Bibliography

3blue1brown (2016). What are vectors.

Arndorfer, M., Blauensteiner, P., Berger, B., Falschlunger, G., Fischerleitner, F., Froihofer, W., Gaber, R., Holzner, W., Kajtna, B., Koller, B., Kriechbaum, M., Machatschek, M., Neunteufel, M., Spitzenberger, F., Michael, S., Stekovics, E., Vogl, C., Vogl-Lukasser, B., Wallner, R. M., Wilfing, A., and Zipser, P. (2010). *Wie viele Arten braucht der Mensch?* Böhlau, Wien, Köln, Weimar.

Bayes, T. and Price, R. (1763). An Essay towards solving a Problem in the Doctrine of Chance. By the late Rev. Mr. Bayes, communicated by Mr. Price, in a letter to John Canton. *Philosophical Transactions of the Royal Society of London*, 53:370—-418.

Bulmer, M. G. (1971). The effect of selection on genetic variability. *Am Nat*, 105:201–211.

Duerst, J. U. (1931). *Grundlagen der Rinderzucht*. Springer, Berlin; Heidelberg.

Falconer, D. S. and Mackay, T. F. C. (1996). *Introduction to Quantitative Genetics*. Addison Wesley Longman Limited, Essex, 4 edition.

Gianola, D. and Fernando, R. L. (1986). Bayesian Methods in Animal Breeding Theory. *Journal of Animal Science*, 63(1):217–244.

Gianola, D. and Foulley, J. L. (1982). Non linear prediction of latent genetic liability with binary expression: An empirical Bayes approach. *Proc. 2nd World Congr. Genet. Appl. Livest. Prod., Madrid, Spain*, 7:293—-303.

Gianola, D. and Rosa, G. J. M. (2015). One Hundred Years of Statistical Developments in Animal Breeding. *Annual Review of Animal Biosciences*, 3:13.1—-13.38.

Hazel, L. N. (1943). The Genetic Basis for Constructing Selection Indexes. *Genetics*, 28(6):476–490.

Hazel, L. N. and Lush, J. L. (1942). The efficiency of three methods of selection. *Journal of Heredity*, 33(11):393–399.

Henderson, C. R. (1953). Estimation of variance and covariance components. *Biometrics*, 9:226—-252.

Henderson, C. R. (1973a). Sire evaluation and genetics trends. In *Proceedings of Animal Breeding and Genetic Symposium in Honor of Dr Jay Lush*, volume 1, pages 10–41.

Henderson, C. R. (1973b). Sire evaluation and genetics trends. *Proceedings of Animal Breeding and Genetic Symposium in Honor of Dr Jay Lush. American Society*, 1:10–41.

Henderson, C. R. (1975). Best linear unbiased estimation and prediction under a selection model. *Biometrics*, 31:423—-449.

Henderson, C. R. (1976). A simple method for computing the inverse of a numerator relationship matrix used in predicting of breeding values. *Biometrics*, 32:69—-83.

Meuwissen, T. H. E. (1997). Maximizing the response of selection with a predefined rate of inbreeding. *Journal of Animal Science*, 75:934—-940.

Meuwissen, T. H. E., Hayes, B. J., and Goddard, M. E. (2001a). Prediction of Total Genetic Value Using Genome-Wide Dense Marker Maps. *Genetics*, 157:1819–1829.

Meuwissen, T. H. E., Hayes, B. J., and Goddard, M. E. (2001b). Prediction of Total Genetic Value Using Genome-Wide Dense Marker Maps. *Genetics*, 157(157):1819–1829.

Moore, G. E. (1965). Cramming more components onto integrated circuits. *Electronics*, 38.

Mrode, R. A. (2005). *Linear Models for the Prediction of Animal Breeding Values.* CABI Publishing, Wallingford, Oxfordshire OX10 8DE, 2nd edition.

Nipp, K. and Stoffer, D. (2002). *Lineare Algebra.* vdf Hochschulverlag, Zurich, 5 edition.

Quaas, R. L. (1976). Computing the diagonal elements and inverse of a large numerator relationship matrix. *Biometrics*, 32:949–953.

R Core Team (2018). R: A language and environment for statistical computing.

Schaeffer, L. R. (1984). Sire and cow evaluation under multiple trait models. *Journal of Dairy Science*, 67:1567—-1580.

Schaeffer, L. R. (2006). Strategy for applying genome-wide selection in dairy cattle. *J Anim Breed Genet*, (123):218–223.

Schaeffer, L. R. (2013). *History of Genetic Evaluation Methods in Dairy Cattle.* self.

Searle, S. R. (1971). *Linear Models.* John Wiley & Sons, New York, wiley clas edition.

