

ESTIMATING THE IMPACTS OF LITTER SIZE AND NON-ADDITIVE GENETIC  
EFFECTS ON EWE LONGEVITY AND STAYABILITY IN A U.S. WESTERN EXTENSIVE  
RANGE PRODUCTION SYSTEM

A Thesis  
Submitted to the Graduate Faculty  
of the  
North Dakota State University  
of Agriculture and Applied Science

By

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In Partial Fulfillment of the Requirements  
for the Degree of  
MASTER OF SCIENCE

Major Department:  
Animal Sciences

March 2021

Fargo, North Dakota

North Dakota State University  
Graduate School

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**Title**

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**MASTER OF SCIENCE**

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## ABSTRACT

Non-additive genetic effects are usually ignored in animal breeding programs due to data structure, computational limitations, and over-parameterization of the models. Non-additive genetic effects play an important role in the expression of complex traits in livestock species, such as longevity and stayability. Components of genetic variance for additive and non-additive genetic effects were estimated for longevity and stayability in U.S. Western ewes using pedigree relationship matrices. Litter size were also investigated for direct and maternal effects. For longevity, a larger proportion of phenotypic variance was explained by non-additive genetic effects than by additive effects for model A+D, indicating that including dominance genetic effects are important. Results suggest that inclusion of non-additive genetic effects in animal models is possible in estimating longevity and stayability and will improve selection accuracy and reduce overestimation of additive genetic effects.

## ACKNOWLEDGMENTS

I would like to thank my Masters committee chair and major professor, Dr. Lauren Hanna, as well as every member of my committee: Dr. Bret Taylor, Prof. Larry Reynolds, and Dr. Megan Orr for their support, advice, and guidance throughout my research. Through her involvement in my research career, Dr. Lauren Hanna has pushed me to new boundaries I did not know existed, and taught me flexibility in learning, teaching, and self-improvement. Without her guidance and enthusiasm, my time here at North Dakota State University would not have been as successful and wonderful as it has been. I would also like to thank the faculty from the Department of Animal Sciences at North Dakota State University for being open and helpful when asked about questions in their expertise. I give my greatest gratitude to my fellow graduate students in the Lauren lab i.e. Nayan, Elfren, and Samuel. Their upbeat attitude, ability to help diffuse stress, and endless opportunities for us to bounce ideas back and forth was a major component in my self-improvement. I am grateful for the funding from USDA that has supported my time here at North Dakota State University.

Finally, I would like to give a heartfelt thanks to my family, my dad, Sir Stephen Oribamise, my mom, Lady Victoria Oribamise, my brothers, Franklin Oribamise and Stephen Oribamise Jnr, my girlfriend, Wiljar Ojuro and my friends. Without these pillars of support and happiness in my life, I would not be who I am today.

## **DEDICATION**

This is dedicated to all the frontline guys ensuring we have food on our tables in a global pandemic.

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## LIST OF ABBREVIATIONS

A + D .....	Additive + Dominance model.
A.....	Additive model.
BYR .....	Birth year.
DIC.....	Deviance information criterion.
DTB.....	Dam's ewe's type of Birth.
DTR.....	Dam's ewe's rearing type.
ESS.....	Effective sample size.
H <sup>2</sup> .....	Broad sense heritability.
h <sup>2</sup> .....	Narrow sense heritability.
LY2 .....	Ewe's lifetime total number of times lambed
LY3 .....	Ewe's lifetime total number of lambs born
LY4 .....	Ewe's lifetime total number of lambs born alive
LY5 .....	Ewe's lifetime total number of lambs raised to weaning.
TB .....	Type of birth.
TR .....	Rearing type.
USSES.....	United States Sheep Experiment Station
YOR .....	Year of record.

## LIST OF SYMBOLS

$\underline{b}$ .....	Vector of birth year effects to be estimated.
$\underline{m}$ .....	Vector of dam's maternal permanent effects to be estimated.
$\underline{u}$ .....	Vector of additive genetic effects to be estimated.
$\underline{y}$ .....	Vector of longevity records.
$\underline{\beta}$ .....	Vector of fixed effects to be estimated.
$\delta_B^2$ .....	Birth year genetic variance.
$\delta_A^2$ .....	Additive genetic variance.
$\delta_D^2$ .....	Dominance genetic variance.
$\delta_{MPE}^2$ .....	Maternal permanent environmental genetic variance.
$\delta_P^2$ .....	Phenotypic variance.
$\delta_e^2$ .....	Error variance.
$\pm$ .....	Plus-or-minus sign
$\mu$ .....	Population mean
$X$ .....	Incidence matrix of fixed effects.
$Z$ .....	Incidence matrix of random effects.
$\varepsilon$ .....	Residual.

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## CHAPTER 1: INTRODUCTION

The success and failure of a sheep operation depend on the ewe's ability to remain in the flock long enough to recoup expenses of lamb development and ewe maintenance in an economical manner (Snelling et al., 1995; Doyle et al., 2000; Cammack et al., 2009). To recoup these investments, the ewe must wean a marketable lamb as a two-year-old or younger and subsequently wean commercial lambs each year after until an age that covers the investment made in the individual ewe. The breakeven point depends on the number of lambs lambled by each ewe (Snelling et al., 1995; Cammack et al., 2009). The ewe's ability to remain in the flock is known as its reproductive life, defined in terms of longevity and stayability. VanRaden and Klaaskate (1993) defined longevity as the amount of time a ewe spends producing lambs to represent the length of its reproductive life. Hudson and Van Vleck (1981) defined stayability as the probability of a ewe to survive to a certain age, given all conditions are kept constant. Litter size selected for reproductive traits like longevity and stayability are more enduring in respect to coping with production challenges than ones not selected for longevity and stayability (Theilgaard et al., 2009).

Genetic variance is broken into two effects: additive and non-additive genetic effects (Hill et al., 2008). The genetic effect is called 'additive' when genes show summing effect on the quantitative trait; this results in deviance from the phenotype mean due to inheritance of a particular allele and its relative effect on the phenotype. Heritability is the magnitude to which individual phenotype differences can be partitioned due to allelic substitutions' additive effects (Lynch and Walsh, 1998). Non-additive genetic effects are the interaction of alleles, genotypes, or both within and across genes (Norris et al., 2010). Interactions between genes at the same loci are called dominance whereas interactions between alleles at different genes are called epistasis. These non-additive genetic effects are not usually included in genetic models because they require a large

dataset with a high ratio of full-sibling relationships (Misztal et al., 1997) and computation of non-additive genetic relationships are always tricky with pedigree-based relationships (Mrode, 2014).

Furthermore, the non-additive component is ignored because it is often confounded with the maternal environment, and estimation would involve large computational requirements (Varona and Misztal, 1999; Aliloo et al., 2017). Even so, it is essential to investigate the impact of including dominance genetic effect in genetic evaluations, as the impact of this effect on longevity and stayability traits in sheep flocks is not well understood (Nazarian and Gezan, 2016). Evidence of non-additive genetic components for reproductive traits has been reported in rabbits (Nagy et al., 2013), poultry (Wei and van der Werf, 1993; Guo et al., 2020), cattle (Hoeschele, 1991, Misztal et al., 1997) and swine (Guo et al., 2016). If non-additive components are unaccounted for, then estimation of heritability is imprecise leading to inaccuracies in selecting individuals as parents for the next generation. Therefore, it is imperative that the non-additive genetic variance for reproductive traits in sheep, such as longevity and stayability, be estimated.

### **Objectives**

The objectives of this study were to:

- Identify familial structure in available data, including full and half-sibling relationships within breeds and across breeds of sheep reared in the western U.S.
- Investigate the effect of genetic covariance matrix model construction on additive and dominance genetic variance components across breeds and within breeds of sheep reared in the western U.S.
- Investigate the role of non-additive genetic effects on stayability and longevity by estimating additive and dominance genetic components using pedigrees of within and across breeds of sheep reared in the western U.S.

- To determine the effect of birth and rearing type of the ewe and ewe's dam on ewe longevity and stayability within and across breeds of sheep reared in the western U.S.

### **Hypothesis**

Dominance effects are often challenging to partition out in genetic evaluations unless appropriate relationships are present to clarify their role in expressing desirable traits (stayability and longevity). Given the dataset available, the expectation is that sufficient full and half-siblings are known to develop and model appropriate dominance effects within breeds and potentially across breeds. Furthermore, if crossbreeds are to be utilized or a multi-breed evaluation is to be run using the entire dataset, the pedigree structure must be investigated. It is expected that an amended relationship matrix can be supplied to the statistical software that will allow modeling across all breeds for the entire dataset. It is expected that dominance effects will be a significant genetic inheritance component for stayability and longevity and that the birth or rearing litter size of the lamb's dam will affect that lamb's stayability and longevity in the flock, specifically that single-born dams will yield offspring with more significant changes of stayability and longevity. Lastly, it is expected that dominance effects will be a significant genetic inheritance component for stayability and longevity.

## **CHAPTER 2: LITERATURE REVIEW**

### **Importance of longevity and stayability in United States sheep flocks**

Sheep are considered an all-purpose animal in that they provide meat, fiber, milk, and skin (Berger et al., 2004). Almost all sheep breeds can be classified based on their abilities to produce a particular product or a combination of these products. The relative economic importance of these products varies from country to country and from one continent to another. Hair sheep breeds in the Middle East's hotter parts dominate because heavy wool fleece is a handicap in high temperatures. On the other hand, wool-producing sheep are favored in the temperate regions because they keep the flock warm during the cold and provide commercial value.

In all production systems, longevity and stayability are economically relevant traits for lamb producers. Longevity is a functional trait positively correlated to farm profitability (Pérez-Cabal and Alenda, 2003). The average longevity will influence economic returns by affecting the proportion of female offspring that must be retained for replacements; this proportion might be available for sale and the annual depreciation cost per ewe will be reduced (Perez-Raso et al., 2004). An increase in a flock's longevity will increase the number of lambs born per ewe (Kenyon et al., 2014). Hence, more lambs will be available for sale, and juvenile stock retention as replacements will be minimized (Castañeda-Bustos et al., 2014). In addition, increasing longevity helps to reduce long-term health care costs (Kizilkaya et al., 2002).

Borg et al. (2009) stated that the average lifespan of a ewe in their commercial sheep production flock is six to seven years before she was culled from the flock. A ewe can be culled from the flock due to voluntary or involuntary reasons (Garcia et al., 2015). Voluntary culling occurs when the main reason for removal is a low performance from the ewe even though she is healthy and might accrue cost (De Vries et al., 2010). On the other hand, involuntary culling occurs

from death, injury, illness, and other environmental challenges, forcing the producer to remove a ewe from the flock (Ahlman et al., 2010). If assuming the productive life of a ewe could be increased to 10 to 11 years, then the lifetime earning capacity of that ewe would increase, and the cost of replacing her would decrease. The ability to make these changes occur, however, depends partially on heritability and related selection response.

Longevity is defined as the amount of time a ewe spends producing lambs in the flock (VanRaden and Klaaskate, 1993). On the other hand, stayability is defined as the probability a ewe survives to a certain age in the flock given all stable conditions, such as ongoing good health and prolonged fecundity (Hudson and Van Vleck, 1981; Cammack et al., 2009; Fortes et al., 2012; Douhard et al., 2016). Some researchers have expanded these definitions by placing age limits based on economic importance (e.g., Brigham et al., 2006; 2009). Others have created variations of these definitions based on species and their production tendencies (Cattle: VanRaden et al., 2006; Rogers et al., 2004; Swine: Serenius and Stalder, 2004; Buzniskas, 2014).

In any case, measuring the trait should show the age that the ewe is most productive, depending on the available information on the ewes so that that selection can lead to profitable outcomes. Attempts at this have been: 1) registering the number of days for which the ewe stays in the flock, 2) a binary trait assigning the value 0 to a ewe that did not survive, and a value of 1 for a ewe that stayed in the flock for a particular time frame; or 3) as the number of offspring birthed or reared during her life (Martinez et al., 2005; Galeazzi et al., 2010). Stayability is a binary trait on the observed scale, i.e., successful lambing (1) after the defined stayability cutoff date (e.g., six years) or failure (0), not lambing in the designated stayability cutoff date. Stayability is considered lowly heritable (Douhard et al., 2016) It has been proven that the number of offspring birthed or reared are genetically the same, and that selection based on the number of offspring

(0.24) is more accurate than ewe age due to higher estimates of heritability compared to stayability to a specific age (0.09) (Martinez et al., 2005).

### **Factors known to influence longevity and stayability**

#### **Breed**

Garcia-Peniche et al. (2006) estimated the effects of breed type on longevity and stayability using Brown Swiss, Holsteins, and Jersey cows. They evaluated the performance during five years of life opportunity of cows born from January 1992 to June 1996 for longevity and stayability. They found out that there was a slight difference in the average stayability proportions of Jersey, Brown Swiss, and Holsteins because of breed differences. They noted that the Jersey breed could stay longer in the herd than the other breeds considered in many instances, but their study did have regional effects. Hohenboken (1977) also estimated the differences between the stayability rates of Columbia and Targhee ewes from 2½ years old to 8½ years old, and found that Columbia ewes had a higher stayability rate in comparison to Targhee ewes.

Iman and Slyter (1996) also evaluated the differences between Finn-Dorset-Targhee (FDT) and Targhee breeds stayability rates in the flock. They opined that FDT ewes had the potential to stay longer in the flock and ultimately could produce more lambs per thousand in comparison to the Targhee ewes. Pellerin and Browning (2012) compared the does of Boer, Kiko, and Spanish goat breeds for stayability. They concluded that it was far better to use the breeds of Spanish with the least-squares values of  $2.62 \pm 0.34$  to  $6.21 \pm 0.61$  or Kiko,  $2.45 \pm 0.31$  to  $6.09 \pm 0.58$  for optimum economic advantage as those breeds stayed more in the flock than that of Boer,  $1.43 \pm 0.18$  to  $3.24 \pm 0.34$ , measured in years. Invariably, it has been shown that there exist levels of differences between each breed's ability to stay in the flock than the other breeds according to the

scientists who have worked on it; therefore, accounting for breeds in multi-breed populations is essential given that Polypay and Rambouillet have not been investigated since the 90s.

### **Birth and rearing type**

The impact of birth and rearing types on reproductive traits is vastly underreported (Tosh and Kemp, 1994). Recently, McHugh et al. (2017) reported that type of rearing when working with Ireland sheep did influence the growth potential of lambs reared as singles, as lambs born and raised as singles had greater birth weight, 40-day weigh, and heavier than multiple-born lambs raised as singles. McHugh et al. (2017) found that type of rearing and type of birth ultimately influence growth traits as single-born lambs raised as twins performed better than triplet-born lambs reared as singles, especially on preweaning and on growth traits. Therefore, producers must record the rearing and birth types to foster proper selection and adequate ewe evaluation as mismanagement of records can lead to bad decision making. Pettigrew et al. (2019), while experimenting on the effects of birth ranks on dual-purpose New Zealand sheep, observed that ewe survival was lowest in ewes that were lambed as singles in comparison to the other ewe groups (lambled as twin, triplet, quartet or quintet and above) with the losses occurring earlier in this group than in other groups. This might have decreased their longevity and weaning weight of lambs produced and concluded that with voluntary culling, ewes that were lambed as singles had lower stayability and longevity than ewes that were lambed as twins.

### **Selection in Animal breeding**

Genetic selection goals in animal breeding are to improve traits of economic importance in the next generation (Ibtisham et al., 2017). Fisher (1918) provided a method of applying concepts from Mendelian genetics to the selection of quantitative phenotypes. He proposed that alleles (Mendelian factors) make a small contribution to producing a phenotype. This method is called



the additive model, summarizing that all these alleles' combined effects are produced by summing up their individual allele effects (Fisher, 1918; Wright, 1931; Wade and Goodnight, 1998). Selection in sheep breeding took advantage of Fisher's assumption of additivity combining phenotypic dataset and pedigree information of individuals and their relatives to generate heritability values, breeding values (EBV), and selection responses using Henderson's 1984 Best Linear Unbiased Predictor (BLUP) method (Kruuk, 2004).

The difficulty of using Fisher's additive model for selecting reproductive traits in sheep arises from low heritability (i.e., small additive genetic variance in proportion to a large phenotypic variance). This has been reported for longevity and stayability traits in literature, ranging from 0.022 in mouse to 0.22 in captive rhesus macaques female (Gagliardi et al., 2010; Vitezica et al., 2013). Non-additive genetic effects have been proposed as the factor that could explain the missing heritability (the portion of heritability not explained by the top associated variants in genome-wide association studies, GWAS) (Visscher et al., 2012). Because of low heritability values for some quantitative traits, Fisher added additional variables to account for non-additive genetic effects. These variables are still considered as 'nuisance' parameters to account for anomalies in the model. Fisher (1918) defined them as 'dominance' (interaction between two alleles at a locus) and 'epistasis' (interaction between two or more loci), which are expected to contribute to variation in fitness (Wright, 1931; Crnokrak and Roff, 1995; Roff, 2012) as well as to determine which additive genetic effects contribute to bottlenecks (Wade and Goodnight, 1998; Turelli and Barton, 2004; Saltz et al., 2014). Researchers have commented that applying the estimates of non-additive genetic effects has not been used frequently in livestock breeding because it is difficult to estimate these effects accurately. Most selection programs aim to estimate just the additive genetic effects (Bolormaa et al., 2015). Many geneticists agree that these non-additive genetic effects exist but do

not agree on how common the phenomenon is and if they should be included in genetic studies (Hill et al., 2008; Powell et al., 2013).

Modeling these non-additive genetic effects might be needed to estimate breeding values, heritability, and proper selection programs. They are often still ignored because the assumption of additivity accounts for more of the genetic variation. To estimate dominance genetic effects based on pedigree-based relationships, a large dataset with a high ratio of full-siblings relationship is needed (Misztal et al., 1997). With pedigree-based relationships, computation of non-additive genetic relationships is always tricky (Mrode, 2014). Even so, not estimating dominance effects can lead to confounding and overestimation of the additive effects (Nagy et al., 2013).

### **Additive genetic effects on longevity and stayability**

Despite the economic importance of longevity and stayability in animal production systems, little attention has been paid to these traits in different sheep breeds. Studies on longevity and stayability heritability estimates are scarce in the United States sheep industry and the world at large because most ewes' life expectancy exceeds the period required to keep them in the flock to be economically viable (Al-Shorepy and Notter, 1996). This is especially true for annually lambing flocks, as there is sufficient time between each lambing period to build up reserves again (Al-Shorepy and Notter, 1996). Longevity and stayability heritability in sheep and cattle vary from low to moderately high ( $<0.10$  to  $\leq 0.30$ ) (Cammack et al., 2009; Fortes et al., 2012). Estimated breeding values (EBV) or expected progeny differences (EPD; EBV divided by 2) are used in breeding programs to improve accuracy by ranking individuals available for selection (Garrick et al., 2009; Hanna et al., 2014). There has been much progress in increasing longevity utilizing selection based on EPD use in cattle production (De Vries, 2017). The use of EPD for stayability as a selection criterion may improve accuracy and selection effectiveness, leading to an increase

in the meantime of stayability in the cattle herd (Van Melis et al., 2007). Even so, this has not been investigated in sheep.

### **Impact of age on longevity and stayability**

Kirschten et al. (2015), in their investigation on Targhee sheep, concluded that the heritability of lambing at one year of age was 0.15. They suggested that ewes should be selected to lamb at one year of age as it will ensure continuous lambing and ewes stay in the flock for a more extended period. Fuerst-Waltl et al. (2004) supported this theory in cattle as they reported that age of dam negatively impacted daughter's longevity. Jamrozik et al. (2013) opined that there was a difference in heritability estimates for calving at an early age (2 years) in comparison to calving at a later age. They found heritability estimates of cows that calved at two years old to be 0.36 for stayability, while cows that calved at later ages had a heritability of 0.12.

Maiwashe et al. (2009) estimated the heritability of South African Angus cows for stayability using a sire threshold model, where estimates ranged from 0.26 (age 4 and 5) to 0.30 (age 6). Shorten et al. (2015) reported that there was a quadratic relationship between the age of a dam at calving and pregnancy rate in Angus cattle. The rates of pregnancy of the cattle reported in the study increased between the ages two and seven and decreased between ages seven and eleven, this was independent of whatever culling strategies employed. Shorten et al. (2015) suggested that rate of pregnancy and overall fertility of dams diminishes once they reach a particular threshold that falls between ages five to seven.

### **Influence of non-additive genetic modeling effects in genetic evaluation models**

#### **Importance of non-additive effects**

Recent studies show that if additive and non-additive genetic effects are considered together, analyses might yield higher statistical power for portioning components of variance for

most livestock species' complex traits (Su et al., 2010). Palucci et al. (2007) found out that the non-additive genetic effects were larger than the additive genetic variance for Canadian Holsteins' fertility traits. Esfandyri et al. (2016) opined that including both additive and dominance effects in their analyses significantly improved prediction accuracy.

### **Challenges to estimating non-additive genetic effects**

Estimating genetic differences due to non-additive genetic effects is possible if we set up breeding programs that maximize favorable allelic combinations (Munoz et al., 2014); additive and non-additive genetic effects differences are orthogonal; therefore, we must separate additive and non-additive effects to avoid problems of selection pressure, and lack of genetic drift (Hill et al., 2010). However, these genetic effects are confounded in breeding populations due to higher sampling variances and shared environmental variances. A portion of variance due to alleles' interaction can be seen as additive genetic variance (Hill et al., 2010; Powell et al., 2013). Thus, ignoring non-additive genetic effects overestimates the additive genetic variance as it inflates breeding values resulting in biased EBV or EPD used in ranking.

Data structure plays a significant role in separating additive and non-additive genetic effects. Munoz et al. (2014) suggested that separating these effects requires a large number of close, full-sibling relatives. Van Tassell et al. (2003) opined that a minimum of 20% full-siblings in the population must be established for successfully estimating non-additive genetic effects. Due to operational challenges, it might be difficult to generate these needed large full-sib families (Munoz et al., 2014). Full-sibling relationships present over several generations can also reduce the confounding effects of additive, and non-additive genetic effects, i.e., inaccurate and inadequate pedigree information can be a limiting factor. Computational requirements can also be a limiting factor in estimating these non-additive genetic effects (Varona and Mistal, 1999;

Wittenburg et al., 2011; Technow et al., 2015). Finally, incomplete model specification due to a lack of computing resources can also be a limiting factor in estimating non-additive genetic effects (Wray et al., 2013). Table 2.1 summarizes experiments on stayability and longevity in sheep. Longevity and stayability studies in other species such as the cow (Rohrer et al., 1988), pig (Koketsu et al., 1999), and goat (Castañeda-Bustos et al., 2014) showed they are complex traits and controlled by many factors.

Table 2.1: Summary of experiments for comparing sheep breeds' estimates of heritability for longevity (LONG) and stayability (STAY)<sup>1</sup>

Traits	Country	Breed	N	Heritability	Method	Reference	
LONG	ZAF	Dorper	42,831	0.05	Linear mixed model (LMM), Restricted maximum likelihood (REML)	Zishiri et al. (2013)	
	ESP	Latxa	1,541	0.13	Linear profit function	Legarra et al. (2007)	
	ITA	Valle del Belice	2,190	0.11	Weibull model	Riggio et al. (2009)	
	NZL	SIL Flock 2638	1,330	0.20 to 0.23	Generalized linear model (GLM), REML	McIntyre et al. (2012)	
	USA	Columbia		4,389	0.06	GLM, REML	Holland (2018)
				213	0.09	GLM, REML	Holland (2018)
				4,534	0.07	GLM, REML	Holland (2018)
				5,922	0.16	GLM, REML	Holland (2018)
				12,154	0.06	Linear animal model, REML	Borg et al., (2009)
STAY	ZAF	Dorper	42,831	0.05 to 0.11	LMM, REML	Zishiri et al. (2013)	
	NZL	SIL Flock 2638	1,330	0.11 to 0.20	GLM, REML	McIntyre et al. (2012)	
	USA	Columbia		4,389	0.08 to 0.22	GLM, REML	Holland (2018)
				6,482	0.17 to 0.32	GLM, REML	Holland (2018)
				213	0.05 to 0.17	GLM, REML	Holland (2018)
				4,534	0.10 to 0.28	GLM, REML	Holland (2018)
				5,922	0.21 to 0.28	GLM, REML	Holland (2018)
				12,154	0.04 to 0.10	Linear animal model, REML	Borg et al. (2009)

<sup>1</sup>SIL Flock 2638: Sheep Improvement Ltd. (SIL) Flock 2638, ZAF: South Africa, NZL: New Zealand, ESP: Spain, ITA: Italy

## **Modeling approaches to understanding the genetic control of longevity and stayability in the flock**

### **Methods of obtaining variance component estimation in animal breeding**

In quantitative genetics, the animal model has been used repeatedly to estimate reproductive parameters, such as additive genetic variance and heritability (Muff et al., 2019). Still, these parameters can have their estimates affected by other factors.

Accurate estimation of breeding values for important economic traits impacts on changing quantitative traits to meet consumers, producers, and breeders' ever-demanding needs. Advances in computer technology, software and hardware, and improved statistical methods have given researchers and producers the ability to recalculate and re-estimate genetic parameters to improve selection strategies for today's market (Gianola and Rosa, 2014). The development of algorithms summarized in Table 2.2 below has helped portion animal variance into direct, maternal, and environmental effects, animal and dam permanent environmental effects, litter effects, and the correlation between these genetic effects. This portioning helps in estimating the contribution of each individual effect on the overall performance of the animal.

### **Bayesian school of thought**

The origin of how Bayesian methodology came to be is founded in a little bit of controversy. In his review of the Bayesian method in animal breeding, Blasco (2001) mentioned that the Bayesian school of thought was in practice founded by Count Laplace. Even so, before Laplace presented his first paper on the subject matter, the new school of thought was named after a priest, rev. Thomas Bayes, the reason for this, I do not know.

Table 2.2: Models for estimating variance components in animal breeding.

Method	Reference	Portioned animal variance
Best linear unbiased predictor	Henderson (1977)	Permanent environmental effects and their correlation
Linear model	Henderson (1984)	Permanent environmental effects
Maximum likelihood	Im et al. (1984)	Litter size
Bayesian method	Gianola and Foulley (1982); Gianola (1986)	Environmental and litter effects
Free derivative restricted maximum likelihood model	Graser et al. (1987)	Litter effects
Restricted maximum likelihood using several random effects model	Meyer (1989)	Dam's permanent environmental effect
Threshold model	Wiggans et al. (2003)	Direct and maternal effects
Random regression model	Schaeffer (2004)	Permanent environmental effects

There are two leading schools of thought in statistics: the Bayesian and the frequentist schools of thought (Gianola and Fernando, 1986). The Bayesian school of thought uses probability distributions to model uncertainty in the value of parameters, treating those parameters as random effects; this then produces a posterior probability that captures our current knowledge regarding the importance of those model parameters (Gianola and Fernando, 1986). The posterior distribution infuses prior knowledge of effects with the information about those effects already established from the observed dataset. In Bayesian analysis, an unobserved dataset is not considered. At the same time, the frequentist approach relies on a frequency definition of probability depending on repeated analysis of the same events, and it is unstable in comparison to the Bayesian approach; both the Bayesian and frequentist schools of thought are concerned with the same objective, which is to analyze unknown quantities of interest then interpret the degree of support for our theories using data.

Bayesian modeling requires the modeler to specify a prior probability distribution for the model under investigation. This prior is an expression of the current knowledge of the model under



study, which is then updated with the observed data's information to producing the posterior distribution. Bayesian inference is majorly influenced by both the prior selected and the empirical data. There are two traditional categories of prior: 1. Informative priors and 2. Non-informative priors. Many scientists use non-informative priors more often because it is considered more objective (Blasco, 2001). This is because the prior distribution contains little information about the model. This, in turn, places much weight on the observed data for proper posterior information, unlike the informative priors that inculcate information from previous knowledge without regards to the data into their distributions. This reduces the importance placed on the empirical data, which might affect the posterior distribution (Datta and Mukerjee, 2004).

Blasco (2001) described a Bayesian model's objective as identifying the uncertainty about the actual value of some parameters based on a given data using probability as the measurement of this uncertainty, i.e., a Bayesian model is driven by assumptions of conditional probability. Blasco (2001) demonstrated that if the parameter of interest is the heritability of a particular trait, the Bayesian model's usefulness estimates a probability density of the heritability given the data,  $f(h^2|\mathbf{y})$ , where  $\mathbf{y}$  is the vector of observations. When our distribution is obtained, we can draw inferences in many ways: 1. We can calculate the probability of  $h^2$  between 0 and 1 by combining these two values' functions. 2. We can also compute the Highest Posterior Density (HPD). The probability of finding  $h^2$  is more than 95% using the Highest Posterior Density (HPD) distributions. We can also calculate the point estimate giving several values of  $h^2$  calculated from the distribution  $f(h^2|\mathbf{y})$ . The mode is the value that maximizes  $f(h^2|\mathbf{y})$  more, no matter the data. The most distinguishing factor between the Bayesian method and other methods is the use of a prior distribution.

## **Bayesian model in animal genetics**

Gianola and Foulley (1982) introduced the Bayesian model in animal genetics when they published their work analyzing threshold traits. This paper discussed and addressed issues regarding Bayesian modeling in animal genetics; their work was further expanded by Gianola (1986 and 1990). He highlighted the possibilities associated with Bayesian models and how they could explain variances in animal models. Mrode (2005) and Gianola and Rosa (2002) supported the use of Bayesian models in animal genetic analyses. This present study is the first attempt at estimating longevity and stayability in sheep using Bayesian models.

## **Markov Chain Monte Carlo (MCMC)**

MCMC combines both properties of Markov chain and Monte-Carlo (Brown and Heathcote, 2008). Monte-Carlo estimates any distribution properties by using random sampling methods to obtain results and calculate the sample mean of those. The Markov chain of the MCMC generates random samples by a unique sequential process where the random samples are used as a seed to produce the next random sample, creating a never-ending chain (Brown and Heathcote, 2008). In a Markov chain, each new random sample depends on its predecessor and independent of its predecessor's predecessor; MCMC estimates samples from distributions which we can use to calculate information about those distributions, such as means, variances, and credible intervals (Bolker, 2008). Specifying a prior for a Bayesian analysis represents the uncertainty about the parameter before the data are examined (Hadfield, 2019). A standard choice for the prior distribution for variance components in Bayesian modeling is an inverse-Gamma distribution.

## **Conclusion**

In summary, the sheep industry has begun to shift its focus towards novel and economically important traits, such as longevity and stayability traits. It is essential to understand the genetic

architecture and control of these traits. One approach is to investigate the impact of including dominance genetic effects in genetic evaluations, as the impact of this effect on longevity and stayability traits in sheep is not well understood, especially those sheep managed in extensive western U.S. ranges. Dominance is essential from an evolutionary perspective and because of its role in the selection response. Therefore, it is expected that separating additive and non-additive genetic components would lead to a more nuanced dissection of the genetic architecture of longevity and stayability traits. Understanding the genetic architecture of these traits could impact the future design and implementation of breeding strategies in the sheep industry.

## CHAPTER 3: MATERIALS AND METHODS

### Reproductive data and processing

North Dakota State University Institutional Animal Care and Use Committee approval was not obtained for this study because the records were extracted from an existing database. All records for this study were from the USDA, ARS, Range Sheep Production Efficiency Research Unit, U.S. Sheep Experiment Station (USSES) located near Dubois, ID that was previously described in Holland (2018). First, lambing (1950 to 2015), weaning (1950 to 2015), ewe productivity (1977 to 2015), and inventory (1955 to 2015) were each parsed together from individual year database files in R software version 4.0.4 (R Core Team, 2021; see Appendix A).

Lambing data was merged with weaning data so that rearing type (TR), weaning weight, and average daily gain were included with lambing records. From this combined lamb data (n = 267,336 records), ewes born before or by 2008 were separated off to be processed further (n = 101,129). The year requirement was set to ensure that a given ewe could be 7 years of age by 2015 (the last year of available data). To do this, formatting for missing data (varied between 0 and “.”) was replaced with NA (missing value in R) for lamb, sire, and dam ID columns. Ewe lambs missing formal ID tags were removed from the data set (n = 5,130). Following this, lamb, sire, and dam ID were used to make unique numeric strings for easier identification of animals across years. The string format followed YYYYBBIIII, where YYYY is a 4-digit birth year, BB is the 2-digit breed code, and IIII is the 4-digit ear tag identifier of that animal. This matched the format of the pedigree provided by the USSES, which was used to check and validate the correct lamb, sire, and dam ID.

Following ID reformatting, the coding system for birth type (TB) was recoded as shown in Table 3.1. This reduced the birth types to four relevant levels rather than 10 used by USSES, most of which would not likely be present for reproduction. As the ewe's dam's birth and rearing type

were also of interest for this project, the dams of ewe’s were extracted from the lamb dataset with their birth and rearing types (DTB and DTR, respectively), then merged with lamb data so that a given ewe’s record included DTB and DTR, if available.

Table 3.1: Birth type code and description provided by the United States Sheep Experiment Station (USSES) after recoding for similar birth types.

New birth type		USSES birth type	
Code	Description	Code	Description
1	Born single	0	1 immature lamb born dead
		1	1 normal lamb born dead
		5	1 live single lamb
2	Born twin	2	2 immature lambs born dead
		4	2 normal lambs born dead
		6	2 born, 1 live, and 1 immature
		7	2 born, 1 live, and 1 born dead
		8	2 live twin lambs
3	Born triplet	9	3, triplet, born in any condition
4	Born quadruplet or higher	3	4-5, quadruplet-quintuplet, born in any condition

Ewe productivity and inventory records were then read into R and had the same ID checks and formatting as described with the lamb data. Each dataset was then summarized using the *dplyr* package (Wickham et al., 2021) *summarize* function (Appendix A). Per ewe, the *summarize* function provided the minimum and maximum of the following columns in the ewe productivity records:

- Ewe’s lifetime total number of times lambed (LY2)
- Ewe’s lifetime total number of lambs born (LY3)
- Ewe’s lifetime total number of lambs born alive (LY4)
- Ewe’s lifetime total number of lambs raised to weaning (LY5)
- Year of record (YOR)

Per animal, the *summarize* function provided the minimum and maximum year of record (YRREC) from inventory records. This summary was then merged with their disposal code, if available. Any data that was not available was set to missing (NA). Both summaries of ewe productivity and inventory records were merged with the lamb data by lamb ID using the base *merge* function, making sure that all lambing data was retained (i.e., setting `all.x = TRUE` in the function). After a review of YOR, YRREC, LY, and disposal traits, it was determined that the maximum LY2 for each ewe would be used as the longevity value. It is not typical for management to lamb more than once a year at USSES, therefore the maximum LY2 would be indicative of the number of years the ewe was productive in the flock. This final combined ewe dataset was saved before independent breed records were analyzed.

