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Technical note

Comparison of machine learning methods for predicting genomic breeding values for growth traits in Braunvieh cattle

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Abstract:

Machine Learning (ML) algorithms have proven advantageous in addressing challenges associated with the quantity and complexity of information, discovering patterns, performing efficient analyses, and serving as a decision-making tool. The objective of this study was to compare four ML methods —artificial neural networks (NN), regression trees (RT), random forests (RF), and support vector machines (SVM)— for predicting genomic value in European Swiss cattle using phenotypic records of birth weight (BW), weaning weight (WW) and yearling weight (YW), as well as genomic information. The results indicate that the predictive ability of the models varies according to the features and the amount of information available. NN, RF, and SVM exhibited similar performances, while RT underperformed. The SVM methodology stood out as the tool with the greatest potential, achieving the highest values of Pearson correlation between corrected phenotypes and

predicted genetic values for WW. Despite its higher computational cost, the NN performed reasonably well, especially for BW and YW. The selection of the final model depends on the specific requirements of the application, as well as on such practical factors as data availability, computational resources, and interpretability; however, in general, the NN and SVM emerged as solid choices in several categories.

Keywords: Neural networks, Predictive capacity, Random forests, Regression trees.

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Genomics has evolved in recent years thanks to advances in DNA sequencing technology. This progress has allowed the generation of large amounts of data at an unprecedented speed. However, the inherent complexity of genomic data, as well as its dimensionality, pose significant obstacles[1]. The diversity of genomic information, ranging from DNA sequences to associated phenotypic data, adds further complexity. In addition, variability in the quality and structure of genomic data can make it difficult to extract useful and meaningful insights. Within this context, machine learning (ML) methods emerge as valuable tools to address these challenges, offering the ability to process and analyze large volumes of data efficiently and accurately[2]. Their ability to identify complex patterns and nonlinear relationships in genomic and phenotypic data makes them a powerful tool for knowledge extraction[2,3].

The application of ML techniques allows for addressing such tasks as the identification of genes relevant to specific traits, prediction of gene functions, detection of genetic variants associated with particular traits, and classification of species based on genomic information[4,5,6]. Recently, ML has become attractive in genomic prediction because of its ability to handle large volumes of data, its flexibility in modeling nonlinear relationships, improving predictive accuracy, and continuous innovations in algorithms and techniques; nevertheless, research is needed to investigate how it compares in predicting genetic values with conventional GBLUP methods[7]. Combining genomic data with ML algorithms would lead the creation of reliable predictive and descriptive models, which in turn would have implications for selective breeding, species conservation, and the understanding of evolution[8,9].

Among the most commonly used ML methods are neural networks, support vector machines, decision trees, linear regression, and clustering methods[3,8-11]. The diversity of available approaches reflects the versatility of these methods in solving challenges involving genomic information, such as DNA sequence classification and protein structure prediction[12]. The

success of the application of these methods in animal genomics depends to a large extent on the availability of information[13], as well as on selecting the optimal ML method, given that several methods have been proposed, each with its own characteristics and specific predictive capabilities with different data sets and features[3,7].

Thus, the objective of this study was to compare the following ML methods —neural networks (NN), regression trees (RT), random forests (RF), and support vector machines (SVM)— to predict genomic breeding values using phenotypic records of birth, weaning and yearling weights, as well as genomic information of a population of Swiss European cattle in Mexico.

The information was drawn from the database of the Mexican Association of Registered Swiss Cattle Breeders (Asociación Mexicana de Criadores de Ganado Suizo de Registro, AMCGSR), which contains phenotypic records and animal identification, ranch of origin or owner, genealogy, and economically important traits such as birth weight (BW), weaning weight (WW) and yearling weight (YW). The data set used was previously analyzed by Valerio-Hernández *et al*[14,15] to fit other models, so that some of the results obtained here compare directly with those of the authors mentioned above. The treatment of phenotypic information for BW, WW, and YW followed the procedure described by Valerio-Hernández *et al*[14,15], i.e., individuals with missing information on maternal age, management, herd of origin, as well as individuals not genetically related were omitted. Contemporary groups (CG) were defined by combining the effects of herd, year, and time of birth. For WW, the CG were formed according to the feeding management given to the herd, as well as adjustment to specific days for weaning. CG with less than three individuals or with zero variance were discarded, according to the methodology cited above[14].

