Application for promotion to
Senior Principal Research Scientist

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Preamble

This application for promotion to Senior Principal Research Scientist is primarily based on my part in the development of ASReml (A S Rem~el). ASReml is a major statistical computing program developed since 1996 and currently used under commercial license in at least 15 countries especially in the disciplines of plant, tree, animal and fish breeding. I have written virtually all the 88000 lines of Fortran code in ASReml. While, I rely heavily on my principal colleagues Brian Cullis and Robin Thompson for theoretical rigor, I am not just a programmer as this application should reveal.

Introduction

I joined NSW Agriculture as a trainee in 1967 while studying Agricultural Science at Sydney University and started work as a biometrician in 1970. I was based in Sydney until 1976 when I moved to Trangie Research Station. I obtained my PhD in Animal Breeding at Massey University in 1980-83 and have worked as a biometrician at Orange Agricultural Institute since 1984.

My research focus is statistical computing in the area of linear models. Three major programs arising from this research are REG (1973-1993), BVEST (1992-1998) and ASREML (1996-present). BVEST is still used by the DPI Advanced (Sheep) Breeding Services although no longer used for LAMBPLAN processing. These programs (and many smaller programs written over the years) arose from needs of fellow researchers to undertake analyses not otherwise available. That is, the theory was available (in general if not specifically) but no software was available to facilitate its application to production data.

My role as a biometrician includes providing statistical designs, consulting with researchers, analysis of data and assistance with reporting. This continuing role provides the stimulus for the software developments. That is, my research is 'data driven', a response to particular problems encountered directly in my consulting, or by my colleagues, to which I provide a general solution rather than just solving the immediate problem. I also have a significant role mentoring in statistics and its application to sheep breeding research.

Recent research

First I refer to the 22 papers that have been published over the past 3 years.

- Thirteen of these are papers were coauthored with Neal Fogarty (retired PRS) and research officers Afolayan, Ingham, Safari and Morgan. These principally arose from the Maternal Central Progeny Test (MCPT) project that Neal conducted and that Raphael Afolayan and Veronica Ingham analysed under my direction and supervision. Similarly, I directed Alex Safari in analyses he conducted for the Sheep CRC reported in these papers. Four of the conference papers (C57, C59, C65 and C67) relate to these papers. The two papers with Jayce Morgan (91 and 94) related to her Masters thesis and were analysed by biometrician Sharon Nielsen with significant direction from me. The conference paper C58 with Peter Worsley was based on analyses of fruit fly populations I performed.
- Two papers (83 and 87) arose directly from PhD studies I supervised.
- I performed the analyses for the three papers (88, 89 and 90) by David Hopkins (PRS, Cowra). These were part of a special volume of AJEA edited by David and my contribution included providing guidelines for the statistical model to be used in all papers in the series.
- Sandra Eady (95) and Kishore Prayaga (105) are scientists with CSIRO who sought my input into their research resulting in these two papers. Both involved sophisticated statistical modeling which ASReml could perform but is beyond the norm. Similarly conference paper C 64 relates to analyses I directed with Schalk Cloete of South Africa.
- The paper with Hogue (97) arose from being asked to referee his paper on the analysis of data on Japanese cattle, and subsequently reanalyzing his data. Paul Arthur (PRS) is another coauthor.

This publication list shows I am still active as a senior biometrician mentoring and directing important production research. I am consulted when there is some particular complex issue with the analysis.

There is one paper (96) on QTL analysis of which I am sole author with 2 related conference papers (C63 and C66). The paper describes a mixed model approach to QTL detection in F2 or backcross populations which I developed and have implemented in ASReml. Simulation studies show that it is more effective than other popular methods in identifying regions where a QTL appears to occur based on mapped marker data. As a mixed model, it can effectively adjust for confounding factors in the data (such as spatial variation) and additive genetic relationships. The conference papers describe its successful application to a cattle breeding mapping experiment.

My major research is associated with ASReml (B45, B46). It includes developing and maintaining the program, training others in its use (W7, W8, W9, W10, W11, Audio tutorials), supporting users from around the world principally by email and to an inadequate degree, documenting the procedures used (96, C60, C61, C62).