The ewe data consists of multiple purebreds and crossbreds, with the largest number of records in Columbia, Polypay, Rambouillet, and Targhee. Each ewe record has a sub-type of mating (STM) column, which indicates the parental cross that ewe originated from. Due to this, STM corresponding to purebred Columbia (06), Polypay (30), Rambouillet (07), and Targhee (02) were used to partition ewe records out by breed. For each breed, any missing data for birth type (TB, DTB, or both), rearing type (TR, DTR, or both), birth weight, and longevity lead to removal. Furthermore, any ewes with dams over the age of 7 were removed as this did not follow typical management protocols. Table 3.2 summarizes record numbers before and after missing record removal. Stayability (STAY; 0 for not present, 1 for present) was assigned from ages 2 to 7 based on the longevity value (e.g., if longevity was 5, then STAY2 to STAY5 were 1, but STAY6 and STAY7 were 0).

To ensure useful and relatively consistent sample sizes for litter size (TB, TR, DTB, DTR) and birth year effects, count per level in each breed were reviewed. Levels that accounted for less

than 1% of the data or did not represent typical management practices by USSES were removed.

Table 3.2 provides total record numbers after removal and Table 3.3 provides summary counts for litter effects before and after removal.

Table 3.2: Record numbers for each major breed from combined ewe data at start, after removal of missing relevant columns, removal of small sample groups (final dataset), and pedigree.

<b>Breed</b>	<b>Start</b>	<b>missing records</b>	<b>final sample size</b>	<b>Pedigree size</b>
Columbia	17,622	3,314	2,251	5,223
Polypay	12,380	3,103	2,599	8,691
Rambouillet	26,018	4,316	2,809	10,711
Targhee	23,597	4,434	2,880	9,661
Combined	79,617	15,167	10,539	24,999

It was uncommon to have lambs raised as orphans, let alone kept as ewes in the flock, based on management at USSES. Therefore, records of ewes with rearing types (TR and DTR) of 2, 4, and 6 were removed across all breeds. The presence of quadruplets or higher was also uncommon for Columbia, Rambouillet, and Targhee, therefore birth type (TB and DTB) of 4 was removed for these 3 breeds, leading to rearing types (TR and DTR) of 0 being absent. Furthermore, management at USSES did not allow these three breeds to raise triplets on extensive rangeland, therefore any ewe with rearing type (TR and DTR) of 9 was due to a specific experiment at the station and not reflective of typical management practices. Ewes with this rearing type were removed for Columbia, Rambouillet, and Targhee.

Polypay, due to the selection pressure placed on them during breed development, is likely to have larger litter sizes and be able to raise them. Even so, birth type of quadruplets or higher (TB or DTB = 4), after year censoring was applied (see later description), accounted for less than 0.1% of the data. Therefore, Polypay ewes with a birth type of 4 (TB and DTB) were removed. Given the breed's ability to raise larger litter sizes, Polypay's rearing type (TR and DTR) of 9

(being raised a triplet) accounted for almost 3% of the breed's data. Due to this, Polypay ewes with TR and/or DTR of 9 were retained.

Table 3.3: Counts per level of litter effect at birth and rearing for ewe (TB, TR) or ewe's dam (DTB, DTR) before and after removal of small groups or uncommon management practices for major breeds present at the United States Sheep Experiment Station (USSES).<sup>1</sup>

Effect	Code	Columbia		Polypay		Rambouillet		Targhee	
		Before	After	Before	After	Before	After	Before	After
TB	1	1,085	625	445	372	1,288	705	1,394	842
	2	1,998	1,367	1,832	1,514	2,757	1,787	2,837	1,809
	3	313	259	829	713	394	317	305	229
	4	11	0	95	0	13	0	8	0
TR	0	3	0	18	0	4	0	4	0
	1	1,037	625	432	372	1,229	705	1,334	842
	2	0	0	0	0	1	0	3	0
	3	479	237	365	290	677	362	738	403
	4	5	0	1	0	12	0	13	0
	5	1,562	1,130	1,480	1,224	2,126	1,425	2,143	1,406
	6	2	0	6	0	3	0	1	0
	7	90	68	176	129	104	78	101	71
	8	222	191	636	507	287	239	193	158
9	7	0	87	77	9	0	14	0	
DTB	1	1,075	573	422	341	1,320	677	1,364	815
	2	2,052	1,448	1,850	1,537	2,751	1,810	2,878	1,843
	3	277	230	843	721	373	322	293	222
	4	3	0	86	0	8	0	9	0
DTR	0	0	0	25	0	5	0	5	0
	1	1,036	573	401	341	1,259	677	1,302	815
	2	0	0	0	0	1	0	5	0
	3	493	290	363	264	695	374	751	400
	4	6	0	0	0	14	0	16	0
	5	1,592	1,158	1,508	1,273	2,102	1,436	2,168	1,443
	6	0	0	5	0	3	0	2	0
	7	64	53	169	124	95	79	95	68
	8	210	177	665	534	274	243	191	154
9	6	0	65	63	4	0	9	0	

<sup>1</sup>Code description for birth type (TB and DTB) include 1 – born single; 2 – born twin; 3 – born triplet; and 4 – born quadruplet or higher. USSES code description for rearing type (TR and DTR) include: 0 – born a quadruplet or quintuplet, weaned any number, minor category; 1 – born single, weaned single; 2 – born single, raised orphan; 3 – born twin, raised single (major) or born single, raised twin (minor); 4 – born twin, raised orphan; 5 – born twin, raised twin; 6 – born triplet, raised orphan; 7 – born triplet, raised single; 8 – born triplet, raised twin; and 9 – born triplet raised triplet.



Rearing type (TR and DTR) of 3 was described as born twin, raised single (major) or born single, raised twin (minor) by USSES files. This was not deemed an appropriate grouping for comparison of litter size effects, therefore singles raised as twins were reassigned to category 2. Even so, singles raised as twins accounted for less than 0.5% of each breed's data. Therefore, all ewes with this rearing type (TR and DTR) were removed. This left TR and DTR 3 to be exclusively twins raised as singles. Lastly, typical management at USSES resulted in ewes being culled following their 7th lambing season. Ewes would only be present at USSES after 7 years for specific experiments. Due to this, any ewe with a longevity value over 7 years was right-censored to be 7 to reflect typical USSES management (n = 38, 39, 111, and 42 for Columbia, Polypay, Rambouillet, and Targhee, respectively).

Ewes with longevity records were present in the dataset as early as 1968 for Columbia, 1969 for Rambouillet and Targhee, and 1978 for Polypay. Even so, management was quite different at that time and was not reflective of current ewe performance in those breeds. Furthermore, years between 1980 and 1985 had inconsistent data sizes within and across breeds. Due to this, years were left-censored to only include 1985 or more recent, which followed Holland (2018). After censoring and adjustments for litter size effects, data records per year accounted for 1.38% to 7.08% for Columbia, 1.75% to 7.42% for Polypay, 1.03% to 6.82% for Rambouillet, and 2.03% to 6.20% for Targhee records, respectively. After these removals, final sample sizes for data are reported in Table 3.2.

Using the lamb ID of each ewe in the remaining breed datasets, pedigree was extracted for each breed to include all available ancestors from the pedigree file supplied by USSES (Appendix A). The four breeds' datasets were combined to create the combined or "across" breed data file for a separate analysis. Only purebred data records were used, but the entire pedigree of purebred and

crossbred animals related to these was extracted from the overall pedigree file. Pedigree size of each breed and across breeds are reported in Table 3.2, which were used for analyses of family size and siblings.

## **Statistical analyses**

### **Descriptive statistics**

Descriptive statistics were run on datasets of longevity and stayability to obtain their means and standard deviation using the *dplyr* package (Wickham et al., 2021) *summarize* function (Appendix D). Scripts in R were further developed to identify characteristics of the population per breed and across breeds related to family statistics such as number of sibling (full or half), overall family size, averages, and ranges. Relevant functions based on availability in current R packages were developed for publication as a pedigree analysis package on The Comprehensive R Archive Network following R manual guidelines (R Core Team, 2021).

### **Animal model**

An animal model using pedigree was run for longevity and stayability using a Bayesian framework in the *MCMCglmm* package of R (Hadfield, 2019). Fixed effects investigated, in a stepwise fashion, were TB, TR, DTB, and DTR on a per breed basis (Table 3.3). In all cases, the age of the ewe's dam ( $n = 7$  levels) at her birth was assessed as either a fixed covariate or class effect. Birth weight of the ewe was also assessed for fit in the model as a fixed covariate. When all breeds and relevant crosses were included, the STM code was also used as a fixed effect to model breed. To this fixed-effect model, random effects for each trait were explored in a stepwise fashion that had additive genetic variance (ID with numerator relationship matrix), maternal permanent environmental variance (ewe's dam without pedigree), birth year, and dominance genetic variance (ID with dominance relationship matrix). Longevity models, including additive

and dominance, were fitted as univariate whereas stayability models (additive and dominance) were fitted as multivariate models using the *MCMCglmm* R package. A univariate model focusing on stayability to 7 years of age was also run to interpret significant fixed effects.

To ensure the data and not the priors were influencing posterior means, several priors were investigated for each trait (Table 3.4). Model outputted from the *MCMCglmm* R package was evaluated to ensure the model met the autocorrelation (less than 0.10) and convergence requirement of fuzzy caterpillar plots (Figure 3.1, Hadfield, 2019). The number of iterations (nitt) ran, number of starting iterations dropped at the beginning (burnin), and number of iterations stored in memory (thin) were evaluated and adjusted based on autocorrelation and convergence output of a given run and recommendations by Hadfield (2019). Lastly, the model fit compared to other models was assessed using the DIC criteria, which is a generalization of the Akaike Information Criterion (Akaike, 1974) in a Bayesian framework (Lynn et al., 2002). Models with lower DIC values were preference over higher values given study objectives.

Table 3.4: Priors investigated when modeling longevity with additive genetic effects using the *MCMCglmm* R package

Prior ID	<sup>1</sup> <i>MCMCglmm</i> prior syntax	Family
A	list(R=list(V=1,nu=0, fix=1), G=list(G1=list(p.var, 0.1), G2=list(p.var, 0.1) , G3=list(p.var, 0.1)))	Threshold
B	list(R=list(V=1,nu=0.002), G=list(G1=list(p.var, 0.1), G2=list(p.var, 0.1), G3=list(p.var, 0.1)))	Poisson
C	list(G=list(G1=list(V=matrix(p.var/2),n=1), G2=list(V=matrix(p.var/2),n=1), G3=list(V=matrix(p.var/2),n=1)), R=list(V=matrix(p.var/2),n=1))	Censored Gaussian
D	list(R=list(V=0.7*p.var,nu=1), G=list(G1=list(0.3*p.var, 1), G2=list(0.3*p.var, 1), G3=list(0.3*p.var, 1)))	Threshold
E	list(R=list(V=1,nu=1), G=list(G1=list(V=1,nu=1,alpha.mu=0,alpha.V=1000), G2=list(V=1,nu=1,alpha.mu=0,alpha.V=1000), G3=list(V=1,nu=1,alpha.mu=0,alpha.V=1000)))	Gaussian
F	list(R=list(V=0.6*p.var,nu=1), G=list(G1=list(0.4*p.var, 1), G2=list(0.4*p.var, 1), G3=list(0.4*p.var, 1)))	Gaussian

<sup>1</sup>*MCMCglmm* prior syntax: R = the prior components for the residual variance, G = list of prior components for the random effect variances that included birth year (1), additive genetic effects (2), and maternal permanent environment effects (3), V= variance, nu= ‘measurement of belief’ parameter, alpha.mu = mean vector, alpha.V = covariance matrix, p.var = phenotypic variation of longevity.

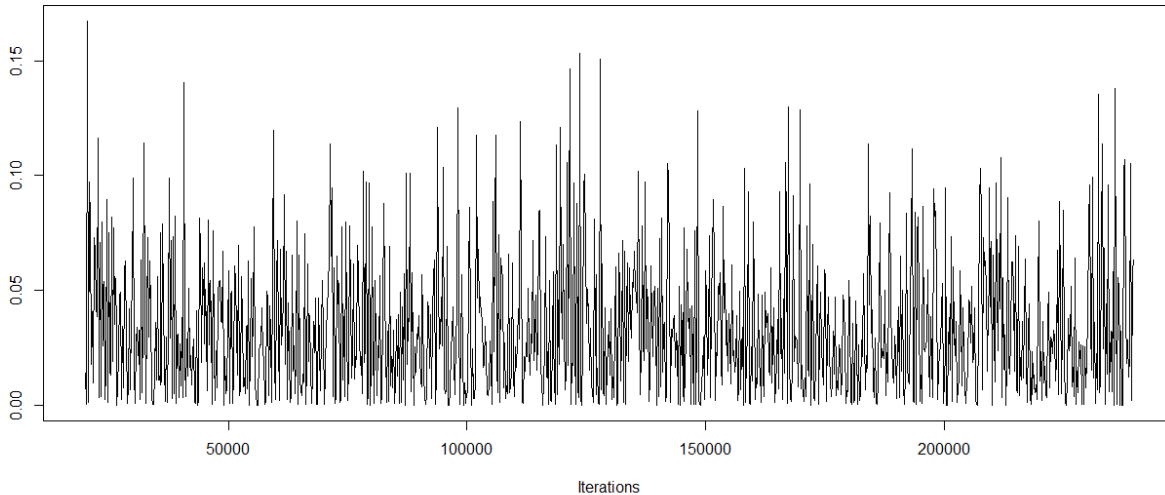


Figure 3.1: Fuzzy caterpillar convergence *MCMCglmm* plot indicating a converged model.

### ***Longevity additive model***

On a per breed basis, the univariate additive model followed:

$$\underline{y} = X\underline{\beta} + Z\underline{a} + Z\underline{m} + Z\underline{b} + e$$

where:

$\underline{y}$  = vector of longevity records;

$X$  = incidence matrix of fixed effects;

$\underline{\beta}$  = vector of fixed effects to be estimated;

$Z$  = incidence matrix for random effects;

$\underline{a}$  = vector of additive random effect to be estimated;

$\underline{m}$  = vector of dam's maternal permanent environmental random effect to be estimated;

$\underline{b}$  = vector of birth year random effect to be estimated;

$e$  = residual.

The expectation of variance for random effects was:

$$\text{var} \begin{pmatrix} a \\ m \\ b \\ e \end{pmatrix} = \begin{pmatrix} A\sigma_a^2 & 0 & 0 & 0 \\ 0 & I_{nd}\sigma_m^2 & 0 & 0 \\ 0 & 0 & I_n\sigma_b^2 & 0 \\ 0 & 0 & 0 & I_n\sigma_e^2 \end{pmatrix}$$

Where:

$\sigma_a^2$  is the additive genetic variance;

$\sigma_m^2$  is the dam's maternal permanent environmental variance;

$\sigma_b^2$  is the birth year variance;

$\sigma_e^2$  is the residual variance;

A is the inverse additive numerator matrix; and

$I_{nd}$  and  $I_n$  are identity matrices of order equal to the number of dams (nd) and to the total number of animals with records (n), respectively.

### ***Longevity dominance model***

On a per breed basis, the univariate dominance model followed:

$$\underline{y} = X\underline{\beta} + Z\underline{a} + Z\underline{d} + Z\underline{m} + Z\underline{b} + e$$

where:

$\underline{y}$  = vector of longevity records;

X = incidence matrix of fixed effects;

$\underline{\beta}$  = vector of fixed effects to be estimated;

Z = incidence matrix for random effects;

$\underline{a}$  = vector of additive random effect to be estimated;

$\underline{d}$  = vector of dominance random effect to be estimated;

$\underline{m}$  = vector of dam's maternal permanent environmental random effect to be estimated;

$\underline{b}$  = vector of birth year random effect to be estimated;

$e$  = residual.

The dominance model expanded the random effects so that the expectation of variance when dominance was included was:

$$\text{var} \begin{pmatrix} a \\ d \\ m \\ b \\ e \end{pmatrix} = \begin{pmatrix} A_a \sigma_a^2 & 0 & 0 & 0 & 0 \\ 0 & D_d \sigma_d^2 & 0 & 0 & 0 \\ 0 & 0 & I_{nd} \sigma_m^2 & 0 & 0 \\ 0 & 0 & 0 & I_n \sigma_b^2 & 0 \\ 0 & 0 & 0 & 0 & I_n \sigma_e^2 \end{pmatrix}$$

Where:

$\sigma_a^2$  is the additive genetic variance;

$\sigma_d^2$  is the dominance genetic variance;

$\sigma_m^2$  is the dam's maternal permanent environmental variance;

$\sigma_b^2$  is the birth year variance;

$\sigma_e^2$  is the residual variance;

A is the inverse additive numerator matrix;

D is the inverse dominance matrix; and

$I_{nd}$  and  $I_n$  are identity matrices of order equal to the number of dams (nd) and to the total number of animals with records (n), respectively.

### ***Stayability model***

On a per breed basis, the stayability additive model followed the multivariate variance expectation as follows:

$$\begin{pmatrix} y_2 \\ y_3 \\ y_4 \\ y_5 \\ y_6 \\ y_7 \end{pmatrix} = \begin{pmatrix} X_2 & X_{2,X_3} & X_{2,X_4} & X_{2,X_5} & X_{2,X_6} & X_{2,X_7} \\ X_{3,X_2} & X_3 & X_{3,X_4} & X_{3,X_5} & X_{3,X_6} & X_{3,X_7} \\ X_{4,X_2} & X_{4,X_3} & X_4 & X_{4,X_5} & X_{4,X_6} & X_{4,X_7} \\ X_{5,X_2} & X_{5,X_3} & X_{5,X_4} & X_5 & X_{5,X_6} & X_{5,X_7} \\ X_{6,X_2} & X_{6,X_3} & X_{6,X_4} & X_{6,X_5} & X_6 & X_{6,X_7} \\ X_{7,X_2} & X_{7,X_3} & X_{7,X_4} & X_{7,X_5} & X_{7,X_6} & X_7 \end{pmatrix} \begin{pmatrix} b_2 \\ b_3 \\ b_4 \\ b_5 \\ b_6 \\ b_7 \end{pmatrix} + \\
\begin{pmatrix} Z_2 & Z_{2,Z_3} & Z_{2,Z_4} & Z_{2,Z_5} & Z_{2,Z_6} & Z_{2,Z_7} \\ Z_{3,Z_2} & Z_3 & Z_{3,Z_4} & Z_{3,Z_5} & Z_{3,Z_6} & Z_{3,Z_7} \\ Z_{4,Z_2} & Z_{4,Z_3} & Z_4 & Z_{4,Z_5} & Z_{4,Z_6} & Z_{4,Z_7} \\ Z_{5,Z_2} & Z_{5,Z_3} & Z_{5,Z_4} & Z_5 & Z_{5,Z_6} & Z_{5,Z_7} \\ Z_{6,Z_2} & Z_{6,Z_3} & Z_{6,Z_4} & Z_{6,Z_5} & Z_6 & Z_{6,Z_7} \\ Z_{7,Z_2} & Z_{7,Z_3} & Z_{7,Z_4} & Z_{7,Z_5} & Z_{7,Z_6} & Z_7 \end{pmatrix} \begin{pmatrix} a_2 \\ a_3 \\ a_4 \\ a_5 \\ a_6 \\ a_7 \end{pmatrix} + \\
\begin{pmatrix} Z_2 & Z_{2,Z_3} & Z_{2,Z_4} & Z_{2,Z_5} & Z_{2,Z_6} & Z_{2,Z_7} \\ Z_{3,Z_2} & Z_3 & Z_{3,Z_4} & Z_{3,Z_5} & Z_{3,Z_6} & Z_{3,Z_7} \\ Z_{4,Z_2} & Z_{4,Z_3} & Z_4 & Z_{4,Z_5} & Z_{4,Z_6} & Z_{4,Z_7} \\ Z_{5,Z_2} & Z_{5,Z_3} & Z_{5,Z_4} & Z_5 & Z_{5,Z_6} & Z_{5,Z_7} \\ Z_{6,Z_2} & Z_{6,Z_3} & Z_{6,Z_4} & Z_{6,Z_5} & Z_6 & Z_{6,Z_7} \\ Z_{7,Z_2} & Z_{7,Z_3} & Z_{7,Z_4} & Z_{7,Z_5} & Z_{7,Z_6} & Z_7 \end{pmatrix} \begin{pmatrix} m_2 \\ m_3 \\ m_4 \\ m_5 \\ m_6 \\ m_7 \end{pmatrix} + \\
\begin{pmatrix} Z_2 & Z_{2,Z_3} & Z_{2,Z_4} & Z_{2,Z_5} & Z_{2,Z_6} & Z_{2,Z_7} \\ Z_{3,Z_2} & Z_3 & Z_{3,Z_4} & Z_{3,Z_5} & Z_{3,Z_6} & Z_{3,Z_7} \\ Z_{4,Z_2} & Z_{4,Z_3} & Z_4 & Z_{4,Z_5} & Z_{4,Z_6} & Z_{4,Z_7} \\ Z_{5,Z_2} & Z_{5,Z_3} & Z_{5,Z_4} & Z_5 & Z_{5,Z_6} & Z_{5,Z_7} \\ Z_{6,Z_2} & Z_{6,Z_3} & Z_{6,Z_4} & Z_{6,Z_5} & Z_6 & Z_{6,Z_7} \\ Z_{7,Z_2} & Z_{7,Z_3} & Z_{7,Z_4} & Z_{7,Z_5} & Z_{7,Z_6} & Z_7 \end{pmatrix} \begin{pmatrix} b_2 \\ b_3 \\ b_4 \\ b_5 \\ b_6 \\ b_7 \end{pmatrix} + \begin{pmatrix} e_2 \\ e_3 \\ e_4 \\ e_5 \\ e_6 \\ e_7 \end{pmatrix}$$

Where:

$y_2$  to  $y_7$  = vector of observations for stayability 2 to stayability 7.

$b_2$  to  $b_7$  = vector of fixed effects for stayability trait.

$a_2$  to  $a_7$  = vector of random additive effects for stayability trait.

$m_2$  to  $m_7$  = vector of random dam's maternal permanent effects for stayability trait.

$b_2$  to  $b_7$  = vector of random birth year effects for stayability trait.

X and Z are incidence matrices relating records of stayability trait to fixed and random animal effects respectively.

Example variance-covariance matrices assumed include:



$$\text{var} \begin{pmatrix} a_2 \\ a_3 \\ a_4 \\ a_5 \\ a_6 \\ a_7 \end{pmatrix} = \begin{pmatrix} A_{a_2}^{\sigma^2} & \text{COV}_{a_2,a_3}^{\sigma^2} & \text{COV}_{a_2,a_4}^{\sigma^2} & \text{COV}_{a_2,a_5}^{\sigma^2} & \text{COV}_{a_2,a_6}^{\sigma^2} & \text{COV}_{a_2,a_7}^{\sigma^2} \\ \text{COV}_{a_3,a_2}^{\sigma^2} & A_{a_3}^{\sigma^2} & \text{COV}_{a_3,a_4}^{\sigma^2} & \text{COV}_{a_3,a_5}^{\sigma^2} & \text{COV}_{a_3,a_6}^{\sigma^2} & \text{COV}_{a_3,a_7}^{\sigma^2} \\ \text{COV}_{a_4,a_2}^{\sigma^2} & \text{COV}_{a_4,a_3}^{\sigma^2} & A_{a_4}^{\sigma^2} & \text{COV}_{a_4,a_5}^{\sigma^2} & \text{COV}_{a_4,a_6}^{\sigma^2} & \text{COV}_{a_4,a_7}^{\sigma^2} \\ \text{COV}_{a_5,a_2}^{\sigma^2} & \text{COV}_{a_5,a_3}^{\sigma^2} & \text{COV}_{a_5,a_4}^{\sigma^2} & A_{a_5}^{\sigma^2} & \text{COV}_{a_5,a_6}^{\sigma^2} & \text{COV}_{a_5,a_7}^{\sigma^2} \\ \text{COV}_{a_6,a_2}^{\sigma^2} & \text{COV}_{a_6,a_3}^{\sigma^2} & \text{COV}_{a_6,a_4}^{\sigma^2} & \text{COV}_{a_6,a_5}^{\sigma^2} & A_{a_6}^{\sigma^2} & \text{COV}_{a_6,a_7}^{\sigma^2} \\ \text{COV}_{a_7,a_2}^{\sigma^2} & \text{COV}_{a_7,a_3}^{\sigma^2} & \text{COV}_{a_7,a_4}^{\sigma^2} & \text{COV}_{a_7,a_5}^{\sigma^2} & \text{COV}_{a_7,a_6}^{\sigma^2} & A_{a_7}^{\sigma^2} \end{pmatrix} = A,$$

$$\text{var} \begin{pmatrix} m_2 \\ m_3 \\ m_4 \\ m_5 \\ m_6 \\ m_7 \end{pmatrix} = \begin{pmatrix} Z_{m_2}^{\sigma^2} & \text{COV}_{m_2,m_3}^{\sigma^2} & \text{COV}_{m_2,m_4}^{\sigma^2} & \text{COV}_{m_2,m_5}^{\sigma^2} & \text{COV}_{m_2,m_6}^{\sigma^2} & \text{COV}_{m_2,m_7}^{\sigma^2} \\ \text{COV}_{m_3,m_2}^{\sigma^2} & Z_{m_3}^{\sigma^2} & \text{COV}_{m_3,m_4}^{\sigma^2} & \text{COV}_{m_3,m_5}^{\sigma^2} & \text{COV}_{m_3,m_6}^{\sigma^2} & \text{COV}_{m_3,m_7}^{\sigma^2} \\ \text{COV}_{m_4,m_2}^{\sigma^2} & \text{COV}_{m_4,m_3}^{\sigma^2} & Z_{m_4}^{\sigma^2} & \text{COV}_{m_4,m_5}^{\sigma^2} & \text{COV}_{m_4,m_6}^{\sigma^2} & \text{COV}_{m_4,m_7}^{\sigma^2} \\ \text{COV}_{m_5,m_2}^{\sigma^2} & \text{COV}_{m_5,m_3}^{\sigma^2} & \text{COV}_{m_5,m_4}^{\sigma^2} & Z_{m_5}^{\sigma^2} & \text{COV}_{m_5,m_6}^{\sigma^2} & \text{COV}_{m_5,m_7}^{\sigma^2} \\ \text{COV}_{m_6,m_2}^{\sigma^2} & \text{COV}_{m_6,m_3}^{\sigma^2} & \text{COV}_{m_6,m_4}^{\sigma^2} & \text{COV}_{m_6,m_5}^{\sigma^2} & Z_{m_6}^{\sigma^2} & \text{COV}_{m_6,m_7}^{\sigma^2} \\ \text{COV}_{m_7,m_2}^{\sigma^2} & \text{COV}_{m_7,m_3}^{\sigma^2} & \text{COV}_{m_7,m_4}^{\sigma^2} & \text{COV}_{m_7,m_5}^{\sigma^2} & \text{COV}_{m_7,m_6}^{\sigma^2} & Z_{m_7}^{\sigma^2} \end{pmatrix} = \text{MPE},$$

$$\text{var} \begin{pmatrix} b_2 \\ b_3 \\ b_4 \\ b_5 \\ b_6 \\ b_7 \end{pmatrix} = \begin{pmatrix} Z_{b_2}^{\sigma^2} & \text{COV}_{b_2,b_3}^{\sigma^2} & \text{COV}_{b_2,b_4}^{\sigma^2} & \text{COV}_{b_2,b_5}^{\sigma^2} & \text{COV}_{b_2,b_6}^{\sigma^2} & \text{COV}_{b_2,b_7}^{\sigma^2} \\ \text{COV}_{b_3,b_2}^{\sigma^2} & Z_{b_3}^{\sigma^2} & \text{COV}_{b_3,b_4}^{\sigma^2} & \text{COV}_{b_3,b_5}^{\sigma^2} & \text{COV}_{b_3,b_6}^{\sigma^2} & \text{COV}_{b_3,b_7}^{\sigma^2} \\ \text{COV}_{b_4,b_2}^{\sigma^2} & \text{COV}_{b_4,b_3}^{\sigma^2} & Z_{b_4}^{\sigma^2} & \text{COV}_{b_4,b_5}^{\sigma^2} & \text{COV}_{b_4,b_6}^{\sigma^2} & \text{COV}_{b_4,b_7}^{\sigma^2} \\ \text{COV}_{b_5,b_2}^{\sigma^2} & \text{COV}_{b_5,b_3}^{\sigma^2} & \text{COV}_{b_5,b_4}^{\sigma^2} & Z_{b_5}^{\sigma^2} & \text{COV}_{b_5,b_6}^{\sigma^2} & \text{COV}_{b_5,b_7}^{\sigma^2} \\ \text{COV}_{b_6,b_2}^{\sigma^2} & \text{COV}_{b_6,b_3}^{\sigma^2} & \text{COV}_{b_6,b_4}^{\sigma^2} & \text{COV}_{b_6,b_5}^{\sigma^2} & Z_{b_6}^{\sigma^2} & \text{COV}_{b_6,b_7}^{\sigma^2} \\ \text{COV}_{b_7,b_2}^{\sigma^2} & \text{COV}_{b_7,b_3}^{\sigma^2} & \text{COV}_{b_7,b_4}^{\sigma^2} & \text{COV}_{b_7,b_5}^{\sigma^2} & \text{COV}_{b_7,b_6}^{\sigma^2} & Z_{b_7}^{\sigma^2} \end{pmatrix} = B,$$

$$\text{var} \begin{pmatrix} e_2 \\ e_3 \\ e_4 \\ e_5 \\ e_6 \\ e_7 \end{pmatrix} = \begin{pmatrix} I_{e_2}^{\sigma^2} & \text{COV}_{e_2,e_3}^{\sigma^2} & \text{COV}_{e_2,e_4}^{\sigma^2} & \text{COV}_{e_2,e_5}^{\sigma^2} & \text{COV}_{e_2,e_6}^{\sigma^2} & \text{COV}_{e_2,e_7}^{\sigma^2} \\ \text{COV}_{e_3,e_2}^{\sigma^2} & I_{e_3}^{\sigma^2} & \text{COV}_{e_3,e_4}^{\sigma^2} & \text{COV}_{e_3,e_5}^{\sigma^2} & \text{COV}_{e_3,e_6}^{\sigma^2} & \text{COV}_{e_3,e_7}^{\sigma^2} \\ \text{COV}_{e_4,e_2}^{\sigma^2} & \text{COV}_{e_4,e_3}^{\sigma^2} & I_{e_4}^{\sigma^2} & \text{COV}_{e_4,e_5}^{\sigma^2} & \text{COV}_{e_4,e_6}^{\sigma^2} & \text{COV}_{e_4,e_7}^{\sigma^2} \\ \text{COV}_{e_5,e_2}^{\sigma^2} & \text{COV}_{e_5,e_3}^{\sigma^2} & \text{COV}_{e_5,e_4}^{\sigma^2} & I_{e_5}^{\sigma^2} & \text{COV}_{e_5,e_6}^{\sigma^2} & \text{COV}_{e_5,e_7}^{\sigma^2} \\ \text{COV}_{e_6,e_2}^{\sigma^2} & \text{COV}_{e_6,e_3}^{\sigma^2} & \text{COV}_{e_6,e_4}^{\sigma^2} & \text{COV}_{e_6,e_5}^{\sigma^2} & I_{e_6}^{\sigma^2} & \text{COV}_{e_6,e_7}^{\sigma^2} \\ \text{COV}_{e_7,e_2}^{\sigma^2} & \text{COV}_{e_7,e_3}^{\sigma^2} & \text{COV}_{e_7,e_4}^{\sigma^2} & \text{COV}_{e_7,e_5}^{\sigma^2} & \text{COV}_{e_7,e_6}^{\sigma^2} & I_{e_7}^{\sigma^2} \end{pmatrix} = R$$

Where:

I is an identity matrix with its dimension equaling the total number of animals evaluated,

Z are the random effect matrices with their dimensions equaling the total numbers of animals evaluated

A is the pedigree-based relationship matrix, and the diagonal elements  $\sigma_a^2$ ,  $\sigma_m^2$ ,  $\sigma_b^2$  and  $\sigma_e^2$  are the genetic, permanent environmental, birth year, and residual effects variances for stayability 1 to nth, having  $COV_{a_2, a_n}^{\sigma^2}$ ,  $COV_{m_2, m_n}^{\sigma^2}$ ,  $COV_{b_2, b_n}^{\sigma^2}$  and  $COV_{e_2, e_n}^{\sigma^2}$  as their corresponding covariances.

The dominance model expanded the random effects so that the expectation of variance when dominance was included, represented as:

$$\text{var} \begin{pmatrix} d_2 \\ d_3 \\ d_4 \\ d_5 \\ d_6 \\ d_7 \end{pmatrix} = \begin{pmatrix} D_{d_2}^{\sigma^2} & COV_{d_2, d_3}^{\sigma^2} & COV_{d_2, d_4}^{\sigma^2} & COV_{d_2, d_5}^{\sigma^2} & COV_{d_2, d_6}^{\sigma^2} & COV_{d_2, d_7}^{\sigma^2} \\ COV_{d_3, d_2}^{\sigma^2} & D_{d_3}^{\sigma^2} & COV_{d_3, d_4}^{\sigma^2} & COV_{d_3, d_5}^{\sigma^2} & COV_{d_3, d_6}^{\sigma^2} & COV_{d_3, d_7}^{\sigma^2} \\ COV_{d_4, d_2}^{\sigma^2} & COV_{d_4, d_3}^{\sigma^2} & D_{d_4}^{\sigma^2} & COV_{d_4, d_5}^{\sigma^2} & COV_{d_4, d_6}^{\sigma^2} & COV_{d_4, d_7}^{\sigma^2} \\ COV_{d_5, d_2}^{\sigma^2} & COV_{d_5, d_3}^{\sigma^2} & COV_{d_5, d_4}^{\sigma^2} & D_{d_5}^{\sigma^2} & COV_{d_5, d_6}^{\sigma^2} & COV_{d_5, d_7}^{\sigma^2} \\ COV_{d_6, d_2}^{\sigma^2} & COV_{d_6, d_3}^{\sigma^2} & COV_{d_6, d_4}^{\sigma^2} & COV_{d_6, d_5}^{\sigma^2} & D_{d_6}^{\sigma^2} & COV_{d_6, d_7}^{\sigma^2} \\ COV_{d_7, d_2}^{\sigma^2} & COV_{d_7, d_3}^{\sigma^2} & COV_{d_7, d_4}^{\sigma^2} & COV_{d_7, d_5}^{\sigma^2} & COV_{d_7, d_6}^{\sigma^2} & D_{d_7}^{\sigma^2} \end{pmatrix} = D$$

Where D is the pedigree-based dominance matrix and the diagonal elements  $\sigma_{d_n}^2$  is the dominance genetic variance for trait stayability to nth, having  $COV_{d_n, d_n}^{\sigma^2}$  as its corresponding covariances.

