Nonparametric C- and D-vine based quantile regression

Marija Tepegjozova, Jing Zhou, Gerda Claeskens and Claudia Czado. February 10, 2021

Abstract

Quantile regression is a field with steadily growing importance in statistical modeling. It is a complementary method to linear regression, since computing a range of conditional quantile functions provides a more accurate modelling of the stochastic relationship among variables, especially in the tails. We introduce a novel non-restrictive and highly flexible nonparametric quantile regression approach based on C- and D-vine copulas. Vine copulas allow for separate modeling of marginal distributions and the dependence structure in the data, and can be expressed through a graph theoretical model given by a sequence of trees. This way we obtain a quantile regression model, that overcomes typical issues of quantile regression such as quantile crossings or collinearity, the need for transformations and interactions of variables. Our approach incorporates a two-step ahead ordering of variables, by maximizing the conditional log-likelihood of the tree sequence, while taking into account the next two tree levels. Further, we show that the nonparametric conditional quantile estimator is consistent. The performance of the proposed methods is evaluated in both low- and high-dimensional settings using simulated and real world data. The results support the superior prediction ability of the proposed models.

Keyword: quantile regression, vine copula, conditional quantile function, nonparametric pair-copulas

1 Introduction

As a robust alternative for the ordinary least squares regression, which estimates the conditional mean, quantile regression (Koenker and Bassett 1978) focuses on the conditional quantiles. This method has been studied extensively in statistics, economics and finance.

^{*}Department of Mathematics, Technische Universität München, Boltzmannstraße 3, 85748 Garching, Germany (email: m.tepegjozova@tum.de (corresponding author), cczado@ma.tum.de)

[†]ORStat and Leuven Statistics Research Center, KU Leuven, Naamsestraat 69-box 3555 Leuven, Belgium (email: jing.zhou@kuleuven.be, gerda.claeskens@kuleuven.be)

The pioneer literature Koenker (2005a) investigated linear quantile regression systematically. It presented properties of the estimators including asymptotic normality and consistency, under various assumptions such as independence of the observations, independent and identically distributed (i.i.d.) errors with continuous distribution and predictors having bounded second moment. Later, the subsequent extensions of linear quantile regression have been intensively studied, see for example adapting quantile regression in the Bayesian framework (Yu and Moyeed 2001), for longitudinal data (Koenker 2004), time-series models (Xiao and Koenker 2009), high-dimensional models with l_1 -regularizer (Belloni and Chernozhukov 2011), nonparametric estimation by kernel weighted local linear fitting (Yu and Jones 1998) and by additive models (Koenker 2011; Fenske et al. 2011), etc. The theoretical analysis of the above-mentioned extensions is based on imposing additional assumptions such as samples that are i.i.d. (see for example Yu and Jones (1998); Belloni and Chernozhukov (2011), or that are generated by a known additive function (see for example Koenker (2011); Koenker (2004)). However, such assumptions, which guarantee the performance of the proposed methods for certain data structure, causes concerns in application due to the uncertainty of the real-world data structures. In addition to the above-mentioned issue, Bernard and Czado (2015) addressed other potential concerns such as quantile crossings and model-misspecification, when the dependence structure of the response variables and the predictive variables does not follow a Gaussian copula. Hence, flexible models without assuming homoscedasticity, or a linear relationship between the response and the predictive variables are of interest. Recent research on dealing with this issue includes quantile forest (Meinshausen 2006; Li and Martin 2017; Athey et al. 2019) inspired by the earlier work of random forest (Breiman 2001). Further, flexible quantile modeling motivates research on modeling conditional quantiles using copulas (see also Noh et al. (2013); Noh et al. (2015); Chen et al. (2009)). Vine copulas in the context of conditional quantile prediction have already been investigated by Kraus and Czado (2017) using drawable (D-vines) vine copulas and Chang and Joe (2019) using regular vines. The approach of Chang and Joe (2019) is based on first finding the locally optimal regular vine structure among all predictors and then adding the response to each selected tree in the vine structure as a leaf, as also followed by Bauer and Czado (2016) in the context of non Gaussian conditional independence testing. The proceeding in Chang and Joe (2019) allows for a recursive determination of the response quantiles, which however is restricted through the prespecified dependence structure among predictor variables. The latter might not be the one maximizing the conditional response likelihood, which is the main focus in regression setup. The approach of Kraus and Czado (2017) is based on optimizing the conditional log-likelihood and selecting predictors sequentially until no improvement of the conditional log-likelihood is achieved. This approach based on the conditional response likelihood is also more suited to determine the associated response quantiles. Therefore, we extend the method of Kraus and Czado (2017) by considering the two-step ahead tree sequence and its conditional log-likelihood for the class of both C- and D-vines. By construction, quantile crossings are avoided. Additionally, all marginal densities and copulas

are estimated nonparametrically, allowing more flexibility than parametric specifications. The benefit of the nonparametric estimation of bivariate copulas in the quantile regression framework is addressed in Kraus and Czado (2017). This construction permits a large variety of dependence structures, resulting in a well-performing conditional quantile estimator. Moreover, extending to the C-vine copula class, in addition to the D-vine copulas, provides greater flexibility.

The paper is organized as follows. Section 2 introduces the general setup and the concept of C-vine and D-vine copulas, while also introducing the nonparametric approach for estimating copula densities. Section 3 describes in detail the vine based approach for quantile regression. The new two-step ahead forward selection algorithms are described in detail in Section 4. Since all densities involved in the model construction are estimated nonparametrically, we investigate in Proposition 4.1 the consistency of the conditional quantile estimator for given variable orders. The finite sample performance of the vine based conditional quantile estimator is evaluated in Section 5 by several quantile related measurements in various simulation settings. Further, we also apply the newly introduced algorithms to low- and high-dimensional real data in Section 6. In Section 7 we conclude and discuss possible directions of future research.

2 Theoretical background

Let $\mathbf{X} = (X_1, \dots, X_d)^T$ be a random vector with observed values denoted as $(x_1, \dots, x_d)^T$. The marginal distribution function of X_j is denoted by F_{X_j} for $j=1,\ldots,d$ and the joint distribution function of the random vector X is denoted by F. Sklar's theorem (Sklar 1959) offers a way to represent any given multivariate distribution in terms of its marginals and the corresponding copula encoding the dependence structure. If we assume that F_{X_j} , and F are continuous, then there exists a copula C associated with the joint distribution of **X** such that $F(x_1, \ldots, x_d) = C(F_{X_1}(x_1), \ldots, F_{X_d}(x_d))$, with the joint density function $f(x_1, ..., x_d) = c(F_{X_1}(x_1), ..., F_{X_d}(x_d)) \cdot f_{X_1}(x_1) \cdot ... \cdot f_{X_d}(x_d)$. To inspect the dependence structure of X, we transform each variable by applying the probability integral transform (PIT). The corresponding transformed variables are defined as $U_i := F_{X_i}(X_i), \ j=1,\ldots,d$, which are uniformly distributed on [0,1]. The observed values of the random vector $\boldsymbol{U} = (U_1, \dots, U_d)^T$ are denoted as $(u_1, \dots, u_d)^T$. The joint distribution of U is a copula denoted by $C_{U_1,...,U_d}$ with copula density function $c_{U_1,...,U_d}$. We utilize notation similar to Czado (2019, Section 5.4). Let $D \subset \{1, \ldots, d\}$ be a subset of indexes such that X_D is a sub-vector of the d-dimensional vector X. Let $i, j \in \{1, \ldots, d\} \setminus D$ be two indices not belonging to the set D. $C_{U_i,U_i;U_D}$ denotes the copula associated with the conditional distribution of (X_i, X_j) conditioned on $X_D = x_D$ with the corresponding copula density $c_{U_i,U_i;U_D}$. The set $U_D = \{F_{X_s}(X_s), s \in D\}$ is called the conditioning set and (U_i, U_j) form the conditioned set. $F_{X_i|X_D}$ denotes the conditional distribution of X_i conditioned on $X_D = x_D$. $C_{U_i|U_D}$ denotes the conditional distribution of the PIT trans-

formed variable U_i conditioned on U_D with corresponding density function $c_{U_i|U_D}$. The so called h-functions are defined as $h_{U_i|U_j}(u_i|u_j) := \frac{\partial}{\partial u_j} C_{U_i,U_j}(u_i,u_j)$. In this case it holds that $h_{U_i|U_j}(u_i|u_j) = C_{U_i|U_j}(u_i|u_j)$. For the conditioned case, we define the h-function as $h_{U_i|U_j;U_D}(u_i|u_j;u_D) := \frac{\partial}{\partial u_j} C_{U_i,U_j;U_D}(u_i,u_j;u_D)$. When the simplifying assumption holds (Czado 2019, Section 5.4), that is, the copula function does not depend on the specific conditioning value, then $h_{U_i|U_j;U_k}(u_i|u_j;u_k) = \frac{\partial}{\partial u_j} C_{U_i,U_j;U_k}(u_i,u_j)$. This assumption is often made due to tractability reasons in higher dimensions, see Haff et al. (2010) and Stoeber et al. (2013). The concept of vine copulas, first introduced in Joe (1996), is that any ddimensional copula can be expressed in terms of d(d-1)/2 bivariate (conditional) copulas. However, this decomposition is not unique. Bedford and Cooke (2002) introduced a graphical method to specify a d-dimensional vine copula in terms of a sequence of trees. The set of trees $\mathcal{V} = (T_1, \dots, T_{d-1})$ is a regular vine tree sequence on d elements if each tree T_i is connected, i.e. T_j contains a path between every pair of nodes; T_1 is a tree with node set $N_1 = \{1, \ldots, d\}$ and edge set E_1 ; for $j \geq 2$, T_j is a tree with node set $N_j = E_{j-1}$ and edge set E_i and if two nodes in T_i are joined by an edge, the corresponding edges in T_{i-1} must share a common node. This condition is also called the proximity condition. In addition to the vine tree sequence, a regular vine copula identifies each edge of the trees with a bivariate pair-copula defined through the set $\mathcal{B}(\mathcal{V}) := \{c_e | e \in E_j, 1 \leq j \leq d-1\}$. Here each c_e corresponds to the density of the pair-copula associated with the corresponding edge e of \mathcal{V} . We consider two different classes of regular vine tree sequences: a C-vine tree sequence and a D-vine tree sequence. A regular vine tree sequence $\mathcal{V} = (T_1, \dots, T_{d-1})$ is called a D-vine tree sequence, if all trees T_1, \ldots, T_{d-1} have degree less or equal to 2, i.e. they are paths, and the nodes with degree 1 are called leaf nodes. Once the first tree T_1 in the tree sequence is defined, then all the other trees T_2, \ldots, T_{d-1} are determined, since the proximity condition has to be satisfied. The right panel of Figure 1 shows an example of a D-vine tree sequence in four dimensions. The construction of the joint density f of a d-dimensional random vector X from a product of (conditional) bivariate copula densities, associated with a D-vine tree sequence, and marginal densities is given as

$$f\left(x_{1},\ldots,x_{d}\right) = \prod_{j=1}^{d-1} \prod_{i=1}^{d-j} c_{U_{s_{i}},U_{s_{i+j}};U_{s_{i+1}},\ldots,U_{s_{i+j-1}}} \left(F_{X_{s_{i}}|X_{s_{i+1}},\ldots,X_{s_{i+j-1}}}(x_{s_{i}}|x_{s_{i+1}},\ldots,x_{s_{i+j-1}}), F_{X_{s_{i+j}}|X_{s_{i+1}},\ldots,X_{s_{i+j-1}}}(x_{s_{i+j}}|x_{s_{i+1}},\ldots,x_{s_{i+j-1}})\right) \cdot \prod_{k=1}^{d} f_{X_{s_{k}}}(x_{s_{k}}),$$

where s_1, \ldots, s_d corresponds to an arbitrary permutation of $1, \ldots, d$. The distribution associated with this density decomposition, if the marginals are uniformly distributed, is called a D-vine copula. We call a regular vine tree sequence $\mathcal{V} = (T_1, \ldots, T_{d-1})$ a C-vine tree sequence if in each tree there is one node connected to all the other nodes, called a root node. This implies that all trees in the C-vine tree sequence are stars. The left panel of Figure 1 shows an example of a C-vine tree sequence in four dimensions. The

construction of the joint density f of a d-dimensional random vector X based on a product of (conditional) bivariate copula densities, associated with a C-vine tree structure, and marginal densities is given as

$$f(x_1, \dots, x_d) = \prod_{j=1}^{d-1} \prod_{i=1}^{d-j} c_{U_{s_j}, U_{s_{j+i}}; U_{s_1}, \dots, U_{s_{j-1}}} \left(F_{X_{s_j} | X_{s_1}, \dots, X_{s_{j-1}}} (x_{s_j} | x_{s_1}, \dots, x_{s_{j-1}}), F_{X_{s_{j+i}} | X_{s_1}, \dots, X_{s_{j-1}}} (x_{s_{j+i}} | x_{s_1}, \dots, x_{s_{j-1}}) \right) \cdot \prod_{k=1}^d f_{X_{s_k}}(x_{s_k}),$$

where s_1, \ldots, s_d corresponds to an arbitrary permutation of $1, \ldots, d$. The distribution associated with this density construction, when the marginals are uniformly distributed, is called a C-vine copula. For more details on the pair-copula construction based on C- and D-vine tree sequences refer to Czado (2019, Section 4.2). When non-simplified pair copulas are used as building blocks, then these constructions are also possible decompositions of an arbitrary multivariate density.

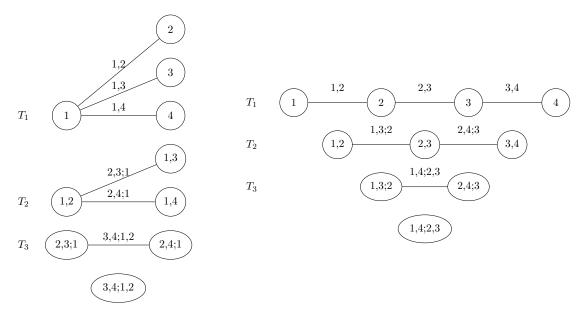


Figure 1: C-vine tree sequence (left panel) and a D-vine tree sequence (right panel) in 4 dimensions.

