Multi-level multi-model data-driven ensemble approach for river bedload formulation

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ABSTRACT

Estimation of bedload transport in rivers is a complex process and needs substantial efforts in pre-processing and ensemble modeling to derive desired level of prediction accuracy. The previous studies used standalone Blackbox models in this case. This paper aims to develop a novel framework to derive explicit formulae for bedload transport in rivers using multi-level Multi-Model Ensemble (MME) approach to derive improved explicit formulations hybridized with multiple pre-processed-based models. Three pre-processing techniques including feature selection by Gamma Test (GT), dimension reduction by principal component analysis (PCA), and data clustering by subset selection of maximum dissimilarity (SSMD) are utilized at level 0. The multi-linear regression (MLR), MLR-PCA, artificial neural network (ANN), ANN-PCA, Gene expression programming (GEP), GEP-PCA, Group method of data handling (GMDH) and GMDH-PCA are used to develop individual explicit formulations at level 1, and the inferred formulas are hybridized with the MME approach at level 2 by Pareto optimality. A newly revised discrepancy ratio (RDR) for error distributions in conjunction with several statistical and graphical indicators were used to evaluate the strategy's performance The proposed multi-model ensemble (MME) achieved the highest predictive performance among all investigated models, with testing values of R^{2}=0.98, NSE = 0.98, RMSE = 0.24, and RAE = 0.10. Compared with the best standalone model (ANN-PCA), the MME improved R^{2}from 0.96 to 0.98, increased NSE from 0.95 to 0.98, and reduced RMSE and RAE by 33.3% (0.36 to 0.24) and 37.5% (0.16 to 0.10), respectively. Results of MME showed that the proposed framework acted as an efficient tool in explicit equation induction for bedload transport (i.e., 33–96% reduction of RMSE; 2-29% increase of R2, 2-138% increase of NSE and 38-98% reduction of RAE in testing step in comparison with the best individual model) and clearly outperformed estimations made by other models. The current study highlights the importance of pre-processing and multi-modelling techniques in deep learning models to encounter the challenges of function finding for complex bedload transport estimations in multiple observed datasets.

KEYWORDS

Multi-model ensembles approach, bedload transport, function finding, equation optimization, machine learning.

1. Introduction

Sediment transport in river flows leads to several challenges for the water resources tasks and is crucial in the context of reservoir sedimentation, flood control, river morphology changes, stable channel design, fish/wild life habitat, and watershed management [1-8].

In sediment transport process, the coarse-grains conveyed by higher discharges and floods immediately above the bed are known as bedload [5]. Sediment transport is a highly complex, stochastic phenomenon with somewhat unknown theory. It is hard to measure in the field due to the time and cost-intensive process. These features of sediment transport produce high uncertainty in predictive equations that made their applicability questionable and makes limitation on employing them [4, 6]. The predictive methods of bedload transport are generally categorized into physical and data driven models [7, 8]. Considering challenges of phenomenon complexity, inaccuracies in the predictive equations of bedload and measuring difficulties with the physical methods, development of new data-driven-based models with an appropriate determination of effective parameters of bedload having easily accessible field variables is vital [9-11,18].

With the emerging applications of machine learning (ML) models, producing effective results in formulation of complex nonlinear challenges in river engineering, researchers have endeavored to use these new techniques to cope with the complicated nature of bedload transport in parallel with the experimental and physical-based studies [6, 12, 13, 18].

Various ML methods were implemented for sediment transport modelling such as artificial neural network: ANN [6-8], The adaptive neural fuzzy inference system: ANFIS [8-13], support vector machine: SVM [14-16], genetic expression programming: GEP [11].

The researchers figured out that these techniques suffer from the generalization capabilities of the results due to inappropriate selection of training set, inaccuracy issues with limited extrapolation abilities when applied to unseen data set extensive than the data used in training phase [17-19]. They suggested pre-processing techniques such as data clustering for subset selection in train and testing steps. The studies in the literature of bedload prediction, have neglected mathematical-based clustering of train and test sets, while this study considered a subset selection of maximum dissimilarity (SSMD) to overcome these challenges.

The data-driven models developed so far for bedload transport estimations are basically black-box type tools such as ANN, ANFIS and suffer from limited interpretability of physical importance of the input parameters and their interactions to the model outputs, inability to capture physical processes. Therefore, the derivation of explicit accurate equations for bedload transport in rivers based on AI models, remains challenging. To address this problem, in the current study a hybridization of four mathematical models including ANN, GEP, The group method of data handling (GMDH), and the multivariable linear regression (MLR) are employed in deriving the explicit predictive equations for bedload using a new multi-model-based strategy. The data-driven models are susceptible to the number of the input variable. To the best of our knowledge, few studies used dimension reduction techniques over the input data space for systematic selection of optimum input variables in bedload prediction with a multi-model ensemble approach. Generally, the bedload rate is chosen as a dependent parameter. The fluid properties, flow conditions, sediment properties, and channel geometry are considered independent parameters in data-driven model developments. In conventional, the ML-based techniques, generally developed based on the investigators' particular "suggesting" variables as the input vector, this individual's subjective reduce the reliability of model results [20-21].

Hence, proposing a sophisticated approach such as dimension reduction using principal component analysis (PCA) and Gamma test (GT) over the input space is valuable for pre-processing of independent variables [19, 22]. The studies in the literature neglected input vector manipulation and data dimension reduction

for ML prediction of bedload. In contrast, the present study used PCA and GT techniques for dimension reduction and effective variable selection. In the current study pre-processing techniques of GT and PCA as dimension reductions are used in conjunction with ANN, GEP, GMDH and MLR.

This literature review confirms that, there are three main challenges and questionable problems in the ML techniques developments for bedload rate, including:

1- The input feature selection, input dimension reduction to infer most effective variables
2- Optimized subset selection of train and test data sets to avoid overfitting, and
3- Multi-model procedure to overcome the weakness of single models using ensembles modeling strategy.

This study aims to address these challenges and efforts to improve the estimation of bedload transport rate through considering techniques implemented in a multi-model-based approach. As powerful ML models, MLR, ANN, GMDH and GEP in conjunction with SSMD, PCA and GT techniques are utilized for modeling.

The contribution of this study lies in the development of a multi-model ensemble framework for predicting dimensionless bed-load transport, which effectively integrates the strengths of individual machine learning models and demonstrates superior accuracy and generalization compared with both standalone and new hybrid models. The main novelty of this study is the development of a transparent multi-model ensemble (MME) framework for predicting dimensionless bed-load transport. Unlike previous machine learning approaches, which are predominantly black-box models, the proposed framework generates explicit mathematical equations by combining the predictive capabilities of multiple individual models. Consequently, the proposed approach not only achieves high prediction accuracy but also provides interpretable and transferable relationships that can be directly implemented in hydraulic engineering analyses without requiring repeated model training. The bedload prediction challenges are improved by a successive strategy including Multiple Models (MM) in three levels as follows:

(i) Level 0: use pre-processing techniques, SSMD, GT and PCA in data PRE-preprocessing, dimension reduction and input feature selection,
(ii) Level 1: developing standalone ML models as base reuse and recursion techniques, that their results are reused as inputs in the next level inputs;
(iii) Level 2: reuse and recursion of base models in a Pareto multi-gene framework by reusing the results of the previous level to the inputs of the present level and the bedload rate as a target for improved accuracy and provide explicit formulas.

The main aim of the current paper is four-fold. First, implementing the SSMD, GT, and PCA-based approaches in input vector manipulation, dimension reduction, and pre-processing of an extensive bedload transport database. Second, the utilized data set includes a wide range of low shear to high shear sediment transport observations. When combined with the pre-processing techniques, will improve the generalization issues of previous studies by dimension reduction. Third utilizing individual MLR, MLR-PCA, ANN, ANN-PCA, GEP, GEP-PCA, GMDH, GMDH-PCA models to derive explicit predictive equations for bedload. Fourth, integrating the output of individual models with the POMGGP procedure as a new multi-model strategy that utilizes individual models' power of and eliminates their weakness in bedload predictions.

To the best of the author's knowledge, the presented multi-model ensembles approach driven by the different techniques is a unique one in the literature concerning bedload rate prediction. This paper is

organized as follows. Section 2 presents the material and method, including data, dimension analysis, preprocessing techniques, stand-alone, and multi-model strategy. Section 3 discusses the results of the study in three pre-defined levels. Section 4 provides summaries and conclusions.