Genomic information was obtained through the analysis of hair samples collected from 300 animals from ranches belonging to the AMCGSR in Colima, Jalisco, and Veracruz. Genotyping was performed by GeneSeek (Lincoln, NE, USA), using the Genomic Profile Bovine LDv.4 chip, which has been used to genotype various *Bos indicus* and *Bos taurus* breeds. A total of 150 animals were genotyped with a chip containing 30,000 markers, and another 150 animals were genotyped using a chip with 50,000 SNP (Single Nucleotide Polymorphism) markers. A total of 12,835 SNP markers present in both chips were selected.

The recoding of additive genetic effects such as AA=0, AB=1, and BB=2 and the quality control of genotypic information carried out by Valerio-Hernández *et al*[15] were based on that performed by Jarquín *et al*[16]. For the imputation of missing genotypes in the present study, it was used the FImpute[17] software (version 2.2), this process yielded 1). A marker map (marker, chromosome, base-pair position), eliminating duplicate markers or markers with unknown positions, and 2) The pedigree of the individuals and their corresponding sex. Monomorphic markers and those with a minor allele frequency (MAF) lower than 0.04 were

eliminated. A total of 9,008 markers were obtained and used to build the genomic relationship matrix **G**; Table 1 shows the number of animals incorporated into the study for each trait after filtering.

Table 1: Number of animals from a Braunvieh cattle population genotyped and phenotyped for three growth traits

Group/Variable	BW	WW	YW
Genotyped	300	300	300
Phenotyped	330	267	232
Phenotyped in $\mathbf{G}^2$	232	218	191

BW= birth weight, WW= weaning weight, YW= yearling weight. $\mathbf{G}^2$ Animals with phenotypes and genomic information.

The genomic relationship matrix **G** was estimated using the methodology described by Pérez-Rodríguez *et al*[18], $\mathbf{G}=\mathbf{WW}^t/p$, where **W** is the centered and standardized marker matrix and p is the total number of markers. Additionally, the relationship matrix **H**, which combines information from the **G** matrix with information from the additive genetic relationship matrix **A**, obtained for pedigree individuals.

Linear mixed models (Base Models). Comparison of the results of predictive power for the BW, WW, and YW breeding values considers the sequence of models and results described by Valerio-Hernández *et al*[15] for linear mixed models versus machine learning models. In order to present all the pertinent information, the linear mixed model used by these authors is described below:

$$\boldsymbol{y} = \boldsymbol{Xb} + \boldsymbol{Z}_1\boldsymbol{c} + \boldsymbol{Z}_2\boldsymbol{a} + \boldsymbol{e}, \ldots (1)$$

where $\boldsymbol{y}$ is the phenotype vector, $\boldsymbol{X}$ is the incidence matrix for fixed effects —which for this study are sex of the animal, age of the mother of each animal, and the contemporaneous group, described above—, $\boldsymbol{b}$ is the vector of fixed effects, $\boldsymbol{Z}_1$ is an incidence matrix connecting phenotypes with contemporaneous groups, whose effects are assumed to be random and represent the variability in phenotypes due to differences between groups of individuals that are subject to the same environmental and management conditions, $\boldsymbol{c} \sim NM(\mathbf{0}, \sigma^2_{gc}\boldsymbol{I})$, where NM denotes the multivariate normal distribution, with mean **0** and associated variance parameter σ^2_{gc}, **I** the identity matrix, $\mathbf{Z_2}$ is an occurrence matrix connecting phenotypes with additive genetic effects which are assumed to be random effects, $\boldsymbol{a} \sim MN(\mathbf{0}, \sigma^2_a\boldsymbol{K})$, with $\boldsymbol{K} \in \{\boldsymbol{A}, \boldsymbol{G}, \boldsymbol{H}\}$, $\boldsymbol{e} \sim MN(\mathbf{0}, \sigma^2_e\boldsymbol{I})$ represents the random error vector, where σ^2_e denotes the variability associated with it. Depending on the data used, model (1) gives rise to three different models, denoted as follows: 1) BLUP, $\boldsymbol{K} = \boldsymbol{A}$, 2) GBLUP, $\boldsymbol{K} =$

$\boldsymbol{G}$, and 3) ssGBLUP (single-step GBLUP) with $\boldsymbol{K} = \boldsymbol{H}$. The linear mixed models described above were fitted by Valerio-Hernández *et al*[15] using the BGLR statistical package[19].

