On Spatial Contagion and mGARCH models

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Abstract

We propose a method for defining and measuring the spatial contagion between two financial markets. Next we investigate which from the large family of multivariate GARCH models is the best tool for modeling spatial contagion.
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1 Introduction

Financial contagion is intuitively defined as a shock to one country's asset market that causes changes in asset prices in another country's financial market. Understanding and describing contagion is essential for coping with financial crises such as the Asian financial crisis of the late 1990's, the subprime mortgage crisis in August 2007 or debt crisis in 2011. For these reasons, financial contagion has recently attracted the attention of several theoretists and practitioners working on finance due to its dramatical effects and many different definitions of contagion have been proposed (compare [1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11]). In fact, the presence of financial contagion among markets can mitigate the effects of diversification of investments precisely when they are needed most. Furthermore it became a great challenge for the international financial institution like The International Monetary Fund or European Central Bank.

In this paper we follow the approach provided by Bradley and Taqqu [3, 4, 2], using copula representations [7]. The idea is that there is a contagion from market X to market Y when dependence between X and Y is stronger when X is in crisis (comparing to normal times). In other words there is more dependence in the loss distribution of X than in the center. We will refer to such type of contagion as *spatial contagion* in order to underline the fact that it relates to areas of the whole distribution of X and Y rather than

time-varying volatility of X. For contagion measurement, the normal copula is chosen as benchmark copula that is contagion free. The investigation of conditional copulas in Gaussian framework is held and some useful theorems of monotonic properties of measures of concordance are proven (with respect to conditioning parameters). The explicit form of the r-*invariant* set on which contagion should be tested is suggested. (where r is parameter of Gaussian copula).

The main goal of this paper is to extend the results obtained by Durante and Jaworski in [7] for time series of multidimensional GARCH type. The assumption that time series follows mGARCH dynamics is made and investigation of the contagion effect is considered. Seven different mGARCH models are considered, including classical multivariate models (BEKK, DCC) as well as copula-GARCH models. All of the models are based more or less on normal or Student distributions and are considered in general fit framework.

The main result is that models with estimation procedure, which could be separated into two steps (first margins, then dependence), provide poor fit for contagion modeling (within the class of models constructed for general fit, rather than contagion modelling). In other words, it is shown that contagion effect in most of the empirically used copula-GARCH models is not strong enough in contrary to BEKK model, which performs quite well.

We also present some general remarks on models constructed for contagion fit. We present some statistics for mGARCH contagion-fit models with Clayton and Survival Gumbel copulas. Using these models one improves the description of the contagion effect but might make the general fit worse.

The paper is so organized. In section 2 we recall some basic facts about copulas and conditioning sets. The formal definition of contagion is presented in Section 3. Section 4 provides useful theorems about limit behavior of conditioned copulas as well as it's monotonic properties for Gaussian family. Here, we also present some tables and graphics which illustrate the theorems. In Section 5 we investigate sets on which contagion should be testes, when taking normal copula as benchmark model. We also provide the explicit form of the set, which is invariant to Gaussian copula correlation parameter, while still being accurate for test purposes. Description of seven mGARCH models on which contagion will be tested is given in Section 6. In Section 7 we examine the presence of contagion effect between two stock indices – FTSE and DAX. We compare contagion fit between standard approach (as in [7]) and the one with mGARCH dynamics. Next we present some statistics for all of the models. We conclude in Section 8, while Section 9 consists of proofs for previously stated Propositions and Theorems.

2 Preliminaries

In this paper we will partially adopt notation used in [7] in further work. Let X and Y be two continuous random variables defined on the same probability space (Ω, Σ, P). $H(x, y) = P[X \leq x, Y \leq y]$ will be their joint distribution function, $F(x) = H(x, \infty)$,

$G(y) = H(\infty, y)$ will be margins and C will be their copula. Using Sklar's theorem we can couple this functions with formula $H(x, y) = C(F(x), G(y))$ (compare [12, 13, 14, 15, 16, 17, 18, 20]). We can also state $C(u, v) = H(F^{[-1]}(u), G^{[-1]}(v))$. It is also worth noticing that C is a joint distribution function with uniform margins. By $F^{[-1]}(\alpha) = \inf\{x : F(x) \geq \alpha\}$ we will understand the quantile function of F (see [14, 19]).

Given a Borel set $\mathscr{B}$ in $\bar{\mathbb{R}}^2$ such that $P(\{\omega \in \Omega : (X(\omega), Y(\omega)) \in \mathscr{B}\}) > 0$ we can define conditional distribution $H_{\mathscr{B}}$ for all $(x, y) \in \mathscr{B}$ by:

$$H_{\mathscr{B}}(x, y) = P[X \leq x, Y \leq y | (X, Y) \in \mathscr{B}]$$

If necessary, we will assume the existence of regular conditional probabilities. In this paper we will assume that $\mathscr{B}$ is a rectangle. For such $\mathscr{B}$ it is very easy to obtain conditional copula from conditional distribution function. Let $\mathscr{B} = [a_1, a_2] \times [b_1, b_2]$ and let $\mathscr{R} = [F^{[-1]}(a_1), F^{[-1]}(a_2)] \times [F^{[-1]}(b_1), F^{[-1]}(b_2)]$. Then we can define conditional copula:

$$C_{\mathscr{R}}(u, v) := H_{\mathscr{B}}(F^{[-1]}_{\mathscr{B}}(u), G^{[-1]}_{\mathscr{B}}(v))$$

It is easy to show that $C_{\mathscr{R}}$ only depends on values of C in $\mathscr{R}$ (see [7] for details).

From now on we will focus on rectangles defined for copula function (that could be expressed as quantiles for H). We will consider two different types of rectangles:

Definition 2.1. Let $\alpha_1, \alpha_2 \in (0, 1)$ and $\beta_1, \beta_2 \in (0, 0.5)$ then:

$$\mathscr{T}_{\alpha_1,\alpha_2} := [0, \alpha_1] \times [0, \alpha_2] \qquad \mathscr{M}_{\beta_1,\beta_2} := [\beta_1, 1 - \beta_1] \times [\beta_2, 1 - \beta_2]$$

We will refer to them with *tail set* and *central set*.

3 Definitions of contagion

As we have said in the introduction, the notion of (spatial) contagion is related to the comparison of the dependence among two financial markets X and Y in some specific regions of the domain of their joint distribution. At a more theoretical level, all these concepts can be translated in terms of comparisons among distribution functions and conditional distribution functions with respect to some meaningful tail and central events, or, equivalently, in terms of copulas and threshold copulas.

The most common way to compare the strength of dependence among two random pairs is to consider the *concordance ordering* (called also positive quadrant dependence (shortly, PQD) ordering) between their respective copulas. We recall that, given two copulas C_1 and C_2, we say that C_1 is *less PQD* than C_2 (and we write $C_1 \preceq_{PQD} C_2$) if,

$$\forall (u, v) \in [0, 1]^2 \quad C_1(u, v) \leq C_2(u, v)$$

(compare [14] Definition 2.8.1). We adopt the symbol $\prec_{PQD}$ in order to indicate the case when $C_1 \preceq_{PQD} C_2$ but $C_1 \neq C_2$ [13, 23]. With respect to this ordering, we have that, for

any copula C, $W \preceq_{PQD} C \preceq_{PQD} M$. Moreover, a copula C is said to be *positive quadrant dependent* if $C \succeq_{PQD} \Pi$.

Now, we are able to formulate the following definitions of contagion. Let X_t and Y_t be the time series representing returns of two financial markets. Suppose that they are stationary and C is the copula of all (X_t, Y_t).

Definition 3.1. We say that there is *contagion* of type 1 (from X to Y) with respect to $\mathscr{M}_{\beta,0}$ and $\mathscr{T}_{\alpha,1}$ if

$$C_{\mathscr{M}_{\beta,0}} \prec_{PQD} C_{\mathscr{T}_{\alpha,1}}.$$

Analogously, we say that there is *contagion* of type 2 (from Y to X) with respect to $\mathscr{M}_{0,\beta}$ and $\mathscr{T}_{1,\alpha}$ if

$$C_{\mathscr{M}_{0,\beta}} \prec_{PQD} C_{\mathscr{T}_{1,\alpha}}.$$

We say that there is *symmetric contagion* of type 3 (between X and Y) with respect to $\mathscr{M}_{\beta,\beta}$ and $\mathscr{T}_{\alpha,\alpha}$ if

$$C_{\mathscr{M}_{\beta,\beta}} \prec_{PQD} C_{\mathscr{T}_{\alpha,\alpha}}.$$

Thus, contagion is defined as an increase of the dependence in some tail regions of the joint distribution of (X_t, Y_t) with respect to some central regions. Moreover, as just copulas describe the dependence among random variables, contagion refers to the comparison among threshold copulas obtained with respect to tail regions or central regions of the unit square.

This definition depends on choice of conditioning sets. As we will see, contagion (defined as increase of dependence in the tails) could be observed in some regions in almost all of the multivariate distributions (like normal or t-student), so choice of $\mathscr{T}$ and $\mathscr{M}$ is crucial.

From practical point of view, checking PQD condition of contagion might be problematic (see [7] for discussion and [24, 25] for possible methods). We will use instead measures of concordance. The two most known measures of concordance are Kendall's τ and Spearman's ρ. Let us remark a simple fact ([14, 26]):

Proposition 3.1. *Let κ be measure of concordance. For any copulas C_1 and C_2 if $C_1 \preceq_{PQD} C_2$ then $\kappa(C_1) \leq \kappa(C_2)$*

Because of it test of contagion could be based on comparison between values of κ of central and tail set conditional copulas.

4 Concordance ordering and Spearman ρ for conditional copulas

4.1 Limits for absolutely continuous copulas

An interesting problem related to threshold copulas given a conditioning set $\mathscr{R}$ is their limit behaviour when $\mathscr{R}$ tends to a degenerate set of 2–Lebesgue measure 0. For threshold

copulas $C_{\mathscr{R}}$, this limit behaviour has been investigated in [27, 28, 29, 30, 31, 32, 33]. Here, we formulate some related results for the threshold copulas corresponding to central sets.

Proposition 4.1. *Let C be an absolutely continuous copula with density c. If c is continuous at the point $\left(\frac{1}{2},\frac{1}{2}\right)$ and $c\left(\frac{1}{2},\frac{1}{2}\right)\neq 0$, then the copula $C_{\mathscr{M}_{\beta,\beta}}$ converges uniformly to Π when β tends to $\frac{1}{2}$, viz.*

$$\forall (u,v)\in[0,1]^2 \qquad C_{\mathscr{M}_{\beta,\beta}}(u,v)\overset{\beta\to\frac{1}{2}}{\longrightarrow} uv.$$

Proposition 4.2. *Let C be an absolutely continuous copula with density c. If c is continuous at all points of the set $\left\{\frac{1}{2}\right\}\times[0,1]$, then the copula $C_{\mathscr{M}_{\beta,0}}$ converges uniformly to Π when $\beta\to\frac{1}{2}$, viz.*

$$\forall (u,v)\in[0,1]^2 \qquad C_{\mathscr{M}_{\beta,0}}(u,v)\overset{\beta\to\frac{1}{2}}{\longrightarrow} uv.$$

Analogous result can be formulated for $C_{\mathscr{M}_{0,\beta}}$.

4.2 Conditioning of a bivariate Gaussian copula

The study of Gaussian copula is important for test construction because it is an example of copula which is contagion free.

We recall that the bivariate Gaussian copula is the copula of the bivariate normal distribution. It depends on one parameter – the correlation r. We have

$$G_r(x,y)=F_r(F^{-1}(x),F^{-1}(y))$$

and

$$\partial_1 G_r(x,y)=F\left(\frac{F^{-1}(y)-rF^{-1}(x)}{\sqrt{1-r^2}}\right),\ \text{for } (x,y)\neq(0,0),$$

where F is a standard univariate normal distribution ($N(0,1)$) and F_r is a bivariate normal distribution $N(0,\Sigma)$ with covariance matrix

$$\Sigma=\begin{pmatrix}1 & r\\ r & 1\end{pmatrix}.$$

Note that the Spearman's ρ depends on r in the following way

$$\rho(G_r)=\frac{6\arcsin(r/2)}{\pi}.$$

Theorem 4.1. *If $r>0$ then the conditional Gaussian copula $G_{r,\mathscr{T}_{\alpha,1}}$ is increasing with α.*

To describe the limiting behaviour of the functions we adopt the symbol $O(*)$. We say that the function $f(q)$ belongs to $O(q^{-n})$ when $q\to-\infty$ if the limit

$$\lim_{q\to-\infty} q^n f(q)$$

exists and is finite.

