

OVIS: A multiple trait breeding value estimation program for genetic evaluation of sheep

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Short title: OVIS Software Version 1.0

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Summary

The *OVIS* software was developed by the Animal Breeding and Genetics Unit (AGBU) at the University of New England (UNE). AGBU has developed multi-trait animal model genetic evaluation software tools and provides technical support and continuing development of similar software for several industries including beef cattle (BREEDPLAN) and pigs (PIGBLUP). The *OVIS* software is designed to suit LAMBPLAN's genetic evaluation requirements.

At present *OVIS* is capable of estimating breeding values for 35 traits. This paper describes the components of the *OVIS* software and the ways in which data are handled. Two example LAMBPLAN runs are also described to illustrate the benefits of *OVIS*. The dimensions of the December 1999 Poll Dorset analysis were; 1,065 flocks with 395,823 animals and 793,365 observations resulting in 15,752,277 equations and 2,029 levels of adjustment for across-flock heterogeneity. The details of an across-breed Terminal Sire analysis is also summarised which further illustrates the analytical capabilities of *OVIS*. This analysis included 1,498 flocks with 527,240 animals and 1,145,956 observations resulting in 21,424,358 equations and 3,381 levels of across-flock variance heterogeneity.

Introduction

LAMBPLAN is a national breeding program and genetic evaluation system for the Australian sheep industry. The aim of LAMBPLAN is to assist commercial sheep breeders to identify the best animals to use in their breeding program according to their breeding objectives.

Prior to *OVIS*, LAMBPLAN utilised BVEST (Gilmour 1993) to produce its estimated breeding values (EBV). Dr. Arthur R. Gilmour from NSW Agriculture developed BVEST in the early 90's, however with the increasing size and complexity of the database and the increasing demands of LAMBPLAN clients there was a need to expand the capabilities of the evaluation system. *OVIS* utilises Best Linear Unbiased Prediction methods (Henderson 1984), as BVEST did, to estimate breeding values for all animals in the pedigree. The *OVIS* Version 1.0 software was constructed using components of BREEDPLAN, which has been extensively used in the beef cattle industry (Johnston *et al.* 1999). The experiences gained from PIGBLUP (Henzell 1995; Crump and Henzell 2000) were also utilised during the development of *OVIS*. The design of *OVIS* offers a range of new features including, an expanded model with maternal and permanent environment components, the ability to analyse a larger number of animals, traits and

breeds, dynamic memory allocation, modified trait adjustment, across-flock variance heterogeneity adjustments and genetic grouping. *OVIS* was also designed so that it would be year 2000 compliant. During the development process, the software has been rigorously tested.

This document is written as an introduction to how *OVIS* Version 1.0 operates and its advantages for estimating breeding values in sheep. The description outlines the fundamental design, models used for the analyses, traits analysed and methods of adjusting data for systematic environmental effects.

Analytical Models

All traits are fitted with the same animal model as follows, which includes components for direct and maternal genetic effects, and animal and maternal environmental effects:

$$y = X_1 \beta + Z_1 a + Z_2 m + Z_2 p + e$$

where \mathbf{y} is the vector of observations,

\mathbf{X}_1 is a known incidence matrix relating observations in \mathbf{y} with contemporary groups fixed effects in β ,

\mathbf{Z}_1 is a known incidence matrix relating observations in \mathbf{y} with random effects in vector \mathbf{a} direct additive genetic effects - breeding values of animals,

\mathbf{Z}_2 is a known incidence matrix relating observations in \mathbf{y} with both the random effects in \mathbf{m} due to additive genetic maternal effects and the random effects in \mathbf{p} due to permanent environmental maternal effects,

\mathbf{e} is the vector of random residuals.