Machine learning models. The input variables for the ML algorithms were the genetic relationship matrix combining genomic information and pedigree information called **H**, as well as the effects of dam's age for each animal, indicator variables for sex, and contemporaneous group described above. In order to include the information of the **H** matrix in the learning models, a spectral decomposition of the matrix was performed, i.e., $\boldsymbol{H} = \boldsymbol{\Gamma\Lambda\Gamma}^{t}$, from which $\boldsymbol{X} = \boldsymbol{\Gamma\Lambda}^{\frac{1}{2}}$ (main components) were obtained and utilized as covariables (explanatory variables) in the models; this and other related computational strategies have been used by other authors in the past[20,21].

Artificial neural network. Neural networks (NN) were initially designed to emulate the functioning of the nervous system and which process input information through mathematical operators, generating output values or the final result[3,22]. Input variables affect model's performance and can generate overfitting if the amount of information is large; therefore, it is important to optimize these variables[23]. One of the advantages of neural networks is their ability to learn nonlinear patterns[3]. The model of an NN with an input layer with p predictors, a hidden layer with S neurons, and an output layer with a continuous response can be expressed as follows:

$$y_i = \beta_0 + \sum_{k=1}^{s} w_k \, g(\beta_0^{(k)} + \sum_{j=1}^{p} \beta_j^{(k)} x_{ij}) + e_i,$$

where $e_i \sim NIID(0, \sigma_e^2)$, with *NIID* denoted by normal, independent, identically distributed random variables; $k = 1, \ldots, S$ (neurons); $j = 1, \ldots, p$ (predictors); $i = 1, \ldots, n$ (observations), and $g(\cdot)$ represents the activation function, according to Bai *et al*[24] and Gianola *et al*[20], where, y_i is the response variable for the i^{th} individual, in this case, the growth weights (BW, WW, YW) of Braunvieh cattle that the network predicts as a function of inputs; β_0 is the bias term or the intercept, which can represent the predicted value when the inputs are equal to zero, and w_k are weights associated with each of the neurons and determine the contribution of each neuron to the final prediction. The hidden layer is an intermediate layer between the input layer and the output layer, it is where most of the processing and feature extraction of the dataset take place; it is composed of a specific number of neurons. (*S*) is a hyperparameter of the model that is adjusted during the training process. A higher value of *S* allows the neural network to capture greater complexity in the data, but may also increase the risk of overfitting. The NN adjusts the parameters $(\beta's, w's)$ during the training process to minimize the prediction error. The activation function, $g(\cdot)$, maps the real line entries to the bounded open interval (-1,1), as described by Pérez-Rodríguez *et al*[25], where $g(x) = 2/[1 + \exp(-2x)] - 1$ is known as the hyperbolic tangent activation function (htaf). The "brnn" function was used to fit the neural network model[26]

included in the package of the same name (version 0.9.3) in the statistical package R[27] (version 4.3.0).

Regression trees. This model is based on the one proposed by Breiman *et al*[28], $y_i = \sum_{j=1}^{J} y_j I(\boldsymbol{x}_i \epsilon\, R_j)$, where y_i is a response variable (BW, WW, and YW), y_j is the regression value associated with a "leaf", $\boldsymbol{x}_i$ is the set of characteristics of the observation, R_j is the region associated with "leaf *j*" defined by characteristics and cutoff values on the path from "root" to "leaf". $I(\cdot)$ is an indicator function that takes the value 1 if observation *i* belongs to the region R_j. The tree identifies the splits that minimize the error in each region and split recursively until a process-stopping criterion is reached, such as the maximum depth of the tree or the minimum number of cases in a leaf. The model fitting was performed with the "rpart" function[29] included in the library of functions of the same name (version 4.1.19) within the statistical package[27] (version 4.3.0).