Theorem 4.2. *The conditional Gaussian copula $G_{r,\mathscr{T}_{\alpha,1}}$ tends to independence copula Π when $\alpha \to 0^+$. Moreover*

$$G_{r,\mathscr{T}_{\alpha,1}}(x,y) = xy + \frac{1}{F^{-1}(\alpha)} \frac{r}{\sqrt{1-r^2}} f(F^{-1}(y)) x \ln x + O((F^{-1}(\alpha))^{-2}).$$

Where f is density of F.

Corollary 4.1.

$$\rho(G_{r,\mathscr{T}_{\alpha,1}}) = \frac{3r}{2\sqrt{\pi}\sqrt{1-r^2}} \frac{1}{|F^{-1}(\alpha)|} + O(F^{-1}(\alpha)^{-2}).$$

Theorem 4.3. *If $r > 0$ then the conditional Gaussian copula $G_{r,\mathscr{M}_{\beta,0}}$ is decreasing with β.*

Theorem 4.4. *The conditional Gaussian copula $G_{r,\mathscr{M}_{\beta,0}}$ tends to Gaussian copula G_r when $\beta \to 0^+$. Moreover for $r > 0$*

$$G_{r,\mathscr{M}_{\beta,0}}(x,y) = G_r(x,y) + [2G_r(x,y) + \partial_1 G_r(x,y)(1-2x) + \partial_2 G_r(x,y)(1-2y) - 1]\,\beta + O(\beta^2).$$

Corollary 4.2. *For $r > 0$*

$$\rho(G_{r,\mathscr{M}_{\beta,0}}) = \rho(G_r) - 6(1-\rho(G_r))\beta + O(\beta^2).$$

For bivariate Gaussian copula with correlation coefficient r, the values of Spearman's ρ for $G_{r,\mathscr{T}_{\alpha,1}}$ and $G_{r,\mathscr{M}_{\beta,0}}$ are presented in Table 1 & 2. For values of Spearman's ρ for $G_{r,\mathscr{T}_{\alpha,\alpha}}$ and $G_{r,\mathscr{M}_{\beta,\beta}}$ see Tables 3 and 4. Note that if $\beta \to 0.5^-$ then $G_{r,\mathscr{M}_{\beta,0}}$ and $G_{r,\mathscr{M}_{\beta,\beta}}$ tend to independence copula Π. Similarly if $\alpha \to 0^+$ then $G_{r,\mathscr{T}_{\alpha,1}}$ tends to independence copula Π. In Fig. 1 one can see plot of $\rho(G_{r,\mathscr{T}_{\alpha,\alpha}})$, $\rho(G_{r,\mathscr{M}_{\beta,\beta}})$ and

$$\Delta\rho(\alpha) := \rho(G_{r,\mathscr{T}_{\alpha,\alpha}}) - \rho(G_{r,\mathscr{M}_{\alpha,\alpha}})$$

as function of α for normal copula with $r = 0.7$.

5 Area of contagiency

In this section we will try to define proper tail and central sets for contagion measurement. We will parametrize them with α and β, according to notation $C_{\mathscr{T}_{\alpha,1}}$, $C_{\mathscr{T}_{1,\alpha}}$, $C_{\mathscr{T}_{\alpha,\alpha}}$ and $C_{\mathscr{M}_{\beta,0}}$, $C_{\mathscr{M}_{0,\beta}}$, $C_{\mathscr{M}_{\beta,\beta}}$ where type of conditioning set should be clear from the contex.

Let $S = \{(\alpha,\beta) : 0 < \alpha \leq \beta < 0.5\}$ be set of all allowable pairs for parameters (inequality comes from the fact, that we want to keep tail and central sets disjoint). For given copula C and concordance measure κ we define the following sets:

Table 1: $\rho(G_{r,\mathscr{T}_{\alpha,1}})$ for normal Copula

$r \diagdown \alpha$	0.01	0.03	0.05	0.075	0.1	0.15	0.2	0.25
0.1	0.03	0.03	0.03	0.04	0.04	0.04	0.04	0.04
0.2	0.06	0.06	0.07	0.07	0.08	0.08	0.09	0.09
0.3	0.09	0.10	0.10	0.11	0.11	0.12	0.13	0.14
0.4	0.12	0.13	0.14	0.15	0.16	0.17	0.18	0.19
0.5	0.15	0.17	0.18	0.20	0.21	0.22	0.24	0.25
0.6	0.20	0.22	0.24	0.25	0.26	0.28	0.30	0.32
0.7	0.26	0.29	0.30	0.32	0.33	0.36	0.38	0.40
0.8	0.34	0.37	0.39	0.41	0.43	0.46	0.48	0.50
0.9	0.47	0.52	0.54	0.57	0.58	0.61	0.64	0.66

Table 2: $\rho(G_{r,\mathscr{M}_{\beta,0}})$ for normal Copula

$r \diagdown \beta$	0.05	0.1	0.15	0.2	0.25	0.3	0.35	0.4
0.1	0.08	0.06	0.05	0.05	0.04	0.03	0.02	0.02
0.2	0.16	0.13	0.11	0.09	0.08	0.06	0.04	0.03
0.3	0.24	0.2	0.17	0.14	0.11	0.09	0.07	0.04
0.4	0.32	0.27	0.23	0.19	0.16	0.13	0.09	0.06
0.5	0.41	0.35	0.3	0.25	0.21	0.17	0.12	0.08
0.6	0.5	0.44	0.38	0.32	0.27	0.21	0.16	0.11
0.7	0.61	0.54	0.48	0.41	0.34	0.27	0.21	0.14
0.8	0.73	0.66	0.6	0.52	0.45	0.36	0.28	0.19
0.9	0.86	0.81	0.76	0.7	0.62	0.52	0.41	0.28

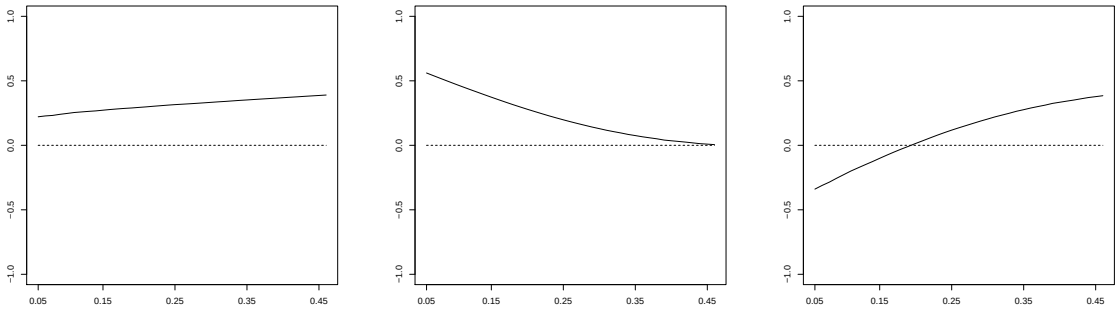

Figure 1: Plot of $\rho(G_{r,\mathscr{T}_{\alpha,\alpha}})$, $\rho(G_{r,\mathscr{M}_{\alpha,\alpha}})$ and $\Delta\rho(\alpha)$ as functions of α for normal copula $(r = 0.7)$, $\alpha \in [0.05, 0.45]$

Table 3: $\rho(G_{r,\mathscr{T}_{\alpha,\alpha}})$ for normal Copula

$r \diagdown \alpha$	0.01	0.03	0.05	0.075	0.1	0.15	0.2	0.25
0.1	0.01	0.02	0.02	0.02	0.02	0.02	0.02	0.02
0.2	0.01	0.02	0.03	0.03	0.04	0.04	0.05	0.05
0.3	0.04	0.05	0.05	0.06	0.06	0.07	0.08	0.08
0.4	0.04	0.07	0.08	0.09	0.09	0.10	0.11	0.12
0.5	0.09	0.10	0.11	0.12	0.13	0.15	0.16	0.17
0.6	0.11	0.14	0.15	0.17	0.18	0.20	0.22	0.24
0.7	0.17	0.20	0.22	0.24	0.25	0.28	0.30	0.32
0.8	0.25	0.29	0.32	0.34	0.35	0.38	0.41	0.43
0.9	0.41	0.46	0.48	0.51	0.53	0.56	0.59	0.61

Table 4: $\rho(G_{r,\mathscr{M}_{\beta,\beta}})$ for normal Copula

$r \diagdown \alpha$	0.05	0.1	0.15	0.2	0.25	0.3	0.35	0.4
0.1	0.06	0.04	0.03	0.02	0.01	0.01	0.00	0.00
0.2	0.13	0.09	0.06	0.04	0.03	0.02	0.01	0.01
0.3	0.19	0.14	0.10	0.07	0.05	0.03	0.02	0.01
0.4	0.27	0.20	0.14	0.10	0.07	0.04	0.02	0.01
0.5	0.35	0.26	0.19	0.14	0.09	0.06	0.03	0.01
0.6	0.45	0.35	0.26	0.19	0.13	0.08	0.04	0.02
0.7	0.56	0.45	0.35	0.26	0.18	0.12	0.07	0.03
0.8	0.69	0.59	0.49	0.38	0.28	0.18	0.10	0.05
0.9	0.84	0.78	0.70	0.60	0.48	0.34	0.21	0.10

$$A_{1,C} := \left\{(\alpha,\beta) \in S : \kappa(C_{\mathscr{T}_{\alpha,1}}) \geq \kappa(C_{\mathscr{M}_{\beta,0}})\right\} \tag{1}$$

$$A_{2,C} := \left\{(\alpha,\beta) \in S : \kappa(C_{\mathscr{T}_{1,\alpha}}) \geq \kappa(C_{\mathscr{M}_{0,\beta}})\right\} \tag{2}$$

$$A_{3,C} := \left\{(\alpha,\beta) \in S : \kappa(C_{\mathscr{T}_{\alpha,\alpha}}) \geq \kappa(C_{\mathscr{M}_{\beta,\beta}})\right\} \tag{3}$$

From now on we will assume that $\kappa := \rho$ (Spearman's ρ). The results for other measures of concordance are similar. For ρ as κ, we will call $A_{1,C}$ and $A_{2,C}$ *contagion sets* of copula C (type 1 and 2 contagion) and $A_{3,C}$ *symmetric contagion set* of copula C (type 3 contagion). The problem is that even for copulas that are considered contagion-free (f.e. normal) the contagion could be observed in some regions (see Fig. 1, plot of $\Delta\rho(\alpha)$). Because of that it might be better to restrict $A_{i,C}$ (for $i = 1, 2, 3$) to subset of S. We will treat normal copula as benchmark model and try to restrict S to subset, where normal copula is contagion

free. Let us point out that such subset might strongly depend on r (where r is correlation parameter from Gaussian copula). Let G_r be a normal copula with $r > 0$. Let

$$S_{i,G_r} = \{(\alpha_1, \beta_1) : \ 0 < \alpha_1 \leq \beta_1 < \inf_{\beta} A_{i,G_r}\} \qquad \text{for } (i = 1, 2, 3)$$

Of course we have then $S_{i,G_r} \cap A_{i,G_r} = \emptyset$, so the Gaussian copula G_r is contagion free (of i-th type) in subset S_{i,G_r}. Now let us approximate the value of $\inf_\beta A_{i,G_r}$ for different $r > 0$.