## Stayability *MCMCglmm* models setup

### *Multivariate model setup*

Running a multivariate stayability model with additive effects, we used a multivariate inverse-Wishart non-informative, weak prior, and a multivariate threshold family distribution repeated six times. For the multivariate model, the prior and model (Appendix C) included a variance of 6, nu, ‘degree of belief,’ 6, fix of 0 for our residual element, and variance of 6 and nu of 6 for our random terms, G1, G2, G3 and G4. The *trait* term in *MCMCglmm* lets us know we want to fit a multivariate mixed model, the *random*=~*us(trait):ID+us(trait):Dam+us(trait):BYR* specifies that *MCMCglmm* should fit an unstructured covariance matrix for the ID, Dam and BYR terms, unstructured here means we are estimating the complete 6 x 6 matrix of covariances (prior). The *rcov*=~*us(trait)units* specify the variance and or covariance among units (individuals). The

*cbind* term means we are exploring and combining many response variables simultaneously, i.e., a multivariate mixed model, which in the model were six terms, stayability two to stayability seven.

### ***Univariate model setup***

In addition to multivariate modeling, a univariate model focused on stayability to age 7 (0 or 1) was used following the same model parameters as longevity, including the inverse-Wishart non-informative prior.

### **Estimation of genetic parameters**

Variance components estimated from final models were used to calculate genetic parameter estimates. Heritability in the narrow sense ( $h^2$ , i.e., additive only) was calculated as follows:

$$h^2 = \frac{V_{ID}}{V_{ID} + V_{DAM} + V_{BYR} + V_R}$$

where:

$V_{ID}$  = between-individual additive genetic variance,

$V_{DAM}$  = maternal variance due to permanent environmental effects,

$V_{BYR}$  = variance due to birth year effects, and

$V_R$  = residual variance.

Heritability in the broad sense ( $H^2$ , i.e., additive and dominance effects) was calculated as follows:

$$H^2 = \frac{(V_{ID} + V_{ID2})}{V_{ID} + V_{ID2} + V_{DAM} + V_{BYR} + V_R}$$

$V_{ID}$  =between-individual additive genetic variance,

$V_{ID2}$  = within-individual dominance genetic variance,

$V_{DAM}$  = maternal variance due to permanent environmental effects,

$V_{BYR}$  = variance due to birth year effects, and

$V_R$  = residual variance.

The codes used to calculate the heritability estimates for both longevity and stayability models are presented in Appendix E.

For multivariate analyses, genetic correlations were estimated from the variance component estimates as:

$$r_g = \frac{COV_g(X, Y)}{\sqrt{VgX \cdot VgY}}$$

where:

- $r_g$  = genetic correlation
- $COV_g(X, Y)$  is the covariance between traits X and Y where X and Y represent stayability 2, 3, 4, 5, 6 and 7, respectively.
- $VgX$  and  $VgY$  are the variances of stayability X and Y where X and Y represent stayability 2, 3, 4, 5, 6 and 7, respectively.

### **Estimated marginal means**

Estimated marginal means are averages from a linear model and they are essential in the analysis of experimental data for summarizing the effects of factors. The Bayesian estimated marginal means were calculated using the R package *emmeans* (Lenth, 2016).

## CHAPTER 4: FAMILY STATISTICS

### R scripts developed

Four functions (Appendix B) were developed in R to understand family statistics and generations based on pedigree as packages with these capabilities were not found prior to project initiation. The first function, *makePed*, was created to ensure that the pedigree was in correct chronological order (i.e., parents came before offspring) and to make sure founding animals (i.e., animals with no parents known) were present and coded correctly. The second function, *GENAssign*, was written to count the numbers of generations in a pedigree following the sorting of the *makePed()* function. The third function, *AssignSibs*, was created to identify full and half-siblings based on sires, dams, and those matings by creating lists of animal identifiers per sire, dam or sire-dam combination. The output from *AssignSibs* was then used in the function *SibCount* to calculate descriptive statistics of siblings and mating from the pedigree provided.

These functions will be used to publish a package in the R CRAN directory called *Sibs* (Oribamise and Hanna, 2020). After creating these functions, additional packages with some of those functionalities were identified (Table 4.1).

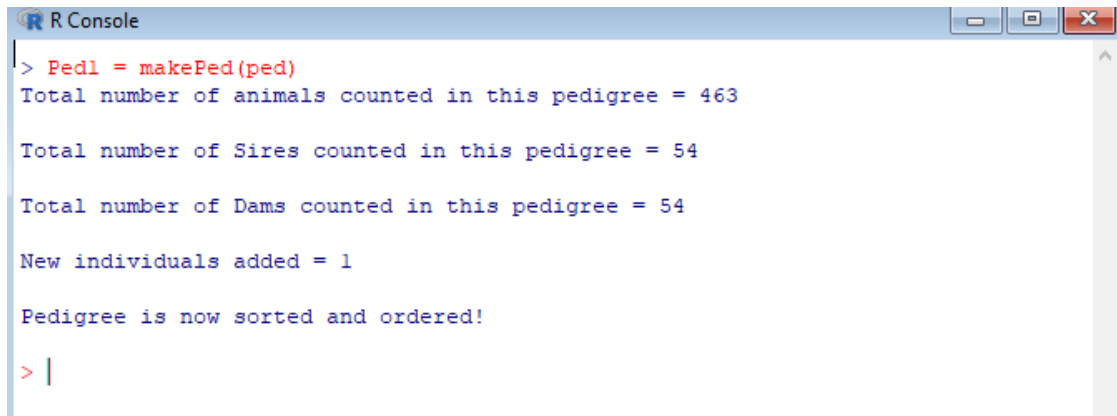
Table 4.1: Available pedigree packages in R and their capabilities

Attributes	R packages							
	<i>Sibs</i>	<i>kinship2</i>	<i>gggroups</i>	<i>AGHmatrix</i>	<i>pedigreemm</i>	<i>pedigree</i>	<i>Nadiv</i>	<i>sequioa</i>
Siblings count	✓		✓			✓		
Assign family	✓	✓						✓
Pedigree sorting	✓	✓	✓	✓	✓	✓	✓	
Generation assignment	✓	✓	✓		✓	✓		

<sup>1</sup>presence of a check mark (✓) indicates function is present in that R package.

Figures 4.1 to 4.6 demonstrate the uses of a given function. Even though some of these functionalities are already present on CRAN through packages listed, the *Sibs* package functions

are faster and more comprehensive than packages indicated in Table 4.1, particularly for large, extensive pedigrees (Oribamise and Hanna, 2020).



```
R Console
> Ped1 = makePed(ped)
Total number of animals counted in this pedigree = 463

Total number of Sires counted in this pedigree = 54

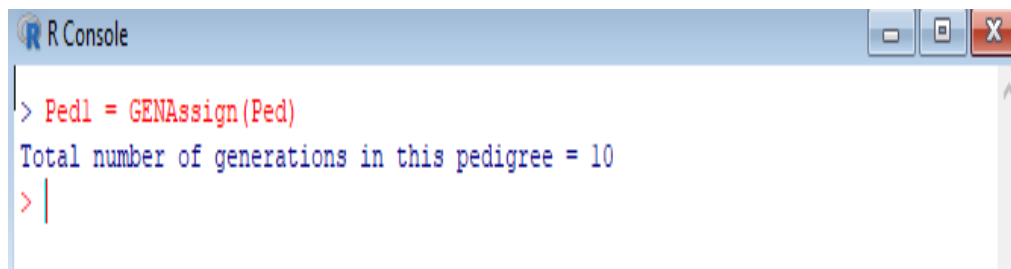
Total number of Dams counted in this pedigree = 54

New individuals added = 1

Pedigree is now sorted and ordered!

> |
```

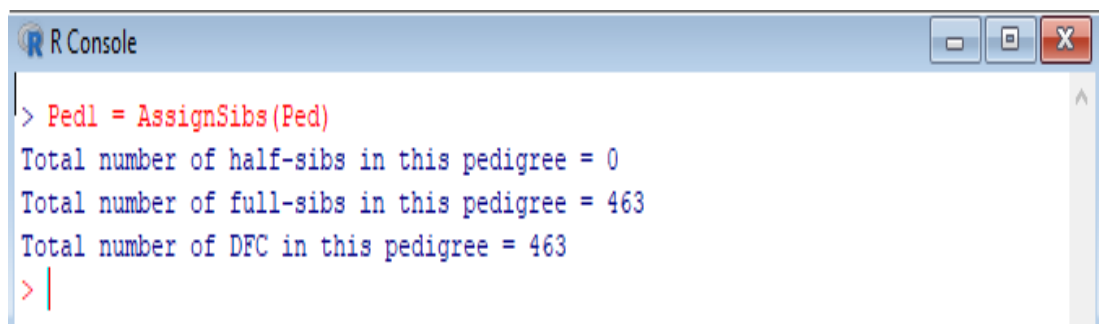
Figure 4.1: General output of *makePed()* function of *Sibs* R .



```
R Console
> Ped1 = GENAssign(Ped)
Total number of generations in this pedigree = 10

> |
```

Figure 4.2: *GENAssign()* function of *Sibs* R package in action



```
R Console
> Ped1 = AssignSibs(Ped)
Total number of half-sibs in this pedigree = 0
Total number of full-sibs in this pedigree = 463
Total number of DFC in this pedigree = 463

> |
```

Figure 4.3: *AssignSibs()* function of *Sibs* R package in action

Show  entries Search:

	ID	Sire	Dam	fullsibs	hsibs	fams
171	171	59	4	170, 172, 173, 174, 175		170, 172, 173, 174, 175
172	172	59	4	170, 171, 173, 174, 175		170, 171, 173, 174, 175
173	173	59	4	170, 171, 172, 174, 175		170, 171, 172, 174, 175
174	174	59	4	170, 171, 172, 173, 175		170, 171, 172, 173, 175
175	175	59	4	170, 171, 172, 173, 174		170, 171, 172, 173, 174
176	176	162	157	177, 178, 179, 180, 181		177, 178, 179, 180, 181
177	177	162	157	176, 178, 179, 180, 181		176, 178, 179, 180, 181
178	178	162	157	176, 177, 179, 180, 181		176, 177, 179, 180, 181
179	179	162	157	176, 177, 178, 180, 181		176, 177, 178, 180, 181
180	180	162	157	176, 177, 178, 179, 181		176, 177, 178, 179, 181

---

Showing 171 to 180 of 463 entries Previous 1 ... 17  19 ... 47 Next

Figure 4.4: Figure showing the familial relationships in a pedigree using *AssignSibs()* function of *Sibs* R package

```

R Console
> Ped1 = SibCount(Ped)
Total number of maternal half-sibs in this pedigree = 110
Total number of paternal half-sibs in this pedigree = 110
Total number of full-sibs in this pedigree = 6050
> |

```

Figure 4.5: *SibCount()* function of *Sibs* R package in action

	Count †	Average †	SD †	Min †	Max †
FullSib	55	8.418	17.934	6	139
PaternalHalfSib	55	8.418	17.934	6	139
MaternalHalfSib	55	8.418	17.934	6	139

Figure 4.6: Figure showing the descriptive statistics of a pedigree using *SibCount()* function of *Sibs* R package

### Pedigree characteristics: Families

The across-breed pedigree used in the analyses consisted of 24,999 animals with related crossbreeds. When sub-setting by breed, the pedigrees averaged 36 generations (Table 4.2). We did not prune the generations used in order to capture all effects, even though it required many computational demands when estimating non-additive genetic effects. Extracting familial records and sizes is essential to ensure that non-genetic effects are not confounded with additive genetic effects, especially for full-siblings, because of shared environmental, additive genetic, and non-additive genetic effects (Munoz et al., 2014).

Table 4.2: Pedigree summary by and across breeds

Breeds	Total animals		Maximum number of generations	Pedigree size
	Sire	Dam		
Across breed <sup>1</sup>	4,644	14,448	39	24,999
Columbia	894	3,074	32	5,223
Polypay	894	3,074	33	8,691
Rambouillet	2,706	6,431	39	10,711
Targhee	2,347	5,704	38	9,661

<sup>1</sup>Across breeds population consisted of purebreds from Columbia, Polypay, Rambouillet, and Targhee, but the pedigree includes related crossbreeds of Friesian, Dorper, Texel, Finnsheep, Dorset, Romanov, and a USMARC-Composite developed in the 1970s.



**Pedigree characteristics: Siblings**

Familial statistics are similar to the suggestions of Van Tassell et al. (2003). They suggested that a minimum of 20% full-sibling relationships must be established in the pedigree to estimate non-additive genetic effects. The presence of full-siblings was well above 20% for within and across breed pedigrees (Table 4.3). Therefore, these full-sibling relationships will help reduce the confounding effects of both additive and non-additive genetic effects.

Table 4.3: Descriptive statistics of familial relationships for Columbia, Polypay, Rambouillet, Targhee, and Across breed pedigrees

Familial relationships	Summary statistics <sup>1</sup>	Breeds				
		Columbia	Polypay	Rambouillet	Targhee	Across breed <sup>2</sup>
Full-siblings	Count	4,482	6,984	9,152	8,134	21,222
	Percent (%)	85.81	80.35	85.44	84.19	84.89
	Mean ± SD	2.03 ± 0.18	2.05 ± 0.24	2.03 ± 0.20	2.05 ± 0.24	2.04 ± 0.27
	Min	2.00	2.00	2.00	2.00	2.00
	Max	4.00	5.00	4.00	4.00	5.00
Paternal Half-siblings	Count	721	1,320	1,979	1,682	3,802
	Percent (%)	13.81	15.18	18.47	17.41	15.21
	Mean ± SD	6.57 ± 5.54	5.35 ± 5.19	4.57 ± 4.31	4.81 ± 4.93	5.90 ± 5.60
	Min	2	2	2	2	2
	Max	41	47	37	57	57
Maternal Half-siblings	Count	1,144	1,578	2,169	1,923	5,484
	Percent (%)	21.91	18.15	20.25	19.90	21.94
	Mean ± SD	2.64 ± 0.99	2.64 ± 1.05	2.60 ± 0.95	2.64 ± 1.01	2.70 ± 1.01
	Min	2	2	2	2	2
	Max	8	11	9.00	9.00	11

<sup>1</sup>Mean: This is the mean number of a given sibling type per sire, dam, or sire x dam combination in a given pedigree. Count: This is the number of individuals marked as either full-sibs or half-sibs (maternal and paternal). Percent (%): The count divided by the total pedigree size and multiplying by 100.

<sup>2</sup>Across breeds population consisted of purebreds from Columbia, Polypay, Rambouillet, and Targhee, but the pedigree includes related crossbreds of Friesian, Dorper, Texel, Finnsheep, Dorset, Romanov, and a USMARC-Composite developed in the 1970s.

## Summary of litter size characteristics

The simple means and standard deviations of litter size effects are reported in Tables 4.4 to 4.6. Longevity, regardless of ewe or ewe's dam, ranged from 3.30 years (Polypay born a twin) to 4.08 years (Rambouillet born a triplet) for birth type. In terms of rearing type, longevity ranged from 3.11 years (Polypay born a twin, raised a single) to 4.10 years (Rambouillet born a triplet, raised a twin). In the same respect, stayability proportions to a given age (STAY) ranged for birth type between 0.08 to 0.86. On a per-year basis, these ranges were: 0.74 to 0.86 (STAY2), 0.56 to 0.72 (STAY3), 0.39 to 0.59 (STAY4), 0.26 to 0.45 (STAY5), 0.17 to 0.30 (STAY6), and 0.08 to 0.17 (STAY7). For rearing types, STAY proportions ranged between 0.05 to 0.88. On a per year basis, these ranges were: 0.65 to 0.88 (STAY2), 0.51 to 0.77 (STAY3), 0.39 to 0.62 (STAY 4), 0.27 to 0.45 (STAY5), 0.16 to 0.33 (STAY6), and 0.05 to 0.21 (STAY7). Differences in mean values for STAY between breeds in each factor may indicate differences in productive and reproductive performance or could indicate differences in the intensities of selection practiced by the breeders.

The STAY proportions are within the range of estimates from other studies. Martinez et al. (2005) reported higher stayability values for Hereford cows for all stayability years except STAY6 with a mean value of 0.26. Van der Westhuizen et al. (2001) reported mean values of 0.56, 0.38, and 0.27 for stayability to ages four, five, and six. The proportion of beef cows that had successful observations to eight years of age in a study by Maiwashe et al. (2009) was 0.37. Stayability mean per breed per traits from our study is similar to that of Lee et al. (2015), whose means for New Zealand rams ranged from 0.73 for stayability to age three to 0.18 for stayability to age six. The choice of the sixth-year cutoff for stayability was selected because of its correlated relationship with herd profitability as it is the year a cow can break-even (Snelling et al., 1995) which was first

reported for breeding programs in 1994 Red Angus Association of America National cattle evaluation for the beef industry. The mean results observed for stayability demonstrates one of the advantages of stayability's definition to consecutive lambing which commanded the study of the different breeds observed in this study regarding this trait.

Table 4.4: Mean and standard deviations of longevity for individual levels of birth and rearing types of ewes (TB, TR) and their dams (DTB, DTR) by breed and across breeds.

Level	Breed									
	Across		Columbia		Polypay		Rambouillet		Targhee	
	TB	DTB	TB	DTB	TB	DTB	TB	DTB	TB	DTB
1	3.53 ± 1.98	3.59 ± 1.98	3.40 ± 1.87	3.46 ± 1.93	3.37 ± 1.98	3.38 ± 1.98	3.88 ± 2.02	3.82 ± 2.03	3.39 ± 1.96	3.57 ± 1.96
2	3.59 ± 2.02	3.54 ± 2.01	3.52 ± 1.98	3.54 ± 1.93	3.40 ± 2.03	3.30 ± 2.01	3.94 ± 2.05	3.93 ± 2.06	3.43 ± 1.95	3.36 ± 1.96
3	3.54 ± 2.03	3.63 ± 2.04	3.69 ± 1.86	3.42 ± 1.99	3.37 ± 2.04	3.59 ± 2.06	3.89 ± 2.16	4.08 ± 2.04	3.38 ± 1.98	3.35 ± 1.92
	TR	DTR	TR	DTR	TR	DTR	TR	DTR	TR	DTR
1	3.53 ± 1.97	3.59 ± 1.98	3.40 ± 1.87	3.46 ± 1.93	3.37 ± 1.98	3.38 ± 1.98	3.88 ± 2.02	3.82 ± 2.03	3.39 ± 1.96	3.57 ± 1.96
3	3.46 ± 2.01	3.57 ± 2.03	3.54 ± 2.04	3.65 ± 2.04	3.11 ± 1.96	3.40 ± 2.13	3.84 ± 2.10	3.89 ± 2.03	3.32 ± 1.88	3.32 ± 1.94
5	3.62 ± 2.02	3.53 ± 2.00	3.52 ± 1.97	3.51 ± 1.91	3.47 ± 2.05	3.28 ± 1.99	3.97 ± 2.04	3.94 ± 2.07	3.47 ± 1.97	3.37 ± 1.96
7	3.49 ± 2.05	3.63 ± 2.10	3.87 ± 1.76	3.59 ± 1.94	3.19 ± 2.11	3.52 ± 2.14	3.81 ± 2.13	4.05 ± 2.14	3.31 ± 2.00	3.37 ± 2.06
8	3.57 ± 2.04	3.61 ± 2.01	3.63 ± 1.89	3.36 ± 2.01	3.42 ± 2.03	3.55 ± 2.03	3.92 ± 2.17	4.10 ± 2.01	3.42 ± 1.98	3.34 ± 1.86
9	NA	NA	NA	NA	3.38 ± 1.93	4.00 ± 2.21	NA	NA	NA	NA

NA: data not available for that level of effect.

<sup>1</sup>Code description for birth type (TB and DTB) include: 1 – born single; 2 – born twin; 3 – born triplet. Code description for rearing type (TR and DTR) include: 1 – born single, raised single; 3 – born twin, raised single; 5 – born twin, raised twin; 7 – born triplet, raised single; 8 – born triplet, raised twin; and 9 – born triplet, raised triplet.

<sup>2</sup>Across breeds population consisted of purebreds from Columbia, Polypay, Rambouillet, and Targhee.

Table 4.5: Mean and standard deviations of stayability (STAY) for individual levels of birth types of ewes (TB) and their dams (DTB) by breed and across breeds.

STAY	Level	Breed									
		Across		Columbia		Polypay		Rambouillet		Targhee	
		TB	DTB	TB	DTB	TB	DTB	TB	DTB	TB	DTB
2	1	0.81 ± 0.39	0.81 ± 0.39	0.81 ± 0.39	0.80 ± 0.40	0.80 ± 0.40	0.78 ± 0.42	0.83 ± 0.37	0.82 ± 0.39	0.79 ± 0.41	0.82 ± 0.38
	2	0.80 ± 0.40	0.79 ± 0.41	0.80 ± 0.40	0.82 ± 0.39	0.75 ± 0.43	0.74 ± 0.44	0.83 ± 0.37	0.82 ± 0.38	0.80 ± 0.40	0.78 ± 0.41
	3	0.78 ± 0.41	0.80 ± 0.40	0.86 ± 0.35	0.79 ± 0.41	0.74 ± 0.44	0.78 ± 0.41	0.79 ± 0.41	0.86 ± 0.35	0.80 ± 0.40	0.80 ± 0.40
3	1	0.62 ± 0.48	0.64 ± 0.48	0.62 ± 0.48	0.62 ± 0.48	0.58 ± 0.49	0.60 ± 0.49	0.70 ± 0.46	0.69 ± 0.46	0.58 ± 0.49	0.63 ± 0.48
	2	0.63 ± 0.48	0.62 ± 0.48	0.62 ± 0.49	0.64 ± 0.48	0.59 ± 0.49	0.56 ± 0.59	0.70 ± 0.46	0.70 ± 0.46	0.60 ± 0.49	0.58 ± 0.49
	3	0.62 ± 0.49	0.63 ± 0.48	0.70 ± 0.46	0.59 ± 0.49	0.58 ± 0.49	0.62 ± 0.49	0.67 ± 0.47	0.72 ± 0.45	0.57 ± 0.50	0.60 ± 0.49
4	1	0.45 ± 0.50	0.47 ± 0.50	0.42 ± 0.49	0.45 ± 0.50	0.39 ± 0.49	0.42 ± 0.49	0.55 ± 0.50	0.53 ± 0.50	0.42 ± 0.49	0.46 ± 0.50
	2	0.48 ± 0.50	0.46 ± 0.50	0.46 ± 0.50	0.46 ± 0.50	0.44 ± 0.50	0.41 ± 0.49	0.56 ± 0.50	0.56 ± 0.50	0.43 ± 0.50	0.42 ± 0.49
	3	0.47 ± 0.50	0.49 ± 0.50	0.49 ± 0.50	0.43 ± 0.50	0.44 ± 0.50	0.49 ± 0.50	0.56 ± 0.50	0.59 ± 0.49	0.42 ± 0.50	0.41 ± 0.49
5	1	0.33 ± 0.47	0.34 ± 0.47	0.30 ± 0.46	0.30 ± 0.46	0.28 ± 0.45	0.30 ± 0.46	0.40 ± 0.49	0.39 ± 0.49	0.31 ± 0.46	0.35 ± 0.48
	2	0.34 ± 0.47	0.33 ± 0.47	0.32 ± 0.47	0.33 ± 0.47	0.31 ± 0.46	0.29 ± 0.45	0.41 ± 0.49	0.41 ± 0.49	0.31 ± 0.46	0.29 ± 0.46
	3	0.33 ± 0.47	0.34 ± 0.48	0.33 ± 0.47	0.31 ± 0.46	0.31 ± 0.46	0.34 ± 0.47	0.41 ± 0.49	0.45 ± 0.50	0.29 ± 0.45	0.26 ± 0.44
6	1	0.21 ± 0.40	0.22 ± 0.41	0.17 ± 0.37	0.20 ± 0.40	0.19 ± 0.40	0.18 ± 0.39	0.27 ± 0.44	0.25 ± 0.44	0.19 ± 0.39	0.22 ± 0.41
	2	0.23 ± 0.42	0.22 ± 0.41	0.21 ± 0.41	0.20 ± 0.40	0.20 ± 0.40	0.19 ± 0.39	0.28 ± 0.45	0.29 ± 0.45	0.20 ± 0.40	0.19 ± 0.39
	3	0.22 ± 0.42	0.23 ± 0.42	0.20 ± 0.40	0.19 ± 0.39	0.20 ± 0.40	0.23 ± 0.42	0.29 ± 0.46	0.30 ± 0.46	0.21 ± 0.41	0.18 ± 0.38
7	1	0.11 ± 0.31	0.11 ± 0.31	0.08 ± 0.27	0.09 ± 0.28	0.12 ± 0.32	0.11 ± 0.31	0.14 ± 0.34	0.13 ± 0.34	0.09 ± 0.29	0.10 ± 0.30
	2	0.12 ± 0.32	0.11 ± 0.32	0.10 ± 0.30	0.10 ± 0.30	0.11 ± 0.32	0.10 ± 0.30	0.15 ± 0.36	0.15 ± 0.36	0.09 ± 0.29	0.09 ± 0.38
	3	0.12 ± 0.32	0.13 ± 0.34	0.10 ± 0.30	0.11 ± 0.39	0.10 ± 0.31	0.13 ± 0.33	0.17 ± 0.38	0.17 ± 0.38	0.09 ± 0.29	0.09 ± 0.29

NA: data not available for that level of effect.

<sup>1</sup>Code description for birth type (TB and DTB) include: 1 – born single; 2 – born twin; 3 – born triplet.

<sup>2</sup>Across breeds population consisted of purebreds from Columbia, Polypay, Rambouillet, and Targhee.

Table 4.6: Mean and standard deviations of stayability (STAY) for individual levels of rearing types of ewes (TR) and their dams (DTR) by breed and across breeds.

STAY	Level	Breeds									
		Across		Columbia		Polypay		Rambouillet		Targhee	
		TR	DTR	TR	DTR	TR	DTR	TR	DTR	TR	DTR
2	1	0.81 ± 0.39	0.81 ± 0.39	0.81 ± 0.39	0.80 ± 0.40	0.80 ± 0.40	0.78 ± 0.42	0.83 ± 0.37	0.82 ± 0.39	0.79 ± 0.41	0.82 ± 0.38
	3	0.77 ± 0.42	0.79 ± 0.41	0.79 ± 0.41	0.81 ± 0.39	0.71 ± 0.45	0.72 ± 0.45	0.80 ± 0.40	0.81 ± 0.39	0.79 ± 0.41	0.80 ± 0.40
	5	0.80 ± 0.40	0.79 ± 0.40	0.81 ± 0.40	0.82 ± 0.38	0.76 ± 0.42	0.75 ± 0.43	0.84 ± 0.37	0.83 ± 0.38	0.80 ± 0.40	0.78 ± 0.41
	7	0.76 ± 0.43	0.80 ± 0.40	0.88 ± 0.32	0.87 ± 0.34	0.67 ± 0.47	0.76 ± 0.43	0.79 ± 0.41	0.85 ± 0.36	0.75 ± 0.44	0.74 ± 0.44
	8	0.79 ± 0.41	0.80 ± 0.40	0.85 ± 0.36	0.76 ± 0.43	0.76 ± 0.43	0.78 ± 0.41	0.78 ± 0.41	0.86 ± 0.35	0.82 ± 0.39	0.83 ± 0.38
	9	NA	NA	NA	NA	0.65 ± 0.43	0.81 ± 0.40	NA	NA	NA	NA
	3	1	0.62 ± 0.48	0.64 ± 0.48	0.62 ± 0.48	0.62 ± 0.48	0.58 ± 0.49	0.60 ± 0.49	0.70 ± 0.46	0.69 ± 0.46	0.58 ± 0.49
3	3	0.60 ± 0.49	0.62 ± 0.49	0.62 ± 0.49	0.63 ± 0.48	0.51 ± 0.50	0.58 ± 0.49	0.67 ± 0.47	0.70 ± 0.46	0.58 ± 0.49	0.56 ± 0.50
	5	0.64 ± 0.48	0.62 ± 0.48	0.62 ± 0.49	0.64 ± 0.48	0.61 ± 0.49	0.56 ± 0.50	0.71 ± 0.45	0.70 ± 0.46	0.61 ± 0.49	0.58 ± 0.49
	7	0.62 ± 0.49	0.62 ± 0.49	0.77 ± 0.43	0.61 ± 0.49	0.53 ± 0.50	0.57 ± 0.50	0.67 ± 0.47	0.72 ± 0.45	0.57 ± 0.50	0.60 ± 0.49
	8	0.62 ± 0.48	0.64 ± 0.48	0.68 ± 0.47	0.59 ± 0.49	0.60 ± 0.49	0.63 ± 0.48	0.67 ± 0.47	0.72 ± 0.45	0.57 ± 0.50	0.59 ± 0.49
	9	NA	NA	NA	NA	0.58 ± 0.50	0.68 ± 0.47	NA	NA	NA	NA
	4	1	0.45 ± 0.50	0.47 ± 0.50	0.42 ± 0.49	0.45 ± 0.50	0.39 ± 0.49	0.42 ± 0.49	0.55 ± 0.50	0.53 ± 0.50	0.42 ± 0.49
4	3	0.46 ± 0.50	0.47 ± 0.50	0.46 ± 0.50	0.48 ± 0.50	0.39 ± 0.49	0.43 ± 0.50	0.54 ± 0.50	0.57 ± 0.50	0.43 ± 0.50	0.40 ± 0.49
	5	0.48 ± 0.50	0.46 ± 0.50	0.46 ± 0.50	0.45 ± 0.50	0.45 ± 0.50	0.41 ± 0.49	0.56 ± 0.50	0.56 ± 0.50	0.43 ± 0.50	0.43 ± 0.49
	7	0.47 ± 0.50	0.47 ± 0.50	0.55 ± 0.50	0.48 ± 0.50	0.40 ± 0.49	0.45 ± 0.50	0.54 ± 0.50	0.51 ± 0.50	0.42 ± 0.50	0.43 ± 0.50
	8	0.47 ± 0.50	0.49 ± 0.50	0.47 ± 0.50	0.42 ± 0.49	0.44 ± 0.50	0.49 ± 0.50	0.57 ± 0.50	0.62 ± 0.49	0.42 ± 0.50	0.41 ± 0.49
	9	NA	NA	NA	NA	0.49 ± 0.50	0.56 ± 0.50	NA	NA	NA	NA
	5	1	0.33 ± 0.47	0.34 ± 0.47	0.30 ± 0.46	0.30 ± 0.46	0.28 ± 0.45	0.30 ± 0.46	0.40 ± 0.49	0.39 ± 0.49	0.31 ± 0.46
5	3	0.32 ± 0.47	0.35 ± 0.48	0.32 ± 0.47	0.37 ± 0.48	0.27 ± 0.44	0.31 ± 0.46	0.40 ± 0.49	0.41 ± 0.49	0.28 ± 0.45	0.29 ± 0.45
	5	0.34 ± 0.48	0.33 ± 0.47	0.32 ± 0.47	0.31 ± 0.46	0.32 ± 0.47	0.29 ± 0.45	0.41 ± 0.49	0.41 ± 0.49	0.31 ± 0.46	0.30 ± 0.46
	7	0.32 ± 0.47	0.35 ± 0.48	0.39 ± 0.49	0.31 ± 0.47	0.27 ± 0.45	0.37 ± 0.48	0.38 ± 0.49	0.43 ± 0.50	0.29 ± 0.46	0.28 ± 0.45
	8	0.33 ± 0.47	0.34 ± 0.47	0.31 ± 0.46	0.30 ± 0.46	0.31 ± 0.46	0.32 ± 0.47	0.42 ± 0.49	0.45 ± 0.50	0.29 ± 0.45	0.26 ± 0.44
	9	NA	NA	NA	NA	0.32 ± 0.47	0.41 ± 0.50	NA	NA	NA	NA
	6	1	0.21 ± 0.40	0.22 ± 0.41	0.17 ± 0.37	0.20 ± 0.40	0.19 ± 0.40	0.18 ± 0.39	0.27 ± 0.44	0.25 ± 0.44	0.19 ± 0.39
6	3	0.21 ± 0.41	0.23 ± 0.42	0.23 ± 0.42	0.24 ± 0.43	0.16 ± 0.37	0.21 ± 0.41	0.28 ± 0.45	0.27 ± 0.44	0.16 ± 0.37	0.19 ± 0.40

Table 4.6: Mean and standard deviations of stayability (STAY) for individual levels of rearing types of ewes (TR) and their dams (DTR) by breed and across breeds (continued).

STAY	Level	Breeds									
		Across		Columbia		Polypay		Rambouillet		Targhee	
		TR	DTR	TR	DTR	TR	DTR	TR	DTR	TR	DTR
6	5	0.23 ± 0.42	0.22 ± 0.41	0.21 ± 0.41	0.19 ± 0.39	0.21 ± 0.41	0.18 ± 0.38	0.29 ± 0.45	0.29 ± 0.46	0.21 ± 0.41	0.19 ± 0.39
	7	0.21 ± 0.41	0.24 ± 0.43	0.20 ± 0.41	0.19 ± 0.39	0.19 ± 0.39	0.22 ± 0.42	0.26 ± 0.44	0.33 ± 0.47	0.19 ± 0.40	0.21 ± 0.41
	8	0.23 ± 0.42	0.22 ± 0.42	0.20 ± 0.40	0.19 ± 0.39	0.21 ± 0.41	0.23 ± 0.42	0.31 ± 0.46	0.29 ± 0.45	0.22 ± 0.41	0.17 ± 0.37
	9	NA	NA	NA	NA	0.17 ± 0.38	0.33 ± 0.48	NA	NA	NA	NA
7	1	0.11 ± 0.31	0.11 ± 0.31	0.08 ± 0.27	0.09 ± 0.28	0.12 ± 0.32	0.11 ± 0.31	0.14 ± 0.34	0.13 ± 0.34	0.09 ± 0.29	0.10 ± 0.30
	3	0.10 ± 0.30	0.11 ± 0.32	0.12 ± 0.33	0.11 ± 0.32	0.07 ± 0.25	0.14 ± 0.35	0.14 ± 0.35	0.13 ± 0.33	0.07 ± 0.25	0.08 ± 0.27
	5	0.12 ± 0.33	0.11 ± 0.31	0.10 ± 0.30	0.09 ± 0.29	0.12 ± 0.33	0.10 ± 0.29	0.16 ± 0.36	0.16 ± 0.37	0.10 ± 0.30	0.09 ± 0.29
	7	0.12 ± 0.32	0.15 ± 0.36	0.07 ± 0.26	0.13 ± 0.34	0.12 ± 0.33	0.14 ± 0.35	0.17 ± 0.38	0.21 ± 0.41	0.08 ± 0.28	0.12 ± 0.32
	8	0.12 ± 0.33	0.12 ± 0.32	0.11 ± 0.32	0.10 ± 0.31	0.11 ± 0.31	0.12 ± 0.32	0.17 ± 0.38	0.16 ± 0.37	0.10 ± 0.30	0.08 ± 0.28
	9	NA	NA	NA	NA	0.05 ± 0.22	0.21 ± 0.41	NA	NA	NA	NA

NA: data not available for that level of effect.

<sup>1</sup>Description for rearing type (TR and DTR) include: 1 – born single, raised single; 3 – born twin, raised single; 5 – born twin, raised twin; 7 – born triplet, raised single; 8 – born triplet, raised twin; and 9 – born triplet, raised triplet.