With $\mathbf{g} = [\mathbf{a} \ \mathbf{m}]$ the covariance matrix among effects is

$$\begin{pmatrix} \mathbf{g} \\ \mathbf{p} \\ \mathbf{e} \end{pmatrix} = \begin{pmatrix} \mathbf{G} & 0 & 0 \\ 0 & \mathbf{P} & 0 \\ 0 & 0 & \mathbf{R} \end{pmatrix}$$

Where ;

$$\mathbf{G} = \mathbf{A} * \mathbf{G}_0$$

$$\mathbf{P} = \mathbf{I} * \mathbf{P}_0$$

$$\mathbf{R} = \mathbf{I} * \mathbf{R}_0$$

* indicates the Kronecker product and \mathbf{G}_0 , \mathbf{P}_0 and \mathbf{R}_0 are the genetic, permanent environment and residual covariance matrices among traits, respectively.

The main approach used by *OVIS* is an implicit representation of the mixed model equations (MME) (Tier and Graser 1991) combined with data augmentation for missing observations and dams in order to produce EBVs. When observations on some traits are missing, new observations are assigned to those animals. These observations are assigned to unique contemporary groups so that the animal is confounded with the contemporary group. Consequently the observation contributes nothing to the animal's EBV. This approach has been proven to yield equivalent solutions while greatly simplifying coding requirements, as only a single \mathbf{R}_o residual covariance matrix is required.

Special considerations are required for the present analytical approach. Some effects are used to model more than one trait (e.g. \mathbf{m} and \mathbf{p} for the post-birth weights). All traits modelled without maternal effects are augmented with both maternal effects that are the same pair for each such trait. The additional \mathbf{m} and \mathbf{p} effects are held close to zero by assigning them minute variances (<0.000001). This augmentation strategy allows all traits to be treated similarly during iteration. This approach has been proven as workable in the multiple continuous trait - single polychotomous trait program used for the analysis of calving ease in beef cattle (BREEDPLAN, Johnston *et al.* 1999).

Traits analysed

LAMBPLAN uses a system of stages based on age of maturity to specify the recording of traits (Table 1). A unique suffix is used to identify traits at different stages of maturity where, B is birth, W is weaning, P is post-weaning, Y is yearling, H is hogget and A is adult. Identifiers are formed by joining an age-related prefix (stage) with a trait specific suffix where weight is abbreviated as wt, C fat depth as cf, GR fat depth as fat and eye muscle depth as emd. For the wool traits, greasy fleece weight is abbreviated as gfw, clean fleece weight as cfw, mean fibre diameter as fd and fibre diameter coefficient of variation as dcv. Faecal egg count is abbreviated as fec and scrotal circumference as sc. *OVIS* version 1.0 analyses thirty five (35) traits which are listed in Table 1.

Accumulated reproductive performance of dams is given as the ratio of number of lambs born (nlb) and the total number of lambs weaned (nlw) to the number of lambing opportunities (lop) for that dam. Thus, if a ewe had weaned 5 lambs in 3 years, then nlw would be given as 5 and lop as 3, and the ratio of 1.67.

Table 1. Trait names, units of measurement, observation and age ranges for the 35 traits analysed by OVIS version 1.0

