# CDVine: An R-package for statistical inference of C- and D-vines

Ulf Schepsmeier & Eike Christian Brechmann

Technische Universität München

May 11, 2011

# Available software for vines

In general...

- "Uncertainty analysis with Correlations" (UNICORN, TU Delft) includes some functionality for vines.

In R...

- Packages for bivariate and multivariate copulas (`copula`, `fCopulae`, `QRMlib`, `nacopula`,...), but nothing regarding vines.
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# Scope of CDVine

CDVine provides functions for bivariate analysis...

- graphical tools
- analytical tools
- selection and estimation of bivariate copulas
- simulation of bivariate copulas

BiCop...

...and for multivariate analysis using canonical (C-) and D-vines.

- sequential and joint maximum likelihood estimation
- simulation of vine copulas
- model selection
- illustration of vine trees

CDVine...

General assumption: Data lies in the unit hypercube $[0,1]^d$.

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# The building blocks: Bivariate copula families

Each family is denoted by a number to shorten notation.

- Elliptical copulas:
  `family` = 1 Gaussian copula
  `family` = 2 Student-t copula
- One parameter Archimedean copulas:
- Two parameter Archimedean copulas:
  `family` = 7 Clayton-Gumbel (BB1) copula
  `family` = 9 Joe-Clayton (BB7) copula

The independence copula is denoted by 0.

Density, distribution & *h*-functions: `BiCopPDF`, `BiCopCDF` & `BiCopHfunc`.

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|  |  |  |
|---|---|---|
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| `family` = | 4 | Gumbel copula |
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| `family` = 13 | survival Clayton copula |
| `family` = 14 | survival Gumbel copula |
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| | | |
|---|---|---|
| `family` = | 23 | rotated Clayton copula (90 degrees) |
| `family` = | 24 | rotated Gumbel copula (90 degrees) |
| `family` = | 5 | Frank copula |
| `family` = | 26 | rotated Joe copula (90 degrees) |

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# Rotation of copulas

- Rotate asymmetric Archimedean copulas to capture negative dependence: if $(U_1, U_2) \sim C_{90^\circ}$, then $(1 - U_1, U_2) \sim C_{0^\circ}$.
- Survival copulas correspond to rotation by 180 degrees.

### Clayton copulas rotated by 0, 90, 180 and 270 degrees

```
> dat0 = BiCopSim(N = 500, family = 3, par = 2)
> dat90 = BiCopSim(N = 500, family = 23, par = -2)
> dat180 = BiCopSim(N = 500, family = 13, par = 2)
> dat270 = BiCopSim(N = 500, family = 33, par = -2)
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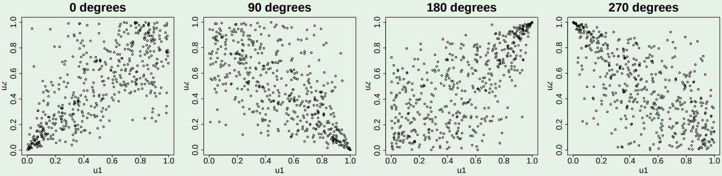

# Two parameter Archimedean copulas

- The BB1 and BB7 copulas can model asymmetric dependence with different non-zero lower and upper tail dependence.
- Density expressions and derivatives are however numerically involved.

### Clayton-Gumbel (BB1) copula

```
> BiCopPar2Tau(family = 7,
+     par = 0.25, par2 = 2.5)

[1] 0.64

> BiCopPar2TailDep(family = 7,
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$lower
[1] 0.33

$upper
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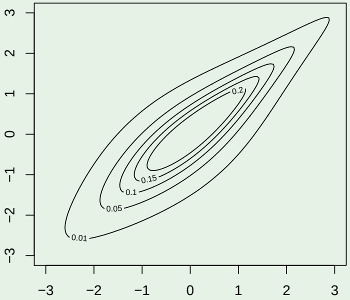
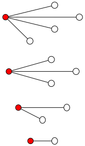
> BiCopMetaContour(family = 7,
+      par = 0.25, par2 = 2.5)
```



# Order of variables in C- and D-vines

- C-vine: specify characteristic order of root nodes for each tree.



- D-vine: specify characteristic order of nodes in the first tree.

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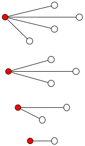

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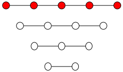

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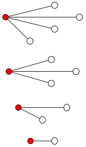

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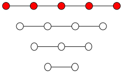

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# Specification of C- and D-vine copula models

Copula families (`family`) and parameters (`par` and `par2`) are specified as vectors of length $d(d-1)/2$ ($d = \#$variables). Entries:

- C-vine:

$$\underbrace{(1,2),(1,3),(1,4),\ldots,(1,d)}_{\text{1st tree}},\underbrace{(2,3|1),(2,4|1),\ldots,(2,d|1)}_{\text{2nd tree}},$$

$$\underbrace{(3,4|1,2),(3,5|1,2),\ldots,(3,d|1,2)}_{\text{3rd tree}},\ldots,\underbrace{(d-1,d|1,\ldots,d-2)}_{(d-1)\text{-th tree}}.$$

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# Example

Transformed residuals of daily log returns of major world stock indices in 2009 and 2010 (396 observations):

- S&P 500
- Nikkei 225
- SSE Composite Index
- DAX
- CAC 40
- FTSE 100 Index

Load into workspace:

```
> data(worldindices)
```

# Copula selection

- Manually using tools for bivariate analysis (e.g., contour plots or goodness-of-fit tests).
- Automatically using AIC or BIC: BiCopSelect (bivariate) or CDVineCopSelect (multivariate).

