

# ASA Experience with Incorporating Genomics into Genetic Evaluation

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# Background

- ◆ Got board approval to initiate development of GE-EPD in January, 2011
- ◆ Already had a DNA repository on heavily used Simmental-influenced bulls
  - ◆ Bull studs
    - ◆ ABS, Accelerated Genetics, Genex, Select Sires
  - ◆ Carcass Merit Program cooperators
  - ◆ Simmental breeders



# Business Model

- ◆ Send samples directly to GeneSeek for genotyping and computation of MBV
- ◆ Share genotypes with NBCEC for development and recalibration of prediction equations and other research
- ◆ Have access to raw genotypes, prediction equations and MBV
- ◆ Gives us flexibility in how we use genotypic data

# Project Collaborators

- USDA
- NBCEC
- Iowa State University
- Montana State University
- University of Illinois
- University Of Missouri
- University of Nebraska
- GeneSeek

# Development of 50K Training Panel

- ◆ 2,703 samples
  - ◆ Mostly purebred Simmental
  - ◆ Included SimAngus and a few Simbrah
- ◆ Genotyped at University of Missouri and GeneSeek
- ◆ Illumina BovineSNP50 BeadChip
  - ◆ 264 with BovineHD

# Development of 50K Training Panel

- ◆ Analyzed by NBCEC/Iowa State (Garrick and Saatchi)
- ◆ Computed deregressed EBV (DEBV) and weighting factors
- ◆ Produced estimates of SNP marker effects using BayesC
- ◆ Derived direct genomic breeding values (DGV)
- ◆ Evaluated accuracy of DGV using K-means clustering and 5-fold cross-validation

# Development of 50K Training Panel

- ◆ Fit DGV and DEBV from all 5 validation sets in weighted bivariate animal model to estimate (co)variance components
- ◆ Used estimated covariance between DGV and DEBV to estimate genetic correlations
- ◆ Genetic correlations represent accuracy of genomic predictions for each trait

Trait	Igenity (Neogen) <sup>a</sup>	Pfizer (Zoetis) <sup>a</sup>	NBCEC <sup>b</sup>
Direct CE	0.47	0.33	0.45
BW	0.57	0.51	0.65
WW	0.45	0.52	0.52
YW	0.34	0.64	0.45
Milk	0.24	0.32	0.34
Maternal CE	NA	NA	0.32
Stayability	NA	NA	0.58
CW	0.54	0.48	0.59
Marbling	0.65	0.57	0.63
REA	0.58	0.60	0.59
BF	0.50	0.56	0.29
WBSF	NA	NA	0.53

<sup>a</sup>When used on the American Angus Association population

<sup>b</sup>When used on American Simmental/SimAngus population



# Incorporation of MBV into MBGE

- ◆ Developed infrastructure in spring/summer of 2012
- ◆ Herdbook interim system
  - ◆ Blending method (Kachman, 2012)
- ◆ MBGE system
  - ◆ External EPD approach (Quaas and Zhang, 2006)

# External EPD Approach

- ◆ Accuracy dependent on pedigree ties in training population
  - ◆ More ties => more accurate
- ◆ External EPD approach takes accuracy of MBV into account
  - ◆ Proper weighting of MBV information
  - ◆ Less biased GE-EPD

# Incorporation of MBV into MBGE

- ◆ First incorporated MBV into fall 2012 MBGE
  - ◆ Weight, CE and carcass traits
  - ◆ 1,263 animals
  - ◆ MBV  $R^2 \leq 0.50$

# Approximation of Prediction Error Variance

- ◆ Noticed higher than expected accuracies on some animals
  - ◆ Also occurs in carcass evaluation
  - ◆ Attributed to method for approximating PEV

# Approximation of Prediction Error Variance

- ◆ Taylor series expansion of inverse matrices (Wang et al., 1995)
  - ◆ Ignores some off-diagonal elements
    - ◆ Decreases PEV
  - ◆ Results in artificially high accuracies on some animals
    - ◆ Low PEV => high accuracy

