INTRODUCTION

The economic results of animal selection based on predictions of breeding value are uncertain and involve a financial risk. Schneeberger et al. (1982) defined risk as the “standard deviation of income” measured in monetary units. As predictions of breeding value using Best Linear Unbiased Prediction (BLUP, Henderson, 1984) are random variables, their variability produces a risk: sires with higher prediction error variances (i.e. lower accuracies) are riskier to use than sires with lower prediction error variances (i.e. higher accuracies; Dematawewa et al., 1998). During the nineties, some of the world’s largest financial institutions have used Value-at-Risk \( \text{VaR} \) (Jorion, 1997) as a method for calculating and controlling market risks. The goal of this presentation is to introduce \( \text{VaR} \) as a methodology to select beef bulls. In doing so, the BLUPs and economic weights in the aggregate genotype are combined with prediction error variances and covariances to generate a new selection criteria that takes into account financial risk.

DEFINITION OF \( \text{VaR} \)

Let \( R \) be a random variable representing the distribution of income (or economic return) due to using a given bull, and let \( B \) be a small probability value (say, \( B = 0.05 \) or \( B = 0.01 \)). Then, \( \text{VaR} \) is defined to be:

\[
P(R \leq \text{VaR}) = \pi
\]

In words : \( \text{VaR} \) is a fixed value of \( R \) such that the probability accumulated to it is \( B \). Therefore, \( \text{VaR} \) represents the value in the distribution of income such that a loss of \( R \) equal or greater to \( \text{VaR} \) will be observed with probability \( B \). In situations such as the one being considered here, the random variable \( R \) is unobservable. However, it is usually assumed (Jorion, 1997) that moments of the distribution of \( R \) can be estimated. Assuming normality of the density of \( R \), \( \text{VaR} \) is calculated by multiplying the standard deviation of \( R \) (\( \Phi \)) by the standard normal deviate \( z \) corresponding to the probability \( B \):

\[
\text{VaR} = z \sigma
\]

MATERIAL AND METHODS

Data used were multiple trait animal model predictions of breeding values of 369 Polled Hereford sires from a purebred herd in Pasteur, western Buenos Aires province, Argentina. The range in EPDs were -3.4 to +3.5 kg for birth weight (BW); -7.2 to +29.2 for weaning weight (WW), -11.3 to +13.9 for maternal weaning weight (MW) and -19.5 to +43.1 kg for 18-month weight (FW). Corresponding values of accuracies were 0.01 to 0.97, 0.01 to 0.97, 0.01 to 0.96 and 0.01 to 0.96 for BW, WW, MW and FW respectively.
In order to calculate \( VaR \) one needs (Jorion, 1997): 1) to define \( R \) for each bull evaluated and 2) to estimate the standard deviation of \( R \). We defined \( R \) to be the aggregate genotype (Hazel, 1943). To obtain economic values, a profit function for a pasture based beef production system in Argentina was developed, using the methodology proposed by Ponzoni and Newman (1989), and the discounted expressions were calculated for a period of 20 years following the method of Brascamp (1978). The final formulae for the economic values were obtained by multiplying the derivatives of the profit function by the total amount of discounted expressions, for each trait. The standard deviation of \( R \) for sire \( i \) was calculated using the formula:

\[
\hat{\sigma}_{ii} = \sqrt{\text{Var}(\hat{a}_i - a_i)} = \sqrt{\text{e}^{\text{C}^{uu}e}} \tag{1}
\]

where \( a_i \) is the vector of breeding values of sire \( i \), \( \hat{a}_i \) is the vector of BLUP of breeding value for \( i \), \( C^{uu} \) is a submatrix of the inverse of the mixed model equations corresponding to \( i \) (Henderson, 1984) and \( e \) is the vector of economic values. Finally, after taking \( B = 0.05 \), the \( VaR \) of each bull was calculated as:

\[
VaR_i = z\hat{\sigma}_{ii} \tag{2}
\]

**RESULTS**

For each trait included in the selection goal, Table 1 displays the \( VaR \) measures plus the predicted aggregate genotypes and the amount of phenotypic information used to predict breeding values. The figures in Table 1 are average aggregate genotypes and \( VaRs \) for quartiles of accuracy: 1) low, from 0.01 to 0.3; medium, from 0.31 to 0.5; high, from 0.51 to 0.75; and very high, with accuracy greater than 0.75.