2.1 Nonparametric estimators of the copula densities and h-functions

We discuss now how the h-functions can be estimated in a nonparametric way, due to their later importance in the estimation of conditional distribution functions. According to the simplifying assumption it holds that $h_{U_i|U_j;U_D}(u_i|u_j;u_D) = \frac{\partial}{\partial u_j} C_{U_i,U_j;U_D}(u_i,u_j)$ can be estimated by the bivariate copula $C_{U_i,U_j;U_D}$ which does not depend on specific values of u_D . Thus, it is sufficient to show the estimation procedure for the h-function $h_{U_i|U_j}$ associated with an arbitrary pair copula. Consider a pair (U_i,U_j) of which the h-function $h_{U_i|U_j} = C_{U_i|U_j}$ can be estimated by the following rescaled estimator

$$\hat{C}_{U_i|U_j}(u_i|u_j) = \int_0^{u_i} \hat{c}_{U_i,U_j}(\tilde{u}_i, u_j) d\tilde{u}_i / \int_0^1 \hat{c}_{U_i,U_j}(\tilde{u}_i, u_j) d\tilde{u}_i,$$

where \hat{c}_{U_i,U_j} is a nonparametric estimator of the bivariate copula density of (U_i,U_j) . Example estimators of the copula density c_{U_i,U_j} are the transformation estimator (Charpentier et al. 2007), the transformation local likelihood estimator (Geenens et al. 2017), the tapered transformation estimator (Wen and Wu 2015), the beta kernel estimator (Charpentier et al. 2007), and the mirror-reflection estimator (Gijbels and Mielniczuk 1990). Among the above-mentioned kernel estimators, the transformation local likelihood estimator (Geenens et al. 2017) was found by Nagler et al. (2017) to have an overall best performance. The estimator is implemented in the R packages kdecopula (Nagler 2018) and rvinecopulib (Nagler and Vatter 2019b) using Gaussian kernels. This is the estimator that we further use. We shortly review its construction in Appendix A.

3 Vine based quantile regression

In a regression framework some variables among the set of potential covariates $\boldsymbol{X}=(X_1,\ldots,X_p)^T$ have predictive ability for the response $Y\in\mathbb{R}$. The main interest of vine based quantile regression is to predict the $\alpha\in(0,1)$ quantile of the response variable Y given \boldsymbol{X} , which can be achieved by a joint modeling of $(Y,\boldsymbol{X})^T$ and by using the conditional quantile function $q_{\alpha}(x_1,\ldots,x_p)=F_{Y|X_1,\ldots,X_p}^{-1}(\alpha|x_1,\ldots,x_p)$. The conditional distribution of Y given \boldsymbol{X} on the u-scale, for $V=F_Y(Y)$ and $U_j=F_{X_j}(X_j),\ j=1,\ldots,p$, as derived in Kraus and Czado (2017), is given as $F_{Y|X_1,\ldots,X_p}(y|x_1,\ldots,x_p)=C_{V|U_1,\ldots,U_p}(v|u_1,\ldots,u_p)$, and its corresponding inverse, the quantile function as

$$F_{Y|X_1,\dots,X_p}^{-1}(\alpha|x_1,\dots,x_p) = F_Y^{-1}\Big(C_{V|U_1,\dots,U_p}^{-1}(\alpha|u_1,\dots,u_p)\Big).$$
(1)

Here $C_{V|U_1,...,U_p}$ is the conditional distribution function of V given $U_j = u_j$ for j = 1, ..., p and $C_{V,U_1,...,U_p}$ is defined as the (p+1)-dimensional copula associated with the joint distribution of $(Y, \mathbf{X})^T$. Compared to Section 1, here it holds that d = p + 1. The above equations indicate that the conditional quantile function of Y given \mathbf{X} can be expressed as a composition of the inverses of the marginal distribution F_Y and the conditional distribution $C_{V|U_1,...,U_p}$. Thus, an estimate of the conditional quantile function can be obtained from the estimated inverses of the marginal distributions, denoted by \hat{F}_Y^{-1} , $\hat{F}_{X_j}^{-1}$, j = 1, ..., p,

and of the conditional distribution function, denoted by $\hat{C}_{V|U_1,...,U_n}^{-1}$, such that

$$\hat{q}_{\alpha}(x_1,\ldots,x_p) = \hat{F}_Y^{-1}\left(\hat{C}_{V|U_1,\ldots,U_p}^{-1}(\alpha|\hat{u}_1,\ldots\hat{u}_p)\right),$$

where $\hat{u}_j = \hat{F}_{X_j}(x_j)$ for $j=1,\ldots,p$. In fact, C_{V,U_1,\ldots,U_p} can be any (p+1)-dimensional multivariate copula. Using C- and D-vine pair-copula constructions this high-dimensional and complex estimation problem can be solved in a sequential and tractable way. Additional flexibility is achieved by allowing for nonparametric pair-copulas as building blocks. In particular, the order of the predictors within the tree sequences itself is a free parameter with direct impact on the target function $C_{V|U_1,\ldots,U_p}$ and thus on the corresponding prediction performance. However, we want to make sure that evaluating the conditional distribution function $C_{V|U_1,\ldots,U_p}$ from the joint copula C_{V,U_1,\ldots,U_p} remains feasible. The pair-copula construction on C- and D-vines provides a strategy how to derive the conditional distribution $C_{V|U_1,\ldots,U_p}$ using specific pair-copulas and the following recursion for conditional distribution functions (Joe 1997). Let $\mathbf{W} = (W_1,\ldots,W_p)^T$ be uniformly distributed random variables with observed values $\mathbf{w} = (w_1,\ldots,w_p)^T$. Further, let $D \subset \{1,\ldots p\}$ and define the set $D_{-j} \coloneqq D \setminus \{j\}$ for some $j \in D$. Then, for any $i \notin D$ and $j \in D$, it holds that

$$C_{W_{i}|\mathbf{W}_{D}}\left(w_{i}|\mathbf{w}_{D}\right) = h_{W_{i}|W_{j};\mathbf{W}_{D-j}}\left(C_{W_{i}|\mathbf{W}_{D-j}}\left(w_{i}|\mathbf{w}_{D-j}\right)|C_{W_{j}|\mathbf{W}_{D-j}}\left(w_{j}|\mathbf{w}_{D-j}\right)\right), \quad (2)$$

where $h_{W_i|W_j;W_{D_{-j}}}$ is the h-function associated with the pair copula $C_{W_i,W_j;\mathbf{W}_{D_{-j}}}$. As shown, for example in Tepegjozova (2019), this implies that $C_{V|U_1,\dots,U_p}$ can be derived using only pair copulas defined by the tree sequence of the vine copula C_{V,U_1,\dots,U_p} if and only if in a D-vine the response V is a leaf node in the first tree of the tree sequence. For a C-vine we need to require that the node containing the response variable V in the conditioned set is not a root node in any tree. More details in Example 3.1.

Example 3.1. Consider the C-vine copula associated to the tree sequence given on the left panel of Figure 1. In the tree sequence $\mathcal{V} = (T_1, T_2, T_3)$ we can see that all trees are stars, where in each tree there a root node connected to all other nodes in that tree level, i.e. 1 is the root node of T_1 while 1, 2 and 2, 3; 1 are the root nodes of trees T_2 and T_3 , respectively. Using (2) the conditional distribution $C_{4|1,2,3}$ can be expressed as

$$C_{4|1,2,3}(u_4|u_1, u_2, u_3) = h_{4|3;1,2} \left(C_{4|1,2}(u_4|u_1, u_2) | C_{3|1,2}(u_3|u_1, u_2) \right)$$

$$= h_{4|3;1,2} \left(h_{4|2;1} \left(C_{4|1}(u_4|u_1) | C_{2|1}(u_2|u_1) \right) | h_{3|2;1} \left(C_{3|1}(u_3|u_1) | C_{2|1}(u_2|u_1) \right) \right)$$

$$= h_{4|3;1,2} \left(h_{4|2;1} \left(h_{4|1}(u_4|u_1) | h_{2|1}(u_2|u_1) \right) | h_{3|2;1} \left(h_{3|1}(u_3|u_1) | h_{2|1}(u_2|u_1) \right) \right).$$
(3)

The corresponding inverse $C_{4|1,2,3}^{-1}$ can be obtained as

$$C_{4|1,2,3}^{-1}(\alpha|u_1,u_2,u_3) = h_{4|1}^{-1} \left(h_{4|2;1}^{-1} \left(h_{4|3;1,2}^{-1} \left(\alpha \middle| h_{3|2;1} \left(h_{3|1}(u_3|u_1) \middle| h_{2|1}(u_2|u_1) \right) \right) \middle| h_{2|1}(u_2|u_1) \right) \middle| u_1 \right).$$

Here, the conditional distribution $C_{4|1,2,3}$ is expressed using only the h-functions $h_{4|3;1,2}$, $h_{4|2;1}$, $h_{3|2;1}$, $h_{4|1}$, $h_{3|1}$ and $h_{2|1}$ which are derived by taking the appropriate derivatives from the pair copulas $C_{3,4;1,2}$, $C_{2,4;1}$, $C_{2,3;1}$, $C_{1,4}$, $C_{1,3}$ and $C_{1,2}$, respectively. With $E(T_i)$ the edge set of tree T_i it holds that $\{(3,4;1,2)\} \subseteq E(T_3)$, $\{(2,3;1), (2,4;1)\} \subseteq E(T_2)$, and $\{(1,2), (1,3), (1,4)\} \subseteq E(T_1)$. Thus, the pair copulas $C_{3,4;1,2}$, $C_{2,3;1}$, $C_{2,4;1}$, $C_{1,2}$, $C_{1,3}$ and $C_{1,4}$ are included in $\mathcal{B}(\mathcal{V})$, the set of pair copula families defining the vine. On the other hand, the conditional distribution function $C_{2|1,3,4}$ can be expressed as

$$C_{2|1,3,4}\left(u_{2}|u_{1},u_{3},u_{4}\right) = \begin{cases} h_{2|1;3,4}\left(C_{2|3,4}\left(u_{2}|u_{3},u_{4}\right)|C_{1|3,4}\left(u_{1}|u_{3},u_{4}\right)\right) \\ h_{2|3;1,4}\left(C_{2|1,4}\left(u_{2}|u_{1},u_{4}\right)|C_{3|1,4}\left(u_{3}|u_{1},u_{4}\right)\right) \\ h_{2|4;1,3}\left(C_{2|1,3}\left(u_{2}|u_{1},u_{3}\right)|C_{4|1,3}\left(u_{4}|u_{1},u_{3}\right)\right) \end{cases}$$

The h-functions $h_{2|1;3,4}$, $h_{2|3;1,4}$ and $h_{2|4;1,3}$ can only be derived from the pair copulas $C_{1,2;3,4}$, $C_{2,3;1,4}$ and $C_{2,4;1,3}$. However, the edges $\{(1,2;3,4)\} \not\subset E(T_3)$, $\{(2,3;1,4)\} \not\subset E(T_3)$, $\{(2,4;1,3)\} \not\subset E(T_3)$ thus the needed pair copulas are not included in $\mathcal{B}(\mathcal{V})$. Using Equation (2) we can derive any of the conditional distributions $C_{1|2,3,4}$, $C_{2|1,3,4}$, $C_{3|1,2,4}$ and $C_{4|1,2,3}$. However, for the conditional distribution $C_{4|1,2,3}$, as seen from Equation (3), this can be done using only pair copulas which are included in $\mathcal{B}(\mathcal{V})$. The same holds for the conditional distribution $C_{3|1,2,4}$. But, for the conditional distributions $C_{2|1,3,4}$ and $C_{1|2,3,4}$ additional pair copulas, which are not included in $\mathcal{B}(\mathcal{V})$, are needed. These are determined by the vine specification, however they require integration over higher dimensional marginal distributions of the vine, which is computationally intractable.

As motivated by Example 3.1, we assume that if $C_{V,U_1,...,U_p}$ is a D-vine, then V is fixed as a leaf node in its first tree, and if C_{V,U_1,\ldots,U_p} is a C-vine, then the node containing the response V in the conditioned set is excluded from being part of the root node specification in any tree of its tree sequence. We introduce the concept of an order of the nodes in a Cand D-vine, as defined in Tepegjozova (2019). A D-vine copula, denoted by \mathcal{C}_D , has order $\mathcal{O}_{D}\left(\mathcal{C}_{D}\right)=\left(V,U_{i_{1}},\ldots,U_{i_{p}}\right)$, if the response V is the first node of the first tree T_{1} and $U_{i_{k}}$ is the (k+1)-th node of T_1 , for $k=1,\ldots,p$. A C-vine copula, denoted by \mathcal{C}_C , has order $\mathcal{O}_C\left(\mathcal{C}_C\right) = \left(V, U_{i_1}, \dots, U_{i_p}\right)$, if U_{i_1} is the root node in the first tree $T_1, U_{i_2}U_{i_1}$ is the root node in the second tree T_2 , and $U_{i_k}U_{i_{k-1}}; U_{i_1}, \ldots, U_{i_{k-2}}$ is the root node in the k-th tree T_k for $k = 3, \ldots, p-1$. The goal of C- and D-vine based quantile regression is finding the model with the optimal order associated to a fit measure, as it has a direct impact on the prediction performance. To be able to compare and quantify the explanatory power of models with different orders of the predictors, we use the conditional log-likelihood function as a fit measure. For N independent identically distributed observations from the random vector $(V, U_1, \ldots, U_p)^T$ denoted by $\boldsymbol{v} := (v^{(1)}, \ldots, v^{(N)})$ and $\boldsymbol{u}_j := (u_j^{(1)}, \ldots, u_j^{(N)}),$ for j = $1,\dots,p,$ with a fitted nonparametric C- or D-vine copula, denoted by $\hat{\mathcal{C}},$ with order is $\mathcal{O}(\hat{\mathcal{C}}) = (V, U_1, \dots, U_p)$, the conditional log-likelihood can be expressed as

$$cll(\hat{C}, \mathbf{v}, (\mathbf{u}_1, \dots, \mathbf{u}_p)) = \sum_{n=1}^{N} \log \hat{c}_{V|U_1, \dots, U_p} \left(v^{(n)} | u_1^{(n)}, \dots, u_p^{(n)} \right).$$

This is for example shown in Tepegjozova (2019), where it also shows that this expression can be rewritten as

$$cll\left(\hat{\mathcal{C}}, \boldsymbol{v}, (\boldsymbol{u}_{1}, \dots, \boldsymbol{u}_{p})\right) = \sum_{n=1}^{N} \left[\log \hat{c}_{V,U_{1}}\left(v^{(n)}, u_{1}^{(n)}\right) + \sum_{j=2}^{p} \log \hat{c}_{V,U_{j}|U_{1},\dots,U_{j-1}}\left(\hat{C}_{V|U_{1},\dots,U_{j-1}}\left(v^{(n)}|u_{1}^{(n)},\dots,u_{j-1}^{(n)}\right), \right. \\ \left. \hat{C}_{U_{j}|U_{1},\dots,U_{j-1}}\left(u_{j}^{(n)}|u_{1}^{(n)},\dots,u_{j-1}^{(n)}\right)\right)\right].$$

Penalizations for model complexity can be added as well.

