Model selection in sparse high-dimensional vine copula models with application to portfolio risk

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Abstract
Vine copulas allow to build flexible dependence models for an arbitrary number of variables using only bivariate building blocks. The number of parameters in a vine copula model increases quadratically with the dimension, which poses new challenges in high-dimensional applications. To alleviate the computational burden and risk of over-fitting, we propose a modified Bayesian information criterion (BIC) tailored to sparse vine copula models. We show that the criterion can consistently distinguish between the true and alternative models under less stringent conditions than the classical BIC. The new criterion can be used to select the hyper-parameters of sparse model classes, such as truncated and thresholded vine copulas. We propose a computationally efficient implementation and illustrate the benefits of the new concepts with a case study where we model the dependence in a large stock stock portfolio.

Keywords: vine copula, BIC, sparsity, model selection, Value-at-Risk

1. Introduction

Following the 2008 financial crisis, academic research and public media identified unrealistic mathematical models for the dependence as one of its key causes.

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(Donnelly and Embrechts, 2010, Salmon, 2009). In the aftermath, modeling the
dependence between financial assets became a hot topic in finance and statistics.
One of most promising tools that emerged are vine copulas (Aas et al., 2009,
Bedford and Cooke, 2001). Vine copula models build the dependence structure
from bivariate building blocks, called pair-copulas. Each pair-copula captures the
dependence between a (conditional) pair of variables. Because each pair-copula
can be parametrized differently, vine copulas allow each pair to have a different
strength and type of dependence. This flexibility is the key reason why vine
copulas became so popular for modeling dependence between financial assets (see,
Aas, 2016, for a review).

The flexibility of vine copulas comes at the cost of a large number of model
parameters. A vine copula on $d$ variables consists of $d(d - 1)/2$ pair-copulas,
and each pair-copula can have multiple parameters. In financial applications,
the number of model parameters quickly exceeds the number of observations.
Suppose each pair-copula can have up to two parameters. Then a model for 50
assets has 2 450 possible parameters, a model for 200 has almost 20 000. On the
other hand, five years of daily stock returns consist of roughly 1 250 observations.

In such situations, there are two major challenges that we want to address: the
risk of overfitting and the computational burden to fit thousands of parameters.
Both issues make it desirable to keep the model sparse. A vine copula model is
called sparse when a large number of pair-copulas are the independence copula.
The key question is now which of the pair-copulas we should select as independence
copula.

The most common strategy is to select the pair-copula family by either AIC
or BIC (Akaike, 1974, Schwarz, 1978). The AIC is known to have a tendency of
selecting models that are too large (e.g., Claeskens and Hjort, 2008), contradicting
our preference for sparsity. The BIC on the other hand is able to consistently
select the true model, but only when the number of possible parameters grows
sufficiently slowly with the sample size $n$. As explained above, this assumption
should be seen critically in a high-dimensional context. Another unpleasantry is
that BIC is derived under the assumption that all models are equally likely. Under
this assumption, we expect only half of the pair-copulas to be independence, a
model we would not consider sparse.

We propose a new criterion called modified Bayesian Information Criterion
for Vines (mBICV) that addresses both issues and is specifically tailored to
vine copula models. It grounds on a modification of the prior probabilities that
concentrates on sparse models and is motivated by statistical practice. This
modification turns out to be enough to relax the restrictions on the rate at
which $d$ diverges. In particular, the criterion will be shown to be consistent
when $d = o(\sqrt{n \ln n})$. The idea behind the mBICV is similar to other modified
versions of the BIC that were developed for linear models (see, Zak-Szatkowska
and Bogdan, 2011).

The mBICV is useful for two things: selecting pair-copulas individually and
selecting hyper-parameters of sparse model classes. One such class are truncated
vine copulas (Brechmann et al., 2012, Kurowicka, 2011). A vine copula model
is called truncated if all pair-copulas that are conditioned on more than $M$ variables are set to independence. We further propose an alternative class of sparse models, \textit{thresholded vine copulas}. They induce sparsity by setting a pair-copula to independence when the encoded strength of dependence falls short of a threshold. This idea has been around for a long time and heavily used, but the threshold was commonly tied to the $p$-value of an independence test (see, e.g. Dissmann et al., 2013). In the more general form, the threshold is a free hyper-parameter. Such classes of sparse models give a computational advantage, since a substantial number of pair-copulas never have to be estimated.

2. Background on vine copulas

This section sets up the notation for vine copula models. For a more thorough introduction, we refer to Stöber and Czado (2012) and Joe (2014).

2.1. Copulas

Copulas are models for the dependence between random variables. By the theorem of Sklar (1959), one can express any multivariate distribution $F$ in terms of the marginal distributions $F_1, \ldots, F_d$ and a function $C$, called the copula:

$$F(x_1, \ldots, x_d) = C\{F_1(x_1), \ldots, F_d(x_d)\}, \quad \text{for all } x \in \mathbb{R}^d. \tag{1}$$

If $F$ is the distribution of a random vector $X$, then $C: [0, 1]^d \rightarrow [0, 1]$ is the distribution of $U = \{F_1(X_1), \ldots, F_d(X_d)\}$. This suggests a two-step approach for estimation. Suppose we have observed data $x_{i,j}, i = 1, \ldots, n, j = 1, \ldots, d$. Then we can proceed as follows: first, obtain estimates of the marginal distributions, say $\hat{F}_1, \ldots, \hat{F}_d$; second, set $u_{i,j} = \hat{F}_j(x_{i,j})$ and estimate estimate $C$ based on $u_{i,j}$, $i = 1, \ldots, n, j = 1, \ldots, d$. Assuming that derivatives exist, a formula similar to (1) can be derived for the density $f$ of $F$:

$$f(x_1, \ldots, x_d) = c\{F_1(x_1), \ldots, F_d(x_d)\} \times \prod_{k=1}^{d} f_k(x_k), \quad \text{for all } x \in \mathbb{R}^d,$$

where $c$ is the density of $C$ and called the \textit{copula density}, and $f_1, \ldots, f_d$ are the marginal densities.

