Statistical inference of vine copulas using the R-package `VineCopula`

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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`,...).
- Daniel Berg (U Oslo/NR): `copulaGOF`/`CopulaLib`.

The R-packages `VineCopula` and `CDVine` fill this gap.

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Scope of VineCopula

VineCopula 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 (simplified) regular vine copulas.

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

RVine...

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

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RVine...

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

The package CDVine

- Functionality for the sub-classes of C- and D-vines.
- Links to the package VineCopula: C2RVine and D2RVine.
- Vignette:

  Brechmann & Schepsmeier (2013).
  Modeling dependence with C- and D-vine copulas:
  The R-package CDVine.
  Journal of Statistical Software 52(3), 1–27.

The building blocks: Bivariate copula families

Each family is denoted by a number to shorten notation (0 = indep.).

- Elliptical copulas:

  `family` = 1 Gaussian copula

  `family` = 2 Student's t copula

- One parameter Archimedean copulas:

- Two parameter Archimedean copulas:

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

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  `family` = 3 Clayton copula
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- Two parameter Archimedean copulas:

  `family` = 7 Clayton-Gumbel (BB1) copula
  `family` = 8 Joe-Gumbel (BB6) copula
  `family` = 9 Joe-Clayton (BB7) copula
  `family` = 10 Joe-Frank (BB8) copula

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  - `family` = 1 Gaussian copula
  - `family` = 2 Student's t copula
- One parameter Archimedean copulas:
  - `family` = 13 survival Clayton copula
  - `family` = 14 survival Gumbel copula
  - `family` = 5 Frank copula
  - `family` = 16 survival Joe copula
- Two parameter Archimedean copulas:
  - `family` = 17 survival BB1 copula
  - `family` = 18 survival BB6 copula
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- One parameter Archimedean copulas:

  `family` = 23 rotated Clayton copula (90 degrees)
  `family` = 24 rotated Gumbel copula (90 degrees)
  `family` = 5 Frank copula
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- Two parameter Archimedean copulas:

  `family` = 27 rotated BB1 copula (90 degrees)
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  `family` = 33 rotated Clayton copula (270 degrees)
  `family` = 34 rotated Gumbel copula (270 degrees)
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  `family` = 37 rotated BB1 copula (270 degrees)
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- Elliptical copulas: (parameters: `par`, `par2` (degrees of freedom))

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- One parameter Archimedean copulas: (parameter: `par`)

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Rotation of copulas

- Rotate 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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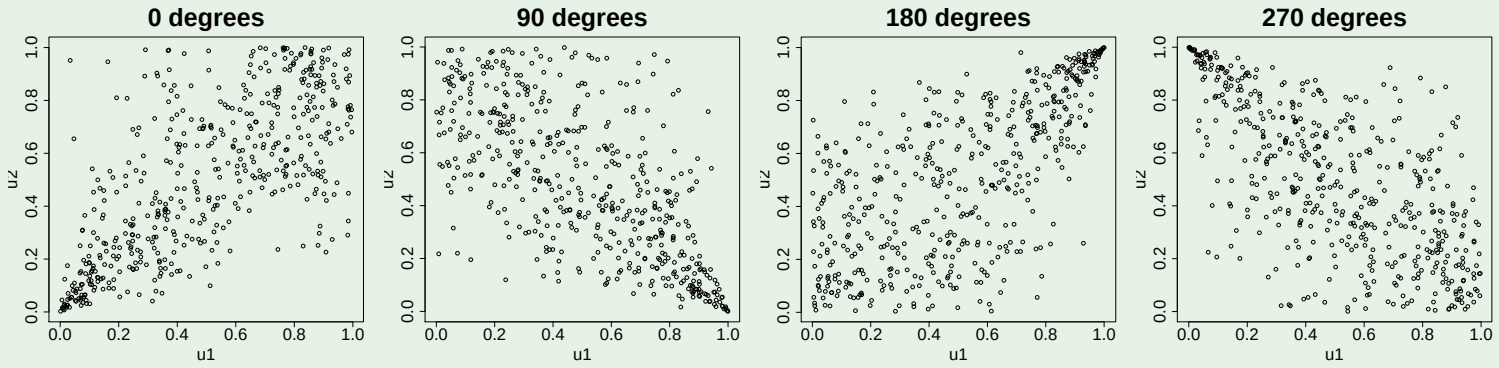

Two parameter Archimedean copulas

- The BB1 and the BB7 copula can model tail-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,
+     par=0.25, par2=2.5)

