

Impact of Data Editing on Fat and Protein Content on Stability of Test Day Model Evaluation

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Abstract

In November 2004 the first Italian genetic evaluation based on Test day random regression model (TDRRM) was published. The model is a Multiple-Trait-Multiple-Lactation model including four milk, fat, protein and somatic cells and three lactations for each trait. When the procedure for data preparation was developed a program to identify abnormal test day records for milk production was developed by Boettcher (2000). Over time milk recording schemes evolved and had an impact on fat and protein %. In order to identify abnormal test day records also for protein and fat % a new program was developed by G.B. Jansen in 2007. The objective of the present study was to implement the new editing program into the routine procedure of genetic evaluation and evaluate its impact on the quality of genetic evaluations. As a first results of the application of the new program new statistical data are now available to monitor the quality of test day records received from the milk recording agency. The impact of the genetic evaluation results was very small, correlation among proofs were higher than 0.99. As expected only bulls newly proven with a small number of daughters were affected but the quality of the evaluation was generally improved.

Introduction

The RRTDM is official in Italy since November 2004.

From that day onward a big amount of time has been devoted to meet farmers and industry people to explain the advantages of the new system and of all the additional information that can be used to better the selection of bulls that will help them increase their profit.

In the meantime research has started in order to improve the system and to address the many questions that users are raising while getting acquainted with the new system.

One of the big issues is the overall stability of proofs from run to run which in Test day model is perceived as much lower compared to the lactation model. One of the reasons of the higher variation from run to run is linked to the fact that RRTDM assumes a more dynamic way of expressing genetic superiority, along the lactation and across lactations, that brings with itself more variation over time in bull proofs.

As part of the official procedure a program to identify abnormal test day records by Boettcher (2000). The program for all lactations with at least three test day records estimates polynomial curves

and discards records that are at least 3 SD over the expected value.

Over time milk recording schemes have been changing: in 2000 a single sampling procedure was introduced in A4 schemes and the percent of AM/PM testing scheme have increased over time. Due to this changes there was a need for a new procedure for the identification of abnormal test day values for fat and protein content.

The objective of this study was therefore:

- to develop a new MT method for the identification of abnormal test day record values for milk, fat and protein %;
- evaluate the impact of the introduction of the new editing on the official genetic evaluation results.

Material and Methods

The method considers milk yield, fat percentage, protein percentage, somatic cell score and optionally casein percentage, of all TD records between 5 and 365 days in milk in a single lactation of one cow. Any of the traits other than milk may be missing on any test day. A flag is set for any trait if the TD value deviates too far from the predicted value computed from other traits on

the same TD and all the traits on other TD records in the same lactation. Acceptable thresholds for deviations in SD units can be defined based on empirical distributions.

Let $z_{ik} = (y_{ik} - \bar{y}_{ik}) / sd_{ik}$ be the standardized trait value for the k^{th} trait on the i^{th} day in milk (DIM). The reference mean and SD are taken from the standard curves for the appropriate parity (first or later) and season of calving. Let \mathbf{z}^* be a vector of standardized observations for all traits on all TD records with the exclusion of z_{ik} . Predicted values are computed as:

$$\hat{z}_{ik} = c_{ik,*} V_*^{-1} \mathbf{z}^*$$

where $c_{ik,*}$ and V_* are appropriate correlations based on the pattern of recorded traits and days in milk for the cow in question. These correlations are selected from much larger matrices of all possible values among all traits on the same day or any pair of days between 5 and 365. The required correlations in $c_{ik,*}$ and V_* are calculated using formulae estimated by Norman *et al.* (1999) from USA TD data. The correlations among traits on the same test day were estimated as raw correlations among $z_{ik} - \hat{z}_{ik}$ values on the same test day using the same data used for the estimation of the reference curves.

Reference lactation curves are estimated for homogeneous group of cows, considering parity group (first parity or later parities) and season of calving. The curves are first computed as raw averages and simple SD of trait values by days in milk within each group and then smoothed using weighted least squares with modified Wilmink functions:

$$b_0 + b_1 DIM + b_2 DIM^2 + b_3 DIM^3 + b_4 \exp(-0.05 DIM)$$

Four seasons were considered (January-March, April-June, July-September, October-December) and closed lactations from January 2004 to December 2006 were considered for the estimation.

A threshold of 2.00 SD was used on the application to data used for the routine genetic evaluation of January 2008. Results were used to

produce general statistics over time, region and type of milk recording scheme.

All TD records flagged for milk production were deleted and for the TD records flagged for fat and protein percentages values those values were set to missing.

A genetic evaluation was run on the edited data for January 2008 and April 2008.

