

To be Connected or not? Answers for Dairy Cattle in International Genetic Evaluations

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Abstract

A method for quantifying connectedness in an international evaluation has recently been proposed. Some new features of this method are presented here. Pedigree information can now be accounted for and the impact of one specific country on the overall connectedness level can now be addressed through a “leave-one-out” procedure. The method is illustrated by an application on the Jersey breed. It was shown to deliver sensible results. It is not computationally demanding, and its use in routine runs maybe envisaged, even for the biggest breeds.

1. Introduction

Connectedness between countries is a critical point for a reliable international evaluation. The criteria for quantifying connectedness in the Interbull context usually rely on the number of common bulls, or on the number of their offspring (Rekaya *et al.*, 1999). Recently, Fouilloux *et al.* (2006) proposed a method that quantifies the connectedness between countries through the ability to estimate a systematic difference between the genetic levels of the countries involved in the evaluation. This method was shown to efficiently analyze exchanges of bulls across countries and to measure the genetic connection created by the common bulls.

The aim of this paper is to present new features of the method, which was improved to be able to consider pedigree information, and measure the impact of a specific country on the overall connectedness of a set of countries.

The method is illustrated by an application on the Jersey breed.

2. Material and Methods

2.1. Principle and procedure

The method relies on the criterion of robustness proposed by Laloë and Phocas

(2003) and was first presented in Fouilloux *et al.* (2006). Its principle is to introduce a systematic difference between the true genetic levels of countries by simulating breeding value (BV) of each sire in pedigree, to run a BLUP and to measure the percent of the initial difference that has been re-estimated.

To present the method, let us consider n sires in pedigree and N countries. Let us suppose we want to assess connectedness between country k and the $(N-1)$ others.

2.1.1 Simulation of the sire's breeding values and performances of their daughters

First, the n sires were chronologically sorted. Then, BV of each base sire was fixed to a_k if it originated from k , a_0 otherwise. BV of a non-base sires was equal to half the sum of BV of its father and a_k if it came from k , a_0 otherwise. Performances of the cows were supposed to be half the BV of their father.

2.1.2. Introduction of a systematic difference

The true genetic level of the country j is given by:

$$u_j = 0,5 \frac{\sum_{i=1}^n n_{ij} \times a_i}{\sum_{i=1}^n n_{ij}} [1],$$

where n_{ij} is the number of progenies of the sire i recorded in the country j and a_i the true BV of the sire i .

The true difference is defined as the difference between the genetic level of the country k and the genetic level of each of the $(N-1)$ countries.

The true genetic level of k informs about the percentage of foreign paternal genes among the performance recorded animals in country k .

2.1.3. BLUP genetic evaluation

A single-trait BLUP was performed using a sire model and considering a heritability of 0.30. The only fixed effect was the country of recording. The BV of each sire was estimated and the estimated genetic level of each country was computed by replacing a_i by \hat{a}_i in [1]. Estimated differences between the genetic levels of the country k and each of the $(N-1)$ countries were calculated.

2.1.4. Measure of the rate of estimation of the initial difference.

The $(N-1)$ ratios of estimated to true differences between the genetic levels of country k and the other ones were calculated. The rate of re-estimation quantifies the ability to estimate a systematic difference, and consequently, the connectedness between the k^{th} country and another. The average of the $(N-1)$ ratios is a global measure of the connectedness of country k , in the context of a given Interbull genetic evaluation.

This procedure (steps 2.1.1 to 2.1.4) was run N times: once for each country.

2.1.5. Measure of the impact of removing one country from the international evaluation.

To evaluate the effect of the absence of a given country in the international genetic evaluation, all records of this country were removed. Moreover, for bulls coming from this country the progeny performances in other countries were also removed. This practice corresponds to the Interbull edit that a bull has to have first crop information included before considering (imported) second crop information.

The whole procedure (steps 2.1.1 to 2.1.4) was run after deleting the relevant records. The impact was measured as the difference between the rates of re-estimation with and without the given country.

2.1.6. Accounting for pedigrees.

The procedure can be run with or without considering pedigree information.

2.2. Data

The data analysed were the international evaluation for milk production of August 2007, for the Jersey breed, where 10 countries participated: AUS: Australia, CAN: Canada, DEU: Germany, DNK: Denmark, GBR: United Kingdom, ITA: Italy, NLD: the Netherlands, NZL: New Zealand, USA: the United States of America and ZAF: Republic of South Africa.

