







**Table 1.** AIC and LRT's of models of Legendre or eigenvector fixed component  $n_f = 9$ , and  $n_r \in \{1, \dots, 5\}$ 

Order $n_r$	Legendre, $n_f = 9$					Eigenvector, $n_f = 9$				
	1	2	3	4	5	1	2	3	4	5
$\ln(L) (\times 10^3)$	-289	-280	-276	-273	-271	-289	-280	-276	-274	-272
AIC ( $+5.7 \times 10^5$ )	13,904	2,533	449	1,051	2,895	14,661	2,930	568	1,217	3,256
LR ( $n_r$ vs. $n_{r-1}$ )		17,169	7,882	5,196	3,954		17,529	8,160	5,148	3,760
$p = 1 - \chi^2$		0	0	1	1		0	0	1	1

**Legendre vs. eigenvector.** Models with a fixed regression component of either Legendre polynomials or eigenvectors of order  $n_f = 9$  were compared via AIC values for their relative merit, for random component of Legendre orders  $n_r \in \{1, \dots, 5\}$ . For any particular random order  $n_r$ , Legendre models had slightly better AIC values than those of the eigenvector models (Table 1). In the absence of a measure of significance for AIC comparison, the default choice of regression function ought to remain as the Legendre polynomials.

**Pedigree information.** Future inclusion of pedigree information ought to improve model fit even more due to increased utilisation of data via pedigree linkages. While the relationship matrix  $\mathbf{A}$  would not be subject to inversion by the block-matrix inversion technique, the use of  $\mathbf{A}^{-1}$  would allow for a similar technique for solving the model. Therefore the use of a full (including pedigree) RR model will have essentially no more computational complexity for random orders  $n_r > 1$ .

## CONCLUSION

In a RR model for WOW data, increasing orders of fixed and random regression components significantly improve the model in general, though these must be tempered by the practical realities of assumed longitudinal relationships and necessary number of parameters per animal. The choice of type of regression function (Legendre polynomials or eigenvectors) is insignificant.

The future inclusion of pedigree relationships ought to ensure a much better depth of data per animal and subsequent model improvement. The use of block-matrix inversion will still ensure that computational complexity is significantly reduced.

## REFERENCES

- Akaike H. (1974) *IEEE Transactions on Automatic Control* **19**(6): 716.  
 Banachiewicz T. (1937) *Acta Astronomica, Series C*, **3**: 41.  
 Jamrozik J. and Schaeffer L. R. (1997) *J. Dairy Sci.* **80**: 762.  
 Kirkpatrick M., Hill W.G. and Thompson R. (1994) *Genet. Res.* **64**: 57.  
 Meyer K. (1999) *J. Anim. Bree. Genet.* **116**: 181.  
 Meyer K. (2004) *Livest. Prod. Sci.* **86**: 69.  
 Mrode R.A. and Thompson R. (2014) '*Linear Models for the Prediction of Animal Breeding Values*', 3<sup>rd</sup> Ed. Cabi Publ., Wallingford, UK. pp130–155.  
 Neyman J. and Pearson E.S. (1933) *Phil. Trans. Royal Soc. A: Math. Phys. Eng. Sci.* **231**(694–706):289.  
 Olori V.E., Hill W.G., McGuirk B.J. and Brotherstone S. (1999) *Livest. Prod. Sci.* **61**: 53.  
 R Core Team (2014). *R: A language and environment for statistical computing*. R Foundation for Statistical Computing, Vienna, Austria. URL <http://www.R-project.org/>  
 Runge C. (1901) *Zeitschrift für Mathematik und Physik* **46**: 224.  
 Schaeffer L.R. and Dekkers J.C.M. (1994) *Proc. 5th World Congr. Genet. Appl. Livest. Prod., Guelph, Canada* **18**: 443.  
 Speidel S.E., Enns R.M. and Crews D.H. Jr. (2010) *Genet. Mol. Res.* **9**: 19.