Trait Identifier	Trait	Units	Observation Range	Age Range (days)	
1	bwt	Birth Weight	kg	1.0 to 10.0	1 to 10
2	wwt	Weaning Weight	kg	15.0 to 60.0	15 to 165
3	pwt	Post-Weaning Weight	kg	25.0 to 90.0	105 to 345
4	ywt	Yearling Weight	kg	30.0 to 110.0	285 to 435
5	hwt	Hogget Weight	kg	35.0 to 120.0	375 to 525
6	awt	Adult Weight	kg	35.0 to 130.0	465 to 2345
7	cwt	Carcass Weight	kg	5.0 to 75.0	100 to 400
8	pcf	Post-Weaning C fat depth	mm	0.1 to 15.0	105 to 345
9	yfc	Yearling C Fat depth	mm	0.1 to 15.0	285 to 435
10	hcf	Hogget C Fat depth	mm	0.1 to 20.0	375 to 525
11	yfat	Yearling Fat depth	mm	5.0 to 30.0	285 to 435
12	cfat	Carcass Fat depth	mm	5.0 to 30.0	100 to 400
13	pemd	Post-Weaning Eye Muscle Depth	mm	11.0 to 49.0	105 to 345
14	yemd	Yearling Eye Muscle Depth	mm	11.0 to 59.0	285 to 435
15	hemd	Hogget Eye Muscle Depth	mm	11.0 to 59.0	375 to 525
16	cemd	Carcass Eye Muscle Depth	mm	11.0 to 59.0	100 to 400
17	ygf	Yearling Greasy Fleece Weight	kg	1.0 to 9.0	285 to 435
18	hg	Hogget Greasy Fleece Weight	kg	1.0 to 10.0	375 to 525
19	ag	Adult Greasy Fleece Weight	kg	1.0 to 11.0	465 to 2345
20	yfcw	Yearling Clean Fleece Weight	kg	0.5 to 7.0	285 to 435
21	hfcw	Hogget Clean Fleece Weight	kg	0.5 to 8.0	375 to 525
22	acfw	Adult Clean Fleece Weight	kg	0.5 to 9.0	465 to 2345
23	yfd	Yearling Fibre Diameter	micron	11.0 to 40.0	285 to 435
24	hfd	Hogget Fibre Diameter	micron	11.0 to 40.0	375 to 525
25	afd	Adult Fibre Diameter	micron	11.0 to 40.0	465 to 2345
26	ydcv	Yearling CV* of Fibre Diameter	%	10.0 to 35.0	285 to 435
27	hdcv	Hogget CV of Fibre Diameter	%	10.0 to 35.0	375 to 525
28	adc	Adult CV of Fibre Diameter	%	10.0 to 35.0	465 to 2345
29	wfec	Weaning Faecal Egg Count	1000 eggs/g	0.0 to 35.0	15 to 165
30	pfec	Post-weaning Faecal Egg Count	1000 eggs/g	0.0 to 35.0	105 to 345
31	yfec	Yearling Faecal Egg Count	1000 eggs/g	0.0 to 35.0	285 to 435
32	ysc	Yearling Scrotal Circumference	mm	15.0 to 49.0	285 to 435
33	hsc	Hogget Scrotal Circumference	mm	15.0 to 59.0	375 to 525
34	nlb	Number of Lambs Born	ratio	0.0 to 5.0	350 to 4500
35	nlw	Number of Lambs Weaned	ratio	0.0 to 5.0	350 to 4500

*CV = Coefficient of variation

Description of LAMBPLAN Data

The LAMBPLAN database currently consists of approximately 77 breeds and in total approximately 800,000 animals. These are combined to form 37 breed analyses for genetic evaluation purposes. The majority of these animals originate from the Poll Dorset, White Suffolk, Texel, Merino, Suffolk, Border Leicester, Corriedale and Coopworth breeds (Table 2). Considerable overlap exists of animals across breeds where sires have been used for purebreeding and crossbreeding purposes.

Table 2 Number of animals recorded by LAMBPLAN breeders by year of birth for the 8 major breeds

Year of Birth	Poll Dorset	White Suffolk	Texel	Merino	Suffolk	Border Leicester	Corriedale	Coopworth
85	2155	607	328	186	609	364	441	209
86	3711	935	467	285	783	631	667	365
87	6969	1357	766	608	1131	785	904	486
88	16779	2402	969	588	1668	1129	1038	640
89	23480	3987	1501	1084	2778	1158	2128	1231
90	22056	5630	1979	3742	3234	1842	2243	1067
91	25229	6791	2506	3078	4074	2136	1923	1137
92	30636	8569	3117	4490	5076	3320	2455	1730
93	35270	11954	5154	4803	6795	4267	3001	2348
94	37660	14274	9580	4994	6953	4267	3410	2804
95	41794	16267	12068	4608	8225	5985	4875	3123
96	46971	19953	13177	3109	8785	6388	5593	3618
97	45192	20115	11691	2938	9746	5907	3995	4396
98	39121	23235	12678	4171	7729	6530	4237	4266
99	26234	17454	6169	1868	4571	5039	1618	4098
Total	403414	153464	83112	81853	72960	47413	40403	31970