<sup>2</sup>Across breeds population consisted of purebreds from Columbia, Polypay, Rambouillet, and Targhee.



## CHAPTER 5: MODEL EXPLORATION FOR LONGEVITY USING BAYESIAN ANALYSIS

### Additive Bayesian model

#### Priors testing

Testing the five priors listed in Table 3.3 on the Columbia dataset, we observed that we could use fewer iterations, burn-in, and smaller thinning intervals while maintaining autocorrelation and convergence criteria with prior E (Table 5.1 and 5.2). This also meant that we could support faster run times. As an example, Table 5.2 demonstrates running model 1 (ewe's age effect only) with different priors. Only prior E found effect sample sizes above 1,000 for all model parameters with lower DIC value than the other priors. Due to these comparisons in Columbia, prior E was used to run longevity models because it gave high effective sample sizes at a very low iteration time, following the directive of Gong and Flegal (2016). Other breeds and across breed tests supported this outcome.

Initially, only a single MCMC chain was considered. However, the addition of the dominance variance-covariance structure slowed the analysis down considerably (over 600 times slower compared to the additive effect only model). Therefore, different number of MCMC chains were investigated along with varying amount of iterations, burn-in, and thinning intervals. Multiple-chain MCMC process does not require communication between different chains during sampling (Gilks et al., 1995). Therefore, as long as a common posterior is found among those chains, saved samples can converge into a single chain for post-analysis summary. Convergence of multiple chains was assessed through visualization of chain posteriors including a convergence plot (`gelman.plot` function based on Gelman and Rubin (1992) statistic in the *coda* R package; Plummer et al., 2006), a cumulative quantile plot (`cumuplot` function of the *coda* R package), and a chain

density overlay plot (`mcmc_dens_overlay` function of the *bayesplot* R package; Gabry et al., 2019) per model effect. Through tests, it was found that running additive models in 10 chains of 10,000 iterations, 1,000 burn-in and a thinning interval of 90 per chain and running additive and dominance models in 10 chains of 20,000 iterations, 11,000 burn-in, and a thinning interval of 90 per chain helped conserve time and met convergence criteria (Appendix C).

Table 5.1: Priors investigated and their results when modeling longevity using the *MCMCglmm* R package<sup>1</sup>

Prior ID	<i>MCMCglmm</i> prior syntax <sup>2</sup>	Family	Results
A	list(R=list(V=1,nu=0, fix=1), G=list(G1=list(p.var, 0.1), G2=list(p.var, 0.1) , G3=list(p.var, 0.1)))	Threshold	Higher run time Small effective sample sizes High autocorrelation values
B	list(R=list(V=1,nu=0.002), G=list(G1=list(p.var, 0.1), G2=list(p.var, 0.1), G3=list(p.var, 0.1)))	Poisson	Higher run time Small effective sample sizes High autocorrelation values
C	list(G=list(G1=list(V=matrix(p.var/2),n=1), G2=list(V=matrix(p.var/2),n=1), G3=list(V=matrix(p.var/2),n=1)), R=list(V=matrix(p.var/2),n=1))	Censored Gaussian	Higher run time Small effective sample sizes High autocorrelation values Zero DIC value
D	list(R=list(V=0.7*p.var,nu=1), G=list(G1=list(0.3*p.var, 1), G2=list(0.3*p.var, 1), G3=list(0.3*p.var, 1)))	Threshold	High run time Slightly high effective sample sizes
E	list(R=list(V=1,nu=1), G=list(G1=list(V=1,nu=1,alpha.mu=0,alpha.V=1000), G2=list(V=1,nu=1,alpha.mu=0,alpha.V=1000), G3=list(V=1,nu=1,alpha.mu=0,alpha.V=1000)))	Gaussian	Lower run time. Large effective sample sizes Lower autocorrelation values
F	list(R=list(V=0.6*p.var,nu=1), G=list(G1=list(0.4*p.var, 1), G2=list(0.4*p.var, 1), G3=list(0.4*p.var, 1)))	Gaussian	High run time Slightly high effective sample sizes High autocorrelation values

<sup>1</sup>The priors were coded using different family distributions ran in multiple chains of 10,000 iterations, burn-in of 1,000, thinning interval of 90, resulting in an expected effective sample size of 1,000 per prior parameter. <sup>2</sup>*MCMCglmm* prior syntax: R = the prior components for the residual variance, G = list of prior components for the random effect variances, V= variance, nu= 'measurement of belief' parameter, alpha.mu = mean vector, alpha.V = covariance matrix, p.var = variation component of longevity. G1= random effect of additive matrix, G2= random effect of dam's permanent environmental variance, G3: random effect of birth year.

Table 5.2: Summary statistics of tested priors<sup>1</sup>

Statistics	Priors					
	A	B	C	D	E	F
<b>ESS</b>						
Intercept	835.6	357.7	26.38	37.19	1,000	1,193
AGE	1,000	114.4	63.03	55.00	890.8	1,067
ID	106.5	71.89	155.4	75.81	895	219.1
MPE	414.5	140.1	59.16	55.17	1,000	605.3
BYR	1,000	550.1	221.1	111.2	1,112	1,000
R	0	45.12	129.9	17.84	1,104	570.9
<b>Autocorrelation</b>						
Intercept	0.0891	0.2901	0.6853	0.7216	0.0418	0.0302
AGE	-0.0059	0.7036	0.8162	0.2937	0.0572	0.0343
ID	0.7558	0.8202	0.6546	0.8139	0.0549	0.6403
MPE	0.3502	0.7035	0.4194	0.5886	0.0229	0.2453
BYR	-0.0129	0.0602	0.2446	0.2023	-0.0537	0.0291
R	NA	0.8638	0.5137	0.9591	-0.0500	0.1782
<b>DIC</b>						
	8,543.95	9,147.33	0	8,321.8	9,300.73	9,289.47
<b>Variance estimate</b>						
ID	0.13	0.03	0.20	0.27	0.24	0.33
MPE	0.08	0.02	0.20	0.18	0.11	0.22
BYR	0.06	0.03	0.29	0.14	0.07	0.17
R	1.00	0.003	0.19	2.70	3.33	3.17
P	1.27	0.0053	0.88	3.29	3.75	3.89
<b>Runtime</b>						
	15mins	16mins	16mins	17 mins	14mins	15.35mins

<sup>1</sup>ESS: Effective sample sizes, DIC: deviance information criterion, BYR: birth year, autocorr: autocorrelation, R: error variance, P: phenotypic variance, MPE: dam's permanent environmental variance, ID: additive genetic variance. The priors were coded using different family distributions ran in multiple chains of 10,000 iterations, burn-in of 1,000, thinning interval of 90, resulting in an expected effective sample size of 1,000 per prior parameter.

### **Additive and additive and dominance models summary**

The best model within individual and across breeds included fixed effects of TB, TR, DTB, and DTR as well as fixed covariate of AGE. A summary of the multichain model, when posterior saved samples were combined to a single chain are presented below (Table 5.3).

Initial model efforts included birth year as a fixed effect rather than a random effect. Model fit criteria (DIC in this case) had slightly lower values when using birth year as a fixed effect, which provided evidence it may be appropriate in this format. Even so, including birth year as a random effect adjusted the additive genetic variance to be comparable to when dominance was included (Table 5.4) and the number of years was large ( $n = 30$ ). Therefore, birth year was included as a random effect for all other analyses to ensure that additive genetic variance was not overestimated and random effects due to environmental differences across years was accounted for.

Continuing with the already established multiple MCMC chains iterations, burn-in and thinning interval, we found out that the effective sample sizes for the fixed effects of TB, TR, DTB and DTR and the fixed covariate of AGE were in the acceptable ranges for both within and across breeds (greater than or equal to 1,000) which showed the models ran, selected and reported below achieved convergence according to the suggestions of Geweke (1992). The autocorrelation values for both the random and fixed effects were within the acceptable ranges of less than 0.10 (Hadfield, 2019) which is shown in figure 5.1. The model reported on achieved convergence based on Geweke (1992) criterion suggestion.

Additive and dominance models were run by extending prior E to include an additional random effect (Dominance genetic effect, Table 5.2). Iterations and burn-in when including the

dominance effect had to be increased to 20,000 and 11,000, respectively, to account for the extra random effect and meeting necessary convergence criteria.

Table 5.3: Summary statistics by breeds using prior E for longevity when including additive genetic effects.

Statistics <sup>1</sup>	Breeds				
	Across <sup>2</sup>	Columbia	Polypay	Rambouillet	Targhee
Effective sample size					
Intercept	1,000	1,111	1,000	838.6	1,000
STM	1,000	--	--	--	--
AGE	1,000	1,141	1,000	1,117.1	1,000
TB	1,000	1,000	1,000	1,000	1,324.7
TR	1,000	1,000	1,000	871.4	1,000
DTB	1,000	1,000	1,000	1,149.2	1,000
DTR	1,000	1,000	1,000	1,149.2	1,000
ID	1,000	1,000	1,000	877.7	1,000
MPE	1,000	1,000	1,000	1,000	1,172
BYR	867.7	1,111	979.9	1,319	1,000
R	1,000	1,000	1,000	822	1,000
Autocorrelation					
Intercept	-0.0029	0.0361	-0.0210	0.0123	0.0417
STM	0.0325	--	--	--	--
AGE	0.0179	-0.0026	0.0431	0.0142	0.0391
TB	0.0010	0.0366	0.0521	-0.0056	-0.0331
TR	-0.010	0.0366	-0.0123	-0.0099	-0.0331
DTB	-0.0018	0.0103	0.0734	-0.0699	-0.0351
DTR	-0.0007	-0.0026	0.0003	-0.0218	-0.0235
ID	-0.0245	0.0049	0.0117	0.0646	-0.0078
MPE	-0.0033	-0.0531	0.0025	0.0025	-0.0798
BYR	0.0765	-0.0352	0.0540	-0.0281	0.0324
R	0.0149	0.0101	-0.0029	0.0971	-0.0020
DIC	44,112.58	9,332.73	10,961.89	11,923.95	11,955.46
Variance Estimate					
ID	0.33	0.15	0.21	0.18	0.09
MPE	0.01	0.15	0.04	0.04	0.05
BYR	0.11	0.07	0.18	0.23	0.14
R	3.54	3.43	3.77	3.90	3.58
P	3.98	3.80	4.20	4.35	3.86

Prior E was coded as list(R = list(V=1,nu=1), G = list(G1=list(V=1,nu=1,alpha.mu=0,alpha.V=1000), G2 = list(V1,nu=1,alpha.mu=0,alpha.V=1000) , G3 = list(V1,nu=1,alpha.mu=0,alpha.V=1000))) using Gaussian family distribution with 10,000 iterations, burn-in of 1,000, thinning interval of 90, resulting in an expected effective sample size of 1,000 per breed when combined into a single chain. <sup>1</sup>Model effects could include fixed effects of intercept (mean), Age of ewe (AGE), ewe birth type (TB), ewe rear type (TR), ewe's dam's birth type (DTB), ewe's dam's rear type (DTR) and random effects of individual ewe (ID) with relationship matrix (additive genetic variance), ewe's dam ID without pedigree (maternal permanent environmental variance), birth year (BYR), residual (R) variance, and phenotypic variance (P). The DIC is the deviance information criterion.

Table 5.4: Example of variance component estimates when birth year was included in the longevity model as fixed or random in Columbia for additive (A) only or additive and dominance (A + D) models.<sup>1</sup>

Effect Type	Model	$V_A$	$V_D$	$V_{MPE}$	$V_{BYR}$	$V_e$	$V_P$
Fixed	A only	0.27	--	0.12	--	3.35	3.74
	A + D	0.23	0.54	0.10	--	2.88	3.75
	Ratio	1.17	--	1.20	--	1.16	0.99
Random	A only	0.25	--	0.11	0.07	3.32	3.75
	A + D	0.22	0.38	0.09	0.06	3.01	3.76
	Ratio	1.14	--	1.22	1.17	1.10	0.99

<sup>1</sup>Prior E was used as `list(R = list(V=1,nu=1), G = list(G1=list(V=1,nu=1,alpha.mu=0,alpha.V=1000), G2 = list(V1,nu=1,alpha.mu=0,alpha.V=1000) , G3 = list(V1,nu=1,alpha.mu=0,alpha.V=1000)))` using Gaussian family distribution with 2,000 iterations, burn-in of 1,000, thinning interval of 10 in multiple chains of 10 MCMC.  $V_A$  = between-individual additive genetic variance,  $V_D$  = within-individual dominance genetic variance,  $V_{MPE}$  = maternal variance due to permanent environmental effects,  $V_{BYR}$  = Birth year variance,  $V_e$  = Error variance,  $V_P$  = Phenotypic variance. The ratio is always variance of A only model to variance of A + D model

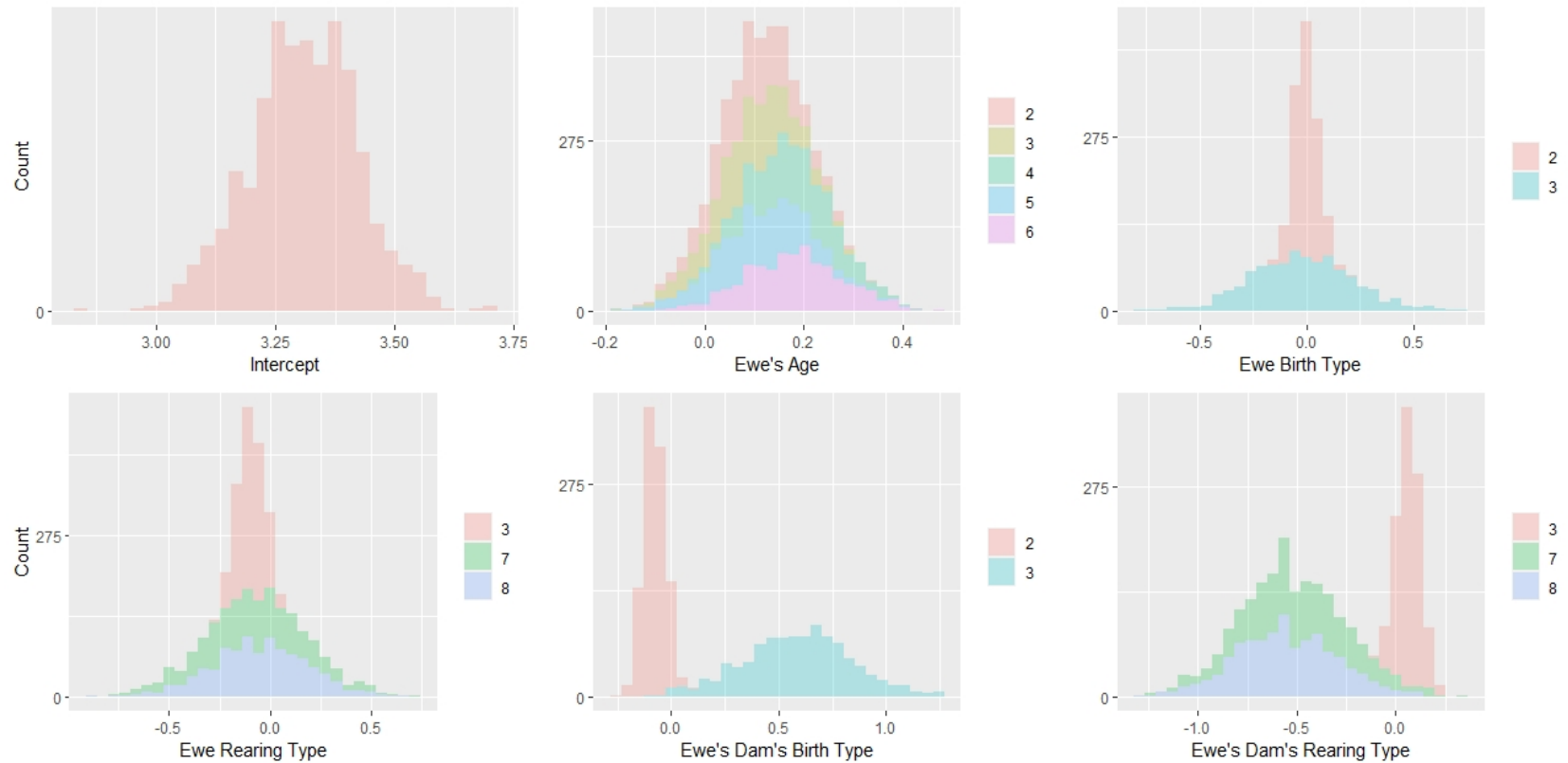


Figure 5.1: Density plots of posterior estimates for fixed effects using Columbia longevity dataset when modeling additive genetic variance only. Density distributions should appear normal or bell-shaped to indicate proper mixing of multiple MCMC chains and convergence in the analysis was met.

## Estimates of genetic parameters

Estimates of additive genetic, maternal permanent environmental, birth year and dominance genetic variances differed among breeds for longevity. Table 5.5 reports variance proportions for the genetic effects of longevity using pedigree. The phenotypic variance reported is the sum of the variance components estimated and provides an avenue of comparison across models. In general, the proportion of phenotypic variance due to additive and dominance genetic variances (A+D) was significantly larger than the proportion of variance due to additive (A) genetic variance, as evident by heritability ratios greater much than 1. Incorporating non-additive genetic effects within breeds reduced the proportion of phenotypic variance due to additive genetic effects for longevity in all cases (i.e., narrow sense heritability).

In contrast to what has been reported in other complex traits (e.g., Muñoz et al., 2014), non-additive genetic effects (dominance effects) estimated from pedigree information in this study represented a large proportion of the total phenotypic variance for both within and across breeds (8.27% to 36.55%) compared to additive genetic, birth year, and maternal permanent environmental variances (Table 5.5, A+D models). Vitezica, Varona, and Legarra (2013) found a large standard error for dominance estimates, which was also seen with the highest posterior density (HPD) interval shown in Table 5.5. The narrow-sense heritability estimates for within breeds (Table 5.5) were similar to those reported for Columbia ( $0.06 \pm 0.022$ ) and Polypay ( $0.07 \pm 0.021$ ) by Holland (2018) and Brash et al. (1994) who reported a heritability estimate of 0.06 for Australian Dorset ewes, which validates our modeling compared to the traditional animal model approach used in his study.

Other studies reported higher additive genetic variances and narrow sense heritability than our study. For example, in crossbred Mule ewe by Mekkawy et al. (2009) while using a univariate



Bayesian method with additive genetic effect fitted as random effect reported 0.27 as crossbred Mule ewes heritability estimate for longevity which was higher than our estimates; this could be due to their analysis based on their 1,500 hill ewes 1998 to 2000 three years of record. The heritability estimates obtained across and within breeds were lower than those obtained for Czech Republic's Suffolk sheep (0.40) in their experiment using records of 20,502 ewes from 137 flocks and fitting birth year as a fixed effect (Milerski et al., 2018).

Table 5.5: Estimates of genetic parameters for Additive (A) models and Additive + Dominance (A+D) Bayesian models for Longevity with lower and upper confidence intervals in brackets<sup>1</sup>

Group	Model	V <sub>A</sub>	V <sub>D</sub>	V <sub>MPE</sub>	V <sub>BYR</sub>	V <sub>e</sub>	V <sub>P</sub>	h <sup>2</sup>	H <sup>2</sup>	H <sup>2</sup> /h <sup>2</sup>
<sup>2</sup> Across	A only	0.33 (0.21, 0.45)	--	0.01 (0.0, 0.04)	0.10 (0.05, 0.18)	3.54 (3.40, 3.68)	3.98	0.09	--	--
	A + D	0.32 (0.21, 0.44)	0.33 (0.0, 0.90)	0.01 (0.0, 0.05)	0.11 (0.05, 0.17)	3.22 (2.62, 3.63)	3.99	0.08	0.17	2.13
	Ratio	1.03	--	1.00	0.90	1.09	0.99	1.13	--	--
Columbia	A only	0.15 (0.0, 0.48)	--	0.15 (0.0, 0.31)	0.07 (0.01, 0.12)	3.43 (3.11, 3.71)	3.80	0.04	--	--
	A + D	0.15 (0.0, 0.49)	0.64 (0.0, 1.68)	0.13 (0.0, 0.30)	0.06 (0.09, 0.14)	2.86 (1.82, 3.68)	3.84	0.03	0.21	7.00
	Ratio	1.00	--	1.15	1.17	1.19	0.99	1.33	--	--
Polypay	A only	0.21 (0.0, 0.67)	--	0.04 (0.0, 0.14)	0.18 (0.07, 0.34)	3.77 (3.50, 4.01)	4.20	0.05	--	--
	A + D	0.16 (0.0, 0.50)	0.82 (0.0, 1.92)	0.03 (0.0, 0.11)	0.17 (0.06, 0.31)	3.06 (2.06, 3.99)	4.24	0.04	0.24	6.00
	Ratio	1.31	--	1.33	1.05	1.23	0.99	1.25	--	--
Rambouillet	A only	0.18 (0.0, 0.55)	--	0.04 (0.0, 0.14)	0.23 (0.08, 0.40)	3.90 (3.60, 4.18)	4.35	0.04	--	--
	A + D	0.17 (0.0, 0.57)	0.90 (0.0, 2.10)	0.03 (0.0, 0.11)	0.22 (0.09, 0.40)	3.07 (1.90, 4.05)	4.39	0.03	0.25	8.33
	Ratio	1.05	--	1.33	1.05	1.27	0.99	1.33	--	--
Targhee	A only	0.09 (0.0, 0.35)	--	0.05 (0.0, 0.14)	0.14 (0.05, 0.25)	3.58 (3.36, 3.84)	3.86	0.03	--	--
	A + D	0.07 (0.0, 0.25)	1.44 (0.05, 2.51)	0.03 (0.0, 0.11)	0.14 (0.05, 0.25)	2.26 (1.15, 3.34)	3.94	0.02	0.38	19
	Ratio	1.29	--	1.67	1.00	1.58	0.97	1.5	--	--

<sup>1</sup>V<sub>A</sub> = between-individual additive genetic variance, V<sub>D</sub> = within-individual dominance genetic variance, V<sub>MPE</sub> = maternal variance due to permanent environmental effects, V<sub>BYR</sub> = Birth year variance, V<sub>e</sub> = Error variance, V<sub>P</sub> = Phenotypic variance, h<sup>2</sup> = narrow-sense heritability, H<sup>2</sup> = broad sense heritability. The ratio is always variance of A only model to variance of A + D model.

<sup>2</sup>Across population consisted of purebreds from Columbia, Polypay, Rambouillet, and Targhee and related crossbreds of Friesian, Dorper, Texel, Finnsheep, Dorset, Romanov, and a USMARC-Composite developed in the 1970s.

Still, they were similar to Riggio et al. (2008) findings for Scottish Blackface sheep (0.06). Hatcher et al. (2007) discovered that the heritability of survival in adult Merino ewes was negligible at two years of age, but it increased as they grew older. The heritability of survival increased at 0 from a two-year-old to 0.13 at five years of age. It has been observed that additive genetic variance can be overestimated when fitting only additive variance because this model captures some non-additive genetic variance (Su et al., 2012; Munoz et al., 2014); our results corroborate these observations as the inclusion of the dominance genetic effect resulted in a reduction of the other genetic variances i.e. additive, birth year and maternal permanent and error effects (Table 5.5), this shows that when dominance effects are included, estimation of additive genetic effects becomes exact. Columbia's heritability ratio compared to the other within breeds' heritability estimates shows that if consideration is put into modeling dominance effects, selection could improve. Our findings are novel because the sheep literature is inadequate on longevity studies for comparison. Still, it enforces Falconer's and Mackay's (1996) postulation that several components influence ewe's productivity. Overall, the inclusion of dominance effects in our models helped to make additive effects more precise, which helped to make the ranking of estimated breeding values better.

Even though it is computationally demanding to estimate non-additive genetic effects, nevertheless the results from this research indicate that non-additive genetic effects do contribute to the variance of complex traits like longevity, and the inclusion of this effect would lead to an improvement in genetic evaluations, even if selecting only using an additive genetic variation.

### **Estimated marginal means**

The estimated marginal means presented in Tables 5.6 and 5.7 are on a per breed basis and none from the across breed analysis. The highest posterior density (HPD) from the *emmeans* function is a 95% confidence region where 95% of the mass (posterior estimates) fall, regardless of the symmetry of the distribution (Hespanhol et al., 2019). Due to convergence criteria established in this study, multimodal posterior distributions per effect were avoided. Therefore, the mean difference and supporting HPD between two comparison groups can be used to determine significant differences (Hespanhol et al., 2019). Furthermore, the inclusion of additive only or additive and dominance genetic effects did not impact differences found among fixed effects.

Based on this, no estimated marginal means were different from each other for birth type in any breed (Tables 5.6 and 5.7). It is evident that breeds often had very different estimated marginal means per effect, even though across breed effects are not reported. Other significant effects are broken down by breed.

### ***Columbia***

Only rearing type and age had significant differences observed among posterior estimates for longevity in Columbia ewes. Columbia ewes born as triplets and either raised as twins or singles were found to have the highest longevity, where triplets raised as singles were different from twins (raised as singles or twins) and singles. Furthermore, Columbia ewes that came from first-time dams had significantly lower longevity than other Columbia ewes with experienced dams (i.e., 2<sup>nd</sup> or higher lambing event). Columbia ewes from dams that were 2 or older had an increasing trend of longevity but were statistically the same. The only exception was ewes with 7-year-old dams, which had higher longevity estimates compared to ewes with 2, 3, or 4-year-old dams.

### ***Polypay***

Rearing type, ewes' dams' type of birth, ewes' dams' type of rearing, and age had significant differences observed among posterior estimates for longevity in Polypay ewes. Polypay ewes born as singles and weaned as single and those born as twin and raised as twin had the highest longevity values statistically recorded where ewes born as twin and raised as single or born as single and raised as twin, ewes born as twin and raised as twin, ewes born triplet raised as twin and ewes born as a triplet and raised as triplet were different from those born triplet and raised as single. In addition, ewes' dams' born as triplets had the highest value for longevity and they were statistically different from those born as singles and twins.

Also, ewes' born as a triplet and raised as triplet had the highest recorded value for longevity and were different statistically from those born as triplet raised as single and those born as a triplet and raised as a twin. Additionally, Polypay ewes that came from fifth-time dams had lower longevity in comparison to other lambing age which was surprising as it did not follow the trend observed in Columbia ewes.

### ***Rambouillet***

Only dam's age of ewes lambing had a significant impact on longevity for Rambouillet ewes. Rambouillet ewes that came from third-time dams had lower longevity in comparison to dams that lambed for the first time. Rambouillet ewes from dams that were 2 or older had a decreasing trend of longevity but were statistically the same.

### ***Targhee***

Only rearing type and age had significant differences observed among posterior estimates for longevity in Targhee ewes. Ewes that were born as a triplet and raised as singles had the lowest recorded value for longevity while those born as single and weaned as single had the highest

longevity value recorded; the other rearing groups were not significantly different from each other. Furthermore, ewes that came from the first time of lambing had lower longevity value than those from second and older lambing ages that had an increasing trend of longevity but were statistically the same.

Not a lot has been reported for how longevity is affected by ewes type of birth, ewes type of rearing, ewes dams' type of birth, ewes' dams' type of rearing, and age of dam at lambing in Columbia, Polypay, Rambouillet, and Targhee ewes but the findings we have reported here suggests that ewes' type of birth does not affect longevity in any of the breeds but ewes type of rearing affects longevity in Columbia, Polypay and Targhee ewes which implies that producers should pay more attention to record-keeping and how the system of rearing undertaken in Columbia, Polypay, and Targhee ewes especially as this could ultimately affect longevity. Additionally, ewes' dams' type of birth only affected longevity in Polypay ewes but did not have any impact on longevity in Columbia, Rambouillet, and Targhee ewes which suggest that longevity in Polypay ewes will be impacted by how their dams' were lambed so producers should pay more attention to how their ewes were lambed in Polypay breed.

Conclusively, producers should pay more attention to how the dams of their ewes were reared and at the age, those dams lambed as they ultimately affect longevity in Columbia, Polypay, Rambouillet, and Targhee ewes, and depending on production goals, dam age may need to be a factor for selecting females with the goal of increased long-term profitability.

Table 5.6: Estimated marginal means and highest posterior density (HPD; lowest and highest in parentheses) for type of birth (TB), type of rearing (TR), ewe's dam's type of birth (DTB), ewe's dam's type of rearing (DTR) and ewe's dam's age (AGE) within breeds when only including additive genetic variance in the model.

Effect	Level	Breeds			
		Columbia	Polypay	Rambouillet	Targhee
TB	1	3.50 (3.26, 3.71)	3.57 (3.33, 3.92)	3.92 (3.63, 4.18)	3.53 (3.31, 3.77)
	2	3.48 (3.28, 3.68)	3.44 (3.22, 3.68)	3.95 (3.72, 4.20)	3.42 (3.21, 3.62)
	3	3.66 (3.37, 3.96)	3.40 (3.08, 3.66)	3.88 (3.55, 4.22)	3.34 (3.00, 3.66)
TR	1	3.50 (3.26, 3.71) <sup>b</sup>	3.57 (3.33, 3.92) <sup>a</sup>	3.92 (3.63, 4.18)	3.53 (3.31, 3.77) <sup>a</sup>
	3	3.47 (3.17, 3.73) <sup>b</sup>	3.35 (3.02, 3.64) <sup>a,b</sup>	3.85 (3.56, 4.15)	3.39 (3.14, 3.66) <sup>a,b</sup>
	5	3.49 (3.32, 3.69) <sup>b</sup>	3.53 (3.34, 3.77) <sup>a</sup>	4.05 (3.79, 4.29)	3.45 (3.25, 3.67) <sup>a,b</sup>
	7	3.79 (3.34, 4.28) <sup>a</sup>	3.25 (2.88, 3.67) <sup>b</sup>	3.89 (3.41, 4.37)	3.30 (2.84, 3.79) <sup>b</sup>
	8	3.56 (3.24, 3.87) <sup>a,b</sup>	3.46 (3.22, 3.73) <sup>a,b</sup>	3.88 (3.53, 4.19)	3.38 (3.04, 3.74) <sup>a,b</sup>
	9	NA	3.49 (3.00, 3.94) <sup>a,b</sup>	NA	NA
DTB	1	3.46 (3.23, 3.72)	3.47 (3.16, 3.85) <sup>a,b</sup>	3.85 (3.54, 4.13)	3.65 (3.40, 3.88)
	2	3.57 (3.31, 3.76)	3.45 (3.12, 3.72) <sup>b</sup>	3.90 (3.60, 4.14)	3.44 (3.21, 3.67)
	3	3.47 (3.11, 3.81)	3.82 (3.48, 4.20) <sup>a</sup>	3.99 (3.64, 4.37)	3.50 (3.17, 3.88)
DTR	1	3.51 (3.29, 3.72)	3.37 (3.04, 3.62) <sup>b,c</sup>	3.84 (3.60, 4.13)	3.55 (3.31, 3.76)
	3	3.70 (3.43, 3.96)	3.41 (3.09, 3.71) <sup>b,c</sup>	3.87 (3.58, 4.15)	3.34 (3.10, 3.60)
	5	3.54 (3.35, 3.72)	3.26 (3.05, 3.49) <sup>c</sup>	3.92 (3.69, 4.18)	3.33 (3.14, 3.55)
	7	3.59 (3.05, 4.11)	3.60 (3.19, 3.98) <sup>b</sup>	4.00 (3.52, 4.48)	3.43 (2.96, 3.92)
	8	3.45 (3.11, 3.76)	3.54 (3.32, 3.84) <sup>b</sup>	3.98 (3.65, 4.33)	3.37 (2.99, 3.74)
	9	NA	4.00 (3.47, 4.53) <sup>a</sup>	NA	NA
AGE	1	3.04 (2.70, 3.34) <sup>c</sup>	3.53 (3.28, 3.90) <sup>a,b</sup>	4.05 (3.74, 4.37) <sup>a</sup>	3.19 (2.87, 3.51) <sup>b</sup>
	2	3.47 (3.21, 3.72) <sup>b</sup>	3.63 (3.32, 3.96) <sup>a</sup>	3.76 (3.48, 4.05) <sup>a,b</sup>	3.49 (3.25, 3.73) <sup>a</sup>
	3	3.42 (3.14, 3.67) <sup>b</sup>	3.62 (3.28, 3.94) <sup>a,b</sup>	3.72 (3.38, 4.02) <sup>b</sup>	3.63 (3.35, 3.90) <sup>a</sup>
	4	3.56 (3.28, 3.85) <sup>a,b</sup>	3.79 (3.45, 4.14) <sup>a</sup>	4.01 (3.65, 4.32) <sup>a,b</sup>	3.46 (3.18, 3.77) <sup>a,b</sup>
	5	3.59 (3.26, 3.92) <sup>a,b</sup>	3.30 (2.92, 3.70) <sup>b</sup>	3.95 (3.58, 4.27) <sup>a,b</sup>	3.59 (3.27, 3.89) <sup>a</sup>
	6	3.54 (3.17, 3.82) <sup>a,b</sup>	3.62 (3.23, 4.03) <sup>a,b</sup>	3.93 (3.54, 4.30) <sup>a,b</sup>	3.72 (3.42, 4.07) <sup>a</sup>

Table 5.6: Estimated marginal means and highest posterior density (HPD; lowest and highest in parentheses) for type of birth (TB), type of rearing (TR), ewe's dam's type of birth (DTB), ewe's dam's type of rearing (DTR) and ewe's dam's age (AGE) within breeds when only including additive genetic variance in the model (continued).

Effect	Level	Breeds			
		Columbia	Polypay	Rambouillet	Targhee
AGE	7	3.86 (3.50, 4.25) <sup>a</sup>	3.56 (3.07, 4.01) <sup>a,b</sup>	3.98 (3.60, 4.42) <sup>a,b</sup>	3.60 (3.23, 3.96) <sup>a</sup>

<sup>1</sup>Levels: USSES code description for rearing type (TR and DTR) include: 0 – born a quadruplet or quintuplet, weaned any number, minor category; 1 – born single, weaned single; 2 – born single, raised orphan; 3 – born twin, raised single (major) or born single, raised twin (minor); 4 – born twin, raised orphan; 5 – born twin, raised twin; 6 – born triplet, raised orphan; 7 – born triplet, raised single; 8 – born triplet, raised twin; and 9 – born triplet raised triplet. NA: Not available.

<sup>a,b,c</sup>Means with different superscripts have evidence based on HPD that they differ ( $P < 0.05$ )



Table 5.7: Estimated marginal means and highest posterior density (HPD; lowest and highest in parentheses) for type of birth (TB), type of rearing (TR), ewe's dam's type of birth (DTB), ewe's dam's type of rearing (DTR) and ewe's dam's age (AGE) within breeds when only including additive and dominance genetic variance in the model.