# Approximation of Prediction Error Variance

- ◆ Developed and implemented a method to temper inflated accuracies for carcass evaluation
  - ◆ Time consuming
  - ◆ Computationally expensive
- ◆ Used blending method only for spring and fall 2013 MBGE

# Scaling of DGV

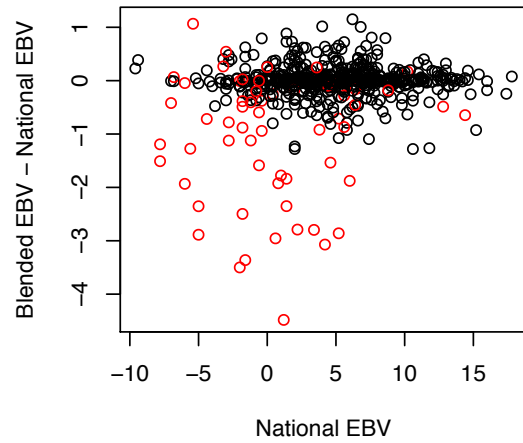
- ◆ DNA test results should have equal chance of increasing or decreasing an animal's EPD
- ◆ Changes in EPD should be independent of previous genetic predictions

# Scaling of DGV

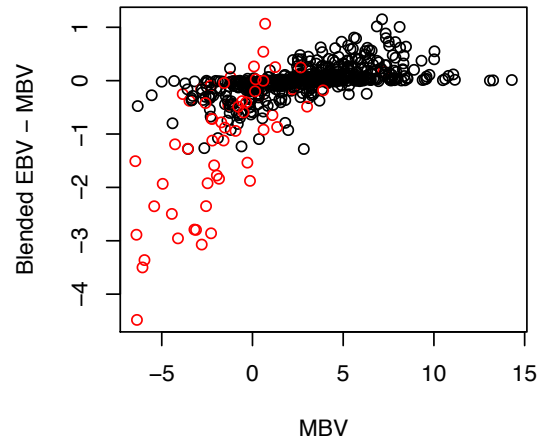
- ◆ Correlation between original EPD and difference between original EPD and GE-EPD should be 0
- ◆ Regression of GE-EPD (more accurate) on original EPD (less accurate) should be 1
  - ◆ Reverter et al., 1994



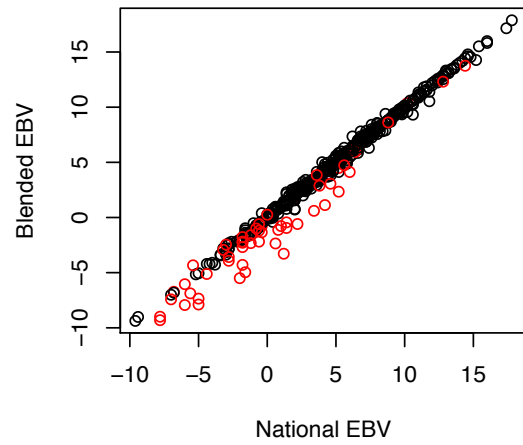
**CORR=0.15**



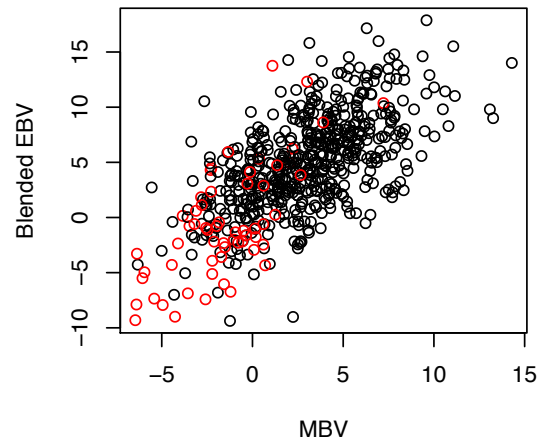
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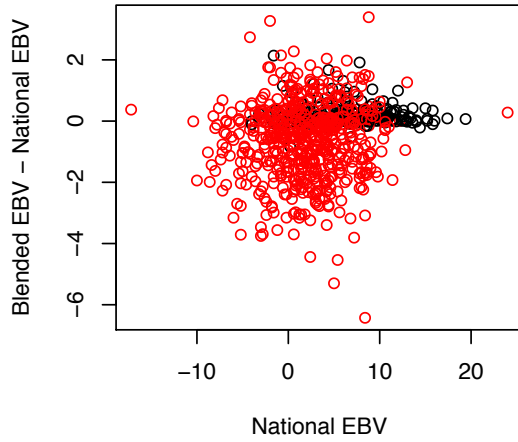
**SLOPE=1.02**