Thompson, R. and Meyer, K. (1986). A review of theoretical aspects in the estimation of breeding values for multi-trait selection. *Livestock Production Science*, 15:299—-313.

VanRaden, P. M. (2008). Efficient methods to compute genomic predictions. *J. Dairy Sci.*, (91):4414—-4423.

Venter, J. C., Adams, M. D., Myers, E. W., Li, P. W., Mural, R. J., Sutton, G. G., Smith, H. O., Yandell, M., Evans, C. A., Holt, R. A., Gocayne, J. D., Amanatides, P., Ballew, R. M., Huson, D. H., Wortman, J. R., Zhang, Q., Kodira, C. D., Zheng, X. H., Chen, L., Skupski, M., Subramanian, G., Thomas, P. D., Zhang, J., Miklos, G. L. G., Nelson, C., Broder, S., Clark, A. G., Nadeau, J., Mckusick, V. A., Zinder, N., Levine, A. J., Roberts, R. J., Simon, M., Slayman, C., Hunkapiller, M., Bolanos, R., Delcher, A., Dew, I., Fasulo, D., Flanigan, M., Florea, L., Halpern, A., Hannenhalli, S., Kravitz, S., Levy, S., Mobarry, C., Reinert, K., Remington, K., Abu-threideh, J., Beasley, E., Biddick, K., Bonazzi, V., Brandon, R., Cargill, M., Chandramouliswaran, I., Charlab, R., Chaturvedi, K., Deng, Z., Francesco, V. D., Dunn, P., Eilbeck, K., Evangelista, C., Gabrielian, A. E., Gan, W., Ge, W., Gong, F., Gu, Z., Guan, P., Heiman, T. J., Higgins, M. E., ru Ji, R., Ke, Z., Ketchum, K. A., Lai, Z., Lei, Y., Li, Z., Li, J., Liang, Y., Lin, X., Lu, F., Merkulov, G. V., Milshina, N., Moore, H. M., Naik, A. K., Narayan, V. A., Neelam, B., Nusskern, D., Rusch, D. B., Salzberg, S., Shao, W., Shue, B., Yao, A., Ye, J., Zhan, M., Zhang, W., Zhang, H., Zhao, Q., Zheng, L., Zhong, F., Zhong, W., Woodage, T., Ali, F., An, H., Awe, A., Baldwin, D., Baden, H., Barnstead, M., Barrow, I., Beeson, K., Busam, D., Carver, A., Cheng, M. L., Curry, L., Danaher, S., Davenport, L., Desilets, R., Dietz, S., Dodson, K., Doup, L., Ferriera, S., Garg, N., Gluecksmann, A., Hart, B., Haynes, J., Haynes, C., Heiner, C., Hladun, S., Hostin, D., Houck, J., Howland, T., Ibegwam, C., Johnson, J., Kalush, F., Kline, L., Koduru, S., Love, A., Mann, F., May, D., Mccawley, S., Mcintosh, T., Mcmullen, I., Moy, M., Moy, L., Murphy, B., Nelson, K., Pfannkoch, C., Pratts, E., Puri, V., Qureshi, H., Reardon, M., Rodriguez, R., hui Rogers, Y., Romblad, D., Ruhfel, B., Scott, R., Sitter, C., Smallwood, M., Stewart, E., Strong, R., Suh, E., Thomas, R., Tint, N. N., Tse, S., Vech, C., Wang, G., Wetter, J., Williams, S., Williams, M., Windsor, S., Winn-deen, E., Wolfe, K., Zaveri, J., Zaveri, K., Abril, J. F., ó, R. G., Campbell, M. J., Blick, L., Caminha, M., Carnes-stine, J., Caulk, P., hui Chiang, Y., Coyne, M., Dahlke, C., Mays, A. D., Dombroski, M., Donnelly, M., Ely, D., Esparham, S., Fosler, C., Gire, H., Glanowski, S., Glasser, K., Glodek, A., Gorokhov, M., Graham, K., Gropman, B., Harris, M., Heil, J., Henderson, S., Hoover, J., Jennings, D., Jordan, C., Jordan, J., Kasha, J., Kagan, L., Kraft, C., Levitsky, A., Lewis, M., Liu, X., Lopez, J., Ma, D., Majoros, W., Mcdaniel, J., Murphy, S., Newman, M., Nguyen, T., Nguyen, N., Nodell, M., Pan, S., Peck, J., Peterson, M., Rowe, W., Sanders, R., Scott,

J., Simpson, M., Smith, T., Sprague, A., Stockwell, T., Turner, R., Venter, E., Wang, M., Wen, M., Wu, D., Wu, M., Xia, A., Zandieh, A., and Zhu, X. (2001). The Sequence of the Human Genome. *Science*, 291(5507):1–38.