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	Autore	Montesinos López Osval Antonio
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	Sommario/riassunto	This book is open access under a CC BY 4.0 license This open access book brings together the latest genome base prediction models currently being used by statisticians, breeders and data scientists. It provides an accessible way to understand the theory behind each statistical learning tool, the required pre-processing, the basics of model building, how to train statistical learning methods, the basic R scripts needed to implement each statistical learning tool, and the output of each tool. To do so, for each tool the book provides background theory, some elements of the R statistical software for its implementation, the conceptual underpinnings, and at least two illustrative examples with data from real-world genomic selection experiments. Lastly, worked-out examples help readers check their own comprehension. The book will greatly appeal to readers in plant (and animal) breeding, geneticists and statisticians, as it provides in a

very accessible way the necessary theory, the appropriate R code, and illustrative examples for a complete understanding of each statistical learning tool. In addition, it weighs the advantages and disadvantages of each tool.