Proposition 5.1. *For given Gaussian copula G_r with $r > 0$, to calculate $\inf_\beta A_{i,G_r}$ (for $i = 1, 2, 3$) we only need to solve equation $\rho(G_{r,\mathscr{T}_{\beta,1}}) = \rho(G_{r,\mathscr{M}_{\beta,0}})$ (for $i = 1, 2$) and $\rho(G_{r,\mathscr{T}_{\beta,\beta}}) = \rho(G_{r,\mathscr{M}_{\beta,\beta}})$ (for $i = 3$) for $\beta \in (0, 0.5)$.*

Proof.
Let us fix $1 > r > 0$. We will prove proposition for $i = 1$. For $i = 2$ the proof is the same (note that Gaussian copula is symmetric so obtained minimal beta will be the same), and for $i = 3$ proof will go in similar way. We know from Theorem 4.1, Theorem 4.3 and Proposition 3.1 that $\rho(C_{r,\mathscr{T}_{\alpha,1}})$ is increasing function of α and $\rho(C_{r,\mathscr{M}_{\beta,0}})$ is decreasing function of β. Because of that and the property $\alpha \leq \beta$:

$$(\alpha, \beta) \in A_{1,G_r} \Rightarrow (\beta, \beta) \in A_{1,G_r}$$
$$\forall h \in [0, 0.5 - \beta) : (\beta, \beta) \in A_{1,G_r} \Rightarrow (\beta + h, \beta + h) \in A_{1,G_r}$$

Because of above observations, to compute $\inf_\beta A_{i,G_r}$ we only need to find minimal β such that $\rho(G_{r,\mathscr{T}_{\beta,1}}) \geq \rho(G_{r,\mathscr{M}_{\beta,0}})$. From above theorems we know also that function

$$\Delta_1(\beta) := \rho(G_{r,\mathscr{T}_{\beta,1}}) - \rho(G_{r,\mathscr{M}_{\beta,0}})$$

is (strictly) increasing. For $\beta \to 0^+$ above inequality is trivially false (as $\rho(\Pi) = 0 \geq \frac{6 \arcsin(r/2)}{\pi} = \rho(G_r)$ is false) and for $\beta \to 0.5^-$ is true (as $\rho(G_{r,\mathscr{T}_{0.5,1}}) \geq \rho(\Pi) = 0$). (This fact follows from Theorem 4.4, Proposition 4.2 and 4.1). Because of that and the fact that function Δ_1 is continuous (as Gaussian copula is absolutely continuous function) we know that Δ_1 will be equal to 0 at exactly one point which will coincide with $\inf_\beta A_{i,G_r}$. □

Using Proposition 5.1 we have computed values of $\inf_\beta A_{i,G_r}$ for various r. In Figure 2 we present empirical results for $r \in (0.05, 0.95)$. As we can see the values of $\inf_\beta A_{i,G_r}$ are almost constant for $(i = 1, 2, 3)$. Therefore we can define *r-invariant* subsets of S:

$$S_1 = S_2 = \{0 < \alpha \leq \beta < 0.21\}, \tag{4}$$
$$S_3 = \{0 < \alpha \leq \beta < 0.18\}. \tag{5}$$

We will also consider sets of the form

$$S_{1a} = S_{2a} = \{0 < \alpha = \beta < 0.21\},$$

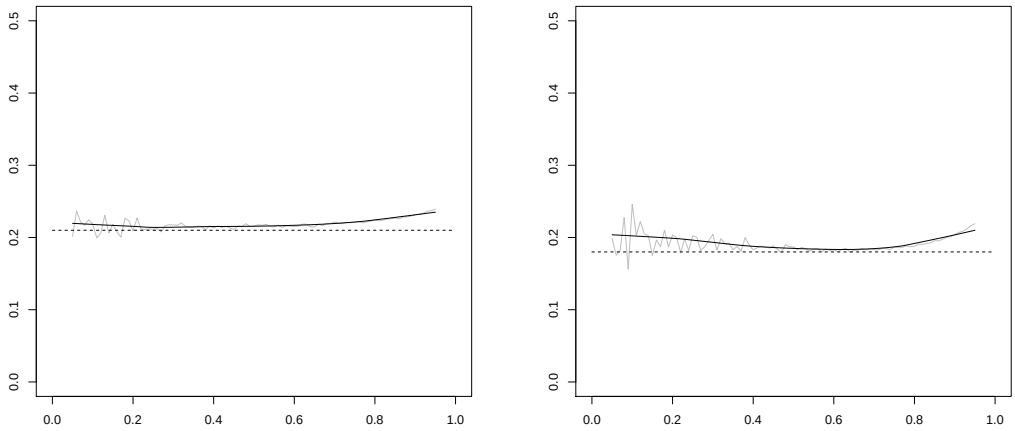

Figure 2: Plot of $\inf_\beta A_{1,G_r}$ and $\inf_\beta A_{3,G_r}$ as functions of r for $r \in [0.05, 0.95]$. (Smoothed and MC-simulated – 1.000.000 copula sample for each r.)

$$S_{3a} = \{0 < \alpha = \beta < 0.18\}.$$

For a broad class of families this should be the limiting case. Let us remark that, the smaller β, the bigger α can be (in S). From empirical point of view, we want to maximize α when sample is of small size. It is also worth noticing, that we could define measure of contagion with respect to S_i . For any copula C and standard Lebesgue measure μ defined on S:

$$\gamma_i(C) := \frac{\mu(A_{i,C} \cap S_i)}{\mu(S_i)}, \tag{6}$$

$$\gamma_{ia}(C) := \frac{\mu_a(A_{i,C} \cap S_{ia})}{\mu_a(S_{ia})} \tag{7}$$

where μ_a is projection of μ. For example, for t-student copula C_{stud} ($r = 0.7$, $df = 3$): $\gamma_1(C_{stud}) \approx 0.10$, $\gamma_{1a}(C_{stud}) \approx 0.12$, $\gamma_3(C_{stud}) \approx 0.70$, $\gamma_{3a}(C_{stud}) \approx 0.48$.

Let us also say that above subsets define proper tail and central sets on which contagion test should be applied.

6 Description of models

We will use seven different mGARCH models to model contagion effect. Standard BEKK(1,1) model, DCC(1,1) (Engle and Shepard), EDCC(1,1), Copula-GARCH(1,1) model (with time-invariant normal/t-student copula), Copula-GARCH(1,1) (with given dynamics for the normal copula parameter) and Markov Switching Copula GARCH(1,1) model (with

Normal and Clayton copulas). For all Copula-GARCH models we will use standard univariate GARCH(1,1) dynamics for margins (with conditional skew t-student distribution). For simplicity, we will write: BEKK, DCC, EDCC, CG1, CG1s, CG2 and MSC. For general description of multivariate GARCH models (BEKK, DCC, EDCC) see [34, 35, 36, 37], for short introduction to extended DCC (EDCC) see [21, 22]. For copula-based models (CG1, CG1s) see [38, 39, 40, 41], description of CG2 could be find in [41, 40], for detailed description of MSC see [11, 42, 9].

In the following we denote by $H^{\frac{1}{2}}$ the lower triangular matrix obtained by Cholesky decomposition of a symmetric positive-definite matrix H.

$$H = H^{\frac{1}{2}}(H^{\frac{1}{2}})',$$

where $\cdot'$ denotes the transposition. When using copula (or MC simulation) from mGARCH model, one must be very cautious and pay attention to ergodic properties of the model. Unfortunately the theory of stationarity for GARCH models is still under development. Nevertheless for BEKK model there is relatively easy condition to check if the model is stationery (concerning eigenvalues of a specific matrix). For details and information about stationarity of mGARCH models see [43]. For interesting theoretical and empirical results concerning mGARCH models see [44].

6.1 BEKK(1,1) model

The BEKK(1,1) process X_t is defined by the following equations:

$$\begin{aligned} X_t &= H_t^{\frac{1}{2}}\nu_t \qquad \nu_t \text{ iid } N_2(0, id) \text{ (white noise)}, \\ H_t &= C'C + A'X_{t-1}X_{t-1}'A + B'H_{t-1}B \end{aligned}$$

where C, A, B are $N \times N$ and C is upper triangle. Of course then we have $E(X_t|\mathscr{F}_{t-1}) = 0$ and $Var(X_t|\mathscr{F}_{t-1}) = H_t$, where the filtration $(\mathscr{F}_t)$ is generated by white noise process ν.

6.2 DCC(1,1) model (Engle)

We define DCC(1,1) model as:

$$\begin{aligned} X_t &= H_t^{\frac{1}{2}} \cdot \nu_t \qquad (\nu_t\text{: white noise}), \\ H_t &= D_t R_t D_t \\ \hat{h}_t &= C + A \cdot \hat{\epsilon}_{t-1} + B \cdot \hat{h}_{t-1} \end{aligned} \tag{8}$$

where

$$\hat{h}_t = \begin{pmatrix} h_{11,t} \\ h_{22,t} \end{pmatrix} \quad D_t = \begin{pmatrix} \sqrt{h_{11,t}} & 0 \\ 0 & \sqrt{h_{NN,t}} \end{pmatrix} \quad \hat{\epsilon}_t = \begin{pmatrix} X_{1,t}^2 \\ X_{2,t}^2 \end{pmatrix}$$

C is 2×1 vector, A and B are diagonal 2×2 matrices with nonnegative coefficients (univariate GARCH(1,1) for all margins) and R_t is time-varying correlation matrix with:

$$R_t = (diag\ Q_t)^{-1/2} Q_t (diag\ Q_t)^{-1/2}, \quad diag\ Q_t = \begin{pmatrix} Q_{11,t} & 0 \\ 0 & Q_{22,t} \end{pmatrix},$$

where Q_t is a sequence of covariance matrices:

$$Q_t = (1 - \alpha - \beta)Q + \alpha X_{t-1} X'_{t-1} + \beta Q_{t-1}$$

with $\alpha + \beta < 1$, $\alpha, \beta > 0$, and Q is covariance matrix of the whole sample.

6.3 EDCC(1,1)

The extended DCC model is a modification of DCC that allows volatility spillovers. In DCC we have assumed that A and B are vectors. In relates to matrices with only diagonal entries. In Extended version we model A and B as $N \times N$ matrices.

6.4 Copula-GARCH(1,1) model (time-invariant copula) – CG1

Copula-GARCH model base on two-step estimation procedure that is similar to DCC estimation. First, we estimate univariate GARCH(1,1) models for the margins (we will use standardized skewed t-Student distribution as conditional distribution, see [45] for details). We get for $i = 1, 2$:

$$\begin{aligned} X_{i,t} &= h_{i,t}^{\frac{1}{2}} \nu_{i,t}, \\ h_{i,t} &= C_i + A_i X_{i,t-1}^2 + B_i h_{i,t-1}, \end{aligned} \tag{9}$$

where ν_t are iid,
$\nu_{i,t}$ has standardized skewed t-Student distribution $t(df_i, skew_i)$
and the dependence between $\nu_{1,t}$ and $\nu_{2,t}$ is described by fixed copula C.

df and *skew* are degrees of freedom and skewness parameters (from marginal GARCH estimation). Now, using conditional variances we get standardized residuals. Using Sklar's theorem we could get empirical copula from the residuals (using CML procedure[1]) and estimate copula C from given copula family. We will use Gaussian and t-Student copula families. From estimation process we get r as dependence parameter (and df_C for t-Student copula). The other possibilities like Clayton or Survival Gumbel families of copulas are discussed in Summary (Section 8).

[1]IFM procedure could be used as well but empirical studies showed that CML provides better fit for empirical data.

6.5 Copula-GARCH(1,1) model (time-varying copula) – CG2

In previous model we had constant copula function over time. We could easily extend it to time-varying copula. Following first step we get standardized residuals from the distribution (with same estimated parameters as in previous model). Now we can define dynamics on the copula parameter. We will use correlation r matrix as parameter matrix for the model (as in normal copula parametrization). We will use dynamics described in [38] that is:

$$r_{(t)} = L\Big(a_1 + a_2 r_{(t-1)} + a_3 \frac{1}{10} \sum_{j=(t-10)}^{t} \big[F^{-1}(u_{1j}) F^{-1}(u_{2j})\big]\Big)$$

where $\{(u_{1t}, u_{2t})\}_{t=1}^{t=T}$ is CML copula sample constructed from standardized residuals, F is standard normal and $L(x) = tanh(\frac{x}{2})$ is function designed to keep r in $[-1, 1]$. As one can see dynamics of the dependence parameter is similar to ARIMA(1,10). We took Φ^{-1} as empirical studies showed that it provides good fit for the financial data. We assume that copula is normal with varying parameter r.

6.6 MSC(1,1) model

Markov-Switching Copula GARCH model (MSC) has also two step estimation procedure, where the first step is similar to the previous models. We assume that the joint conditional distribution of $\epsilon_t|\mathscr{F}_{t-1} \sim C_{S_t}(F_1(\cdot), \ldots, F_N(\cdot)|\mathscr{F}_{t-1})$, where S_t is homogeneous Markov chain with two states $\{1, 2\}$, and F_t, G_t are margins with dynamics described with univariate GARCH(1,1) (we took standardized skewed t-student distribution). Markov chain is described with transition probabilities:

$$\mathbf{P} = \begin{pmatrix} p_{11} & 1 - p_{11} \\ 1 - p_{22} & p_{22} \end{pmatrix}$$

where, for example $p_{11} = P(S_t = 1|S_{t-1} = 1)$. Conditional probabilities are calculated using Hamilton's filter:

$$P(S_t = k|\mathscr{F}_{t-1}) = p_{1k} P(S_{t-1} = 1|\mathscr{F}_{t-1}) + p_{2k} P(S_{t-1} = 2|\mathscr{F}_{t-1})$$

$$P(S_t = k|\mathscr{F}_t) = \frac{c_k(u_t|S_t = k, \mathscr{F}_{t-1}) P(S_t = k|\mathscr{F}_{t-1})}{c_1(u_t|S_t = 1, \mathscr{F}_{t-1}) P(S_t = 1|\mathscr{F}_{t-1}) + c_2(u_t|S_t = 2, \mathscr{F}_{t-1}) P(S_t = 2|\mathscr{F}_{t-1})}$$

for $k = 1, 2$. $u_t = \big(F_1(r_{1,t}), \ldots, F_N(r_{N,t})\big)'$ (IFM copula sample constructed from standardized residuals) and c_1, c_2 are densities of conditional copula. We will use Normal and Joe-Clayton (BB7) as conditional copulas. r will be the parameter of Normal copula and (θ, δ) will be parameters of Joe-Clayton copula. For details and construction of log-likelihood function see [9].

