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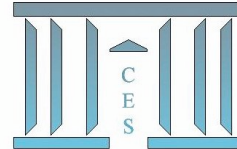


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New Prospects on Vines

Dominique GUEGAN, Pierre André MAUGIS

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New Prospects on Vines

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Abstract

In this paper, we present a new methodology based on vine copulas to estimate multivariate distributions in high dimensions, taking advantage of the diversity of vine copulas. Considering the huge number of vine copulas in dimension n , we introduce an efficient selection algorithm to build and select vine copulas with respect to any test T . Our methodology offers a great flexibility to practitioners to compute VaR associated to a portfolio in high dimension.

Keywords: Vine copulas - Multivariate copulas - Model Selection - VaR

1 Introduction

For almost ten years now, copulas have been used in econometrics and finance. They became an essential tool for pricing complex products, managing portfolios and evaluating risks in banks and insurance companies. For instance, they can be used to compute VaR (Value at Risk) and ES (Expected shortfall), Artzner et al. (1997). Moreover, copulas appear to be a very flexible tool, allowing for semi-parametric estimation, fast parameter optimisation and time varying parameters. These advantages make them a very interesting tool, although one major shortcoming is their use in high dimensions. Indeed, elliptical copulas can be expended to higher dimension, but they are unable to represent financial tail dependences (Patton, 2009), and the Archimedean copulas are not satisfactory as models to describe multivariate dependence in dimensions higher than 2 (Joe, 1997). In this paper we present a solution to this problem by using the vine copulas.

Recently, Aas et al. (2009) produced a seminal paper presenting a method to build high dimension copulas using pair-copulas as building blocks. Such decompositions are called vine copulas. To build these copulas, the authors recursively

decomposed the dependence of the variables as done in Joe (1997) and Bedford and Cooke (2002, 2001). Another possible way to build multivariate copulas is to use nested copulas. This last notion is defined as follows: if $C_1(\cdot, \cdot)$ and $C_2(\cdot, \cdot)$ are two bivariate copulas, then $C_1(C_2(\cdot, \cdot), \cdot)$ is a trivariate nested copula. In this paper we only consider vine copulas, which appear richer than nested copulas for multivariate analysis, following (Berg and Aas, 2009) who show that nested copulas are less efficient than vine copulas to estimate densities and risk measures such as the *VaR*.

Our purpose is to build all possible vine copulas in order to capture as much information as possible from a dataset. Indeed, a practitioner aims to find the vine copula that characterises correctly the behavior of the dataset under study: we call this true copula C^0 . However finding C^0 is almost impossible for any real dataset. On the other hand, a vine copula could be described as a decomposition of an n -variate vector's density using bivariate copula densities as building blocks. Such vine decomposition is not unique, and many different vine copulas exist in each dimension. Through an example in Section 4 we show that, given a dataset, each vine decomposition estimates specific dependence between the variables.

This result highlights the importance of defining a strategy to find the vine copula that is closest to the true copula C^0 according to any criterion retained by the practitioner. To do so we generated a large number of vine copulas using a simple algorithm that produces $N = \frac{n!}{2} \prod_{i=1}^{n-3} i!$ different vine copulas in dimension n . Previously cited papers use $n!$ vine copulas, but as our purpose is to find a copula closest to the copula C^0 , increasing the number of vine copula under consideration is crucial. The size of the set of possible vine copulas necessitates a computationally efficient selection algorithm. We present an algorithm that has the advantage of selecting the best vine copula within a set of vine copulas according to any criterion chosen by the practitioner without the requirement of having to test all the copulas. This algorithm is based on an underlying lattice structure inside the set of vine copulas.

The paper is organised as follows: in Section 2, we introduce a new method to build vine copulas. Section 3 provides some characteristics of vine copulas that motivated our work. In Section 4, we describe the model selection procedure, relying on a lattice structure on the set of vine copulas. Section 5 presents a numerical application and Section 6 concludes.

2 The Vine Set

In this section, we introduce a new algorithm to build vine copulas. It consists of a step-by-step factorisation of the density function in a product of bivariate copulas. Our approach is different from the methods developed by Bedford and

Cooke (2002, 2001) and is not related to them in any obvious way. Indeed, in Bedford and Cooke (2002, 2001) vine copulas are introduced as decomposition of the multivariate random vector density based on a type of graph structure called "vines", from which comes their denomination. Our approach has the advantage of being able to coherently describe a large set of vine copulas – N in dimension n – while also being a simple recursive algorithm.

