(Ancca),sd=AnccaS,mean=AnccaM, lower.tail = T)
#Limousin with a=stirks and c=calves.
LmcccB<- qnorm(cumsum(Lmccc),sd=LmcccS,mean=LmcccM, lower.tail = T)
LmccaB<- qnorm(cumsum(Lmcca),sd=LmccaS,mean=LmccaM, lower.tail = T)

```

Then I define the shares with the changed mean.

```

#Shares second mean carcass conformation
#Angus with a=stirks and c=calves.
Anccc2<- diff(c(0,pnorm(AncccB,sd=AncccS,mean=AncccM2, lower.tail = T)))
Ancca2<- diff(c(0,pnorm(AnccaB,sd=AnccaS,mean=AnccaM2, lower.tail = T)))
#Limousin with a=stirks and c=calves.
Lmccc2<- diff(c(0,pnorm(LmcccB,sd=LmcccS,mean=LmcccM2, lower.tail = T)))
Lmcca2<- diff(c(0,pnorm(LmccaB,sd=LmccaS,mean=LmccaM2, lower.tail = T)))

```

To compute the mean difference in revenue with the shift of population mean, I need the price differences of the carcass conformation classes

Prices

The stirks prices will be a mean of three different carcass categories, but calves prices come from a single category, CV. Stirks can be MT, OB or RG.

```

# Mean price minus stirks / kg carcass weight
# mean price plus or minus for different carcass fat classes from Proviande 2018, week 33.
z <- data.frame(class=c("X","A","T-","T","T+","H","C"))
x<-data.frame(MT=c(7.9,8.2,8.6,8.8,9.1,9.3,9.55),
              OB=c(7.9,8.2,8.6,8.8,9.1,9.4,9.65), RG=c(6.9,7.5,8.2,8.8,9.2,9.5,9.75))
y<-as.matrix(x)
#compute mean over categories
x$mean<-rowMeans(y)
x<-cbind(z,x)
#defintion of variable
ccap <- x$mean

```

```
#Mean price minus calves / kg carcass weight
cccp <- c(11.2,12.7,13.6,14.2,14.7,15.2,15.7)
```

The combination of shares and price will result in the economical weights per change of mean in the population.

Economical weights

```
#Economic weights
#Angus with a=stirks and c=calves.
AncccEW<- t(cccp)%*%Anccc2-t(cccp)%*%Anccc
AnccaEW<- t(ccap)%*%Ancca2-t(ccap)%*%Ancca
#Limousin with a=stirks and c=calves.
LmcccEW<- t(cccp)%*%Lmccc2-t(cccp)%*%Lmccc
LmccaEW<- t(ccap)%*%Lmcca2-t(ccap)%*%Lmcca
AncccEW
```

```
##           [,1]
## [1,] 0.00484011
```

```
AnccaEW
```

```
##           [,1]
## [1,] 0.002626938
```

```
LmcccEW
```

```
##           [,1]
## [1,] 0.004072617
```

```
LmccaEW
```

```
##           [,1]
## [1,] 0.002097717
```

Carcass weight

The trait carcass weight has the unit kg. For carcass weight the price plus per kg is the same on the whole scale. Therefore I do not need to assume a standard deviation in the population. I just need the mean for the first scenario and the function that will tell me how much the profit will change when I change the carcass weight is one kg more. Important: Here I assume that the carcass weight changes, without a change of age at slaughter. The profit will be here defined as the revenue minus the fixed and variable costs.

```
#profit per animal in Sfr. from @Burkard2013
VersProfitAnimal<- 438
KontrProfitAnimal<- 384
#mean carcass weight in kg as mean September of categories Stiere, Ochsen and Rinder of Agristat S.33.
k<-mean(c(298,256,260))
k
VersMeancw<- k
KontrMeancw<- k
#profit per mean kg carcass weight in Sfr.
cwEW<- KontrProfitAnimal/VersMeancw
pCW
```

Annex/Jnk