4 Forward selection algorithms

Given a response variable V and a set of p predictors, U_1, \ldots, U_p , the goal of the proposed vine based quantile regression is to find the cll-optimal C- or D-vine copula, i.e. the C- or D-vine with the highest conditional log-likelihood. The definition of the order of a C- or D-vine implies that the order uniquely determines the underlying tree sequence and vice versa. Further, since the response variable is fixed as the first element of the order, while the other elements can be any permutation of the predictors, there are p!different orders. This implies that there are p! different C-vines and p! different D-vines that can be fitted. However, in practice, fitting all possible C- or D-vines and comparing the conditional log-likelihood values would be computationally inefficient. Thus, the idea is to have an algorithm that will sequentially choose the elements of the order one by one, so that at every step the resulting model for the prediction of the conditional quantiles has the highest conditional log-likelihood. The first algorithm of this type is the one-step ahead D-vine quantile regression introduced by Kraus and Czado (2017). The idea of the one-step ahead algorithm is to sequentially update the order of the D-vine by adding the predictor that yields the highest improvement in the conditional log-likelihood at each step. Building upon the idea of Kraus and Czado (2017), we propose an algorithm which allows for more flexibility and which in particular is less greedy, given the intention to obtain a globally optimal C- or D-vine fit. The algorithm builds the C- or D-vine step by step, starting with an order consisting of only the response variable, V. In each step it adds one of the predictors to the order based on the improvement of the conditional log-likelihood, while taking into account the possibility of future improvement, i.e. extending our view two steps ahead in the order. Further, as already discussed in Section 2.1, the pair copulas at each step are estimated nonparametrically in contrast to the parametric approach by Kraus and Czado (2017). We present the implementation for both C-vine and D-vine based quantile regression as a single algorithm, in which we can choose whether we want a C-vine, or D-vine model fitted, based on the given data set and background knowledge of dependency structures in the data. Furthermore, since implementing the algorithm on a large data set is computationally expensive, we introduce some randomization in the algorithm, so that it remains computationally tractable in high dimensions.

4.1 Two-step ahead forward selection algorithm for C- and D-vine based quantile regression

Input and data preprocessing:

Let there be given a data set of N independent and identically distributed observations, denoted by $\mathbf{y} \coloneqq (y^{(1)}, \dots, y^{(N)})$ and $\mathbf{x}_j \coloneqq (x_j^{(1)}, \dots, x_j^{(N)})$, for $j = 1, \dots, p$, from the random vector $(Y, X_1, \dots, X_p)^T$. The raw input data are on the x-scale, but in order to fit bivariate copulas to the data we need to transform them to the u-scale. To achieve the desired transformation the probability integral transform is employed. However, since the marginal distributions are usually unknown estimates need to be acquired. F_Y and F_{X_j} , for $j = 1, \dots, p$, are estimated using a univariate nonparametric kernel density estimator, as implemented in the R package kdeld (Nagler and Vatter 2019a). With the marginals estimated, the pseudo copula data are obtained as $\hat{v}^{(n)} \coloneqq \hat{F}_Y(y^{(n)})$ and $\hat{u}_j^{(n)} \coloneqq \hat{F}_{X_j}(x_j^{(n)})$, for $n = 1, \dots, N$, $j = 1, \dots, p$. Also, assume that the normalized marginals are defined as $Z_j \coloneqq \Phi^{-1}(U_j)$ for $j = 1, \dots, p$, and $Z_V \coloneqq \Phi^{-1}(V)$, where Φ denotes the cumulative distribution function of a standard Gaussian distribution.

Step 1:

In the first step of the algorithm, to reduce computational complexity, we perform a preselection of the predictors based on the Kendall's τ correlation values. The motivation of this choice is based on the fact that Kendall's τ is rank-based, therefore invariant with respect to monotone transformations of the marginals and can be expressed in terms of pair copulas. Using the pseudo copula data

$$(\hat{\boldsymbol{v}}, \hat{\boldsymbol{u}}_j) = \left\{ \hat{v}^{(n)}, \hat{u}_j^{(n)} | n = 1, \dots, N \right\}$$

estimates $\hat{\tau}_{VU_j}$ of the Kendall's τ values between the response V, and all possible predictors U_j for $j=1,\ldots,p$, are obtained. Further, for a given $k\leq p$, the k largest estimates of $|\hat{\tau}_{VU_j}|$ are selected and the corresponding indices q_1,\ldots,q_k are identified such that

$$|\hat{\tau}_{VU_{q_1}}| \ge |\hat{\tau}_{VU_{q_2}}| \ge \ldots \ge |\hat{\tau}_{VU_{q_k}}| \ge |\hat{\tau}_{VU_{q_{k+1}}}| \ge \ldots \ge |\hat{\tau}_{VU_{q_p}}|.$$

The k candidate predictors and the corresponding candidate index set of step 1 are defined as U_{q_1}, \ldots, U_{q_k} and the set $K_1 = \{q_1, \ldots, q_k\}$, respectively.

Next, for all $c \in K_1$ and $j \in \{1, ..., p\} \setminus \{c\}$ the candidate two-step ahead C- or D-vine copulas are defined as the 3-dimensional copulas $\mathcal{C}^1_{c,j}$ with order $\mathcal{O}(\mathcal{C}^1_{c,j}) = (V, U_c, U_j)$. The first predictor is added to the order based on the conditional log-likelihood of the candidate two-step ahead C- or D-vine copulas, $\mathcal{C}^1_{c,j}$, given as

$$cll\left(\mathcal{C}_{c,j}^{1}, \hat{\boldsymbol{v}}, (\hat{\boldsymbol{u}}_{c}, \hat{\boldsymbol{u}}_{j})\right) = \sum_{n=1}^{N} \left[\log \hat{c}_{V,U_{c}}\left(\hat{v}^{(n)}, \hat{u}_{c}^{(n)}\right) + \log \hat{c}_{V,U_{j}|U_{c}}\left(\hat{h}_{V|U_{c}}\left(\hat{v}^{(n)}|\hat{u}_{c}^{(n)}\right), \hat{h}_{U_{j}|U_{c}}\left(\hat{u}_{j}^{(n)}|\hat{u}_{c}^{(n)}\right)\right)\right].$$

For each candidate predictor U_c the maximal two-step ahead conditional log-likelihood at step 1, cll_c^1 , is defined as

$$cll_c^1 \coloneqq \max_{j \in \{1, \dots, p\} \setminus \{c\}} cll\left(\mathcal{C}_{c,j}^1, \hat{\boldsymbol{v}}, (\hat{\boldsymbol{u}}_c, \hat{\boldsymbol{u}}_j)\right), \ \forall c \in K_1.$$

Finally, based on the maximal two-step ahead conditional log-likelihood at step 1, cll_c^1 , the index t_1 is chosen as

$$t_1 \coloneqq \underset{c \in K_1}{\operatorname{arg\,max}} \ cll_c^1,$$

and the corresponding candidate predictor U_{t_1} is selected as the first predictor added to the order. An illustration of the vine tree structure of the candidate two-step ahead copulas $C_{c,j}^1$, in the case of fitting a D-vine model, with order $\mathcal{O}_D(C_{c,j}^1) = (V, U_c, U_j)$ is given in Figure 2. Finally, the current optimal fit after the first step is the C-vine or D-vine copula, C_1 with order $\mathcal{O}(C_1) = (V, U_{t_1})$.

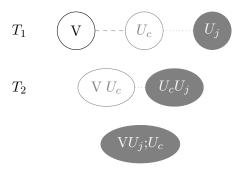


Figure 2: V is fixed as the first node of T_1 and the first candidate predictor to be included in the model, U_c (gray), is chosen based on the conditional log-likelihood of the two-step ahead copula including the predictor U_j (gray filled).

Step r:

After r-1 steps, the current optimal fit is the C- or D-vine copula \mathcal{C}_{r-1} with order $\mathcal{O}\left(\mathcal{C}_{r-1}\right) = \left(V, U_{t_1}, \ldots, U_{t_{r-1}}\right)$. At each previous step i, the order of the current optimal fit is sequentially updated with the predictor U_{t_i} for $i=1,\ldots,r-1$. At the r-th step the next predictor candidate is to be included. In order to do so, the set of potential candidates is narrowed based on a partial correlation measure. Thus, estimates of the empirical Pearson's partial correlation, $\hat{\rho}_{Z_V,Z_j;Z_{t_1},\ldots,Z_{t_{r-1}}}$, between the normalized response variable V and available predictors U_j for $j \in \{1,2,\ldots,p\} \setminus \{t_1,\ldots,t_{r-1}\}$ are obtained. Similar to the first step, a set of candidate predictors of size k is selected based on the largest values of $|\hat{\rho}_{Z_V,Z_j;Z_{t_1},\ldots,Z_{t_{r-1}}}|$ and the corresponding indices q_1,\ldots,q_k are identified such that it holds

$$|\hat{\rho}_{Z_{V},Z_{q_{1}};Z_{t_{1}},\dots,Z_{t_{r-1}}}| \geq \dots \geq |\hat{\rho}_{Z_{V},Z_{q_{k}};Z_{t_{1}},\dots,Z_{t_{r-1}}}| \geq \dots \geq |\hat{\rho}_{Z_{V},Z_{q_{n-r+1}};Z_{t_{1}},\dots,Z_{t_{r-1}}}|.$$

The k candidate predictors and the corresponding candidate index set of step r are defined as U_{q_1}, \ldots, U_{q_k} and the set $K_r = \{q_1, \ldots, q_k\}$, respectively. Next, for all $c \in K_r$ and $j \in \{1, 2, \ldots, p\} \setminus \{t_1, \ldots, t_{r-1}, c\}$ the candidate two-step ahead C- or D-vine copulas are defined as the copulas $\mathcal{C}^r_{c,j}$ with order $\mathcal{O}(\mathcal{C}^r_{c,j}) = (V, U_{t_1}, \ldots, U_{t_{r-1}}, U_c, U_j)$. At this point there are $k \times (p-r)$ different candidate two-step ahead C- or D-vine copulas

At this point there are $k \times (p-r)$ different candidate two-step ahead C- or D-vine copulas $\mathcal{C}_{c,j}^r$ and their corresponding conditional log-likelihood is given as

$$cll\left(\mathcal{C}_{c,j}^{r},\ \hat{\boldsymbol{v}},\left(\hat{\boldsymbol{u}}_{t_{1}}\dots\hat{\boldsymbol{u}}_{t_{r-1}},\hat{\boldsymbol{u}}_{c},\hat{\boldsymbol{u}}_{j}\right)\right) = cll\left(\mathcal{C}_{r-1},\hat{\boldsymbol{v}},\left(\hat{\boldsymbol{u}}_{t_{1}}\dots\hat{\boldsymbol{u}}_{t_{r-1}}\right)\right)$$

$$+\sum_{n=1}^{N}\log\hat{c}_{VU_{c};U_{t_{1}},\dots,U_{t_{r-1}}}\left(\hat{C}_{V|U_{t_{1}},\dots,U_{t_{r-1}}}\left(\hat{v}^{(n)}|\hat{u}_{t_{1}}^{(n)},\dots,\hat{u}_{t_{r-1}}^{(n)}\right),$$

$$\hat{C}_{U_{c}|U_{t_{1}},\dots,U_{t_{r-1}}}\left(\hat{u}_{c}^{(n)}|\hat{u}_{t_{1}}^{(n)},\dots,\hat{u}_{t_{r-1}}^{(n)}\right)\right)$$

$$+\sum_{n=1}^{N}\log\hat{c}_{VU_{j};U_{t_{1}},\dots,U_{t_{r-1}},U_{c}}\left(\hat{C}_{V|U_{t_{1}},\dots,U_{t_{r-1}},U_{c}}\left(\hat{v}^{(n)}|\hat{u}_{t_{1}}^{(n)},\dots,\hat{u}_{t_{r-1}}^{(n)},\hat{u}_{c}^{(n)}\right),$$

$$\hat{C}_{U_{j}|U_{t_{1}},\dots,U_{t_{r-1}},U_{c}}\left(\hat{u}_{j}^{(n)}|\hat{u}_{t_{1}}^{(n)},\dots,\hat{u}_{t_{r-1}}^{(n)},\hat{u}_{c}^{(n)}\right)\right).$$

The r-th predictor is then added to the order based on the maximal two-step ahead conditional log-likelihood at Step r, cll_c^r , defined as

$$cll_c^r := \max_{j \in \{1, 2, \dots, p\} \setminus \{t_1, \dots, t_{r-1}, c\}} cll\left(\mathcal{C}_{c, j}^r, \hat{\boldsymbol{v}}, \left(\hat{\boldsymbol{u}}_{t_1} \dots \hat{\boldsymbol{u}}_{t_{r-1}}, \hat{\boldsymbol{u}}_c, \hat{\boldsymbol{u}}_j\right)\right), \ \forall c \in K_r.$$

$$(4)$$

Namely, the index t_r is chosen as

$$t_r := \underset{c \in K_r}{\operatorname{arg \, max}} \ cll_c^r,$$

and the corresponding candidate predictor U_{t_r} is selected as the r-th predictor of the order. An illustration of the vine tree structure of the candidate two-step ahead copulas

 $C_{c,j}^r$, in the case of fitting a D-vine model, with order $\mathcal{O}_D(C_{c,j}^r) = (V, U_{t_1}, \dots, U_{t_{r-1}}, U_c, U_j)$ is given in Figure 3. At this step, the current optimal fit is the C-vine or D-vine copula C_r , with order

$$\mathcal{O}\left(\mathcal{C}_r\right) = \left(V, U_{t_1}, \dots U_{t_r}\right).$$

The iterative procedure is repeated until all predictors are included in the order of the Cor D-vine copula model.