```
> DV = CDVineCopSelect(data = worldindices[, c(1,4,5,6,2,3)],
+      familyset = NA, type = "DVine", selectioncrit = "AIC")

$family
 [1]  9  2  2  9  9  1  2 14 14  3 24  5  5  2  6

$par
 [1]  1.91  0.96  0.94  1.17  1.15  0.15  0.07  1.09
 [9]  1.08  0.13 -1.08 -0.39 -0.27 -0.01  1.04

$par2
 [1]  1.21 14.93 13.76  0.22  0.32  0.00  8.71  0.00
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# Parameter estimation

- Sequential estimation (based on `BiCopEst`)
  - either using bivariate inversion of Kendall's $\tau$:

    ```
    > CDVineSeqEst(data, family, type, method="itau")
    ```
  - or bivariate maximum likelihood estimation:

    ```
    > CDVineSeqEst(data, family, type, method="mle")
    ```
- Maximum likelihood estimation of all parameters jointly (log-likelihood computation: `CDVineLogLik`).

```
> DV.mle = CDVineMLE(data = worldindices[, c(1,4,5,6,2,3)],
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# Discrimination among vine models

- AIC and BIC: `CDVineAIC` and `CDVineBIC`.
- Tests by Vuong (1989) and by Clarke (2007) for non-nested comparisons of two models.

```
> CDVineVuongTest(worldindices,
+     Model1.order = c(1,4,5,6,2,3), Model2.order = c(5,2,6,1,4,3),
+     Model1.family = DV$family, Model2.family = CV$family, ...)

$statistic
[1] 0.05

$statistic.Akaike
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$statistic.Schwarz
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$p.value
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# Illustrating C- and D-vine trees

Respective first trees of the C- and D-vine copulas models:

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> CDVineTreePlot(family = DV$family, ..., tree = 1,
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+     edge.labels = c("family", "theotau"))
> CDVineTreePlot(family = CV$family, ...)
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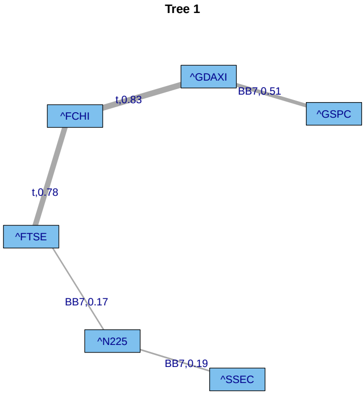

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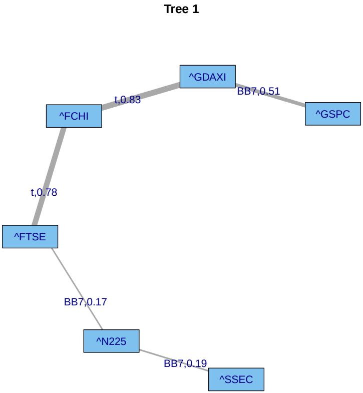
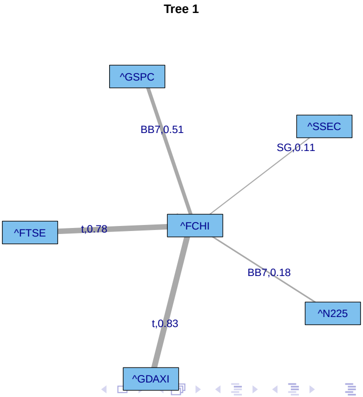


Tree 1



Tree 1

# Summary & conclusion

- Strong (positive) dependence among European indices.
- European indices central to explaining overall dependence.
- Indication of medium to strong tail dependence.
- Asymmetric (conditional) dependencies.
- No significant difference between C- and D-vine copula models.
  → Different interpretations possible based on tree structures.

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# Bibliography

Aas, K., C. Czado, A. Frigessi, and H. Bakken (2009).
Pair-copula constructions of multiple dependence.
*Insurance: Mathematics and Economics 44*(2), 182–198.

Clarke, K. A. (2007).
A simple distribution-free test for nonnested model selection.
*Political Analysis 15*(3), 347–363.

Czado, C., U. Schepsmeier, and A. Min (2011).
Maximum likelihood estimation of mixed C-vines with application to exchange rates.
*To appear in Statistical Modelling*.

Vuong, Q. H. (1989).
Ratio tests for model selection and non-nested hypotheses.
*Econometrica 57*(2), 307–333.

**Thank you very much for your attention!**

Visit: `http://cran.r-project.org/web/packages/CDVine/`