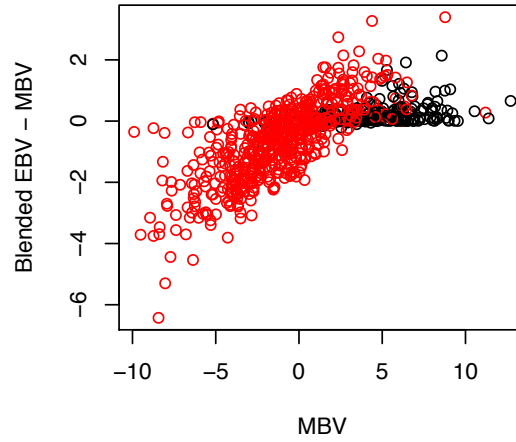
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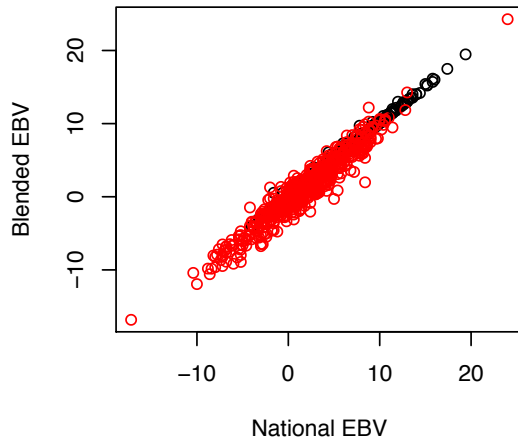
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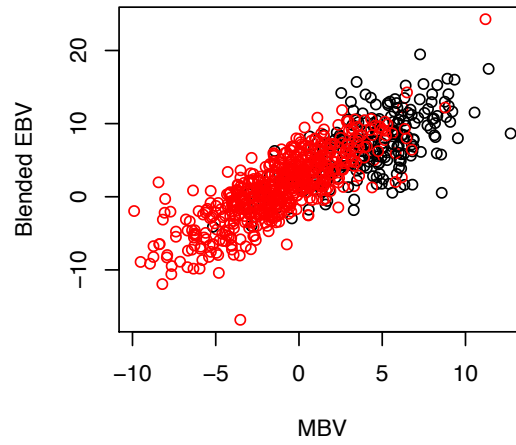
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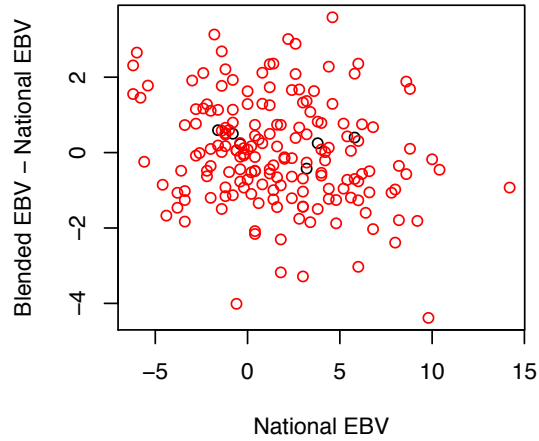
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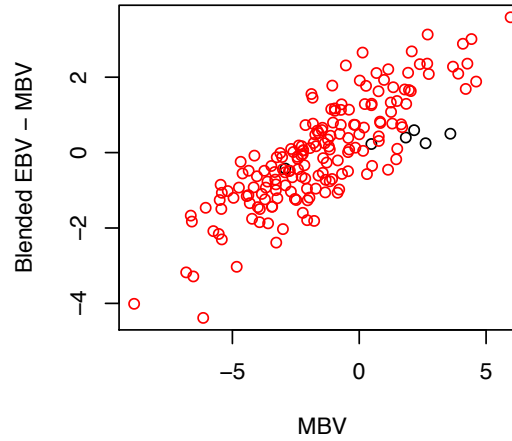
**SLOPE=0.69**