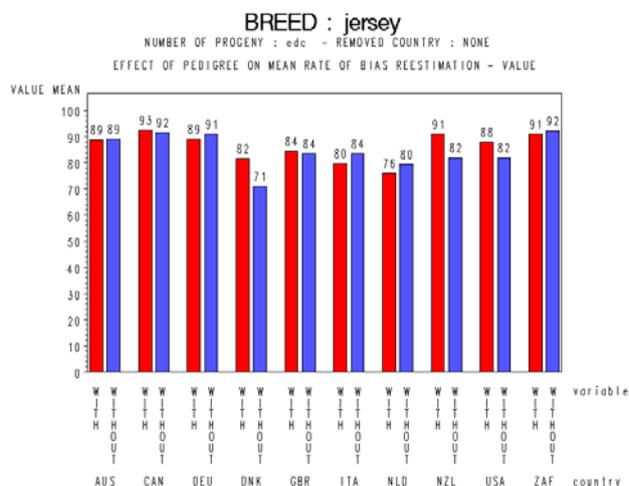
Effective Daughters Contributions were used as n_{ij} in [1]. Origin of sires of recorded daughters was determined by the country of test (type of proof 11 or 12, and if there was more than one country, the one with the most daughters). Origins of other sires in the pedigree file were their natal countries.

3. Results and Discussion

Description of connectedness

Ignoring pedigree information, CAN, DEU and ZAF were the most connected countries: more than 90% of initial differences were re-estimated (Figure 1). DNK appeared to be the least connected country, with a bias re-estimation rate of only 71%.

Figure 1. Mean rates of bias re-estimation.



Accounting for pedigree did not dramatically change the re-estimation rates. The magnitude of change varied between countries. The averaged re-estimation rate increased for DNK (+11%), NZL (+9%), USA (+6%) and CAN (+1%). It was stable for AUS and GBR, and it decreased for ITA (-4%), NLD (-4%), DEU (-2%) and ZAF (-1%).

Differences in results from both approaches (with or without pedigree) result of a redistribution of paternal gene origins through pedigree. Hence, the decrease in the rate re-estimation may be due to an increase in the pedigree of the weight of paternal genes coming from a country less connected with the others.

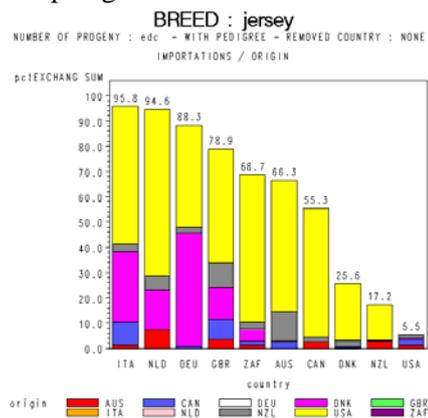
Relation with the structure of the data

Figures 2a and 2b give the origin of the paternal genes of the cows of a country, in- or excluding pedigree. ITA was the country that has imported the most, both considering pedigree or not, with 95.77% (91.54%

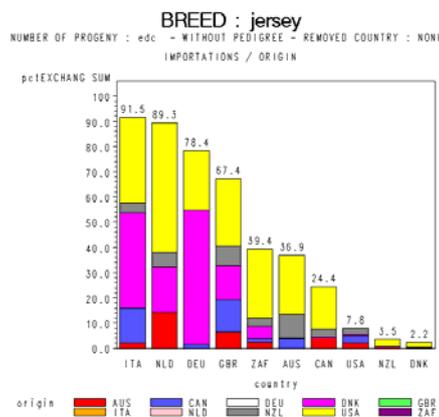
respectively) of paternal genes coming from foreign bulls among the Italian cows. The percentage of foreign paternal genes for DNK and NZL was very low when pedigree was ignored (respectively 2.24% and 3.46% of the cows of the country had a foreign sire).

Figures 2a 2b. Foreign origin of paternal genes of cows in the countries

2a. with pedigree:



2b. without pedigree



However, when pedigree was taken into account, percentage of cows paternal genes coming from foreign bulls increased in a large proportion and reached 25.6% for DNK and 17.2% for NZL, mostly in favor of US origin. These extra links provided by US animals in pedigree could probably explain the increase in the rates of re-estimation for DNK and NZL when pedigree is included (Figure 1).