7 Empirical study

For empirical analysis we have used data set that consists of FTSE100 and DAX indices. For daily log-returns, we have chosen period from 26.11.1990 to 21.10.2011 and considered the days where both markets were operating. There are 5206 observations from this sample. In Fig. 3 one can see plot for daily returns. Computations were done using **R 2.13.2** (64-bit). We have used libraries **fGarch** (for marginal GARCH simulation), **copula** (for copula function estimation and fitting), **mgarchBEKK** (for BEKK estimation and simulation), **ccgarch** (for DCC and EDCC estimation and simulation) and **doSMP** (for symmetric multicore processing to speed up Monte Carlo simulation). For estimated parameters we have simulated 1000 (standard) Monte Carlo samples (each of size 5206) for each model.

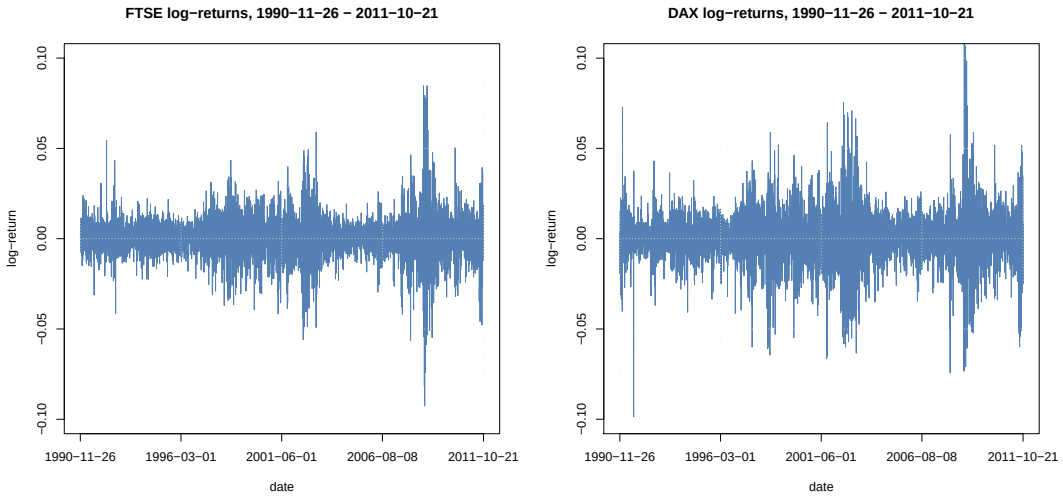

Figure 3: FTSE100 (left) and DAX (right) daily log returns from 26.11.1990 to 21.10.2011.

7.1 Estimation

We will try to fit copulas from certain families (i.e. normal and t-copula) as well as several mGARCH models (described in Section 6). For copula estimation we have used CML procedure (with function fitCopula from **copula** R library) and obtained $\hat{r} = 0.73$ for normal copula and ($\hat{r} = 0.73$, $\hat{df} = 3.48$) for t-copula. The results of estimation for all mGARCH models can be seen in Table 5.

For general fitting information, AIC and BIC (standard and normalized) for all mGARCH models are presented in Table 6. Let us point out that it tells us nothing about the contagion of the fitted model. In package ccgarch (as well as many others), estimation is based on **optim** function which does not (always) guarantee convergence to the global solution (i.e. set of parameters with maximal likelihood). Because of that the loglikelihood of the EDCC model is smaller than the loglikelihood of the DCC model, so estimation results as well as values of AIC and BIC should be treated carefully. Increase in the number of

Table 5: mGARCH models estimated parameters for FTSE-DAX sample

Model	Estimation results
BEKK(1,1)	$\mathbf{C} = \begin{pmatrix} -1.137 \times 10^{-3} & -1.617 \times 10^{-3} \\ 0 \times 10^{0} & -1.872 \times 10^{-3} \end{pmatrix}$, $\mathbf{A} = \begin{pmatrix} -2.449 \times 10^{-1} & 1.977 \times 10^{-1} \\ -1.051 \times 10^{-1} & -4.647 \times 10^{-1} \end{pmatrix}$, $\mathbf{B} = \begin{pmatrix} 9.84 \times 10^{-1} & 1.05 \times 10^{-1} \\ -5.331 \times 10^{-2} & 8.551 \times 10^{-1} \end{pmatrix}$
DCC(1,1)	$C = (3.611 \times 10^{-7}, 5.508 \times 10^{-6})$, $A = (5.441 \times 10^{-2}, 8.349 \times 10^{-2})$, $B = (9.372 \times 10^{-1}, 8.708 \times 10^{-1})$, $\mathbf{Q} = \begin{pmatrix} 1.000 & 0.701 \\ 0.701 & 1.000 \end{pmatrix}$, $\alpha = 0.022$, $\beta = 0.975$
EDCC(1,1)	$C = (1.488 \times 10^{-7}, 1.804 \times 10^{-5})$, $\mathbf{A} = \begin{pmatrix} 5.448 \times 10^{-2} & 1.294 \times 10^{-2} \\ 4.669 \times 10^{-2} & 6.509 \times 10^{-3} \end{pmatrix}$, $\mathbf{B} = \begin{pmatrix} 9.181 \times 10^{-1} & 4.713 \times 10^{-3} \\ 1.435 \times 10^{0} & 1.410 \times 10^{-3} \end{pmatrix}$, $\mathbf{Q} = \begin{pmatrix} 1.000 & 0.692 \\ 0.692 & 1.000 \end{pmatrix}$, $\alpha = 0.032$, $\beta = 0.965$
CG1(1,1)	$C = (1.032 \times 10^{-6}, 1.476 \times 10^{-6})$, $A = (8.123 \times 10^{-2}, 8.217 \times 10^{-2})$, $B = (9.128 \times 10^{-1}, 9.126 \times 10^{-1})$, $df = (10, 9.06)$, $skew = (0.925, 0.911)$, $r = 0.698$
CG1s(1,1)	$C = (1.032 \times 10^{-6}, 1.476 \times 10^{-6})$, $A = (8.123 \times 10^{-2}, 8.217 \times 10^{-2})$, $B = (9.128 \times 10^{-1}, 9.126 \times 10^{-1})$, $df = (10, 9.06)$, $skew = (0.925, 0.911)$, $r = 0.707$, $df_C = 5.522$
CG2(1,1)	$C = (1.032 \times 10^{-6}, 1.476 \times 10^{-6})$, $A = (8.123 \times 10^{-2}, 8.217 \times 10^{-2})$, $B = (9.128 \times 10^{-1}, 9.126 \times 10^{-1})$, $df = (10, 9.06)$, $skew = (0.925, 0.911)$, $(a_1 = 0.582, a_2 = 1, a_3 = 0.65)$
MSC(1,1)	$C = (1.032 \times 10^{-6}, 1.476 \times 10^{-6})$, $A = (8.123 \times 10^{-2}, 8.217 \times 10^{-2})$, $B = (9.128 \times 10^{-1}, 9.126 \times 10^{-1})$, $df = (10, 9.06)$, $skew = (0.925, 0.911)$, $\mathbf{P} = \begin{pmatrix} 0.993 & 0.007 \\ 0.009 & 0.991 \end{pmatrix}$, $r = 0.55$, $\theta = 2.54$, $\delta = 2.01$

parameters might make a solution worse fitted to data due to loglikelihood maximization algorithm imperfectness (or convergence speed).

Nevertheless the DCC model was chosen according to both AIC and BIC criteria (for general fit).

Table 6: AIC and BIC values for fitted mGARCH models

Model	AIC	AIC (norm.)	BIC	BIC (norm.)
BEKK(1,1)	-67967.42	-13.0556	-67888.73	-13.0405
DCC(1,1)	**-71624.29**	**-13.7581**	**-71572.46**	**-13.7480**
EDCC(1,1)	-70380.57	-13.5191	-70301.88	-13.5040
CG1(1,1)	-68169.98	-13.0945	-68097.8400	-13.0806
CG1s(1,1)	-68376.29	-13.1341	-68297.60	-13.1190
CG2(1,1)	-68453.72	-13.1490	-68368.47	-13.1326
MSC(1,1)	-68798.34	-13.2152	-68699.97	-13.1963

7.2 Contagion modelling

In Fig. 4 we can see plots of $\hat{\rho}_{emp}(C_{\mathscr{T}_{\alpha,\alpha}})$, $\hat{\rho}_{emp}(C_{\mathscr{M}_{\alpha,\alpha}})$ and $\Delta\hat{\rho}_{emp}(\alpha) := \hat{\rho}_{emp}(C_{\mathscr{T}_{\alpha,\alpha}}) - \hat{\rho}_{emp}(C_{\mathscr{M}_{\alpha,\alpha}})$ for FTSE-DAX sample, $\alpha \in [0.05, 0.45]$. Empirical values of $\hat{\rho}_{emp}$ are presented in Table 7.

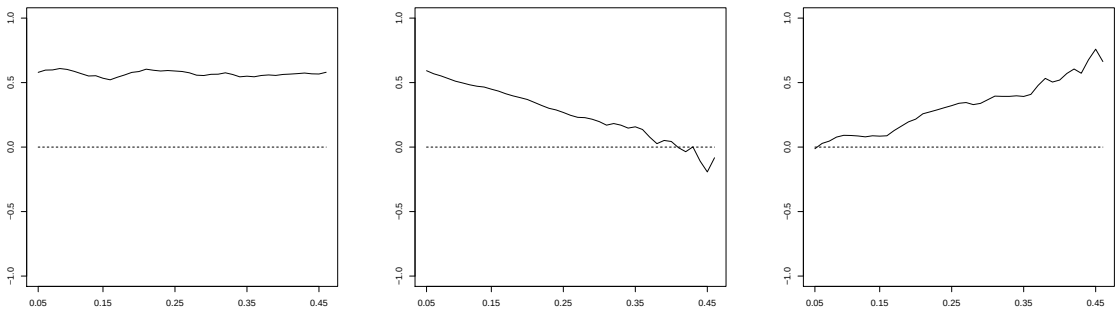

Figure 4: Plot of $\hat{\rho}_{emp}(C_{\mathscr{T}_{\alpha,\alpha}})$, $\hat{\rho}_{emp}(C_{\mathscr{M}_{\alpha,\alpha}})$ and $\Delta\hat{\rho}_{emp}(\alpha)$ as functions of α for real stock-market data FTSE-DAX, $\alpha \in [0.05, 0.45]$

Before comparing mGARCH models, we will see how general copula fits work for the data and compare it to BEKK model. Starting with copulas obtained from CML procedure, for $(j = 1, \ldots, 1000)$ we have sampled 5206 observations from estimated copulas and for every α we computed upper and lower 0.05 quantile of $\{\hat{\rho}(C^j_{\mathscr{T}_{\alpha,\alpha}})\}_{j=1}^{1000}$, $\{\hat{\rho}(C^j_{\mathscr{M}_{\alpha,\alpha}})\}_{j=1}^{1000}$ and $\{\hat{\Delta\rho}^j(\alpha)\}_{j=1}^{1000}$. Results are presented in Fig. 5 and Fig. 6.