2.1 Formula

Let us consider a vector $\mathbf{X} = (X_1, X_2, \dots, X_n)$ of random variables characterised by a joint distribution function $F_{\mathbf{X}}$ that we assume has a density function $f_{\mathbf{X}}$. We introduce the following notations:

- $\mathbf{X}_{-\alpha} = (X_1, \dots, X_{\alpha-1}, X_{\alpha+1}, \dots, X_n)$ is the set of variables except the α -th.
- We denote f_{α} the density of X_{α} . In the same fashion $f_{\alpha|\beta}$ is the density of $(X_{\alpha}|X_{\beta})$, $f_{-\alpha}$ is the density of $\mathbf{X}_{-\alpha}$ and $f_{\alpha|-\beta}$ is the density of $\mathbf{X}_{\alpha}|\mathbf{X}_{-\beta}$.
- $c_{\alpha,\beta|\gamma} = c_{X_{\alpha},X_{\beta}|X_{\gamma}}(F_{X_{\alpha}|X_{\gamma}}(X_{\alpha}|X_{\gamma}), F_{X_{\beta}|X_{\gamma}}(X_{\beta}|X_{\gamma}))$ is the copula density of $(X_{\alpha}, X_{\beta}|X_{\gamma})$ as defined in Sklar (1959)'s theorem. Similarly $c_{\alpha,\beta|-(\alpha,\beta)} = c_{X_{\alpha},X_{\beta}|\mathbf{X}_{-(\alpha,\beta)}}(F_{X_{\alpha}|\mathbf{X}_{-(\alpha,\beta)}}(X_{\alpha}|\mathbf{X}_{-(\alpha,\beta)}), F_{X_{\beta}|\mathbf{X}_{-(\alpha,\beta)}}(X_{\beta}|\mathbf{X}_{-(\alpha,\beta)}))$.

Our objective is to compute $c_{1,\dots,n}$, the copula density associated with the vector \mathbf{X} . This will be done by factorizing $f_{\mathbf{X}}$ in the following form:

$$f_{\mathbf{X}} = \prod_{i=1,\dots,n} f_i \cdot c_{1,\dots,n}.$$

By construction for $n = 2$ we have: $f_{\alpha,\beta} = f_{\alpha} \cdot f_{\beta} \cdot c_{\alpha,\beta}$. Using this property we consider the following factorisation of the joint density $f_{\mathbf{X}}$:

$$\forall \alpha, \beta \in \{1, \dots, n\}^2, \alpha \neq \beta$$

$$\begin{aligned} f_{\mathbf{X}} &= f_{-\alpha} \cdot f_{\alpha|-\alpha} = f_{-\alpha} \cdot \frac{f_{\alpha,\beta|-(\alpha,\beta)}}{f_{\beta|-(\alpha,\beta)}} = f_{-\alpha} \cdot \frac{f_{\alpha|-(\alpha,\beta)} \cdot f_{\beta|-(\alpha,\beta)}}{f_{\beta|-(\alpha,\beta)}} \cdot c_{\alpha,\beta|-(\alpha,\beta)} \\ &= \frac{f_{-\alpha} \cdot f_{-\beta}}{f_{-(\alpha,\beta)}} \cdot c_{\alpha,\beta|-(\alpha,\beta)}. \end{aligned} \tag{1}$$

Formula (1) allows the computation of an n -variate density with a bivariate copula, two $(n-1)$ -and one $(n-2)$ -variate densities. Using this factorisation recursively, insuring that the denominators cancel at each step, we produce a factorisation of the n -variate density as a product of univariate and bivariate

copula densities. Using this algorithm we can produce all N possible vine copulas (Napoles, 2007)^{1,2}.

2.2 Example

In this example, we illustrate the unwinding of the previous algorithm for $n = 4$, providing the joint density function $f_{1,2,3,4}$. Our aim is to compute $c_{1,2,3,4}$: the joint copula density. We describe the two steps of the algorithm using the previous notations.