The pedigree used in the Poll Dorset analysis consists of 403,414 animals of which approximately 76% have their sire recorded while 60% have their dam recorded. The proportion of animals with pedigree recorded is increasing over time as breeders record greater amounts of more accurate information. The majority of observations are for liveweight and carcass traits (see Table 3 for the Poll Dorset details as at December 1999). A small number of records for fleece weight, fibre diameter, scrotal circumference and the fertility traits are also available.

Data validation

Prior to genetic evaluation data are tested to validate their accuracy. All observations need to lie within a biologically meaningful range and data should have been observed within the age ranges specified in Table 1. LAMBPLAN management performs preliminary data validation by confirming with the breeder observations beyond three standard deviations from the management group mean. All observations taken outside those ranges are reported. The stage specified for the measurement must also be one of those listed in Table 1.

Table 3 Summary statistics for the observations recorded for each observed trait from the December 1999 Poll Dorset analysis

Trait	Count	Mean	Minimum	Maximum	Adjusted Mean
bwt	31031	4.51	0.90	10.80	5.07
wwt	89907	34.14	8.00	74.00	36.64
pwt	5362	56.27	27.00	108.50	54.82
ywt	94660	59.08	13.50	132.50	61.46
hwt	60543	68.86	24.50	148.00	70.65
awt	5367	68.82	20.50	138.50	70.10
pcf	84387	3.13	0.50	16.00	2.76
ycf	78642	3.71	0.20	19.00	3.86
hcf	53105	4.47	0.50	17.00	4.62
yfat	78642	11.13	0.60	57.00	11.13
pepd	55694	28.34	9.00	47.00	26.26
yemd	49414	31.03	11.80	53.00	30.61
hemd	36041	33.66	11.40	58.00	33.53
ygfw	220	2.95	1.04	4.26	3.04
hgfw	63	3.72	3.10	5.62	3.56
yfd	220	32.10	27.80	38.40	31.48
ysc	384	28.46	23.00	34.50	28.39
hsc	34	33.74	28.00	37.00	32.98
nlb	1171	1.72	0.10	7.00	1.72
nlw	1171	1.56	0.10	4.24	1.56

Animal information needs to be biologically consistent. Animals need to retain the same sex throughout their life and cannot be their own ancestors (or progeny). Basic information about the animal must also meet minimum requirements, such as the sex and breed codes correctly specified. For animals where these errors occur, all their data are rejected from the analysis. Some other examples of problems that will be detected include scrotal circumference measurements on ewes, date of birth missing or incorrect and breeder unknown.

Data Adjustments

The only fixed effect fitted in the mixed linear model used in *OVIS* is the contemporary group which is defined to be the group of animals that have been treated alike. Observations of different traits appear in different contemporary groups. *OVIS* handles all other systematic effects by pre-adjusting the data using a number of adjustment processes. This system enables the use of non-linear adjustment methods for traits that are not suited to linear methods, which reduces computational demands as a result of a simpler model and quicker solving times. Adjustment of performance records for known environmental effects aims at reducing the non-genetic or environmental components of phenotypic variance (Raymond 1982). All the adjustment methods utilised by *OVIS* are multiplicative in nature and can be applied in any order.