As we can clearly see (and what has been many times proven in literature), normal copula underestimates tail dependence, while being good model for central set conditional copula. On the other hand, t-copula provides better fit for the tails, but it is still not very accurate. The resulting benchmark (Δ) shows us, that both models underestimates dependence in specific regions of copula. It tells us, that there is contagion effect in the sample (stronger than in normal, or t copula model). Because of that the standard test

Table 7: FTSE-DAX Sample

FTSE-DAX/ α	0.01	0.03	0.05	0.075	0.1	0.15	0.2	0.25
$\rho(C_{\mathscr{T}_{\alpha,1}})$	0.34	0.55	0.58	0.56	0.61	0.58	0.56	0.55
Sample size:	52	156	260	390	520	780	1041	1301
$\rho(C_{\mathscr{T}_{1,\alpha}})$	0.3	0.63	0.52	0.54	0.52	0.53	0.57	0.55
Sample size:	52	156	260	390	520	780	1041	1301
$\rho(C_{\mathscr{T}_{\alpha,\alpha}})$	0.33	0.62	0.58	0.62	0.59	0.52	0.6	0.59
Sample size:	33	92	153	239	316	485	651	849
FTSE-DAX/ α	0.05	0.1	0.15	0.2	0.25	0.3	0.35	0.4
$\rho(C_{\mathscr{M}_{\beta,0}})$	0.62	0.55	0.5	0.43	0.36	0.28	0.22	0.09
Sample size:	4685	4165	3645	3123	2603	2083	1561	1041
$\rho(C_{\mathscr{M}_{0,\beta}})$	0.63	0.55	0.49	0.43	0.34	0.26	0.18	0.11
Sample size:	4685	4165	3645	3123	2603	2083	1561	1041
$\rho(C_{\mathscr{M}_{\beta,\beta}})$	0.59	0.5	0.43	0.35	0.25	0.17	0.14	0
Sample size:	4452	3733	3034	2368	1765	1204	726	351
FTSE-DAX α	0.1	0.15	0.17	0.2	0.21	0.25	0.3	0.35
$\rho(C_{\mathscr{T}_{\alpha,1}}) - \rho(C_{\mathscr{M}_{\alpha,0}})$	0.05	0.07	0.1	0.13	0.13	0.19	0.27	0.31
$\rho(C_{\mathscr{T}_{1,\alpha}}) - \rho(C_{\mathscr{M}_{0,\alpha}})$	-0.03	0.04	0.1	0.14	0.15	0.21	0.3	0.36
$\rho(C_{\mathscr{T}_{\alpha,\alpha}}) - \rho(C_{\mathscr{M}_{\alpha,\alpha}})$	0.09	0.09	0.16	0.26	0.27	0.34	0.4	0.41

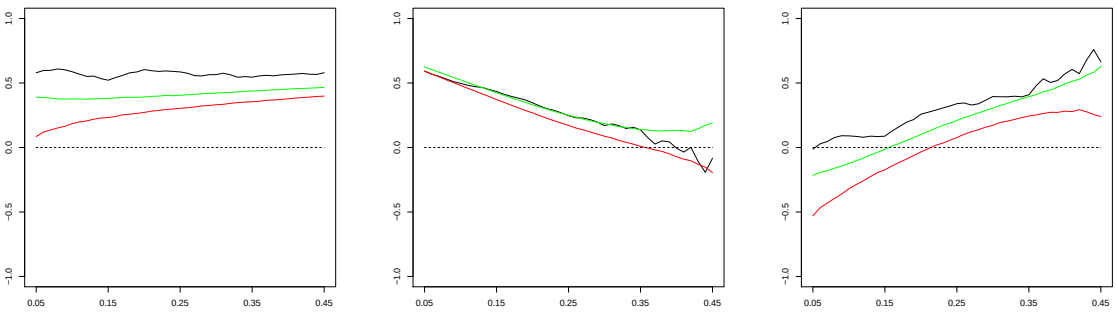

Figure 5: Plot of 0.05 and 0.95 α quantiles for $\{\hat{\rho}(C^j_{\mathscr{T}_{\alpha,\alpha}})\}_{j=1}^{1000}$, $\{\hat{\rho}(C^j_{\mathscr{M}_{\alpha,\alpha}})\}_{j=1}^{1000}$ and $\{\Delta\hat{\rho}^j(\alpha)\}_{j=1}^{1000}$ from MC-simulation of normal copula, $r = 0.73$

for contagion should be positive. See [7] for details.

Sampling from normal and t-copula we assumed that the observations are independent, which simplifies sampling procedure, but does not have strong foundations in reality. Now we will try, to sample 5206 observations from various mGARCH models with estimated parameters.

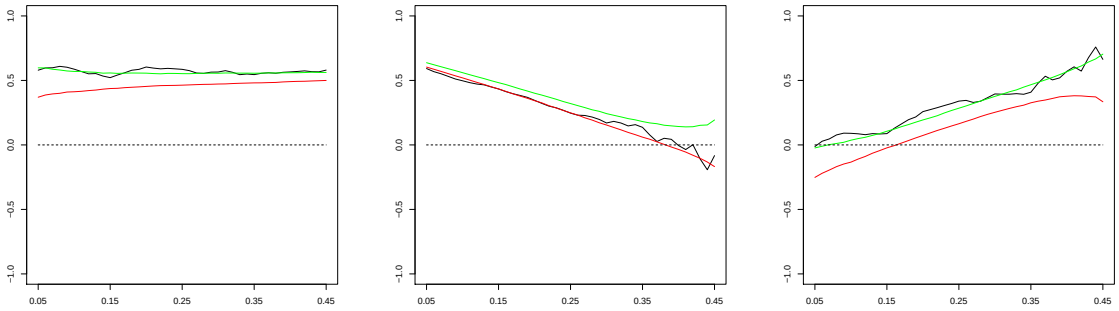

Figure 6: Plot of 0.05 and 0.95 α quantiles for $\{\hat{\rho}(C^j_{\mathscr{T}_{\alpha,\alpha}})\}_{j=1}^{1000}$, $\{\hat{\rho}(C^j_{\mathscr{M}_{\alpha,\alpha}})\}_{j=1}^{1000}$ and $\{\hat{\Delta\rho}^j(\alpha)\}_{j=1}^{1000}$ from MC-simulation of t-student copula, $r = 0.73$, $df = 3.48$

For BEKK(1,1) model (with normal residuals) and estimated parameters we simulated sample of size 5206. We repeated this procedure 1000 times and computed α quantiles as in previous approach. The result can be seen in Fig. 7.

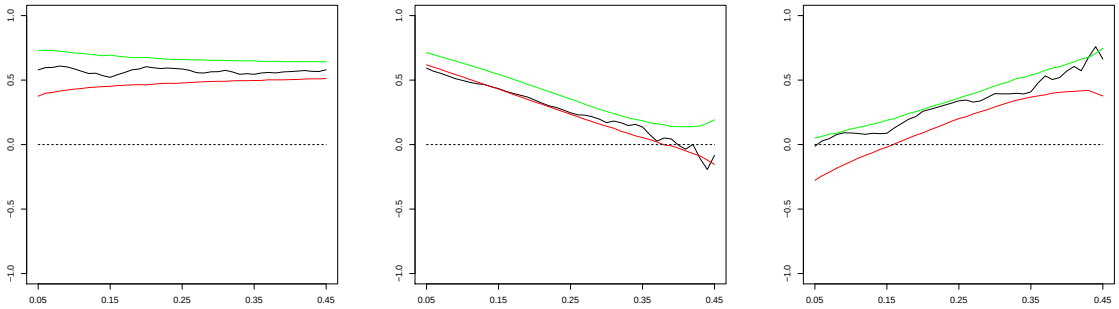

Figure 7: Plot of 0.05 and 0.95 α quantiles for $\{\hat{\rho}(C^j_{\mathscr{T}_{\alpha,\alpha}})\}_{j=1}^{1000}$, $\{\hat{\rho}(C^j_{\mathscr{M}_{\alpha,\alpha}})\}_{j=1}^{1000}$ and $\{\hat{\Delta\rho}^j(\alpha)\}_{j=1}^{1000}$ from MC-simulation of BEKK model (FTSE-FAX estimated parameters)

As one can see BEKK model fits better for the data. For a large 1.000.000 BEKK(1,1) sample (with estimated parameters) the values of $\rho(C_{\mathscr{T}_{\alpha,\alpha}})$, $\rho(C_{\mathscr{M}_{\alpha,\alpha}})$ and $\Delta\rho(\alpha)$ for $\alpha \in [0.05, 0.45]$ are presented in Fig. 8. The values of conditional Spearman's $\hat{\rho}$ are presented in Table 8.

Now we will compute some basic MC-statistics for various central and tail sets for previously estimated mGARCH models. We propose four different statistics for valuation of model. Statistics are based on Monte Carlo simulation. For each mGARCH model we simulate sample of size 5206 (with given estimates) and repeat this procedure 1000 times. For each simulation we compute empirical copula and it's $\Delta(\hat{\rho})$ for various tail and central sets. Then we compute the following MC-statistics for given tail set $\mathscr{T}$ and central set $\mathscr{M}$ which are based on $\Delta(\rho) := \rho(C_{\mathscr{T}}) - \rho(C_{\mathscr{M}})$. For given mGARCH model and 1000 Monte Carlo simulations:

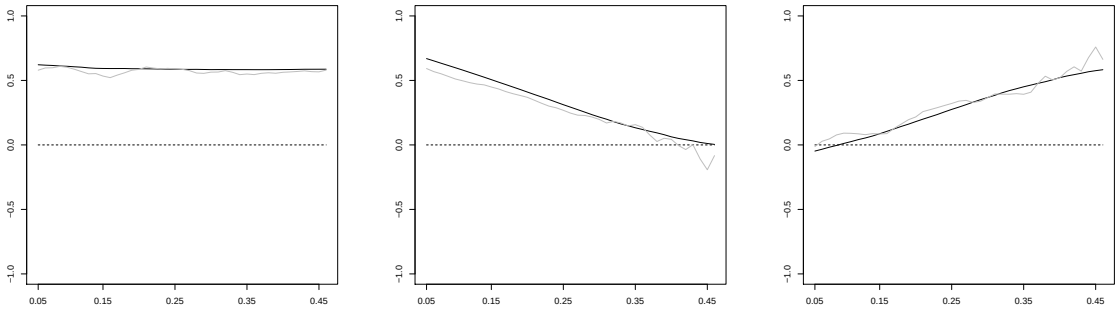

Figure 8: Plot of $\rho(C_{\mathscr{T}_{\alpha,\alpha}})$, $\rho(C_{\mathscr{M}_{\alpha,\alpha}})$ and $\Delta\rho(\alpha)$ as functions of α for BEKK 1.000.000 sample (FTSE-FAX estimated parameters), $\alpha \in [0.05, 0.45]$

Table 8: Conditional Spearman's ρ values for estimated BEKK model (1.000.000 sample size, parameters estimated from FTSE-DAX)

BEKK α	0.01	0.03	0.05	0.075	0.1	0.15	0.2	0.25
$\rho(C_{\mathscr{T}_{\alpha,1}})$	0.57	0.55	0.54	0.54	0.54	0.54	0.55	0.55
Sample size	9999	29999	49999	74999	99999	149999	199999	249999
$\rho(C_{\mathscr{T}_{1,\alpha}})$	0.62	0.59	0.58	0.57	0.57	0.57	0.57	0.57
Sample size	9999	29999	49999	74999	99999	149999	199999	249999
$\rho(C_{\mathscr{T}_{\alpha,\alpha}})$	0.66	0.64	0.62	0.61	0.61	0.59	0.59	0.59
Sample size	6259	18271	30378	45799	61890	95132	130614	168330
BEKK β	0.05	0.1	0.15	0.2	0.25	0.3	0.35	0.4
$\rho(C_{\mathscr{M}_{\beta,0}})$	0.69	0.63	0.56	0.49	0.42	0.34	0.26	0.17
Sample size	899999	799999	699999	599999	499999	399999	299999	199999
$\rho(C_{\mathscr{M}_{0,\beta}})$	0.69	0.62	0.55	0.48	0.41	0.33	0.25	0.17
Sample size	899999	799999	699999	599999	499999	399999	299999	199999
$\rho(C_{\mathscr{M}_{\beta,\beta}})$	0.67	0.58	0.49	0.39	0.29	0.2	0.12	0.05
Sample size	861109	724685	592411	466199	347152	237836	142432	66453
BEKK α	0.1	0.15	0.17	0.2	0.21	0.25	0.3	0.35
$\rho(C_{\mathscr{T}_{\alpha,1}}) - \rho(C_{\mathscr{M}_{\alpha,0}})$	-0.09	-0.02	0.01	0.05	0.07	0.13	0.22	0.3
$\rho(C_{\mathscr{T}_{1,\alpha}}) - \rho(C_{\mathscr{M}_{0,\alpha}})$	-0.05	0.01	0.04	0.08	0.1	0.16	0.24	0.32
$\rho(C_{\mathscr{T}_{\alpha,\alpha}}) - \rho(C_{\mathscr{M}_{\alpha,\alpha}})$	0.03	0.11	0.14	0.2	0.22	0.29	0.38	0.46

1. μ and σ are mean and standard deviation of the MC-sample (i.e. $\Delta(\hat{\rho})_{j=1}^{1000}$).

2. $p_1 = P_{MC}[\Delta(\rho) \geq 0)]$. It refers to probability under which the contagion in observed in the model (i.e. dependence in the tail is stronger than in the center of copula). By default it will be $1 - ecdf(0)$, where *ecdf* is MC-distribution function constructed

from values of $\Delta(\hat{\rho})_{j=1}^{1000}$ (obtained from MC-simulations).

3. $p_2 = P_{MC}[\Delta(\rho) \geq \Delta(\rho)_{emp})]$ where $\Delta(\rho)_{emp}$ is value of $\Delta(\rho)$ in given real-stock data sample. It refers to the probability that the contagion effect is stronger in the model, than in the sample. Also here we use MC-distribution function.

We will also consider some global benchmarks based on contagion measures γ_i and γ_{ia} (for $i = 1, 2, 3$) defined as (6) and (7). For given mGARCH model and 1000 Monte Carlo simulations:

4. μ_2 and σ_2 are mean and standard deviation of the MC-sample (i.e. $\gamma_i(C)_{j=1}^{1000}$ or $\gamma_{ia}(C)_{j=1}^{1000}$).