Random forests. This model combines multiple RTs averaging the predictions of each to obtain a final optimized prediction, $y_i = \frac{1}{N}\sum_{j=1}^{N} y_{ij}$, where *N* is the number of trees in the random forest, y_i is an observed random variable (BW, WW, and YW), and y_{ij} is the prediction of the *j*th RF for the observation *i*. The random forests algorithm was implemented using the "randomForest" function[30] included in the library of functions of the same name (version 4.7-1.1) within the statistical package R[27] (version 4.3.0).

Support vector machine. The Support Vector Machine Model (SVM) was used for classification and regression[31]. Within the context of regression, given a data set $\{y_1, \boldsymbol{x}_1\}, \ldots, \{y_n, \boldsymbol{x}_n\}$, where y_i represents the value of the continuous response variable for the *i*th individual, and $\boldsymbol{x}_i$, the value of the associated covariates, the objective is to obtain a function $f(\boldsymbol{x})$ such that the distance with y is no larger than ε for each of the training points. According to Hastie et al.[32] the regression function is approximated in terms of basis functions $\{h_m(\boldsymbol{x})\}, m = 1, \ldots, M$ as follows:

$$f(\boldsymbol{x}) = \beta_0 + \sum_{m=1}^{M} \beta_m h_m(\boldsymbol{x}),$$

where $\beta = (\beta_0, \beta_1, \ldots, \beta_M)^t$ are coefficients obtained by minimizing: $Q(\boldsymbol{\beta}) = \sum_{i=1}^{n} L\big(y_i - f(\boldsymbol{x}_i)\big) + \frac{\lambda}{2}\sum \beta_m^2$, in which $L(\cdot)$ is called loss function (e.g. quadratic or absolute value), and λ is a positive regularization parameter. For any selection of $L(\cdot)$, the solution has the form: $\hat{f}(\boldsymbol{x}) = \sum_{i=1}^{n} \hat{a}_i K(\boldsymbol{x}, \boldsymbol{x}_i)$, with $K(\cdot,\cdot)$ known as kernel function. Kernels are fundamental components of the model; they serve as functions that allow transforming the data and generating a higher dimensional space; they help to model complex relationships in the data. The most common kernels are the linear $(\boldsymbol{x}_i^t \boldsymbol{x}_j)$, polynomial $(\boldsymbol{x}_i^t \boldsymbol{x}_j + coef_0)^d, d = 2,3, \ldots,$

radial $\left(e^{-\gamma\left|\left|x_i-x_j\right|\right|^2}\right)$, and sigmoid (htaf($\gamma \boldsymbol{x}_i^t \boldsymbol{x}_j$), $+coef_0$), where γ is known as the bandwidth that is adjusted in the training process through cross-validation, and $coef_0$ is a constant that can be adjusted during the model training process, although it is usually set to 1. The model was fitted using the "e1071" package[33] (version 1.7-13), with the help of the SVM function in the statistical package R[27] (version 4.3.0). Codes for model fitting are available upon request to the author for correspondence.

Cross-validation. Cross-validation is a widely used data re-sampling method to estimate the true prediction error of models and to adjust model parameters[20,34]. Therefore, in order to obtain the predictive capability of the models NN, RT, RF, and SVM, and thus make the comparison, the cross-validation was carried out using as a reference the procedures performed by Valerio-Hernández *et al*[15] These authors randomly divided the data into percentages, allotting 80 % to the training set and 20 % to the validation set, and the process was repeated 100 times. The ML models were fitted, and the correlations between the observed vs. predicted values were estimated by observing the values of the response variable corrected for fixed effects and other random effects. Pearson's correlation coefficient was estimated for the corrected phenotypes and predicted genetic values for each one of the partitions, and averages were obtained for each model.

Table 2 presents the averages of the 100 Pearson correlations (based on cross-validation) between corrected and predicted values for the BW, WW, and YW traits, using the four ML algorithms compared in the study. For WW, the SVM algorithm achieved the highest values for the Pearson's correlation coefficient between corrected and predicted values in the validation sets (WW= 0.256). By this method, the best fit for the three characteristics was obtained with the "Radial Kernel" by optimizing the hyperparameters γ (gamma) and cost (BW: 0.045 and 0.05; WW and YW: 0.05 and 0.01, respectively). Tests performed using the Artificial NN method determined the number of neurons in the hidden layer of the model to be 3 neurons for BW and 2 for WW and YW when appropriate parameter estimators of weights were obtained generating a parsimonious model. The best performance of this method was estimated at 0.402 for the BW and 0.195 for the YW.