$lower
[1] 0.33

$upper
[1] 0.68
```

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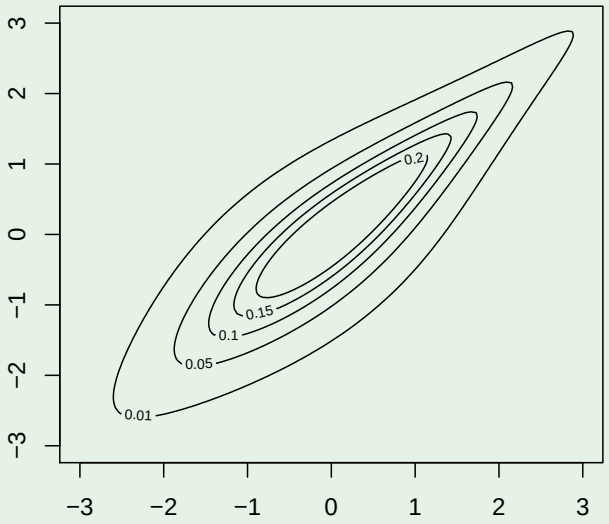
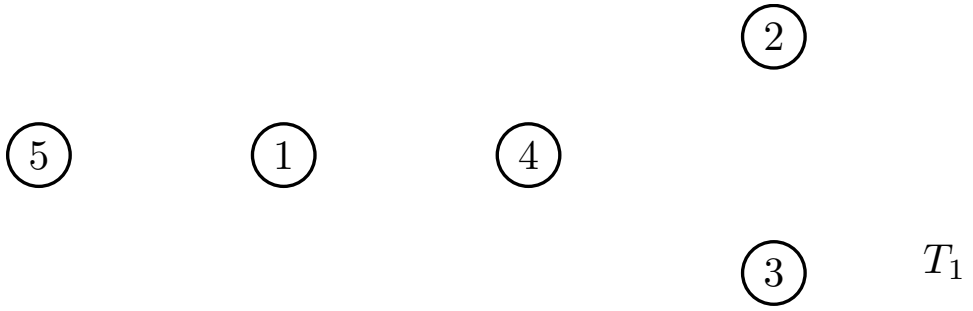
```

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



Reminder: R-vine copulas

Three components: vine trees, pair copulas, copula parameters



Density

$$c = c_{14} \cdot c_{15} \cdot c_{24} \cdot c_{34} \cdot c_{12;4} \cdot c_{13;4} \cdot c_{45;1} \cdot c_{23;14} \cdot c_{35;14} \cdot c_{25;134}$$

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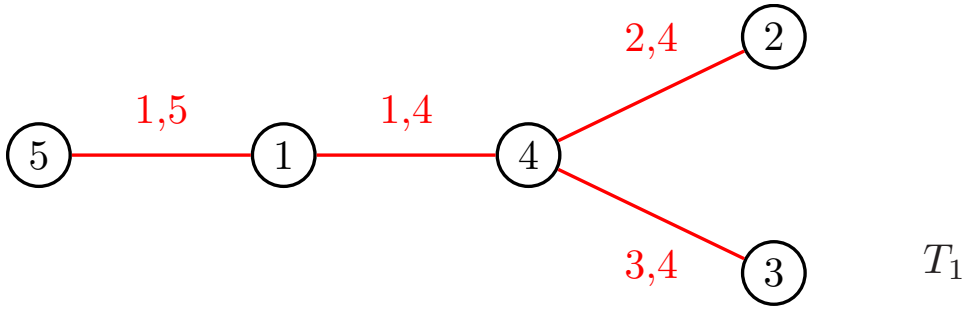