5. $p_3 = P_{MC}[\gamma_i(C) > \gamma_i(C_{emp})] = p$, where C_{emp} will be real-stock data empirical copula and $\gamma_i(C)$ will be random variable with MC-distribution of $\gamma_i(C)_{j=1}^{1000}$ from 1000 copulas obtained with Monte Carlo simulations . That will refer to probability that contagion is more thorough in the model, than in the sample.

6. Similarly $p_4 = P_{MC}[\gamma_{ia}(C) > \gamma_{ia}(C_{emp})]$.

The results for various types of contagion (type 1, 2 (asymmetric) and 3 (symmetric) as in Section 5) are presented in Tables 9, 10 and 11 while overall contagion statistics are presented in Table 12. We have checked statistics for α,$\beta \in \{0.1, 0.15, 0.18, 0.21\}$ with inequality ($\alpha \leq \beta$). Let us point out that for type 3 contagion the last part of the table could be misleading (see (4) and (5) in Section 5). Apart from values of test statistics, every table contain empirical value over which the test statistics is based on. (do not confuse it with value of statistics – it is not comparable).

Table 9: Statistics for contagion type 1, FTSE-DAX

$\mathscr{M} = (1, \beta)$	β	0.1	0.15		0.18			0.21			
$\mathscr{T} = (0, \alpha)$	α	0.1	0.1	0.15	0.1	0.15	0.18	0.1	0.15	0.18	0.21
emp Δ		0.054	0.021	0.074	0.016	0.069	0.110	0.002	0.054	0.096	0.134
BEKK		-0.104	-0.097	-0.032	-0.093	-0.028	0.014	-0.089	-0.024	0.018	0.061
DCC		-0.222	-0.195	-0.134	-0.182	-0.121	-0.083	-0.170	-0.109	-0.071	-0.033
EDCC		-0.086	-0.077	-0.019	-0.071	-0.013	0.021	-0.068	-0.010	0.025	0.060
CG1	μ	-0.279	-0.251	-0.192	-0.234	-0.175	-0.139	-0.218	-0.160	-0.123	-0.086
CG1s		-0.244	-0.216	-0.159	-0.200	-0.144	-0.109	-0.186	-0.130	-0.095	-0.058
CG2		-0.242	-0.216	-0.155	-0.200	-0.140	-0.103	-0.188	-0.128	-0.091	-0.053
MSC		-0.220	-0.189	-0.129	-0.172	-0.112	-0.075	-0.157	-0.097	-0.060	-0.023
BEKK		0.061	0.050	0.051	0.045	0.047	0.047	0.041	0.043	0.043	0.043
DCC		0.068	0.057	0.056	0.052	0.052	0.051	0.049	0.049	0.049	0.048
EDCC		0.109	0.094	0.096	0.088	0.090	0.090	0.082	0.085	0.086	0.085
CG1	σ	0.068	0.057	0.057	0.052	0.053	0.052	0.048	0.050	0.050	0.049
CG1s		0.064	0.055	0.055	0.050	0.051	0.051	0.046	0.047	0.048	0.047
CG2		0.067	0.056	0.056	0.050	0.051	0.051	0.047	0.048	0.048	0.047
MSC		0.085	0.070	0.071	0.064	0.066	0.066	0.058	0.060	0.060	0.060
BEKK		0.047	0.025	0.263	0.020	0.281	0.613	0.013	0.288	0.652	0.923
DCC		0.001	0.002	0.010	0.001	0.008	0.040	0.001	0.009	0.073	0.243
EDCC		0.185	0.183	0.388	0.189	0.404	0.575	0.180	0.421	0.592	0.777
CG1	p_1	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.000	0.003	0.026
CG1s		0.001	0.000	0.001	0.000	0.002	0.006	0.000	0.000	0.012	0.094
CG2		0.000	0.000	0.001	0.000	0.001	0.013	0.000	0.001	0.019	0.127
MSC		0.000	0.000	0.023	0.000	0.030	0.119	0.000	0.031	0.156	0.373
BEKK		0.009	0.009	0.022	0.006	0.027	0.027	0.011	0.039	0.036	0.044
DCC		0.000	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001
EDCC		0.103	0.140	0.158	0.149	0.165	0.152	0.173	0.203	0.184	0.177
CG1	p_2	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
CG1s		0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
CG2		0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
MSC		0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.001	0.001

Table 10: Statistics for contagion type 2, FTSE-DAX

$\mathscr{M} = (\beta, 1)$	β	0.1	0.15		0.18			0.21			
$\mathscr{T} = (\alpha, 0)$	α	0.1	0.1	0.15	0.1	0.15	0.18	0.1	0.15	0.18	0.21
emp Δ		-0.035	-0.023	0.044	0.016	0.083	0.115	0.005	0.072	0.104	0.152
BEKK		-0.069	-0.069	-0.002	-0.068	0.000	0.042	-0.066	0.002	0.045	0.088
DCC		-0.232	-0.207	-0.146	-0.192	-0.131	-0.094	-0.179	-0.118	-0.080	-0.043
EDCC		-0.143	-0.126	-0.070	-0.116	-0.060	-0.026	-0.108	-0.052	-0.017	0.017
CG1	μ	-0.280	-0.251	-0.193	-0.235	-0.177	-0.140	-0.220	-0.162	-0.126	-0.089
CG1s		-0.249	-0.220	-0.165	-0.206	-0.150	-0.115	-0.191	-0.136	-0.101	-0.064
CG2		-0.247	-0.220	-0.160	-0.206	-0.146	-0.109	-0.192	-0.132	-0.095	-0.058
MSC		-0.225	-0.194	-0.135	-0.177	-0.117	-0.080	-0.161	-0.101	-0.064	-0.027
BEKK		0.064	0.051	0.052	0.045	0.046	0.046	0.041	0.042	0.043	0.043
DCC		0.054	0.045	0.044	0.043	0.042	0.040	0.040	0.040	0.039	0.037
EDCC		0.102	0.091	0.091	0.084	0.085	0.085	0.078	0.079	0.079	0.079
CG1	σ	0.067	0.058	0.057	0.054	0.055	0.054	0.049	0.051	0.051	0.050
CG1s		0.068	0.057	0.057	0.053	0.054	0.054	0.048	0.050	0.050	0.050
CG2		0.071	0.061	0.061	0.056	0.057	0.056	0.051	0.052	0.053	0.052
MSC		0.086	0.070	0.071	0.063	0.065	0.065	0.058	0.060	0.060	0.060
BEKK		0.128	0.092	0.480	0.066	0.492	0.831	0.053	0.528	0.861	0.979
DCC		0.000	0.000	0.000	0.000	0.001	0.010	0.000	0.002	0.023	0.117
EDCC		0.082	0.078	0.207	0.082	0.221	0.337	0.081	0.229	0.361	0.557
CG1	p_1	0.000	0.000	0.001	0.000	0.000	0.002	0.000	0.000	0.003	0.023
CG1s		0.000	0.000	0.000	0.000	0.000	0.004	0.000	0.000	0.011	0.076
CG2		0.000	0.000	0.002	0.000	0.002	0.020	0.001	0.004	0.026	0.115
MSC		0.001	0.000	0.019	0.001	0.022	0.087	0.000	0.032	0.132	0.346
BEKK		0.289	0.167	0.177	0.033	0.033	0.066	0.039	0.045	0.080	0.069
DCC		0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
EDCC		0.142	0.127	0.098	0.066	0.056	0.059	0.072	0.067	0.071	0.058
CG1	p_2	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
CG1s		0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
CG2		0.001	0.000	0.000	0.000	0.000	0.000	0.001	0.001	0.001	0.001
MSC		0.005	0.002	0.002	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Table 11: Statistics for contagion type 3, FTSE-DAX

$\mathscr{M} = (\beta, \beta)$	β	0.1	0.15		0.18			0.21			
$\mathscr{T} = (\alpha, \alpha)$	α	0.1	0.1	0.15	0.1	0.15	0.18	0.1	0.15	0.18	0.21
emp Δ		0.090	0.024	0.088	0.082	0.145	0.196	0.098	0.162	0.212	0.273
BEKK		-0.012	-0.011	0.081	-0.009	0.083	0.141	-0.009	0.083	0.141	0.199
DCC		-0.205	-0.175	-0.087	-0.162	-0.073	-0.021	-0.149	-0.060	-0.008	0.040
EDCC		-0.060	-0.028	0.044	-0.013	0.059	0.103	-0.002	0.070	0.113	0.157
CG1	μ	-0.263	-0.228	-0.145	-0.212	-0.128	-0.078	-0.197	-0.113	-0.063	-0.014
CG1s		-0.193	-0.155	-0.082	-0.140	-0.067	-0.021	-0.127	-0.054	-0.008	0.038
CG2		-0.220	-0.193	-0.106	-0.178	-0.091	-0.039	-0.164	-0.077	-0.025	0.024
MSC		-0.119	-0.096	-0.022	-0.083	-0.009	0.035	-0.073	0.001	0.045	0.089
BEKK		0.077	0.064	0.065	0.056	0.057	0.058	0.050	0.051	0.052	0.053
DCC		0.082	0.064	0.062	0.056	0.054	0.054	0.051	0.049	0.048	0.048
EDCC		0.120	0.107	0.105	0.103	0.100	0.098	0.097	0.094	0.092	0.090
CG1	σ	0.097	0.076	0.077	0.068	0.069	0.070	0.061	0.061	0.062	0.064
CG1s		0.092	0.073	0.074	0.063	0.065	0.065	0.058	0.058	0.059	0.060
CG2		0.094	0.074	0.076	0.067	0.069	0.070	0.062	0.063	0.064	0.065
MSC		0.098	0.078	0.081	0.070	0.072	0.074	0.063	0.066	0.067	0.069
BEKK		0.422	0.404	0.896	0.414	0.926	0.995	0.404	0.948	0.999	1.000
DCC		0.006	0.004	0.085	0.003	0.085	0.350	0.001	0.103	0.430	0.814
EDCC		0.281	0.342	0.651	0.397	0.712	0.861	0.445	0.766	0.912	0.981
CG1	p_1	0.003	0.001	0.032	0.000	0.031	0.123	0.001	0.026	0.150	0.423
CG1s		0.017	0.015	0.134	0.016	0.152	0.369	0.011	0.168	0.455	0.755
CG2		0.013	0.010	0.072	0.009	0.089	0.269	0.005	0.089	0.344	0.656
MSC		0.103	0.103	0.424	0.109	0.460	0.697	0.121	0.520	0.759	0.897
BEKK		0.091	0.268	0.450	0.052	0.140	0.169	0.023	0.068	0.098	0.086
DCC		0.000	0.004	0.004	0.000	0.000	0.000	0.000	0.000	0.000	0.000
EDCC		0.111	0.284	0.306	0.158	0.175	0.158	0.135	0.146	0.133	0.098
CG1	p_2	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000
CG1s		0.000	0.008	0.011	0.000	0.001	0.000	0.000	0.000	0.000	0.000
CG2		0.003	0.004	0.008	0.000	0.001	0.000	0.000	0.000	0.000	0.000
MSC		0.012	0.060	0.087	0.008	0.013	0.009	0.002	0.007	0.005	0.005

Table 12: Statistics of global contagion type 1,2 and 3, FTSE-DAX

Measure		γ_1	γ_2	γ_3	γ_{1a}	γ_{2a}	γ_{3a}
emp value		0.772	0.755	0.935	0.913	0.790	0.975
BEKK		0.541	0.594	0.749	0.706	0.758	0.861
DCC		0.394	0.376	0.518	0.553	0.537	0.653
EDCC		0.582	0.496	0.770	0.718	0.643	0.801
CG1	μ_2	0.316	0.310	0.441	0.482	0.478	0.587
CG1s		0.351	0.344	0.535	0.517	0.509	0.654
CG2		0.360	0.355	0.493	0.525	0.520	0.631
MSC		0.427	0.419	0.624	0.574	0.566	0.730
BEKK		0.084	0.089	0.090	0.089	0.095	0.087
DCC		0.082	0.064	0.065	0.072	0.053	0.067
EDCC		0.189	0.167	0.154	0.155	0.142	0.111
CG1	σ_2	0.069	0.067	0.076	0.063	0.062	0.080
CG1s		0.070	0.071	0.090	0.064	0.063	0.084
CG2		0.072	0.076	0.083	0.065	0.069	0.083
MSC		0.096	0.095	0.116	0.084	0.084	0.104
BEKK		0.009	0.046	0.030			
DCC		0.001	0.000	0.000			
EDCC		0.172	0.083	0.204			
CG1	p_3	0.000	0.000	0.000		–	
CG1s		0.000	0.000	0.000			
CG2		0.000	0.001	0.000			
MSC		0.000	0.000	0.007			
BEKK					0.035	0.283	0.132
DCC					0.001	0.000	0.000
EDCC					0.139	0.146	0.065
CG1	p_4		–		0.000	0.000	0.000
CG1s					0.000	0.000	0.002
CG2					0.000	0.001	0.002
MSC					0.000	0.006	0.017

8 Summary

From test statistics and previous observations the following general conclusions could be derived:

- In all mGARCH models (within the models based on normal or Student distribution for general data fit), the contagion effect is too small (in comparison with the sample).
- From given mGARCH models, BEKK provides the best fit for contagion effect and is vitally better than other mGARCH models. EDCC and MSC models could be taken into consideration as well.