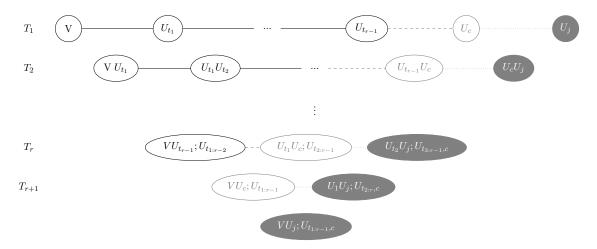


Figure 3: In step r, the current optimal fit, C_{r-1} (black), is extended by one more predictor, U_c (gray), to obtain the new current optimal fit C_r (black and gray), based on the conditional log-likelihood of the two-step ahead copula $C_{c,j}^r$ which also includes the predictor U_j (gray filled). (In the figure, we use the shortened notation $U_{t_{1:r-1}}$ instead of writing $U_{t_1}, \ldots, U_{t_{r-1}}$ and we use $U_{t_1:r-1}, c$ instead of $U_{t_1}, \ldots, U_{t_{r-1}}, U_{c}$.)

4.1.1 Additional variable reduction in higher dimensions

The search procedure described above requires calculating p-(r-1) conditional log-likelihoods for each candidate predictor at a given step r. This leads to calculating a total of $(p-r+1) \times k$ conditional log-likelihoods, where k denotes the number of candidates. In cases where p is large, this search procedure would cause a heavy computational burden. Hence, the idea is to reduce the number of conditional log-likelihoods calculated for each candidate predictor. This is done by reducing the size of the set over which the maximal two-step ahead conditional log-likelihood, cll_c^r in Equation 4, is computed. Instead of taking the maximum over the set $\{1, 2, \ldots, p\} \setminus \{t_1, \ldots, t_{r-1}, c\}$, it can be taken over an appropriate subset. This subset can be then chosen either based on the largest Pearson's partial correlations in absolute value, $|\hat{\rho}_{Z_V,Z_j;Z_{t_1},\ldots,Z_{t_{r-1}},Z_c}|$, by random selection or a combination of the two, where the selection method and the size of reduction are user-decided.

4.2 Consistency of the conditional quantile estimator

Example 3.1 gives an intuition on expressing the conditional quantile function $C_{V|U_1,...,U_p}^{-1}$ recursively by the inverses of h-functions for fixed variable orders. The conditional quantile function on the original scale in Equation (1) requires the inverse of the marginal distribution function of Y. Following Kraus and Czado (2017); Noh et al. (2013), the marginal cumulative distribution functions F_Y and F_{X_j} , for $j=1,\ldots p$, are estimated nonparametrically to reduce the bias caused by model misspecification. Examples of nonparametric estimators for the marginal distributions F_Y and F_{X_j} , for $j=1,\ldots p$, are the continuous kernel smoothing estimator (Parzen 1962) and the transformed local likelihood estimator in the univariate case (Geenens 2014). Using a Gaussian kernel, the above two estimators of the marginal distribution are strong uniformly consistent. When also all inverses of the h-functions are estimated nonparametrically, we establish the consistency of the conditional quantile estimator $\hat{F}_{Y|X_1,\ldots,X_p}^{-1}$ in Proposition 4.1 for fixed variable orders. Appendix B contains the proof.

Proposition 4.1. Let the inverse of the marginal distribution functions F_Y and F_{X_j} $j=1,\ldots,p$ be uniformly continuous and estimated nonparametrically, and let the inverse of the h-functions expressing the conditional quantile estimator $C_{V|U_1,\ldots,U_p}^{-1}$ be uniformly continuous and estimated nonparametrically in the interior of the support of bivariate copulas, i.e., $[\delta, 1-\delta]^2, \delta \to 0_+$.

- 1. If estimators of the inverse of marginal functions \hat{F}_Y^{-1} , $\hat{F}_{X_j}^{-1}$, $j=1,\ldots,p$, are strong uniformly consistent on the support $[\delta,1-\delta],\delta\to 0_+$, and the estimators of the inverse of h-functions composing the conditional quantile estimator $C_{V|U_1,\ldots,U_p}^{-1}$ are strong uniformly consistent, then the estimator $\hat{F}_{Y|X_1,\ldots,X_p}^{-1}(\alpha|x_1,\ldots,x_p)$ is also strong uniformly consistent.
- 2. If estimators of the inverse of marginal functions \hat{F}_{Y}^{-1} , $\hat{F}_{X_{j}}^{-1}$, $j=1,\ldots,p$, are at least weak consistent, and the estimators of the inverse of h-functions are also at least weak consistent, then the estimator $\hat{F}_{Y|X_{1},\ldots,X_{p}}^{-1}(\alpha|x_{1},\ldots,x_{p})$ is weak consistent.

For more details about uniform continuous functions see Bartle and Sherbert (2000, Section 5.4), Kolmogorov and Fomin (1970, p.109,Def. 1). For a definition of strong uniform consistency or convergence with probability one, see Ryzin (1969); Silverman (1978) and Durrett (2010, p.16), while for a definition for weak consistency or convergence in probability, see Durrett (2010, p.53). The strong uniform consistency result in Proposition 1 requires additionally that all estimators of \hat{F}_Y^{-1} , $\hat{F}_{X_j}^{-1}$, for $j=1,\ldots p$, are strong uniformly consistent on a truncated compact interval $[\delta, 1-\delta], \delta \to 0_+$. Although not directly used in the proof of Proposition 4.1 in Appendix B, the truncation is an essential condition for guaranteeing the strong uniform consistency of all estimators of the inverse of the marginal distributions (i.e. estimators of quantile functions), see Cheng (1995); Van Keilegom and

Veraverbeke (1998); Cheng (1984). The inverse of h-functions can be obtained through a nested sequence of bivariate copula densities. Here, we consider the transformed local likelihood estimator in Geenens et al. (2017), which inherits uniformly (weak or strong) consistency from the estimator $\tilde{f}_{S,T}$ in (8). Using a product of univariate Gaussian kernels for the kernel function K in (9) for estimating $\tilde{f}_{S,T}$ is discussed in Geenens et al. (2017) and implemented in the R packages kdecop and rvinecopulib. Proposition 4.1 shows the uniform consistency and gives an indication on the performance of the conditional quantile estimator $\hat{F}_{Y|X_1,...,X_p}^{-1}$ for fixed variable orders, while combining the consistent estimators of F_Y , F_{X_j} 's, and bivariate copula densities. Extensive studies on numerical performance of $\hat{F}_{Y|X_1,...,X_p}^{-1}$ are presented in Section 5.

5 Simulation study

The proposed two-step ahead forward selection algorithms for C- and D-vine based quantile regression, from Section 4.1, are implemented in the statistical language R (R Core Team 2020). The D-vine one-step ahead algorithm is implemented in the R package vinereq (Nagler 2019). In the simulation study from Kraus and Czado (2017), it is shown that the D-vine one-step ahead forward selection algorithm performs better or similar, compared to other state of the art quantile methods, boosting additive quantile regression (Koenker 2005b; Fenske et al. 2011), nonparametric quantile regression (Li et al. 2013), semi-parametric quantile regression (Noh et al. 2015) and the linear quantile regression (Koenker and Bassett 1978). Thus we use the one-step ahead algorithm as the benchmark competitive method in the simulation study. The following simulation settings are used. Each setting is replicated for R = 100 times. In each simulation replication, we randomly generate N_{train} samples used for fitting the appropriate nonparametric vine based quantile regression models. Additionally, another $N_{\text{eval}} = \frac{1}{2} N_{\text{train}}$ samples for settings (a) – (f) and $N_{\text{eval}} = N_{\text{train}}$ for settings (g) and (h) are generated for predicting conditional quantiles from the models. Settings (a) - (f) are designed to test quantile prediction accuracy of nonparametric C- or D-vine quantile regression in cases where $p \leq N$; hence, we set $N_{\text{train}} = 1000 \text{ or } 300.$ Settings (g) and (h) test quantile prediction accuracy in cases where p > N; hence, we set $N_{\text{train}} = 100$.

- (a) Simulation setting M5 from Kraus and Czado (2017):
 - $Y = \sqrt{|2X_1 X_2 + 0.5|} + (-0.5X_3 + 1)(0.1X_4^3) + \sigma\varepsilon,$

with $\varepsilon \sim N(0,1)$, $\sigma \in \{0.1,1\}$, $(X_1,X_2,X_3,X_4)^T \sim N_4(0,\Sigma)$, and the (i,j)th component of the covariance matrix given as $(\Sigma)_{i,j} = 0.5^{|i-j|}$.

(b) $(Y, X_1, ..., X_5)^T$ follows a mixture of two 6-dimensional t copulas with degrees of freedom equal to 3 and mixture probabilities 0.3 and 0.7. Association matrices R_1 , R_2 and marginal distributions are recorded in Table 1.

$$R_{1} = \begin{pmatrix} 1 & 0.6 & 0.5 & 0.6 & 0.7 & 0.1 \\ 0.6 & 1 & 0.5 & 0.5 & 0.5 & 0.5 \\ 0.5 & 0.5 & 1 & 0.5 & 0.5 & 0.5 \\ 0.6 & 0.5 & 0.5 & 1 & 0.5 & 0.5 \\ 0.7 & 0.5 & 0.5 & 0.5 & 1 & 0.5 \\ 0.1 & 0.5 & 0.5 & 0.5 & 0.5 & 1 \end{pmatrix} \quad R_{2} = \begin{pmatrix} 1 & -0.3 & -0.5 & -0.4 & -0.5 & -0.1 \\ -0.3 & 1 & 0.5 & 0.5 & 0.5 & 0.5 \\ -0.5 & 0.5 & 1 & 0.5 & 0.5 & 0.5 \\ -0.4 & 0.5 & 0.5 & 1 & 0.5 & 0.5 \\ -0.5 & 0.5 & 0.5 & 0.5 & 1 & 0.5 \\ -0.1 & 0.5 & 0.5 & 0.5 & 0.5 & 1 \end{pmatrix}$$

Table 1: Association matrices of the multivariate t-copula and marginal distributions for simulation setting (b)

(c) Linear and heteroscedastic (Chang and Joe 2019):

$$Y = 5(X_1 + X_2 + X_3 + X_4) + 10(U_1 + U_2 + U_3 + U_4)\varepsilon,$$

where $(X_1, X_2, X_3, X_4)^T \sim N(0, \Sigma)$, $\Sigma_{i,j} = 0.5^{I\{i \neq j\}}$, $\varepsilon \sim N_4(0, 0.5)$, and U_j , $j = 1, \ldots, 4$ are obtained from X_j 's by the probability integral transform.

(d) Nonlinear and heteroscedastic (Chang and Joe 2019):

$$Y = U_1 U_2 e^{1.8U_3 U_4} + 0.5(U_1 + U_2 + U_3 + U_4)\varepsilon,$$

where $U_j, j = 1, ..., 4$ are probability integral transformed from $N_4(0, \Sigma)$, $\Sigma_{i,j} = 0.5^{I\{i \neq j\}}$, and $\varepsilon \sim N(0, 0.5)$.

- (e) R-vine copula (Czado 2019): $(V, U_1, \dots, U_4)^T$ follows an R-vine distribution with pair copulas given in Table 2.
- (f) D-vine copula (Tepegjozova 2019): $(V, U_1, \dots, U_5)^T$ follows a D-vine distribution with pair copulas given in Table 3.
- (g) Similar to setting (a),

$$Y = \sqrt{|2X_1 - X_2 + 0.5|} + (-0.5X_3 + 1)(0.1X_4^3) + (X_5, \dots, X_{110})(0, \dots, 0)^T + \sigma\varepsilon,$$

where $(X_1,\ldots,X_{110})^T \sim N_{110}(0,\Sigma)$ with the (i,j)th component of the covariance matrix $(\Sigma)_{i,j} = 0.5^{|i-j|}$, $\varepsilon \sim N(0,1)$, and $\sigma \in \{0.1,1\}$.

(h) Similar to (g),

$$Y = (X_1^3, \dots, X_{110}^3)\boldsymbol{\beta} + \varepsilon,$$

where $(X_1, ..., X_{10})^T \sim N_{10}(0, \Sigma_A)$ with the (i, j)th component of the covariance matrix $(\Sigma_A)_{i,j} = 0.8^{|i-j|}, (X_{11}, ..., X_{110})^T \sim N_{100}(0, \Sigma_B)$ with $(\Sigma_B)_{i,j} = 0.4^{|i-j|}$.

Tree	Edge	Conditioned	;	Conditioning	Family	Parameter	Kendall's τ
1	1	U_1, U_3	;		Gumbel	3.9	0.74
1	2	U_2, U_3	;		Gauss	0.9	0.71
1	3	V, U_3	;		Gauss	0.5	0.33
1	4	V, U_4	;		Clayton	4.8	0.71
2	1	V, U_1	;	U_3	Gumbel(90)	6.5	-0.85
2	2	V, U_2	;	U_3	Gumbel(90)	2.6	-0.62
2	3	U_3, U_4	;	V	Gumbel	1.9	0.48
3	1	U_1, U_2	;	V , U_3	Clayton	0.9	0.31
3	2	U_2, U_4	;	V, U_3	Clayton(90)	5.1	-0.72
4	1	U_1, U_4	;	V, U_2, U_3	Gauss	0.2	0.13

Table 2: Pair copulas of the R-vine C_{V,U_1,U_2,U_3,U_4} , with their family parameter and Kendall's τ for simulation setting (e).

The first 10 entries of β are a descending sequence between (2, 1.1) with increment of 0.1 respectively, and the rest are equal to 0. We assume $\varepsilon \sim N(0, \sigma)$ and $\sigma \in \{0.1, 1\}$.