ASReml 1 was commercially released in 2003, ASReml 2 was released in 2006 and the release of ASReml 3 is anticipated in July 2008. I will briefly recap the background to ASREML before describing the recent developments.

The theory behind Restricted Maximum Likelihood (REML) was published by Patterson and Thompson in 1971. I met Robin Thompson in 1981 in New Zealand and have collaborated with him since then. REML was recognized as valuable but was limited in application by computing strategies and computer limitations. During a visit in 1992, Robin proposed a new computing strategy (using an Average Information matrix, Gilmour et al 1995) which I implemented and found very effective. Along-side this development was work by Dr Cullis and others on spatial analysis of field experiments which utilized the concept of separability. This I disseminated in my program TwoD (Gilmour 1992). ASREML was conceived to exploit the average information algorithm using sparse matrix computing strategies and a general variance model specification based on the principle of separability to accommodate multivariate analysis of animal genetics data, multi-site analysis of field data with spatial variation as well as traditional variance component models. Consequently, it caters to a wide range of applications covering animal breeding, livestock production over time, forestry trials, plant breeding, fish breeding as well as applications in economics and medical statistics.

The decision by NSW DPI to commercialize ASReml is two edged. VSN International was contracted to be the commercial partner. Under the Contract, NSW has 51% of IP and Rothamsted Research has 49% of IP. VSN is a venture company set up my Rothamsted and NAG principally to distribute Genstat, a major statistical software system developed at Rothamsted and formerly distributed by NAG. ASReml is the only other product VSN distribute. Note that Genstat actually uses the core of ASReml for its REML processing. Under the contract, NSW DPI receives one third of sales revenue. NSWDPI received $63,736 in royalties from sales in 2007. The advantage of commercialization is that we know ASReml is currently licensed in over 15 countries by over 170 individuals and organizations. Most of these are multiple user licenses. Over 280 individuals are currently registered on the ASReml discussion list. There are an unknown number of users with licensed copies of ASReml 1 (who have not updated) and early versions (pre 2002) which did not require a license.

David Butler of QDPI has developed an S language version of ASReml for the R and S statistical environments. R is a free (public domain) reimplementation of the S language. Both provide comprehensive statistical analysis environments with a huge number of statistical methods including some procedures for mixed models. ASReml-R has been formally distributed by VSN over the last few years and is much more comprehensive than the other mixed model procedures otherwise available. However, R users are generally resistant to paying for software and the R developers will not promote procedures like ASReml-R that require a license.

Since commercialization, ASReml has not been available to third world users without western funds. I am hopeful that this restriction will be removed with the release of a

'Discovery' version when ASReml 3 is released. From my perspective, income from sales is less important than facilitating efficient analysis, wherever the need.

ASReml has had a huge direct impact in many areas of Agricultural Research, especially plant and animal breeding. This impact was recognized early in relation to animal breeding when I was appointed a Fellow of the Association for the Advancement of Animal Breeding and Genetics at its meetings in New Zealand in 2001. In several years, over a third of the papers to their conferences cited ASReml, indicating the need that existed for such a product. So, while others had developed the statistical ideas, scientists were frustrated in not being able to implement them until ASReml appeared.

Without deprecating the contribution of others, and especially my colleagues Brian Cullis (SPRS) and Robin Thompson (former head of statistics at Rothamsted), I see my role has been to make new ideas in the area of mixed models accessible to general researchers so they can effectively explore their data. The novel contribution I made was to achieve economies in computation which meant models could be fitted to large bodies of data which previously were too large or complex to be handled.

However, it is in plant breeding that ASReml has facilitated a paradigm shift, not only to the application of new statistical models, but too their development.   My close association with Brian Cullis has made it possible for him to revolutionize the statistical analysis of plant breeding data. Thus, in the last 20 years, broadacre plant breeding in particular has moved from simple averaging of results from diverse trials to integrated analysis incorporating spatial adjustment and appropriate trial weighting based on individual trial variability. Brian has overseen the development of new models and their deployment across Australia through the GRDC funded National Statistics Program. It has been my role to provide the principal tool, ASReml.