It is worth noticing that better performance of BEKK and EDCC might be the result of the so-called volatility spillover effect. Also, models other than BEKK in some way separate the estimation procedure into two steps. In the beginning the marginal densities are derived and then the multivariate dependence structure is taken into consideration. It could lead to serious loss of information (when dynamic model is considered). Most of copula-based GARCH models are strongly connected with that idea (two step estimation) and because of that they are not very good for modelling contagion.

According to the knowledge of the authors there are no models which could efficiently join the dynamic behaviour of the margins, with dynamics of the copula (simultaneously guaranteeing any substantial benefit from using copula function). Also, the theory of dynamic copula is still not very-well developed.

Perhaps, the most promising class of models (for copulas) are MSC models which provide Markov switching in the margins and assume dynamics in every class (i.e. state) of copula. Still, the estimation procedure must not be separated (as switches in the copula is too strongly associated with switches in the tails) so further development of that models in needed. Also extreme value copulas might play important role as (crisis-time) conditional copulas.

We want to underline the fact, that our study was held within the class of models designed for general fit for the data. When we consider specific class for copulas, which are designed to catch contagion effect – like Clayton copula – then the results may vary. For example, in Table 13 we present previously considered statistics for contagion type 1 for CG1sg (Survival-Gumbel-GARCH(1,1)) and CG1c (Clayton-GARCH(1,1)) models (MLE fitted parameters as in previous models). Let us point out that such copulas usually provide good fit for contagion effect but they might lack good overall fit for the data. In fact, for mGARCH models (CG1), ML (i.e. maximum log-likelihood of copula) for model based on normal copula is equal to 1741, t-Student copula – 1845, Clayton – 1557, Survival-Gumbel – 1805. As we can see CG1c lacks good overall fit. On the other hand CG1sg provides general fit but contagion-fit is worse than in BEKK model. It is also worth mentioning

that fit for the upper tail (associated with boom period), is very poor both in Clayton and Survival-Gumbel.

In future's work authors will show how mGARCH models behave (in copula framework) when temporal copula contagion is considered (i.e. copula is conditioned over sample volatility value – time-space is divided into sets with high and low volatility).

Table 13: Statistics for contagion-fit copulas, contagion type 1, FTSE-DAX

$\mathscr{M}=(1,\beta)$	β	0.1	0.15		0.18			0.21			
$\mathscr{T}=(0,\alpha)$	α	0.1	0.1	0.15	0.1	0.15	0.18	0.1	0.15	0.18	0.21
emp Δ		0.054	0.021	0.074	0.016	0.069	0.110	0.002	0.054	0.096	0.134
BEKK		-0.104	-0.097	-0.032	-0.093	-0.028	0.014	-0.089	-0.024	0.018	0.061
CG1c	μ	-0.096	-0.057	-0.004	-0.037	0.017	0.050	-0.020	0.034	0.067	0.100
CG1sg		-0.165	-0.129	-0.073	-0.112	-0.055	-0.019	-0.096	-0.040	-0.004	0.033
BEKK		0.061	0.050	0.051	0.045	0.047	0.047	0.041	0.043	0.043	0.043
CG1c	σ	0.078	0.063	0.063	0.057	0.057	0.057	0.051	0.052	0.052	0.052
CG1sg		0.073	0.058	0.059	0.053	0.054	0.054	0.048	0.049	0.050	0.050
BEKK		0.047	0.025	0.263	0.020	0.281	0.613	0.013	0.288	0.652	0.923
CG1c	p_1	0.089	0.181	0.503	0.259	0.631	0.820	0.352	0.750	0.911	0.966
CG1sg		0.003	0.004	0.089	0.005	0.148	0.391	0.010	0.213	0.495	0.772
BEKK		0.009	0.009	0.022	0.006	0.027	0.027	0.011	0.039	0.036	0.044
CG1c	p_2	0.018	0.099	0.098	0.181	0.185	0.142	0.342	0.354	0.290	0.252
CG1sg		0.000	0.000	0.000	0.000	0.001	0.000	0.008	0.019	0.014	0.009

9 Proofs

Proof of Proposition 4.1.
Let (U,V) be a pair of random variables with distribution function C. Consider the set $\mathscr{M}_{\beta,\beta}=[\beta,1-\beta]\times[\beta,1-\beta]$. Set $\beta=\frac{1}{2}-t$. Let $F_{\mathscr{M}_{\beta,\beta}}$ be the conditional distribution function of $[(U,V)\mid\mathscr{M}_{\beta,\beta}]$. For every $(x,y)\in[-1,1]^2$ we have

$$\begin{aligned} F_{\mathscr{M}_{\beta,\beta}}\left(\frac{1}{2}+tx,\frac{1}{2}+ty\right) &= \frac{V_C([\frac{1}{2}-t,\frac{1}{2}+tx]\times[\frac{1}{2}-t,\frac{1}{2}+ty])}{V_C([\frac{1}{2}-t,\frac{1}{2}+t]\times[\frac{1}{2}-t,\frac{1}{2}+t])} \\ &= \frac{\int_{-1}^{y}\int_{-1}^{x}c(\frac{1}{2}+tu,\frac{1}{2}+tv)dudv}{\int_{-1}^{1}\int_{-1}^{1}c(\frac{1}{2}+tu,\frac{1}{2}+tv)dudv}. \end{aligned} \tag{10}$$

For $t\to 0$, we obtain that the above expression tends to

$$\frac{\int_{-1}^{y}\int_{-1}^{x}c(\frac{1}{2},\frac{1}{2})dudv}{\int_{-1}^{1}\int_{-1}^{1}c(\frac{1}{2},\frac{1}{2})dudv}=\frac{(x+1)(y+1)c(\frac{1}{2},\frac{1}{2})}{4c(\frac{1}{2},\frac{1}{2})}=\frac{(x+1)(y+1)}{4}.$$

This fact can be seen by using the Dominated Convergence Theorem and the continuity of c at the point $\left(\frac{1}{2}, \frac{1}{2}\right)$,

$$c\left(\frac{1}{2}+tu, \frac{1}{2}+tv\right) \xrightarrow{t\to 0} c\left(\frac{1}{2}, \frac{1}{2}\right),$$

for all $(u, v) \in [-1, 1]^2$. Since the conditional distribution function $F_{\mathscr{M}_{\beta,\beta}}$ tends to the product of univariate distribution functions (after a linear transformation of its arguments as in (10)), the limiting copula of $C_{\mathscr{M}_{\beta,\beta}}$ is Π.

□

Proof of Proposition 4.2.

As in the previous proof, let (U, V) be a pair of random variables with distribution function C. Consider the set $\mathscr{M}_{\beta,0} = [\beta, 1-\beta] \times [0, 1]$. Set $\beta = \frac{1}{2} - t$. Let $F_{\mathscr{M}_{\beta,0}}$ be the conditional distribution function of $[(U, V) \mid \mathscr{M}_{\beta,0}]$. For every $(x, y) \in [-1, 1] \times [0, 1]$, we have

$$\begin{aligned} F_{\mathscr{M}_{\beta,0}}\left(\frac{1}{2}+tx, y\right) &= \frac{V_C([\frac{1}{2}-t, \frac{1}{2}+tx] \times [0, y])}{2t} \\ &= \frac{1}{2}\int_0^y \int_{-1}^x c\left(\frac{1}{2}+tu, v\right) dudv. \end{aligned} \tag{11}$$

As $t \to 0$, the above expression tends to

$$\frac{1}{2}\int_0^y \int_{-1}^x c\left(\frac{1}{2}, v\right) dudv = \frac{x+1}{2}\int_0^y c\left(\frac{1}{2}, v\right) dv,$$

for all $(u, v) \in [-1, 1] \times [0, 1]$. This fact can be seen by using the Dominated Convergence Theorem and the continuity of c at all points of the set $\left\{\frac{1}{2}\right\} \times [0, 1]$. Since the conditional distribution function $F_{\mathscr{M}_{\beta,0}}$ tends to the product of univariate distribution functions (after a linear transformation of its first argument as in (11)), then the limiting copula of $C_{\mathscr{M}_{\beta,0}}$ is Π. □

Proof of Theorem 4.1.

We recall that

$$C_{\mathscr{T}_{\alpha,1}}(x, y) = \frac{C(\alpha x, \Phi_\alpha^{-1}(y))}{\alpha},$$

where

$$\Phi_\alpha(y) = \frac{C(\alpha, y)}{\alpha}.$$

For fixed y and α the function

$$H(x) = \frac{\partial}{\partial \alpha} G_{r,\mathscr{T}_{\alpha,1}}(x, y)$$

is vanishing for $x = 0$ and $x = 1$. Since Gaussian copulas are analytic on the open square $(0, 1)^2$, we get

$$\begin{aligned} H'(x) &= \frac{\partial}{\partial x}\frac{\partial}{\partial \alpha} G_{r,\mathscr{T}_{\alpha,1}}(x, y) = \frac{\partial}{\partial \alpha}\frac{\partial}{\partial x} G_{r,\mathscr{T}_{\alpha,1}}(x, y) = \frac{\partial}{\partial \alpha}\partial_1 G_r(\alpha x, \Phi_\alpha^{-1}(y)) \\ &= \frac{\partial}{\partial \alpha} F\left(\frac{F^{-1}(\Phi_\alpha^{-1}(y)) + rF^{-1}(\alpha x)}{\sqrt{1-r^2}}\right) \\ &= \frac{1}{\sqrt{1-r^2}} f\left(\frac{F^{-1}(\Phi_\alpha^{-1}(y)) - rF^{-1}(\alpha x)}{\sqrt{1-r^2}}\right)\left(\frac{\partial}{\partial \alpha} F^{-1}(\Phi_\alpha^{-1}(y))) - r\frac{x}{f(F^{-1}(\alpha x))}\right), \end{aligned}$$

where f is a density of F.

The density f is positive everywhere and $\frac{\partial}{\partial \alpha} F^{-1}(\Phi_\alpha^{-1}(y)))$ is not depending on x. We will show that $\frac{x}{f(F^{-1}(\alpha x))}$ is increasing in x.

Let $x = \frac{F(q)}{\alpha}$. We have

$$\frac{x}{f(F^{-1}(\alpha x))} = \frac{F(q)}{\alpha f(q)}.$$

$$\frac{\partial}{\partial q}\frac{F(q)}{f(q)} = 1 - \frac{F(q)f'(q)}{f(q)^2} = 1 + \frac{qF(q)}{f(q)}.$$

Obviously for $q \geq 0$ the derivative is positive. For $q < 0$ positivity follows from the standard estimate

$$F(q) < \frac{f(q)}{-q}.$$

Since $\frac{F(q)}{f(q)}$ is increasing in q, $\frac{x}{f(F^{-1}(\alpha x))}$ is increasing in x. Therefore the derivative $H'(x)$ is vanishing only in one point, at which it changes sign from + to -. Hence $H(x)$ is non-negative.

□

Proof of Theorem 4.2.
First we observe that the product of the standard Gaussian distribution function and its density $F(q)/f(q)$ admits an asymptotic expansion

$$-q^{-1} + q^{-3} - 3q^{-5} + \cdots + (-1)^{k+1}\frac{(2k)!}{2^k k!}q^{-2k-1} + \ldots$$

for $q \to -\infty$. Indeed:

Lemma 9.1. *For every $n > 0$*

$$\lim_{x\to 0^+} x^{-n}\left[\frac{F(x^{-1})}{f(x^{-1})} - \sum_{0\leq k\leq \frac{n-1}{2}} (-1)^{k+1}\frac{(2k)!}{2^k k!}x^{2k+1}\right] = 0$$

PROOF.
We apply the l'Hôspital's rule and the equality

$$f'(x) = -xf(x).$$

Let $m = \left[\frac{n}{2}\right]$. We get

$$\lim_{x\to 0^+} x^{-n}\left[\frac{F(x^{-1})}{f(x^{-1})} - \sum_{k=0}^{m}(-1)^{k+1}\frac{(2k)!}{2^k k!}x^{2k+1}\right]$$

$$= \lim_{x\to 0^+} \frac{F(x^{-1}) - f(x^{-1})\sum_{k=0}^{m}(-1)^{k+1}\frac{(2k)!}{2^k k!}x^{2k+1}}{f(x^{-1})x^n}$$

$$\stackrel{H}{=} \lim_{x\to 0^+} \frac{-f(x^{-1})x^{-2} - f(x^{-1})x^{-3}\sum_{k=0}^{m}(-1)^{k+1}\frac{(2k)!}{2^k k!}x^{2k+1} - f(x^{-1})\sum_{k=0}^{m}(-1)^{k+1}\frac{(2k)!}{2^k k!}(2k+1)x^{2k}}{f(x^{-1})nx^{n-1} + x^{-3}f(x^{-1})x^n}$$

$$= \lim_{x\to 0^+} \frac{-1 - \sum_{k=0}^{m}(-1)^{k+1}\frac{(2k)!}{2^k k!}x^{2k} - \sum_{k=1}^{m+1}(-1)^{k}\frac{(2k-2)!}{2^{k-1}(k-1)!}(2k-1)x^{2k}}{x^{n-1} + nx^{n+1}}$$

$$= \lim_{x\to 0^+} \frac{(-1)^{m+1}\frac{(2m)!}{2^m(m)!}(2m+1)x^{2m}}{x^{n-1} + nx^{n+1}} = 0$$

□

Basing on the above lemma we get two more estimates.