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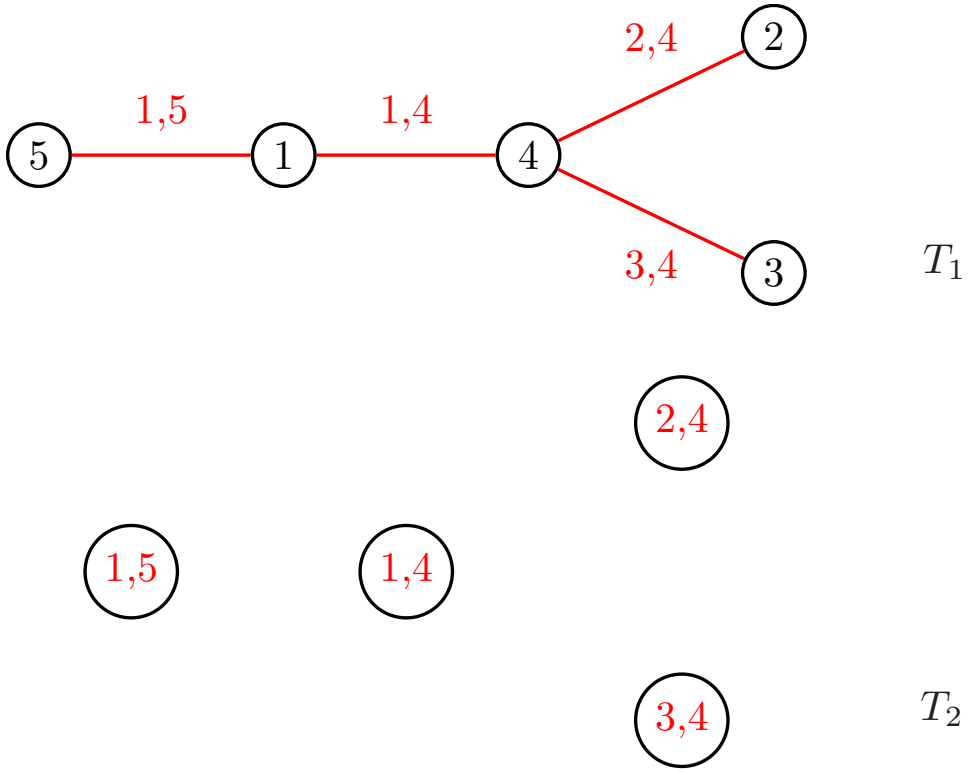

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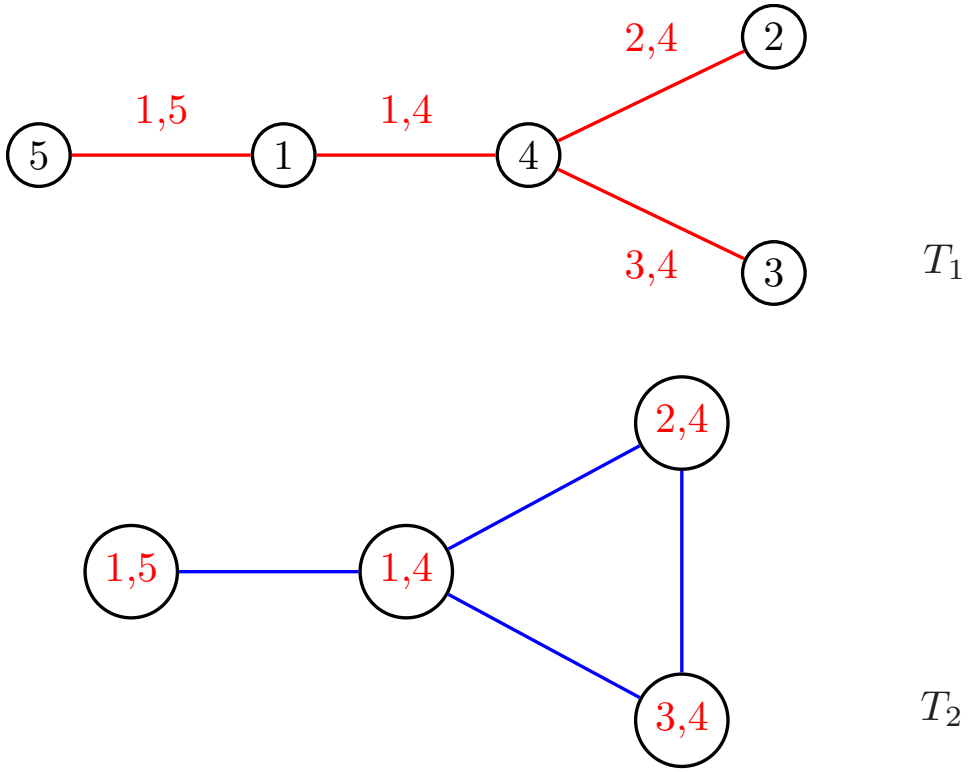