- First step:

$$f_{1,2,3,4} = \frac{f_{1,2,3} \cdot f_{1,2,4}}{f_{1,2}} \cdot c_{3,4|1,2} = \frac{f_{1,2,3} \cdot f_{1,2,4}}{f_1 \cdot f_2 \cdot c_{1,2}} \cdot c_{3,4|1,2}. \quad (2)$$

- Second step: we apply the relationship (1) to the densities $f_{1,2,3}$ and $f_{1,2,4}$:

$$f_{1,2,3} = \frac{f_{1,2} \cdot f_{1,3}}{f_1} \cdot c_{2,3|1} = \frac{f_1 \cdot f_2 \cdot c_{1,2} \cdot f_1 \cdot f_3 \cdot c_{1,3}}{f_1} \cdot c_{2,3|1} = f_1 \cdot f_2 \cdot f_3 \cdot c_{1,2} \cdot c_{1,3} \cdot c_{2,3|1}, \quad (3)$$

and

$$f_{1,2,4} = \frac{f_{1,2} \cdot f_{2,4}}{f_2} \cdot c_{1,4|2} = \frac{f_1 \cdot f_2 \cdot c_{1,2} \cdot f_2 \cdot f_4 \cdot c_{2,4}}{f_2} \cdot c_{1,4|2} = f_1 \cdot f_2 \cdot f_4 \cdot c_{1,2} \cdot c_{2,4} \cdot c_{1,4|2}. \quad (4)$$

By merging formulas (2),(3) and (4), we obtain the following factorisation:

$$f_{1,2,3,4} = f_1 \cdot f_2 \cdot f_3 \cdot f_4 \cdot c_{1,3} \cdot c_{1,2} \cdot c_{2,4} \cdot c_{2,3|1} \cdot c_{1,4|2} \cdot c_{3,4|1,2}. \quad (5)$$

We have now factorised the density $f_{1,2,3,4}$ into a product of four univariate densities and six bivariate copula densities. By construction, this means that the copula density of (X_1, X_2, X_3, X_4) can be factorised as follows:

$$c_{1,2,3,4} = c_{1,3} \cdot c_{1,2} \cdot c_{2,4} \cdot c_{2,3|1} \cdot c_{1,4|2} \cdot c_{3,4|1,2}.$$

The unwinding of this algorithm can yield other vine copulas if other parameters are used. For instance the copula density $c_{1,2,3,4}$ has also the following decomposition:

$$c_{1,2,3,4} = c_{2,3} \cdot c_{3,4} \cdot c_{1,4} \cdot c_{2,4|3} \cdot c_{1,3|4} \cdot c_{1,2|3,4}.$$

¹ N is the number of "vine" type graphs with n nodes, which is also the number of vine copulas (see Bedford and Cooke (2002, 2001)). The proof of the formula relies heavily on the graph structure of vines.

²Our algorithm can produce more varied decomposition, however we do not consider them as they are not efficient estimators, Bedford and Cooke (2002, 2001).

3 The Vine Copula Estimator

Using the previous algorithm for an n -variate density, we can construct the N different vine copulas in dimension n . In the following, using a real dataset as example, we show how each vine copula can yield different representations of the same dataset. We proceed in the following way.

We estimate two different trivariate vine copulas from the same dataset and compare the tail dependence of the two estimated densities by observing in which quadrant of $[0, 1]^3$ the densities evolves³. The dataset is the daily Morgan Stanley evaluation of the French, German and British price indexes from 01/01/06 to 01/12/08 (Datastream). We denote them respectively as X , Y and Z . In a first step, for X , Y and Z we estimate separately $GARCH(1,1)$ models using pseudo-maximum likelihood methods, Ghysels et al. (1995). In a second step, using the residuals, we estimate the parameters of the vine copula using maximum likelihood, Chen and Fan (2006). For each bivariate copula in the estimation procedure, we select among the Gaussian, Student, Clayton and Gumbel copula, the one with higher likelihood. We choose these copulas because they characterise the main features detected in economic and financial time-series (Patton, 2009)⁴. In Figure 1, we plot the estimated copulas with uniform margins in three cases: $(X, Y|z = 0.1)$, $(X, Y|z = 0.5)$ and $(X, Y|z = 0.9)$ (from left to right).