Since the true regression quantiles are difficult to obtain in most settings, we consider the averaged check loss (Kraus and Czado 2017; Komunjer 2013) and the interval score (Chang and Joe 2019; Gneiting and Raftery 2007), instead of the out-of-sample mean averaged square error in Kraus and Czado (2017), to evaluate the performance of the estimation methods. For a chosen $\alpha \in (0,1)$, the averaged check loss is defined as

$$\widehat{\mathrm{CL}}_{\alpha} = \frac{1}{R} \sum_{r=1}^{R} \left\{ \frac{1}{N_{\text{eval}}} \sum_{n=1}^{N_{\text{eval}}} \left\{ \gamma_{\alpha} \left(Y_{r,n}^{\text{eval}} - \hat{q}_{\alpha}(X_{r,n}^{\text{eval}}) \right) \right\} \right\}, \tag{5}$$

where the check loss function γ_{α} is given as

$$\begin{split} \gamma_{\alpha} \left(Y_{r,n}^{\text{eval}} - \hat{q}_{\alpha}(X_{r,n}^{\text{eval}}) \right) &= \left(Y_{r,n}^{\text{eval}} - \hat{q}_{\alpha}(X_{r,n}^{\text{eval}}) \right) \left(\alpha - I(\left(Y_{r,n}^{\text{eval}} - \hat{q}_{\alpha}(X_{r,n}^{\text{eval}}) \right) < 0) \right) \\ &= \begin{cases} \left(Y_{r,n}^{\text{eval}} - \hat{q}_{\alpha}(X_{r,n}^{\text{eval}}) \right) \alpha, & \left(Y_{r,n}^{\text{eval}} - \hat{q}_{\alpha}(X_{r,n}^{\text{eval}}) \right) \geq 0 \\ \left(Y_{r,n}^{\text{eval}} - \hat{q}_{\alpha}(X_{r,n}^{\text{eval}}) \right) (\alpha - 1), & \left(Y_{r,n}^{\text{eval}} - \hat{q}_{\alpha}(X_{r,n}^{\text{eval}}) \right) < 0. \end{cases} \end{split}$$

The interval score, for the $(1-\alpha) \times 100\%$ prediction interval, is defined as

$$\widehat{IS}_{\alpha} = \frac{1}{R} \sum_{r=1}^{R} \left\{ \frac{1}{N_{\text{eval}}} \sum_{n=1}^{N_{\text{eval}}} \left\{ \left(\hat{q}_{\alpha/2}(X_{r,n}^{\text{eval}}) - \hat{q}_{1-\alpha/2}(X_{r,n}^{\text{eval}}) \right) + \frac{2}{\alpha} \left(\hat{q}_{1-\alpha/2}(X_{r,n}^{\text{eval}}) - Y_{r,n}^{\text{eval}} \right) I\{Y_{r,n}^{\text{eval}} \le \hat{q}_{1-\alpha/2}(X_{r,n}^{\text{eval}}) \} + \frac{2}{\alpha} \left(Y_{r,n}^{\text{eval}} - \hat{q}_{\alpha/2}(X_{r,n}^{\text{eval}}) \right) I\{Y_{r,n}^{\text{eval}} > \hat{q}_{\alpha/2}(X_{r,n}^{\text{eval}}) \} \right\},$$
(6)

Tree	Edge	Conditioned	;	Conditioning	Family	Parameter	Kendall's τ
1	1	V, U_1	;		Clayton	3.00	0.60
1	2	U_1, U_2	;		Joe	8.77	0.80
1	3	U_{2}, U_{3}	;		Gumbel	2.00	0.50
1	4	U_{3}, U_{4}	;		Gauss	0.20	0.13
1	5	U_4, U_5	;		Indep.	0.00	0.00
2	1	V, U_2	;	U_1	Gumbel	5.00	0.80
2	2	U_1, U_3	;	U_2	Frank	9.44	0.65
2	3	U_{2}, U_{4}	;	U_3	Joe	2.78	0.49
2	4	U_3, U_5	;	U_4	Gauss	0.20	0.13
3	1	V, U_3	;	U_1, U_2	Joe	3.83	0.60
3	2	U_{1}, U_{4}	;	U_2, U_3	Frank	6.73	0.55
3	3	U_{2}, U_{5}	;	U_3, U_4	Gauss	0.29	0.19
4	1	V, U_4	;	U_1, U_2, U_3	Clayton	2.00	0.50
4	2	U_1, U_5	;	U_2, U_3, U_4	Gauss	0.09	0.06
5	1	V, U_5	;	U_1, U_2, U_3, U_4	Indep.	0.00	0.00

Table 3: Pair copulas of the D-vine $C_{V,U_1,U_2,U_3,U_4,U_5}$, with their family parameter and Kendall's τ for simulation setting (f).

and smaller interval scores are better. For setting (a) – (f), the estimation procedure for the two-step ahead C- or D-vine quantile regression follows exactly Section 4.1 where the candidate sets at each step include all possible remaining predictors. The additional variable reduction described in Section 4.1.1 is not applied, thus we calculate all possible conditional log-likelihoods in each step. On the contrary, due to computational burden in Settings (g) and (h), we set the number of candidates to be k=5 and the additional variable reduction from Section 4.1.1 is applied. The chosen subset contains 20% of all possible choices, where 10% are predictors having the highest Pearson's partial correlation with the response and the remaining 10% are chosen randomly from the remaining predictors. Performance of the C- and D-vine two-step ahead quantile regression is compared with the C- and D-vine one-step ahead quantile regression. The performance of the competitive methods, evaluated by the averaged check loss at 5%, 50%, 95% quantile levels and interval score for the 95% prediction interval, are recorded in Tables 4, 5 and 6. All densities are estimated nonparametrically for fair comparison. Tables 4 and 5 show that the C- and D-vine two-step ahead regression models outperform the C- and D-vine one-step ahead regression models in five out of seven settings, with the exception of settings (b) and (e), in which all models perform quite similarly to each other. Further, when comparing regression models within the same vine copula class, again in five out of seven settings the C-vine two-step ahead regression models outperform the C-vine one-step ahead models. Similarly, the D-vine two-step ahead models outperform the D-vine one-step ahead models in six out of seven scenarios, with the exception of setting (b) only. Thus, in scenarios where there is no significant improvement through the second step, both one-step and two-step ahead approaches perform very similar. All of that implies that the two-step ahead vine based quantile regression greatly improves the performance of the one-step ahead quantile regression. Table 6 indicates that in the high dimensional settings where the two-step ahead quantile regression was used in combination with the additional variable selection from Section 4.1.1, in three out of four simulation settings the two-step ahead models outperform the one-step ahead models. In the simulation setting (g) we can see that all models show similar performance. However, in the setting (g) with noise of $\sigma = 0.1$, the Dvine one-step ahead model outperforms the other models, while in the setting (g) with noise of $\sigma = 1$ the D-vine two-step ahead model shows a better performance. In the simulation setting (h) we see that there is a significant improvement in the two-step ahead models, compared to the one-step ahead models. For both $\sigma = 0.1$ and $\sigma = 1$ the best performing model is the C-vine two-step ahead model. These results indicate that the newly proposed method improves the accuracy of the one-step ahead quantile regression in high dimensions, even with an attempt to ease the computational complexity of the two-step ahead model with a low number of candidates, compared to the number of predictors.

6 Real data examples

We test the proposed methods on two real data sets, i.e., the concrete data set from Yeh (1998) corresponding to $p \leq N$, and the riboflavin data set from Bühlmann and van de Geer (2011) corresponding to p > N. For both data sets, performances of the four competitive algorithms is evaluated by the averaged check loss defined in Equation (5) at 5%, 50% and 95% quantile levels, as well as the 95% prediction interval score defined in Equation (6), by randomly splitting the data set into training and evaluation sets 100 times.

6.1 Concrete data set

The concrete data set was originaly used in Yeh (1998), and is available at the UCI Machine Learning Repository (Dua and Graff 2017). The data set has in total 1030 samples. Our objective is quantile predictions of the concrete compressive strength, which is a highly nonlinear function of age and ingredients. The predictors are age (AgeDay, counted in days) and 7 physical measurements of the concrete ingredients (given in kg in a m^3 mixture): cement (CementComp), blast furnace slag (BlastFur), fly ash (FlyAsh), water (WaterComp), superplastizer (Superplastizer), coarse aggregate (CoarseAggre) and fine aggregate (FineAggre). We randomly split the data set into training set with 830 samples and evaluation set with 200 samples; the random splitting is repeated for 100 times. Performance of the proposed C- and D-vine two-step ahead quantile regression, compared with the C- and D-vine one-step ahead quantile regression, is evaluated by several measurements reported in Table 7 after 100 repetitions of fitting the models. The results are quite close to each other, but given the small number of predictors, that is what

Setting	Model	$\widehat{\mathrm{IS}}_{0.05}$	$\widehat{\mathrm{CL}}_{0.05}$	$\widehat{\mathrm{CL}}_{0.5}$	$\widehat{\mathrm{CL}}_{0.95}$
(a)	D-vine One-step	55.541	0.655	0.157	0.507
$\sigma = 0.1$	D-vine Two-step	43.333	0.468	0.104	0.407
**	C-vine One-step	53.509	0.635	0.157	0.489
	C-vine Two-step	42.013	0.454	0.101	0.401
(a)	D-vine One-step	154.352	1.625	0.451	1.615
$\sigma = 1$	D-vine Two-step	148.527	1.569	0.448	1.563
**	C-vine One-step	151.599	1.606	0.453	1.596
	C-vine Two-step	148.410	1.563	0.448	1.564
(b)	D-vine One-step	118.748	1.289	0.417	1.300
*	D-vine Two-step	119.103	1.296	0.417	1.301
	C-vine One-step	119.084	1.297	0.414	1.301
	C-vine Two-step	118.896	1.295	0.417	1.300
(c)	D-vine One-step	2908.904	30.539	8.551	30.422
**	D-vine Two-step	2853.517	30.208	8.699	29.950
	C-vine One-step	2859.232	30.238	8.586	29.946
	C-vine Two-step	2850.103	30.191	8.642	29.837
(d)	D-vine One-step	86.396	0.916	0.238	0.914
**	D-vine Two-step	83.538	0.897	0.236	0.878
	C-vine One-step	84.985	0.908	0.240	0.900
	C-vine Two-step	83.326	0.900	0.237	0.871
(e)	D-vine One-step	10.587	0.108	0.028	0.109
*	D-vine Two-step	10.323	0.096	0.026	0.113
	C-vine One-step	10.233	0.107	0.026	0.102
	C-vine Two-step	10.345	0.100	0.025	0.109
(f)	D-vine One-step	13.787	0.158	0.043	0.137
**	D-vine Two-step	8.437	0.091	0.023	0.079
	C-vine One-step	12.624	0.139	0.038	0.129
	C-vine Two-step	9.093	0.098	0.024	0.085

Table 4: Out-of-sample predictions $\widehat{\mathrm{IS}}_{0.5}$, $\widehat{\mathrm{CL}}_{0.05}$, $\widehat{\mathrm{CL}}_{0.95}$ for settings (a) – (f) with $N_{train}=300$. Lower values, indicating better performance, are highlighted in gray. With ** we denote the scenarios in which there is an improvement through the second step and with * we denote scenarios in which the models perform similar.

Setting	Model	$\widehat{\mathrm{IS}}_{0.05}$	$\widehat{\mathrm{CL}}_{0.05}$	$\widehat{\mathrm{CL}}_{0.5}$	$\widehat{\mathrm{CL}}_{0.95}$
(a)	D-vine One-step	55.891	0.673	0.150	0.498
$\sigma = 0.1$	D-vine Two-step	40.736	0.445	0.088	0.373
**	C-vine One-step	54.516	0.661	0.151	0.485
	C-vine Two-step	40.043	0.436	0.086	0.368
(a)	D-vine One-step	162.122	1.697	0.431	1.663
$\sigma = 1$	D-vine Two-step	156.772	1.632	0.419	1.619
**	C-vine One-step	160.775	1.684	0.432	1.653
	C-vine Two-step	156.794	1.634	0.419	1.617
(b)	D-vine One-step	125.327	1.365	0.395	1.361
*	D-vine Two-step	125.242	1.363	0.399	1.360
	C-vine One-step	125.122	1.364	0.395	1.359
	C-vine Two-step	125.298	1.364	0.398	1.361
(c)	D-vine One-step	3064.781	31.692	8.147	31.474
**	D-vine Two-step	3041.950	31.607	8.195	31.259
	C-vine One-step	3046.516	31.639	8.182	31.247
	C-vine Two-step	3042.458	31.617	8.195	31.225
(d)	D-vine One-step	91.105	0.963	0.223	0.945
**	D-vine Two-step	89.558	0.957	0.222	0.920
	C-vine One-step	90.401	0.961	0.223	0.935
	C-vine Two-step	89.465	0.956	0.222	0.920
(e)	D-vine One-step	10.493	0.105	0.025	0.106
*	D-vine Two-step	10.264	0.091	0.023	0.114
	C-vine One-step	10.023	0.104	0.024	0.097
	C-vine Two-step	10.334	0.097	0.023	0.110
(f)	D-vine One-step	13.700	0.156	0.040	0.137
**	D-vine Two-step	8.279	0.086	0.020	0.077
	C-vine One-step	12.233	0.134	0.036	0.126
	C-vine Two-step	8.928	0.093	0.021	0.083

Table 5: Out-of-sample predictions $\widehat{\text{IS}}_{0.5}$, $\widehat{\text{CL}}_{0.05}$, $\widehat{\text{CL}}_{0.05}$, $\widehat{\text{CL}}_{0.95}$ for settings (a) – (f) with $N_{train}=1000$. Lower values, indicating better performance, are highlighted in gray. With ** we denote the scenarios in which there is an improvement through the second step and with * we denote scenarios in which the models perform similar.