2. Material and methods

2.1. The data set and input features

Literature review revealed that bedload material properties, cross-section geometry features, and flow conditions are the main properties that affect the sediment transport in streams [11, 12] and can be used as the input variables for predictive models, as:

$$q_b = f_1(U, H, W, R, D_s, S, g, \rho_s, \rho_w, \mu, u_*, u_{*c}) \quad (1)$$

Where $q_b$is the bedload transport rate (**kg s⁻¹** or **m³ s⁻¹**), $U$is the mean flow velocity (**m s⁻¹**), $H$is the flow depth (**m**), $W$is the river width (**m**), $R$is the hydraulic radius (**m**), $D_s$is the representative sediment particle diameter (**m**), $S$is the bed slope (–, dimensionless), $g$is the gravitational acceleration (**m s⁻²**), $\rho_s$and $\rho_w$are the sediment and water densities (**kg m⁻³**), respectively, μ is the dynamic viscosity (**Pa·s** or **kg m⁻¹ s⁻¹**), $u_*$is the shear velocity (**m s⁻¹**), and $u_{*c}$is the critical shear velocity (**m s⁻¹**).The dimensionless form of bedload transport with dimensionless parameters including particle mobility parameter $\emptyset$, Slope S , dimensionless grain diameter D_{gr}, relative depth $\frac{R}{D_s}$, critical velocity ratio $\frac{U}{u_{*c}}$, depth ratio $\frac{H}{D_S}$, aspect ratio $\frac{H}{W}$, Froud number F_r, densimetric Froud number F_{rg}, Reynold number R_e, densimetric Reynold number R_{e*}, shields parameter θ, velocity ratio $\frac{U}{u_*}$, defined by

$$\emptyset = \frac{q_b}{D_S\sqrt{g(s-1)D_s}},\ D_{gr} = D_s\left[\frac{(S-1)g}{\vartheta^2}\right]^{1/3},$$
$$R_{e*} = \frac{u_* D_s}{\vartheta},\ R_e = \frac{UH}{\vartheta},\ F_r = \frac{U}{\sqrt{gH}}, \quad (2)$$
$$F_{rg} = \frac{U}{\sqrt{gD_S(s-1)}},\ \theta = \frac{\gamma HS}{gD_S(s-1)}$$

In the current study datasets are collected from the literature [23-25]. A total of 1280 data points are used in this current study that are provided in the paper's supplementary material. The sediment diameter ranges from 0.274 mm to 44.3 mm. The bed sloped varies from 0.01 % to 20 %, flow depth from 0.00084 m to 1.0921 m, flow velocity from 0.193 m/s to 2.88 m/s, Froud number from 0.41 to 5.19 and bed material load from 0.01 g/m^3 to 1356 g/m^3.

2.2. Modeling Framework for explicit Bedload Transport modelling

In this study, a novel multi-level modeling framework based on a Multiple Models (MM) strategy was developed to overcome the persistent challenges associated with accurate bedload transport prediction. The proposed framework consists of three successive levels, as presented in Fig.1. At Level 0, the original bedload database was systematically processed using advanced data manipulation and dimensionality reduction techniques, including SSMD, GT, and PCA, to enhance input feature representation, eliminate redundant information, and improve model generalization capability. At Level 1, a comprehensive set of standalone predictive models, including MLR, MLR-PCA, ANN, ANN-PCA, GEP, GEP-PCA, GMDH, and GMDH-PCA, were developed to derive explicit relationships between hydraulic–sediment variables and bedload transport rate. The generated outputs of these individual models were subsequently recycled as additional informative predictors for the next modeling stage. At Level 2, a Pareto-based multi-gene genetic programming framework (POMGGP) was employed to integrate the complementary strengths of the individual models while mitigating their inherent limitations. Through this recursive multi-model architecture, the final model was optimized to achieve enhanced prediction accuracy and, simultaneously, provide transparent

and explicit mathematical expressions for bedload transport estimation. The proposed framework represents a transition from conventional single-model approaches toward an interpretable ensemble learning paradigm, offering improved robustness, generalization, and physical interpretability for complex sediment transport prediction problems.

2.3. Level 0: Pre-Processing techniques

2.3.1. Feature selection using Gamma test

In the current study the GT is used to select the best input variables in ML-based bedload predictions. The GT assumes that if points x' and x are close together in input space, their corresponding bedload rate in output points φ' and φ would stand close, otherwise the noise term caused the differences. In each data set $\{(x_i, \emptyset_i) \in R^m, 1 \leq i \leq M\}$ the GT shows that the functional form of bedload transport is $\emptyset = \emptyset(x_1, \dots x_m) + r$, where $\emptyset$ is a smooth function, and r is the random noise term. In mathematics a function could be considered "smooth" if it is differentiable everywhere (hence continuous) and in the Gamma test procedure the $\emptyset$ is smooth if it has constrained first partial derivatives. For a function to be smooth, it must have continuous derivatives up to a certain order, say k. We say that function is k^{th} order smooth. Now the domain of possible simulation model is smooth functions $\emptyset$ that have bounded first partial derivatives. The Gamma indicator Γ is an approximation of that part of the variance of the simulations that cannot be attained by a smooth function. The Euclidean distance of input and outputs δ and γ of k^{th} nearest neighbour x_N [i, k] from $x_i(1 \leq i \leq M)$, $(1 \leq k \leq p)$ the Γ is calculated using $\gamma = A\delta + \Gamma$. The slope A shows the difficulty of the model. More details about GT techniques is presented in the literature [26].

2.3.2. Data Clustering and Subset Selection by SSMD

According to Montes et al. [18] and Safari [12], the range of dissimilarity in the training dataset directly influences the model generality, overfitting problem, extrapolation ability and accuracy. The SSMD is utilized for daa clustering and selection of train / test sets. Suppose that X is the dataset as $X = (x_1, x_2, \dots, x_p)$ and a collection of $m = 1,2,..,N$ points selected for the training stage. The minimum distance for selection of x_i and x_j from applicant point of N to k points calculated by:

$$D_{ij}^2 = \|x_i - x_j\|^2 = \sum_{k=1}^{p} (x_{ki} - x_{kj})^2 \quad (3)$$

The $(k+1)^{th}$ candidate for selection as the train is selected from remaining $(N-k)$ points with the highest distance from selected point. In this study, the SSMD code is developed in MATLAB environment.

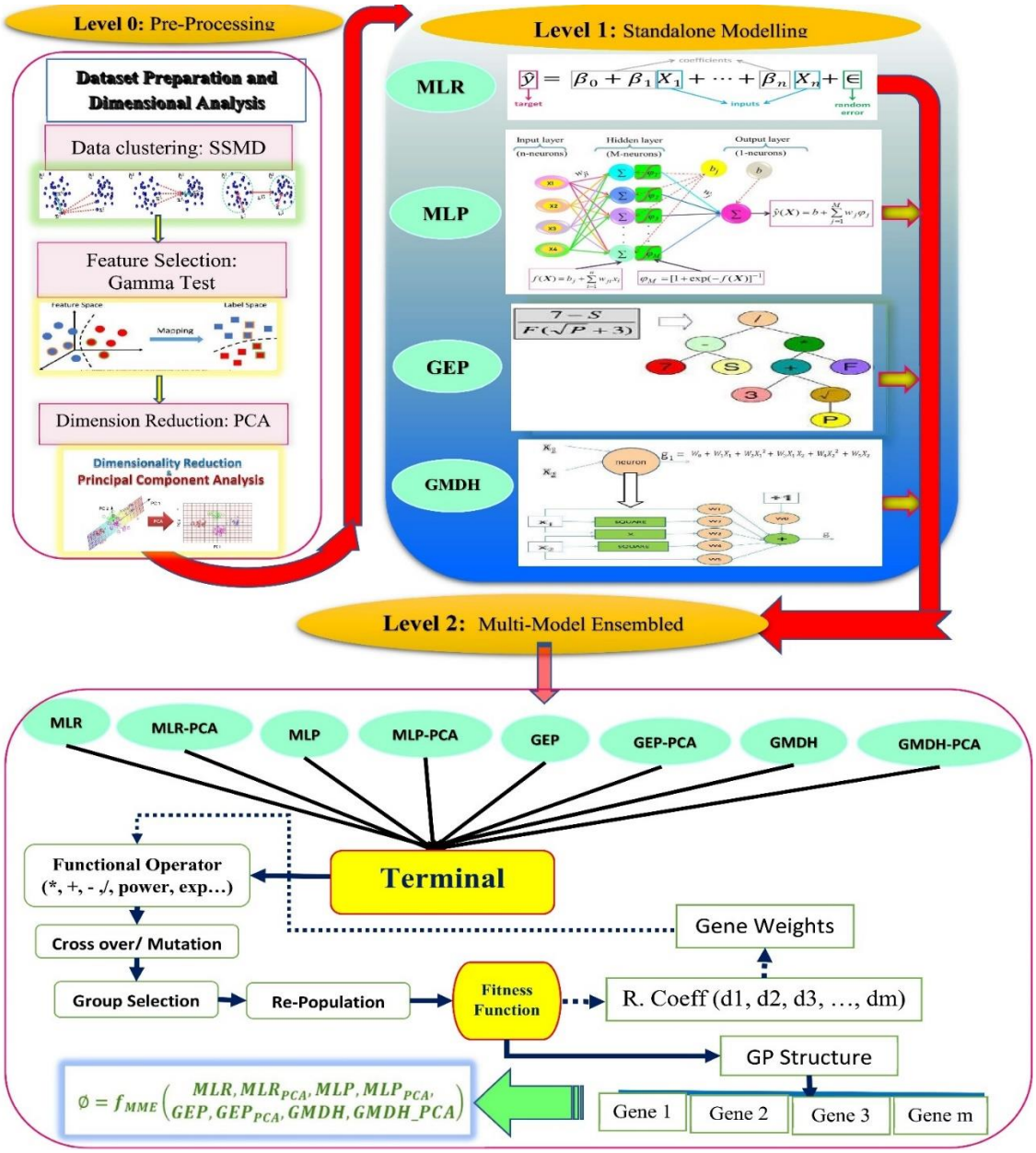


Figure 1. Flowchart of the developed multi-model ensembles approach for function finding in bedload prediction

2.3.4. Component selection and dimension reduction using PCA

In the PCA method for pre-processing of variables, the primary variables are scaled and concentrated to less principal components (PCs) using the orthogonal projection into uncorrelated PCs [27]. In this method, collection of the P original variable, $X_1,\ldots,X_p$, implemented in the P independent principal components, $PC_1,\ldots,PC_p$ equal to the number of primary parameters.