Effect	Level	Breeds			
		Columbia	Polypay	Rambouillet	Targhee
TB	1	3.50 (3.30, 3.71)	3.58 (3.28, 3.88)	3.91 (3.66, 4.19)	3.51 (3.29, 3.73)
	2	3.48 (3.29, 3.69)	3.44 (3.19, 3.69)	3.94 (3.69, 4.19)	3.40 (3.20, 3.62)
	3	3.68 (3.35, 3.95)	3.40 (3.12, 3.67)	3.87 (3.55, 4.22)	3.31 (3.01, 3.64)
TR	1	3.50 (3.30, 3.71) <sup>b</sup>	3.58 (3.28, 3.88) <sup>a</sup>	3.91 (3.66, 4.19)	3.51 (3.29, 3.73) <sup>a</sup>
	3	3.46 (3.16, 3.73) <sup>b</sup>	3.35 (3.03, 3.69) <sup>a,b</sup>	3.84 (3.54, 4.15)	3.37 (3.12, 3.64) <sup>a,b</sup>
	5	3.50 (3.29, 3.68) <sup>b</sup>	3.53 (3.30, 3.76) <sup>a</sup>	4.03 (3.81, 4.28)	3.43 (3.23, 3.64) <sup>a,b</sup>
	7	3.80 (3.29, 4.28) <sup>a</sup>	3.24 (2.88, 3.65) <sup>b</sup>	3.89 (3.41, 4.38)	3.25 (2.76, 3.71) <sup>b</sup>
	8	3.58 (3.25, 3.92) <sup>a,b</sup>	3.46 (3.18, 3.71) <sup>a,b</sup>	3.86 (3.51, 4.17)	3.38 (3.03, 3.70) <sup>a,b</sup>
	9	NA	3.48 (3.00, 4.01) <sup>a,b</sup>	NA	NA
DTB	1	3.47 (3.24, 3.70)	3.48 (3.13, 3.82) <sup>a,b</sup>	3.85 (3.57, 4.14)	3.63 (3.39, 3.85)
	2	3.57 (3.35, 3.78)	3.45 (3.13, 3.76) <sup>b</sup>	3.90 (3.63, 4.17)	3.41 (3.17, 3.63)
	3	3.47 (3.11, 3.78)	3.82 (3.48, 4.19) <sup>a</sup>	3.99 (3.63, 4.35)	3.49 (3.17, 3.84)
DTR	1	3.53 (3.28, 3.71)	3.36 (3.05, 3.63) <sup>b</sup>	3.84 (3.58, 4.10)	3.52 (3.30, 3.73)
	3	3.71 (3.41, 3.96)	3.40 (3.09, 3.72) <sup>b</sup>	3.87 (3.55, 4.15)	3.31 (3.07, 3.57)
	5	3.53 (3.37, 3.71)	3.26 (3.05, 3.48) <sup>b</sup>	3.92 (3.68, 4.15)	3.31 (3.12, 3.51)
	7	3.60 (3.10, 4.20)	3.62 (3.24, 4.04) <sup>a,b</sup>	4.00 (3.52, 4.53)	3.44 (2.96, 3.92)
	8	3.44 (3.12, 3.75)	3.53 (3.26, 3.80) <sup>b</sup>	3.97 (3.64, 4.30)	3.34 (2.96, 3.65)
	9	NA	3.99 (3.50, 4.57) <sup>a</sup>	NA	NA
AGE	1	3.03 (2.75, 3.37) <sup>c</sup>	3.55 (3.21, 3.83) <sup>a,b</sup>	4.06 (3.74, 4.37) <sup>a</sup>	3.17 (2.88, 3.52) <sup>b</sup>
	2	3.47 (3.21, 3.70) <sup>b</sup>	3.64 (3.29, 3.94) <sup>a</sup>	3.78 (3.49, 4.06) <sup>a,b</sup>	3.47 (3.21, 3.71) <sup>a,b</sup>
	3	3.42 (3.17, 3.68) <sup>b</sup>	3.61 (3.27, 3.98) <sup>a,b</sup>	3.72 (3.40, 4.05) <sup>b</sup>	3.62 (3.33, 3.88) <sup>a</sup>
	4	3.55 (3.29, 3.83) <sup>a,b</sup>	3.80 (3.44, 4.16) <sup>a</sup>	4.02 (3.69, 4.33) <sup>a,b</sup>	3.47 (3.16, 3.74) <sup>a,b</sup>
	5	3.60 (3.31, 3.90) <sup>a,b</sup>	3.28 (2.87, 3.64) <sup>b</sup>	3.93 (3.56, 4.26) <sup>a,b</sup>	3.56 (3.20, 3.85) <sup>a</sup>

Table 5.7: Estimated marginal means and highest posterior density (HPD; lowest and highest in parentheses) for type of birth (TB), type of rearing (TR), ewe’s dam’s type of birth (DTB), ewe’s dam’s type of rearing (DTR) and ewe’s dam’s age (AGE) within breeds when only including additive and dominance genetic variance in the model (continued).

Effect	Level	Breeds			
		Columbia	Polypay	Rambouillet	Targhee
AGE	6	3.54 (3.23, 3.87) <sup>a,b</sup>	3.63 (3.24, 4.06) <sup>a,b</sup>	3.92 (3.55, 4.29) <sup>a,b</sup>	3.69 (3.33, 3.99) <sup>a</sup>
	7	3.86 (3.50, 4.25) <sup>a</sup>	3.56 (3.07, 4.01) <sup>a,b</sup>	3.98 (3.60, 4.42) <sup>a,b</sup>	3.60 (3.23, 3.96) <sup>a</sup>

<sup>1</sup>Levels: USSES code description for rearing type (TR and DTR) include: 0 – born a quadruplet or quintuplet, weaned any number, minor category; 1 – born single, weaned single; 2 – born single, raised orphan; 3 – born twin, raised single (major) or born single, raised twin (minor); 4 – born twin, raised orphan; 5 – born twin, raised twin; 6 – born triplet, raised orphan; 7 – born triplet, raised single; 8 – born triplet, raised twin; and 9 – born triplet raised triplet. NA: Not available.

<sup>a,b,c</sup>Means with different superscripts have evidence based on HPD that they differ ( $P < 0.05$ )

**CHAPTER 6: MODEL EXPLORATION FOR STAYABILITY USING BAYESIAN  
ANALYSIS**

**Priors used**

Building off of modeling procedures described for longevity in Chapter 5, the priors used to run multivariate and univariate stayability analyses are shown in Table 6.1. The idea behind using different priors for stayability and longevity stemmed from the fact that they are different traits following different family distributions. The family distribution used to run the models was the “threshold” family distribution, this is because the response variable is binary (successful lambing (1) after the defined stayability cutoff date (e.g., seven years) or failure (0), not lambing in the designated stayability cutoff date).

Table 6.1: Priors used to run stayability

<b>Model</b>	<b>Prior</b>	<b>Family</b>	<b>Type of run</b>
Additive	list(R=list(V=diag(6),nu=6, fix=0),G=list(G1=list(V=diag(6), nu=6), G2=list(V=diag(6), nu=6), G3=list(V=diag(6), nu=6)))	Threshold	Multivariate
Additive	list(G=list(G1=list(V=1,nu=1000), G3=list(V=1,nu=1000), G3=list(V=1,nu=1000)),R = list(V =1, nu =1000))	Threshold	Univariate
Dominance	list(R=list(V=diag(6),nu=6, fix=0),G=list(G1=list(V=diag(6), nu=6), G2=list(V=diag(6), nu=6), G3=list(V=diag(6), nu=6), G4=list(V=diag(6), nu=6)))	Threshold	Multivariate
Dominance	list(G=list(G1=list(V=1,nu=1000), G3=list(V=1,nu=1000), G3=list(V=1,nu=1000), G4=list(V=1,nu=1000)),R = list(V =1, nu =1000))	Threshold	Univariate

## Summary of additive (A) and additive and dominance stayability Bayesian models

Models were run in multivariate and univariate analyses using *MCMCglmm* to explore the within and across breed datasets. All models followed effects outlined for longevity in Chapter 5, including random effects of ID with pedigree (additive genetic variance), birth year effect (BYR), and maternal permanent environment (MPE). These models also used the same chain and iteration criteria previously discussed for longevity (additive genetic only model: 10 chains, 10,000 iterations, 1,000 burn-in, and 90 thinning interval; additive and dominance genetic model: 10 chains, 20,000 iterations, 11,000 burn-in, and 90 thinning interval). The *MCMCglmm* summary presented below is for stayability to age seven (7) only (Tables 6.2 and 6.3). The R codes used to run stayability models are presented in Appendix B. The effective sample sizes for all fixed and random effects exceeded the recommended value of 1000 and the autocorrelation values for both the random and fixed effects were less than 0.1. Figures 6.1 and 6.2 provide examples showing that all chains achieved convergence via the criterion of Geweke (1992).

Table 6.2: Summary statistics of *MCMCglmm* models by breeds for univariate additive stayability to age seven models.

Statistics <sup>1</sup>	Breeds				
	Across <sup>2</sup>	Columbia	Polypay	Rambouillet	Targhee
<b>Effective sample size</b>					
Intercept	1,064.6	1,000	1,000	1,000	874.7
STM	1,000	--	--	--	--
AGE	1,000	1,000	1,000	1,000	910.3
TB	1,000	1,000	1,261.7	1,000	871.7
TR	1,000	1,000	892.8	1,000	1,000
DTB	1,000	1,151	1,000	1,000	1,092.9
DTR	1,000	1,000	1,000	1,026	1,000
ID	1,000	843.1	1,000	1,000	1,000
MPE	1,148	1,000	1,000	1,000	1,000
BYR	648.5	1,000	1,000	1,000	1,000
R	1,000	839.8	1,000	1,000	1,000
<b>Autocorrelation</b>					
Intercept	0.0337	-0.0041	-0.0173	-0.0023	0.0151
STM	0.0372	--	--	--	--
AGE	0.0133	-0.0232	-0.0069	-0.0351	0.0071
TB	0.0264	-0.0191	0.0547	0.0245	-0.0011
TR	0.0025	0.0373	-0.0401	0.0200	-0.0231
DTB	-0.0020	-0.0085	0.0122	-0.0461	-0.0449
DTR	-0.0113	-0.0046	0.0306	-0.0126	-0.0128
ID	0.0163	0.0846	<0.0001	-0.0060	0.0007
MPE	-0.0023	-0.0364	-0.0047	-0.0413	-0.0127
BYR	0.0499	0.0071	0.0324	-0.0100	-0.0084
R	-0.0184	0.0484	-0.0415	-0.0251	-0.0026
<b>DIC</b>	<b>6,698.27</b>	<b>1,255.46</b>	<b>1,641.1</b>	<b>2,177</b>	<b>1,562.71</b>
<b>Variance Estimate</b>					
ID	1.01	1.00	1.01	1.01	1.00
MPE	0.92	0.99	0.97	0.96	0.99
BYR	0.98	0.98	0.99	0.99	0.98
R	1.14	1.03	1.05	1.06	1.05
P	4.05	4.00	4.02	4.02	4.02

The models were ran with univariate threshold prior coded as `list(G=list(G1=list(V=1,nu=1000), G3=list(V=1,nu=1000), G3=list(V=1,nu=1000)),R = list(V=1, nu =1000))` using 10,000 iterations, burn-in of 1,000, thinning interval of 90, resulting in an expected effective sample size of 1,000 per breed parameter. <sup>1</sup>Model effects could include fixed effects of intercept (mean), Age of ewe (AGE), ewe birth type (TB), ewe rear type (TR), ewe's dam's birth type (DTB), ewe's dam's rear type (DTR) and random effects of individual ewe (ID) with relationship matrix (additive genetic variance), ewe's dam ID without pedigree (maternal permanent environmental variance), birth year (BYR), residual (R) variance, and phenotypic variance (P). The DIC is the deviance information criterion. <sup>2</sup>Across population consisted of purebreds from Columbia, Polypay, Rambouillet, and Targhee and related crossbreds of Friesian, Dorper, Texel, Finnsheep, Dorset, Romanov, and a USMARC-Composite developed in the 1970s.

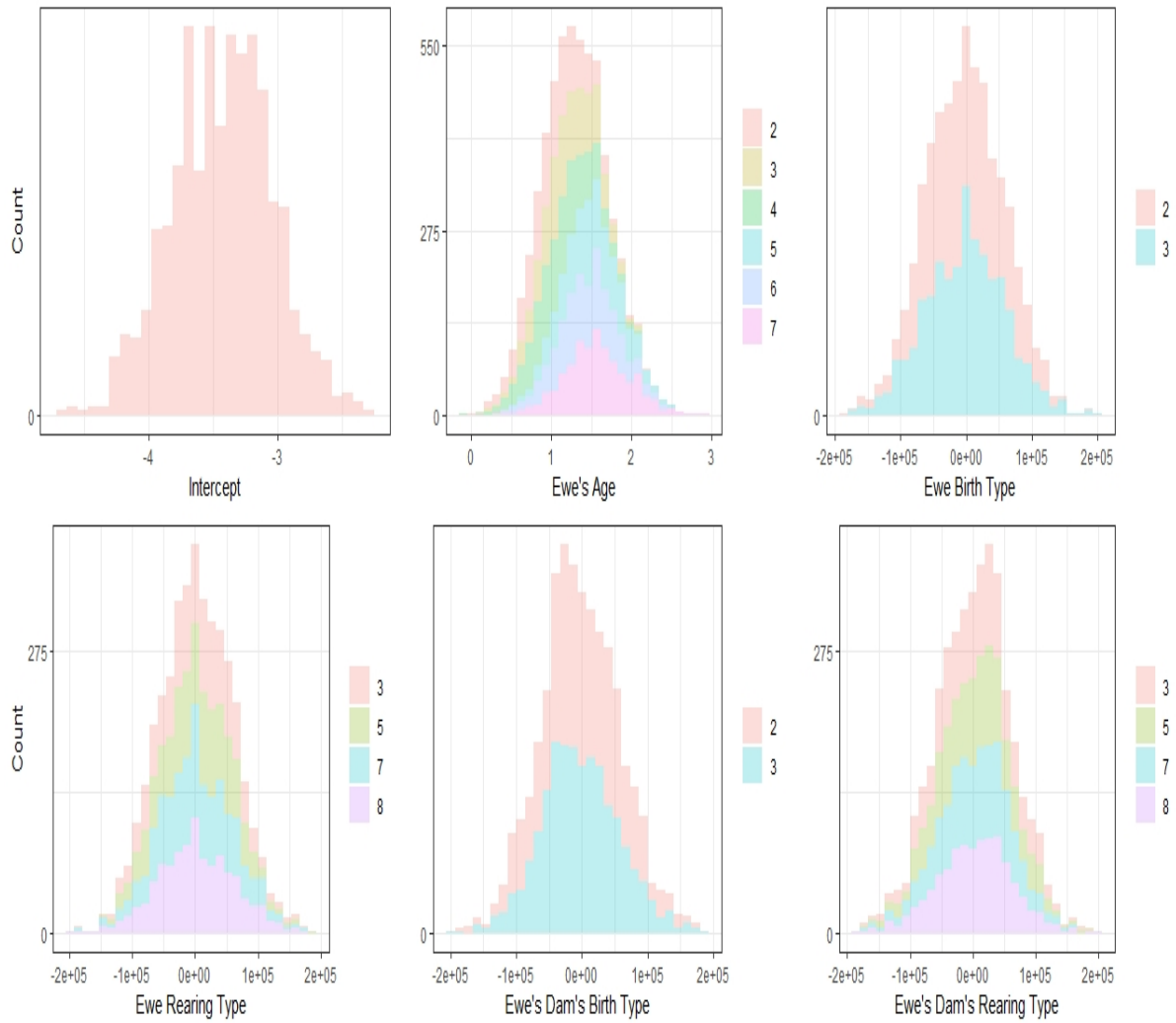


Figure 6.1: Density plots of posterior estimates for fixed effects using Columbia longevity dataset when modeling additive genetic variance only using a multiple chain MCMC model. Density distributions should appear normal or bell-shaped to indicate proper mixing and convergence in the analysis was met.

## Summary of additive + dominance stayability univariate Bayesian models

Table 6.3: Summary statistics of additive and dominance univariate stayability to age seven models

Statistics <sup>1</sup>	Breeds				
	Across <sup>2</sup>	Columbia	Polypay	Rambouillet	Targhee
Effective sample size					
Intercept	1,000	1,000	1,000	1,000	1,000
STM	1,000	--	--	--	--
AGE	1,076	1,000	1,000	1,230	1,072.6
TB	1,139	1,141.7	910.9	1,000	959.9
TR	1,000	1,000	1,000	1,000	1,000
DTB	1,000	891.5	794.2	1,175	1,000
DTR	1,000	1,000	1,000	1,000	1,000
ID	1,000	1,000	1,000	1,000	1,000
ID2	1,000	1,000	1,000	1,000	1,000
MPE	1,000	1,000	1,000	1,000	1,000
BYR	1,000	1,000	1,000	1,000	1,000
R	1,000	1,000	1,000	783.7	1,000
Autocorrelation					
Intercept	-0.0008	0.0026	-0.0131	-0.0156	0.0235
STM	-0.0764	--	--	--	--
AGE	-0.0210	0.0568	0.0001	-0.0495	0.0222
TB	-0.0652	-0.0666	-0.0081	-0.0011	0.0004
TR	0.0224	0.0187	0.0256	0.0126	0.0499
DTB	0.0052	0.0568	0.0146	0.0458	-0.0069
DTR	0.0140	-0.0038	0.0376	-0.0324	0.0002
ID	0.0275	-0.0035	-0.0362	0.0114	-0.0089
ID2	0.0135	-0.0418	-0.0432	0.0217	0.0342
MPE	0.0201	0.0341	-0.0361	-0.0211	0.0129
BYR	0.0212	-0.0049	0.0103	-0.0223	0.0349
R	0.0265	0.0214	-0.0157	-0.0030	-0.0207
DIC	5,875.81	1,129.35	1,478.16	1,973.84	1,403.68
Variance Estimate					
ID	0.97	1.00	1.00	1.00	0.99
ID2	1.06	1.02	1.02	1.03	1.02
MPE	0.95	1.00	0.98	0.97	0.99
BYR	0.98	0.98	0.99	0.99	0.98
R	1.07	1.01	1.03	1.05	1.02
P	5.03	5.01	5.02	5.04	5.00

The models were ran with univariate threshold prior coded as list(G=list(G1=list(V=1,nu=1000), G3=list(V=1,nu=1000), G3=list(V=1,nu=1000)), R=list(V=1, nu=1000)) using 20,000 iterations, burn-in of 11,000, thinning interval of 90, resulting in an expected effective sample size of 1,000 per breed parameter. <sup>1</sup>Model effects could include fixed effects of intercept (mean), Age of ewe (AGE), ewe birth type (TB), ewe rear type (TR), ewe's dam's birth type (DTB), ewe's dam's rear type (DTR) and random effects of individual ewe (ID) with relationship matrix (additive genetic variance), individual ewe (ID2) with relationship matrix (dominance genetic variance), ewe's dam ID without pedigree (maternal permanent environmental variance), birth year (BYR), residual (R) variance, and phenotypic variance (P). The DIC is the deviance information criterion. <sup>2</sup>Across population consisted of purebreds from Columbia, Polypay, Rambouillet, and Targhee and related crossbreds of Friesian, Dorper, Texel, Finnsheep, Dorset, Romanov, and a USMARC-Composite developed in the 1970s.

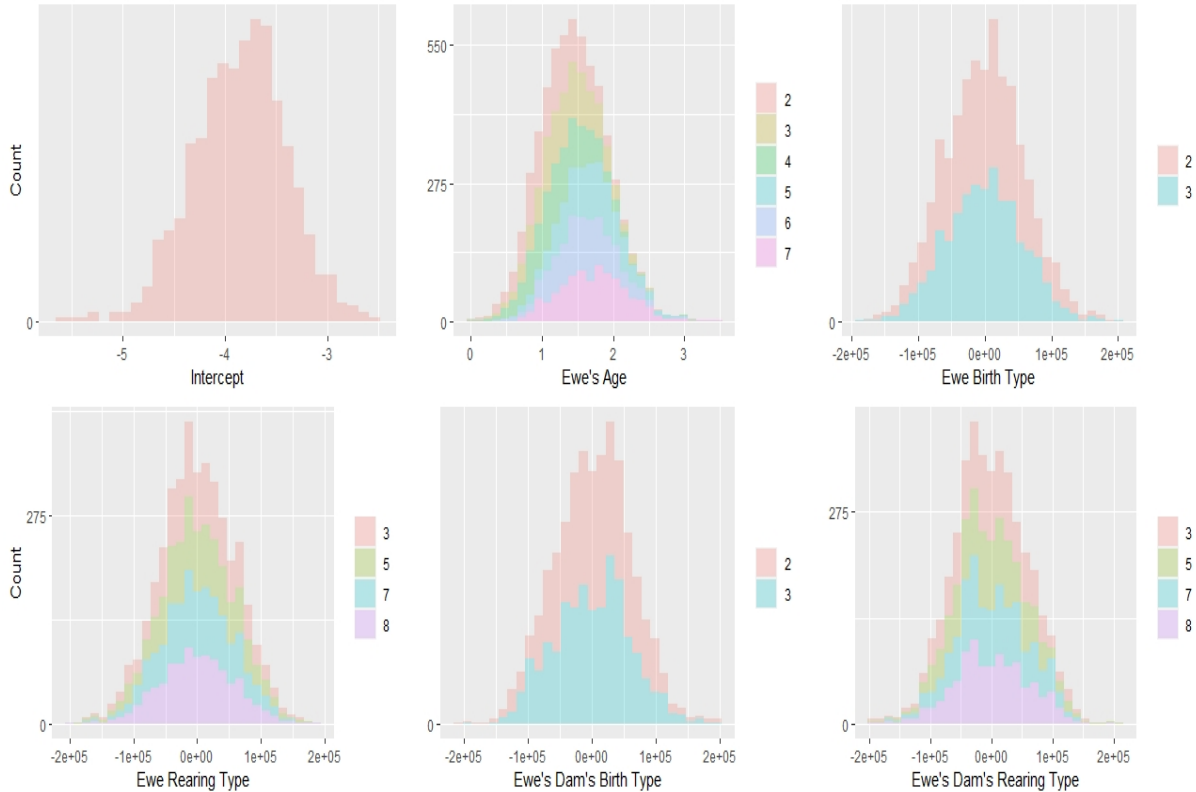


Figure 6.2: Density plots of posterior estimates for fixed effects using Columbia longevity dataset when modeling additive genetic variance and dominance genetic variance when using a multiple MCMC chain. Density distributions should appear normal or bell-shaped to indicate proper mixing and convergence in the analysis was met.

## Genetic parameters

### Estimates of heritability for models

Estimates of heritability for within breeds analyses using a multivariate Bayesian model were lower for Polypay ewe stayability to different ages than other breeds (Table 6.4). Estimates for stayability across breeds for the dominance model were not estimated because of computational demands. The values obtained for A models are lower than those reported by Martinez et al. (2005), where a heritability estimate of  $0.30 \pm 0.14$  for the ability of a female to remain in the flock until six years of age was observed. These estimates recorded are similar to that of Borg et al. (2009) in their single-trait evaluations experiment for stayability, which ranged from 0.00 to 0.09 for stayability 5|2 to 6|5. These estimates of stayability were equally lower than those recorded for



Columbia, Polypay, Rambouillet, and Targhee by Holland (2018). Conington et al. (2001) reported a heritability estimate of 0.08 similar to our additive model estimates for removal from the flock in Scottish Blackface hill sheep. Brash et al. (1994) reported a heritability estimate of 0.06 for age at last breeding in an Australian Dorset flock. These estimates for heritability for the additive model are similar to that of Lee et al. (2015) when they reported heritability estimates for commercial New Zealand flock for STAY3 to STAY6 ranging from 0.048 to 0.082. Lower heritability values have equally been reported for stayability in other species; Hudson and Van Vleck (1981) reported heritability estimates ranging from 0.02 to 0.05 using a linear model in Holstein cows for stayability of 36 to 84 months of age, respectively. Doormaal et al. (1984) reported low heritability estimates for stayability to 42, 54, 66, and 78 months of total life for Canadian Holsteins which were 0.051, 0.040, 0.045, and 0.059, respectively. Stayability in Large White and Landrace sows evaluated by Lopez-Serrano et al. (2000) were reported to be 0.07 and 0.11 before culling. Estimates of heritability for additive univariate models for stayability to age seven (7) were similar to those reported by Holland (2018) for STAY6 for within breeds and across breeds (Table 6.5). The heritability estimates reported for additive models (Table 6.5) are similar to those reported by Quiroz et al. (2007) in their experiment on Caracu cows whose heritability estimates were 0.28, 0.27, and 0.23 for stayability to 48, 60, and 72 months, respectively. Heritability estimates of a similar proportion to those reported in this present study were observed for beef cattle; in Nellore cattle, Van Melis et al. (2007) reported a heritability estimate of 0.28 for stayability to age seven (Table 6.5). Estimates of heritability for dominance multivariate models are not yet reported. Inclusion of dominance genetic effects tends to increase the heritability values (Table 6.5), which supports the assertion that including non-additive genetic effects in genetic evaluation models could improve EBVs and heritability and ultimately lead to better selection

decisions (Aliloo et al. 2016). This shows that stayability is a heritable trait, and when dominance effects are included in the models, the heritability estimates increased (Table 6.5).

Table 6.4: Estimates of heritability and their standard error for an additive model (A) for stayability

<b>Breed</b>	<b>Model</b>	<b>Stayability to age</b>					
		2	3	4	5	6	7
Columbia	A	0.02 ±	0.01 ±	0.02 ±	0.01 ±	0.02 ±	0.03 ±
		0.01	0.008	0.008	0.006	0.01	0.01
Polypay	A	0.02 ±	0.01 ±	0.009 ±	0.009 ±	0.02 ±	0.01 ±
		0.01	0.01	0.007	0.005	0.01	0.01
Rambouillet	A	0.03 ±	0.01 ±	0.007 ±	0.01 ±	0.01 ±	0.02 ±
		0.01	0.007	0.004	0.007	0.009	0.01
Targhee	A	0.03 ±	0.01 ±	0.009 ±	0.009 ±	0.01 ±	0.03 ±
		0.01	0.009	0.005	0.004	0.007	0.02

Table 6.5: Estimates of genetic parameters for Additive (A) models and Additive + Dominance (A+D) Bayesian models for Univariate stayability models with lower and upper confidence intervals in brackets<sup>1</sup>

Group	Model	V <sub>A</sub>	V <sub>D</sub>	V <sub>MPE</sub>	V <sub>BYR</sub>	V <sub>c</sub>	V <sub>P</sub>	h <sup>2</sup>	H <sup>2</sup>	H <sup>2</sup> /h <sup>2</sup>
Across <sup>2</sup>	A only	1.01 (0.93, 1.11)	--	0.92 (0.84, 0.99)	0.98 (0.90, 1.07)	1.14 (1.05, 1.25)	4.05	0.25	--	--
	A + D	0.99 (0.91, 1.08)	0.99 (0.91, 1.07)	0.95 (0.88, 1.03)	0.98 (0.91, 1.08)	1.12 (1.08, 1.22)	5.03	0.20	0.39	1.95
	Ratio	1.02	--	0.97	1.00	1.01	0.80	1.25	--	--
Columbia	A only	1.00 (0.92, 1.09)	--	0.99 (0.91, 1.08)	0.98 (0.91, 1.07)	1.03 (0.93, 1.11)	4.00	0.25	--	--
	A + D	1.00 (0.91, 1.08)	1.02 (0.93, 1.11)	1.00 (0.92, 1.09)	0.98 (0.91, 1.07)	1.01 (0.93, 1.10)	5.01	0.19	0.40	2.11
	Ratio	1.00	--	0.99	1.00	1.02	0.79	1.31	--	--
Polypay	A only	1.01 (0.93, 1.10)	--	0.97 (0.89, 1.06)	0.99 (0.89, 1.07)	1.06 (0.97, 1.15)	4.03	0.25	--	--
	A + D	1.00 (0.92, 1.09)	1.01 (0.92, 1.09)	0.98 (0.90, 1.07)	0.98 (0.91, 1.08)	1.05 (0.95, 1.14)	5.02	0.19	0.40	2.11
	Ratio	1.01	--	0.98	1.01	1.00	0.81	1.25	--	--
Rambouillet	A only	1.01 (0.93, 1.10)	--	0.96 (0.88, 1.05)	0.99 (0.91, 1.08)	1.06 (0.97, 1.16)	4.02	0.25	--	--
	A + D	1.00 (0.92, 1.09)	1.03 (0.94, 1.11)	0.97 (0.88, 1.05)	0.99 (0.91, 1.08)	1.03 (0.94, 1.12)	5.02	0.19	0.40	2.11
	Ratio	1.01	--	0.99	1.00	1.03	0.80	1.33	--	--
Targhee	A only	1.00 (0.91, 1.09)	--	0.99 (0.89, 1.08)	0.98 (0.91, 1.07)	1.05 (0.96, 1.15)	4.02	0.25	--	--
	A + D	0.99 (0.91, 1.09)	1.02 (0.93, 1.11)	0.99 (0.92, 1.08)	0.98 (0.91, 1.07)	1.02 (0.94, 1.11)	5.00	0.20	0.40	2.00
	Ratio	1.01	--	1.00	1.00	1.03	0.80	1.25	--	--

<sup>2</sup>Across population consisted of purebreds from Columbia, Polypay, Rambouillet, and Targhee and related crossbreds of Friesian, Dorper, Texel, Finnsheep, Dorset, Romanov, and a USMARC-Composite developed in the 1970s

## **Genetic correlation**

The genetic correlation values reported (Table 6.6) are similar to the findings of Hudson and Van Vleck (1981). Estimates of genetic correlation for stayability to age two (2) to stayability to age seven (7) ranged from 0.004 to 0.16 for Columbia, -0.003 to 0.32 for Polypay, -0.03 to 0.21 for Rambouillet, -0.09 to 0.19 for Targhee, and 0.37 to 0.59 for Across breed, for additive multivariate model. Our study suggests that selection of ewes on a stayability basis will have a positive response in improvement for stayability because moderate genetic correlation with stayability to ages 6 and 7 was observed for Columbia (0.19 to 0.24), Polypay (0.18 to 0.30), Rambouillet (0.13 to 0.31), Targhee (0.11 to 0.21) and for across breeds (0.60 to 0.64) for additive models. This means that selecting either of these breeds will result in selecting improvements in stayability despite how long it takes to achieve genetic progress because it takes a longer time to achieve due to the low heritability estimates associated with stayability (Table 6.5) our research is novel because there is a dearth in the sheep literature on stayability studies for comparison.

Table 6.6: Genetic correlation for stayability to age for within breeds for additive (A) multivariate models

Breed	Stayability to age							Model
	2	3	4	5	6	7		
Columbia	2	-	0.16	0.06	0.08	0.15	0.04	A
	3	0.16	-	0.21	0.09	0.08	0.06	
	4	0.06	0.21	-	0.24	0.08	0.11	
	5	0.08	0.09	0.24	-	0.25	0.19	
	6	0.15	0.08	0.08	0.25	-	0.24	
	7	0.004	0.06	0.11	0.19	0.24	-	
	Polypay	2	-	0.32	0.15	0.06	-0.04	
3		0.32	-	0.27	0.09	0.05	0.06	
4		0.15	0.27	-	0.20	0.13	0.15	
5		0.06	0.09	0.20	-	0.27	0.18	
6		-0.04	0.05	0.13	0.27	-	0.30	
7		-0.03	0.06	0.15	0.18	0.30	-	
Rambouillet		2	-	0.21	0.09	0.02	0.01	-0.03
	3	0.21	-	0.27	0.07	0.07	0.06	
	4	0.09	0.27	-	0.16	0.08	0.04	
	5	0.02	0.07	0.16	-	0.29	0.13	
	6	0.01	0.07	0.08	0.29	-	0.31	
	7	-0.03	0.06	0.04	0.13	0.31	-	
	Targhee	2	-	0.19	0.09	0.04	-0.05	-0.09
3		0.19	-	0.22	0.12	-0.009	-0.011	
4		0.09	0.22	-	0.20	0.09	-0.03	
5		0.04	0.12	0.20	-	0.17	0.11	
6		-0.05	-0.009	0.09	0.17	-	0.21	
7		-0.09	-0.011	-0.03	0.11	0.21	-	
<sup>1</sup> Across		2	-	0.59	0.52	0.47	0.43	0.37
	3	0.59	-	0.66	0.58	0.54	0.49	
	4	0.52	0.66	-	0.67	0.60	0.55	
	5	0.47	0.58	0.67	-	0.68	0.60	
	6	0.43	0.54	0.60	0.68	-	0.64	
	7	0.37	0.49	0.55	0.60	0.64	-	

<sup>1</sup>Across population consisted of purebreds from Columbia, Polypay, Rambouillet, and Targhee and related crossbreds of Friesian, Dorper, Texel, Finnsheep, Dorset, Romanov, and a USMARC-Composite developed in the 1970s.

## **Estimated marginal means**

The estimated marginal means presented in Tables 6.7 and 6.8 are on a per breed basis and none from the across breed analysis. The estimated marginal means obtained for the univariate stayability to age seven (7) were log-transformed using the “logit” function of the *emmeans* R package (Lenth, 2016) (Appendix E). The highest posterior density (HPD) is used to determine significant differences between two comparison groups as obtained in the longevity model (Hespanhol et al., 2019). Furthermore, the inclusion of additive only or additive and dominance genetic effects did not impact differences found among fixed effects. Based on this, no estimated marginal means were different from each other for birth type in any breed (Tables 6.7 and 6.8). It is evident that breeds often had very different estimated marginal means per effect, even though across breed effects are not reported. Therefore, other significant effects are broken down by breed.

### ***Columbia***

Only age of dam was significant to stayability at age seven for Columbia ewes; noticeably, ewes that were lambed by first time dams recorded lower stayability to age seven value from the rest of the group. There was an observable increasing trend of stayability values as we move from dams that lambed for the first time to those that lambed for the seventh time.

### ***Polypay***

Ewes’ dams’ type of rearing affected stayability to age seven in Polypay ewes. Ewes’ dams’ that were born as triplets and raised as triplets were significantly different from those born as triplets and raised as twins. Ewes’ dams’ that were born as triplets and raised as orphans had the lowest value for stayability to age seven. Dams that lambed for the fourth and sixth times had the highest value for stayability to age seven and were significantly different from the rest of the group.

### ***Rambouillet***

Only ewes' dams' type of rearing impacted stayability to age seven in Rambouillet ewes; ewes' dams' that were born as triplets and raised as singles had the highest value for stayability to age seven and were highly significant to the rest of the rearing groups.

### ***Targhee***

Ewes' dams' type of rearing and age of dam impacted stayability to age seven in Targhee ewes; ewes' dams' that were born as triplets and raised as singles had the highest value for stayability to age seven and were highly significant to the rest of the rearing groups and ewes that were lambled by first time dams recorded the lowest value for stayability to age seven (7).