2.2. Vine copulas

Vine copula models are based on the idea of Joe (1996) to decompose the dependence into a cascade of dependencies between (conditional) pairs. However, the decomposition is not unique. Bedford and Cooke (2002) introduced a graphical model, called \textit{regular vine}, that organizes all valid decompositions. A regular vine on $d$ variables consists of a sequence of linked trees $T_m = (V_m, E_m)$,
A vine copula model identifies each edge in the vine with a bivariate copula. This is best explained by an example. Figure 1 shows a regular vine tree sequence on five variables. The nodes in the first tree represent the random variables $U_1, \ldots, U_5$. The edges are identified with a bivariate copula (called pair-copula), where edge $(j_e, k_e)$ described the dependence between $U_{j_e}$ and $U_{k_e}$. In the second tree, the nodes are just the edges of the first tree. The edges are annotated by $(j_e, k_e; D_e)$ and describe the dependence between $U_{j_e}$ and $U_{k_e}$ conditional on $U_{D_e}$. In subsequent trees, the number of conditioning variables increases.

Bedford and Cooke (2001) showed that this naturally leads to a decomposition of the copula density $c$:

$$c(u) = \prod_{m=1}^{d-1} \prod_{e \in E_m} c_{j_e,k_e;D_e} \{ G_{j_e|D_e}(u_{j_e}|u_{D_e}), G_{k_e|D_e}(u_{k_e}|u_{D_e}); u_{D_e} \},$$

where $u_{D_e} := (u_{l})_{l \in D_e}$ and $G_{j_e|D_e}$ is the conditional distribution of $U_{j_e}|U_{D_e} = u_{D_e}$. The pair-copula density $c_{j_e,k_e;D_e}$ is the joint density of the bivariate conditional random vector

$$(G_{j_e|D_e}(U_{j_e}|U_{D_e}), G_{k_e|D_e}(U_{k_e}|U_{D_e})) | U_{D_e} = u_{D_e}.$$

Equation 2 holds for any copula density, but note that the functions $c_{j_e,k_e;D_e}$ take a third argument $u_{D_e}$. This indicates that, in general, the conditional dependence between $U_{j_e}$ and $U_{k_e}$ may be different for different values of $u_{D_e}$. To facilitate tractability of the models, it is customary to ignore this influence and simplify
the model to
\[ c(u) = \prod_{m=1}^{d-1} \prod_{e \in E_m} c_{j,e,D,e}(u_{j,e} | u_{D,e}), G_{k,e,D,e}(u_{k,e} | u_{D,e}) \].

In this case the pair copula density \( c_{j,e,D,e}(u_{j,e} | u_{D,e}), G_{k,e,D,e}(u_{k,e} | u_{D,e}) \) encodes the partial dependence between \( U_{j,e} \) and \( U_{k,e} \) conditional on \( U_{D,e} \) (cf., Gijbels et al., 2015, Spanhel and Kurz, 2015a). This simplifying assumption is often valid for financial data and even if it is violated, it may serve as a useful approximation to the truth. For further discussions, see Acar et al. (2012), Kraus and Czado (2017), Kurz and Spanhel (2017), Nagler and Czado (2016), Spanhel and Kurz (2015b), Stöber et al. (2013), Vatter and Nagler (2018), and references therein. Since tractability is vital in very high dimensions, we shall assume that the simplifying assumption holds for the remainder of this paper.

3. A modified BIC for sparse vine copula models

Consider a vine copula model with density \( c^n \) that is characterized by a finite dimensional parameter \( \eta \). We denote the number of parameters in the model by \( \nu \). To simplify our arguments, we assume that there is only one parameter per pair-copula, i.e., \( \eta = (\eta_e)_{e \in E_m,m=1,...,d-1} \), and that \( \eta_e \) is zero if and only if the pair-copula at edge \( e \) is independence. However, we formally distinguish between the number of non-zero parameters \( \nu \) and the number of non-independence pair-copulas \( q \) to maintain validity of the formulas in the general context.

The maximal model contains \( q_{\text{max}} = d(d - 1)/2 \) non-independence copulas. A sparse vine copula model contains many independence copulas and, thus, only few non-zero parameters. Let \( q = \# \{ \eta_e : \eta_e \neq 0, e \in E_1, \ldots, E_{d-1} \} \) be the number of non-independence copulas in the model. We speak of a sparse model if \( q \ll q_{\text{max}} \) or, asymptotically, \( q/q_{\text{max}} \to 0 \).

3.1. The BIC and why it is inappropriate for sparse models

Let \( u_i \in [0, 1]^d \), \( i = 1, \ldots, n \), be iid observations and \( \hat{\eta} \) be the maximum likelihood estimate of the model parameter. The \textit{Bayesian information criterion (BIC)} is defined as
\[ \text{BIC}(c^{\hat{\eta}}) = -2\ell(c^{\hat{\eta}}) + \hat{\nu} \ln n, \]
where \( \ell(c^{\hat{\eta}}) = \sum_{i=1}^{n} \ln c^{\hat{\eta}}(u_i) \) denotes the log likelihood and \( \hat{\nu} \) is the number of non-zero parameters in \( \hat{\eta} \). The lower the BIC, the more favorable we see a model.

The BIC of a vine copula model decomposes to
\[ \text{BIC}(c^{\hat{\eta}}) \]
\[= -2 \sum_{m=1}^{d-1} \sum_{e \in E_m} \sum_{i=1}^{n} \ln c^e_{j_e,k_e;D_e} \{ G^\eta_{j_e|D_e}(u_{i,j_e}; u_{i,D_e}) \}, G^\eta_{k_e|D_e}(u_{i,k_e}; u_{i,D_e}) \} + \hat{\nu}_e \ln n \]

where \(\hat{\nu}_e\) is the number of parameters for edge \(e\). On a first glance, this looks like the sum over the BICs for all individual edges. This would imply that the global BIC can be minimized by sequentially minimizing the BIC of individual pair-copulas. But there is a subtle issue: the log likelihood for an edge in tree \(e \in E_m, m \geq 2\) also depends on estimated parameters \(\eta_{e'}\), from previous trees \((e' \in E_{m'}, m' < m)\). However, if the model is correctly specified, this effect is asymptotically negligible as \(n\) tends to infinity. Hence, we can write more simply

\[\text{BIC}(c^\eta) \approx \sum_{m=1}^{d-1} \sum_{e \in E_m} \{ -2\ell(c^\eta_{j_e,k_e;D_e}) + \hat{\nu}_e \ln n \} = \sum_{m=1}^{d-1} \sum_{e \in E_m} \text{BIC}(c^\eta_{j_e,k_e;D_e}),\]

where \(\ell(c^\eta_{j_e,k_e;D_e})\) and \(\text{BIC}(c^\eta_{j_e,k_e;D_e})\) are the log likelihood and BIC of \(c^\eta_{j_e,k_e;D_e}\) when all parameters in lower trees are correctly specified. This representation justifies the common practice of selecting the pair-copulas individually in sequential estimation (e.g., Dissmann et al., 2013).