The major enhancements I have implemented in ASReml 2 and 3 are as follows:
- Testing of fixed effects is not simple in mixed models. I have implemented 2 methods for calculating the denominator degrees of freedom making significance testing of fixed effects possible
- QTL methods are implemented from two perspectives. I have implemented several traditional methods as well as my new method (96). More recently, users have thousands of markers to explore and methods have been implemented to handle this.
- Pedigree extensions: Animal breeders have traditionally used additive genetic relationships based on the pedigree and a diploid genetic structure. I have recently extended this to handle varying degrees of inbreeding typically found in plant pedigrees.
- Generalized linear mixed models was the subject of my PhD (1983) and I have implemented these basic forms in ASReml. More recently I have implemented multiple threshold models for ordered multinomial data.
- Tabulation and various other data exploration procedures have been added to help users explore/verify the structure of their data prior to analysis.
- Prediction of means and trends has proved a challenge for some of the more complex models that can be fitted in ASReml. Recent work has facilitated prediction in hierarchal models.
- Merge is a facility to combine data from several files for integrated analysis.
- Model extensions allow for more sophisticated testing of effects and variances.

ASReml3 consists of some 88000 lines of Fortran code, nearly all of which I have written. Documentation includes a User Guide (400 pages), an online help system of some 158 HTML pages, and a tutorial series consisting of 4 hours of audio. I drafted and maintain the User Guide with significant input from collaborators in formatting and the text of some sections. I have prepared all of the HELP system and the audio tutorials.

To summarize, my current involvement with ASREML includes

Maintenance: With any major statistical package, there is a continual need for maintenance as users find novel ways to use the package. ASREML provides for a very wide range of models and users sometimes discover bugs or limitations as they invoke combinations of options never previously used.

Commercialization: As well as providing the product, documentation and test examples to VSN, I provide support to users both directly and as requested by VSN.

Training and consultancies: I periodically conduct courses for new and experienced ASReml users, present details of statistical models and methods at national and international conferences, and undertake minor and major consultancies for commercial users,

Developments: Ideas for developments come from three primary sources: my own ideas for making ASReml better arising from my own use of it in consulting and from user applications, requirements arising from needs of the National Statistics project (Brian Cullis) and ideas developed by Robin Thompson. I periodically meet with Brian and Robin to review these ideas to establish priorities and formalize them more. The list is long with more sophisticated modeling of vatriances being high on the agenda.

One rough measure of the importance of ASReml is that a Web of Science citation report identifies 879 citations over 11 years (1996 to 2007). There are 507 other citations of my work including 130 to my 1997 JABES paper describing single site spatial analysis.

Other Activities

While I have little line management responsibility, I continue to provide support to several PhD students, to review papers in several statistical journals and mentor colleagues and junior scientists.

Student Supervision: I am not formally supervising any students at present but have had significant input into the PhD studies of Helena Oakey (University of Adelaide), Alison Kelly (University of Brisbane) and Meimei Ding (University of New England, Armidale) in the last 3 years.
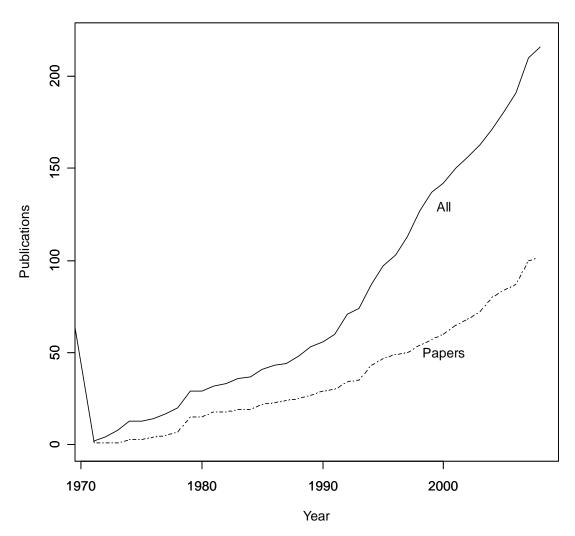
Peer review: I have refereed papers for Australian Journal of Agricultural Research, Biometrics, Journal of Agricultural Science Cambridge, Genetics Selection and Evolution, Journal of Agricultural, Biological and Environmental Science, Crop Science, Journal of Animal Breeding and Communications in Statistics.

