

# Determining relatedness between South African and Australian Merino populations according to a genomic relationship matrix and its principal components

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## Introduction

- Genomic prediction of breeding value takes place in Australia but not in South Africa (SA)
- Combining genomic resources across countries could benefit evaluation of Merinos in SA, depending on relatedness of reference populations in the two countries
- The relatedness of Merino populations across countries was determined by genomic methods

## Methods

- Resource flocks (Elsenburg (400), Grootfontein (115), Cradock (127) and commercial ‘Industry’ animals (41) represented SA Merinos
- Australian samples were grouped by strain: Ultrafine (270), Fine Medium 1 (224), Fine Medium 2 (133) and Strong (291)
- Recent across-country links were all in the Cradock flock
- Four Australian sires were used in 1988, 2 in 1996 and 2 Ultrafine rams in 2002-2003

## Results

- Internal relationships for South African flocks were low, but positive
- Australian bloodlines were negatively related
- The highest relatedness was between the Cradock flock and the Australian Ultrafine bloodline (Figure 1)
- The first two principal components showed discernable clusters by population group
- More distant separations were seen for the Fine Medium 1 and Strong lines
- The SA Cradock flock plotted close to the Australian Fine Medium 2 and Ultrafine bloodlines (Figure 2)

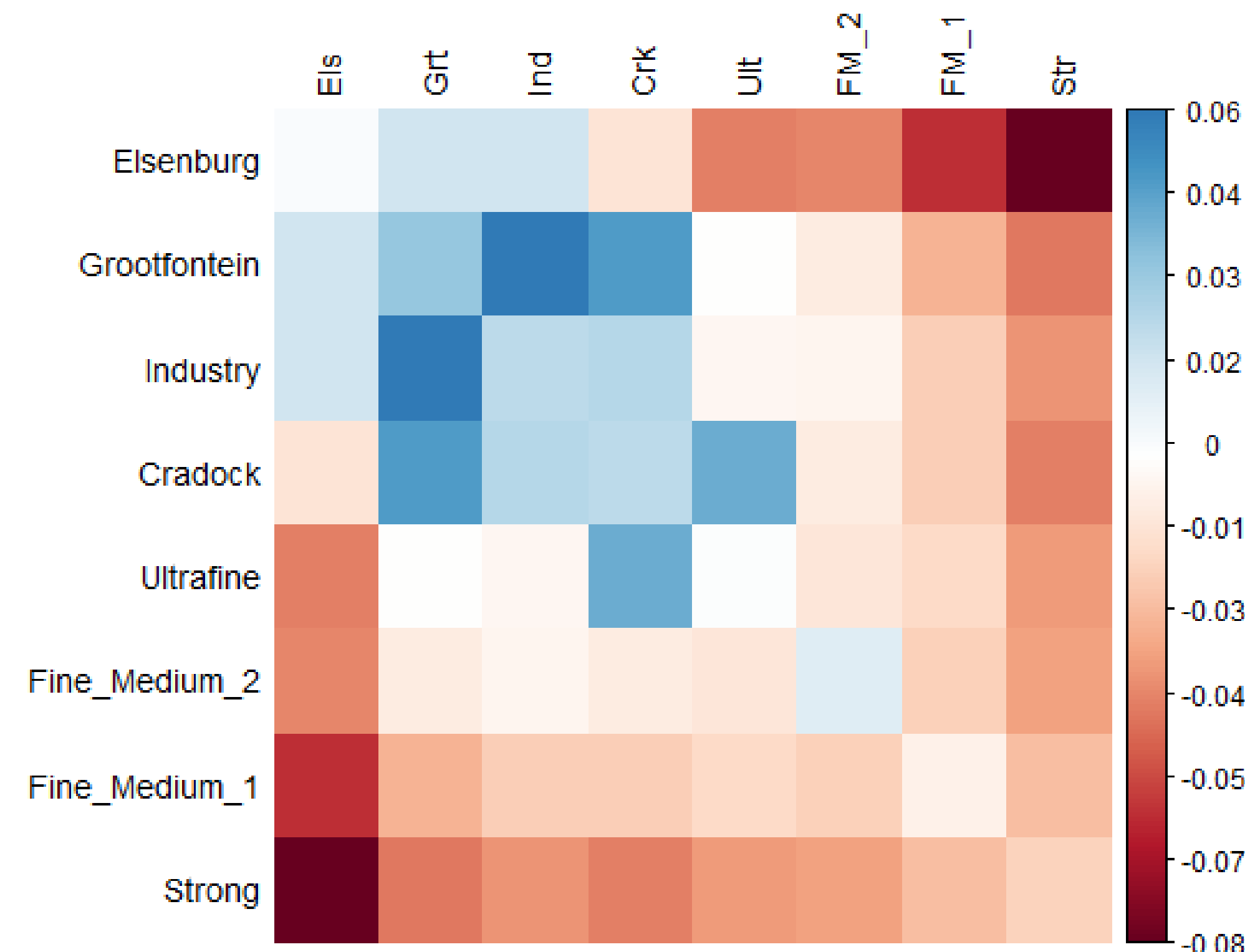


Figure 1 – Relatedness across populations calculated from the mean of the off-diagonal of the GRM