The BIC is derived from a Bayesian argument that states that the posterior log probability of a model is proportional to

\[-2\ell(e^\eta) + \hat{\nu} \ln n - 2 \ln \psi(e^\eta) + O_p(n), \quad (3)\]

where \(\psi(e^\eta)\) is the prior probability of the model \(e^\eta\) and the \(O_p(n)\) term is independent of the model choice. The simpler form of the BIC is then a consequence of the assumption that all models are equally likely \(a\) priori. A well-known result is that the BIC selects the true model with probability going to 1 as \(n\) tends to infinity while \(q_{\text{max}}\) (hence \(d\)) is fixed (e.g., Claeskens and Hjort, 2008). In high-dimensional vine copula models, \(q_{\text{max}}\) is often of the same order or much larger than \(n\). In such situations, “large \(n\), fixed \(d\)” asymptotics are at least questionable.

Since all models are equally likely, we expect the number of parameters in the true model to be \(q_{\text{max}}/2\) which stands in contrast to the sparsity assumption \(q/q_{\text{max}} \to 0\). In fact, one can show with arguments similar to those in Section 3.3 that the BIC cannot distinguish the true from an incorrect model when \(q_{\text{max}} \geq \sqrt{n \ln n}\) or equivalently \(d \geq \sqrt{n \ln n}\). In terms of the number of variables \(d\), this restriction is much more severe for vine copula models compared to (generalized) linear models, where the BIC has been studied most extensively (e.g. Zak-Szatkowska and Bogdan, 2011).

### 3.2. A modified criterion

Several authors considered modifications of the BIC to make it more suitable for high-dimensional problems (e.g., Bogdan et al., 2004, Chen and Chen, 2008,
The unifying idea is to adjust the prior probabilities in (3) such that sparse models are more likely than dense models. We shall follow the same path and assign each pair-copula a prior probability $\psi_e$ of not being independent.

More precisely, we assume that the indicators $I_e = 1(\eta_e \neq 0)$ are independent Bernoulli variables with mean $\psi_e$ and propose to choose $\psi_e = \psi_0^m$ for any edge in tree $m$, i.e., $e \in E_m$. The resulting prior probability of a vine copula model $c^\eta$ is

$$\psi(c^\eta) = \prod_{m=1}^{d-1} \psi_0^{mq_m} (1 - \psi_0^m)^{d-1-q_m},$$

where $q_m$ is the number of non-independence copulas in tree $m$. Now (3) suggests the criterion

$$\text{mBICV}(c^\eta) = -2\ell(c^\eta) + \hat{\nu} \ln n - 2 \sum_{m=1}^{d-1} \left\{ \hat{q}_m \ln \psi_0^m + (d - 1 - \hat{q}_m) \ln(1 - \psi_0^m) \right\},$$

where $\hat{q}_m$ is the number of non-independence copulas in tree $m$ of the fitted model $\hat{\eta}$.

The choice $\psi_e = \psi_0^m$ implies that higher-order pairs are more likely to be independent, a feature that is motivated by statistical practice. All popular structure selection algorithms try to capture strong dependence relationships in the first few trees (see, e.g., Brechmann and Joe, 2015, Dissmann et al., 2013, Müller and Czado, 2017). Although there is no guarantee, this typically leads to models where there is no or only little dependence left in higher trees. Further, the parameters of a vine copula are typically estimated sequentially starting from the first tree. Because estimation errors accumulate over the trees, estimates in higher trees are less reliable. And the less reliable the estimates are, the more conservatively we should choose our model.

The mBICV decomposes similarly to the BIC:

$$\text{mBICV}(c^\eta) \approx \sum_{m=1}^{d-1} \sum_{e \in E_m} \left\{ -2\ell(c_j,e;D_e c^\eta_e) + \hat{\nu}_e \ln n - 2 \left\{ I_e \ln \psi_0^m + (1 - I_e) \ln(1 - \psi_0^m) \right\} \right\} = \sum_{m=1}^{d-1} \sum_{e \in E_m} \text{mBICV}(c_j,e;D_e),$$

suggesting that mBICV is a suitable criterion for sequential selection of the pair-copulas.

Under the prior used for the mBICV, $q_m$ is a binomial experiment of $(d - m)$ trials with success probability $\psi_0^m$. Therefore, the expected number of non-independence copulas in tree $m$ is $E(q_m) = (d - m)\psi_0^m$ and the expected total
number is

\[ E(q) = \sum_{m=1}^{d-1} (d - m) \psi_m^m = \frac{\psi_0^d + d(1 - \psi_0) - 1}{(1 - \psi_0)^2}. \]

Recalling that \( q_{\text{max}} \sim d^2 \), we obtain \( E(q)/q_{\text{max}} \to 0 \) and, thus, expect the true model to be sparse.

### 3.3. Properties

We will argue that the mBICV can consistently distinguish between a finite number of models provided that \( d = o(\sqrt{n \ln n}) \), which is a less stringent condition compared to BIC. We should emphasize that this is only a weak form of consistency: when \( d \to \infty \), this does not automatically imply that the criterion finds the best among all possible candidate models. Because the number of possible candidates grows rapidly with \( d \), results on this stronger form of consistency are considerably more difficult to derive and have only recently emerged in the simpler context of linear models (Fan and Tang, 2013, Wang et al., 2009, Wang, 2011).