2.4. Level 1: Standalone predictive models

2.4.1. Multiple linear regression (MLR)

If we have n observations of the p-dimensional independent variable X and want to establish a linear relationship with the response variable $\emptyset$, we can use the following MLR model [28]:

$$\emptyset = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \cdots + \beta_p x_p + \varepsilon \quad (4)$$

The parameters β_j, $j = 0, 1, \ldots, p$ are called regression coefficients. The least-squares method is commonly used to estimate the regression coefficients.

2.4.2. ANN-MLP

The Multi-Layer Perceptron (MLP) models are the most popular NN tools used in most of research and literature [20]. By determining the weights and biases of NN architecture, and simplifying the MLP, the predictive equation of model can be derived. The ANN is developed using the MATLAB toolbox.

2.4.3. Pareto Optimal GEP and MGEP

The innovative technique of gene expression programming (GEP) utilized with Darwinian theory of evolution by natural selection to automatically solve optimization problems based on its two main components, the chromosomes and expression trees. A new sophisticated version of GEP is the Multigene-GEP(MGEP), that the population generated by GP trees having selected gens from1 and G_{max}. In the MGEP approach two conflict goals are considered. The first is the selection of the bedload predictive equation with lowest complexity and the second is the highest accuracy. These two conflict objects solved using Pareto optimality combined with multi-genetic programming. In the multi-model-based framework the Pareto optimization is sued in order to balance between the complexity of model and the accuracy. Suppose that X_1 and X_2 are two feasible solutions. In the dominance relationship, two solutions must satisfy the constraints of [29]: $f_d(X_1) \le f_d(X_2), \forall d \in \{1,2,\ldots,D\}$ and $f_i(X_1) \le f_i(X_2), \exists i \in \{1,2,\ldots,D\}$, In which f_d is the fitness value of d solution, and D is the number of the optimization goals.

If the feasible solution X* satisfies the above conditions and there isn't any sequence solution X while X< X*, so that the solution X* will be preserved and is called the Pareto optimal solution.

2.4.4. Group Method of Data Handling (GMDH)

GMDH is one of the meta-heuristic data-driven models based on multivariate analysis for complex systems without the need to have a special basic knowledge. The GMDH develops an analytic function using a progressive network with binomial transfer functions [30]. The mathematical form of GMDH that maps inputs (x_1, x_2, x_3, …, x_n) to the predicted output ($\widehat{\emptyset}$) is written as:

$$\widehat{\emptyset} = a_o + \sum_{i=1}^{n} a_1 x_i + \sum_{i=1}^{n}\sum_{j=1}^{n} a_{ij} x_i x_j + \sum_{i=1}^{n}\sum_{j=1}^{n}\sum_{k=1}^{n} x_j a_{ijk} x_i x_j x_k + \cdots \quad (5)$$

The least-squares error rule is utilized for coefficient determination of GMDH in MATLAB environment.

2.5. Level 2: Multi-model ensembles (MME) approach

In the present study, in addition to the individual predictive models, an innovative multi-model ensembles approach is presented. This feeds the output of standalone models into the POMGGP as a multi-model technique to improve the predictive capability of models.

This new contribution in bedload rate prediction as an ensembles approach consists of two primary levels: Level 1 in which the original input variables or pre-processed (PCs) are used to estimate bedload transport rate in standalone models of MLR, MLR-PCA, ANN, ANN-PCA, GMDH, GMDH-PCA, GEP, GEP-PCA; Level 2 in which the outputs of level 1 models are used as inputs to the POMGGP along with the original bedload rate as output.

In this framework, as presented in Fig.1 the POMGGP is used to run models at level 1 based on Pareto optimality analysis. Observed values of bedload rate serve as the target output in both levels. The strength of the developed framework is learning at two levels, automatic individual model selection by natural evolution in multi-gene GEP, balancing surrogate model complexity and accuracy via Pareto optimality.

The idea behind the multi-model ensembles approach has been inspired by the hierarchical recursion of models, that teamworking of models in parallel can help achieve a more accurate prediction [31].

The models in level 1 and 2 are comparatively evaluated using performance metrics coefficient of determination (R^2), root mean square error (RMSE), mean absolute error (MAE), Nash Sutcliffe efficiency (NSE), and graphical analysis including scatter plots, importance probability, Pareto front and Taylor diagrams. Furthermore, a newly revised discrepancy ratio (RDR) for error distributions developed by the authors [32] is used to overcome non-normality, zero or negative value predictions with a rectified linear unit (ReLu) function [33]. The RDR is calculated by:

$$RDR = Sign(\emptyset_{p,i} - \emptyset_{o,i}) \left| log \left| \frac{\emptyset_{p,i}}{\emptyset_{o,i}} \right| \right| \quad (6)$$

In which the $\emptyset_{o,i}$ is measured value $\emptyset_{p,i}$ is the estimated model output. In the case of over-predictions by POMGGP, the value of RDR>0 and in the case of under-prediction RDR<0 and for exact predictions RDR is equal to zero. The multi-model ensemble is developed using MATLAB environment.

3. Results and discussion

3.1. Level 0: Pre-processing

The results obtained using the pre-processing techniques are presented here, in the level 0. The train (80%) and test (20%) sets are selected using the SSMD approach. For a sizeable sediment transport data as used in the current paper, the SSMD expands the covering bounds of train subset case more applicability of model results and encompasses outlier data in the training set. The GT is utilized for optimum feature selection of the complex process in bedload transport. In the first configuration, all 12 input parameters are used. Then in the next GT execution, the first variable removed and masked and the GT executed again given in the second row. This iterative process of removing and entering input variables continued for all selected variables one by one and in each step the Γ value is calculated. The masking of the most influential variables in bedload prediction results in increases in the Γ (V ratio) versus the non-masking trial. The highest Γ value indicates that the removed variable is essential and should be selected as the input variable of models. Finally based on the results of GT , the most important variables with the highest Γ value are S, D_{gr}, U/u^*_c, H/W, F_r, Re_*, Q, U/u_* as shown in bold style and input dimension from 12 reduced to 8 as:

$$\emptyset = f_3(S, D_{gr}, \frac{U}{u_{*c}}, \frac{H}{W}, F_r, R_{e*}, \theta, \frac{U}{u_*}) \quad (7)$$

The PCA is used for reduction of 8 selected inputs from GT as a linear combination of primitive dimensionless variables and resulted as:

$$PC_1 = 0.069S_n + 0.310D_{gr,n} - 0.256\left(\frac{U}{u_{*c}}\right)_n + 0.012\left(\frac{H}{W}\right)_n - 0.042(F_r)_n + 0.293(R_{e*})_n - 0.151(\theta)_n - 0.253\left(\frac{U}{u_*}\right)_n$$

$$PC_2 = 0.314S_n - 0.143D_{gr,n} - 0.051\left(\frac{U}{u_{*c}}\right)_n + 0.064\left(\frac{H}{W}\right)_n + 0.39(F_r)_n - 0.081(R_{e*})_n + 0.382(\theta)_n - 0.059\left(\frac{U}{u_*}\right)_n \quad (8)$$

$$PC_3 = -0.113S_n + 0.289D_{gr,n} + 0.267\left(\frac{U}{u_{*c}}\right)_n + 0.683\left(\frac{H}{W}\right)_n + 0.037(F_r)_n + 0.289(R_{e*})_n + 0.266(\theta)_n + 0.264\left(\frac{VU}{u_*}\right)_n$$

where, the n footnote indicates the normalized parameters in PCA. The selected PCs represents 85 % of total variances in the bedload transport datasets as shown in Table 3. PC1 has an eigenvalue of 3.526 that explains 44.071 % of the total variance, PC2 has an eigenvalue of 2.049 with 25.614 % of total variance presented and PC with an eigenvalue of 1.16 has an eigenvalue of 14.505 %. The next section presents the results of standalone models I predictions.

3.2. Level 1: Performance of standalone models

The results obtained by using the presented standalone models are presented and discussed here. A comprehensive evaluation of the model predictions should include at least 'goodness-of-fit' such as R^2, NSE and error indices such as RMSE, or RAE. The comprehensive comparison of the best single model results using the selected input variables by the GT and the quantitative values of performance evaluation indices of the MLR, MLR-PCA, ANN, ANN-PCA, GEP, GEP-PCA, GMDH, GMDH-PCA are presented in Table 1. In the training step, the ensembles ANN-PCA model showed a relatively accurate estimation of bedload with (R^2=1≈0.996), RMSE=0.71 when compared with the ANN (R^2=0.98, RMSE=1.66), GEP-PCA (R^2=0.95, RMSE=2.94) and the others. Based on the classification of model performances by the R^2 metric, all models in Table 1 had an outstanding performance (0.7>R^2>1) in bedload predictions, except the MLR-PCA. In the test stag, the same performance trend and accuracy improvement when combined the standalone models with the PCA were declared.

