Supplementary File 1: *Notes on Tutorials and Software*

<u>**Running the tutorials**</u>

The tutorials and accompanying data files are provided separately for four different software packages: **ASReml**, **ASReml-R**, **WOMBAT** and **MCMCglmm**. You will need to carefully follow the instructions below to download the correct supporting files for the tutorials in each software package and, in some cases, re-name files so that they will work in the tutorials.

For the tutorial in **ASReml** download the supporting following files:

- "Supplementary File 2 - Tutorial ASReml.pdf"
- "gryphon.dat"
- "gryphonRM.dat"
- "gryphon.ped"
-

For the tutorials in **ASReml-R** or in **MCMCglmm** download the supporting following files:

- "Supplementary File 3 - Tutorial ASReml-R.pdf" or "Supplementary File 5 - Tutorial MCMCglmm.pdf" as appropriate
- "gryphon.txt"
- "gryphonRM.txt"
- "gryphonped.txt"

For the tutorial in **WOMBAT** download the supporting following files:

- "Supplementary File 4 - Tutorial WOMBAT.pdf"
- "gryphon_uni.dat"
- "gryphon_bi.dat"
- "gryphonRM.dat"
- "gryphonRM_pe.dat"
- "gryphon.ped_WOMBAT"

Before beginning the tutorial, we assume the reader has successfully installed the chosen software on their computer and has saved the required data files to an appropriate directory from which they will be read. Full instructions for how to do this are provided with software distributions.

Once downloaded the pedigree file for the WOMBAT tutorial "gryphon.ped_WOMBAT" should be renamed as simply "gryphon.ped".

Software notes

ASReml and **ASReml-R** are commercial software applications published by VSN international (http://www.vsni.co.uk/software/asreml/). At the time of writing a free 30-day trial is available. Users of the stand-alone version of **ASReml** will require an appropriate text editor for preparation of input files and viewing of output files. Although all readers will probably have a workable text editor on their

computers already, we recommend using **CONTEXT** (freeware available at http://www.contexteditor.org/) as this program can be set up to interface nicely with ASReml.

Instructions to do this can be found in the ASReml user guide and on the VSN website which hosts a lot of useful material for the novice user (see http://www.vsni.co.uk/software/asreml/user-area/tutorials/#tutorialA). Other important resources include the ASReml reference user guide itself (Gilmour et al. 2006), and the "ASReml cookbook" written by Luis Apiolaza and posted at http://uncronopio.org/ASReml/HomePage. The cookbook is an extremely helpful place to start for any reader interested in learning more about running mixed models with ASReml

Reference: Gilmour, A.R., Gogel, B.J., Cullis, B.R., & Thompson, R. (2006) *ASReml User Guide Release 2.0.* VSN International Ltd, Hemel Hempstead.

WOMBAT is a slightly less flexible but free alternative to ASReml, written by Karen Meyer (2006). It can be downloaded via http://agbu.une.edu.au/~kmeyer/wombat.html. 32-bit and 64-bit Linux executables, capable of analysing complex models and large amounts of data, as well as a less powerful and efficient Windows version are available. As is the case for ASReml, users will require a simple text editor to generate the input files. A manual covering all the basics as well as a number of more advanced options can be downloaded at http://agbu.une.edu.au/~kmeyer/download.php?file=WombatManual.pdf. Additional information related to running **WOMBAT** and REML estimation in general can also be found at the WOMBAT Wiki (http://agbu.une.edu.au/~kmeyer/dokuwiki/doku.php).

Reference: Meyer, K. (2006). WOMBAT – Digging deep for quantitative genetic analyses by restricted maximum likelihood. *Proc. 8th World Congr. Genet. Appl. Livest. Prod., Communication.* **27**: 4.

MCMCglmm is an R package for Bayesian mixed model analysis written by Jarrod Hadfield. It is freeware distributed through CRAN (http://cran.r-project.org/). Information about the package, together with a user manual and vignettes are available at http://cran.r-project.org/web/packages/MCMCglmm/index.html.

Reference: Hadfield J.D. (2009) MCMC methods for Multi-response Generalised Linear Mixed Models: The MCMCglmm R Package.

Users of both **MCMCglmm** and **ASReml-R** will require an up to date installation of the statistical package **R** (obtained http://cran.r-project.org/).

It is always important to take time to think carefully about the strengths and potential limitations of your pedigree information before embarking on quantitative genetic analyses. **Pedigree Viewer**, written by Brian Kinghorn, is an extremely useful application for visualising pedigrees, and can be downloaded from: http://www-personal.une.edu.au/~bkinghor/pedigree.htm. **Pedantics** an R package written by Michael Morrissey and distributed through CRAN (http://cran.r-project.org/) can also be used for this and offers some nice additional features for visualising pedigree structures and generating associated statistics. Before you begin running through the tutorials, we advise taking a moment to look at the pedigree files provided with them using **Pedigree Viewer** or **Pedantics**.