Owing to the applied focus of this article, we will not concern ourselves with regularity conditions required for consistency of (sequential) maximum-likelihood analysis, but simply work under the assumption that \( \| \hat{\eta} - \eta \| = o_p(1) \). Even if the model is correctly specified, this is no longer a consequence of the regularity conditions given in Hobæk Haff (2013) when \( d \) diverges with \( n \). To our best knowledge, the consistency of parameter estimates in copula models of diverging size has not been investigated so far. Results from other model classes Liang and Du (2012), Wang (2011) give hope that consistency continues to hold, but likely with a slower rate. However, we acknowledge that this leaves an open end to the arguments given below.

We start by approximating error probabilities for individual pair-copulas. Our null hypothesis is that the true pair-copula at edge \( e \in E_m \) corresponds to independence, i.e., \( \eta_e = 0 \). Denote by \( \alpha_{n,e} \) the probability of a type I error (selecting the non-independence model \( \eta_e \neq 0 \) although the true model has \( \eta_e = 0 \)), i.e.,

\[ \alpha_{n,e} = P\{\text{mBICV}(\hat{c}_{j_e,k_e,D_e}) < \text{mBICV}(c_{j_e,k_e,D_e}^0) \mid \eta_e = 0\}, \]

and by \( \beta_{n,e} \) the probability of a type II error (selecting the independence model \( \eta_e = 0 \) although the true model has \( \eta_e \neq 0 \)), i.e.,

\[ \beta_{n,e} = P\{\text{mBICV}(\hat{c}_{j_e,k_e,D_e}) > \text{mBICV}(c_{j_e,k_e,D_e}^0) \mid \eta_e \neq 0\}. \]

**Proposition 1.** It holds

\[ \alpha_{n,e} = 1 - 2\Phi\left\{ \sqrt{\nu_e \ln n} - 2 \ln \psi_0^m + 2 \ln(1 - \psi_0^m) \right\} + o(1), \]
\[
\beta_{n,e} = 1 - \Phi\left\{ \sqrt{n} \ell^*(c_{j,e}^{m_e}; D_e) - \frac{\widehat{\nu} \ln n - 2 \ln \psi_0^m + 2 \ln(1 - \psi_0^m)}{2\sqrt{n}\sigma_e} \right\} + o(1),
\]
where \( \Phi \) denotes the standard normal distribution function,
\[
\ell^*(c_{j,e}^{m_e}; D_e) = \int_{[0,1]^2} c_{j,e}^{m_e}(u,v) \ln c_{j,e}^{m_e}(u,v) dudv
\]
is the mutual information (or entropy) and
\[
\sigma_e^2 = \int_{[0,1]^2} c_{j,e}^{m_e}(u,v)\left\{ \ln c_{j,e}^{m_e}(u,v) \right\}^2 dudv - \ell^*(c_{j,e}^{m_e}; D_e)^2.
\]
The proof is given in Section A.1. The type I error probability \( \alpha_{n,e} \) decreases with \( \psi_0 \), the parameter controlling the prior probability of a non-independence model. Lower values shift our expectations to sparser models and the probability of overfitting decreases. Furthermore, \( \alpha_{n,e} \) is decreasing in the tree level \( m \), because the mBICV expects more independence copulas at higher tree levels. The type II error probability \( \beta_{n,e} \) decreases in the mutual information \( \ell^*(c_{j,e}^{m_e}; D_e) \) which confirms our intuition that stronger dependence relationships are easier to detect. Further, \( \beta_{n,e} \) converges to a strictly positive constant when \( \ell^*(c_{j,e}^{m_e}; D_e) \sim 1/\sqrt{n} \), indicating an opportunity for power analysis under local alternatives.

We should emphasize that the error probabilities in Proposition 1 are only valid asymptotically, and usually require large sample sizes to be realistic. Nevertheless, their qualitative interpretation remains valid even for small samples. More important for our following result is that Proposition 1 quantifies the rate with which the error probabilities vanish as \( n \to \infty \). Thanks to the decomposition (4), the error probabilities in Proposition 1 can now be aggregated over the whole vine. Consistency of the mBICV is then a consequence of a bound on Gaussian tail probabilities.

**Theorem 1.** With probability tending to one, the mBICV selects the true vine copula model among a finite number of alternatives when \( d = o(\sqrt{n \ln n}) \).

The proof, given in Section A.2, suggests that one can relax the condition on \( d \) further by replacing \( \ln n \) in the mBICV penalty by a sequence that diverges faster. For example, replacing \( \ln n \) with \( \ln(nd) \) and using the same arguments, we expect consistency when \( d = o(n \ln n) \). However, we will not pursue this path any further and turn to more practical issues.

### 4. Special classes of sparse vine copula models and their selection

The mBICV can be used to decide which pair-copulas in the model are set to independence. But in order to calculate the mBICV, one first needs to
estimate a model. In high-dimensional vine copula models, there is a huge number of pair-copulas. Estimating all of them will be computationally demanding. This predicament is solved by focusing on sparse model classes that set a large proportion of pair-copulas to independence before a model is fit. Below we discuss two such classes, truncated and thresholded vine copula models. Both classes have a sparsity inducing hyper-parameter that can be selected by mBICV.

4.1. Truncated vine copulas

Truncated vine copula models induce sparsity by setting all pair-copulas after a certain tree level \( M \in \{1, \ldots, d-1\} \) to the independence copula. The lower the truncation level \( M \), the higher the degree of sparsity: an \( M \)-truncated vine copula model allows for only \( M(2d-M-1)/2 \) non-independence copulas. Since the density of the independence copula is 1 everywhere, the density of an \( M \)-truncated vine copula model can be written as

\[
c(u) = \prod_{m=1}^{M} \prod_{e \in E_m} c_{j_e,k_e:D_e} \{G_{j_e:D_e}(u_{j_e:D_e}), G_{k_e:D_e}(u_{k_e:D_e})\}.
\]

(5)

The logic behind truncated vine copulas is closely related to the structure selection heuristic of Dissmann et al. (2013). Its goal is to capture most of the dependence in the first couple of trees. If this would allow to capture all dependence in the first \( M \) trees, the truncated model arises naturally. If this is not the case, one can at least hope that the dependence in higher trees is practically irrelevant.