An interesting case: DNK (without pedigree)

DNK had the lowest rate of re-estimation, when pedigree was not taken into account

(71%). At first sight, this result could be related to the small percent of importation in DNK (Figure 2b), but it was not the only reason, because USA and NZL have not imported so much either but had higher rates of re-estimation (both 82%). US bulls have largely been used by all the countries, which could explain the better connectedness of USA. But bulls coming from DNK have also been used in all the countries, and represent 13.6% of daughters in GBR, 17.8% in NLD, 37.8% in ITA and 53.4% in DEU. It is surprising that these considerable exportations did not improve connectedness. Looking deeper in the data structure (Table 1) shows that for DNK the ratio between numbers of bulls with daughters in at least one other country than DNK (115) to the number of bulls with daughters in DNK (1492) is only 0.08. It was much lower than for other countries. The low number of Danish bulls used in several countries compared to the total number of bulls in Denmark decreased its global connectedness.

Table 1. Structure of the data (without pedigree).

	N° bulls	N° common bulls	CB/TB *	Reestimation rate
AUS	1130	409	0.36	89
CAN	329	191	0.58	92
DEU	63	54	0.86	91
DNK	1491	115	0.08	71
GBR	324	135	0.42	84
ITA	90	80	0.89	84
NLD	56	42	0.75	80
NZL	2752	412	0.15	82
USA	2477	485	0.20	82
ZAF	446	185	0.41	92

* CB/TB: ratio between numbers of bulls with daughters in at least one other country on total number of bulls in the country

Impact of removing one country

Removing US records and bulls tested in USA from the Jersey dataset had the largest effect: on average, the rate of re-estimation decreases by 5.02% among the remaining countries (Figure 3). That means that USA provides an important contribution for global connectedness. The second most important country is AUS (-1.11%). On the opposite,

removing DEU, NLD or ITA data did not affect connectedness. This kind of analyses and results could be very useful for deciding whether it is relevant to run an international evaluation without the participation of one specific country.

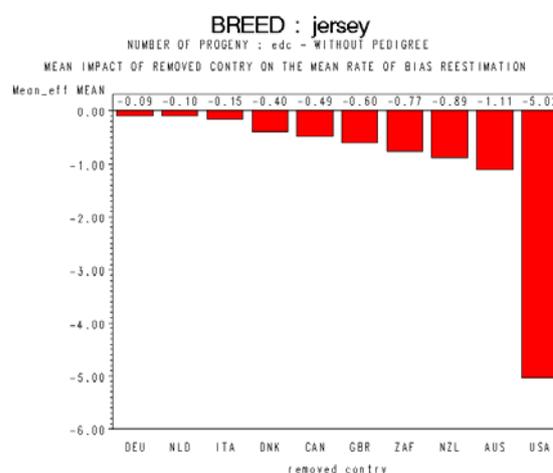


Figure 3. Mean impact of removing a country on rate of re-estimation (without pedigree).

4. Conclusion

This method was carried out for all the breeds participating to the International Evaluation for milk production of August 2007 (Brown Swiss, Guernsey, Holstein, Jersey, Red Dairy Cattle and Simmental). Results of other breeds are available for consultation on Web site (http://www-sgqa.jouy.inra.fr/article.php3?id_article=93).

Not surprisingly, the most computationally demanding analysis concerned the Holstein breed. However, the computing time was moderate (less than 5 minutes to calculate mean rate of bias reestimation of the 25 countries, with pedigree) and does not prevent this method to be routinely performed. Software with several options had been developed by Fouilloux M.N. to compute and to present all the results.

This method has several major interests. It is able to account for pedigree information in the analysis of connectedness. It uses indirect links between countries, i.e. when 2 countries have no common bulls but both have bulls in common with a third country. The “leave-one-out” procedure which consists in removing a

country from the analysis could be very useful to study the importance of a specific country on the global connectedness between countries.

Some other applications of the method are planned: to study the impact of “imported semen bulls” on connectedness, study evolution of connectedness with time, to simulate extra links between some countries to analyse consequence on connectedness of a potential joint progenies testing program.

5. Acknowledgements

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