Impact on bull ranking was evaluated looking at top 100 bulls and at correlations among proofs in comparison with the official evaluation. Impact on stability of bull proofs was assessed looking at average differences on group of bulls stratified by date of first publication, between two genetic evaluation runs with edited data when compared to the corresponding official runs.

Results and discussion

Figure 1 reports an example of output of the program when run on the lactations whose TD records were received in between two runs of genetic evaluation. The TD record values that are flagged more frequently are related to fat percentage. Figure 2 and 3 show some statistics on frequency of TD flagged as abnormal from 1992 to 2007.

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Date 2008-03-20 21:21:54 TDFLAG2...

breed=02 maxDIM=305 maxLACT=3

3281798 = TD records in
  0 = TD skipped (beyond maxDIM or maxLACT)
42852 = TD singleton records skipped
3238946 = TD records checked
203370 = TD records flagged for at least one trait (6.28%)
506795 = lactations checked
160481 = lactations with flagged TD (31.67%)

Stats on 3238946 checked TD records (THRESHOLD=2.00)

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	Milk	Fat%	Pro%	SCS
Missing	0 0.00%	82051 2.53%	9262 0.29%	13120 0.41%
Normal	3219481 99.40%	3069233 94.76%	3180944 98.21%	3156462 97.45%
Flagged	19465 0.60%	87662 2.71%	48740 1.50%	69364 2.14%
1 z-zhat >=2.00	8143 0.25%	28667 0.89%	14659 0.45%	23423 0.72%
2 z-zhat >=2.25	4706 0.15%	19627 0.61%	9799 0.30%	16213 0.50%
3 z-zhat >=2.50	2715 0.08%	13000 0.40%	6589 0.20%	10877 0.34%
4 z-zhat >=2.75	1565 0.05%	8637 0.27%	4802 0.15%	7431 0.23%
5 z-zhat >=3.00	922 0.03%	5773 0.18%	3327 0.10%	4755 0.15%
6 z-zhat >=3.25	549 0.02%	3883 0.12%	2432 0.08%	2891 0.09%
7 z-zhat >=3.50	339 0.01%	2701 0.08%	1730 0.05%	1731 0.05%
8 z-zhat >=3.75	202 0.01%	1876 0.06%	1250 0.04%	992 0.03%
9 z-zhat >=4.00	324 0.01%	3498 0.11%	4152 0.13%	1051 0.03%

```

Mean and SD of z-zhat by parity
parity 1 0.01 0.58 -0.01 0.83 0.00 0.75 0.00 0.75
parity 2 0.01 0.56 -0.00 0.88 0.00 0.74 0.00 0.73

Date 2008-03-20 21:33:29

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Figure 1. Example of summary output from the program.

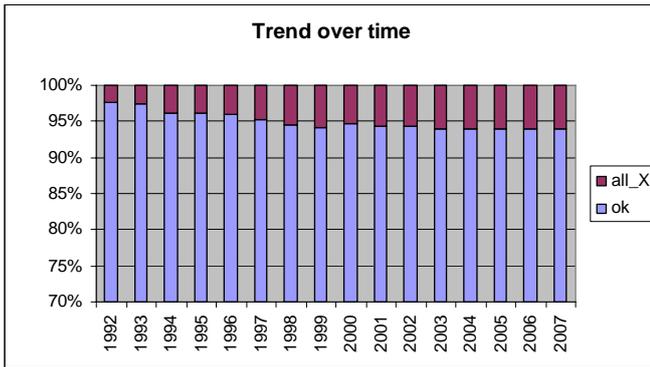


Figure 2. Trend over time of TD flagged as abnormal.

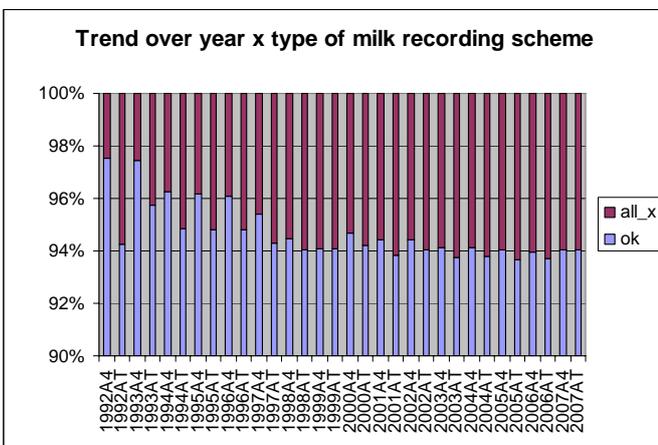


Figure 3. Trend over time of TD flagged as abnormal by type of milk recording scheme (A4 Versus AM/PM).

There is a general increase of the frequency of abnormal TD records from around 2% in 1992 to around 6% in 2007. The impact of sampling from one milking only (alternatively as in AM/PM milk recording scheme) also in A4 scheme that was introduced around year 2000 is evident. From the year 2000 onward the frequency of abnormal test day records shows no difference between A4 and AM/PM milk recording schemes.