Conclusively, stayability to age seven is impacted by age of the dam at lambing, ewes' dams' type of birth, and ewe's dams' type of rearing in Columbia, Polypay, Rambouillet and Targhee ewes which suggests that proper record keeping should be maintained by the producers. There is not a lot of research done on estimating the impact of ewe's type of birth, ewe's type of rearing, ewes' dams' type of birth, ewes' dams' type of rearing and age of dam on stayability to age seven (7) in Columbia, Polypay, Rambouillet and Targhee ewes so we could not compare our research work to other research works.

Table 6.7: Estimated marginal means mean estimates for all breeds and their highest posterior densities (HPD) for univariate additive (A) models for stayability to age seven (7).

Effect	Level	Breeds			
		Columbia	Polypay	Rambouillet	Targhee
TB	1	0.11 (0.07, 0.16)	0.14 (0.08, 0.21)	0.14 (0.09, 0.20)	0.11 (0.07, 0.15)
	2	0.10 (0.06, 0.15)	0.12 (0.08, 0.17)	0.15 (0.09, 0.21)	0.09 (0.06, 0.13)
	3	0.08 (0.05, 0.13)	0.10 (0.06, 0.16)	0.15 (0.09, 0.22)	0.10 (0.05, 0.15)
TR	1	0.11 (0.07, 0.16)	0.14 (0.09, 0.21)	0.14 (0.09, 0.20)	0.11 (0.07, 0.15)
	3	0.12 (0.06, 0.17)	0.09 (0.05, 0.14)	0.14 (0.08, 0.21)	0.09 (0.05, 0.13)
	5	0.09 (0.06, 0.14)	0.14 (0.09, 0.19)	0.15 (0.11, 0.21)	0.10 (0.06, 0.14)
	7	0.07 (0.03, 0.12)	0.12 (0.07, 0.20)	0.16 (0.09, 0.26)	0.09 (0.03, 0.16)
	8	0.09 (0.05, 0.15)	0.12 (0.07, 0.18)	0.14 (0.09, 0.22)	0.09 (0.05, 0.16)
	9	NA	0.08 (0.04, 0.16)	NA	NA
DTB	1	0.09 (0.05, 0.14)	0.13 (0.07, 0.19)	0.13 (0.08, 0.19)	0.11 (0.07, 0.16)
	2	0.10 (0.06, 0.16)	0.13 (0.07, 0.19)	0.13 (0.08, 0.19)	0.10 (0.07, 0.15)
	3	0.12 (0.06, 0.18)	0.17 (0.09, 0.25)	0.15 (0.09, 0.23)	0.12 (0.05, 0.18)
DTR	1	0.09 (0.05, 0.13)	0.11 (0.07, 0.16) <sup>b,c</sup>	0.14 (0.08, 0.19) <sup>b</sup>	0.09 (0.07, 0.15) <sup>b</sup>
	3	0.11 (0.06, 0.16)	0.14 (0.08, 0.21) <sup>b</sup>	0.13 (0.08, 0.19) <sup>b</sup>	0.09 (0.06, 0.14) <sup>b</sup>
	5	0.08 (0.05, 0.13)	0.08 (0.06, 0.13) <sup>c</sup>	0.15 (0.09, 0.21) <sup>b</sup>	0.09 (0.05, 0.12) <sup>b</sup>
	7	0.11 (0.04, 0.21)	0.15 (0.07, 0.23) <sup>a,b</sup>	0.19 (0.08, 0.30) <sup>a</sup>	0.13 (0.05, 0.23) <sup>a</sup>
	8	0.11 (0.06, 0.16)	0.11 (0.07, 0.16) <sup>b,c</sup>	0.14 (0.08, 0.20) <sup>b</sup>	0.09 (0.04, 0.15) <sup>b</sup>
	9	NA	0.19 (0.08, 0.31) <sup>a</sup>	NA	NA
AGE	1	0.04 (0.014, 0.06) <sup>b</sup>	0.14 (0.08, 0.21)	0.14 (0.08, 0.21)	0.06 (0.04, 0.10) <sup>b</sup>
	2	0.09 (0.05, 0.15) <sup>a</sup>	0.15 (0.09, 0.21)	0.12 (0.07, 0.18)	0.11 (0.06, 0.16) <sup>a</sup>
	3	0.12 (0.07, 0.17) <sup>a</sup>	0.15 (0.08, 0.22)	0.13 (0.08, 0.20)	0.11 (0.07, 0.17) <sup>a</sup>
	4	0.10 (0.05, 0.16) <sup>a</sup>	0.16 (0.09, 0.25)	0.15 (0.09, 0.22)	0.11 (0.07, 0.16) <sup>a</sup>
	5	0.15 (0.08, 0.22) <sup>a</sup>	0.11 (0.06, 0.17)	0.16 (0.09, 0.23)	0.11 (0.07, 0.18) <sup>a</sup>
	6	0.14 (0.07, 0.22) <sup>a</sup>	0.17 (0.09, 0.25)	0.13 (0.08, 0.21)	0.13 (0.07, 0.20) <sup>a</sup>



Table 6.7: Estimated marginal means mean estimates for all breeds and their highest posterior densities (HPD) for univariate additive (A) models for stayability to age seven (7) (continued).

		<b>Breeds</b>			
Effect	Level	Columbia	Polypay	Rambouillet	Targhee
AGE	7	0.15 (0.08, 0.25) <sup>a</sup>	0.12 (0.06, 0.21)	0.12 (0.06, 0.20)	0.14 (0.08, 0.22) <sup>a</sup>

<sup>1</sup>Levels: TB and DTB represent ewe's or ewe's dams being born a single (1), twin (2), triplets (3), and quadruplets or higher (4). TR and DTR represent ewes or ewe's dam's born a quadruplet or quintuplet and weaned as any number (0), born single, weaned as single (1), born single and raised as an orphan (2), born as twin raised single (major) or born single and raised as a twin (minor) (3), born twin, raised orphan (4), born twin, raised twin (5), born triplet raised orphan (6), born triplet raised single (7), born triplet raised twin (8) and born triplet raised triplet (9).

NA: Not available.

<sup>a,b,c</sup>Means with different superscripts have evidence based on HPD that they differ ( $P < 0.05$ )

Table 6.8: Estimated marginal means mean estimates for all breeds and their highest posterior densities (HPD) for univariate additive and dominance (A+D) models for stayability to age seven (7).

		<b>Breeds</b>			
Effect	Level	Columbia	Polypay	Rambouillet	Targhee
TB	1	0.08 (0.05, 0.13)	0.12 (0.06, 0.17)	0.11 (0.06, 0.16)	0.08 (0.05, 0.12)
	2	0.08 (0.06, 0.13)	0.09 (0.05, 0.13)	0.11 (0.07, 0.16)	0.07 (0.04, 0.01)
	3	0.06 (0.04, 0.10)	0.08 (0.05, 0.13)	0.12 (0.07, 0.18)	0.07 (0.03, 0.11)
TR	1	0.08 (0.05, 0.13)	0.12 (0.06, 0.17)	0.11 (0.06, 0.16)	0.08 (0.05, 0.12)
	3	0.09 (0.05, 0.15)	0.07 (0.03, 0.12)	0.11 (0.06, 0.16)	0.06 (0.03, 0.01)
	5	0.07 (0.04, 0.11)	0.11 (0.07, 0.16)	0.12 (0.07, 0.17)	0.07 (0.04, 0.10)
	7	0.05 (0.02, 0.09)	0.01 (0.05, 0.17)	0.13 (0.06, 0.22)	0.06 (0.03, 0.13)
	8	0.08 (0.04, 0.13)	0.01 (0.06, 0.15)	0.11 (0.06, 0.17)	0.07 (0.03, 0.11)
	9	NA	0.06 (0.02, 0.13)	NA	NA
DTB	1	0.07 (0.04, 0.11)	0.10 (0.06, 0.17)	0.01 (0.06, 0.15)	0.08 (0.05, 0.12)
	2	0.08 (0.05, 0.12)	0.11 (0.06, 0.16)	0.01 (0.06, 0.15)	0.07 (0.04, 0.10)
	3	0.09 (0.04, 0.16)	0.14 (0.08, 0.22)	0.12 (0.06, 0.19) <sup>a</sup>	0.09 (0.03, 0.14)
DTR	1	0.06 (0.04, 0.01)	0.08 (0.05, 0.14) <sup>b</sup>	0.10 (0.07, 0.16) <sup>b</sup>	0.07 (0.04, 0.11)
	3	0.09 (0.05, 0.14)	0.11 (0.06, 0.17) <sup>b</sup>	0.01 (0.05, 0.15)	0.06 (0.04, 0.10)
	5	0.07 (0.04, 0.01)	0.07 (0.04, 0.10)	0.12 (0.08, 0.17) <sup>b</sup>	0.06 (0.04, 0.09)
	7	0.09 (0.03, 0.18)	0.12 (0.06, 0.21) <sup>b</sup>	0.16 (0.08, 0.28) <sup>a</sup>	0.09 (0.03, 0.18)
	8	0.08 (0.04, 0.14)	0.09 (0.05, 0.13)	0.10 (0.05, 0.16) <sup>b</sup>	0.07 (0.03, 0.12)
	9	NA	0.16 (0.07, 0.30) <sup>a</sup>	NA	NA
AGE	1	0.02 (0.009, 0.05)	0.12 (0.06, 0.18) <sup>b</sup>	0.11 (0.06, 0.17) <sup>b</sup>	0.04 (0.02, 0.07)
	2	0.07 (0.04, 0.12)	0.12 (0.07, 0.19) <sup>b</sup>	0.09 (0.05, 0.14)	0.08 (0.05, 0.12)
	3	0.09 (0.05, 0.14)	0.12 (0.07, 0.20) <sup>b</sup>	0.10 (0.06, 0.16) <sup>b</sup>	0.09 (0.05, 0.13)
	4	0.08 (0.04, 0.13)	0.14 (0.07, 0.22) <sup>b,a</sup>	0.11 (0.06, 0.17) <sup>b</sup>	0.08 (0.04, 0.13)
	5	0.12 (0.06, 0.19) <sup>a</sup>	0.08 (0.04, 0.14) <sup>c</sup>	0.12 (0.07, 0.20) <sup>a</sup>	0.08 (0.04, 0.13)
	6	0.11 (0.06, 0.18) <sup>a,b</sup>	0.14 (0.06, 0.22) <sup>a</sup>	0.10 (0.05, 0.16) <sup>b</sup>	0.09 (0.05, 0.15)
	7	0.12 (0.06, 0.21) <sup>a</sup>	0.01 (0.04, 0.17) <sup>c</sup>	0.09 (0.05, 0.16)	0.11 (0.06, 0.19) <sup>a</sup>

<sup>1</sup>Levels: TB and DTB represent ewe's or ewe's dams being born a single (1), twin (2), triplets (3), and quadruplets or higher (4). TR and DTR represent ewes or ewe's dam's born a quadruplet or quintuplet and weaned as any number (0), born single, weaned as single (1), born single and raised as an orphan (2), born as twin raised single (major) or born single and raised as a twin (minor) (3), born twin, raised orphan (4), born twin, raised twin (5), born triplet raised orphan (6), born triplet raised single (7), born triplet raised twin (8) and born triplet raised triplet (9).

NA: Not available.

<sup>a,b,c</sup>Means with different superscripts have evidence based on HPD that they differ ( $P < 0.05$ ).

### **Limitations to running stayability models**

In analyzing multivariate non-additive models, it is computationally demanding to fit non-additive multivariate Bayesian models as the models take time to analyze and a majority of the time, the computer crashes while analyzing these models. The limitation is that the computational requirements for both models with both additive and non-additive genetic effects are always high since both additive and non-additive relationship matrices are most dense. This requires more powerful computers and more efficient algorithms.

Furthermore, running multivariate analyzes might not be that important for stayability to producers if the end-goal is to select for stayability to age seven (7).

## CHAPTER 7: CONCLUSION

The main goal of genetic selection in breeding programs is to improve economically important traits in the next generation; longevity and stayability are of utmost economic importance to the sheep industry. The current study was based on data from the USDA, ARS, Range Sheep Production Efficiency Research Unit, U.S. Sheep Experiment Station located near Dubois, ID. including Columbia, Polypay, Rambouillet, Targhee, and a combined pool of those breeds.

Recently, scientists have suggested the importance of estimating non-additive genetic effects for complex traits; if additive and non-additive genetic effects are considered together, results obtained tends to yield a higher ability to efficiently partition components of variance for economically important traits in animal breeding (Su et al. 2012; Bolormaa et al. 2015; Lopes et al. 2015). Estimating non-additive genetic effects in breeding models has been shown to reduce bias and overestimation of additive genetic effects (Su et al. 2012). This is why this thesis set out to determine how important non-additive genetic effects are really in estimating longevity and stayability in Columbia, Polypay, Rambouillet, and Targhee breeds as well as if the inclusion of non-additive genetic effects in variance component estimation will improve our understanding of longevity and stayability.

Chapter 4 focused on family statistics where we developed an R package, '*Sibs*' that could be used to organize pedigrees, assign and count generations of individuals in the pedigree, assign siblings to individuals in the pedigree, and output the summary statistics of the inputted pedigree. Chapter 4 is important to our study as it has been suggested in the literature by Van Tassell et al. (2003) that a minimum of 20% full-sibling relationships must be established in the pedigree before

we can estimate non-additive genetic effects which were established for every pedigree used for this analyses.

Chapter 5 investigated the role of including non-additive genetic effects in estimating longevity using a univariate Bayesian model. We discovered that the proportion of phenotypic variance due to dominance models was higher than the proportion of variance due to additive models only across all breeds; we also discovered that incorporating non-additive genetic effects within breeds reduced the proportion of phenotypic variance due to additive genetic effects for longevity in all cases. The heritability estimates observed for dominance models were also higher than that observed for just additive models only which suggests that the inclusion of dominance effects in our models will improve selection for longevity.

In chapter 6, we investigated the role of including non-additive genetic effects in estimating stayability using both univariate and multivariate Bayesian models, we discovered that including dominance effects in univariate models helped to increase our phenotypic variance-ratio and including dominance effects will help to improve selection and increase heritability estimates.

Selecting for longevity and stayability will have a direct impact on the future design and proper planning and implementation of breeding strategies in the sheep industry, which is why including non-additive genetic effects in animal models will help to estimate heritability well and help selection programs in the near future.

In conclusion, it was possible to unravel the estimates of heritability and genetic correlation for additive and non-additive genetic effects for longevity and stayability in the U.S. Western sheep. Bayesian estimates of additive and non-additive genetic variance components were obtained, which can be used as a baseline for defining the type of epistasis that is involved in the longevity and stayability traits in the U.S. Western sheep. Thus, this research emphasizes the need

for a re-examination of our modeling to help understand these methods which will be inevitably incorporated into selection indices in the near future.

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## APPENDIX A: DATA PROCESSING AND FILTERING R SCRIPT

### Script to combine *.dbf* files

```
library(foreign)

#BIRTH WEIGHT DATA
setwd("PATH TO FILES HERE")
temp<- list.files(pattern = ".DBF")

for(i in 1:length(temp)){
  assign(temp[i], read.dbf(temp[i],as.is=TRUE))
  A =
eval(parse(text=paste0(temp[i],"[,c('YR','DAM','DBRD','SIRE','SBRD','AGE','TB','SEX','BRWT'
,'LAMB','LBRD','STM','DISP']"))))
  if(i == 1){
    write.table(A,paste0(getwd(),"/EDLAMB.csv"),quote = FALSE,row.names = FALSE,sep =
",")
  }else{
    write.table(A,paste0(getwd(),"/EDLAMB.csv"),quote = FALSE,row.names = FALSE,sep =
",",col.names=FALSE,append=TRUE)
  }
  print(paste0(i, " ",temp[i]))
}

#WEAN DATA
setwd("PATH TO FILES HERE ")
temp<- list.files(pattern = ".DBF")

for(i in 1:length(temp)){
  assign(temp[i], read.dbf(temp[i],as.is=TRUE))
  A =
eval(parse(text=paste0(temp[i],"[,c('YR','ETAG','LBRD','DAM','DBRD','TBRE','SEX','WNWT','
ADG']"))))
  if(i == 1){
    write.table(A,paste0(getwd(),"/EDWEAN.csv"),quote = FALSE,row.names = FALSE,sep =
",")
  }else{
    write.table(A,paste0(getwd(),"/EDWEAN.csv"),quote = FALSE,row.names = FALSE,sep =
",",col.names=FALSE,append=TRUE)
  }
  print(paste0(i, " ",temp[i]))
}

##EWE PRODUCTIVITY
setwd("PATH TO FILES HERE ")
```



```

temp<- list.files(pattern = ".DBF")

for(i in 1:length(temp)){
  assign(temp[i], read.dbf(temp[i],as.is=TRUE))
  A =
eval(parse(text=paste0(temp[i],"[,c('YR','DAM','DBRD','AGE','STM','LY2','LY3','LY4','LY5','Y
OR')]")))
  if(i == 1){
    write.table(A,paste0(getwd(),"/EDEWEPROD.csv"),quote = FALSE,row.names = FALSE,sep
= ",")
  }else{
    write.table(A,paste0(getwd(),"/EDEWEPROD.csv"),quote = FALSE,row.names = FALSE,sep
= ",",col.names=FALSE,append=TRUE)
  }
  print(paste0(i, " ",temp[i]))
}

##INVENTORY
setwd("PATH TO FILES HERE ")
temp<- list.files(pattern = ".DBF")

for(i in 1:length(temp)){
  assign(temp[i], read.dbf(temp[i],as.is=TRUE))
  A = eval(parse(text=paste0(temp[i],"[,c('YR','ETAG','BRD','SEX','DISP','YRREC')]")))
  if(i == 1){
    write.table(A,paste0(getwd(),"/EDINVENTORY.csv"),quote = FALSE,row.names =
FALSE,sep = ",")
  }else{
    write.table(A,paste0(getwd(),"/EDINVENTORY.csv"),quote = FALSE,row.names =
FALSE,sep = ",",col.names=FALSE,append=TRUE)
  }
  print(paste0(i, " ",temp[i]))
}

```

### **Script to process and edit ewe data for analyses**

```

library(dplyr)
library(foreign)

setwd("PATH TO FILE HERE")
Ped = read.dbf("PEDIGREE.dbf",as.is=TRUE)
#0 is missing, replace as NA
Ped[which(Ped$SIREID==0),"SIREID"]=NA
Ped[which(Ped$DAMID==0),"DAMID"]=NA

lamb = read.table(paste0(getwd(),"/Lamb/EDLAMB.csv"),sep=" ",header=TRUE)

```

```

wean = read.table(paste0(getwd(), "/Wean/EDWEAN.csv"), sep=",", header=TRUE)

sort(unique(lamb$YR))
lamb[which(lamb$YR=="e"), "YR"]="07" #based on dam records in lambing
lamb[which(lamb$YR=="\\"), "YR"]="12" #found in weaning records

##Correcting birth year format in records
lamb[which(as.numeric(lamb$YR)>20), "YR"]=paste0("19", lamb[which(as.numeric(lamb$YR)>
20), "YR"])
lamb[which(as.numeric(lamb$YR)<20), "YR"]=paste0("20", lamb[which(as.numeric(lamb$YR)<
20), "YR"])

#remove lambs missing ear tags
lamb[which(lamb$LAMB=="." | lamb$LAMB==0), "LAMB"]=NA
lamb = lamb[which(!is.na(lamb$LAMB)),]
lamb = lamb[which(!is.na(lamb$LBRD)),]

sort(unique(wean$YR))
##Correcting birth year format in records
wean[which(as.numeric(wean$YR)>20), "YR"]=paste0("19", wean[which(as.numeric(wean$YR)
>20), "YR"])
wean[which(as.numeric(wean$YR)<20 and
as.numeric(wean$YR)>9), "YR"]=paste0("20", wean[which(as.numeric(wean$YR)<20 and
as.numeric(wean$YR)>9), "YR"])
wean[which(as.numeric(wean$YR)<10), "YR"]=paste0("200", wean[which(as.numeric(wean$YR)
<10), "YR"])

#Making lambid in lambing data (nchar is between 4 and 5 for lamb tag, need 4)
lamb[which(nchar(lamb$LAMB)==5), "LAMB"]=substr(lamb[which(nchar(lamb$LAMB)==5), "
LAMB"], 2, 5)
lamb$LAMB=paste0(lamb$YR, lamb$LBRD, lamb$LAMB)

#making lambid in weaning data
wean[which(nchar(wean$LBRD)==1), "LBRD"]=paste0("0", wean[which(nchar(wean$LBRD)==
1), "LBRD"])
wean[which(nchar(wean$ETAG)==5), "ETAG"]=substr(wean[which(nchar(wean$ETAG)==5), "
ETAG"], 2, 5)
wean$LAMBID = paste0(wean$YR, wean$LBRD, wean$ETAG)

#Checking for duplication
lambdup = lamb[which(duplicated(lamb)),]
weandup = wean[which(duplicated(wean)),]

#getting rid of duplications
lamb = lamb[which(!duplicated(lamb)),]

```

```

wean = wean[which(!duplicated(wean)),]

lambcomb = merge(lamb,wean,by="LAMBID",all.x = TRUE)

#cleaning up:
lambcomb =
lambcomb[,c("LAMBID","YR.x","DAM.x","DBRD.x","SIRE","SBRD","AGE","SEX.x","STM
","BRWT","WNWT","ADG","TB","TBRE","DISP")]
colnames(lambcomb) =
c("LAMBID","BYR","DAM","DBRD","SIRE","SBRD","AGE","SEX","STM","BRWT","WN
WT","ADG","TB","TBRE","DISP")
write.table(lambcomb,paste0(getwd(),"/lambcomb.txt"),row.names=FALSE,quote=FALSE)

remove(lamb,wean,lambdup,weandup)

justewes = lambcomb[which(lambcomb$SEX==2 and lambcomb$BYR<=2008),]

#cleaning up sires and dams labeled as "." and "0" to be missing (NA)
justewes[which(justewes$SIRE=="." | justewes$SIRE==0),"SIRE"]=NA
justewes[which(justewes$DAM=="." | justewes$DAM==0),"DAM"]=NA

#Making sure format is consistent
#SIRE
justewes[which(nchar(justewes$SIRE,keepNA=TRUE)==1),"SIRE"]=paste0("000",justewes[wh
ich(nchar(justewes$SIRE,keepNA=TRUE)==1),"SIRE"])
justewes[which(nchar(justewes$SIRE,keepNA=TRUE)==2),"SIRE"]=paste0("00",justewes[whi
ch(nchar(justewes$SIRE,keepNA=TRUE)==2),"SIRE"])
justewes[which(nchar(justewes$SIRE,keepNA=TRUE)==3),"SIRE"]=paste0("0",justewes[whic
h(nchar(justewes$SIRE,keepNA=TRUE)==3),"SIRE"])
justewes[which(nchar(justewes$SIRE,keepNA=TRUE)==5),"SIRE"]=substr(justewes[which(nc
har(justewes$SIRE,keepNA=TRUE)==5),"SIRE"],2,5)
justewes[which(nchar(justewes$SBRD,keepNA=TRUE)==1),"SBRD"]=paste0("0",justewes[wh
ich(nchar(justewes$SBRD,keepNA=TRUE)==1),"SBRD"])

#DAM
justewes[which(nchar(justewes$DAM,keepNA=TRUE)==1),"DAM"]=paste0("000",justewes[w
hich(nchar(justewes$DAM,keepNA=TRUE)==1),"DAM"])
justewes[which(nchar(justewes$DAM,keepNA=TRUE)==2),"DAM"]=paste0("00",justewes[whi
ch(nchar(justewes$DAM,keepNA=TRUE)==2),"DAM"])
justewes[which(nchar(justewes$DAM,keepNA=TRUE)==3),"DAM"]=paste0("0",justewes[whic
h(nchar(justewes$DAM,keepNA=TRUE)==3),"DAM"])
justewes[which(nchar(justewes$DAM,keepNA=TRUE)==5),"DAM"]=substr(justewes[which(nc
har(justewes$DAM,keepNA=TRUE)==5),"DAM"],2,5)
justewes[which(nchar(justewes$DBRD,keepNA=TRUE)==1),"DBRD"]=paste0("0",justewes[w
hich(nchar(justewes$DBRD,keepNA=TRUE)==1),"DBRD"])

```

```

#Add Full ID
JEPed = Ped[which(Ped$LAMBID%in%justewes$LAMBID),]
justewes2 = merge(justewes,JEPed,by="LAMBID",all.x=TRUE)
justewes2$dam = paste0(justewes2$DBRD,justewes2$DAM)
justewes2$sire = paste0(justewes2$SBRD,justewes2$SIRE)

#Fixing remaining ped issues:
dam = unique(justewes2[which(is.na(justewes2$DAMID) and !is.na(justewes2$DAM) and
!is.na(justewes2$DBRD)), "dam"])
dams =
data.frame(DAMID=sort(unique(Ped[which(substr(Ped$DAMID,5,10)%in%dam), "DAMID"])))
dams = cbind(dam=substr(dams$DAMID,5,10),dams)
justewes2[which(is.na(justewes2$DAMID) and
!is.na(justewes2$DAM)), "DAMID"]=with(dams,DAMID[match(justewes2[which(is.na(justewes
2$DAMID) and !is.na(justewes2$DAM)), "dam"],dam)])

sire = unique(justewes2[which(is.na(justewes2$SIREID) and !is.na(justewes2$SIRE) and
!is.na(justewes2$SBRD)), "sire"])
sires =
data.frame(SIREID=sort(unique(Ped[which(substr(Ped$SIREID,5,10)%in%sire), "SIREID"])))
sires = cbind(sire=substr(sires$SIREID,5,10),sires)
justewes2[which(is.na(justewes2$SIREID) and
!is.na(justewes2$SIRE)), "SIREID"]=with(sires,SIREID[match(justewes2[which(is.na(justewes2
$SIREID) and !is.na(justewes2$SIRE)), "sire"],sire)])

#Reorganize
justewes2 =
justewes2[,c("LAMBID", "SIREID", "DAMID", "STM.x", "BYR", "AGE", "SEX", "BRWT", "WN
WT", "ADG", "TB", "TBRE", "DISP")]

remove(dam,dams,sire,sires,justewes,lambcomb,JEPed)

#TBrecode
justewes2[which(justewes2$TB==0 | justewes2$TB==1 | justewes2$TB==5), "TB_recode"]=1
justewes2[which(justewes2$TB==2 | justewes2$TB==4 | justewes2$TB==6 | justewes2$TB==7
| justewes2$TB==8), "TB_recode"]=2
justewes2[which(justewes2$TB==9), "TB_recode"]=3
justewes2[which(justewes2$TB==3), "TB_recode"]=4

#Identify if any ewes are duplicated
justewes2[which(duplicated(justewes2$LAMBID)==TRUE),]
#None found

#Add DTB and DTR

```

```

dams =
justewes2[which(justewes2$LAMBID%in%array(justewes2$DAMID)),c("LAMBID","TB_recode",
"TBRE"),drop=FALSE]
colnames(dams) = c("DAMID","DTB","DTR")
justewes2 = merge(justewes2,dams,by="DAMID",all.x=TRUE)

#Reorganize
justewes2 =
justewes2[,c("LAMBID","SIREID","DAMID","STM.x","BYR","AGE","SEX","BRWT","WN
WT","ADG","TB","TB_recode","TBRE","DTB","DTR","DISP")]
colnames(justewes2)
=c("LAMBID","SIREID","DAMID","STM","BYR","AGE","SEX","BRWT","WNWT","ADG",
"TB_USSES","TB_recode","TBRE","DTB","DTR","WNDISP")
#Tidy up environment
remove(dams)

#Work with ewe productivity
eweprod = read.table(paste0(getwd(),"/EDEWEPROD.csv"),head=TRUE,sep=",")
#Create ID like lamb ID
eweprod[which(nchar(eweprod$DAM,keepNA=TRUE)==1),"DAM"]=paste0("000",eweprod[w
hich(nchar(eweprod$DAM,keepNA=TRUE)==1),"DAM"])
eweprod[which(nchar(eweprod$DAM,keepNA=TRUE)==2),"DAM"]=paste0("00",eweprod[whi
ch(nchar(eweprod$DAM,keepNA=TRUE)==2),"DAM"])
eweprod[which(nchar(eweprod$DAM,keepNA=TRUE)==3),"DAM"]=paste0("0",eweprod[whic
h(nchar(eweprod$DAM,keepNA=TRUE)==3),"DAM"])
eweprod[which(nchar(eweprod$DAM,keepNA=TRUE)==5),"DAM"]=substr(eweprod[which(nc
har(eweprod$DAM,keepNA=TRUE)==5),"DAM"],2,5)
eweprod[which(nchar(eweprod$DBRD,keepNA=TRUE)==1),"DBRD"]=paste0("0",eweprod[w
hich(nchar(eweprod$DBRD,keepNA=TRUE)==1),"DBRD"])

eweprod[,"DAMID"]=paste0(eweprod[,"BYR"],eweprod[,"DBRD"],eweprod[,"DAM"]) #no NA
here

eweprodsummary = eweprod %>%
  group_by(DAMID) %>%

summarize(minLY2=min(LY2),maxLY2=max(LY2),minLY3=min(LY3),maxLY3=max(LY3),
minLY4=min(LY4),maxLY4=max(LY4),minLY5=min(LY5),maxLY5=max(LY5),minYOR=mi
n(YOR),maxYOR=max(YOR))

#merging
justewes3 = merge(justewes2,eweprodsummary,by.x="LAMBID",by.y="DAMID",all.x=TRUE)

#Tidy up environment
remove(justewes2,eweprod,eweprodsummary)

```

```

#Work with inventory
invent = read.table(paste0(getwd(),"/EDINVENTORY.csv"),head=TRUE,sep=",")
#just females
invent = invent[which(invent$SEX==2),]
invent = invent[which(!is.na(invent$BRD)),]
#create ID to match lamb data
invent[which(nchar(invent$ETAG,keepNA=TRUE)==1),"ETAG"]=paste0("000",invent[which(
nchar(invent$ETAG,keepNA=TRUE)==1),"ETAG"])
invent[which(nchar(invent$ETAG,keepNA=TRUE)==2),"ETAG"]=paste0("00",invent[which(n
char(invent$ETAG,keepNA=TRUE)==2),"ETAG"])
invent[which(nchar(invent$ETAG,keepNA=TRUE)==3),"ETAG"]=paste0("0",invent[which(nc
har(invent$ETAG,keepNA=TRUE)==3),"ETAG"])
invent[which(nchar(invent$ETAG,keepNA=TRUE)==5),"ETAG"]=substr(invent[which(nchar(i
nvent$ETAG,keepNA=TRUE)==5),"ETAG"],2,5)
invent[which(nchar(invent$BRD,keepNA=TRUE)==1),"BRD"]=paste0("0",invent[which(nchar(
invent$BRD,keepNA=TRUE)==1),"BRD"])

invent[,"ETAGID"]=paste0(invent[,"BYR"],invent[,"BRD"],invent[,"ETAG"]) #no NA here

inventsummary = invent %>%
  group_by(ETAGID) %>%
  summarize(minYYREC=min(YRREC),maxYYREC=max(YRREC))

DISP = unique(invent[,c("ETAGID","DISP")])
inventsummary$DISP=with(DISP,DISP[match(inventsummary$ETAGID,ETAGID)])

#merging
justewes4 = merge(justewes3,inventsummary,by.x="LAMBID",by.y="ETAGID",all.x=TRUE)

#Tidy up environment
remove(justewes3,invent,inventsummary,DISP)

write.table(justewes4,paste0(getwd(),"/JustEwes.txt"),row.names=FALSE,quote=FALSE)

#Separating out breeds
COLUMBIA = justewes4[which(justewes4$STM=="06"),] #17622 records #
POLYPAY = justewes4[which(justewes4$STM=="30"),] #12380 records #
RAMBOUILLET = justewes4[which(justewes4$STM=="07"),] #26018 records #
TARGHEE = justewes4[which(justewes4$STM=="02"),] #23597 records #

#Using maxLY2 as longevity record

####COLUMBIA###
#COLUMBIA -> LY2 = 0 has no meaning (they were never allowed to be productive) - affects
570 records
COLUMBIA$Longevity=COLUMBIA$maxLY2