Research leadership: I continue to play a significant mentoring role among my biometrical colleagues being involved in giving statistical guidance and support, internal review of draft publications, monitoring the internal consulting report series and advising on software and hardware upgrades. I do not have any formal line management responsibilities.

External funding: I had a major role in the GRDC project *Statistical support for plant improvement programs* just completed and have a major commitment to *Integrated genetic parameter estimation of sheep production traits* with the Australian Sheep Industry CRC.

Conferences: I presented an invited paper (C60, C61, C62, C63, C64) to the *8th World Congress on Genetics Applied to Livestock Production*, held in Brazil in 2006. I regularly contribute to local applied statistical meetings and the Association for the Advancement of Animal Breeding and Genetics biennial meetings (C57, C65, C66, C67).

Publications 1971 - 2008

Future Research

I will be eligible to formally retire in 2009 but do not expect to cease involvement in ASReml. Three persons, Simon Harding of VSN, David Butler of QDPI and Damian Collins of NSW DPI have started collaborating to rewrite the core of ASReml with a view to better documenting its procedures, implementing more modern programming techniques and improving algorithms where possible. The goal is that the new core will better handle the new developments required. I am integral to that process as the aim is to document and transfer my knowledge and skill while I am available. I expect I will continue to work on the ASReml program, incorporating the new core in due course, but also implementing more of the developments that have been proposed.

The most interesting idea for future development is the development of hyper models for the variance parameters.

Summary of Claim

Research and Publication:
My research represented in ASReml has made and continues to have a huge impact in both the efficiency and soundness of statistical analysis with linear mixed models in NSW DPI, Australia and globally. The impact of ASreml is both direct and indirect as people are stimulated by ASREML to develop new models and applications of mixed models.

I have maintained a steady publication rate (Figure 1) with 22 papers published since my last interview.

Transfer of Skills: I constantly support biometricians, statisticians and research officers from both within and outside NSW Agriculture and Australia in the application of linear mixed models.

International Standing: I have very high standing internationally, particularly in the animal breeding discipline and among other users of ASReml, people needing to perform complex statistical analysis by linear mixed models.

Recent Publications

The following publications appeared since 2005 (the two paper with * were listed previously as in press).

Papers

(83)   Fischer, T.M., van der Werf, J.H.J, Banks, R.G., Ball, A.J. and **Gilmour, A.R**. (2005) Genetic analysis of weight, fat and muscle depth in growing lambs using random regression models. *Animal Science* **82:** 13-22.

(84)   * N.M. Fogarty, V.M. Ingham, **A.R. Gilmour**, L. P. Cummins, G.M. Gaunt, J. Stafford, J.E. Hocking Edwards and R.G. Banks (2005) Genetic evaluation of crossbred lamb production. 1. Breed and fixed effects for birth and weaning weight of first cross lambs, gestation length and reproduction of base ewes. *Australian Journal of Agricultural Research* **56**: 443-453.

(85)   * N.M. Fogarty, V.M. Ingham, **A.R. Gilmour**, L. P. Cummins, G.M. Gaunt, J. Stafford, J.E. Hocking Edwards and R.G. Banks (2005) Genetic evaluation of crossbred lamb production. 2. Breed and fixed effects for post-weaning growth, carcase and wool of first cross lambs. *Australian Journal of Agricultural Research* 56: 455-463.

(86)   Safari, E., Fogarty, N.M. and **Gilmour, A.R.** (2006) Sensitivity of response of multi-trait index selection to changes in genetic correlations between production traits in sheep. *Australian Journal of Experimental Agriculture* **46**(3):283-290.