4.2. Thresholded vine copulas

The idea of thresholded regular vines is different. The ultimate goal is to set all conditional pair-copulas that are practically irrelevant to independence. Arguably, ‘practical relevance’ is a vague concept and we need to rely on a proxy measure for it. A natural choice are measures for the strength of dependence. On such measure is Kendall’s \( \tau \). It is a measure of concordance and, as such, is a functional of the copula only. In particular, it does not depend on the marginal distributions (see, e.g., Nelsen, 2006). In the remainder of this article we take Kendall’s \( \tau \) as our target measure, although other choices are equally valid.

Similar to the truncation level \( M \) before, thresholded vine copulas have a hyper-parameter \( \theta \), called threshold. Denote the Kendall’s \( \tau \) associated with the pair-copula \( c_{j_e,k_e:D_e} \) by \( \tau_e \) and define \( E_{m}^{\theta} = \{e \in E_m : |\tau_e| > \theta\} \) for any edge set \( E_m \) in the vine. Then the the density of a thresholded vine copula model becomes

\[
c(u) = \prod_{m=1}^{d-1} \prod_{e \in E_{m}^{\theta}} c_{j_e,k_e:D_e} \{G_{j_e:D_e}(u_{j_e:D_e}), G_{k_e:D_e}(u_{k_e:D_e})\}.
\]

(6)
The number of non-independence copulas in the model can be controlled by the threshold parameter $\theta$. But in contrast to the truncated model, the number also depends on the actual dependence in the random vector $U$. To illustrate this, we fix $\theta$ and consider a few interesting boundary cases:

- If $|\tau_e| > \theta$ for all $e \in E_1, \ldots, E_{d-1}$, the thresholded model is equal to the full model.
- If for $1 \leq M < d - 1$, it holds $|\tau_e| > \theta$ for all $e \in E_1, \ldots, E_M$ and $|\tau_e| \leq \theta$ for all $e \in E_M, \ldots, E_d$, the thresholded model is equal to the $M$-truncated model.
- If $|\tau_e| \leq \theta$ for all $e \in E_1, \ldots, E_{d-1}$, the thresholded model contains only independence pair-copulas and, thus, is equal to the independence model.

The thresholded model generalizes the truncated model: whenever a model is truncated, it can be represented as a thresholded model with $\theta < \min_{e \in \{E_1, \ldots, E_{d-1}\}} |\tau_e|$. If this is not the case, the thresholded model can still adapt to the sparsity patterns of the truth and is therefore more flexible.

The thresholding idea is not new. Several authors used a similar idea (e.g., Brechmann et al., 2012, Czado et al., 2012, Dissmann et al., 2013), but tied the value of $\theta$ to the critical value of a significance test for an empirical version of Kendall’s $\tau$. The idea is to perform a statistical test for independence and set the pair-copula to independence whenever the null hypothesis cannot be rejected. This procedure is only heuristic: in general, the test based on the empirical Kendall’s $\tau$ is not consistent for the null hypothesis of independence and there is no correction for multiple testing. Treating the threshold as a free hyper-parameter brings additional flexibility and allows to tailor the threshold to a specific application.

### 4.3. Automatic hyper-parameter selection based on mBICV

The mBICV allows us to compare models for various thresholds and decide which is the best. The natural way to select the best model is to fit several models for a fine grid of $\theta$ values and select the one with lowest mBICV. This strategy can be extremely time-consuming in high dimensions, where a single fit of the full model often takes hours. An advantage of sparse vine copula models is that only a fraction of the pair-copulas needs to be estimated (all others are set to independence). This motivates the following strategy to automatically select the threshold parameter $\theta$:

1. Start with a large threshold and fit the model.
2. Reduce the threshold and fit a new model.
3. If the new model improves the mBICV, continue with 2. Stop if there is no improvement.
This approach has several computational advantages. Since we start with a large threshold, only a few pair-copulas have to be estimated in the first iteration. For all following iterations, only a few pair-copulas will change from one iteration to the next. By keeping the result from the previous fit in memory, we can re-use most of the fitted pair-copulas and only need to estimate a few additional parameters. Upon termination of the algorithm, most of the non-independent pair-copulas have only been estimated once. Thus, the overall time spent on model fitting and selection will be comparable to the time required for fitting only the mBICV-optimal model. Depending on the dimension $d$ and the level of sparsity in the data, this can be several times faster than fitting the full model.

The same strategy can be used for selecting the truncation level: start with a low truncation level and gradually add more tree levels until the mBICV fails to improve. It is similarly straightforward to select the threshold and the truncation level simultaneously by using an outer loop for the threshold and an inner loop for the truncation level.

4.4. Implementation

We propose to reduce the threshold in a data-driven manner. For the initial threshold, we choose the maximum of all pair-wise absolute empirical Kendall’s $\tau$. In this case, the initial model consists of only independence copulas and mBICV = 0. To reduce the threshold from one iteration to the next, we choose the threshold such that about 5% of the previously independent pairs may become non-independent in the new model. To be more precise, let $\theta_k$ denote the threshold in iteration $k$, $T_k = \{\tau_e : |\tau_e| \leq \theta_k\}$ and $N_k = |T_k|$. Then we set $\theta_{k+1}$ to the $\lceil 0.05N_k \rceil$-th largest value in $T_k$.

To check if a pair-copula from the last iteration can be re-used, we need to check if the pseudo-observations have changed. In very high-dimensional models it is also important to make efficient use of memory. We should not store the pseudo-observations of each conditional pair in the vine. Because of the large number of pair-copulas, this will quickly exceed the memory of customary computers. Instead, one can store a summary statistic (like a weighted sum) of the pseudo-observations and only check if this summary statistic has changed.

The selection algorithm is implemented in C++ and will shortly be published as part of the vinecopulib library and its interface to R (Nagler and Vatter, 2018).