By examining Figure 1, we observe that the two vine copulas describe different tail dependences. According to the first vine copula there is strong upper tail dependence (top-right plot) but no lower dependence (top-left plot). However the second vine copula describes strong lower tail dependence (bottom left plot) but no upper tail dependence (bottom right plot). This difference in terms of tail dependence is solely caused by the vine copula, since in both cases we used the same estimation procedure and the same dataset.

Taking this fact into account and to attain our purpose of finding the copula that is closest to the true one C^0 according to a criterion chosen by the practitioner, we decided to consider the whole set of possible vine copulas. However, as there are N different vine copulas in dimension n , estimating and testing all of them is computationally intractable, thus we needed to develop an efficient search strategy. In the next section, we describe such an algorithm using a lattice structure. We denote T the test retained by the practitioner to make the selection.

³The two copulas used are: $Vine\ 1 = c_{1,2} \cdot c_{1,3} \cdot c_{2,3|1}$ and $Vine\ 2 = c_{1,3} \cdot c_{2,3} \cdot c_{1,2|3}$

⁴All computations are done in *MatLab*.

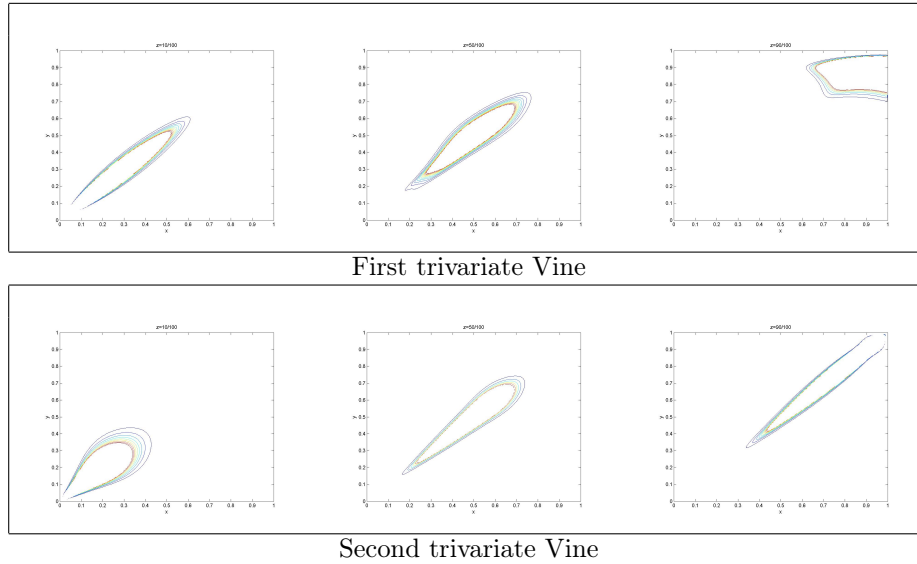


Figure 1: Two vines estimated on the same data set: slices at $z = 10\%$, 50% , 90%

4 Model Selection

In this section, we describe the search algorithm that finds the set of vine copulas accepted by the test T among all possible vine copulas. To this end, we introduce a lattice which is a partial order on the set of vine copulas. We proceed in two steps: we first introduce lattice theory and the implemented lattice structure, and then we describe the search algorithm. We illustrate our approach with an example in dimension $n = 3$.

Lattice Theory A lattice is a set and a partial order. A partial order is a binary relation, for instance denoted \leq , that is reflexive, antisymmetric and transitive, i.e for all a , b , and c , we have that:

- $a \leq a$ (reflexivity)
- if $a \leq b$ and $b \leq a$ then $a = b$ (antisymmetric)
- if $a \leq b$ and $b \leq c$ then $a \leq c$ (transitive)

For instance the set \mathbb{R} with binary relation \leq is a lattice.

The lattice structure we build from the set of all possible vines is based on increasing independence hypotheses. For instance, in the trivariate case when

the random variables $(X_1|X_2)$ and $(X_3|X_2)$ are independent, the vine copula $c_{1,2,3} = c_{1,2} \cdot c_{2,3} \cdot c_{1,3|2}$ becomes $c_{1,2,3} = c_{1,2} \cdot c_{2,3}$. Thus, we will consider $c_{1,2,3} = c_{1,2} \cdot c_{2,3}$ as being a vine copula and insert it into the lattice structure⁵.