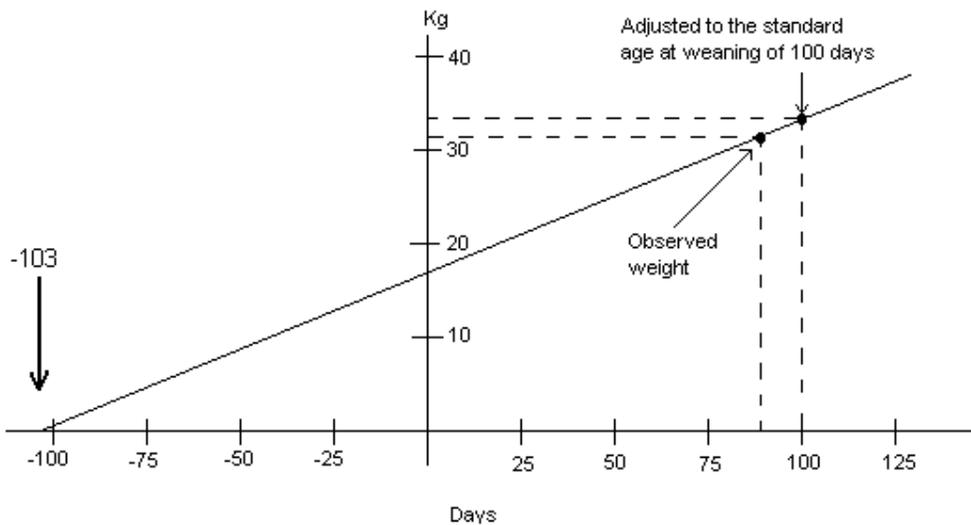
Adjustment Processes

Date of Birth and Age: Date of measurement for each trait is used to compute the age when measurements are taken. Age is then used to adjust weight and scrotal circumference to a standard age for that stage of measurement. The X-intercept method (Raymond 1982) is used to adjust the remaining liveweight observations for age (Figure 1). The adjusted age (standard age) and x-intercept values have been estimated using LAMBPLAN data. The following formula is used;

$$Y_a = Y_o (A_a - A_i) / (A_o - A_i)$$

- Where:
- Y_a = Adjusted weight
 - Y_o = Observed weight
 - A_a = Adjusted age (100 days)
 - A_i = Age intercept
 - A_o = Observed age

Figure 1. Illustration of x-intercept adjustments of weight for age



Birth and Rearing type: These traits are used solely for making percentage (multiplicative) adjustments to liveweight, greasy fleece weight and fibre diameter measurements. The actual adjustments range between 100% and 137%. Birth Type and Rearing Type are coded 1, 2, 3, or 4 for single, twin, triplets and quadruplets or more lambs, respectively. Since newborn lambs may be fostered, rearing type may be different to birth type.

Age of Dam: Dam age is used solely for making quadratic adjustments of liveweight measurements. Liveweight is adjusted to the standard dam age of 4.5 years at which the dam is

expected to be at a point of maximum production. If the dam is younger or older than this standard age the liveweight will be adjusted up to compensate accordingly (Figure 2). The range in age of dam accepted is 0.8 to 12 years old, progeny with dams outside these ranges will have their observations rejected from the analysis. The formula used is;

$$\text{Adjustment Factor} = I + Lx + Qx^2 / I$$

where $x = \text{Age of Dam} - 4.5$

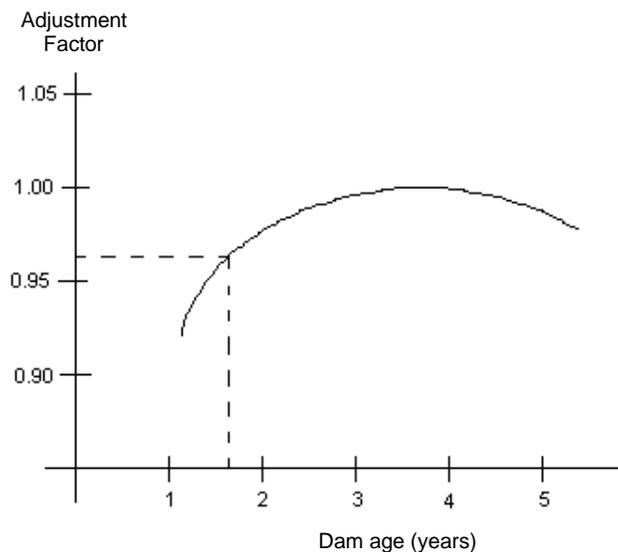
I = Intercept value

L = Coefficient for the linear component

Q = Coefficient for the quadratic component

The I,L and Q components are re-estimated for each breed and trait combination and as a result are common for all animals in each analysis.