The best results were comparatively obtained by the ANN-PCA, GEP-PCA and ANN models. In this regard the ANN-PCA model with R^2=0.96, RMSE=0.38, RAE=0.16 and NSE=0.95 have the best predictions for the bedload in the test stage. The NSE values of the GEP-PCA, ANN-PCA, GEP and ANN models in the train and testing steps confirmed excellent predictions for the bedload transport in the test stage with NSE>0.75. The best accuracy of the GEP-PCA and ANN PCA-based models confirmed their ability in the emerging non-linear system indentation when combined GT and PCA's pre-processing model-free techniques. The hierarchical accuracy of models follows the order of ANN-PCA> ANN> GEP-PCA> GEP> GMDH-PCA> GMDH> MLR-PCA> MLR in terms of the R^2, RMSE, RAE and NSE values for the test stage, as given in Table 1. The percent of prediction improvements by utilizing the PCA as input dimension reduction in RMSE reduction was 57% and 3% in ANN-PCA, 4% and 4% in GEP-PCA, 9% and 45% in GMDH-PCA for train and testing steps, respectively. The explicit form of predictive equations based on the trained above eight models are as follows:

MLR:

$$MLR = -3{,}39S + 0{,}02D_{gr} - 2{,}02\frac{U}{u_{*c}} - 5{,}4\frac{H}{W} - 8{,}3F_r - 0{,}002R_{e*} - 46{,}2\theta + 1{,}8\ \frac{U}{u_*} + 4{,}81 \quad (9)$$

MLR-PCA:

$$MLR - PCA = 1{,}95 - 2{,}81PC_1 + 6{,}35PC_2 + 3{,}65PC_3 \quad (10)$$

GMDH:

$$\begin{aligned} G_1 &= 1.9Se^{0.27(\theta+0.64)} + 0.16S^2 + 12e^{0.27(\theta+0.64)} - 2.84S - 11.44 \\ G_2 &= 411.52 * e^{0.002(G_1+1.73)} - 411.4 \\ G_3 &= 115671.3e^{0.000009(G_2+1.35)} - 115671.3 \\ GMDH &= 970.9e^{0.000956(G_3+1.36)} - 970.79 \end{aligned} \quad (11)$$

GMDH-PCA:

$$GMDH - PCA = \frac{504{,}35}{1+e^{4{,}55PC_3-17{,}7}} + 1{,}78e^{0{,}998+0{,}3008PC_3+0{,}55PC_2-0{,}225PC_1} + 0{,}01e^{-(3{,}71PC_1+10{,}83)} - 0{,}61PC_3 + 0{,}44PC_3 \times PC_1 - 506{,}39 \quad (12)$$

GEP:

$$GEP = \theta \times Fr + e^{Fr-2.21} + 6.2e^{\theta} - \theta - S - 7.14 \quad (13)$$

GEP-PCA:

$$GEP - PCA = 33{,}6e^{-\frac{(PC_2-7{,}81)^2}{2PC_3^2}} + 1479391{,}4e^{-\frac{(PC_2-24{,}13)^2}{2PC_3^2}} - 1{,}75e^{-0{,}37(PC_2-PC_1)^2} + 2^{(PC_2-PC_1)} + 0{,}73 \quad (14)$$

ANN:

$$\begin{aligned} ANN &= \frac{530.2}{1+e^{-2(T_1+T_2+T_3+T_4)-28.3}} - 265.1 \\ T_1 &= \frac{16.36}{1+e^{0.66S-12.94D_{gr}+5.18\frac{U}{u_{*c}}+0.2\frac{H}{W}+5.44F_r+7.66R_{e*}-4.34\theta-5.18\frac{U}{u_*}-5.86}} - 8.18 \\ T_2 &= \frac{-41.46}{1+e^{31.22S+1.74D_{gr}+109.78\frac{U}{u_{*c}}-165.86\frac{H}{W}+136.76F_r+2.3R_{e*}+92.44\theta+117.63\frac{U}{u_*}-271.4}} + 20.73 \\ T_3 &= \frac{-2.98}{1+e^{1.26S-12.64D_{gr}+4.8\frac{U}{u_{*c}}+0.1\frac{H}{W}+5.28F_r+7.44R_{e*}-2.68\theta-4.72\frac{U}{u_*}-4.2}} + 1.49 \\ T_4 &= \frac{0.24}{1+e^{26S-4.78D_{gr}-2.52\frac{U}{u_{*c}}+9.24\frac{H}{W}+6.06F_r-0.3R_{e*}-38.42\theta-0.38\frac{U}{u_*}+9.38}} - 0.12 \end{aligned} \quad (15)$$

ANN-PCA:

$$\begin{aligned} ANN - PCA &= \frac{530.2}{1+e^{-2(T_1+T_2+T_3)-68.43}} - 265.1 \\ T_1 &= \frac{-5.065}{1+e^{-37PC_1+34.63PC_2-2PC_3-30.2}} + \frac{0.09}{1+e^{20.2PC_1-16.9PC_2+2.75PC_3+9.68}} + 2.48 \\ T_2 &= \frac{68.9}{1+e^{1025.7PC_1+34.7PC_2+195.9PC_3+347.4}} + \frac{5.64}{1+e^{-36.4PC_1+18.4PC_2-8.6PC_3-18.6}} - 37.3 \\ T_3 &= \frac{-0.03}{1+e^{-9.75PC_1+17.1PC_2+0.3PC_3+3.6}} + 0.013 \end{aligned} \quad (16)$$

The scatter plots of the measured bedload rate against predicted by the models are presented in Fig.2. it shows that MLR, MLR-PCA, GMDH and GMDH-PCA model have underestimations for the bedload rate. As the results in this figure confirmed, the GEP-PCA, ANN-PCA models are most consistent with the 1:1 line and provide superior predictions for bedload transport rate in rivers compared to the standalone models of ANN, GEP, MLR, and GMDH. As the first main motivation and contribution of the current study was to introduce the feasibility of utilizing the pre-processing model-free techniques of SSMD, GT and PCA and their ensemble ability with standalone models for bedload transport rate prediction in rivers, these techniques show an improved generalization capacity than non-preprocessed predictions and is confirmed with high estimation accuracy obtained. In the next section the results of ensembled multi model provided.

Table 1. The statistical measures of standalone models in the train and testing steps

	Train								
	MLR	MLR-PCA	ANN	ANN-PCA	GEP	GEP-PCA	GMDH	GMDH-PCA	MME
R^2	0.76	0.37	0.98	0.996	0.94	0.95	0.80	0.55	0.997
RMSE	6.27	10.27	1.66	0.71	3.06	2.94	12.77	9.39	0.6
RAE	0.90	1.39	0.10	0.08	0.24	0.20	2.28	1.26	0.06
NSE	0.76	0.37	0.98	0.996	0.94	0.95	0.02	0.47	0.997

	Test								
	MLR	MLR-PCA	ANN	ANN-PCA	GEP	GEP-PCA	GMDH	GMDH-PCA	MME
R^2	0.78	0.76	0.96	0.96	0.93	0.92	0.88	0.89	0.98
RMSE	5.66	4.75	0.37	0.36	0.56	0.54	6.16	3.37	0.24
RAE	3.06	2.83	0.18	0.16	0.34	0.25	4.21	2.16	0.1
NSE	-9.03	-6.07	0.96	0.95	0.90	0.91	-10.91	-2.57	0.98

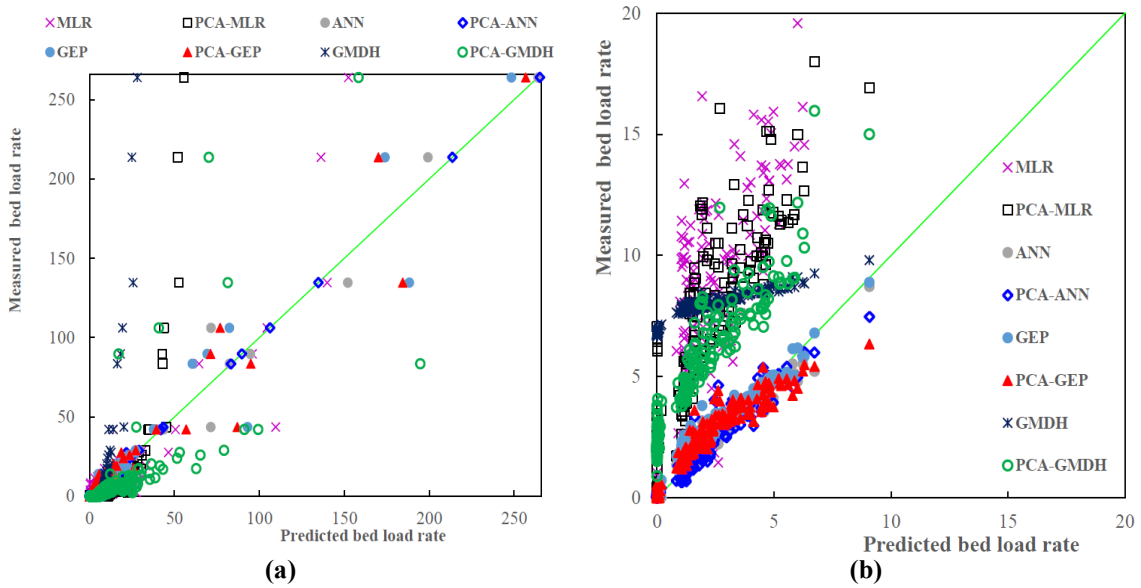


Figure 2. Scatter plots of observed bedload rates versus prediction by standalone models in A) tarin and B) test data sets

3.3. Level 2: Results of EMM approach: Ensembles-POMGGP

In the developed new strategy of EMM approach for bedload transport predictions, the Pareto optimality in conjunction with the multi-gene genetic programming is used to predict bedload transport by considering the output of standalone models. In this strategy the MLR, MLR-PCA, ANN, ANN-PCA, GEP, GEP-PCA, GMDH and GMDH-PCA predictions are used as the input vector to the POMGGP model and the feasible inputs are selected automatically by the geniting programming.