Scenario	Model	$\widehat{\mathrm{IS}}_{0.05}$	$\widehat{\mathrm{CL}}_{0.05}$	$\widehat{\mathrm{CL}}_{0.5}$	$\widehat{\mathrm{CL}}_{0.95}$
(g)	D-vine One-step	19.625	0.260	0.245	0.231
$\sigma = 0.1$	D-vine Two-step	20.475	0.260	0.256	0.252
*	C-vine One-step	19.733	0.252	0.247	0.241
	C-vine Two-step	19.789	0.249	0.247	0.246
(g)	D-vine One-step	53.381	0.688	0.667	0.646
$\sigma = 1$	D-vine Two-step	52.166	0.675	0.652	0.629
**	C-vine One-step	53.616	0.694	0.670	0.646
	C-vine Two-step	52.353	0.666	0.654	0.643
(h)	D-vine One-step	558.359	6.922	6.979	7.037
$\sigma = 0.1$	D-vine Two-step	529.508	6.456	6.619	6.781
**	C-vine One-step	514.08	6.047	6.426	6.805
	C-vine Two-step	479.655	5.873	5.996	6.119
(h)	D-vine One-step	554.175	6.869	6.927	6.985
$\sigma = 1$	D-vine Two-step	531.296	6.643	6.641	6.639
**	C-vine One-step	512.964	6.386	6.412	6.438
	C-vine Two-step	483.921	6.050	6.049	6.048

Table 6: Out-of-sample predictions $\widehat{\text{IS}}_{0.5}$, $\widehat{\text{CL}}_{0.05}$, $\widehat{\text{CL}}_{0.05}$, $\widehat{\text{CL}}_{0.95}$ for settings (g) – (h) with $N_{train} = 100$. Lower values, indicating better performance, are highlighted in gray. With ** we denote the scenarios in which there is an improvement through the second step and with * we denote scenarios in which the models perform similar.

one would expect of the forward sequential algorithm. However, there is an improvement in the performance of the two-step ahead approach compared to the one-step ahead approach for both C- and D-vine based models. Also, the C-vine model seems more appropriate for modelling the dependency structure in the data set. Finally, out of all models, the C-vine two-step ahead algorithm is the best performing algorithm in terms of out-of-sample predictions $\widehat{\text{IS}}_{0.5}$, $\widehat{\text{CL}}_{0.05}$, $\widehat{\text{CL}}_{0.05}$, $\widehat{\text{CL}}_{0.95}$ on the concrete data set, as seen in Table 7. In order to explain the different approaches of the one-step ahead and the two-step ahead algorithms, we consider the order of the predictors which the algorithms provide. The order of the predictors enter the model is based on maximising the conditional log-likelihood, thus it provides a descending order of influence of the predictors on the conditional quantile function of the response. Figure 4 shows the individual distribution of positions for each predictor in the four different models, i.e. each individual bar plot has all the possible positions in the order on the x-axis and the counts of how many times the given predictor appeared on a specific position of the order on the y-axis out of the 100 repeated model

Model	$\widehat{\mathrm{IS}}_{0.05}$	$\widehat{\mathrm{CL}}_{0.05}$	$\widehat{\mathrm{CL}}_{0.5}$	$\widehat{\mathrm{CL}}_{0.95}$
D-vine One-step	1032.319	10.751	2.759	10.520
D-vine Two-step	987.101	10.543	2.778	9.815
C-vine One-step	976.750	10.649	2.696	9.454
C-vine Two-step	967.002	10.519	2.639	9.453

Table 7: Concrete data set: Out-of-sample predictions $\widehat{IS}_{0.5}$, $\widehat{CL}_{0.05}$, $\widehat{CL}_{0.05}$, $\widehat{CL}_{0.95}$. The best performing model is highlighted in gray.

fits.

From Figure 4 we can indeed see the greedy approach of the one-step algorithms. Both onestep ahead C- and D- vine models always choose the same predictor as the first predictor to enter the model. That is because the pair copula between the response and the predictor AgeDay has the biggest likelihood, out of the possible pair copulas between the response and each of the predictors. Next, as second predictor both one-step ahead algorithms always choose the predictor CementComp, because, similarly as before, the bivariate copula between the response and CementComp conditioned on the already chosen AgeDay has the biggest likelihood out of the possible pair copulas between the response and the other possible predictors conditioned on AgeDay. Note that in only 3 dimensions the models for both C- and D-vines are equivalent (in 3 dimensions a path is also a star, and vice versa). On other side, the two-step ahead approaches do not make such a uniform decision about the first predictor to be included. Instead of choosing AgeDay as first predictor, the algorithms consider the future possible improvement and based on that, they choose the predictor CementComp as the first to enter the model. The most influential predictor from the one-step ahead models, AgeDay, is chosen to be the second or third predictor of the two-step ahead models, which turns out to be a better ordering. Next, the influence of the predictors is ranked sequentially by choosing the predictor with the highest frequency of each position in the order excluding the predictor chosen in the previous steps. As already stated, the predictors that take the first positions in the order have the biggest contribution to the conditional log-likelihood, thus they influence the conditional quantile function the most and we are interested in finding them. For instance, the most influential predictor is chosen as the one most frequently ranked first; the second most important is chosen as the most frequently ranked second, excluding the most important one selected in the previous step. Following this approach, the three most influential predictors, based on the most accurate C-vine two-step model, on the concrete compressive strength are CementComp, WaterComp and AgeDay. In Figure 5 the marginal effect plots based on the fitted quantiles, from the C-vine two-step model, for the three most influential predictors are given. The marginal effect of a predictor variable is its expected impact on the quantile estimator, where the expectation is taken over all other predictor variables.

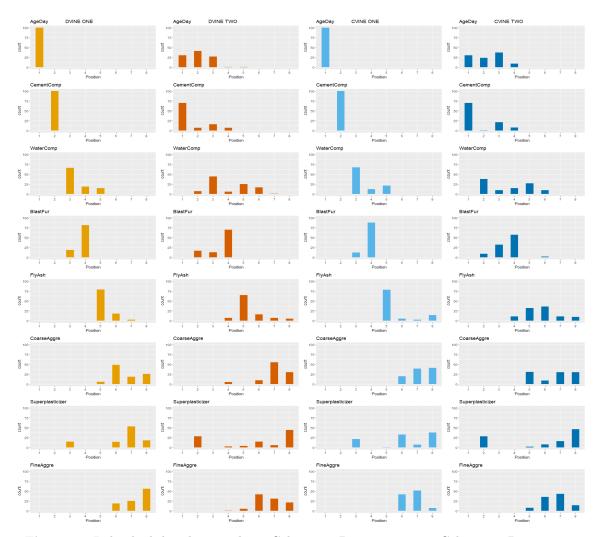


Figure 4: Individual distribution plots. Column 1: D-vine one-step, Column 2: D-vine two-step, Column 3: C-vine one-step, Column 4: C-vine two-step.

This is estimated using all fitted conditional quantiles and smoothed over the predictor variables considered.

6.2 Riboflavin data set

The riboflavin data set, available in the R package hdi, aims at quantile predictions of log-transformed production rate of Bacillus subtilis using log-transformed expression levels of 4088 genes. To reduce the computational burden, we perform a pre-selection of the top 100 genes with the highest variance (Bühlmann and van de Geer 2011), resulting in

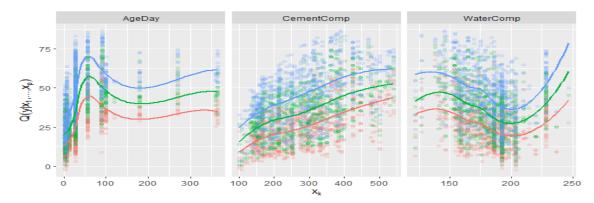


Figure 5: Marginal effect plots for the 3 most influential predictors on the concrete compressive strength for α values of 0.05 (red colour), 0.5 (green colour) and 0.95 (blue color).

a subset with p=100 log-transformed gene expressions and N=71 samples. Random splitting of the subset into training set with 61 samples and evaluation set with 10 samples, is repeated for 100 times. For the C- and D-vine two-step ahead quantile regression the number of candidates is set to k=10. Additionally, to further reduce the computational burden the additional variable selection from Section 4.1.1 is applied with the chosen subset containing 25% of all possible choices, where 15% are predictors having the highest partial correlation with the log-transformed Bacillus subtilis production rate and the remaining 10% are chosen randomly from the remaining predictors. Performance of competitive quantile regression models is reported in Table 8, where we see that the proposed C-vine two-step ahead quantile regression is the best performing model and outperforms both the D-vine one-step ahead quantile regression from Kraus and Czado (2017) and the C-vine one-step ahead quantile regression to a large extent. Further, the second best performing method is the D-vine two-step ahead model which, while performing slightly worse than the C-vine two-step ahead models. Further, since the predictors entering the C- and

Model	$\widehat{\mathrm{IS}}_{0.05}$	$\widehat{\mathrm{CL}}_{0.05}$	$\widehat{\mathrm{CL}}_{0.5}$	$\widehat{\mathrm{CL}}_{0.95}$
D-vine One-step	33.826	0.438	0.423	0.408
D-vine Two-step	30.574	0.436	0.382	0.328
C-vine One-step	34.516	0.485	0.431	0.378
C-vine Two-step	28.590	0.413	0.357	0.302

Table 8: Out-of-sample predictions $\widehat{IS}_{0.5}$, $\widehat{CL}_{0.05}$, $\widehat{CL}_{0.05}$, $\widehat{CL}_{0.95}$. The best performing model is highlighted in gray.

D-vine models yield a descending order of the predictors contributing to maximizing the

conditional log-likelihood, the order indicates the influence of the predictors to the response variable. It is often of practical interest to know which gene expressions are of the highest importance for prediction. Similarly as before, since we repeat the random splitting of the subset for R=100 times, the importance of the gene expressions is ranked sequentially by choosing the one with the highest frequency of each element in the order excluding the gene expressions chosen in the previous steps. For instance, the most important gene expression is chosen as the one most frequently ranked first; the second most important gene is chosen as the one most frequently chosen as the second element in the order, excluding the most important gene selected in the previous step. The top ten most influential gene expressions using the C- and D-vine one- or two-step ahead models are recorded in Table 9. Figure 6 shows the marginal effects plots based on the fitted quantiles, from the C-vine two-

Model/Position	1	2	3	4	5	6	7	8	9	10
D-vine One-step	GGT	YCIC	MTA	RPSE	YVAK	THIK	ANSB	SPOVB	YVZB	YQJB
D-vine Two-step	MTA	RPSE	THIK	YMFE	YCIC	sigM	PGM	YACC	YVQF	YKPB
C-vine One-step	GGT	YCIC	MTA	RPSE	HIT	BFMBAB	PHRC	YBAE	PGM	YHEF
C-vine Two-step	MTA	RPSE	THIK	YCIC	YURU	PGM	sigM	YACC	YKRM	ASNB

Table 9: The 10 most influential gene expressions on the conditional quantile function, ranked based on their position in the order.

step model, for the 10 most influential predictors on the log-transformed Bacillus subtilis production rate.

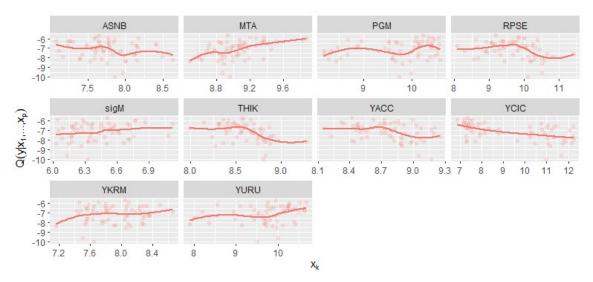


Figure 6: Marginal effect plots for the 10 most influential predictors on the log-transformed Bacillus subtilis production rate for $\alpha = 0.5$.

7 Summary and discussion

In this paper, we introduce a novel two-step ahead forward selection algorithm for nonparametric C- and D-vine copula based quantile regression. Inclusion of future information, obtained through considering the next tree in the two-step ahead algorithm, yields a significantly less greedy sequential selection procedure in comparison to the already existing one-step ahead algorithm for D-vine based quantile regression in Kraus and Czado (2017). We extend the vine-based quantile regression framework to include C-vine copulas, giving an additional choice for the dependence structure. Further, for the first time nonparametric bivariate copulas are used in the construction of vine copula based quantile regression models. This overcomes the problem of possible family misspecification in the parametric estimation of bivariate copulas, and allows for even more flexibility in dependence estimation. As an additional result, under mild regularity conditions the nonparametric conditional quantile estimator is shown to be consistent.

The extensive simulation study, including several different settings and data sets with different dimensions, strengths of dependence and tail dependencies, shows that the two-step ahead algorithm outperforms the one-step ahead algorithm in the majority of scenarios. Especially interesting are the results for the Concrete and Riboflavin data sets, as the C-vine two-step ahead algorithm has a significant improvement in comparison to the other algorithms. These findings provide strong evidence for the need of modeling the dependence structure following a C-vine copula. In addition, the two-step ahead algorithm allows to control the computational intensity independently of the data dimensions, through the number of candidate predictors and the additional variable selection discussed in Section 5. Thus, fitting a vine based quantile regression models in high dimensions becomes feasible. As seen in a number of simulation settings, there is a significant gain by introducing additional dependence structures in the vine based quantile regression. An area of further research is developing similar forward selection algorithms for R-vine tree structures.

At each step of the vine building stage we compare equal-sized models with the same number of variables. The conditional log-likelihood is suited for such a comparison. For other questions such as choosing between a C-vine, D-vine or R-vine information criteria might come in handy. When maximum likelihood estimation is employed at all stages, the selection criteria by Akaike (AIC) (Akaike 1973), the Bayesian information criterion (BIC) (Schwarz 1978) and the focussed information criterion (FIC) (Claeskens and Hjort 2003) might be used immediately. Ko et al. (2019) studied FIC and AIC specifically for the selection of parametric copulas. The copula information criterion in the spirit of the Akaike information criterion by Grønneberg and Hjort (2014) can be used for selection among copula models with empirically estimated margins, while Ko and Hjort (2019) studied such a criterion for parametric copula models. We plan a deeper investigation of the use of information criteria for nonparametrically estimated copulas and for vines in particular. Such a study is beyond the scope of this paper, but could be interesting to study stopping criteria too for building vines.

Nonparametrically estimated vines are offering a large flexibility. Their parametric counterparts, on the other hand, are enjoying simplicity. An interesting route for further research is to combine parametric and nonparametric components in the construction of the vines in an efficient way to bring most benefit, which should be made tangible by means of some criterion such that guidance can be provided about which components should be modelled nonparametrically and which others are best modeled parametrically. For some types of models, such choice between a parametric and a nonparametric model has been investigated by Jullum and Hjort (2017) via the focussed information criterion. This and alternative methods taking the effective degrees of freedom into account are worthwhile to further investigate for vine copula models.

Acknowledgments

This work was supported by the Deutsche Forschungsgemeinschaft[DFG CZ 86/6-1], the Research Foundation Flanders and KU Leuven internal fund C16/20/002. The resources and services used in this work were provided by the VSC (Flemish Supercomputer Center), funded by the Research Foundation-Flanders (FWO) and the Flemish Government.