**Table 1. Averages of aggregate genotype and \( VaR \) for different quartiles of accuracy**

<table>
<thead>
<tr>
<th>Trait</th>
<th>Offspring/grand offs.</th>
<th>Aggregate genotype ( $)</th>
<th>Value-at-risk ( $)</th>
<th>Accuracy</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Low</td>
<td>Medium</td>
<td>Medium/high</td>
<td>Very high</td>
</tr>
<tr>
<td>Birth weight</td>
<td>4</td>
<td>14</td>
<td>46</td>
<td>199</td>
</tr>
<tr>
<td>Weight</td>
<td>23,917</td>
<td>26,506</td>
<td>52,586</td>
<td>58,701</td>
</tr>
<tr>
<td>Value-at-risk</td>
<td>189,576</td>
<td>172,491</td>
<td>142,042</td>
<td>94,034</td>
</tr>
<tr>
<td>Weaning</td>
<td>5</td>
<td>14</td>
<td>20</td>
<td>217</td>
</tr>
<tr>
<td>Weight</td>
<td>23,576</td>
<td>32,600</td>
<td>60,109</td>
<td>44,316</td>
</tr>
<tr>
<td>Value-at-risk</td>
<td>189,025</td>
<td>176,920</td>
<td>146,126</td>
<td>89,097</td>
</tr>
<tr>
<td>Maternal</td>
<td>3</td>
<td>8</td>
<td>19</td>
<td>223</td>
</tr>
<tr>
<td>Weaning weight</td>
<td>29,930</td>
<td>39,957</td>
<td>56,495</td>
<td>34,671</td>
</tr>
<tr>
<td>Value-at-risk</td>
<td>187,792</td>
<td>171,611</td>
<td>148,965</td>
<td>92,854</td>
</tr>
<tr>
<td>Final weight</td>
<td>4</td>
<td>12</td>
<td>32</td>
<td>211</td>
</tr>
<tr>
<td>Value-at-risk</td>
<td>23,955</td>
<td>29,193</td>
<td>55,682</td>
<td>51,667</td>
</tr>
<tr>
<td></td>
<td>190,337</td>
<td>175,430</td>
<td>144,362</td>
<td>90,484</td>
</tr>
</tbody>
</table>

Prediction error variances were obtained by full inversion of the multiple trait coefficient matrix of the mixed model equations. To evaluate the impact of individual accuracies on \( VaR \), the correlations between both sets of measures were calculated, as accuracies were used as measures of risk due to bull usage (Schneeberger et al., 1982; Klieve et al., 1993). All correlations were highly significant \((P < 0.01)\) and negative: -0.86, -0.92, -0.86 and –0.92 for
BW, WW, MW and FW respectively. This indicates that the higher the accuracies, the lower
the risk measured as $VaR$. The relationship between accuracies and $VaR$ is depicted in Figure 1
only for FW as the trend was similar for the other traits. Lines in the figure correspond to either
using the complete $C_{uu}$ (full) or using the diagonal elements of $C_{uu}$ (dashed) to calculate $VaR$.
In the latter case, the correlation coefficients were still significant ($P < 0.01$) but of smaller
magnitude: -0.54, -0.56, -0.53 and –0.56 for BW, WW, MW and FW respectively.

![Figure 1. VaR and accuracy of final weight](image)

**DISCUSSION**

The main utility of $VaR$ is to introduce risk into the selection goal, and this generalizes the
economic approach of selection indices using economic weights, as originally developed by
Hazel (1943). Dematawewa et al. (1998) pointed out that selection criteria using predicted
aggregate genotypes do not account for financial risk. Therefore, animals with the same
predicted values and different accuracies for all traits will have the same predicted aggregate
genotype. However, their $VaR$s will be different.

The concept and the use of $VaR$ in the financial literature is discussed at length in Jorion
(1997), and the time horizon for which the risk measures apply ranges in days or months. By
contrast, animal breeding applications require larger time horizons as returns are realized when
progeny and further descendants are sold. As the period chosen in the present research is 20
years, a loss of $R$ equal or greater than $VaR$ will be observed with probability of 5% in 20
years, assuming normality of the distribution of returns. The extreme $VaR$s calculated with
these data were 200,000 $ and 47,000 $. The last number belonged to a bull that had the
highest number of progeny (968 calves) distributed in a large number of contemporary groups
for all traits. The difference between the two $VaR$ numbers can be seen in Figure 2. The wider
distribution corresponds to the bull with the largest $VaR$, thus indicating the greatest risk. On
the other hand, the tighter distribution corresponds to the sire with the smallest $VaR$ and the
lowest risk.

Looking at equation [1], it is worth noting that PEV is the main factor that enters into the $VaR$
to discriminate among the different sires, as the economic values are the same for all selection
candidates. This reflects the fact that $R$ varies mainly due to differences in prediction errors and
not due to variations in future prices. The latter factor affects all selection candidates the same
way without altering the ranking (Dematawewa et al., 1998). Schneeberger et al. (1982) also used PEV to estimate the variance of R. The impact of estimating VaR, either with the complete PEV matrix for each selection candidate, or with a diagonal PEV (i.e. covariance of prediction errors assumed to be zero), was evidenced in Figure 1. The differences in VaR calculated with either method were larger the smaller the accuracies. These latter values are usually calculated by approximating diagonal elements of the PEV matrix (Harris and Johnson, 1998). As the inversion of the coefficient matrix of the mixed model equations is generally prohibitive, both diagonal and off-diagonal elements of PEV are not available. Therefore, further research is needed to calculate those elements, maybe as in García-Cortés et al. (1992).

To conclude, we have applied VaR methodology to combine predictions of breeding values and corresponding PEV matrices in order to generalize the selection goal. This single number for each selection candidate is expressed in terms of money, and it is easy to use and to interpret by breeders. It also allows to select animals for increasing profit with minimum risk.

Figure 2. Distribution of returns for two bulls with extreme VaRs

REFERENCES
Brascamp, E.W. (1978) "Course in economic breeding planning". Univ. of Helsinki, Helsinki, Finland.