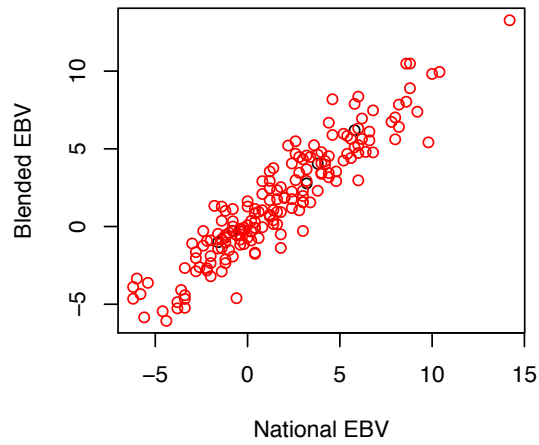
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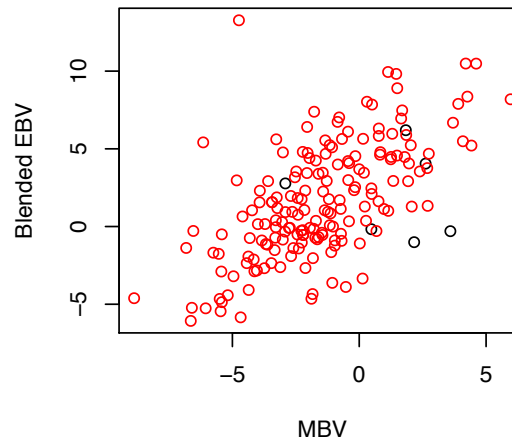
**CORR=0.82**