(87)   Dutkowski, G.W., Costa e Silva, J., **Gilmour, A.R.**, Wellendorf, H. and Aguiar, A. (2006) Spatial analysis enhances modelling of a wide variety of traits in forest genetic trials   *Canadian Journal of Forest Research* **36** :

(88)   Hopkins, D.L., Stanley, D.S., Martin, L.C. and **Gilmour, A.R.** (2007) Genotype and age effects on sheep meat production. 1. Meat quality. *Australian Journal of Experimental Agriculture*, **47**, -.

(89)   Hopkins, D.L., Stanley, D.S., Martin, L.C. and **Gilmour, A.R.** (2007) Genotype and age effects on sheep meat production. 1. Production and growth. *Australian Journal of Experimental Agriculture*, **47**, 1119-1127.

(90)   Hopkins, D.L., Stanley, D.S., Martin, L.C., Toohey, E.S., and **Gilmour, A.R.** (2007) Genotype and age effects on sheep meat production. 3. Meat quality. *Australian Journal of Experimental Agriculture*, **47**, 1155-1164.

(91)   Morgan, J, N.M. Fogarty, S.M. Nielsen, **A.R. Gilmour**, (2006) Milk yield and milk composition from grazing primiparous crossbred ewes. *Australian Journal of Agricultural Research* **57**: 377-387.

(92)   Safari E, Fogarty NM, Gilmour AR, Atkins KD, Mortimer SI, Swan AA, Brien F, Greeff JC, van der Werf, JHJ (2007) Across population genetic parameters for wool, growth and reproduction in Australian Merino sheep 1. Data structure and non-genetic effects. *Australian Journal of Agricultural Research.* **58,** 169–175.

(93)   Safari E, Fogarty NM, Gilmour AR, Atkins KD, Mortimer SI, Swan AA, Brien F, Greeff JC, van der Werf, JHJ (2007) Across population genetic parameters for wool, growth and reproduction in Australian Merino sheep 2. Estimates of heritability and variance components. *Australian Journal of Agricultural Research.* **58,** 177–184.

(94)   Morgan, J, Fogarty, N.M., Nielsen, S.M., **Gilmour**, **A.R.** (2007) The relationship of lamb growth from birth to weaning and the milk production of their primiparous crossbred dams. *Australian Journal of Experimental Agriculture* **47**: 899-904.

(95)   Eady, S.J., Garreau, H.S., and **Gilmour, A.R.** (2007) Heritability of resistance to bacterial infection in meat rabbits. *Livestock Science*, **112:** 90-98.

(96)   **Gilmour, A.R.** (2007) Mixed model regression mapping for QTL detection in experimental crosses. *Computational Statistics and Data Analysis* **51**:3749-3764

(97)   Hogue, M.A., Arthur, P.F., Hiramoto, K., **Gilmour, A.R.,** and Oikawa, T. (2007) Variance components due to direct genetic, maternal genetic and permanent environmental effect for growth and feed efficiency traits in young male Japanese Black cattle. *Journal of Animal Breeding and Genetics.* **124**: 102-107.

(98)   Rejected

(99)   Safari, E., Fogarty, N. M., **Gilmour, A. R**., Atkins, K. D., Mortimer, S. I., Swan, A. A., Brien, F., Greeff, J. C., and van der Werf, J. H. J.. (2007) Genetic correlations among and between wool, growth and reproduction traits in Merino sheep. *Journal of Animal Breeding and Genetics.* **124**:65-72.

(100)   Afolayan, R. A., N. M. Fogarty, N. M., Ingham, V. M., **Gilmour, A. R**., Gaunt, G. M., Cummins, L. J., and Pollard, T.. (2007) Genetic evaluation of crossbred lamb production. 3. Growth and carcass performance of second cross lambs. *Australian Journal of Agricultural Research* **58**: 457-466.

(101)   Ingham, V.M., Fogarty, N.M., **Gilmour, A.R.,** Afolayan, R.A., Cummins, L.J., Gaunt, G.M., Stafford, J., and Hocking Edwards, J.E. (2007) Genetic evaluation of crossbred lamb production. 4. Genetic parameters for first cross animal performance. *Australian Journal of Agricultural Research* **58**: 839-846.