```

```
COLUMBIA[which(COLUMBIA$maxLY2==0),"Longevity"]=NA
COLUMBIA[which(COLUMBIA$Longevity > 7),"Longevity"]=7
```

```
#Getting rid of missing data at important points
```

```
COLUMBIA = COLUMBIA[which(!(is.na(COLUMBIA$Longevity))),]
COLUMBIA = COLUMBIA[which(!(is.na(COLUMBIA$DTR))),]
COLUMBIA = COLUMBIA[which(!(is.na(COLUMBIA$DTB))),]
COLUMBIA = COLUMBIA[which(!(is.na(COLUMBIA$TBRE))),]
COLUMBIA = COLUMBIA[which(!(is.na(COLUMBIA$TB_recode))),] COLUMBIA =
COLUMBIA[which(!(COLUMBIA$BRWT==0.0)),]
COLUMBIA = COLUMBIA[which(!(COLUMBIA$AGE>7)),]
```

```
#Adding Stayability code
```

```
COLUMBIA[,"STAY2"]=ifelse(COLUMBIA$Longevity>=2,1,0)
COLUMBIA[,"STAY3"]=ifelse(COLUMBIA$Longevity>=3,1,0)
COLUMBIA[,"STAY4"]=ifelse(COLUMBIA$Longevity>=4,1,0)
COLUMBIA[,"STAY5"]=ifelse(COLUMBIA$Longevity>=5,1,0)
COLUMBIA[,"STAY6"]=ifelse(COLUMBIA$Longevity>=6,1,0)
COLUMBIA[,"STAYABILITY TO AGE SEVEN (7)"]=ifelse(COLUMBIA$Longevity>=7,1,0)
```

```
####POLYPAY####
```

```
#Same approach as Columbia, LY2 = 0 dropped
```

```
POLYPAY[,"Longevity"]=POLYPAY$maxLY2
POLYPAY[which(POLYPAY$maxLY2==0),"Longevity"]=NA
POLYPAY[which(POLYPAY$Longevity > 7),"Longevity"]=7
POLYPAY = POLYPAY[which(!(is.na(POLYPAY$Longevity))),]
POLYPAY = POLYPAY[which(!(is.na(POLYPAY$DTR))),]
POLYPAY = POLYPAY[which(!(is.na(POLYPAY$DTB))),]
POLYPAY = POLYPAY[which(!(is.na(POLYPAY$TBRE))),]
POLYPAY = POLYPAY[which(!(is.na(POLYPAY$TB_recode))),]
POLYPAY = POLYPAY[which(!(POLYPAY$BRWT == 0.0)),]
POLYPAY = POLYPAY[which(!(POLYPAY$AGE>7)),]
POLYPAY[,"STAY2"]=ifelse(POLYPAY$Longevity>=2,1,0)
POLYPAY[,"STAY3"]=ifelse(POLYPAY$Longevity>=3,1,0)
POLYPAY[,"STAY4"]=ifelse(POLYPAY$Longevity>=4,1,0)
POLYPAY[,"STAY5"]=ifelse(POLYPAY$Longevity>=5,1,0)
POLYPAY[,"STAY6"]=ifelse(POLYPAY$Longevity>=6,1,0)
POLYPAY[,"STAYABILITY TO AGE SEVEN (7)"]=ifelse(POLYPAY$Longevity>=7,1,0)
```

```
####RAMBOUILLET####
```

```
#Same approach as Columbia, maxLY2 = 0 dropped
```

```
RAMBOUILLET[,"Longevity"]=RAMBOUILLET$maxLY2
RAMBOUILLET[which(RAMBOUILLET$maxLY2==0),"Longevity"]=NA
RAMBOUILLET[which(RAMBOUILLET$Longevity > 7),"Longevity"]=7
RAMBOUILLET = RAMBOUILLET[which(!(is.na(RAMBOUILLET$Longevity))),]
RAMBOUILLET = RAMBOUILLET[which(!(is.na(RAMBOUILLET$DTR))),]
```

```

RAMBOUILLET = RAMBOUILLET[which(!(is.na(RAMBOUILLET$DTB))),]
RAMBOUILLET = RAMBOUILLET[which(!(is.na(RAMBOUILLET$TBRE))),]
RAMBOUILLET = RAMBOUILLET[which(!(is.na(RAMBOUILLET$TB_recode))),]
RAMBOUILLET = RAMBOUILLET[which(!(RAMBOUILLET$BRWT == 0.0)),]
RAMBOUILLET = RAMBOUILLET[which(!(RAMBOUILLET$AGE>7)),]
RAMBOUILLET[, "STAY2"]=ifelse(RAMBOUILLET$Longevity>=2,1,0)
RAMBOUILLET[, "STAY3"]=ifelse(RAMBOUILLET$Longevity>=3,1,0)
RAMBOUILLET[, "STAY4"]=ifelse(RAMBOUILLET$Longevity>=4,1,0)
RAMBOUILLET[, "STAY5"]=ifelse(RAMBOUILLET$Longevity>=5,1,0)
RAMBOUILLET[, "STAY6"]=ifelse(RAMBOUILLET$Longevity>=6,1,0)
RAMBOUILLET[, "STAYABILITY TO AGE SEVEN
(7)"]=ifelse(RAMBOUILLET$Longevity>=7,1,0)

####TARGHEE####
#Same approach as Columbia, LY2 = 0 dropped
TARGHEE[, "Longevity"]=TARGHEE$maxLY2
TARGHEE[which(TARGHEE$maxLY2==0), "Longevity"]=NA
TARGHEE[which(TARGHEE$Longevity > 7), "Longevity"]=7
TARGHEE = TARGHEE[which(!(is.na(TARGHEE$Longevity))),]
TARGHEE = TARGHEE[which(!(is.na(TARGHEE$DTR))),]
TARGHEE = TARGHEE[which(!(is.na(TARGHEE$DTB))),]
TARGHEE = TARGHEE[which(!(is.na(TARGHEE$TBRE))),]
TARGHEE = TARGHEE[which(!(is.na(TARGHEE$TB_recode))),]
TARGHEE = TARGHEE[which(!(TARGHEE$BRWT == 0.0)),]
TARGHEE = TARGHEE[which(!(TARGHEE$AGE > 7)),]
TARGHEE[, "STAY2"]=ifelse(TARGHEE$Longevity>=2,1,0)
TARGHEE[, "STAY3"]=ifelse(TARGHEE$Longevity>=3,1,0)
TARGHEE[, "STAY4"]=ifelse(TARGHEE$Longevity>=4,1,0)
TARGHEE[, "STAY5"]=ifelse(TARGHEE$Longevity>=5,1,0)
TARGHEE[, "STAY6"]=ifelse(TARGHEE$Longevity>=6,1,0)
TARGHEE[, "STAYABILITY TO AGE SEVEN (7)"]=ifelse(TARGHEE$Longevity>=7,1,0)

#####FIXING TB/DTB#####
#COLUMBIA
#Cleaning up the data
COLUMBIA = COLUMBIA[which(!(COLUMBIA$TB_recode==4)),]
COLUMBIA = COLUMBIA[which(!(COLUMBIA$DTB==4)),]

#RAMOUILLET
#Cleaning up the data
RAMBOUILLET = RAMBOUILLET[which(!(RAMBOUILLET$TB_recode==4)),]
RAMBOUILLET = RAMBOUILLET[which(!(RAMBOUILLET$DTB==4)),]

#TARGHEE
#Removing Quad+, like other breeds
TARGHEE = TARGHEE[which(!(TARGHEE$TB_recode==4)),]

```



```

TARGHEE = TARGHEE[which(!(TARGHEE$DTB==4)),]

#####FIXING TR/DTR#####
#COLUMBIA:
#Removing levels 2, 4, 6, and 9
#Level 0 gone after TB fix
COLUMBIA = COLUMBIA[which(!(COLUMBIA$TBRE==2)),]
COLUMBIA = COLUMBIA[which(!(COLUMBIA$TBRE==4)),]
COLUMBIA = COLUMBIA[which(!(COLUMBIA$TBRE==6)),]
COLUMBIA = COLUMBIA[which(!(COLUMBIA$TBRE==9)),]
COLUMBIA = COLUMBIA[which(!(COLUMBIA$DTR==2)),]
COLUMBIA = COLUMBIA[which(!(COLUMBIA$DTR==4)),]
COLUMBIA = COLUMBIA[which(!(COLUMBIA$DTR==6)),]
COLUMBIA = COLUMBIA[which(!(COLUMBIA$DTR==9)),]

#Split level 3 so that "singles raised as twins" goes in category 2
COLUMBIA[which(COLUMBIA$TB_recode==1 and COLUMBIA$TBRE==3),"TBRE"]=2
COLUMBIA[which(COLUMBIA$DTB==1 and COLUMBIA$DTR==3),"DTR"]=2

###RERUN COUNTS FOR TB and TR with revised data
#Ewes born single and raised a twin only accounted for 43 records (2.3% of data).
#Twins were never raised as triplets, so this group does not make
#sense to keep. Dropping those records.
COLUMBIA = COLUMBIA[which(!(COLUMBIA$TBRE==2)),]
COLUMBIA = COLUMBIA[which(!(COLUMBIA$DTR==2)),]

###Reduce years
COLUMBIA = COLUMBIA[which(COLUMBIA$BYR>=1985),]

#POLYPAY:
#Removing levels 2, 4, and 6
POLYPAY = POLYPAY[which(!(POLYPAY$TBRE==2)),]
POLYPAY = POLYPAY[which(!(POLYPAY$TBRE==4)),]
POLYPAY = POLYPAY[which(!(POLYPAY$TBRE==6)),]
POLYPAY = POLYPAY[which(!(POLYPAY$DTR==2)),]
POLYPAY = POLYPAY[which(!(POLYPAY$DTR==4)),]
POLYPAY = POLYPAY[which(!(POLYPAY$DTR==6)),]

#Split level 3 so that "singles raised as twins" goes in category 2
POLYPAY[which(POLYPAY$TB_recode==1 and POLYPAY$TBRE==3),"TBRE"]=2
POLYPAY[which(POLYPAY$DTB==1 and POLYPAY$DTR==3),"DTR"]=2
#Same issue with category 2, dropping records
POLYPAY = POLYPAY[which(!(POLYPAY$TBRE==2)),]
POLYPAY = POLYPAY[which(!(POLYPAY$DTR==2)),]

```

```

POLYPAY_ISSUES = POLYPAY[which((POLYPAY$TB_recode==3 and
POLYPAY$TBRE==1) | (POLYPAY$TB_recode==4 and POLYPAY$TBRE==7) |
(POLYPAY$TB_recode==4 and POLYPAY$TBRE==8) | (POLYPAY$TB_recode==4 and
POLYPAY$TBRE==9) | (POLYPAY$DTB==4 and POLYPAY$DTR==7) |
(POLYPAY$DTB==4 and POLYPAY$DTR==8) | (POLYPAY$DTB==4 and
POLYPAY$DTR==9)),]
write.table(POLYPAY_ISSUES,paste0(getwd(),"/Polypay_Issues.txt"),row.names=FALSE,quot
e=FALSE)

```

```

#get rid of problem animals
POLYPAY =
POLYPAY[which(!(POLYPAY$LAMBID%in%POLYPAY_ISSUES$LAMBID)),]

```

```

#removing remaining Quad+
POLYPAY = POLYPAY[which(!(POLYPAY$TB_recode==4 | POLYPAY$DTB==4)),]

```

```

##Reduce years
POLYPAY = POLYPAY[which(POLYPAY$BYR>=1985),]
#no more issues

```

```

#RAMBOUILLET
#Need to clean up levels 0, 2, 4, 6, and 9
#No more level 0 after TB cleanup
RAMBOUILLET = RAMBOUILLET[which(!(RAMBOUILLET$TBRE==2)),]
RAMBOUILLET = RAMBOUILLET[which(!(RAMBOUILLET$TBRE==4)),]
RAMBOUILLET = RAMBOUILLET[which(!(RAMBOUILLET$TBRE==6)),]
RAMBOUILLET = RAMBOUILLET[which(!(RAMBOUILLET$TBRE==9)),]
RAMBOUILLET = RAMBOUILLET[which(!(RAMBOUILLET$DTR==2)),]
RAMBOUILLET = RAMBOUILLET[which(!(RAMBOUILLET$DTR==4)),]
RAMBOUILLET = RAMBOUILLET[which(!(RAMBOUILLET$DTR==6)),]
RAMBOUILLET = RAMBOUILLET[which(!(RAMBOUILLET$DTR==9)),]

```

```

#Split level 3 so that "singles raised as twins" goes in category 2
RAMBOUILLET[which(RAMBOUILLET$TB_recode==1 and
RAMBOUILLET$TBRE==3),"TBRE"]=2
RAMBOUILLET[which(RAMBOUILLET$DTB==1 and
RAMBOUILLET$DTR==3),"DTR"]=2
#Dropping category 2 for same reason as Columbia and Polypay
RAMBOUILLET = RAMBOUILLET[which(!(RAMBOUILLET$TBRE==2)),]
RAMBOUILLET = RAMBOUILLET[which(!(RAMBOUILLET$DTR==2)),]

```

```

##Reduce years
RAMBOUILLET = RAMBOUILLET[which(RAMBOUILLET$BYR>=1985),]

```

```

#TARGHEE
#No more level 0 after TB cleanup

```

```

#Need to clean up levels 2, 4, 6, and 9
TARGHEE = TARGHEE[which(!(TARGHEE$TBRE==2)),]
TARGHEE = TARGHEE[which(!(TARGHEE$TBRE==4)),]
TARGHEE = TARGHEE[which(!(TARGHEE$TBRE==6)),]
TARGHEE = TARGHEE[which(!(TARGHEE$TBRE==9)),]
TARGHEE = TARGHEE[which(!(TARGHEE$DTR==2)),]
TARGHEE = TARGHEE[which(!(TARGHEE$DTR==4)),]
TARGHEE = TARGHEE[which(!(TARGHEE$DTR==6)),]
TARGHEE = TARGHEE[which(!(TARGHEE$DTR==9)),]

#Split level 3 so that "singles raised as twins" goes in category 2
TARGHEE[which(TARGHEE$TB_recode==1 and TARGHEE$TBRE==3),"TBRE"]=2
TARGHEE[which(TARGHEE$DTB==1 and TARGHEE$DTR==3),"DTR"]=2
#Dropping category 2 for same reason as other breeds
TARGHEE = TARGHEE[which(!(TARGHEE$TBRE==2)),]
TARGHEE = TARGHEE[which(!(TARGHEE$DTR==2)),]

##Reduce years
TARGHEE = TARGHEE[which(TARGHEE$BYR>=1985),] #2950 remain

#####Counting Work#####
red = XXXX #replace XXXX for each breed

TBlevels = array(c(1:4))
LevelCount = matrix(0,nrow = dim(TBlevels),ncol=3,dimnames =
list(c(1:dim(TBlevels)),c("Level","TB","DTB")))
LevelCount[, "Level"] = TBlevels

for(i in 1:dim(TBlevels)){
  LevelCount[i,"TB"] = dim(red[which(red$TB_recode == TBlevels[i]),,drop=FALSE])[1]
  LevelCount[i,"DTB"] = dim(red[which(red$DTB == TBlevels[i]),,drop=FALSE])[1]
}
LevelCount

TRlevels = array(c(0:9))
LevelCount = matrix(0,nrow = dim(TRlevels),ncol=3,dimnames =
list(c(1:dim(TRlevels)),c("Level","TR","DTR")))
LevelCount[, "Level"] = TRlevels
for(i in 1:dim(TRlevels)){
  LevelCount[i,"TR"] = dim(red[which(red$TBRE == TRlevels[i]),,drop=FALSE])[1]
  LevelCount[i,"DTR"] = dim(red[which(red$DTR == TRlevels[i]),,drop=FALSE])[1]
}
LevelCount

BYRlevels = array(sort(unique(red$BYR)))

```

```

LevelCount = matrix(0,nrow = dim(BYRlevels),ncol=2,dimnames =
list(c(1:dim(BYRlevels)),c("Level","Count")))
LevelCount[, "Level"] = BYRlevels
for(i in 1:dim(BYRlevels)){
  LevelCount[i,"Count"] = dim(red[which(red$BYR == BYRlevels[i]),,drop=FALSE])[1]
}
LevelCount

#Columbia:
#All data present and read for Columbia, outputting data:
write.table(COLUMBIA,paste0(getwd(),"/Columbia.txt"),sep="\t",row.names=FALSE,quote=FALSE)

#Polypay:

##All data present and read for Polypay, outputting current dataset:
write.table(POLYPAY,paste0(getwd(),"/Polypay.txt"),sep="\t",row.names=FALSE,quote=FALSE)

#RAMBOUILLET:
write.table(RAMBOUILLET,paste0(getwd(),"/Rambouillet.txt"),sep="\t",row.names=FALSE,quote=FALSE)

#TARGHEE
#No issues with BYR found, distributed adequately across years of 1986 to 2008
write.table(TARGHEE,paste0(getwd(),"/Targhee.txt"),sep="\t",row.names=FALSE,quote=FALSE)

```

### Script to extract pedigree from final datasets

```

#Function
PedExtract = function(Ped,extractlist,keep=TRUE){
  if(missing(Ped)){
    stop("Pedigree was not provided.")
  }
  if(missing(extractlist)){
    stop("List of individuals to extract pedigree for was not provided.")
  }
  NewPed = Ped[which(Ped[,1]%in%extractlist),]
  sires = array(na.omit(unique(NewPed[,2])))
  sires = sires[which(!(sires %in% NewPed[,1]))]
  dams = array(na.omit(unique(NewPed[,3])))
  dams = dams[which(!(dams %in% NewPed[,1]))]
  newparents = array(c(sires,dams))
  while(dim(newparents)>0){

```

```

PedAdd = Ped[which(Ped[,1]%in%c(newparents)),]
if(dim(PedAdd)[1] < dim(newparents)){
  miss = array(c(newparents[which(!(newparents%in%array(PedAdd[,1])))]))
  PedAdd =
rbind(PedAdd,data.frame(LAMBID=miss,SIREID=NA,DAMID=NA,ID10=NA,STM=NA,SIR
E4=NA,DAM4=NA))
}
NewPed = rbind(PedAdd,NewPed)
sires = array(na.omit(unique(PedAdd[,2])))
sires = sires[which(!(sires %in% NewPed[,1]))]
dams = array(na.omit(unique(PedAdd[,3])))
dams = dams[which(!(dams %in% NewPed[,1]))]
newparents = array(c(sires,dams))
}
if(keep==FALSE){
  NewPed = NewPed[,1:3]
}
return(NewPed)
}

#processing data
library(foreign)
Ped = read.dbf("PEDIGREE.dbf",as.is=TRUE)
Ped[which(Ped$SIREID==0),"SIREID"]=NA
Ped[which(Ped$DAMID==0),"DAMID"]=NA

#SireIssues = array(c("200500 595","200600 629","200400 426","200600 661"))
Ped[which(substr(Ped$SIREID,7,7)==
),"SIREID"]=paste0(substr(Ped[which(substr(Ped$SIREID,7,7)==
),"SIREID"],1,6),"0",substr(Ped[which(substr(Ped$SIREID,7,7)==
),"SIREID"],8,10))
write.table(Ped,paste0(getwd(),"/PedUpdated.txt"),sep="\t",row.names=FALSE,quote=FALSE)

Columbia = read.table("Columbia.txt",header=TRUE,sep="\t")
extractlist = array(Columbia$LAMBID)

PedC = PedExtract(Ped,extractlist,keep=FALSE)
PedC = PedC[order(PedC$LAMBID),]
write.table(PedC,paste0(getwd(),"/PedC.txt"),sep="\t",row.names=FALSE,quote=FALSE)

remove(Columbia,PedC,extractlist)

Polypay = read.table("Polypay.txt",header=TRUE,sep="\t")
extractlist = array(Polypay$LAMBID)
PedP = PedExtract(Ped,extractlist,keep=FALSE)
PedP = PedP[order(PedP$LAMBID),]
write.table(PedP,paste0(getwd(),"/PedP.txt"),sep="\t",row.names=FALSE,quote=FALSE)

```

```

remove(Polypay,PedP,extractlist)

Rambouillet = read.table("Rambouillet.txt",header=TRUE,sep="\t")
extractlist = array(Rambouillet$LAMBID)
PedR = PedExtract(Ped,extractlist,keep=FALSE)
PedR = PedR[order(PedR$LAMBID),]
write.table(PedR,paste0(getwd(),"/PedR.txt"),sep="\t",row.names=FALSE,quote=FALSE)

remove(Rambouillet,PedR,extractlist)

Targhee = read.table("Targhee.txt",header=TRUE,sep="\t")
extractlist = array(Targhee$LAMBID)
PedT = PedExtract(Ped,extractlist,keep=FALSE)
PedT = PedT[order(PedT$LAMBID),]
write.table(PedT,paste0(getwd(),"/PedT.txt"),sep="\t",row.names=FALSE,quote=FALSE)

remove(Targhee,PedT,extractlist)

Columbia = read.table("Columbia.txt",header=TRUE,sep="\t")
Polypay = read.table("Polypay.txt",header=TRUE,sep="\t")
Rambouillet = read.table("Rambouillet.txt",header=TRUE,sep="\t")
Targhee = read.table("Targhee.txt",header=TRUE,sep="\t")
Across = rbind(Columbia,Polypay,Rambouillet,Targhee)

extractlist = array(Across$LAMBID)
PedA = PedExtract(Ped,extractlist,keep=FALSE)
PedA = PedA[order(PedA$LAMBID),]
write.table(PedA,paste0(getwd(),"/PedA.txt"),sep="\t",row.names=FALSE,quote=FALSE)
write.table(Across,paste0(getwd(),"/Across.txt"),sep="\t",row.names=FALSE,quote=FALSE)

```

## APPENDIX B: *SIBS* PACKAGE R CODE BY FUNCTION

### Generation assignment

```
GENAssign = function(Ped, ID=1, Sire=2, Dam=3, st = TRUE, header=TRUE) {Ped =
  cbind(Ped, matrix(0, nrow=dim(Ped)[1], ncol=1))
  colnames(Ped)=array(c("ID", "Sire", "Dam", "GEN"))
  Ped[which(Ped[,2]==0 and Ped[,3]==0),4]=1
  fpl=array(c(unique(Ped[which(Ped[,2]>0),2]), unique(Ped[which(Ped[,3]>0),3])))
  i=1
  while(dim(fpl)>0) {
    pl = array(Ped[which(Ped[,4]==i),1])
    fpl=array(subset(fpl,!(fpl%in%pl)))
    Ped[which((Ped[,2]%in%pl and Ped[,3]%in%pl) | (Ped[,2]%in%pl and
      !(Ped[,3]%in%pl) and !(Ped[,3]%in%fpl)) | (Ped[,3]%in%pl and !(Ped[,2]%in%pl) and
      !(Ped[,2]%in%fpl))),4]=i+1
    i=i+1
  }
  if (st == TRUE) {
    Ped = Ped[order(Ped[,4],Ped[,2],Ped[,3],)]
  }
  return(Ped)
}
```

### Sibling assignment

```
AssignSibs = function(Ped, colnames = c("ID", "Sire", "Dam"), st = TRUE, savefiles = TRUE) {
  library(data.table)
  Ped <- data.table(Ped)
  sibDT = Ped[!is.na(Sire) and !is.na(Dam),
    CJ(ID = ID, fullsibs = ID)[ID != fullsibs], by=.(Sire, Dam)]
  hsibDT = melt(Ped, id.vars = "ID")[!is.na(value), CJ(ID = ID, hsid = ID)[ID !=
    hsid], by=.(ptype = variable, pid = value)][!sibDT, on=.(ID, hsid = fullsibs)]
  Ped[sibDT[, .(fullsibs = toString(fullsibs)), by=ID], on=.(ID), fullsibs := i.fullsibs,
    by=.EACHI ]
  Ped[hsibDT[, .(hsibs = toString(hsid)), by=ID], on=.(ID), hsibs := i.hsibs, by=.EACHI ]
  Ped[rbind(sibDT[, .(ID, oid = fullsibs)], hsibDT[, .(ID, oid = hsid)]), .(fams =
    toString(oid)), by=.(ID), on = .(ID), fams := i.fams, by = .EACHI]
  message(paste0("Total number of half-sibs in this pedigree = ",
    length(table(Ped[, "hsibs"])), sep=""))
  message(paste0("Total number of full-sibs in this pedigree = ",
    length(table(Ped[, "fullsibs"])), sep=""))
}
```

```

message(paste0('Total number of DFC in this pedigree = ', length(table(Ped[, "fams"])),
sep=""))
return(Ped)
}

```

### Sibling count

```

SibCount = function(Ped,coln = c("ID","Sire","Dam"),st = TRUE,savefiles = TRUE){
  Stats = matrix(0,nrow=3,ncol=5,byrow=TRUE,dimnames =
list(c("FullSib","PaternalHalfSib","MaternalHalfSib"),c("Count","Average","SD","Min",
"Max")))
  FSCount = cbind(unique(Ped[,c("Sire","Dam")]),data.frame(0))
  colnames(FSCount) = c("Sire","Dam","NuFullSib")
  FSCount = FSCount[!rowSums(is.na(FSCount[,c("Sire","Dam")])),]
  for(i in 1:dim(FSCount)[1]){
    FSCount[i,"NuFullSib"]=nrow(Ped[which(Ped[, "Sire"]==FSCount[i,"Sire"] and
Ped[, "Dam"]==FSCount[i,"Dam"]),])
    FullSibs = FSCount[which(FSCount[, "NuFullSib"]>=2),]
    Stats[1,] =
c(nrow(FullSibs),round(mean(FullSibs[, "NuFullSib"]),3),round(sd(FullSibs[, "NuFullSib"
]),3),min(FullSibs[, "NuFullSib"]),max(FullSibs[, "NuFullSib"]))
    PHSCount = cbind(unique(Ped[, "Sire"]),data.frame(0))
    colnames(PHSCount) = c("Sire","NuPHalfSib")
    PHSCount = PHSCount[!is.na(PHSCount[, "Sire"]),]
    for(i in 1:dim(PHSCount)[1]){
      PHSCount[i,"NuPHalfSib"]=nrow(Ped[which(Ped[, "Sire"]==PHSCount[i,"Sire"]),])
      PHSCount = PHSCount[which(PHSCount[, "NuPHalfSib"]>=2),]
      Stats[2,] =
c(nrow(PHSCount),round(mean(PHSCount[, "NuPHalfSib"]),3),round(sd(PHSCount[, "N
uPHalfSib"]),3),min(PHSCount[, "NuPHalfSib"]),max(PHSCount[, "NuPHalfSib"]))
    MHSCount = cbind(unique(Ped[, "Dam"]),data.frame(0))
    colnames(MHSCount) = c("Dam","NuMHalfSib")
    MHSCount = MHSCount[!is.na(MHSCount[, "Dam"]),]
    for(i in 1:dim(MHSCount)[1]){
      MHSCount[i,"NuMHalfSib"]=nrow(Ped[which(Ped[, "Dam"]==MHSCount[i,"Da
m"]),])
    }
    MHSCount = MHSCount[which(MHSCount[, "NuMHalfSib"]>=2),]
    Stats[3,] =
c(nrow(MHSCount),round(mean(MHSCount[, "NuMHalfSib"]),3),round(sd(MHSCount[,
"NuMHalfSib"]),3),min(MHSCount[, "NuMHalfSib"]),max(MHSCount[, "NuMHalfSib"
]))
  }
}

```



```

message(paste0('Total number of maternal half-sibs in this pedigree = ',
length(table(MHSCount)), sep=""))
message(paste0('Total number of paternal half-sibs in this pedigree = ',
length(table(PHSCount)), sep=""))
message(paste0('Total number of full-sibs in this pedigree = ', length(table(FSCount)),
sep=""))
li = list(FSCount=as.data.frame(FSCount),PHSCount=as.data.frame(PHSCount),
MHSCount= as.data.frame(MHSCount), Stats=as.data.frame(Stats))
return(li)
}

```

### Building pedigree

```

makePed <- function (pedigree, ID=1, Sire=2, Dam=3, rmsingle = FALSE, verbose = TRUE) {

anim = unique(as.character(pedigree[,ID]))
Sires = unique(as.character(pedigree[,Sire]))
Dams = unique(as.character(pedigree[,Dam]))

#check for duplicated IDs
if(anyDuplicated(pedigree[,ID]))
{
message("Duplicated IDs were detected and removed.\n")
ord <- order(!is.na(pedigree[,2])+!is.na(pedigree[,3]))
pedigree <- pedigree[ord,]
message("This includes: \n")
print(head(pedigree[duplicated(pedigree[,1]),]))
pedigree <- pedigree[!duplicated(pedigree[,1]),]
}
rownames(pedigree)<-pedigree[,1]

Sireclean = Sires[Sires!="0"]
Damclean = Dams[Dams!="0"]
wrongsex = Sireclean %in% Damclean

if(TRUE %in% wrongsex) {
warning (" looks like some Sires appear as Dams, assumed selfing")
}

# remove singleton animals (no parents or progeny in the pedigree)
if(rmsingle == TRUE){
singleton.vec <- pedigree[,1][pedigree[,2] == 0 and pedigree[,3]== 0 and !(pedigree[,1] %in%
c(pedigree[,2], pedigree[,3]))]

if(length(singleton.vec) > 0) {
pedigree = pedigree[-(pedigree[,1] %in% singleton.vec),]
}
}
}

```

```

    if (verbose == TRUE) message("A total of", length(singleton.vec), "found and removed. \n")
  }
}

#Run check for individuals in Sire/Dam that are not in ID and add them as founders
if(any(!pedigree[,2] %in% pedigree[,1]))
  Sirenew <- data.frame(ID = pedigree[which(!pedigree[,2] %in% pedigree[,1]), 2],
    Sire = 0, Dam = 0)
if(any(!pedigree[,3] %in% pedigree[,1]))
  Damnew <- data.frame(ID = pedigree[which(!pedigree[,3] %in% pedigree[,1]), 3],
    Sire = 0, Dam = 0)
Sirenew <- unique(subset(Sirenew, ID != 0))
Damnew <- unique(subset(Damnew, ID != 0))

newPed <- as.data.frame(rbind(Sirenew, Damnew, pedigree))

addFounders = TRUE

if(length(newPed) > length(pedigree)) {
  addFounders == TRUE
  message("individuals appearing as Sire/Dam but not as individuals were added as founders.
\n")
}

# wraps up pedigree stats and output information
message(paste0("Total number of animals counted in this pedigree = ", length(anim),sep=""),'\n')
message(paste0("Total number of Sires counted in this pedigree = ',
length(Sireclean),sep="),'\n')
message(paste0("Total number of Dams counted in this pedigree = ',
length(Damclean),sep="),'\n')
message("New individuals added = ", length(addFounders),'\n')
message('Pedigree is now sorted and ordered! \n')
if (addFounders == TRUE) {
  return(newPed)
}
else return(pedigree)
}

```

## APPENDIX C: BAYESIAN ANALYSIS *MCMCglmm* R CODES

### Longevity additive *MCMCglmm* models R codes

```
prior<-
list(R=list(V=1,nu=1),G=list(G1=list(V=1,nu=1,alpha.mu=0,alpha.V=1000),G2=list(V=1,nu=1,alp
lpha.mu=0,alpha.V=1000), G3=list(V=1,nu=1,alpha.mu=0,alpha.V=1000)))

Phen$ID2 = Phen$ID
Phen$Dam = as.character(Phen$Dam)

M1dim = dim(array(na.omit(unique(Phen$Dam))))
M1 = matrix(0,nrow=M1dim,ncol=M1dim,
            dimnames=list(array(na.omit(unique(Phen$Dam))),array(na.omit(unique(Phen$Dam))))
diag(M1) = 1
M1 = as(M1, "dgCMatrix")

Phen$BYR = as.character(Phen$BYR)
BYdim = dim(array(na.omit(unique(Phen$BYR))))
BY =
matrix(0,nrow=BYdim,ncol=BYdim,dimnames=list(array(na.omit(unique(Phen$BYR))),array(n
a.omit(unique(Phen$BYR))))
diag(BY) = 1
BY = as(BY, "dgCMatrix")

Ainv1 = inverseA(Ped)$Ainv

Model 1<- mclapply(1:10, function(i)
{MCMCglmm(Longevity~AGE,random=~ID+Dam+BY,data=Phen,ginverse=list(ID=
Ainv1,Dam=M1, BY=BYR),prior=prior, nitt=10000, burnin=1000,
thin=90, pr=T, family="gaussian", verbose=T, slice=T, singular.ok = T) },
mc.cores=10)

Model 2<- mclapply(1:10, function(i)
{MCMCglmm(Longevity~AGE+TB,random=~ID+Dam+BY,data=Phen,ginverse=list(ID=
Ainv1,Dam=M1, BY=BYR),prior=prior, nitt=10000, burnin=1000,
thin=90, pr=T, family="gaussian", verbose=T, slice=T, singular.ok = T) },
mc.cores=10)

Model 3<- mclapply(1:10, function(i)
{MCMCglmm(Longevity~AGE+TB+TR,random=~ID+Dam+BY,data=Phen,ginverse=list(ID=
Ainv1,Dam=M1, BY=BYR),prior=prior, nitt=10000, burnin=1000,
thin=90, pr=T, family="gaussian", verbose=T, slice=T, singular.ok = T) },
mc.cores=10)
```

```

Model 4<- mclapply(1:10, function(i)
{MCMCglmm(Longevity~AGE+TB+TR+DTB,random=~ID+Dam+BY,data=Phen,ginverse=list(ID=
      Ainv1,Dam=M1, BY=BYR),prior=prior, nitt=10000, burnin=1000,
thin=90, pr=T, family="gaussian", verbose=T, slice=T, singular.ok = T) },
mc.cores=10)

```

```

Model 5<- mclapply(1:10, function(i)
{MCMCglmm(Longevity~AGE+TB+TR+DTB+DTR,random=~ID+Dam+BY,data=Phen,ginverse=list(ID=
      Ainv1,Dam=M1, BY=BYR),prior=prior, nitt=10000, burnin=1000,
thin=90, pr=T, family="gaussian", verbose=T, slice=T, singular.ok = T) },
mc.cores=10)

```

```

Model 6<- mclapply(1:10, function(i)
{MCMCglmm(Longevity~factor(AGE),random=~ID+Dam+BY,data=Phen,ginverse=list(ID=
      Ainv1,Dam=M1, BY=BYR),prior=prior, nitt=10000, burnin=1000,
thin=90, pr=T, family="gaussian", verbose=T, slice=T, singular.ok = T) },
mc.cores=10)

```

```

Model 7<- mclapply(1:10, function(i)
{MCMCglmm(Longevity~factor(AGE)+factor(TB),random=~ID+Dam+BY,data=Phen,ginverse=list(ID=
      Ainv1,Dam=M1, BY=BYR),prior=prior, nitt=10000, burnin=1000,
thin=90, pr=T, family="gaussian", verbose=T, slice=T, singular.ok = T) },
mc.cores=10)

```

```

Model 8<- mclapply(1:10, function(i)
{MCMCglmm(Longevity~factor(AGE)+factor(TB)+factor(DTB),random=~ID+Dam+BY,data=Phen,ginverse=list(ID=
      Ainv1,Dam=M1, BY=BYR),prior=prior, nitt=10000, burnin=1000,
thin=90, pr=T, family="gaussian", verbose=T, slice=T, singular.ok = T) },
mc.cores=10)

```

```

Model 9<- mclapply(1:10, function(i)
{MCMCglmm(Longevity~factor(AGE)+factor(TB)+factor(DTB)+factor(DTR),random=~ID+Dam+BY,data=Phen,ginverse=list(ID=
      Ainv1,Dam=M1, BY=BYR),prior=prior, nitt=10000, burnin=1000,
thin=90, pr=T, family="gaussian", verbose=T, slice=T, singular.ok = T) },
mc.cores=10)

```

## Dominance longevity models *MCMCglmm* R codes

```
prior2<-
list(R=list(V=1,nu=1),G=list(G1=list(V=1,nu=1,alpha.mu=0,alpha.V=1000),G2=list(V=1,nu=1,alpha.mu=0,alpha.V=1000),G3=list(V=1,nu=1,alpha.mu=0,alpha.V=1000),G4=list(V=1,nu=1,alpha.mu=0,alpha.V=1000)))

Phen$ID2 = Phen$ID
Phen$Dam = as.character(Phen$Dam)

M1dim = dim(array(na.omit(unique(Phen$Dam))))
M1 = matrix(0,nrow=M1dim,ncol=M1dim,
            dimnames=list(array(na.omit(unique(Phen$Dam))),array(na.omit(unique(Phen$Dam)))))
diag(M1) = 1
M1 = as(M1, "dgCMatrix")

Phen$BYR = as.character(Phen$BYR)
BYdim = dim(array(na.omit(unique(Phen$BYR))))
BY =
matrix(0,nrow=BYdim,ncol=BYdim,dimnames=list(array(na.omit(unique(Phen$BYR))),array(na.omit(unique(Phen$BYR)))))
diag(BY) = 1
BY = as(BY, "dgCMatrix")

Ainv1 = inverseA(Ped)$Ainv
Dinv1 = nadv::makeD(Ped)$Dinv

Model 1dom<- mclapply(1:10, function(i)
  {MCMCglmm(Longevity~AGE,random=~ID+Dam+BY+ID2,data=Phen,ginverse=list(ID=
    Ainv1,Dam=M1, BY=BYR, ID2=Dinv1),prior=prior2, nitt=20000,
    burnin=11000, thin=90, pr=T, family="gaussian", verbose=T, slice=T,
    singular.ok = T) }, mc.cores=10)

Model 2dom<- mclapply(1:10, function(i)
  {MCMCglmm(Longevity~AGE+TB,random=~ID+Dam+BY+ID2,data=Phen,ginverse=list(ID=
    Ainv1,Dam=M1, BY=BYR, ID2=Dinv1),prior=prior2, nitt=20000,
    burnin=11000, thin=90, pr=T, family="gaussian", verbose=T, slice=T,
    singular.ok = T) }, mc.cores=10)

Model 3dom<- mclapply(1:10, function(i)
  {MCMCglmm(Longevity~AGE+TB+TR,random=~ID+Dam+BY+ID2,data=Phen,ginverse=list(
    ID=
    Ainv1,Dam=M1, BY=BYR, ID2=Dinv1),prior=prior2, nitt=20000,
    burnin=11000, thin=90, pr=T, family="gaussian", verbose=T, slice=T,
    singular.ok = T) }, mc.cores=10)
```

```

Model 4dom<- mclapply(1:10, function(i)
{MCMCglmm(Longevity~AGE+TB+TR+DTB,random=~ID+Dam+BY+ID2,data=Phen,ginvers
e=list(ID=
          Ainv1,Dam=M1, BY=BYR, ID2=Dinv1),prior=prior2, nitt=20000,
burnin=11000, thin=90, pr=T, family="gaussian", verbose=T, slice=T,
singular.ok = T) }, mc.cores=10)