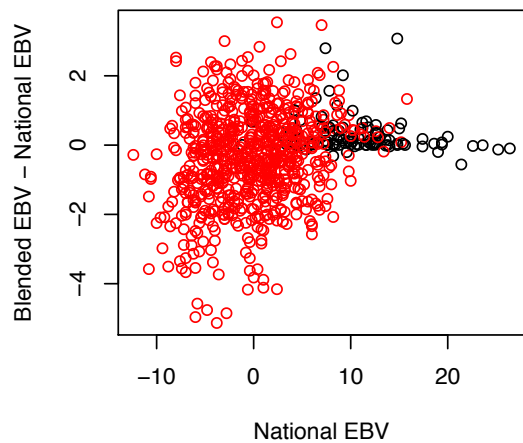
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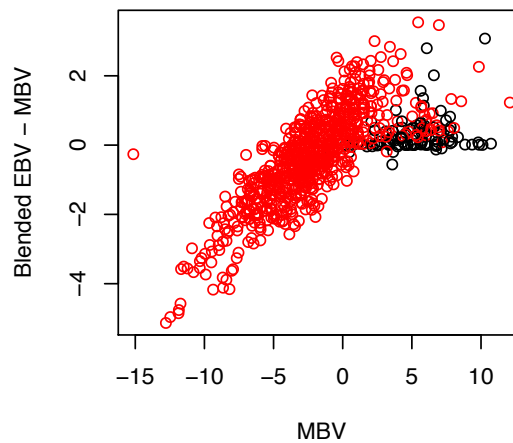
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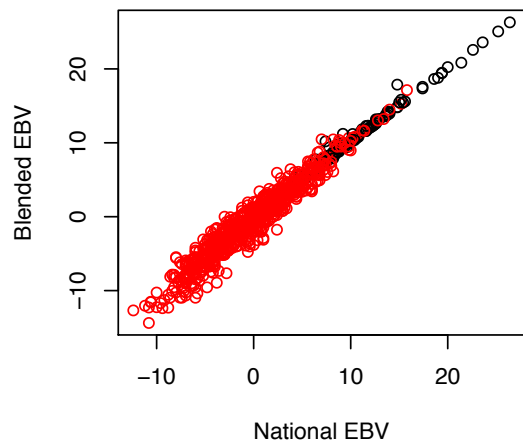
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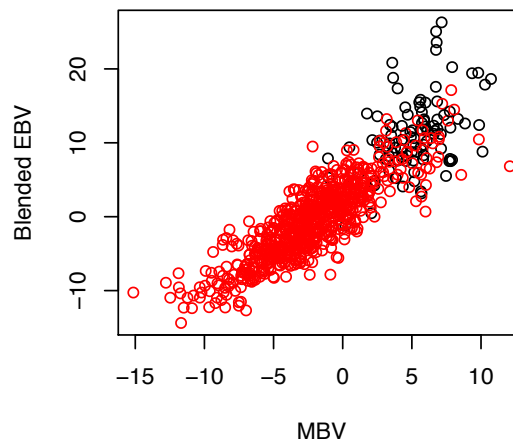
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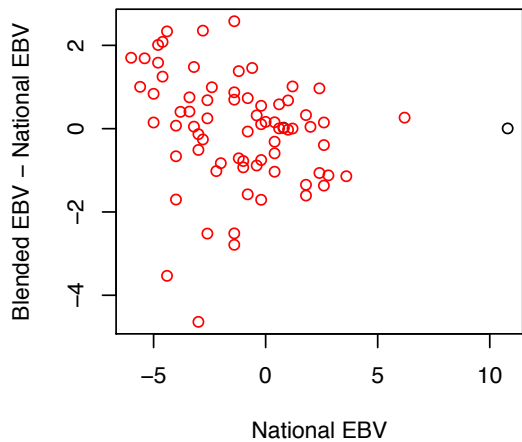
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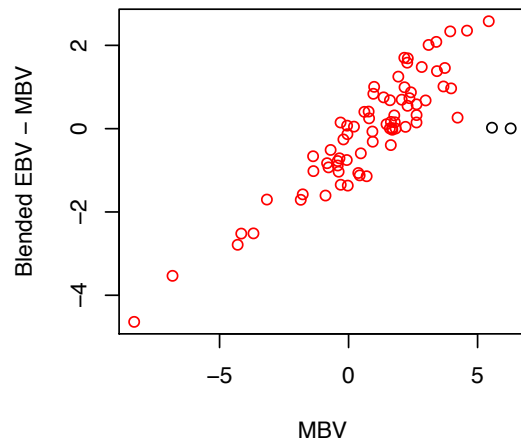
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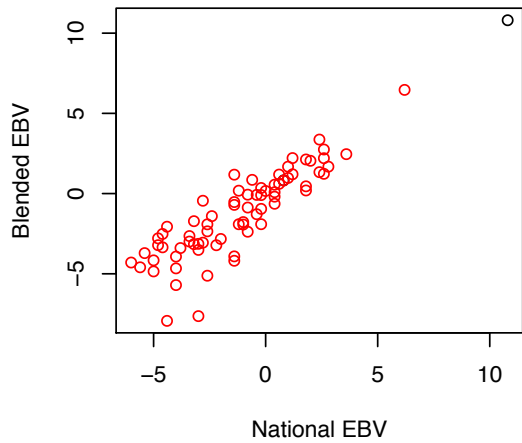
**CORR=-0.2**