(102)   N. M. Fogarty, N. M., Ingham, V. M., **Gilmour, A. R**., Afolayan, R. A., Cummins, L. J., Hocking Edwards, J. E. and Gaunt, G. M. (2007) Genetic evaluation of crossbred lamb production. 5. Age of puberty and lambing performance of yearling crossbred ewes. *Australian Journal of Agricultural Research* **58**: 928-934.

(103)   R.A. Afolayan, N.M. Fogarty, **A.R. Gilmour**, V.M. Ingham, G.M. Gaunt and L.J. Cummins (2008) Genetic correlations between reproduction traits and growth and wool production in crossbred ewes. *Australian Journal of Experimental Agriculture* **48**: 8

(104)   Afolayan RA, Fogarty NM, **Gilmour AR**, Ingham VM, Gaunt GM, Cummins LJ (2008) Reproductive performance and genetic parameters in first cross ewes from different maternal genotypes. *Journal of Animal Science* **86,** 804-814.

(105)   Prayaga KC. Henshall JM. Swain DL. and **Gilmour A.R.** (2008) Estimation of maternal variance components considering cow-calf contacts under extensive pastoral systems *Journal of Animal Science.* 86(5):1081-1088

Reference Manuals

(B45)   **Gilmour, A.R.**, Cullis, B., Gogel, B.J., Welham, S. and Thompson, R.(2006) ASReml User Guide. Release 2. VSN International, UK 324 pp

(B46)   Butler, D., Cullis, B.R., **Gilmour, A.R.,** and Gogel, B.J. (2007) Analysis of mixed models for S language environments. ASReml-R reference manual. Release 2 (2007) Queensland Department of Primary Industries and Fisheries, GPO Box 46, Brisbane, QLD, 4001, Australia.

Scientific Conferences

(C57)   Safari, E., Fogarty, N.M., **Gilmour, A.R.,** Atkins, K.D., Mortimer, S.I., Swan, A.A., Brien, F., Greeff, J.C. and van der Werf, J.H.J. (2005) Preliminary genetic parameters for clean fleece weight, fibre diameter, hogget weight and number of lambs born in Merinos. *Proceedings of the Association for the Advancement of Animal Breeding and Genetics*, **16**: 180-183

(C58)   Worsley, P.M., Dominiak, B.C., **Gilmour, A.R.** and James, D.G. (2005) Pilot study of Intra-town dynamics of Queensland Fruit Fly (*Bactrocera tryoni*). *Proceedings of SSC 2005 Spatial Intelligence, Innovation and Praxis: The national biennial Conference of the Spatial Sciences Institute, September 2005. Melbourne: Spatial Sciences Institute.* 1248:1254

(C 59) Fogarty, NM, Safari, E, **Gilmour, A.R.**, Ingham, VI, Atkins, KD, Mortimer, SI, Swan, AA, Brien, F, Greeff, JC, van der Werf, JHJ (2006) Wool and meat genetics – the joint possibilities. In: PB Cronje and D Maxwell (eds.) Wool Meets Meat – Tools for a modern sheep enterprise. Proceedings of the 2006 Australian Sheep Industry CRC Conference, Orange, Australia pp. 36-41.

(C 60) **Gilmour, A.R.**, (2006). Statistical models for multidimensional (longitudinal/spatial) data. *Proceedings of the 8th World Congress on Genetics Applied to Livestock Production*, Brazil, CD Paper 25-1

(C 61) **Gilmour, A.R.**, Butler, D., Cullis, B.R. and Thompson, R. (2006). ASReml 2 and SAMM 2 – Mixed models for many. *Proceedings of the 8th World Congress on Genetics Applied to Livestock Production*, Brazil, CD Paper 27-2

(C 62) **Gilmour, A.R.**, and Thompson, R. (2006). Equation ordering for Average Information REML. *Proceedings of the 8th World Congress on Genetics Applied to Livestock Production*, Brazil, CD Paper 27-13