Lemma 9.2. *For $x > 0$ and $q \to -\infty$*

$$\frac{F\left(q - \frac{\ln x}{q}\right)}{xF(q)} = 1 + O(q^{-2}).$$

PROOF.

$$\frac{F\left(q - \frac{\ln x}{q}\right)}{xF(q)} = \frac{f(q - q^{-1}\ln x)(q - q^{-1}\ln x)^{-1}(-1 + O(q^{-2})}{xf(q)q^{-1}(-1 + O(q^{-2})}$$

$$= \frac{1}{x}\exp\left(-\frac{1}{2}(-2\ln x + q^{-2}\ln^2 x)\right)\frac{1 + O(q^{-2})}{1 - q^{-2}\ln x} = 1 + O(q^{-2}).$$

□

Lemma 9.3. *For $x, v \in \mathbb{R}$, $x > 0$ and $q \to -\infty$*

$$\frac{G_r\left(F(q - q^{-1}\ln x), F(r(q + q^{-1}) + \sqrt{1-r^2}v)\right)}{F(q)} = xF\left(v + \frac{r\ln x}{\sqrt{1-r^2}}q^{-1}\right) + O(q^{-2}).$$

Proof.
We apply the l'Hôspital's rule and the equalities

$$\partial_1 G_r(x,y) = F\left(\frac{F^{-1}(y) - rF^{-1}(x)}{\sqrt{1-r^2}}\right),$$

$$\partial_2 G_r(x,y) = F\left(\frac{F^{-1}(x) - rF^{-1}(y)}{\sqrt{1-r^2}}\right).$$

We get

$$\begin{aligned}
&\lim_{q\to-\infty} q^2\left(\frac{G_r(F(q-q^{-1}\ln x), F(r(q+q^{-1})+\sqrt{1-r^2}v))}{F(q)} - xF\left(v+\frac{r\ln x}{\sqrt{1-r^2}}q^{-1}\right)\right)\\
&= \lim_{q\to-\infty} \frac{G_r(F(q-q^{-1}\ln x), F(r(q+q^{-1})+\sqrt{1-r^2}v)) - xF(v+\frac{r\ln x}{\sqrt{1-r^2}}q^{-1})F(q)}{F(q)q^{-2}}\\
&\overset{H}{=} \lim_{q\to-\infty} \frac{1}{f(q)q^{-2}-2F(q)q^{-3}}\left[F\left(v+\frac{r(1+\ln x)}{\sqrt{1-r^2}}q^{-1}\right) f(q-q^{-1}\ln x)(1+q^{-2}\ln x)\right.\\
&\quad +F\left(\sqrt{1-r^2}q - rv - \frac{r^2+\ln x}{\sqrt{1-r^2}}q^{-1}\right) f\left(r(q+q^{-1})+\sqrt{1-r^2}v\right) r(1-q^{-2})\\
&\quad \left.-xF\left(v+\frac{r\ln x}{\sqrt{1-r^2}}q^{-1}\right) f(q) - xf\left(v+\frac{r\ln x}{\sqrt{1-r^2}}q^{-1}\right)\frac{-r\ln x}{\sqrt{1-r^2}}q^{-2}F(q)\right]\\
&= \lim_{q\to-\infty} \frac{1}{q^{-2}-2q^{-4}+O(q^{-6})}\left[F\left(v+\frac{r(1+\ln x)}{\sqrt{1-r^2}}q^{-1}\right)x(1+O(q^{-2})) - xF\left(v+\frac{r\ln x}{\sqrt{1-r^2}}q^{-1}\right)\right.\\
&\quad \left.+\frac{f\left(\sqrt{1-r^2}q - rv - \frac{r^2+\ln x}{\sqrt{1-r^2}}q^{-1}\right) f\left(r(q+q^{-1})+\sqrt{1-r^2}v\right) r(1+O(q^{-2}))}{f(q)\left(\sqrt{1-r^2}q - rv - \frac{r^2+\ln x}{\sqrt{1-r^2}}q^{-1}\right)} + O(q^{-3})\right]\\
&= \lim_{q\to-\infty} \frac{1}{q^{-2}-O(q^{-4})}\left[xf\left(v+\frac{r\ln x}{\sqrt{1-r^2}}q^{-1}\right)\frac{r}{\sqrt{1-r^2}}q^{-1} - O(q^{-2})\right.\\
&\quad \left.-\frac{r}{\sqrt{1-r^2}}\frac{1}{\sqrt{2\pi}}\exp\left(-\frac{1}{2}v^2+\ln x - \frac{rv(1+\ln x)}{\sqrt{1-r^2}}q^{-1}+O(q^{-2})\right)\frac{q^{-1}}{1-O(q^{-1})}\right]\\
&= \lim_{q\to-\infty} q^2\left[xf(v)\frac{r}{\sqrt{1-r^2}}q^{-1} - \frac{r}{\sqrt{1-r^2}}f(v)xq^{-1} + O(q^{-2})\right].
\end{aligned}$$

The above limit exists and is finite.

□

Now we are in position to prove the theorem. Besides the above lemmas we will use the fact that copulas are Lipschitz functions and for $q \to -\infty$ we get

$$G_r(x+O(q^{-2}), y+O(q^{-2})) = G_r(x,y) + O(q^{-2}).$$

We put $q = F^{-1}(\alpha)$.

$$G_{r,\mathscr{T}_{\alpha,1}}(x, F(v)) = G_{r,\mathscr{T}_{\alpha,1}}\left(x, \frac{G_r\left(F(q), F(r(q+q^{-1}) + \sqrt{1-r^2}v)\right)}{F(q)} + O(q^{-2})\right)$$

$$= G_{r,\mathscr{T}_{\alpha,1}}\left(x, \frac{G_r\left(F(q), F(r(q+q^{-1}) + \sqrt{1-r^2}v)\right)}{F(q)}\right) + O(q^{-2})$$

$$= \frac{G_r\left(xF(q), F(r(q+q^{-1}) + \sqrt{1-r^2}v)\right)}{F(q)} + O(q^{-2})$$

$$= \frac{G_r\left(F\left(q - \frac{\ln x}{q}\right) - xF(q) + O(q^{-2}), F(r(q+q^{-1}) + \sqrt{1-r^2}v)\right)}{F(q)} + O(q^{-2})$$

$$= \frac{G_r\left(F\left(q - \frac{\ln x}{q}\right), F(r(q+q^{-1}) + \sqrt{1-r^2}v)\right)}{F(q)} + O(q^{-2}) =$$

$$= xF\left(v + \frac{r\ln x}{\sqrt{1-r^2}}q^{-1}\right) + O(q^{-2})$$

$$= xF(v) + xf(v)\frac{r\ln x}{\sqrt{1-r^2}}q^{-1} + O(q^{-2}).$$

Hence

$$G_{r,\mathscr{T}_{\alpha,1}}(x, y) = xy + xf(F^{-1}(y))\frac{r\ln x}{\sqrt{1-r^2}}q^{-1} + O(q^{-2}).$$

□

Proof of Theorem 4.3.
We recall that

$$C_{\mathscr{M}_{\beta,0}}(x, y) = \frac{C\left((1-2\beta)x + \beta, \Phi_\beta^{-1}(y)\right) - C\left(\beta, \Phi_\beta^{-1}(y)\right)}{1-2\beta},$$

where

$$\Phi_\beta(v) = \frac{C(1-\beta, v) - C(\beta, v)}{1-2\beta}.$$

For fixed y and α the function

$$H(x) = \frac{\partial}{\partial\beta}C_{\mathscr{M}_{\beta,0}}(x, y)$$

is vanishing for $x = 0$ and $x = 1$. Since Gaussians copulas are analytic on the open square $(0, 1)^2$, we get

$$H'(x) = \frac{\partial}{\partial x}\frac{\partial}{\partial\beta}G_{r,\mathscr{M}_{\beta,0}}(x, y)$$

$$= \frac{\partial}{\partial\beta}\frac{\partial}{\partial x}G_{r,\mathscr{M}_{\beta,0}}(x,y) = \frac{\partial}{\partial\beta}\partial_1 G_r((1-2\beta)x+\beta, \Phi_\beta^{-1}(y))$$

$$= \frac{\partial}{\partial\beta}F\left(\frac{F^{-1}(\Phi_\beta^{-1}(y)) + rF^{-1}((1-2\beta)x+\beta)}{\sqrt{1-r^2}}\right)$$

$$= f\left(\frac{F^{-1}(\Phi_\beta^{-1}(y)) - rF^{-1}((1-2\beta)x+\beta)}{\sqrt{1-r^2}}\right)\left(\frac{\partial}{\partial\beta}F^{-1}(\Phi_\beta^{-1}(y))) - r\frac{1-2x}{f(F^{-1}((1-2\beta)x+\beta))}\right).$$

The density f is positive everywhere and $\frac{\partial}{\partial\beta}F^{-1}(\Phi_\beta^{-1}(y)))$ is not depending on x. We will show that $\frac{1-2x}{f(F^{-1}((1-2\beta)x+\beta))}$ is increasing in x.

Let $q = F^{-1}((1-2\beta)x+\beta)$. We have

$$\frac{1-2x}{f(F^{-1}((1-2\beta)x+\beta))} = \frac{1-2F(q)}{(1-2\beta)f(q)}.$$

$$\frac{\partial}{\partial q}\frac{1-2F(q)}{f(q)} = -2 - \frac{(1-2F(q))f'(q)}{f(q)^2} = -2 + \frac{q(1-2F(q))}{f(q)}.$$

Obviously for every q the derivative is negative. Since $\frac{1-2F(q)}{f(q)}$ is decreasing in q,

$$\frac{1-2x}{f(F^{-1}((1-2\beta)x+\beta))}$$

is decreasing in x. Therefore the derivative $H'(x)$ is vanishing only in one point, at which it changes sign from - to +. Hence $H(x)$ is nonpositive.

□

Proof of Theorem 4.4.

Basing on the fact that the Gaussian distribution function is an analytic function on $(0,1)^2$ we apply the Taylor expansion. We recall that

$$G_{r,\mathscr{M}_{\beta,0}}(x,y) = \frac{G_r\left((1-2\beta)x+\beta, \Phi_\beta^{-1}(y)\right) - G_r\left(\beta, \Phi_\beta^{-1}(y)\right)}{1-2\beta},$$

where

$$\Phi_\beta(v) = \frac{G_r(1-\beta, v) - G_r(\beta, v)}{1-2\beta}.$$

Since $\Phi_0(v) = v$, we get

$$\Phi_\beta(v) - v = [2(G_r(1,v) - G_r(0,v)) - \partial_1 G_r(1,v) - \partial_1 G_r(0,v)]\beta + O(\beta^2) = (2v-1)\beta + O(\beta^2)$$

and

$$\Phi_\beta^{-1}(y) - y = (1-2y)\beta + O(\beta^2).$$

Therefore

$$G_{r,\mathscr{M}_{\beta,0}}(x,y) = \left(G_r\left((x+(1-2x)\beta, y+(1-2y)\beta\right) - G_r\left(\beta, y+(1-2y)\beta\right)\right)(1+2\beta)+O(\beta^2)$$

$$= G_r(x,y) + \left(2G_r(x,y) + \partial_1 G_r(x,y)(1-2x) + \partial_2 G_r(x,y)(1-2y) - \partial_1 G_r(0,y)\right]\beta + O(\beta^2).$$

Note that for $y > 0$ and $r > 0$

$$\partial_1 G_r(0,y) = F\left(\frac{F^{-1}(y) - rF^{-1}(0)}{\sqrt{1-r^2}}\right) = F(+\infty) = 1$$

□

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