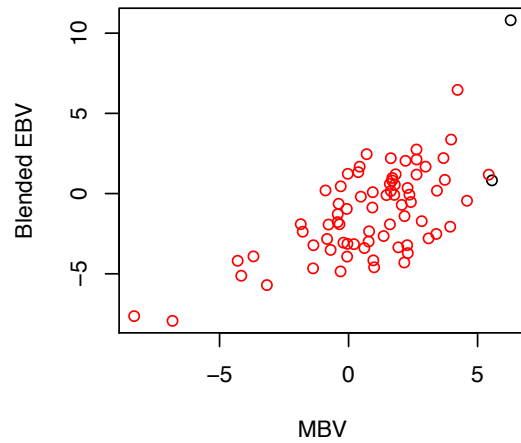
**CORR=0.87**



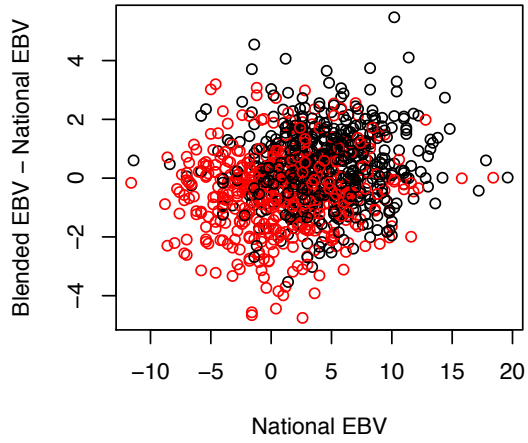
**SLOPE=0.91**



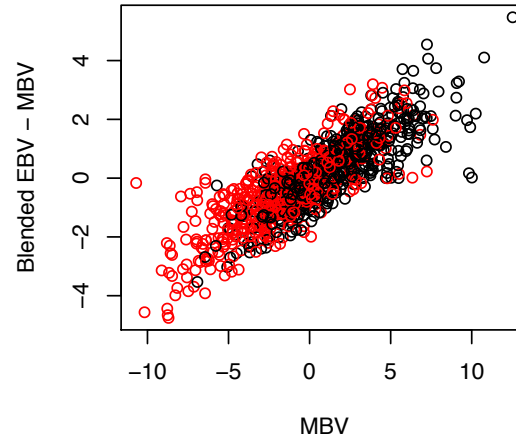
**SLOPE=0.6**



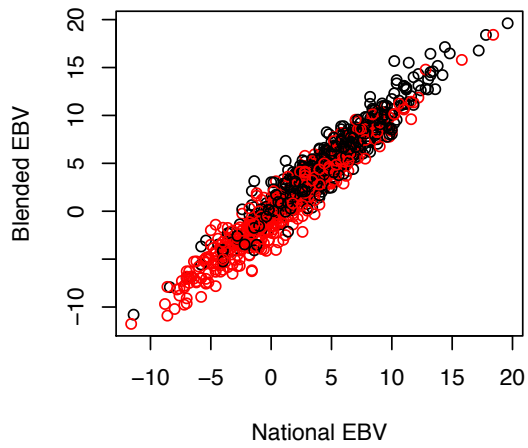
**CORR=0.19**



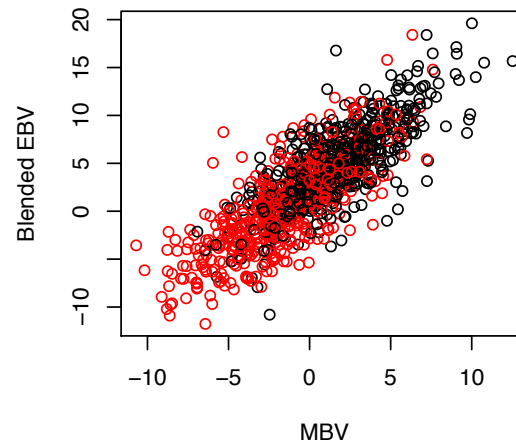
**CORR=0.83**



**SLOPE=1.06**



**SLOPE=0.69**



# Scaling of DGV

- ◆ Inappropriate scaling of DGV
- ◆ Double counting of information in DGV and EPD

# Scaling of DGV

- ◆ Derived multiplicative rescaling factors within fold for each trait
- ◆ Moved correlations closer to 0 and regressions closer to 1



# Scaling of DGV

- ◆ Re-released blended EPD on over 5,000 Simmental-influenced animals on November 1
- ◆ Spring 2014 evaluation currently in the works
  - ◆ May have to derive another set of stayability rescaling factors

# Conclusion

- ◆ ASA has had some negative experiences incorporating genomics into MBGE

**BUT . . .**

- ◆ Expect to have kinks after implementing new technology
- ◆ Firmly believe in potential of genomics to advance beef cattle breeding