5. Case study: Modeling dependence in a large stock portfolio

To illustrate the concepts introduced in the previous section, we use the new methodology to model the dependence between a large number of stocks. Our data set contains daily stock returns from the S&P 100 constituents from the period of 1 January 2010 to 31 December 2016 ($n = 1756$). Only stocks that were traded over the whole period are included, leaving us with $d = 96$. Note that
we have \( d < \sqrt{n \ln n} \approx 115 \), which is in line with the condition \( d = o(\sqrt{n \ln n}) \) derived in Section 3.3. On the other hand, the BIC is likely inappropriate since \( d \gg \sqrt{n \ln n} \approx 11 \).

5.1. Modeling

Models for the marginal time series

A stylized fact about stock returns is that the squared time-series exhibit strong inter-serial dependence. A popular model that takes this fact into account is the ARMA-GARCH model (see, e.g., Francq and Zakoian, 2011). Let \( x_{t,k}, t = 1, \ldots, T \) be the returns of stock \( k \) at time \( t \). The ARMA(1, 1)-GARCH(1, 1) model for this time series is

\[
\begin{align*}
x_{t,k} &= \mu_k + \phi_k x_{t-1,k} + \psi_k a_{t-1,k} + a_{t,k} \\
a_{t,k} &= \sigma_{t,k} \epsilon_{t,k} \\
\sigma_{t,k}^2 &= \omega_k + \beta_k \sigma_{t-1,k}^2 + \alpha_k \epsilon_{t-1,k}^2,
\end{align*}
\]

where \( \epsilon_{t,k} \) are iid Student t variables with zero mean, unit variance, and \( \nu_k \) degrees of freedom. The parameters of this model can be estimated with maximum likelihood, for example using the R package \texttt{fGarch} (Wuertz et al., 2016). In addition to parameter estimate, this also gives us estimates \( \hat{\epsilon}_{t,k} \) and \( \hat{\sigma}_{t,k} \) of the unobserved innovation process \( \epsilon_{t,k} \) and volatility process \( \sigma_{t,k} \).

Dependence model

The cross-sectional dependence between stocks is modeled by a vine copula underlying the residual time series \( \epsilon_t = (\epsilon_{t,1}, \ldots, \epsilon_{t,d}), t = 1, \ldots, T \). We assume that the dependence in \( \epsilon_t \) is induced by a vine copula model \( C \). Define \( u_{t,k} = \Psi(\epsilon_{t,k}; \nu_k) \), where \( \Psi(\cdot; \nu_k) \) is the cumulative distribution function of a Student t distribution with zero mean, unit variance, and degrees of freedom \( \nu_k \). Then, \( u_t = (u_{t,1}, \ldots, u_{t,d}), t = 1, \ldots, T \), are independent observations from a random vector with distribution \( C \).

In practice, we do not observe \( u_t \). Suppose that \( \hat{\epsilon}_t \) are the observed residual series and \( \hat{\nu}_k \) are the estimated degrees of freedom parameters of the fitted ARMA-GARCH models. Then \( \hat{u}_{t,k} = \Psi(\hat{\epsilon}_{t,k}; \hat{\nu}_k), k = 1, \ldots, d, t = 1, \ldots, T \), act as pseudo-observations of the copula \( C \). Based on these, a thresholded vine copula model can be estimated for any fixed value of the threshold \( \theta \). We only allow for parametric pair-copulas, and choose the family of each pair-copula from the Gaussian, Student t, Clayton, Gumbel, Frank, and Joe families by the mBICV criterion. The prior probability \( \psi_0 \) is set to 0.84, which asymptotically controls the type I error for a pair-copula in the first tree at a level of approximately 5% (see Proposition 1). The vine structure is selected by the algorithm of Dissmann et al. (2013).
5.2. Illustration of the new concepts

To assess the influence of the sparsity hyper-parameters in thresholded and truncated vine copula models, we shall first estimate the marginal and dependence models using the full data from 1 January 2010 to 31 December 2016. This allows us to make a direct connection between the hyper-parameters and the mBICV, which helps us to understand their relation. In particular, we fit vine copula models to the pseudo-observations $\hat{u}_t$, $t = 1, \ldots, T$, for a range of values for the hyper-parameters and investigate how they affect the mBICV, model sparsity, and computation time. The results are shown in Figure 2, where thresholded models are in the left and truncated models in the right column.

mBICV optimal hyper-parameters

The mBICV is shown in the upper panel of Figure 2. We observe that the mBICV is a decreasing function of the threshold $\theta$ and becomes flat around $\theta = 0.04$. At this stage almost all pair-copulas that would be selected by mBICV are already contained in the model and further reducing the threshold does not improve the fit. The value $\theta_{\text{auto}} \approx 0.037$ is the threshold selected by the automatic algorithm proposed in Section 4. It is small enough to include the relevant non-independence copulas, but allows to omit fitting models for many other pairs that would be selected out anyway. The threshold that would result from a Kendall’s $\tau$ based independence test at the 5% level is $\theta_{\tau} \approx 0.31$, which is slightly smaller than the one suggested by mBICV.

As we would expect, the mBICV increases with the truncation level, but flattens around $M = 25$. The truncation level selected by the automatic procedure is $M_{\text{auto}} = 28$. The fact that the mBICV reduces further until around $M = 65$ indicates that there were several trees full of independence copulas before additional non-independence copulas enter the model. In this sense, the automatic procedure stopped to early, but the loss in mBICV compared to $M = 65$ is only marginal.

The two models $\theta_{\text{auto}}$ and $M_{\text{auto}}$ end up with approximately equal values for mBICV. Hence, none of the two models classes can be regarded better than the other. However, this conclusion is only valid for this particular data set. Since the class of thresholded vine copulas nests the class of truncated models, thresholded models will likely outperform truncated ones in other situations.

Level of sparsity

The sparsity of a vine copula model is characterized by the number of independence copulas. The middle panel in Figure 2 shows the proportion of non-independence copulas among all pair copulas ($q/q_{\text{max}}$) in the model as function of the hyper-parameters.