```

```

Model 5dom<- mclapply(1:10, function(i)
{MCMCglmm(Longevity~AGE+TB+TR+DTB+DTR,random=~ID+Dam+BY+ID2,data=Phen,
ginverse=list(ID=
          Ainv1,Dam=M1, BY=BYR, ID2=Dinv1),prior=prior2, nitt=20000,
burnin=11000, thin=90, pr=T, family="gaussian", verbose=T, slice=T,
singular.ok = T) }, mc.cores=10)

```

```

Model 6dom<- mclapply(1:10, function(i)
{MCMCglmm(Longevity~factor(AGE)+factor(TB),random=~ID+Dam+BY+ID2,data=Phen,gin
verse=list(ID=
          Ainv1,Dam=M1, BY=BYR, ID2=Dinv1),prior=prior2, nitt=20000,
burnin=11000, thin=90, pr=T, family="gaussian", verbose=T, slice=T,
singular.ok = T) }, mc.cores=10)

```

```

Model 7dom<- mclapply(1:10, function(i)
{MCMCglmm(Longevity~factor(AGE)+factor(TB)+factor(TR),random=~ID+Dam+BY+ID2,da
ta=Phen,ginverse=list(ID=
          Ainv1,Dam=M1, BY=BYR, ID2=Dinv1),prior=prior2, nitt=20000,
burnin=11000, thin=90, pr=T, family="gaussian", verbose=T, slice=T,
singular.ok = T) }, mc.cores=10)

```

```

Model 8dom<- mclapply(1:10, function(i)
{MCMCglmm(Longevity~factor(AGE)+factor(TB)+factor(TR)+factor(DTB),random=~ID+Da
m+BY+ID2,data=Phen,ginverse=list(ID=
          Ainv1,Dam=M1, BY=BYR, ID2=Dinv1),prior=prior2, nitt=20000,
burnin=11000, thin=90, pr=T, family="gaussian", verbose=T, slice=T,
singular.ok = T) }, mc.cores=10)

```

```

Model 9dom<- mclapply(1:10, function(i)
{MCMCglmm(Longevity~factor(AGE)+factor(TB)+factor(TR)+factor(DTB)+factor(DTR),rand
om=~ID+Dam+BY+ID2,data=Phen,ginverse=list(ID=

```

```
Ainv1,Dam=M1, BY=BYR, ID2=Dinv1),prior=prior2, nitt=20000,
burnin=11000, thin=90, pr=T, family="gaussian", verbose=T, slice=T,
singular.ok = T) }, mc.cores=10)
```

### An example of parallel in windows operating system

```
library(parallel)
setCores<-round(detectCores()*0.8) #80% of cores
cl <- makeCluster(getOption("cl.cores",setCores))
cl.pkg <- clusterEvalQ(cl,library(MCMCglmm))

clusterExport(cl,"prior2")
clusterExport(cl,"Phen")
clusterExport(cl,"Ainv1")
clusterExport(cl,"Dinv1")
clusterExport(cl,"M1")
clusterExport(cl,"BYR")

test8<-parLapply(cl=cl,1:5, function(i) {
  MCMCglmm(Longevity~factor(AGE)+factor(TB)+factor(TR)+factor(DTB)+factor(DTR
  ), random=~ID+Dam+BY+ID2, ginverse=list(ID=Ainv1, Dam=M1, BY=BYR,
  ID2=Dinv1), data=Phen, prior=prior2, verbose=T,nitt=20000, burnin=11000, thin=90,
  pr=T, family="gaussian", slice=T, singular.ok = T)
})
stopCluster(cl)
```

### Stayability multivariate additive models

```
priorb<- list(R=list(V=diag(6),nu=6, fix=0),G=list(G1=list(V=diag(6), nu=6),
G2=list(V=diag(6), nu=6), G3=list(V=diag(6), nu=6)))

stay1<- mclapply(1:10,
function(i){MCMCglmm(cbind(STAY2,STAY3,STAY4,STAY5,STAY6,STAY7)~trait+1+trait
:AGE,random= ~us(trait):ID+us(trait):Dam+us(trait):BYR, ginverse=list(ID=Ainv1, Dam=M1,
BYR= BY),family=rep("threshold", 6),pr=T, prior=priorb, data=Phen,nitt=10000, burnin=1000,
thin=90, rcov=~us(trait):units, verbose=T, slice=T, singular.ok = T, scale=T)}, mc.cores=10)

stay2<- mclapply(1:10,
function(i){MCMCglmm(cbind(STAY2,STAY3,STAY4,STAY5,STAY6,STAY7)~trait+1+trait
:AGE+trait:TB,random= ~us(trait):ID+us(trait):Dam+us(trait):BYR, ginverse=list(ID=Ainv1,
Dam=M1, BYR= BY),family=rep("threshold", 6),pr=T, prior=priorb, data=Phen,nitt=10000,
burnin=1000, thin=90, rcov=~us(trait):units, verbose=T, slice=T, singular.ok = T, scale=T)},
mc.cores=10)

stay3<- mclapply(1:10,
function(i){MCMCglmm(cbind(STAY2,STAY3,STAY4,STAY5,STAY6,STAY7)~trait+1+trait
:AGE+trait:TB+trait:TR,random= ~us(trait):ID+us(trait):Dam+us(trait):BYR,
```

```
ginverse=list(ID=Ainv1, Dam=M1, BYR= BY),family=rep("threshold", 6),pr=T, prior=priorb,
data=Phen,nitt=10000, burnin=1000, thin=90, rcov=~us(trait):units, verbose=T, slice=T,
singular.ok = T, scale=T)}, mc.cores=10)
```

```
stay4<- mclapply(1:10,
function(i){MCMCglmm(cbind(STAY2,STAY3,STAY4,STAY5,STAY6,STAY7)~trait+1+trait
:AGE+trait:TB_recode+trait:TBRE+trait:DTB,random=
~us(trait):ID+us(trait):Dam+us(trait):BYR, ginverse=list(ID=Ainv1, Dam=M1, BYR=
BY),family=rep("threshold", 6),pr=T, prior=priorb, data=Phen,nitt=10000, burnin=1000,
thin=90, rcov=~us(trait):units, verbose=T, slice=T, singular.ok = T, scale=T)}, mc.cores=10)
```

```
stay5<- mclapply(1:10,
function(i){MCMCglmm(cbind(STAY2,STAY3,STAY4,STAY5,STAY6,STAY7)~trait+1+trait
:AGE+trait:TB_recode+trait:TBRE+trait:DTB+trait:DTR,random=
~us(trait):ID+us(trait):Dam+us(trait):BYR, ginverse=list(ID=Ainv1, Dam=M1, BYR=
BY),family=rep("threshold", 6),pr=T, prior=priorb, data=Phen,nitt=10000, burnin=1000,
thin=90, rcov=~us(trait):units, verbose=T, slice=T, singular.ok = T, scale=T)}, mc.cores=10)
```

### Stayability dominance models

```
priora<- list(R=list(V=diag(6),nu=6, fix=0),G=list(G1=list(V=diag(6), nu=6),
G2=list(V=diag(6), nu=6), G3=list(V=diag(6), nu=6), G4=list(V=diag(6), nu=6)))
```

```
stay1d<- mclapply(1:10,
function(i){MCMCglmm(cbind(STAY2,STAY3,STAY4,STAY5,STAY6,STAY7)~trait+1+trait
:AGE,random= ~us(trait):ID+us(trait):Dam+us(trait):BYR+us(trait):ID2,
ginverse=list(ID=Ainv1, Dam=M1, BYR= BY, ID2=Dinv1),family=rep("threshold", 6),pr=T,
prior=priora, data=Phen,nitt=20000, burnin=11000, thin=90, rcov=~us(trait):units, verbose=T,
slice=T, singular.ok = T, scale=T)}, mc.cores=10)
```

```
stay2d<- mclapply(1:10,
function(i){MCMCglmm(cbind(STAY2,STAY3,STAY4,STAY5,STAY6,STAY7)~trait+1+trait
:AGE+trait:TB,random= ~us(trait):ID+us(trait):Dam+us(trait):BYR+us(trait):ID2,
ginverse=list(ID=Ainv1, Dam=M1, BYR= BY, ID2=Dinv1),family=rep("threshold", 6),pr=T,
prior=priora, data=Phen,nitt=20000, burnin=11000, thin=90, rcov=~us(trait):units, verbose=T,
slice=T, singular.ok = T,
```

```
scale=T)}, mc.cores=10)
```

```
stay3d<- mclapply(1:10,
function(i){MCMCglmm(cbind(STAY2,STAY3,STAY4,STAY5,STAY6,STAY7)~trait+1+trait
:AGE+trait:TB+trait:TR,random= ~us(trait):ID+us(trait):Dam+us(trait):BYR+us(trait):ID2,
ginverse=list(ID=Ainv1, Dam=M1, BYR= BY, ID2=Dinv1),family=rep("threshold", 6),pr=T,
prior=priora, data=Phen,nitt=20000, burnin=11000, thin=90, rcov=~us(trait):units, verbose=T,
slice=T, singular.ok = T,
```

```
scale=T)}, mc.cores=10)
```



```

stay4d<- mclapply(1:10,
function(i){MCMCglmm(cbind(STAY2,STAY3,STAY4,STAY5,STAY6,STAY7)~trait+1+trait
:AGE+trait:TB+trait:TR+trait:DTB,random=
~us(trait):ID+us(trait):Dam+us(trait):BYR+us(trait):ID2, ginverse=list(ID=Ainv1, Dam=M1,
BYR= BY, ID2=Dinv1),family=rep("threshold", 6),pr=T, prior=priora, data=Phen,nitt=20000,
burnin=11000, thin=90, rcov=~us(trait):units, verbose=T, slice=T, singular.ok = T,
scale=T)}, mc.cores=10)

stay5d<- mclapply(1:10,
function(i){MCMCglmm(cbind(STAY2,STAY3,STAY4,STAY5,STAY6,STAY7)~trait+1+trait
:AGE+trait:TB+trait:TR+trait:DTB+trait:DTR,random=
~us(trait):ID+us(trait):Dam+us(trait):BYR+us(trait):ID2, ginverse=list(ID=Ainv1, Dam=M1,
BYR= BY, ID2=Dinv1),family=rep("threshold", 6),pr=T, prior=priora, data=Phen,nitt=20000,
burnin=11000, thin=90, rcov=~us(trait):units, verbose=T, slice=T, singular.ok = T,
scale=T)}, mc.cores=10)

```

### Stayability univariate additive model

```

prior.reml<-list(G=list(G1=list(V=1,nu=1000), G3=list(V=1,nu=1000),
G3=list(V=1,nu=1000)),R = list(V =1, nu =1000))

model9 <- mclapply(1:10, function(i) {MCMCglmm(STAY7~factor(TB) +factor(TR) +
factor(DTB) + factor(DTR) + factor(AGE), random=~ID+Dam+BYR, data=Phen,
family="threshold",ginverse=list(ID=Ainv1, Dam=M1, BYR=BY), prior=prior.reml, pr = T,
slice = T, singular.ok = T, scale=T, nitt=10000, burnin=1000, thin=90, verbose=T)},
mc.cores=10)

```

### Stayability univariate dominance model

```

prior.rem<-list(G=list(G1=list(V=1,nu=1000), G3=list(V=1,nu=1000), G3=list(V=1,nu=1000),
G4=list(V=1,nu=1000)),R = list(V =1, nu =1000))

model9 <- mclapply(1:10, function(i) {MCMCglmm(STAY7~factor(TB) + factor(TR) +
factor(DTB) + factor(DTR) + factor(AGE), random=~ID+Dam+BYR+ID2, data=Phen,
family="threshold",ginverse=list(ID=Ainv1, Dam=M1, BYR=BY, ID2=Dinv1), prior=prior.rem,
pr = T, slice = T, singular.ok = T, scale=T, nitt=20000, burnin=11000, thin=90, verbose=T)},
mc.cores=10)

```

## Parallel chains combination codes

```
testSol <- lapply(model9, function(m) m$Sol[,1:19])
testSol <- do.call(mcmc.list, testSol)
testVCV = lapply(model9, function(m) m$VCV)
testVCV = do.call(mcmc.list, testVCV)
aSOL = autocorr.diag(testSol) #average across chains
aVCV = autocorr.diag(testVCV) #average across chains
#Effective sample sizes across chains
keptchains = attributes(model9[[1]]$VCV)$dim[1]*10
effratioSOL = round(effectiveSize(testSol)/keptchains,2)
effratioVCV = round(effectiveSize(testVCV)/keptchains,2)
SOL = summary(testSol)
VCV = summary(testVCV)
Summary =
matrix(c(round(effectiveSize(testSol),2),round(effectiveSize(testVCV),2),effratioSOL,effratioVCV,
t(round(aSOL[2,],4)),t(round(aVCV[2,],4)),round(SOL$statistics,3),round(VCV$statistics,3)
),byrow=FALSE,ncol=7)
rownames(Summary)=names(c(effratioSOL,effratioVCV))
colnames(Summary)=c("ESS", "Ratio", "Autocorrelation", "Mean", "SD", "NaiveSE", "Time-
SeriesSE")
DIC=c(round(model9[[1]]$DIC,2),round(model9[[2]]$DIC,2),round(model9[[3]]$DIC,2),round(
model9[[4]]$DIC,2),round(model9[[5]]$DIC,2),round(model9[[6]]$DIC,2),round(model9[[7]]$
DIC,2),round(model9[[8]]$DIC,2),round(model9[[9]]$DIC,2),round(model9[[10]]$DIC,2))
paste("Sample size = ",keptchains)
Summary
paste("DIC per
chain:",DIC[1],DIC[2],DIC[3],DIC[4],DIC[5],DIC[6],DIC[7],DIC[8],DIC[9],DIC[10],".
Average DIC is:",round(mean(DIC),2))
test_1CSol =
as.mcmc(rbind(model9[[1]]$Sol,model9[[2]]$Sol,model9[[3]]$Sol,model9[[4]]$Sol,model9[[5]]
$Sol,model9[[6]]$Sol,model9[[7]]$Sol,model9[[8]]$Sol,model9[[9]]$Sol,model9[[10]]$Sol))
test_1CVCV =
as.mcmc(rbind(model9[[1]]$VCV,model9[[2]]$VCV,model9[[3]]$VCV,model9[[4]]$VCV,mod
el9[[5]]$VCV,model9[[6]]$VCV,model9[[7]]$VCV,model9[[8]]$VCV,model9[[9]]$VCV,mode
l9[[10]]$VCV))
combMod = list(Sol = test_1CSol, Lambda = NULL, VCV = test_1CVCV, CP = NULL, Liab =
NULL, Fixed = model9[[1]]$Fixed, Random = model9[[1]]$Random, Residual =
model9[[1]]$Residual, Deviance =
as.mcmc(c(model9[[1]]$Deviance,model9[[2]]$Deviance,model9[[3]]$Deviance,model9[[4]]$D
eviance,model9[[5]]$Deviance,model9[[6]]$Deviance,model9[[7]]$Deviance,model9[[8]]$Devi
ance,model9[[9]]$Deviance,model9[[10]]$Deviance)),DIC = round(mean(DIC),2), X =
model9[[1]]$X, Z = model9[[1]]$Z, ZR = model9[[1]]$ZR, XL = NULL, ginverse =
model9[[1]]$ginverse,
error.term = model9[[1]]$error.term, family = model9[[1]]$family, Tune = model9[[1]]$Tune,
meta = model9[[1]]$meta, y.additional = model9[[1]]$y.additional)
```

```
class(combMod) = "MCMCglmm"
```

## APPENDIX D: SUMMARY STATISTICS R CODES

### Longevity summary statistics codes

```
longs <- Phen %>% group_by(TB_recode) %>%  
  summarise(mean = mean(Longevity), sd=sd(Longevity))  
longs <- Phen %>% group_by(TBRE) %>%  
  summarise(mean = mean(Longevity), sd=sd(Longevity))  
longs <- Phen %>% group_by(DTB) %>%  
  summarise(mean = mean(Longevity), sd=sd(Longevity))  
longs <- Phen %>% group_by(DTR) %>%  
  summarise(mean = mean(Longevity), sd=sd(Longevity))
```

### Stayability summary statistics codes

```
stats <- Phen %>% group_by(TB_recode) %>%  
  summarise(mean = mean(STAY2), sd=sd(STAY2))  
stats <- Phen %>% group_by(TB_recode) %>%  
  summarise(mean = mean(STAY3), sd=sd(STAY3))  
stats <- Phen %>% group_by(TB_recode) %>%  
  summarise(mean = mean(STAY4), sd=sd(STAY4))  
stats <- Phen %>% group_by(TB_recode) %>%  
  summarise(mean = mean(STAY5), sd=sd(STAY5))  
stats <- Phen %>% group_by(TB_recode) %>%  
  summarise(mean = mean(STAY6), sd=sd(STAY6))  
stats <- Phen %>% group_by(TB_recode) %>%  
  summarise(mean = mean(STAY7), sd=sd(STAY7))  
stats <- Phen %>% group_by(TBRE) %>%
```

```

        summarise(mean = mean(STAY2), sd=sd(STAY2))
stats <- Phen %>% group_by(TBRE) %>%
        summarise(mean = mean(STAY3), sd=sd(STAY3))
stats <- Phen %>% group_by(TBRE) %>%
        summarise(mean = mean(STAY4), sd=sd(STAY4))
stats <- Phen %>% group_by(TBRE) %>%
        summarise(mean = mean(STAY5), sd=sd(STAY5))
stats <- Phen %>% group_by(TBRE) %>%
        summarise(mean = mean(STAY6), sd=sd(STAY6))
stats <- Phen %>% group_by(TBRE) %>%
        summarise(mean = mean(STAY7), sd=sd(STAY7))
stats <- Phen %>% group_by(DTB) %>%
        summarise(mean = mean(STAY2), sd=sd(STAY2))
stats <- Phen %>% group_by(DTB) %>%
        summarise(mean = mean(STAY3), sd=sd(STAY3))
stats <- Phen %>% group_by(DTB) %>%
        summarise(mean = mean(STAY4), sd=sd(STAY4))
stats <- Phen %>% group_by(DTB) %>%
        summarise(mean = mean(STAY5), sd=sd(STAY5))
stats <- Phen %>% group_by(DTB) %>%
        summarise(mean = mean(STAY6), sd=sd(STAY6))
stats <- Phen %>% group_by(DTB) %>%
        summarise(mean = mean(STAY7), sd=sd(STAY7))
stats <- Phen %>% group_by(DTR) %>%
        summarise(mean = mean(STAY2), sd=sd(STAY2))

```

```
stats <- Phen %>% group_by(DTR) %>%  
  summarise(mean = mean(STAY3), sd=sd(STAY3))  
stats <- Phen %>% group_by(DTR) %>%  
  summarise(mean = mean(STAY4), sd=sd(STAY4))  
stats <- Phen %>% group_by(DTR) %>%  
  summarise(mean = mean(STAY5), sd=sd(STAY5))  
stats <- Phen %>% group_by(DTR) %>%  
  summarise(mean = mean(STAY6), sd=sd(STAY6))  
stats <- Phen %>% group_by(DTR) %>%  
  summarise(mean = mean(STAY7), sd=sd(STAY7))
```

## APPENDIX E: HERITABILITY R CODES

### Longevity additive model heritability codes

```
library(MCMCglmm)
Model8 = function(Model81){Model81= mcmc(data =cbind(
ID_variance = Model81$VCV[,1],
MPE_variance = Model81$VCV[,2],
BYR_variance = Model81$VCV[,3],
unit_variance = Model81$VCV[,4],
phen_variance = (Model81$VCV[,1] +Model81$VCV[,2] + Model81$VCV[,3] +
Model81$VCV[,4])))
Model81 = mcmc(data =cbind(Model81, heritability =
Model81["ID_variance"]/Model81["phen_variance"]))
return(Model81)
heri = summary(Model8(mcmcmodel)) $statistics
heri = round(heri, 4)
print(heri)
```

### Longevity additive + dominance model heritability codes

```
library(MCMCglmm)
Model8 = function(Model81){Model81= mcmc(data =cbind(ID_variance = Model81$VCV[,1],
ID2_variance = Model81$VCV[,2],
MPE_variance = Model81$VCV[,3],
BYR_variance = Model81$VCV[,4],
unit_variance = Model81$VCV[,5],
phen_variance = (Model81$VCV[,1] + Model81$VCV[,2]+Model81$VCV[,3] +
Model81$VCV[,4] + Model81$VCV[,5])))
Model81 = mcmc(data =cbind(Model81, heritability = Model81["ID_variance"]
+Model81["ID2_variance"]/Model81["phen_variance"]))
return(Model81)
domheri = summary(Model8(mcmcmodel)) $statistics
domheri = round(heri, 4)
print(domheri)
```

### Genetic correlation codes

```
corr23 <- round((multivariatestaymodel$VCV[, 'traitSTAY3:traitSTAY2.ID'] )/
sqrt((multivariatestaymodel$VCV[, 'traitSTAY2:traitSTAY2.ID'] ) *
(multivariatestaymodel$VCV[, 'traitSTAY3:traitSTAY3.ID'])), 4)
summary(corr23)
```

```
corr24 <- round((multivariatestaymodel$VCV[, 'traitSTAY4:traitSTAY2.ID'] )/
sqrt((multivariatestaymodel$VCV[, 'traitSTAY2:traitSTAY2.ID'] ) *
(multivariatestaymodel$VCV[, 'traitSTAY4:traitSTAY4.ID'])), 4)
summary(corr24)
```

```
corr25 <- round((multivariatestaymodel$VCV[, 'traitSTAY5:traitSTAY2.ID'] )/  
sqrt((multivariatestaymodel$VCV[, 'traitSTAY2:traitSTAY2.ID'] ) *  
(multivariatestaymodel$VCV[, 'traitSTAY5:traitSTAY5.ID'])), 4)  
summary(corr25)
```

```
corr26 <- round((multivariatestaymodel$VCV[, 'traitSTAY6:traitSTAY2.ID'] )/  
sqrt((multivariatestaymodel$VCV[, 'traitSTAY2:traitSTAY2.ID'] ) *  
(multivariatestaymodel$VCV[, 'traitSTAY6:traitSTAY6.ID'])), 4)  
summary(corr26)
```

```
corr27 <- round((multivariatestaymodel$VCV[, 'traitSTAY7:traitSTAY2.ID'] )/  
sqrt((multivariatestaymodel$VCV[, 'traitSTAY2:traitSTAY2.ID'] ) *  
(multivariatestaymodel$VCV[, 'traitSTAY7:traitSTAY7.ID'])), 4)  
summary(corr27)
```

```
corr34 <- round((multivariatestaymodel$VCV[, 'traitSTAY4:traitSTAY3.ID'] )/  
sqrt((multivariatestaymodel$VCV[, 'traitSTAY3:traitSTAY3.ID'] ) *  
(multivariatestaymodel$VCV[, 'traitSTAY4:traitSTAY4.ID'])), 4)  
summary(corr34)
```

```
corr35 <- round((multivariatestaymodel$VCV[, 'traitSTAY5:traitSTAY3.ID'] )/  
sqrt((multivariatestaymodel$VCV[, 'traitSTAY3:traitSTAY3.ID'] ) *  
(multivariatestaymodel$VCV[, 'traitSTAY5:traitSTAY5.ID'])), 4)  
summary(corr35)
```

```
corr36 <- round((multivariatestaymodel$VCV[, 'traitSTAY6:traitSTAY3.ID'] )/  
sqrt((multivariatestaymodel$VCV[, 'traitSTAY3:traitSTAY3.ID'] ) *  
(multivariatestaymodel$VCV[, 'traitSTAY6:traitSTAY6.ID'])), 4)  
summary(corr36)
```

```
corr37 <- round((multivariatestaymodel$VCV[, 'traitSTAY7:traitSTAY3.ID'] )/  
sqrt((multivariatestaymodel$VCV[, 'traitSTAY3:traitSTAY3.ID'] ) *  
(multivariatestaymodel$VCV[, 'traitSTAY7:traitSTAY7.ID'])), 4)  
summary(corr37)
```

```
corr45 <- round((multivariatestaymodel$VCV[, 'traitSTAY5:traitSTAY4.ID'] )/  
sqrt((multivariatestaymodel$VCV[, 'traitSTAY4:traitSTAY4.ID'] ) *  
(multivariatestaymodel$VCV[, 'traitSTAY5:traitSTAY5.ID'])), 4)  
summary(corr45)
```

```
corr46 <- round((multivariatestaymodel$VCV[, 'traitSTAY6:traitSTAY4.ID'] )/  
sqrt((multivariatestaymodel$VCV[, 'traitSTAY4:traitSTAY4.ID'] ) *  
(multivariatestaymodel$VCV[, 'traitSTAY6:traitSTAY6.ID'])), 4)  
summary(corr46)
```



```
corr47 <- round((multivariatestaymodel$VCV[, 'traitSTAY7:traitSTAY4.ID'] )/
sqrt((multivariatestaymodel$VCV[, 'traitSTAY4:traitSTAY4.ID'] ) *
(multivariatestaymodel$VCV[, 'traitSTAY7:traitSTAY7.ID'])), 4)
summary(corr47)
```

```
corr56 <- round((multivariatestaymodel$VCV[, 'traitSTAY6:traitSTAY5.ID'] )/
sqrt((multivariatestaymodel$VCV[, 'traitSTAY5:traitSTAY5.ID'] ) *
(multivariatestaymodel$VCV[, 'traitSTAY6:traitSTAY6.ID'])), 4)
summary(corr56)
```

```
corr57 <- round((multivariatestaymodel$VCV[, 'traitSTAY7:traitSTAY5.ID'] )/
sqrt((multivariatestaymodel$VCV[, 'traitSTAY5:traitSTAY5.ID'] ) *
(multivariatestaymodel$VCV[, 'traitSTAY7:traitSTAY7.ID'])), 4)
summary(corr57)
```

```
corr67 <- round((multivariatestaymodel$VCV[, 'traitSTAY7:traitSTAY6.ID'] )/
sqrt((multivariatestaymodel$VCV[, 'traitSTAY6:traitSTAY6.ID'] ) *
(multivariatestaymodel$VCV[, 'traitSTAY7:traitSTAY7.ID'])), 4)
summary(corr67)
```

### Estimated marginal means codes

```
pol = readRDS("read in MCMCglmm model")
Phen = read.delim2("read in phenotype data")
library(dplyr)
library(foreach)
library(emmeans)
Phen$ID2 = Phen$ID
Phen$Longevity[Phen$Longevity > 7] <- 7
Phen=Phen %>% filter(AGE <= 7)
Phen= Phen %>%filter(BRWT > 0)
Phen$Dam = as.character(Phen$Dam)
gridemm <- update(ref_grid(pol, data = Phen, type = "response"), tran = "logit") #log-
transformed line for stayability to age seven models
emmeans(gridemm, "TB_recode")
gridemm1 <- ref_grid(pol, data = Phen) #longevity models
emmeans(gridemm1, "TB_recode")
```

Table E.1: Summary statistics for Additive + Dominance (A+D) models

Statistics <sup>1</sup>	Breeds				
	Across <sup>2</sup>	Columbia	Polypay	Rambouillet	Targhee
Effective sample size					
Intercept	1,000	1,000	1,000	903.7	1,000
STM	912.6	--	--	--	--
AGE	1,000	1,000	1,184.1	1,114.3	1,177
TB	1,000	1,000	1,000	1,000	1,000
TR	1,142.2	1,000	1,000	1,000	1,000
DTB	1,000	1,000	1,000	1,000	1,000
DTR	1,000	1,000	1,000	1,000	1,000
ID	1,000	1,000	614.3	684.4	819.5
ID2	79.62	314.6	137.2	140.4	102.9
MPE	817.4	750.4	1,000	770.9	912
BYR	861.1	1,106	1,000	913.3	911.2
R	89.75	304	140.7	127.7	101.3
Autocorrelation					
Intercept	-0.0106	-0.0343	0.0316	0.0501	-0.0306
STM	0.0451	--	--	--	--
AGE	-0.0109	-0.0146	0.0452	0.0014	-0.0174
TB	0.0333	0.0040	0.0288	-0.0383	0.0277
TR	-0.0145	0.0040	0.0629	0.0280	0.0027
DTB	-0.0600	0.0095	0.0293	-0.0056	-0.0609
DTR	0.0702	-0.0157	0.0658	0.0237	0.0286
ID	-0.0018	0.0327	0.2384	0.1868	0.0986
ID2	0.8381	0.5209	0.7584	0.7534	0.7957
MPE	0.0999	0.0558	-0.0036	0.0823	0.0455
BYR	0.0741	-0.0508	-0.0003	0.0447	0.0459
R	0.8153	0.4921	0.7276	0.7409	0.7980
DIC	43,913.82	9,187.47	10,798.83	11,702.46	11,452.04
Variance Estimate					
ID	0.32	0.15	0.16	0.17	0.07
ID2	0.33	0.64	0.82	0.90	1.44
MPE	0.01	0.13	0.03	0.03	0.03
BYR	0.11	0.06	0.17	0.22	0.14
R	3.22	2.86	3.06	3.07	2.26
P	3.99	3.84	4.24	4.39	3.94

Prior E was coded as list(R = list(V=1,nu=1), G = list(G1=list(V=1,nu=1,alpha.mu=0,alpha.V=1000), G2 = list(V1,nu=1,alpha.mu=0,alpha.V=1000) , G3 = list(V1,nu=1,alpha.mu=0,alpha.V=1000) , G4 = list(V1,nu=1,alpha.mu=0,alpha.V=1000))) using Gaussian family distribution with 20,000 iterations, burn-in of

11,000, thinning interval of 90, resulting in an expected effective sample size of 1,000 per breed parameter. <sup>1</sup>Model effects could include fixed effects of intercept (mean), Age of ewe (AGE), ewe birth type (TB), ewe rear type (TR), ewe's dam's birth type (DTB), ewe's dam's rear type (DTR) and random effects of individual ewe (ID) with relationship matrix (additive genetic variance), ewe's dam ID without pedigree (maternal permanent environmental variance), individual ewe's (ID2) with relationship matrix (dominance genetic variance), birth year (BYR), residual (R) variance, and phenotypic variance (P). The DIC is the deviance information criterion.

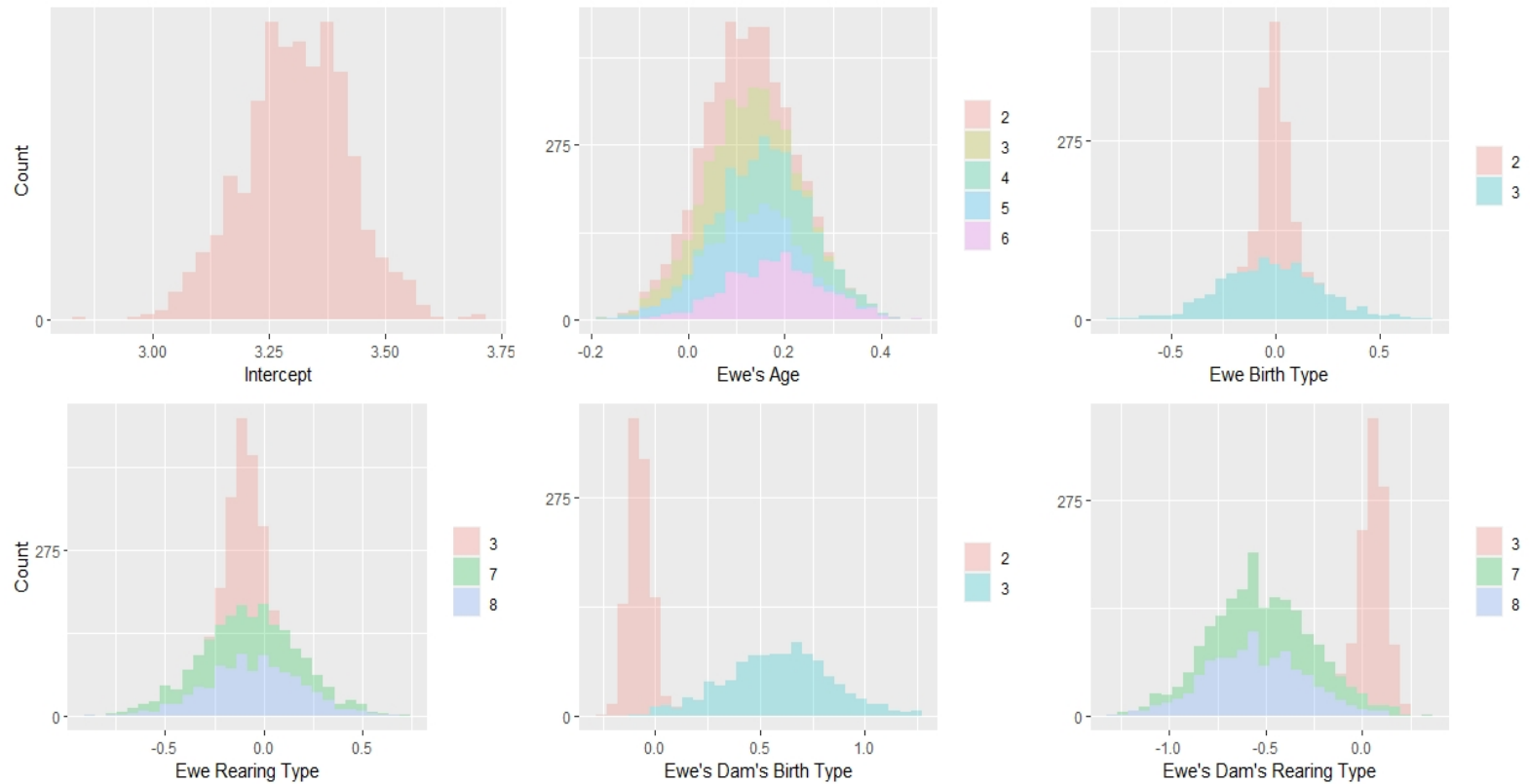


Figure E.1: Density plots of posterior estimates for fixed effects using Columbia longevity dataset when modeling additive genetic variance and dominance genetic variance. Density distributions should appear normal or bell-shaped to indicate proper mixing and convergence in the analysis was met.