



DISCIPLINA	Tópicos Especiais: Genomic analyses with emphasis on single-step					
CÓDIGO	DZO4188					
NÍVEL	Mestrado/Doutorado					
CARGA HORÁRIA	45					
NÚMERO DE CRÉDITOS	Teóricos:	3	Práticos:		Total:	3

EMENTA

Genomic selection in breeding plans using the Single-step method.

PROGRAMA

1. Introduction to BLUPF90 family of programs: Animals model, Multiple trait model, Maternal models and Genomic model
2. Introduction to genomic selection: simple models
 - 2.1 - Data simulation (including genomics)
 - 2.2 - Methods based on SNP estimation (BLUP_SNP and BayesA, BayesB, BayesC etc.)
3. Genomic relationship matrix (G)
4. Theory of Single-step
 - 4.1 - Single-step for populations under selection. Bias, inflation, accuracy
 - 4.2 - Forming Single-step equations
 - 4.3 - Quality control for G
5. Practical results with Single-step
6. Experiences and future with ssGBLUP
7. GWAS in Single Step

BIBLIOGRAFIA

- RESENDE, M. D. V. Genômica quantitativa e seleção no melhoramento de plantas perenes e animais. Colombo: Embrapa Florestas, 2008. 330p.
- Aguilar, I., I. Misztal, D. L. Johnson, A. Legarra, S. Tsuruta, and T. J. Lawlor. 2010. Hot topic: A unified approach to utilize phenotypic, full pedigree, and genomic information for genetic evaluation of Holstein final score. *Journal of Dairy Science* 93: 743-752.
- Chen, C. Y., I. Misztal, I. Aguilar, A. Legarra, and W. M. Muir. 2011. Effect of different genomic relationship matrices on accuracy and scale. *J. Anim. Sci.* 89: 2673-2679.
- Fragomeni, B. O., D. A. L. Lourenco, S. Tsuruta, Y. Masuda, I. Aguilar, A. Legarra, T. J. Lawlor, and I. Misztal. 2015. Use of genomic single-step genomic BLUP with a large number of genotypes. *J. Dairy Sci.* 98: 4090-4094.
- Legarra, A., I. Aguilar, and I. Misztal. 2009. A relationship matrix including full pedigree and genomic information. *J. Dairy Sci.* 92: 4656-4663.
- Legarra, A., O. F. Chistensen, I. Aguilar, and I. Misztal. 2014. Single step, a general approach for genomic selection. *Livest. Prod. Sci.* 166: 54-65.
- Lourenco, D. A. L., I. Misztal, S. Tsuruta, I. Aguilar, E. Ezra, M. Ron, A. Shirak, and J. Weller. 2014. Methods for genomic evaluation of a relatively small genotyped dairy population and effect of genotyped cow information in multiparity analyses. *Journal of Dairy Science* 97: 1742-1752.
- Lourenco, D. A. L., B. O. Fragomeni, S. Tsuruta, I. Aguilar, B. Zumbach, R. J. Hawken, A. Legarra, and I. Misztal. 2015a. Accuracy of estimated breeding values with genomic information on males, females, or both: an example in broiler chicken. *Genet. Sel. Evol.* 47: 56.
- Lourenco, D. A. L., S. Tsuruta, B. O. Fragomeni, Y. Masuda, I. Aguilar, A. Legarra, J. K. Bertrand, T. Amen, L. Wang, D. W. Moser, and I. Misztal. 2015b. Genetic evaluation using single-step genomic best linear unbiased predictor in American Angus. *Journal of Animal Science* 93: 2653-2662.
- Misztal, I., A. Legarra, and I. Aguilar. 2009. Computing procedures for genetic evaluation including phenotypic, full pedigree, and genomic information. *Journal of Dairy Science* 92: 4648-4655.
- Misztal, I., I. Aguilar, A. Legarra, and T. J. Lawlor. 2010. Choice of parameters for single-step genomic evaluation for type. *J. Dairy Sci.* 93(Suppl. 1): 533.
- Misztal, I., A. Legarra, and I. Aguilar. 2014a. Using recursion to compute the inverse of the genomic relationship matrix. *J. Dairy Sci.* 97: 3943-3952.
- Misztal, I. 2016. Inexpensive computation of the inverse of the genomic relationship matrix in populations with small effective population size. *Genetics* 202: 401-409.
- Pocrnic, I., D. A. L. Lourenco, Y. Masuda, A. Legarra, and I. Misztal. 2016. The dimensionality of genomic information and its effect on genomic prediction. *Genetics* 203: 573-581.
- Sargolzaei, M., and F. S. Schenkel. 2009. QMSim: A large-scale genome simulator for livestock. *Bioinformatics* 25: 680-681.
- VanRaden, P. M. 2008. Efficient methods to compute genomic predictions. *Journal of Dairy Science* 91: 4414-4423.
- VanRaden, P. M., C. P. VanTassel, G. R. Wiggans, T. S. Sonstegard, R. D. Schnabel, J. F. Taylor, and F. S. Schenkel. 2009. Invited review: Reliability of genomic predictions for North American Holstein bulls. *J. Dairy Sci.* 92: 16-24.
- Wang, H., I. Misztal, I. Aguilar, A. Legarra, and W. M. Muir. 2012. Genome-wide association mapping including phenotypes from relatives without genotypes. *Genetics Research* 94: 73-83.

CRITÉRIO DE AVALIAÇÃO

- Avaliação por meio de atividades (exercícios) propostas em sala de aula;