The higher the threshold, the more independence copulas the model contains. Again around $\theta = 0.04$, the proportion has a kink and stays flat for lower values. The automatic selection procedure ends up slightly below this kink. At this stage,
Figure 2: The mBICV, proportion of non-independence copulas, and time required to fit the model as functions of the sparsity hyper-parameters. The dotted lines indicate the values of the hyper-parameter that have been selected by the automatic selection procedure from Section 4.3.
roughly 82% of the pairs are independent, indicating a sparse model. On the other hand, the proportion of non-independence copulas increases with the truncation level and smoothly flattens around $M_{\text{auto}} = 28$, where, again, approximately 82% of the pairs are independent.

**Computation time**

As explained in Section 4, sparse vine copulas have a side benefit in terms of computation time, because a large number of pair-copulas are never estimated (but directly set to independence). We can see this effect in the lower panel of Figure 2, where the threshold is plotted against the time required to fit the model.\(^1\)

The larger the threshold, the less time it takes to fit the model. The full model ($\theta = 0$) takes 3.6 hours; the mBICV-optimal model only takes around 1 hour. However, there is an overhead for selecting the threshold. Finding the optimal threshold and fitting the model takes 1.7 hours in total, which is still considerably faster than fitting the full model. The difference between the two can be expected to increase with the dimension and level of sparsity. Similarly, truncated models with a larger truncation level take more time to fit. The model selected by the automatic procedure ($M = 28$) takes 1.8 hours which is similar to selecting the optimal thresholded model (for truncated models, there is no overhead for mBICV selection).

### 5.3. Out-of-sample Value-at-Risk forecasts

We now turn to a more realistic setup and analyze the models’ ability to accurately forecast the Value-at-Risk out-of-sample. We fit the marginal and vine copula

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\(^1\)All times were recorded on a single thread of a 8-way Opteron (Dual-Core, 2.6 GHz) CPU with 64GB RAM.
Table 1: Exceedance frequencies of out-of-sample Value-at-Risk forecast and \( p \)-values of the conditional coverage test of Christoffersen (1998) for three models: the one selected by BIC, and thresholded and truncated models selected by the procedure described in Section 4.

|        | BIC | \( \theta_{\text{auto}} \) | \( M_{\text{auto}} \) |
|--------|-----|-----------------|----------------|
| exceedances | 0.042 0.007 | 0.044 0.009 | 0.043 0.009 |
| \( p \)-value  | 0.169 0.114 | 0.319 0.302 | 0.212 0.302 |

Table 1: Exceedance frequencies of out-of-sample Value-at-Risk forecast and \( p \)-values of the conditional coverage test of Christoffersen (1998) for three models: the one selected by BIC, and thresholded and truncated models selected by the procedure described in Section 4.

models on a training period period \( t = t^* - T_{\text{train}} \), \ldots, \( t^* \), and predict the Value-at-Risk for subsequent days \( t = t^* + 1 \), \ldots, \( t^* + T_{\text{test}} \). To ensure that a reasonable amount of data is available, we choose \( T_{\text{train}} = 1260 \) (five years) and \( T_{\text{test}} = 252 \) (one year). After each year, the marginal and vine copula models are fit again to the previous five years of data. To make the results comparable to the in-sample analysis, we want to use the same period for evaluating out-of-sample forecasts. To achieve this, we augment the data by five more years of data for the period 2005-2009. Four more stocks have to be dropped, leaving us with \( d = 92 \).

The fitted models can be used to forecast the one-day-ahead Value-at-Risk (VaR) of an equally weighted portfolio of all \( d = 96 \) stocks. The portfolio return at time \( t \) is then \( y_t = d^{-1} \sum_{k=1}^{d} x_{t,k} \). The theoretical \( \alpha \)-level portfolio VaR on day \( t + 1 \) is defined as the \((1 - \alpha)\)-quantile of \( y_{t+1} \),

\[
\text{VaR}_{t+1,\alpha} = \inf\{y \in \mathbb{R}: P(y_{t+1} \leq y) \geq 1 - \alpha\}, \quad \alpha \in (0, 1).
\]

Our goal is to forecast \( \text{VaR}_{t+1,\alpha} \), based on fitted marginal and vine copula models, and only using past observations of the processes \( \hat{\epsilon}_t \) and \( \hat{\sigma}_t \). We proceed as follows:

1. Simulate \( u_{t+1}^{(r)} \), \( r = 1, \ldots, R = 10^6 \), from the fitted vine copula model.

2. For all \( k = 1, \ldots, d, r = 1, \ldots, R \), set

\[
\begin{align*}
\hat{\epsilon}_{t+1,k}^{(r)} &= \Psi^{-1}(u_{t+1}^{(r)}; \hat{\nu}_k), \\
\hat{\sigma}_{t+1,k} &= \hat{\omega}_k + \hat{\beta}_k \hat{\sigma}_{t,k}^2 + \hat{\alpha}_k \hat{\epsilon}_{t,k}^2, \\
x_{t+1,k}^{(r)} &= \hat{\mu}_k + \hat{\phi}_k x_{t,k} + \hat{\psi}_k \hat{\sigma}_{t,k} + \hat{\sigma}_{t+1,k} \hat{\epsilon}_{t+1,k}^{(r)}, \\
y_{t+1}^{(r)} &= \frac{1}{d} \sum_{k=1}^{d} x_{t+1,k}^{(r)}.
\end{align*}
\]

3. The forecast \( \hat{\text{VaR}}_{t+1,\alpha} \) is the empirical \( \alpha \)-quantile of \((y_{t+1}^{(r)})_{r=1,\ldots,R}\).

Figure 3 shows the observed time series \( y_t \) along with VaR predictions from an exemplary model.

In the following we focus on three models: thresholded and truncated models selected by the automatic procedure from Section 4 (\( \theta_{\text{auto}} \) and \( M_{\text{auto}} \)), and the
model selected by BIC. We consider two common levels for the Value-at-Risk, $\alpha = 0.95, 0.99$. The second row of Table 1 shows the frequencies with which the Value-at-Risk forecasts were exceeded. For an optimal model we expect these frequencies to be $1 - \alpha$, which (along with independence of exceedance indicators) is the null hypothesis of the conditional coverage test (Christoffersen, 1998). Corresponding $p$-values are listed in the third row.