The impact of introducing the new editing strategy on genetic evaluation results was very small. Genetic correlations with official proofs were higher than 0,99.

It is expected that for some cows TD records flagged in one evaluation as abnormal can become acceptable due to additional information on the same lactation record or vice versa and this aspect, that can have an impact on stability of cow breeding values is currently under investigation.

On the variability of bulls from one run to the next the evaluations with edited data on January 2008 and April 2008 genetic evaluations were compared to the corresponding official evaluations.

Italian proven bulls were grouped by date of first publication and average difference and its standard deviation between the subsequent runs was analyzed.

Figures 4 to 6 report the average difference only because there was no difference in SD of differences as expected.

The impact on average difference for milk was very little but milk is the trait for which an editing procedure is already in place so no changes were expected. An improvement on stability is visible especially for fat kg and a little less for protein. Since the majority of abnormal values were found for fat this was also expected.

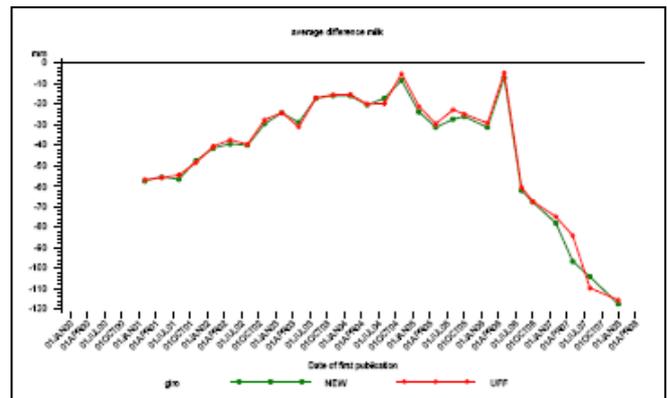


Figure 4. Average difference between two subsequent runs in EBVs of bulls by date of first publication (milk kg).

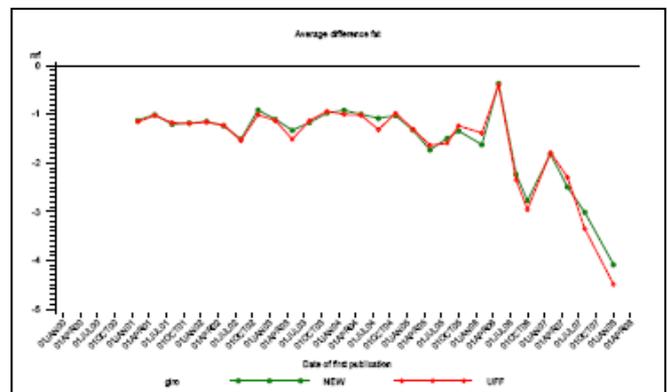


Figure 5. Average difference between two subsequent runs in EBVs of bulls by date of first publication (fat kg).

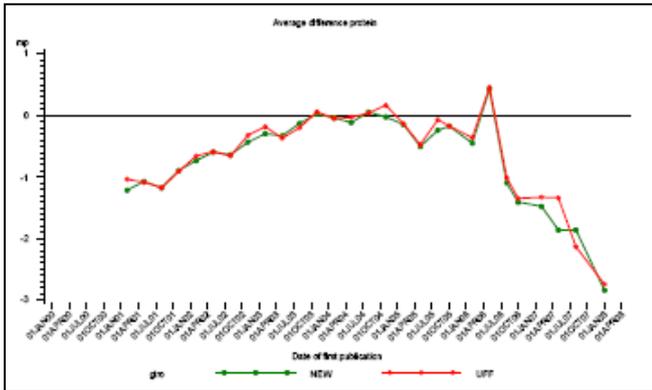


Figure 6. Average difference between two subsequent runs in EBVs of bulls by date of first publication (protein kg).

Conclusions

The new program that has been developed is an useful tool to monitor the quality of data received from the milk recording agency. This will provide useful information especially now that it seems that the majority of herds will move to AM/PM milk recording scheme before the end of the year.

Its impact on genetic evaluation results is very small overall: there is no significant impact on EBVs correlations, no significant impact on bull and cow trend and a small improvement on stability of proofs over time especially for fat yield.

Its introduction in routine genetic evaluation procedure will improve the quality of the resulting EBVs and their stability in time.

It is planned to introduce the new editing in the next genetic evaluation in August 2008 and this will be another step in the improvement of stability of test day model evaluation.

Research is ongoing in order to improve the model that will have larger impact on stability.

Acknowledgements

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References

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