The Multi-Model input variable importance is shown in Fig. 3. As this figure shows, the most important sub-model is the ANN with an importance probability of 0.301, followed by the ANN-PCA sub-model with an importance probability of 0.286, and the MLR model with an importance probability of 0.225. Less important sub-models in the ensembles multi-model for predicting the dimensionless bedload transport rate follows the order of GMDH (probability=0.075)> GEP (probability=0.071)> GMDH-PCA (probability=0.029)> GEP-PCA (probability=0.014)> and MLR-PCA (probability=0.0).

The importance probability graph of sub-models in Fig. 3 shows that using the results of ANN, ANN-PCA, MLR, GMDH and GEP models, we are able to derive a predictive equation with an importance probability of 95.8%. So, in order to reduce the complexity of the final multi-model, and increase the application feasibility of the results, the Pareto optimality is used to derive the equation of final multi-model.

The parameters in Table 2 are determined by trial and error and using those suggested in the literature. The multi-gene genetic programming is trained and optimized by the least square error, the RMSE as the fitness function, basic math operators in function set, and Pareto optimality as the selection criteria. The Pareto graph of the evolved multi-models for bedload predictions using all sub-models as inputs, i.e: MLR, MLR-PCA, ANN, ANN-PCA, GEP, GEP-PCA, GMDH, and GMDH-PCA are shown in Fig. 4.

The Pareto-optimal solution of different multi-models on the Pareto front are chosen not more than 10% decrease occurred in model accuracy neither in the train nor at testing step. In this figure, the Pareto front is demonstrated with green circles, the best final multi-model is displayed by a red perimeter circle with green fill color. The structural properties of the final multi-model include the overall complexity of 367, with 89 nodes in the selected symbolic expression, 4 individual genes, depth value 6 and -7.77 as the bias term, with MLR, ANN, ANN-PCA, GEP-PCA, GMDH as selected optimum input sub-models in agreement with probability importance graph in Fig. 3.

complexities and depths are presented in Table 3.

As shown in Table 3, The bias term with weight=-7.77, Gene 2 that includes ANN and ANN-PCA with weight=7.6, Gene 4 with weight= -3.86 added the MLR, GMDH followed by Gene 1, has the highest weight and importance in the multi-gene model solution. To evaluate the statistical significance of individual genes the p-value of each gene calculated and the p-values in all of the genes were smaller than 0.00001, confirms and indicates the statistical importance of individual genes in the multigene model. Finally, by applying the coefficients of individual genes and simplifying the final Pareto solution of multi-gene equation, the final explicit predictive equation for dimensionless bedload rate resulted from the developed multi-model strategy with its effective sub-models is derived as:

$$\emptyset = 1.13\mathrm{ANN}_{\mathrm{PCA}} - 0.079ANN - 0.073GEP_{PCA} + 0.027MLR + 7.6e^{(Exp(-3.34Exp(ANN_{PCA}{}^2))} + \frac{3.93ANN}{GMDH} - \frac{4ANN_{PCA}}{GMDH} + \frac{0.073MLR}{GMDH} - \frac{ANN_{PCA}}{13.74GMDH - 3.82ANN_{PCA} + \frac{13.74MLR}{ANN}} - 7.77 \quad (20)$$

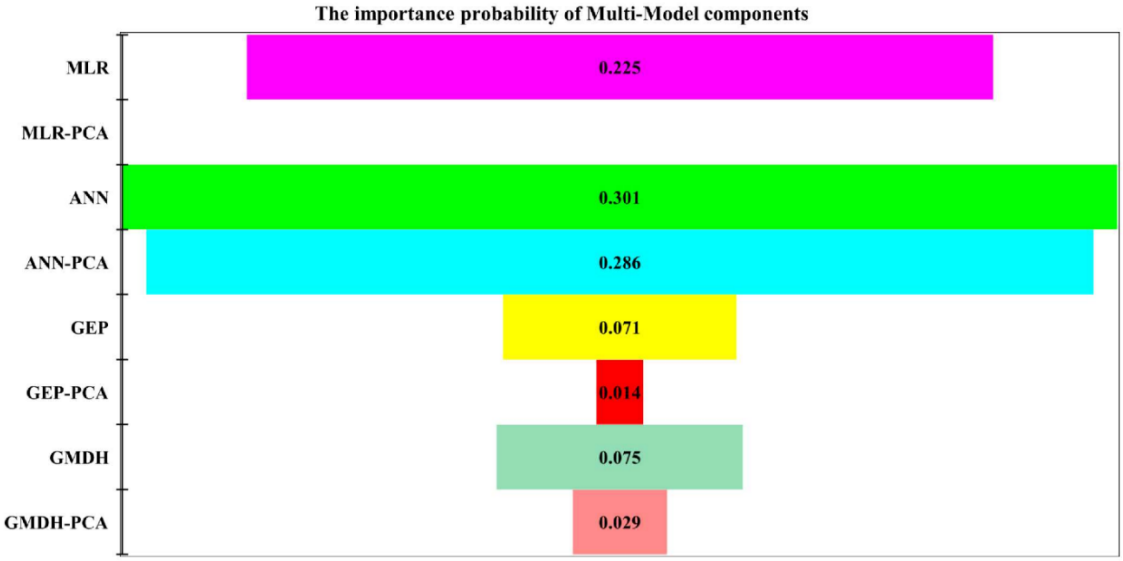


Figure 3. The multi-model input variable (standalone models) importance

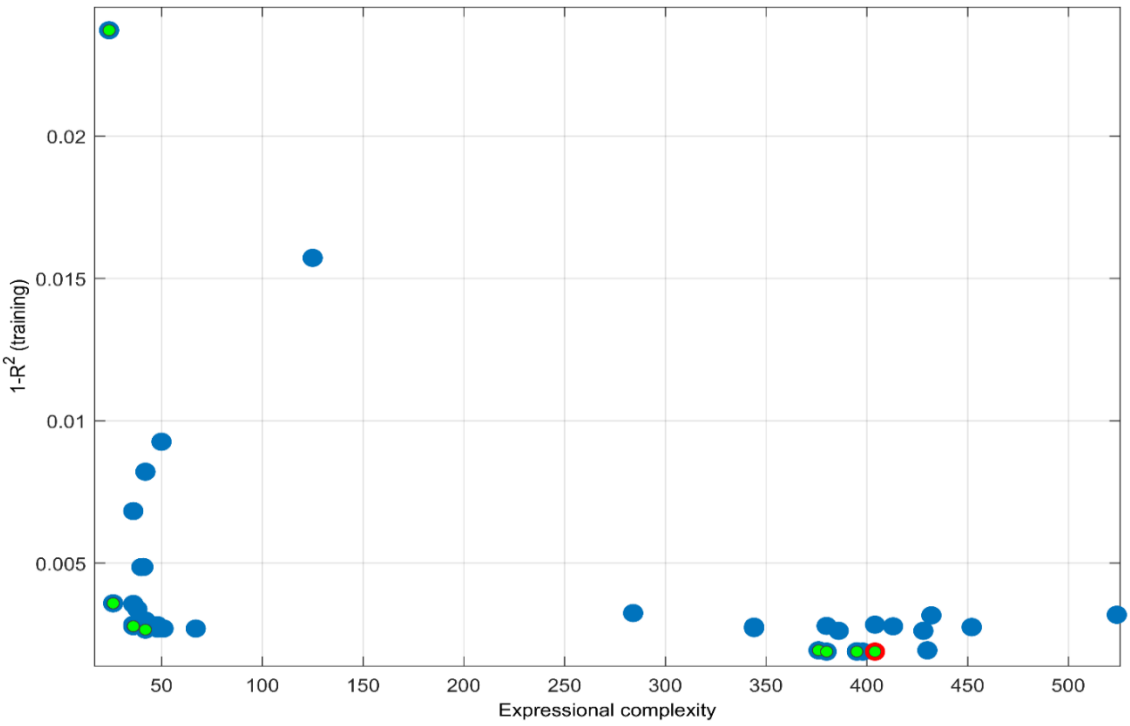


Figure 4. Pareto graph of the best evolved multi-models

The final parse tree of the Pareto selected multi-model is presented in Fig. 5. This figure presents the symbolic expression of each gene in the multi-gene model. The final equation and simplified gene's expression, the individual weights, the number of nodes, individual

Performance indices of the final MME predictions for bedload are compared in Table 3 in train and test stages. Graphically, the results of Eq. 34 as the final multi-model solution are presented in Figs. 6 and 7 for the test stage and in Figs. 8 and 9 for the train stage. The scatter plots and series plots show the multi-model is accurately capable of capturing low and high values of bedload with different conditions in input observations. This is one remarkable aspect of our multi-model in mimicking low and high flows.

These results revealed that the multi-model approach improved the generalization capacity of single standalone single models, as confirmed with better estimation accuracy obtained in this extensive dataset (Train: R^2=0.997, RMSE=0.6, RAE=0.06, NSE=0.997, and in test Train: R^2=0.98, RMSE=0.1, RAE=0.24, NSE=0.98. Comparing the results of the training period of multi-model with the greatest improvement, about 16% in RMSE, and 25% in RAE was obtained compared to the best standalone model, ANN-PCA.