Appendix

A Construction of the transformation local likelihood estimator of the copula density

Let the $N \times 2$ transformed sample matrix be

$$D = (S, T), \tag{7}$$

where the transformed samples $D_n = (S_n = \Phi^{-1}(U_i^{(n)}), T_n = \Phi^{-1}(U_j^{(n)})), n = 1, ..., N$, and Φ denotes the cumulative distribution function of a standard Gaussian distribution. The logarithm of the density $f_{S,T}$ of the transformed samples $(S_n, T_n), n = 1, ..., N$ is approximated locally by a bivariate polynomial expansion P_{a_m} of order m with intercept $\tilde{a}_{m,0}$ such that the approximation is denoted by

$$\tilde{f}_{S,T}(\Phi^{-1}(u_i^{(n)}), \Phi^{-1}(u_j^{(n)})) = \exp\big\{\tilde{a}_{m,0}(\Phi^{-1}(u_i^{(n)}), \Phi^{-1}(u_j^{(n)}))\big\}.$$

The transformation local likelihood estimator is then defined as

$$\tilde{c}(u_i^{(n)}, u_j^{(n)}) = \frac{\tilde{f}_{S,T}(\Phi^{-1}(u_i^{(n)}), \Phi^{-1}(u_j^{(n)}))}{\phi(\Phi^{-1}(u_i^{(n)}))\phi(\Phi^{-1}(u_j^{(n)}))}.$$
(8)

To get the local polynomial approximation, we need a kernel function K with 2×2 bandwidth matrix B_N . For some pair (\check{s},\check{t}) close to (s,t), $\log f_{ST}(\check{s},\check{t})$ is assumed to be well approximated, locally, by for instance a polynomial with m=1 (log-linear)

$$P_{\mathbf{a}_1}(\check{s} - s, \check{t} - t) = a_{1,0}(s, t) + a_{1,1}(s, t)(\check{s} - s) + a_{1,2}(s, t)(\check{t} - t),$$

or m=2 (log-quadratic)

$$P_{a_2}(\check{s} - s, \check{t} - t) = a_{2,0}(s, t) + a_{2,1}(s, t)(\check{s} - s) + a_{2,2}(s, t)(\check{t} - t) + a_{2,3}(s, t)(\check{s} - s)^2 + a_{2,4}(s, t)(\check{t} - t)^2 + a_{2,5}(s, t)(\check{s} - s)(\check{t} - t).$$

The coefficient vector of the polynomial expansion P_{a_m} is denoted by $a_m(s,t)$, where $a_1(s,t) = (a_{1,0}(s,t), a_{1,1}(s,t), a_{1,2}(s,t))$ for the log-linear approximation and $a_2(s,t) = (a_{2,0}(s,t), \ldots, a_{2,5}(s,t))$ for the log-quadratic. The estimated coefficient vector $\tilde{\boldsymbol{a}}_m(s,t)$ is obtained by a maximization problem in Equation (9)

$$\tilde{\boldsymbol{a}}_{m}(s,t) = \arg\max_{a_{m}} \left\{ \sum_{n=1}^{N} \boldsymbol{K} \left(\boldsymbol{B}_{N}^{-1/2} \begin{pmatrix} s - S_{n} \\ t - T_{n} \end{pmatrix} \right) P_{\boldsymbol{a}_{m}}(S_{n} - s, T_{n} - t) - N \left\{ \int \int_{\mathbb{R}^{2}} \boldsymbol{K} \left(\boldsymbol{B}_{N}^{-1/2} \begin{pmatrix} s - \check{s} \\ t - \check{t} \end{pmatrix} \right) \exp\left(P_{\boldsymbol{a}_{m}} (\check{s} - s, t - t) \right) d\check{s} d\check{t} \right\} \right\}.$$
(9)

While it is well-known that kernel estimators suffer from the curse of dimensionality, in the vine construction only two-dimensional functions need to be estimated, this thus avoids problems with high-dimensionality.

We next explain as in Geenens et al. (2017) how a bandwidth selection is obtained. Consider the principal component decomposition for the $N \times 2$ sample matrix D = (S, T) in Equation (7), such that the $N \times 2$ matrix (Q, R) follows

$$(Q,R)^T = WD^T, (10)$$

where each row of W is an eigenvector of D^TD . We obtain an estimator of f_{ST} through the density estimator of f_{QR} , which can be estimated based on a diagonal bandwidth matrix diag (h_Q^2, h_R^2) . Selecting the bandwidths h_Q uses samples $Q_n, n = 1, ..., N$ as

$$h_Q = \arg\min_{h>0} \left\{ \int -\infty^{\infty} \left\{ \tilde{f}_Q^{(p)} \right\}^2 dq - \frac{2}{N} \sum_{n=1}^N \tilde{f}_{Q(-n)}^{(p)}(\hat{Q}_n) \right\}, \tag{11}$$

where $\tilde{f}_Q^{(p)}(p=1,2)$ are the local polynomial estimators for f_Q , and $\tilde{f}_{Q(-n)}^{(p)}$ is the "leave-one-out" version of $\tilde{f}_Q^{(p)}$ computed by leaving out Q_n . The procedure of selecting h_R is similar. The bandwidth matrix for the bivariate copula density is then given by $\boldsymbol{B}_N = K_N^{(p)}W^{-1}\mathrm{diag}(h_Q^2,h_R^2)W^{-1}$ where $K_N^{(p)}$ takes $N^{1/45}$ to ensure an asymptotic optimal bandwidth order for the local log-quadratic case (p=2), see Geenens et al. (2017, Section 4) for details. Selection for the k-nearest-neighbour type bandwidth is similar. The k-nearest-neighbour bandwidths denoted as h_Q' and h_R' are obtained by restricting the minimization in Equation (11) in the interval (0,1), i.e.,

$$h'_{Q} = \arg\min_{h'_{Q} \in (0,1)} \left\{ \int_{-\infty}^{\infty} \left\{ \tilde{f}_{Q}^{(p)} \right\}^{2} dq - \frac{2}{N} \sum_{n=1}^{N} \tilde{f}_{Q(-n)}^{(p)}(\hat{Q}_{n}) \right\}.$$

Estimating f_{QR} at any (q, r) is obtained by using its $k = K_N^{(p)} \cdot h_Q' \cdot N$ nearest neighbours where $K_N^{(p)}$ takes $N^{-4/45}$ for p = 2. The R package rvinecopulib only implemented the bandwidth in Equation (11) for the quadratic case with p = 2.

B Proof of Proposition 4.1

Proof. We first show statement 1. By Equation (1), the estimator

$$\hat{F}_{Y|X_1,\dots,X_p}^{-1}(\alpha|x_1,\dots,x_p) = \hat{F}_Y^{-1}\Big(\hat{C}_{V|U_1,\dots,U_p}^{-1}(\alpha|\hat{u}_1,\dots,\hat{u}_p)\Big),$$

where $\hat{u}_j = \hat{F}_j(x_j), j = 1, \dots, p$ denote variables on the u-scale. To avoid heavy notation, N referring to the sample size will be omitted here. Following Wied and Weißbach (2012); Silverman (1978), to show the uniformly strong consistency of $\hat{F}_Y^{-1}(\hat{C}_{V|U_1,\dots,U_p}^{-1}(\alpha|\hat{u}_1,\dots,\hat{u}_p))$,

we show

$$\sup_{\alpha} \left| \hat{F}_{Y}^{-1} \Big(\hat{C}_{V|U_{1},\dots,U_{p}}^{-1} (\alpha | \hat{u}_{1},\dots,\hat{u}_{p}) \Big) - F_{Y}^{-1} \Big(C_{V|U_{1},\dots,U_{p}}^{-1} (\alpha | u_{1},\dots,u_{p}) \Big) \right| \to 0 \ a.s.$$

For all $\epsilon \geq 0$,

$$1 \geq P\left(\sup_{\alpha} \left| \hat{F}_{Y}^{-1} \left(\hat{C}_{V|U_{1},...,U_{p}}^{-1} (\alpha | \hat{u}_{1}, ..., \hat{u}_{p}) \right) - F_{Y}^{-1} \left(C_{V|U_{1},...,U_{p}}^{-1} (\alpha | u_{1}, ..., u_{p}) \right) \right| \leq \epsilon \right)$$

$$= P\left(\sup_{\alpha} \left| \hat{F}_{Y}^{-1} \left(\hat{C}_{V|U_{1},...,U_{p}}^{-1} (\alpha | \hat{u}_{1}, ..., \hat{u}_{p}) \right) - \hat{F}_{Y}^{-1} \left(C_{V|U_{1},...,U_{p}}^{-1} (\alpha | u_{1}, ..., u_{p}) \right) \right)$$

$$+ \hat{F}_{Y}^{-1} \left(C_{V|U_{1},...,U_{p}}^{-1} (\alpha | u_{1}, ..., u_{p}) \right) - F_{Y}^{-1} \left(C_{V|U_{1},...,U_{p}}^{-1} (\alpha | u_{1}, ..., u_{p}) \right) \right| \leq \epsilon \right)$$

$$\geq P\left(\sup_{\alpha} \left\{ \left| \hat{F}_{Y}^{-1} \left(\hat{C}_{V|U_{1},...,U_{p}}^{-1} (\alpha | \hat{u}_{1}, ..., \hat{u}_{p}) \right) - \hat{F}_{Y}^{-1} \left(C_{V|U_{1},...,U_{p}}^{-1} (\alpha | u_{1}, ..., u_{p}) \right) \right| \right\}$$

$$+ \left| \hat{F}_{Y}^{-1} \left(C_{V|U_{1},...,U_{p}}^{-1} (\alpha | u_{1}, ..., u_{p}) \right) - F_{Y}^{-1} \left(C_{V|U_{1},...,U_{p}}^{-1} (\alpha | u_{1}, ..., u_{p}) \right) \right| \right\}$$

$$= P\left(\sup_{\alpha} \left| \hat{F}_{Y}^{-1} \left(\hat{C}_{V|U_{1},...,U_{p}}^{-1} (\alpha | \hat{u}_{1}, ..., \hat{u}_{p}) \right) - \hat{F}_{Y}^{-1} \left(C_{V|U_{1},...,U_{p}}^{-1} (\alpha | u_{1}, ..., u_{p}) \right) \right| \right\}$$

$$\geq P\left(\left(\sup_{\alpha} \left| \hat{F}_{Y}^{-1} \left(\hat{C}_{V|U_{1},...,U_{p}}^{-1} (\alpha | \hat{u}_{1}, ..., \hat{u}_{p}) \right) - \hat{F}_{Y}^{-1} \left(C_{V|U_{1},...,U_{p}}^{-1} (\alpha | u_{1}, ..., u_{p}) \right) \right| \right) \right\}$$

$$\geq P\left(\left(\sup_{\alpha} \left| \hat{F}_{Y}^{-1} \left(\hat{C}_{V|U_{1},...,U_{p}}^{-1} (\alpha | \hat{u}_{1}, ..., \hat{u}_{p}) \right) - \hat{F}_{Y}^{-1} \left(C_{V|U_{1},...,U_{p}}^{-1} (\alpha | u_{1}, ..., u_{p}) \right) \right| \right) \right\}$$

$$\geq P\left(\left(\sup_{\alpha} \left| \hat{F}_{Y}^{-1} \left(\hat{C}_{V|U_{1},...,U_{p}}^{-1} (\alpha | \hat{u}_{1}, ..., \hat{u}_{p}) \right) - \hat{F}_{Y}^{-1} \left(C_{V|U_{1},...,U_{p}}^{-1} (\alpha | u_{1}, ..., u_{p}) \right) \right) \right| \right\}$$

$$= P\left(\sup_{\alpha} \left| \hat{F}_{Y}^{-1} \left(\hat{C}_{V|U_{1},...,U_{p}}^{-1} (\alpha | \hat{u}_{1}, ..., \hat{u}_{p}) \right) - \hat{F}_{Y}^{-1} \left(C_{V|U_{1},...,U_{p}}^{-1} (\alpha | u_{1}, ..., u_{p}) \right) \right| \right\}$$

$$= P\left(\sup_{\alpha} \left| \hat{F}_{Y}^{-1} \left(\hat{C}_{V|U_{1},...,U_{p}}^{-1} (\alpha | u_{1}, ..., u_{p}) \right) - \hat{F}_{Y}^{-1} \left(C_{V|U_{1},...,U_{p}}^{-1} (\alpha | u_{1}, ..., u_{p}) \right) \right| \right\}$$

$$= P\left(\sup_{\alpha} \left| \hat{F}_{Y}^{-1} \left(\hat{C}_{V|U_{1},...,U_{p}}^{-1} (\alpha | u_{1}, ..., u_{p}) \right) - \hat{F}_{Y}^{-1} \left(C_{V|U_{1},...,U_{p}}^{-1} (\alpha | u_{1}, ..$$