For the RF method, tests were conducted with different numbers of "trees" as model parameters; 150 of these obtained optimal prediction values for BW and WW, and 250, for YW. The third-best performance values were predicted for WW and YW. The RT methodology showed lower predictive capacity for WW and YW in this study. Based on these results, the following set of hypotheses were proposed to test the significance of the estimated correlation coefficients: $H_0: \mu_r \leq 0$ *vs* $H_1: \mu_r > 0$, where μ_r is the mean of the distribution of the Pearson correlation coefficient and it was to test whether the association is positive or not. The set of hypotheses was tested using the 1-sample t-test, first verifying

the assumption of normality in each of the cases[35]; in all cases, it was concluded that the assumption of normality is appropriate ($P - value > 0.05$).

Table 2: Average Pearson's correlation estimators and standard deviation between corrected phenotypes and predicted genetic values with the 100 cross-validations for the three growth characteristics and the compared algorithms

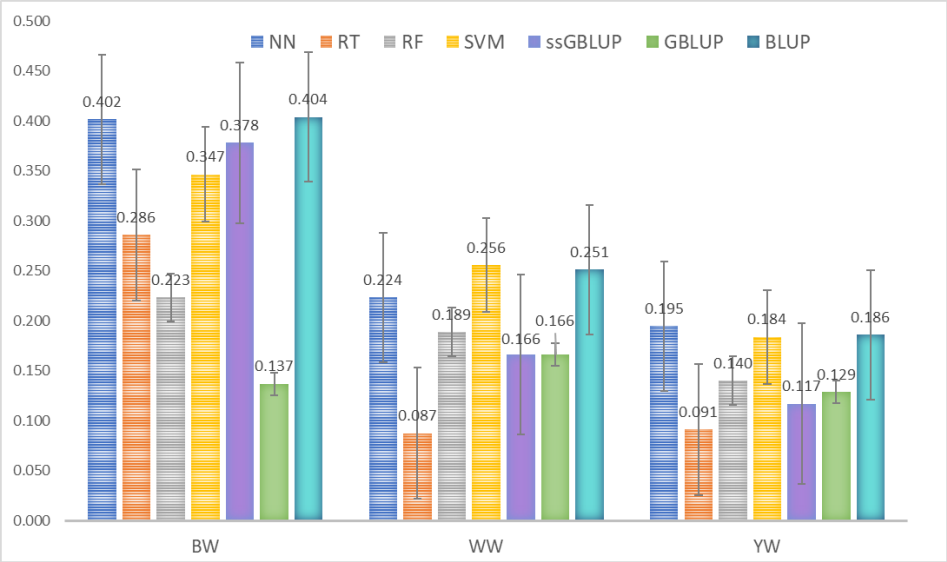
Characteristic	Algorithm	PCC	SD
BW	Neural network	0.402	0.160
	Regression tree	0.286	0.153
	Random forests	0.223	0.163
	Support Vector Machine	0.347	0.129
WW	Neural network	0.224	0.126
	Regression tree	0.087	0.163
	Random forests	0.189	0.117
	Support Vector Machine	0.256	0.144
YW	Neural network	0.195	0.152
	Regression tree	0.091	0.178
	Random forests	0.140	0.128
	Support Vector Machine	0.184	0.160

BW = birth weight, WW = weaning weight, YW = yearling weight; PCC = Pearson correlation coefficient; SD= standard deviation of the 100 correlation estimators for randomly selected partitions.