In dimension three we get the following lattice structure:

"1" is the root of the lattice, and the arrow points from a general vine copula to a more specific one. We say that the vine copula " $c_{1,3}$ " is more general than the vine copula " $c_{1,2} \cdot c_{1,3}$ " because the former vine copula defines a simpler relation between the variables and requires fewer parameters than the latter one. This kind of specification of the vine copulas is different from that introduced by Czado et al. (2009), which is based on a Bayesian selection framework.

We proceed now to construct the search algorithm based on the lattice structure in the general case. The use of lattices to organise large sets of models is not new, but lattice selection has never been used on vine copulas. Gabriel (1969) developed the principles and provided the theoretical groundwork for such a method. It relies on two tools, first a test T to decide whether a model is accepted or rejected⁶, second on the rule of coherence: "one ought not to accept a model while rejecting a more general model." When we apply the test T on a model, if the null of the model being the true model is retained then we accept all generalisations of this model, and if the null is rejected we reject all specifications of this model. In our case, the term "model" refers to vine copulas, and the rule of coherence could be restated as follows: "the gain in increased specification does not compensate for the loss of requiring more parameters."

We now develop the search algorithm based on the rule of coherence. Within the set of models, it selects the subset of all possible vine copulas composed of the most complex models accepted by a test T :

1. We randomly build a set S of possible models and classify them into two sets according to the test T : A , the accepted models and R , the rejected models.
2.
 - i If $A \neq \emptyset$: let D_A be the set composed of the most complex models that are not in A or R . If $D_A = \emptyset$ we stop; otherwise we test with T the models in D_A . If we do not retain any models, we stop. Otherwise, we update A and R accordingly and iterate.
 - ii If $A = \emptyset$: let D_R be the set composed of the most simple models that are not in A or R . If $D_R = \emptyset$ we stop; otherwise we test with T the models in D_R . If we accept all models, we stop. Otherwise, we update A and R accordingly and iterate.

⁵This imply that the number of copulas we consider is greater than N .

⁶We do not specify T in this section, and instead describe the procedure for any test chosen by the practitioner, but we specify a possible test in Section 5.

Edwards and Havranek (1987) study a similar algorithm and prove that the algorithm reaches its purpose efficiently. This means that given a set of models of size p it will only require $o(\log(p))$ steps to find the optimum.

We give a step-by-step illustration of how the previous algorithm could unwind in the case of our trivariate example. Let X be a trivariate dataset and T a test. First, two vine copulas are selected randomly to be tested, $c_{1,3}.c_{2,3}$ and $c_{1,2}.c_{1,3}$. The former one is accepted (solid line) while the latter one is rejected (in black) by the test T , as can be seen in the upper left diagram.

The consequence of $c_{1,3}.c_{2,3}$ being accepted according to the rule of coherence is that three more vine copulas are accepted: 1, $c_{2,3}$ and $c_{1,3}$ (dashed lines in the upper right diagram). Similarly, the consequence of $c_{1,2}.c_{1,3}$ being rejected is that $c_{1,2}.c_{1,3}.c_{2,3|1}$ is also rejected (in grey in the upper right diagram). The next step of the algorithm is to test using T the most complex vine copulas that are not accepted or rejected: $c_{1,3}.c_{2,3}.c_{1,2|3}$ and $c_{1,2}.c_{2,3}.c_{1,3|2}$ (underlined in the upper right diagram). The former copula is refused, and the latter one is accepted (in the lower left diagram) by the test T . By the rule of coherence, we accept: $c_{1,2}$ and $c_{1,2}.c_{2,3}$. In summary, the research algorithm keeps the most complex among the accepted vine copulas, which is $c_{1,2}.c_{2,3}.c_{1,3|2}$ (double lines in the lower right diagram).

The advantage of this lattice structure is that it presents a high connectivity inside the set of all possible vine copulas. For instance, $c_{1,2}$ is connected directly or indirectly to five other vine copulas. This means that each step of the algorithm is very useful for the search, because it allows us to accept or reject many other copulas by using the rule of coherence.

5 Application to the *CAC40* index

Here we estimate the joint density of the five main assets composing the *CAC40*, the French leading index, using the methodology described above, and we use this estimated joint density to compute the *VaR* of a portfolio composed of the five assets.