Figure 2. Illustration of quadratic adjustments of liveweight for age of dam



Liveweight: Fat depth and eye muscle depth are adjusted by quadratic functions using the corresponding liveweight measurement. This is achieved in a similar manner to that described for age of dam.

OVIS Design and operation

Fundamental Design

All programs are written in Fortran 90 that allows both dynamic allocation of memory and intrinsic matrix operations. Dynamic memory allocation allows one program to be configured for different sized sets of data at run-time. It also makes more efficient use of memory as memory

can be allocated and de-allocated as required instead of reserving all the memory that the program will use at the start. The intrinsic matrix operators found in Fortran 90 help simplify the code and can be considerably faster than the traditional coding method of using loops.

Input Information

Three main types of input data are required;

1. The observations for the traits that are included in a genetic analysis,
2. The pedigree information,
3. The variables required for data adjustment and EBV estimation.

File formats for input and output of data to and from *OVIS* have been specified jointly by LAMBPLAN and AGBU. Adjustment factors are specified in a parameter file that is a list of ranges and adjustment factors for each trait. This file also details trait codes (1 – 35 in *OVIS* Version 1.0), names, standard age at measurement, adjustment codes (0 to 6), allowable observation and age ranges, birth-type adjustment factors, rear-type adjustment factors, X-intercept values for age adjustment of weight (separate for each sex) and coefficients for a second degree polynomials to adjust for age of dam and individual weight. *OVIS* utilises a second parameter file containing variance components. These parameters originated from the BVEST parameter files (Gilmour, 1993; Fogarty 1995), research conducted at UNE (van der Werf and Wheaton 1999) and results of research conducted by AGBU staff. At present this file contains the breed specific genetic parameters that are used for the 8 breeds listed in Table 2. This file lists the following components: genetic variance (direct and maternal), genetic correlations, residual variance, residual correlations, sire by flock variances (not operational in *OVIS* Version 1.0) and maternal permanent environment variance for the 2 traits with maternal components analysed. A third parameter file lists the major breeds and the details of which variance components, adjustment factors, genetic groups to use for the analysis. A heterosis table is also included with maternal and individual components. In *OVIS* Version 1.0 all heterosis effects are zero.

LAMBPLAN supplies the input files that contain pedigree and other animal information and performance records for the 35 direct traits.

Animal grouping

Specification of Contemporary Grouping: The breeder defines contemporary group so that it only contains animals that were treated alike. *OVIS* also allocates different traits to different

contemporary groups. Animals in a group should be of similar age and management history and they will be split into subgroups if the age range exceeds 70 days. The number of lambing opportunities is also used to specify contemporary group for fertility traits (nlb and nlw).

Formation of Genetic Groups: Genetic grouping is a unique feature of OVIS. At present genetic groups in the four major meat sire breeds (Poll Dorset, Texel, White Suffolk and Suffolk) are formed with base animals born in different years being assigned to different groups. Years within groups vary between breeds depending on the number of base animals present. Genetic groups in the Merino breed are formed on a fibre diameter basis. Flocks are grouped according to their average fibre diameter if they have enough base animals to form a group otherwise they join the nearest fibre diameter group. In across-breed analyses, breed is also included in the definition of genetic group.

Testing and Validation of the OVIS software

The *OVIS* software has been subjected to a large series of tests. During the developmental stages the analytical component was checked with a number of different sets of data against the BVEST software configured with the same data and similar models.