To determine the predictive ability of the ML models, Pearson correlation coefficient estimators between corrected phenotypes and predicted genetic values were compared with those obtained from the analyzed models[36] in the test sets for each characteristic of the cross-validation methodology described above; unlike the previous studies, this study maintained consistency in the data used in the analyses. This ensures consistency in the comparisons made and provides a solid basis for evaluating the relative performance of traditional methods and ML algorithms. The problem of inferring genetic values and predicting phenotypes for quantitative traits governed by complex forms of gene interactions is difficult to solve using the routinely used linear mixed models[37,38], Therefore, the use of ML algorithms is an alternative to model complex functions by identifying nonlinear relationships between the covariates and the response variable[20]. The correlations between corrected phenotypes and predicted values with the methodologies used made it possible to evaluate the NN, RT, RF, and SVM machine learning algorithms for the growth characteristics BW, WW, and YW in bovines. Figure 1 illustrates that the NN, RF, and SVM algorithms generally showed a similar predictive performance to that of the methodologies assessed by Valerio-Hernandez *et al*[15] using the same variables. In a study comparing the predictive capacity of nonlinear neural networks (NLNN) with linear models, these were found to be potentially useful to predict complex characteristics based on genomic information, a situation in which the number of

parameters to be estimated usually exceeds the sample size[20]. Rodríguez-Alcántar[3] compared ML algorithms using different sets of SNPs generated from chromosomes with a high number of QTLs associated with high milk production. This author found that classification accuracy ranged between 90.9 and 94.5 % with decision trees, and between 79.0 and 87.3 % with neural networks. The author concludes that both the neural network method for binary classification and decision trees are efficient tools for the early identification of highly producing dairy cows.

Figure 1: Comparison of correlation coefficients (average of 100 validations) of corrected phenotypes and predicted genetic values



Genetic values obtained with machine learning methods, artificial neural networks (NN), regression trees (RT), random forests (RF), and support vector machines (SVM) with the methodologies applied by Valerio-Hernández *et al*[15], best linear unbiased predictor (BLUP), genomic BLUP (GBLUP) and single-step GBLUP (ssGBLUP) for birth weight (BW), weaning weight (WW) and yearling weight (YW) of a population of Braunvieh cattle.

The results suggest that the performance of the models varies according to the feature and the amount of information[20], among other factors. This suggests that better results can be obtained with these models by including more variable and covariate information to fit the training model[39,40]; despite the low correlations and large variances of the predictions, these can be attributed to several genetic and methodological factors. Consistently with the findings of Cuyabano *et al*[41], it is important to consider genetic differences between reference and target populations when calculating the accuracy of predictions. Furthermore, it is suggested that there is a theoretical upper limit to the accuracy of these predictions, determined by the square root of the heritability. Zhang *et al*[42] mention that various factors can influence the accuracy of genomic breeding value predictions; heritability (using the model described as BLUP, Valerio-Hernandez *et al*[15] report 0.260 for BW; 0.223 for WW, and 0.231 for YW), the density of genetic markers, the minor allele frequency (MAF) utilized during the data

cleaning process, and the statistical model used are just some factors that can affect the accuracy of genomic breeding value predictions. This poses significant challenges in the prediction of complex traits.

The SVM, NN, and RF methodologies showed similar performance in terms of Pearson correlation coefficients of corrected phenotypes and predicted values for the three growth characteristics used; these results were subsequently compared with the values obtained by Valerio-Hernández *et al*[15] using traditional BLUP, GBLUP, and ssGBLUP methodologies. The computational cost of the BW was higher than that of the other three compared algorithms; it was determined by measuring the runtime required to train and validate each one of the algorithms on this training and test data sets, recording the time elapsed from the start of the training to the completion of the validation process. This result is similar to that reported by Zhao *et al*[43], who mentioned that NR adjustment is more complicated and time-consuming. The SVM algorithm stood out as a promising tool for prediction based on genomic information, considering the amount of information and the parameters used with this methodology. Like the Kernel[31], this algorithm contributes to ML applications for the analysis of datasets derived from genetic and genomic information[44,45].

The results obtained in this study prove that ML algorithms have the potential to generate useful predictions even under constrained information conditions, such as a small sample size and low density of genetic markers. This finding highlights their applicability in practical scenarios where resources are limited. Nevertheless, significant challenges were identified, such as high computational cost and dependence on sufficient quality data to maximize predictive capability. Despite these limitations, algorithms such as NN and SVM showed consistent performance, suggesting that they may be valuable tools for genomic analysis. These results not only provide practical insights on the use of ML algorithms, but also open the door to future research focused on evaluating their behavior with larger and more detailed databases, optimizing both their implementation and their predictive capacity within different contexts.

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Conflict of interest

The authors declare that they have no conflicts of interest.

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