(C 63) Esmailizadeh Koshkoih, A. Pitchford W.S., Bottema C.D.K., Verbyla, A.P., and **Gilmour, A.R.** (2006). MAPPING MULTIPLE QTL FOR BIRTH WEIGHT IN CATTLE USING A MIXED MODEL APPROACH.. *Proceedings of the 8th World Congress on Genetics Applied to Livestock Production*, Brazil, CD Paper 20-17

(C 64) Cloete, S.W.P., van Wyk, J.B., Scholtz, A.J., and **Gilmour, A.R.**, (2006). GENETIC PARAMETERS AND TRENDS FOR LAMB BEHAVIOUR. *Proceedings of the 8th World Congress on Genetics Applied to Livestock Production*, Brazil, CD Paper 17-07

(C 65) Safari, E., Fogarty, N.M., Mortimer, S.I., Greeff, J.C., Hatcher, S., Lee, G.J., and **Gilmour, A.R.,** (2007) Feed Intake and its Genetic Relationship with growth traits in Merino sheep. *Proceedings of the Association for the Advancement of Animal Breeding and Genetics*, **17**: 199-202.

(C 66) Pitchford W.S., Esmailizadeh Koshkoih, A., and **Gilmour, A.R.,** (2007) Combining information across traits using a factor analytic model increases the power of QTL detection. *Proceedings of the Association for the Advancement of Animal Breeding and Genetics*, **17**: 368-375.

(C 67)   Afolayan, R.A., **Gilmour, A.R.,** and Fogarty, N.M., (2007) Selection indexes for crossbred ewe reproduction and productivity. *Proceedings of the Association for the Advancement of Animal Breeding and Genetics*, **17**: 491-494.

ASREML WORKSHOP/CONSULTANCIES

(W7)   Pioneer, Des Moines, 5 days, 2006

(W8)   VSN, Hemel Hemsted 2 days, 2006

(W9)   CSIRO, Armidale, 2 days, 2007

(W10)   South Africa and Kenya, 2 weeks , 2007

(W11)   Pioneer, Des Moines, 1 week, 2008

Travel Reports

(R18)   **Gilmour, A.R.**, (2005) Overseas travel report 2005 Pioneer - Iowa, Monsanto – Missouri, Rothamsted Research 22pp

(R19)   **Gilmour, A.R.**, (2006) Overseas travel report January 2006 Rothamsted Research 9pp

(R20)   **Gilmour, A.R.**, (2006) Overseas travel report August 2006 Pioneer - Iowa, WCGALP in Brazil, Rothamsted Research 37pp

(R21)   **Gilmour, A.R.**, (2007) Overseas travel report 2007 ILRI in Kenya, Workshops in South Africa 11pp

(R22)   **Gilmour, A.R.**, (2008) Overseas travel report January 2008 Pioneer - Iowa, Rothamsted Research 5pp

ASREML Tutorials

Set of 16 audio tutorials running for 15 to 20 minutes each.

Table 1 Summary of publications over time

YEAR	Scientific Collaborative	Scientific Statistical	Conferences Collaborative	Conferences Statistical	Other	Total
71	1				1	2
72					2	2
73			1		3	4
74	2			1	2	5
75						0
76	1					1
77	1			1	1	3
78	2			1		3
79	8			1		9
80						0
81	3					3
82				1		1
83	1				2	3
84					1	1
85	1	2			1	4
86	1			1		2
87		1				1
88	1		1	1	1	4
89	2				3	5
90	2				1	3
91	1			2	1	4
92	3	1	5	1	1	11
93	1			1	1	3
94	6	2	1	3	1	13
95	2	2	1	2	3	10
96		2		1	3	6
97		1	3	2	4	10
98	4		3	6	1	14
99	2	1	3	1	3	11
2000	0	3	0	0	2	5
2001	4	1	0	0	3	8
2002	2	1	1	1	1	6
2003	2	2	2	1	0	7
2004	5	3	0	0	0	8
2005	4	0	5	1	0	10
2006	3	0	4	2	1	10
2007	12	1	3	0	1	18
2008	2	1	1	2	1	7

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