Initially EBVs produced by *OVIS* were compared to those from BVEST. *OVIS* was shown to produce very similar EBVs to that of BVEST over all major sheep breeds (ie correlations greater than 0.85 for the vast majority of traits). A large number of animals with significant differences in EBVs between *OVIS* and BVEST were also examined. In all cases *OVIS* was shown to be performing as anticipated given the data and the models. In November 1999 LAMBPLAN changed over to the *OVIS* Version 1.0 software to produce its EBVs. The major differences between *OVIS* Version 1.0 and BVEST are listed below.

1. Data acceptance criteria
2. Data adjustment factors
3. Contemporary group definition
4. Genetic grouping
5. Model characteristics
6. Genetic parameters
7. Number of traits and trait combinations.

Some of the differences arise due to changes in the parameter files and were present in BVEST. These have simply been updated to suite the data now being analysed. The majority of changes

arise due to differences in the capability of the software and the methods it utilises. As a result of these differences any further comparison of OVIS with BVEST became invalid.

An example LAMBPLAN run

Each month LAMBPLAN runs separate analyses for 32 breeds of sheep. The Poll Dorset breed is the largest within breed analysis that is performed. The dimensions of the Poll Dorset December 1999 *OVIS* analysis illustrate the potential of the *OVIS* software. This analysis incorporated 1065 flocks, with data recorded between 1974 and 1999. There were 395,823 animals in the pedigree. Although *OVIS* Version 1.0 is already capable of analysing 35 traits, only 16 traits were included in the analysis. These were the traits with sufficient data to be analysed (observations on 1% of animals with data). This combination of animals and traits resulted in 15,752,277 equations being solved. The number of equations built in the analysis represents approximately the number of animals by the number of traits times 3 (direct, maternal and permanent environment components). The analysis also included 11 genetic groups and 2029 levels of adjustment for across-flock heterogeneity of variance. This analysis took approximately 10.1 hours CPU time to complete on a COMPAQ Alpha station XP1000 running Digital Unix with 2 gigabytes of memory.

At certain times throughout the year a large across breed terminal sire analysis is also performed. This analysis consists of all the breeds that are used as terminal sires (typically Poll Dorset, White Suffolk, Suffolk and Texel breeds). This large analysis consisted of a pedigree with 527,240 animals, 1,145,956 observations, 2,029 flocks and 21,424,358 equations to solve. There were also 15 genetic groups and 3,381 levels of adjustment for heterogeneity of variance. This analysis used approximately 14.1 hours of CPU time to complete on the same computer.

Future Development

The main areas of future development will involve the estimation of heterosis components to develop appropriate across breed analysis, increasing the number of direct and maternal traits analysed and extensive and accurate estimation of variance components and adjustment factors based on the LAMBPLAN data for all the major breeds.

There are seven main very important properties of *OVIS* that are utilised by BREEDPLAN but that are as yet not functional in the current operational version of *OVIS*. With appropriate

research and data these properties may be readily implemented into OVIS. These are;

1. Interactions in the performance of sires across different flocks
2. Permanent environment effects for all traits
3. Incorporation of genetic information from external analyses
4. Embryo transfer and artificial insemination information
5. Fostered animals
6. Genetic evaluation of crossbred animals.

OVIS has the necessary code to facilitate the incorporation of these features, however at present the appropriate information and estimates for these effects are unavailable and/or not recorded by LAMBPLAN breeders.

Conclusions

OVIS has been designed to give sheep breeders a range of important benefits which has been possible by utilising the experiences gained from BREEDPLAN and PIGBLUP. There are also many more features and components of *OVIS* that await data and development. With these components in operation and improved data quality and parameter estimates Australian sheep breeders will have access to a very efficient means for selecting their best animals for breeding purposes. The example analyses highlight the analytical power of the *OVIS* software.

Acknowledgments

This project was funded by Meat and Livestock Australia (MLA), LAMBPLAN, UNE and NSW Agriculture.

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