Denote the event $A = \sup_{\alpha} \left| \hat{F}_{Y}^{-1} \left(C_{V|U_{1},...,U_{p}}^{-1} (\alpha | u_{1},...,u_{p}) \right) - F_{Y}^{-1} \left(C_{V|U_{1},...,U_{p}}^{-1} (\alpha | u_{1},...,u_{p}) \right) \right| \leq \frac{1}{4}\epsilon$, then P(A) = 1 holds by the uniform strong consistency of the estimator of F_{Y}^{-1} . We now show that the conditional probability in (12) is equal to 1. We start by rewriting the

conditional probability as

$$\begin{split} P\bigg(\sup_{\alpha} \left| \hat{F}_{Y}^{-1} \Big(\hat{C}_{V|U_{1},\dots,U_{p}}^{-1} (\alpha | \hat{u}_{1},\dots,\hat{u}_{p}) \Big) - \hat{F}_{Y}^{-1} \Big(C_{V|U_{1},\dots,U_{p}}^{-1} (\alpha | u_{1},\dots,u_{p}) \Big) \right| &\leq \frac{3}{4} \epsilon \bigg| A \bigg) \\ &= P\bigg(\sup_{\alpha} \left| \hat{F}_{Y}^{-1} \Big(\hat{C}_{V|U_{1},\dots,U_{p}}^{-1} (\alpha | \hat{u}_{1},\dots,\hat{u}_{p}) \Big) - F_{Y}^{-1} \Big(\hat{C}_{V|U_{1},\dots,U_{p}}^{-1} (\alpha | \hat{u}_{1},\dots,\hat{u}_{p}) \Big) \right. \\ &+ F_{Y}^{-1} \Big(\hat{C}_{V|U_{1},\dots,U_{p}}^{-1} (\alpha | \hat{u}_{1},\dots,\hat{u}_{p}) \Big) - \hat{F}_{Y}^{-1} \Big(C_{V|U_{1},\dots,U_{p}}^{-1} (\alpha | u_{1},\dots,u_{p}) \Big) \\ &+ F_{Y}^{-1} \Big(C_{V|U_{1},\dots,U_{p}}^{-1} (\alpha | u_{1},\dots,u_{p}) \Big) - F_{Y}^{-1} \Big(C_{V|U_{1},\dots,U_{p}}^{-1} (\alpha | u_{1},\dots,u_{p}) \Big) \bigg| \leq \frac{3}{4} \epsilon \bigg| A \bigg) \\ &\geq P\bigg(\sup_{\alpha} \left| \hat{F}_{Y}^{-1} \Big(\hat{C}_{V|U_{1},\dots,U_{p}}^{-1} (\alpha | \hat{u}_{1},\dots,\hat{u}_{p}) \Big) - F_{Y}^{-1} \Big(\hat{C}_{V|U_{1},\dots,U_{p}}^{-1} (\alpha | u_{1},\dots,\hat{u}_{p}) \Big) \bigg| \\ &+ \sup_{\alpha} \left| F_{Y}^{-1} \Big(\hat{C}_{V|U_{1},\dots,U_{p}}^{-1} (\alpha | \hat{u}_{1},\dots,u_{p}) \Big) - \hat{F}_{Y}^{-1} \Big(C_{V|U_{1},\dots,U_{p}}^{-1} (\alpha | u_{1},\dots,u_{p}) \Big) \right| \\ &+ \sup_{\alpha} \left| F_{Y}^{-1} \Big(\hat{C}_{V|U_{1},\dots,U_{p}}^{-1} (\alpha | \hat{u}_{1},\dots,\hat{u}_{p}) \Big) - F_{Y}^{-1} \Big(C_{V|U_{1},\dots,U_{p}}^{-1} (\alpha | u_{1},\dots,u_{p}) \Big) \right| \leq \frac{3}{4} \epsilon \bigg| A \bigg). \end{split}$$

This conditional probability is equal to 1, since the first and second supremum are less than or equal to $\frac{1}{4}\epsilon$ by conditioning on A and due to the uniform consistency of \hat{F}_Y^{-1} . The last supremum is less than or equal to $\frac{1}{4}\epsilon$ by Bartle and Joichi (1961, Thm.2) on almost uniform convergence, applied to the continuous inverse distribution function F_Y^{-1} , and taking the measurable space to be the probability space. First, $P\bigg(\sup_{\alpha} \bigg| \Big(\hat{C}_{V|U_1,\dots,U_p}^{-1}(\alpha|\hat{u}_1,\dots,\hat{u}_p)\Big) - \Big(C_{V|U_1,\dots,U_p}^{-1}(\alpha|u_1,\dots,u_p)\Big)\bigg| \leq \frac{1}{4}\epsilon\bigg) = 1$, which can be argued similar to (12) using the uniform consistency and continuity of the inverse of the h-functions. Next, (12) states

$$P\bigg(\sup_{\alpha} \left| \hat{F}_{Y}^{-1} \Big(\hat{C}_{V|U_{1},...,U_{p}}^{-1} (\alpha | \hat{u}_{1}, ..., \hat{u}_{p}) \Big) - \hat{F}_{Y}^{-1} \Big(C_{V|U_{1},...,U_{p}}^{-1} (\alpha | u_{1}, ..., u_{p}) \Big) \right| \le \epsilon \bigg) = 1.$$

We conclude that $\hat{F}_Y^{-1}(\hat{C}_{V|U_1,\dots,U_p}^{-1}(\alpha|\hat{u}_1,\dots,\hat{u}_p))$ is uniformly strong consistent. To prove the weak consistency in 2, by Wied and Weißbach (2012); Silverman (1978), we only need to show

$$P\left(\left|\hat{F}_{Y}^{-1}\left(\hat{C}_{V|U_{1},\dots,U_{p}}^{-1}(\alpha|\hat{u}_{1},\dots,\hat{u}_{p})\right) - F_{Y}^{-1}\left(C_{V|U_{1},\dots,U_{p}}^{-1}(\alpha|u_{1},\dots,u_{p})\right)\right| \leq \epsilon\right) \to 1.$$

Using the same technique in Equation (12) and a similar argument for proving statement 2 of Proposition 4.1 with Theorem 2 on convergence in measure in Bartle and Joichi (1961), the weak consistency can be obtained.

References

- Akaike, H. (1973). Information theory and an extension of the maximum likelihood principle. In Petrov, B. and Csáki, F., editors, *Second International Symposium on Information Theory*, pages 267–281. Akadémiai Kiadó, Budapest.
- Athey, S., Tibshirani, J., Wager, S., et al. (2019). Generalized random forests. *The Annals of Statistics*, 47(2):1148–1178.
- Bartle, R. G. and Joichi, J. T. (1961). The preservation of convergence of measurable functions under composition. *Proceedings of the American Mathematical Society*, 12(1):122–126.
- Bartle, R. G. and Sherbert, D. R. (2000). Introduction to real analysis. Wiley New York.
- Bauer, A. and Czado, C. (2016). Pair-copula bayesian networks. *Journal of Computational and Graphical Statistics*, 25(4):1248–1271.
- Bedford, T. and Cooke, R. M. (2002). Vines–a new graphical model for dependent random variables. *The Annals of Statistics*, 30(4):1031–1068.
- Belloni, A. and Chernozhukov, V. (2011). ℓ 1-penalized quantile regression in high-dimensional sparse models. The Annals of Statistics, 39(1):82–130.
- Bernard, C. and Czado, C. (2015). Conditional quantiles and tail dependence. *Journal of Multivariate Analysis*, 138:104–126.
- Breiman, L. (2001). Random forests, machine learning 45. J. Clin. Microbiol, 2(30):199–228.
- Bühlmann, P. and van de Geer, S. (2011). Statistics for high-dimensional data: methods, theory and applications. Springer Science & Business Media.
- Chang, B. and Joe, H. (2019). Prediction based on conditional distributions of vine copulas. Computational Statistics & Data Analysis, 139:45–63.
- Charpentier, A., Fermanian, J.-D., and Scaillet, O. (2007). The estimation of copulas: Theory and practice. In Rank, J., editor, *Copulas: from theory to application in finance*, pages 35–64. London: Risk Books.
- Chen, X., Koenker, R., and Xiao, Z. (2009). Copula-based nonlinear quantile autoregression. *The Econometrics Journal*, 12:S50–S67.
- Cheng, C. (1995). Uniform consistency of generalized kernel estimators of quantile density. The Annals of Statistics, 23(6):2285–2291.

- Cheng, K.-F. (1984). On almost sure representation for quantiles of the product limit estimator with applications. Sankhyā: The Indian Journal of Statistics, Series A.
- Claeskens, G. and Hjort, N. (2003). The focused information criterion. *Journal of the American Statistical Association*, 98:900–916. With discussion and a rejoinder by the authors.
- Czado, C. (2019). Analyzing Dependent Data with Vine Copulas: A Practical Guide With R. Lecture Notes in Statistics. Springer International Publishing.
- Dua, D. and Graff, C. (2017). UCI machine learning repository.
- Durrett, R. (2010). Probability: theory and examples. Cambridge university press.
- Fenske, N., Kneib, T., and Hothorn, T. (2011). Identifying risk factors for severe childhood malnutrition by boosting additive quantile regression. *Journal of the American Statistical Association*, 106(494):494–510.
- Geenens, G. (2014). Probit transformation for kernel density estimation on the unit interval. *Journal of the American Statistical Association*, 109(505):346–358.
- Geenens, G., Charpentier, A., and Paindaveine, D. (2017). Probit transformation for nonparametric kernel estimation of the copula density. *Bernoulli*, 23(3):1848–1873.
- Gijbels, I. and Mielniczuk, J. (1990). Estimating the density of a copula function. Communications in Statistics-Theory and Methods, 19(2):445–464.
- Gneiting, T. and Raftery, A. E. (2007). Strictly proper scoring rules, prediction, and estimation. *Journal of the American Statistical Association*, 102(477):359–378.
- Grønneberg, S. and Hjort, N. L. (2014). The copula information criteria. *Scandinavian Journal of Statistics*, 41(2):436–459.
- Haff, I. H., Aas, K., and Frigessi, A. (2010). On the simplified pair-copula construction—simply useful or too simplistic? *Journal of Multivariate Analysis*, 101(5):1296–1310.
- Joe, H. (1996). Families of m-variate distributions with given margins and m (m-1)/2 bivariate dependence parameters. *Lecture Notes-Monograph Series*, pages 120–141.
- Joe, H. (1997). Multivariate models and multivariate dependence concepts. CRC Press.
- Jullum, M. and Hjort, N. L. (2017). Parametric or nonparametric: The FIC approach. Statistica Sinica, 27(3):951–981.
- Ko, V. and Hjort, N. L. (2019). Copula information criterion for model selection with two-stage maximum likelihood estimation. *Econometrics and Statistics*, 12:167 180.

- Ko, V., Hjort, N. L., and Hobæk Haff, I. (2019). Focused information criteria for copulas. Scandinavian Journal of Statistics, 46(4):1117–1140.
- Koenker, R. (2004). Quantile regression for longitudinal data. Journal of Multivariate Analysis, 91(1):74–89.
- Koenker, R. (2005a). Quantile Regression. Cambridge University Press.
- Koenker, R. (2005b). *Quantile Regression*. Econometric Society Monographs. Cambridge University Press.
- Koenker, R. (2011). Additive models for quantile regression: Model selection and confidence bandaids. *Brazilian Journal of Probability and Statistics*, 25(3):239–262.
- Koenker, R. and Bassett, G. (1978). Regression quantiles. *Econometrica: journal of the Econometric Society*.
- Kolmogorov, A. N. and Fomin, S. (1970). Introductory real analysis. Prentice-Hall.
- Komunjer, I. (2013). Quantile Prediction, Chapter 17 in Handbook of Financial Econometrics, edited by Yacine Ait-Sahalia and Lars Peter Hansen. Elsevier.
- Kraus, D. and Czado, C. (2017). D-vine copula based quantile regression. *Computational Statistics & Data Analysis*, 110:1–18.
- Li, A. H. and Martin, A. (2017). Forest-type regression with general losses and robust forest. In *International Conference on Machine Learning*, pages 2091–2100.
- Li, Q., Lin, J., and Racine, J. S. (2013). Optimal bandwidth selection for nonparametric conditional distribution and quantile functions. *Journal of Business & Economic Statistics*, 31(1):57–65.
- Meinshausen, N. (2006). Quantile regression forests. *Journal of Machine Learning Research*, 7(Jun):983–999.
- Nagler, T. (2018). kdecopula: An R package for the kernel estimation of bivariate copula densities. *Journal of Statistical Software*, 84(7):1–22.
- Nagler, T. (2019). vinereq: D-Vine Quantile Regression. R package version 0.7.0.
- Nagler, T., Schellhase, C., and Czado, C. (2017). Nonparametric estimation of simplified vine copula models: comparison of methods. *Dependence Modeling*, 5(1):99–120.
- Nagler, T. and Vatter, T. (2019a). kde1d: Univariate Kernel Density Estimation. R package version 1.0.2.

- Nagler, T. and Vatter, T. (2019b). rvinecopulib: High Performance Algorithms for Vine Copula Modeling. R package version 0.5.1.1.0.
- Noh, H., Ghouch, A. E., and Bouezmarni, T. (2013). Copula-based regression estimation and inference. *Journal of the American Statistical Association*, 108(502):676–688.
- Noh, H., Ghouch, A. E., and Van Keilegom, I. (2015). Semiparametric conditional quantile estimation through copula-based multivariate models. *Journal of Business & Economic Statistics*, 33(2):167–178.
- Parzen, E. (1962). On estimation of a probability density function and mode. *The Annals of Mathematical Statistics*, 33(3):1065–1076.
- R Core Team (2020). R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna, Austria.
- Ryzin, J. V. (1969). On strong consistency of density estimates. The Annals of Mathematical Statistics, 40(5):1765–1772.
- Schwarz, G. (1978). Estimating the dimension of a model. The Annals of Statistics, 6(2):461–464.
- Silverman, B. W. (1978). Weak and strong uniform consistency of the kernel estimate of a density and its derivatives. *The Annals of Statistics*, pages 177–184.
- Sklar, M. (1959). Fonctions de repartition an dimensions et leurs marges. *Publ. inst. statist.* univ. Paris, 8:229–231.
- Stoeber, J., Joe, H., and Czado, C. (2013). Simplified pair copula constructions—limitations and extensions. *Journal of Multivariate Analysis*, 119:101–118.
- Tepegjozova, M. (2019). D- and c-vine quantile regression for large data sets. Masterarbeit, Technische Universität München, Garching b. München.
- Van Keilegom, I. and Veraverbeke, N. (1998). Bootstrapping quantiles in a fixed design regression model with censored data. *Journal of Statistical Planning and Inference*, 69(1):115–131.
- Wen, K. and Wu, X. (2015). An improved transformation-based kernel estimator of densities on the unit interval. *Journal of the American Statistical Association*, 110(510):773–783.
- Wied, D. and Weißbach, R. (2012). Consistency of the kernel density estimator: a survey. Statistical Papers, 53(1):1–21.

- Xiao, Z. and Koenker, R. (2009). Conditional quantile estimation for generalized autoregressive conditional heteroscedasticity models. *Journal of the American Statistical Association*, 104(488):1696–1712.
- Yeh, I.-C. (1998). Modeling of strength of high-performance concrete using artificial neural networks. *Cement and Concrete research*, 28(12):1797–1808.
- Yu, K. and Jones, M. (1998). Local linear quantile regression. *Journal of the American* statistical Association, 93(441):228–237.
- Yu, K. and Moyeed, R. A. (2001). Bayesian quantile regression. *Statistics & Probability Letters*, 54(4):437–447.