The dataset is taken from Datastream, daily quotes from Total, BNP - Paribas, Sanofi - Synthelabo, GDF-Suez and France Telecom from 25/4/08 to 21/11/08. This period is marked by the 2008 crisis, and our purpose is to test the resilience of our model to this shock and change of regimes. We estimate the parameters and select the vine copula based on the data ranging from 25/4/08 to 9/12/08, while the *VaR* is computed from the remaining dates. The portfolio we consider is as follows: Total (33%), BNP - Paribas (20%), Sanofi - Synthelabo (20%), GDF-Suez (14%) and France Telecom (13%).

For each dataset a *GARCH*(p, q) process is selected using the *AIC* criterion (Akaike, 1974) and estimated using pseudo likelihood. On the residual we estimated the vine copula parameters using maximum likelihood. The parametric copula families used in this exercise are the Clayton, Gumbel, Student and Gaussian copulas.

The selection process has been described in Section 4. The test T we used is an

Anderson-Darling (A-D) type test modified for use with copulas in high dimension. It is described in Chen et al. (2004) and shown through Monte-Carlo simulation of possessing significant power even in high dimension. We recall that this test associates to each estimated density a χ^2 sample. A complete presentation of the test is detailed in the Annex.

In dimension five, the lattice structure contains 8536 different vine copulas. Using our lattice-based algorithm in order to select the best vine copula according to the A-D test, we only needed to test 1423 vine copulas (less than 17% of them). In fine, the retained vine copula is⁷:

$$c_{1,2,3,4,5} = c_{2,5} \cdot c_{4,5} \cdot c_{1,3} \cdot c_{1,5} \cdot c_{1,5|4} \cdot c_{1,2|5}.$$

The fact that this vine copula was selected imply that the vines copulas presented in Aas et al. (2009) were rejected by the test, and hence were unable to represent the dependence between the five assets properly. This example shows the necessity of using the whole set of vine copulas for times series applications.

Our final objective is to use this estimated vine copula density to compute the 10% VaR ⁸. We computed it from 9/12/08 to 21/11/08 using Monte-Carlo based integration and optimisation, see Figure 2. We compared it to a univariate $GARCH(p, q)$ model-based estimate of the VaR computed directly on the portfolio value time series. To discriminate between the two approaches, we use the Kupiec test (Kupiec, 1995). The Kupiec statistic is the number Q of time the out-sample time-series is below the predicted 10% VaR . Under the null of the prediction being a true 10% VaR the sampling distribution of the statistic follows a binomial distribution of parameter 0.1.

In our example the vine copula- VaR has a p -value of 0.96 for the Q statistic, so it is accepted as a true VaR , while the $GARCH-VaR$ has a p -value of 0.00 and is rejected according to this test⁹. Nevertheless, the vine copula approach fails to predict the major drop during the crisis, but the prediction remains solid before and after the crisis. These results make the vine copula methodology we described an interesting approach for risk management in order to estimate the multivariate ($n > 2$) density of a portfolio and to compute its associated VaR .

6 Conclusion

In this paper, we estimated multivariate distributions in high dimensions using a new vine copula-based approach that builds upon the work of Aas et al. (2009) by taking advantage of the diversity of vine copulas. We introduced an algorithm using a large number of vine copulas from which we were able to retain the "best" one according to a predefined test T , using a lattice structure, which makes the research simple and fast. The methodology we developed offers great flexibility for the practitioners in

⁷The computation took one hour on a 1.5Ghz processor computer.

⁸Given a random variable X , the 10% VaR of X is the value $VaR(X)$ such that:

$$P(X < VaR(X)) = 0.1.$$

⁹ Q for the vine copula- VaR is equal to 5 and for the $GARCH-VaR$ is equal to 21.