Based on the results in training step, the Multi-model had a decrease of 90% (in RMSE, RAE) and an increase of 31% (in NSE, R^2) compared to MLR. Multi-Model also showed a decrease of 95% (in RMSE, RAE) and an increase of 169% (in NSE, R^2) compared to MLR-PCA; a decrease of 63% and 40%% (in RMSE, RAE) and an increase of 2% (in NSE, R^2) compared to ANN, a decrease of 80% and 75%% (in RMSE, RAE) and an increase of 6% (in NSE, R^2) compared to GEP; a decrease of 79% and 70% (in RMSE, RAE) and an increase of 5% (in NSE, R^2) compared to GEP-PCA in train stages.

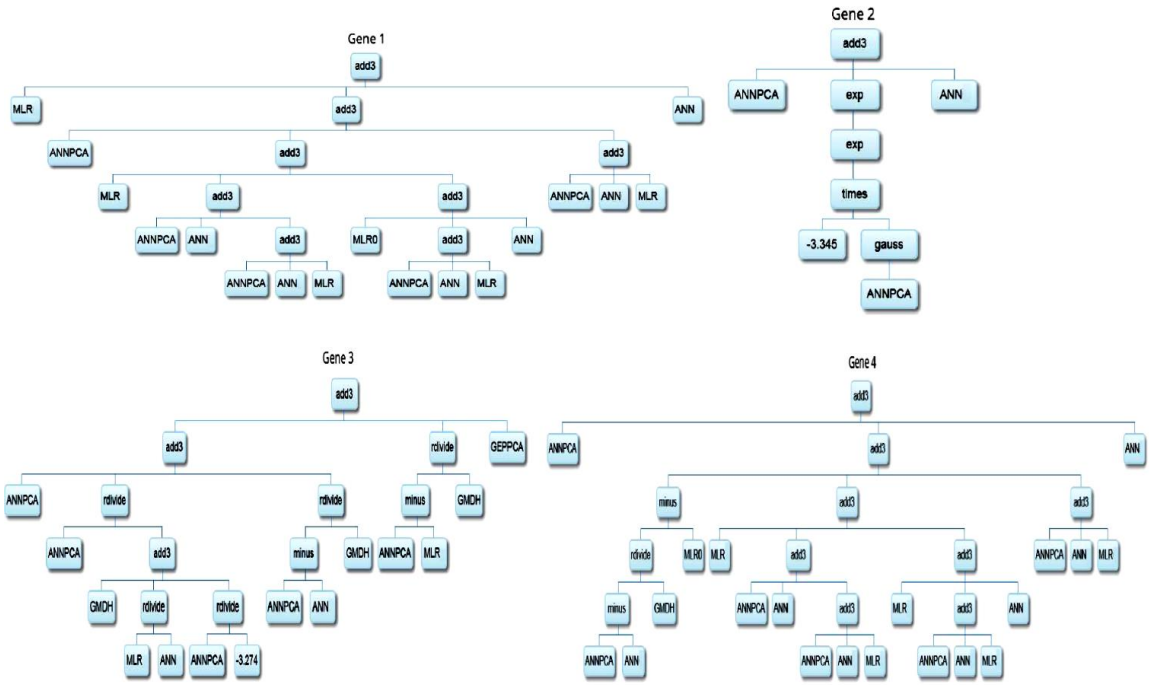


Figure 5. The final parse tree of the Pareto selected multi-model

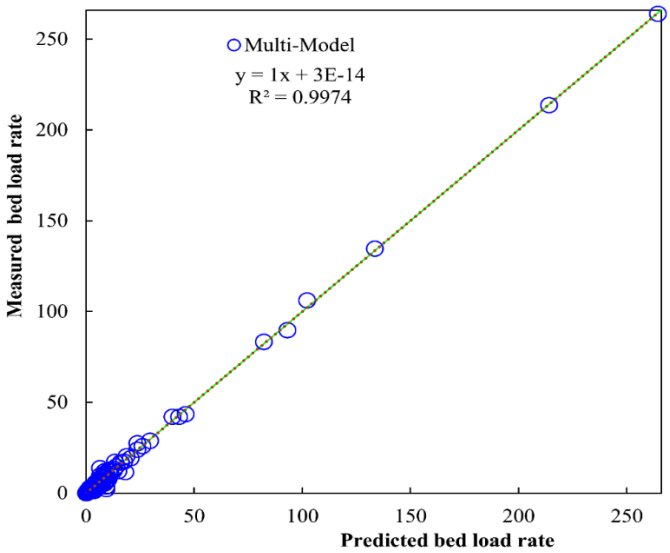


Figure 6. Scatter plot of multi-model in training step

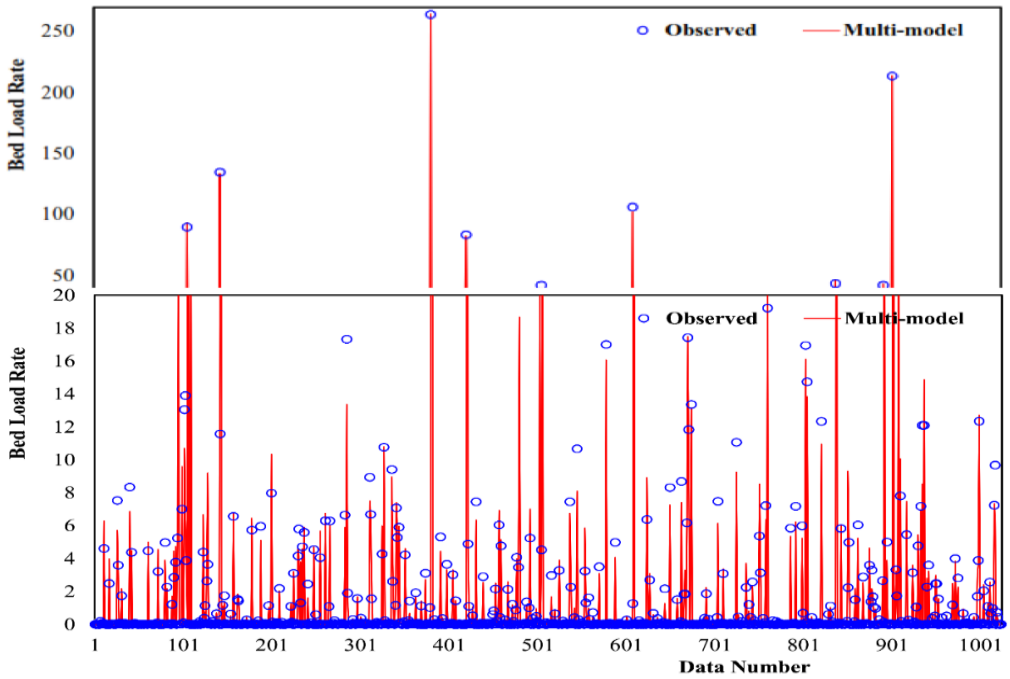


Figure 7. Comparison of observed versus predicted bedload transport in training step

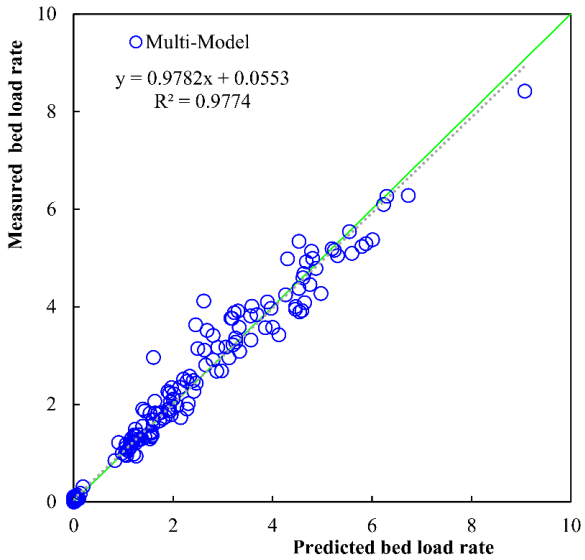


Figure 8. Scatter plot of multi-model in testing step

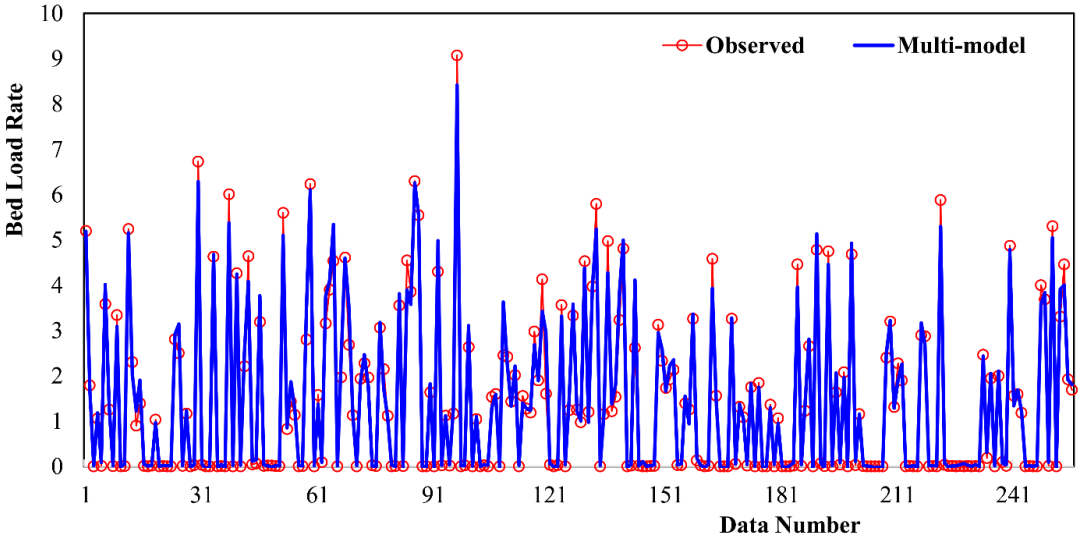


Figure 9. Comparison of observed versus predicted bedload transport in testing step

The percentage of improvements in the test stage of multi-Model when these results are compared with other standalone predictions, are presented in Table 2. The improvement percentages in this table indicates that utilizing the multi-model strategy the RMSE and RAE values, as major error indices are decreased from 33% in ANN-PCA up to 96% in MLR and GMDH. In the R^2 measure the improvement varies from 2% up to 29%, and in the NSE, the gain varies from 2 up to 138%. These values confirm the superiority of the developed strategy in the generalization of bedload prediction.