We observe that all models show exceedance frequencies close to our expectation. All methods seem to overestimate the Value-at-Risk by a small margin. The two sparse models are slightly closer, with $\theta_{\text{auto}}$ being closest. This is also reflected in the $p$-values, which indicate that no model can be rejected. However, the two sparse models are not only less complex, they were also substantially faster to fit. These two benefits would become even more striking for portfolios of larger size.

6. Conclusion

This article was concerned with model selection in high-dimensional vine copula models. We proposed the mBICV as a selection criterion tailored to sparse vine copula models. It can be used to sequentially select individual pair-copula or automatically select hyper-parameters in sparse model classes. The benefits of the mBICV were illustrated by a case study modeling the dependence in a large stock portfolio. The mBICV-optimal sparse models were shown to produce valid out-of-sample forecasts for the Value-at-Risk and to be computationally more efficient than models selected by BIC.

We took a first step towards “large $n$, diverging $d$” asymptotics in vine copula models by showing that the selection criterion is consistent when $d = o(\sqrt{n \ln n})$. However, our arguments require a (so far) unverified assumption on the consistency of parameter estimates as $d \to \infty$. Result from other model classes give hope that this assumption is valid under reasonable conditions, although we should expect a slower convergence rate compared to “fixed $d$” asymptotics. A formal study of such properties is an interesting direction for future research.

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A. Proofs

A.1. Proof of Proposition 1

First note that the independence model, \( c^0_{j_e,k_e; D_e} \equiv 1 \), yields

\[
mBICV(c^0_{j_e,k_e; D_e}) = -2 \ln(1 - \psi^m_0).
\]

Therefore, the alternative model \( c^\hat{\eta}_{j_e,k_e; D_e} \) is selected if

\[
2\ell(c^\hat{\eta}_{j_e,k_e; D_e}) > \hat{\nu}_e \ln n - 2 \ln \psi^m_0 + 2 \ln(1 - \psi^m_0). \tag{7}
\]

We start by approximating the type I error \( \alpha_{n,e} \). Since \( \ell(c^0_{j_e,k_e; D_e}) = 0 \), the left hand side of (7) is a classical likelihood ratio statistic and, as \( n \to \infty \), converges in distribution to a \( \chi^2_1 \) random variable if the null hypothesis of independence is true. Hence,

\[
\alpha_{n,e} = 2P\left(Z > \sqrt{\hat{\nu}_e \ln n - 2 \ln \psi^m_0 + 2 \ln(1 - \psi^m_0)}\right) + o(1),
\]

where \( Z \sim N(0, 1) \).

For the type II error, we have

\[
\beta_{n,e} = P\left\{2\ell(c^\hat{\eta}_{j_e,k_e; D_e}) < \hat{\nu}_e \ln n - 2 \ln \psi^m_0 + 2 \ln(1 - \psi^m_0) \mid \eta_e \neq 0\right\}.
\]

A Taylor expansion around \( \eta_e \) implies \( \ell(c^\hat{\eta}_{j_e,k_e; D_e}) = \ell(c^{\eta_e}_{j_e,k_e; D_e}) + o_p(\sqrt{n}) \). In combination with the central limit and Slutsky’s lemma we obtain

\[
\sqrt{n}\left\{\frac{1}{n}\ell(c^\hat{\eta}_{j_e,k_e; D_e}) - \ell^*(c^{\eta_e}_{j_e,k_e; D_e})\right\} \overset{d}{\to} N(0, \sigma^2_e),
\]

where \( \sigma^2_e = \text{var}_{\eta_e} \{\ln c^{\eta_e}_{j_e,k_e; D_e}(U, V)\} \). For large \( n \), this implies

\[
\beta_{n,e} = P\left\{Z > \sqrt{n}\ell^*(c^{\eta_e}_{j_e,k_e; D_e}) - \frac{\hat{\nu}_e \ln n - 2 \ln \psi^m_0 + 2 \ln(1 - \psi^m_0)}{2\sqrt{n}\sigma_e}\right\} + o(1). \quad \square
\]

A.2. Proof of Theorem 1

We first bound \( \alpha_{n,e} \) and \( \beta_{n,e} \) using the following tail approximation for normal variates:

\[
P(Z > z) \leq \frac{1}{\sqrt{2\pi}} \frac{1}{x} \exp\left(-\frac{x^2}{2}\right).
\]

This gives

\[
\alpha_{n,e} \leq \frac{2}{\sqrt{2\pi n}} \frac{\psi^m_0 (1 - \psi^m_0)^{-1}}{\sqrt{\ln n - 2 \ln \psi^m_0 + 2 \ln(1 - \psi^m_0)}} + o(1) \tag{8}
\]
and by using
\[ \frac{\hat{\nu} \ln n - 2 \ln \psi_0^m + 2 \ln (1 - \psi_0^m)}{2\sqrt{n}\sigma} = o(1), \]
we obtain
\[ \beta_{n,e} \leq \frac{1}{\sqrt{2\pi n}} \exp \left\{ -nE^* \left( e_{j_e,k_e:D_e}^\eta \right)^2 / 2 \right\} + o(1). \]

We now consider the family-wise error rates (FWER), i.e., the probability of selecting the wrong model for at least one among a collection of edges. Denote by \( \alpha_n \) the FWER of a type error over the whole vine copula model and similarly \( \beta_n \) for the type II error. Using Bonferroni’s inequality, we get
\[ \alpha_n \leq \sum_{m=1}^{d-1} \sum_{e \in E_m : \eta_e = 0} \alpha_{n,e}, \quad \beta_n \leq \sum_{m=1}^{d-1} \sum_{e \in E_m : \eta_e \neq 0} \beta_{n,e}. \]

By expanding the sum and using (8), we obtain \( \alpha_n = O(d/\sqrt{n \ln n}) \). Thus, the mBICV consistently selects independence pair-copulas when \( d = o(\sqrt{n \ln n}) \). Similarly, using (9), we get \( \beta_n = O(d^2 e^{-n} / \sqrt{n}) \). Hence, the mBICV consistently selects non-independence pair-copulas if \( d = o(e ^{n/2} \sqrt{n}) \). Combining the results for type I and type II error proves our claim.

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