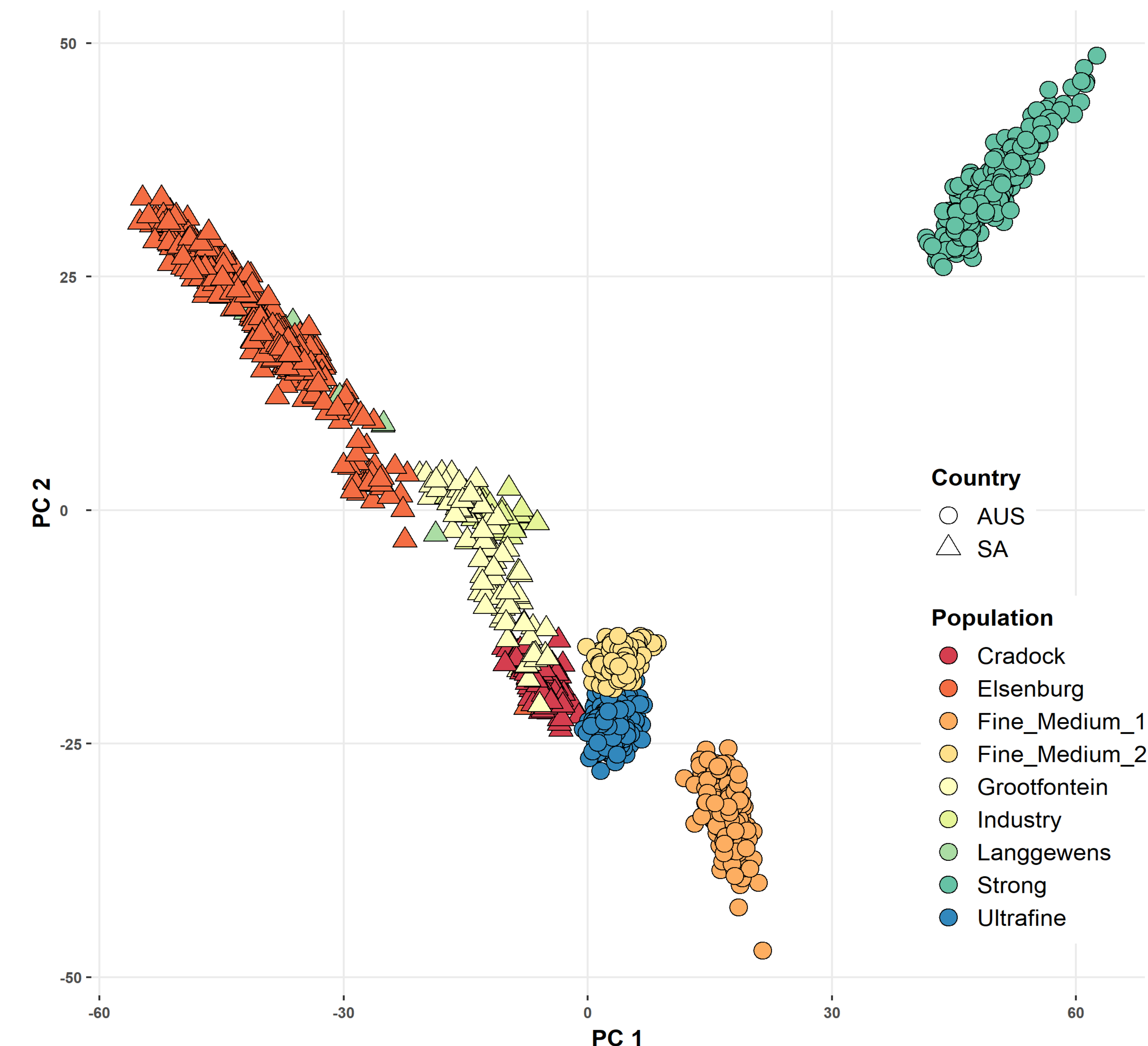


Figure 2 – The first (PC1) and second (PC2) principal components of the GRM with animals identified by flock and country of origin.

## Conclusions

- The relatedness among Merinos by country and subpopulation expanded knowledge of within-breed genetic variation
- The Cradock – Ultrafine comparison indicated that few recent genetic links could increase overall relatedness
- Research in across-country genomic prediction is recommended