To compare the underestimation or overestimation of the multi-model with the other models, in Figs. 10 and 11 the standardized error distribution of prediction in terms of RDR versus probability and the Taylor diagram of all models in train and test stages are shown. As these figures show the MLR, MLR-PCA, ANN and GEP models have underestimated and the GMDH-PCA, GMDH, ANN-PCA and GEP-PCA models overestimated for the bedload, while the multi-Model have reasonable estimates in training step. In the

testing step, the RDR graph in Fig. 9, declares that the multi-Model strategy provides more generalities in the predictions and the RDR distribution is accurately around the 0, while the ANN, GEP, MLR and MLR-PCA have considerable underestimates and ANN-PCA, GEP-PCA, GMDH-PCA and GMDH have high overestimate in bedload. Reasonable accuracy and generality and parsimonious structure, endorse the developed multi-model approach for bedload transport estimation in practice. The leading cause behind the improvement in MME originates from the inherent multi-process nature and different patterns of bedload transport in the extremely low flows up to high flows is that the sediment transport is a mixture of a laminar, turbulent, linear and nonlinear phenomenon in rivers that would be taken into account by integration of linear and nonlinear models.

Table 2. Parameter setting for the MME development.

Run parameter	Value	Run parameter	Value
Population size	100	Gaussian perturbation of constant	0.05
Max. generations	500	Max. genes	4
Generations elapsed	500	Max. tree depth	6
Input variables	8	Max. total nodes	Inf
Training instances	1024	ERC probability	0.3
Tournament size	50	Crossover probability	0.84
High level Crossover	0.2	Low level Crossover	0.8
Elite fraction	0.75	Mutation probabilities	0.14
Sub-tree mutation	0.9	Input Mutation probabilities	0.05
Lexicographic selection pressure	On	Complexity measure	Expressional
Function set	*, -, +, /, ^,$\sqrt{\ }$, exp, ln, multi3, cub, gauss, add3, square,		

Table 3. The Multi-gene results of Pareto solution in MME.

Term	Value	Gene weights	Nodes	Depth	Complexity
Bias	-7.77	-7.71	-	-	-
Gene 1	15.4 ANN + 12.9 ANN_{PCA} + 15.4 MLR	2.57	34	6	151
Gene 2	7.6 ANN + 7.6 ANN_{PCA} + 7.6 Exp(Exp(-3.34 gauss(ANN_{PCA})))	7.6	30	6	125
Gene 3	(0.0728 ANN)/GMDH - 0.0728 GEP_{PCA} - (ANN_{PCA})/(13.74 GMDH – 4.2 ANN_{PCA} + (13.74 MLR)/ANN) - 0.0728 ANN_{PCA} - (0.146 ANN_{PCA})/GMDH + (0.0728 MLR)/GMDH	-0.0728	9	6	31
Gene 4	-(3.86 (ANN_{PCA} -ANN + 6.0 ANN× GMDH + 5.0 ANN_{PCA} ×GMDH + 4.0GMDH ×MLR))/GMDH	-3.86	23	6	97
Overall Structure of Multi-Model: Genes:4; Nodes:89; Complexity: 367; Depth:6; Inputs selected: MLR, ANN, ANN-PCA, GEP-PCA, GMDH					