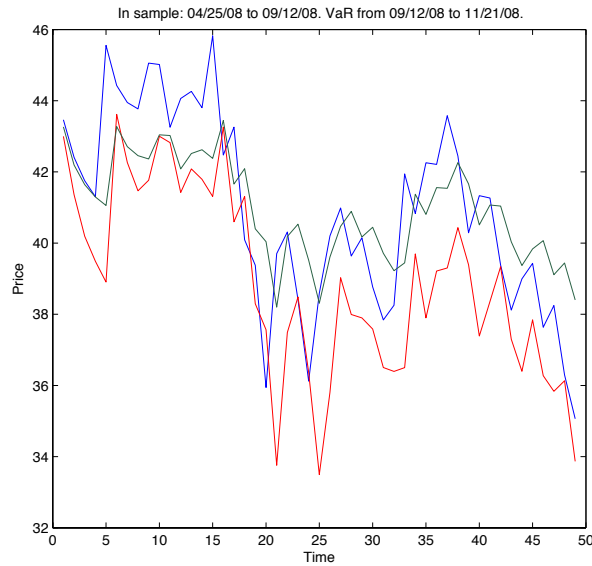


Figure 2: In Blue: The CAC40, In Red: Vine VaR Estimation, In Green: GARCH VaR Estimation.

terms of the choice of the set of vine copulas, choice of bi-variate copulas, usefulness of the lattice structure, and the test T for the selection procedure.

It appears necessary to have a great number of vine copulas to be able to take into account the most important features of the dataset to be analysed: indeed, through a simple example we have highlighted the importance of finding the vine copula that takes into account most of the information contained in the dataset, particularly the behaviour of the tails. Finally, the VaR computation based on our methodology provides interesting results compared with the classical parametric approach.

However, some questions remain. First is the problem of devising a test to decide whether a vine copula represents a dataset dependence correctly or not. Chen et al. (2004) and Chen and Fan (2006) produced interesting tests, but for an optimum use of vine copulas a simpler and more efficient test needs to be built. Another question concerns the quality of the estimates, on which we did not focus in this paper. Instead, we applied a classical maximum likelihood estimation approach as developed for instance in Aas et al. (2009) to estimate the vine copula parameters. Results on the efficiency of the estimates have to be established. We address this question in a companion paper, Guégan and Maugis (2009).

7 Acknowledgment

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8 Annex

8.1 The modified Anderson-Darling test, Chen et al. (2004)

The test is the following: we are testing the null hypothesis H_0 against the alternative hypothesis H_1 :

$$H_0 : Pr(C(U_1, \dots, U_n) = C_0(U_1, \dots, U_n)) = 1$$

$$H_1 : Pr(C(U_1, \dots, U_n) = C_0(U_1, \dots, U_n)) < 1$$

where C is the true copula and C_0 the estimated copula. We define $\{Z_i\}_{i < n}$ and W as:

$$Z_i = F(U_i | U_1, \dots, U_{i-1}) \text{ and } W = \sum_1^n [\Phi^{-1}(Z_j)]^2,$$

where Φ is the standard normal distribution function. Then W follows a χ_d^2 distribution; our test will be based on this result. For this purpose we use the univariate boundary kernel $K_h(x, y)$

$$K_h(x, y) = \begin{cases} k(\frac{x-y}{h}) / \int_{-\frac{x}{h}}^1 k(u) du & \text{if } x \in [0, h) \\ k(\frac{x-y}{h}) & \text{if } x \in [h, 1-h] \\ k(\frac{x-y}{h}) / \int_{-\frac{x}{h}}^1 k(u) du & \text{if } x \in (1-h, 1] \end{cases}$$

in which $k(\cdot)$ is the quartic kernel: $k(u) = \frac{15}{16}(1-u^2)^2 \mathbf{1}_{|u| < 1}$ and h is fixed using the rule of thumb: $h = \sqrt{Var(W)} n^{-1/5}$. Then we define g_W as a kernel estimation of the inverse density of W :

$$g_W(\omega) = \frac{1}{n \cdot h} \sum_t^T K_h(\omega, F_{\chi_d^2}(W_t))$$

Finally the test is based on the statistics J_n :

$$J_n = \int_0^1 [g_W(\omega) - 1]^2 d\omega$$

Then under the null we have that:

$$Stat_n = \frac{(nh^{1/2}J_n - r_n)}{\sigma} \rightarrow N(0,1) \text{ in distribution.}$$

Where:

$$r_n = h1/2 \left[(h^{-1} - 2) \int_{-1}^1 k^2(\omega) d\omega + 2 \int_0^1 \int_{-1}^z k_z^2(y) dy dz \right]$$

$$\sigma^2 = 2 \int_{-1}^1 \left[\int_{-1}^1 k(u+v)k(v) dv \right]^2 du$$

$$k_z(y) = k(y) / \int_{-1}^z k(u) du$$