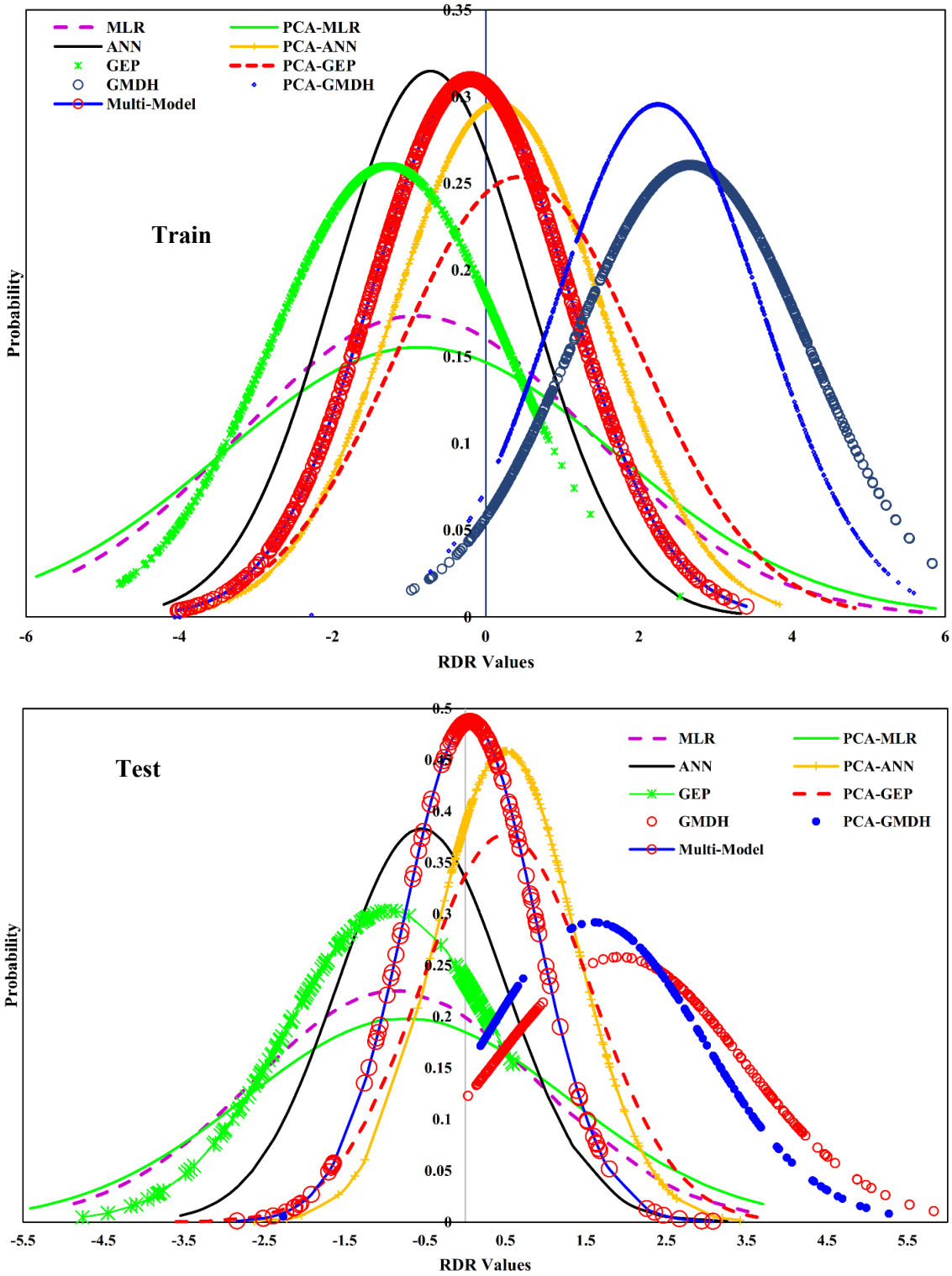


Figure 10. The RDR graph in train and test stages of the MME

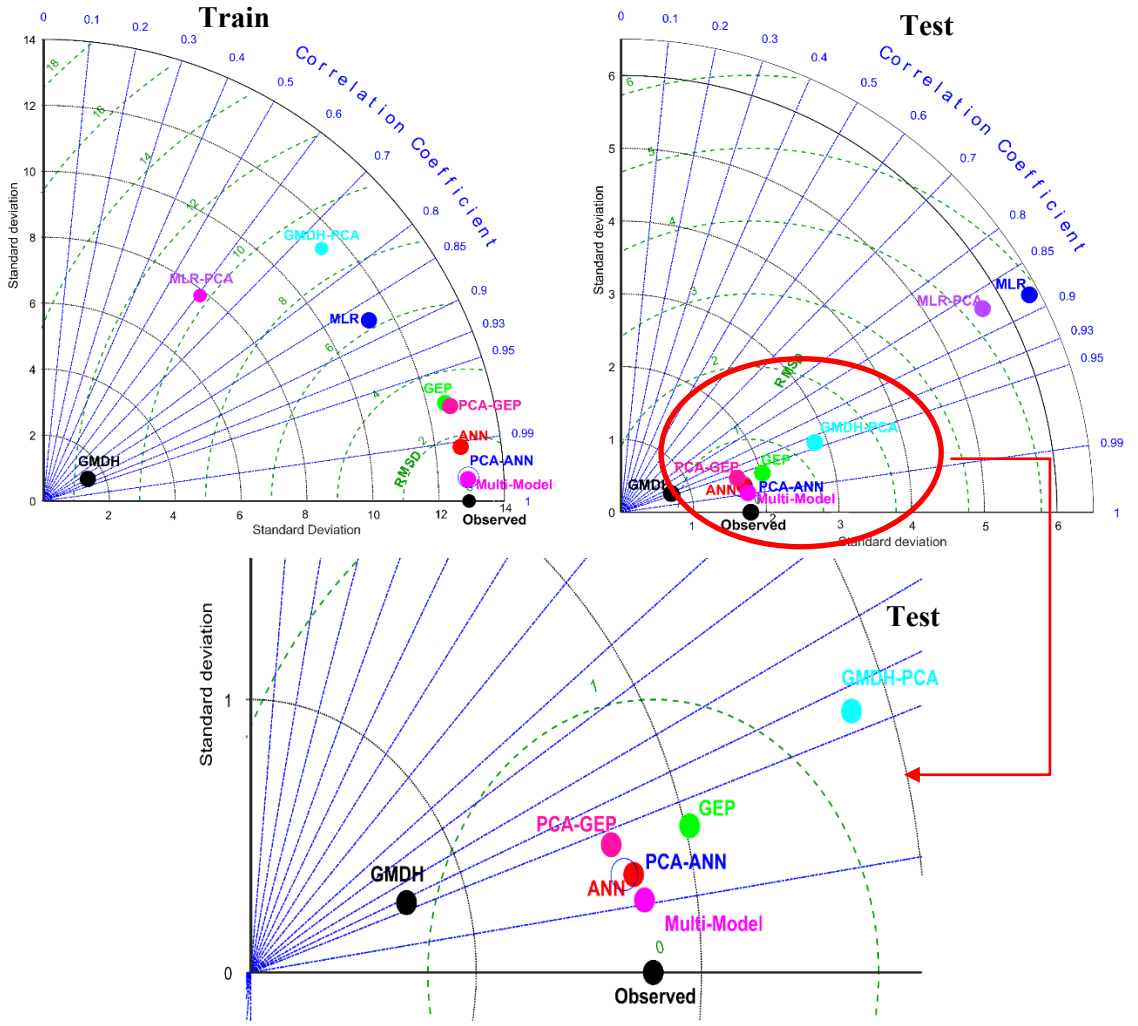


Figure 11. The Taylor diagram in train and test stages

Table 4. The percentage of improvements in bedload rate prediction with multi-Model strategy in testing step

	MLR	MLR-PCA	ANN	ANN-PCA	GEP	GEP-PCA	GMDH	GMDH-PCA
R^2	26	29	2	2	5	7	11	10
RMSE	-96	-95	-35	-33	-57	-56	-96	-93
RAE	-97	-96	-44	-38	-71	-60	-98	-95
NSE	111	116	2	3	9	8	109	138

3.4. Comparison with previous studies, Limitations, Recommendations, and Implications

To further evaluate the predictive capability of the proposed model, its performance was compared with those reported in previous studies on bed-load transport prediction using data-driven approaches. As shown in Table X, the proposed MME model achieved a testing performance of R^2 = 0.98, NSE = 0.98, RMSE = 0.24, and RAE = 0.10, indicating excellent agreement between the observed and predicted dimensionless bed-load transport rates. Compared with previous studies, the proposed model demonstrates a highly competitive predictive capability. For instance, Khosravi et al. (2020) reported

that the hybrid Bagging–M5P model achieved R^2 = 0.943, NSE = 0.945, and RMSE = 0.061, whereas Roshangar and Javalizadeh (2022) obtained the best results using an LSTM model with R = 0.95, DC = 0.90, and RMSE = 0.024 kg m^{-1} s^{-1} for bed-load prediction. Likewise, Riahi-Madvar and Seifi (2018) reported that the best ANFIS model yielded R^2 = 0.70 and RMSE = 0.27 kg s^{-1} during the testing phase, while the corresponding ANN model showed even lower prediction accuracy, confirming the superior capability of neuro-fuzzy systems over conventional neural networks for bed-load estimation. Similar improvements achieved by advanced hybrid and machine learning approaches over conventional empirical sediment transport equations have also been reported by Samantaray et al. (2022), Bhattacharya et al. (2007), Kitsikoudis et al. (2020), and Bonakdari and Ebtehaj (2019). More recently, Mir et al. (2024) demonstrated that an XGBoost model achieved a testing accuracy of approximately R^2 = 0.99, representing one of the best performances reported for sediment transport prediction. Overall, the proposed MME model exhibits predictive accuracy among the highest reported in the literature and substantially improves upon most previously published ANN-, ANFIS-, GEP-, and hybrid machine learning models for predicting bed-load transport.

The superior performance of the proposed MME model can be attributed to its ensemble learning strategy, which combines the complementary strengths of multiple individual learners while reducing prediction variance and improving generalization capability. Ensemble methods have consistently been shown to achieve higher predictive accuracy and robustness than single learning algorithms because they reduce overfitting and improve model stability through the aggregation of multiple predictors (Dietterich, 2000; Zhou, 2025). In addition, ensemble learning is particularly effective for modeling highly nonlinear and complex hydrological processes, where interactions among hydraulic and sediment variables are difficult to capture using individual models (Mosavi et al., 2018). Therefore, the proposed MME framework provides a robust and competitive approach for predicting dimensionless bed-load transport and demonstrates considerable potential for practical sediment transport applications.

Despite the significant improvements achieved by the proposed multi-level multi-model framework, some limitations should be considered. The heterogeneity of the compiled global database, including variations in measurement techniques, experimental conditions, sediment properties, and reporting protocols, may introduce uncertainties into the model development process. Moreover, the present framework mainly relies on hydraulic and sedimentological variables commonly available in previous studies; therefore, additional physical factors such as sediment shape, gradation, bedforms, and turbulence characteristics were not explicitly incorporated. Furthermore, the applicability of the developed explicit equation beyond the range of the training dataset requires further validation under diverse river conditions.

The findings demonstrate that integrating data preprocessing, dimensionality reduction, and recursive ensemble learning provides an effective pathway for developing accurate and interpretable bedload transport models. The proposed framework can serve as a robust modeling strategy for extracting explicit predictive relationships from complex and heterogeneous sediment transport datasets. Future research should focus on expanding field-based databases, incorporating additional physical descriptors, and combining the proposed approach with uncertainty analysis and physics-informed machine learning techniques to further improve model reliability and transferability to data-limited river systems

4. Conclusions

In this study, a new multi-Model strategy integrated with pre-processing techniques of

SSMD, GT, and PCA is developed to derive an explicit predictive equation for the bedload transport in rivers with extensive dataset. The framework of enhanced multi-modelling improves the accuracy and heuristic capability to learn tendencies within residuals of individual model results and gain an insight into the nature of bedload transport in three-level strategy.

At level 0, the pre-processing, input selection and dimension reduction are carried out by SSMD, GT, PCA. At level 1, the standalone models MLR, MLR-PCA, ANN, ANN-PCA, GEP, GEP-PCA, GMDH, GMDH-PCA are used to derive explicit predictive equations. At level 2, the EMM is developed by utilizing the output of individual models as an external input to the multigene genetic programming with Pareto optimality to derive explicit predicting models. The main conclusions of this ensemble modeling are as follows:

1. The hierarchical accuracy of models follows the order of ANN-PCA> ANN> GEP-PCA> GEP> GMDH-PCA> GMDH> MLR-PCA> MLR in terms of the R^2, RMSE, RAE and NSE values for the test stage.
2. The percent of prediction improvements by utilizing the PCA as input dimension reduction in terms of RMSE reduction was 57% and 3% in ANN-PCA, 4% and 4% in GEP-PCA, 9% and 45% in GMDH-PCA for training and testing steps respectively.
3. The MME had a decrease of 90% (in RMSE, RAE) and an increase of 31% (in NSE, R^2) compared to MLR, a reduction of 95% (in RMSE, RAE) and an increase of 169% (in NSE, R^2) compared to MLR-PCA; a decrease of 63% and 40%% (in RMSE, RAE) and an rise of 2% (in NSE, R^2) compared to ANN, a decrease of 80% and 75%% (in RMSE, RAE) and an increase of 6% (in NSE, R^2) compared to GEP; a reduction of 79% and 70% (in RMSE, RAE) and an increase of 5% (in NSE, R^2) compared to GEP-PCA.
4. The explicit predictive equation based on EMM approach has resulted in the gaining of a robust system with significant predictive accuracy improvement, (i.e., 33–96% in terms of RMSE; 2-29% in terms of R^2, 2-138% in terms of NSE and 38-98% in terms of RAE in testing step).

Finally, the authors would like to acknowledge the not always subtle differences in the previous studies' data measurement/collection methods. These differences constitute a limitation of the current research and a potential source of error when compiling the data set for machine learning. However, most of the sources used for compiling the comprehensive data set needed for the training and testing of the machine learning models have followed similar data measurement methods and standard data analysis, and reporting protocols to serve a truly global international community of researchers in this field.

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During the preparation of this work the author used check spelling tools in order to grammar correct. After using this tool, the author reviewed and edited the content as needed and takes full responsibility for the content of the publication.

Author Contributions:
All authors contributed to the study conception and design. Material preparation, data collection, and analysis were performed by H. R-M. The first draft of the manuscript was written by H. R-M

and the final revised version prepared by A. S. All The author reads and approved the final manuscript.

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