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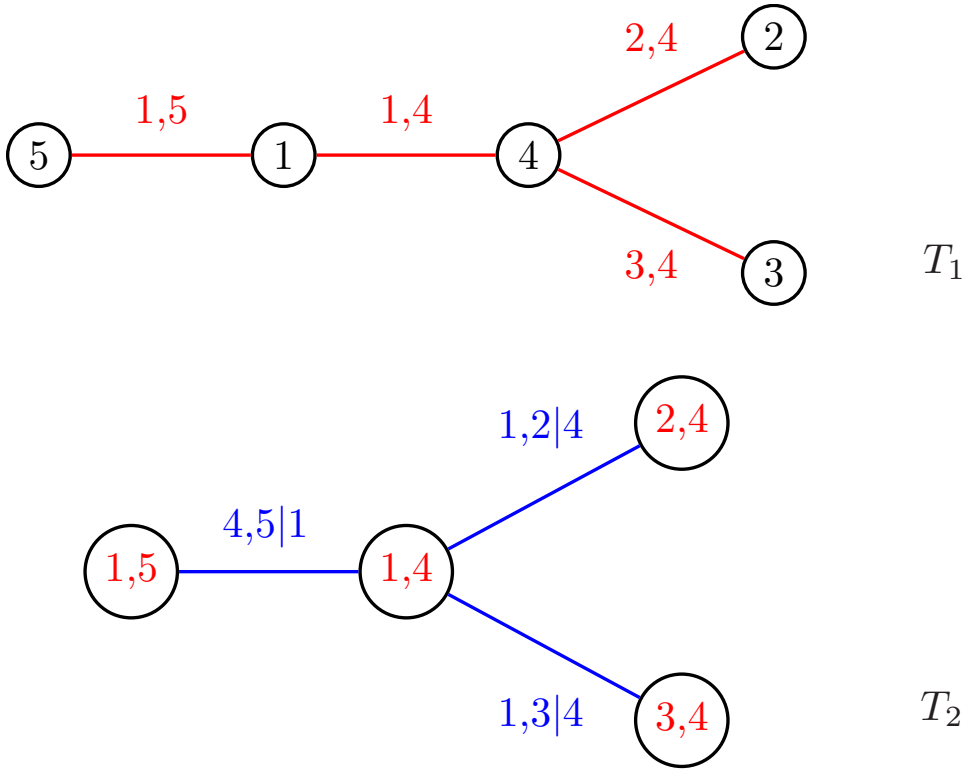

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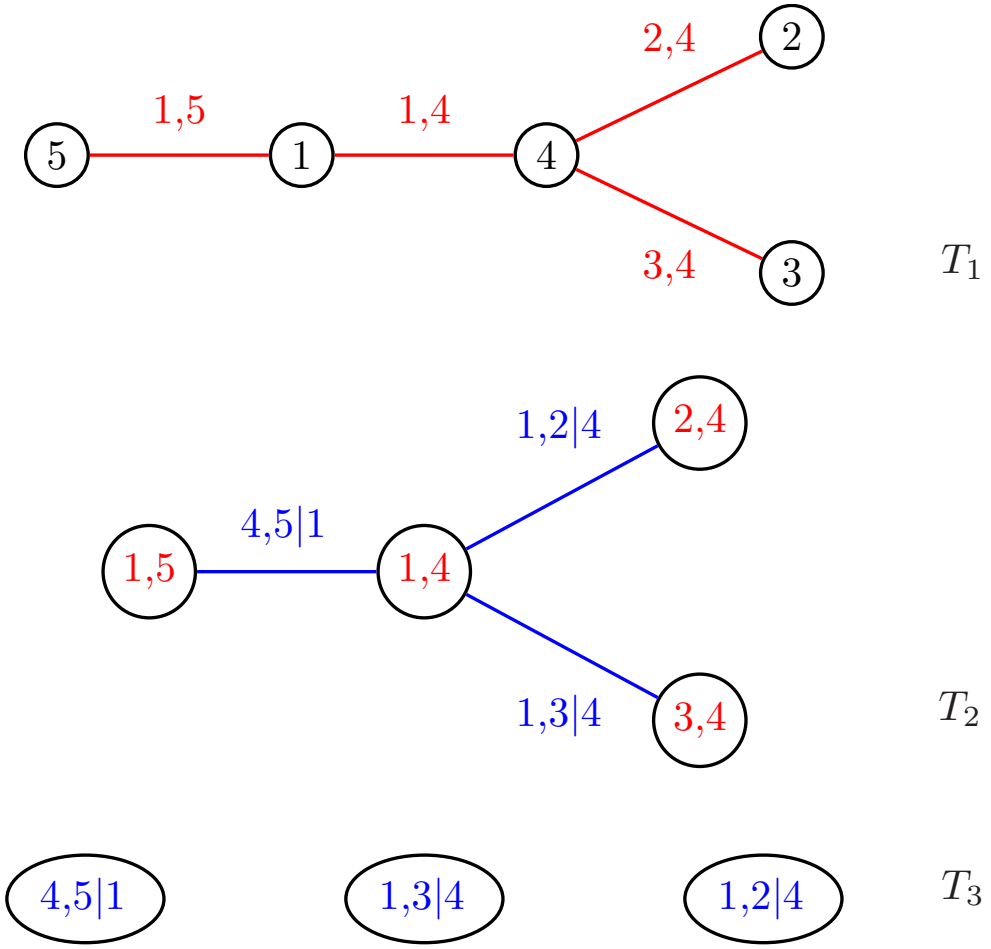

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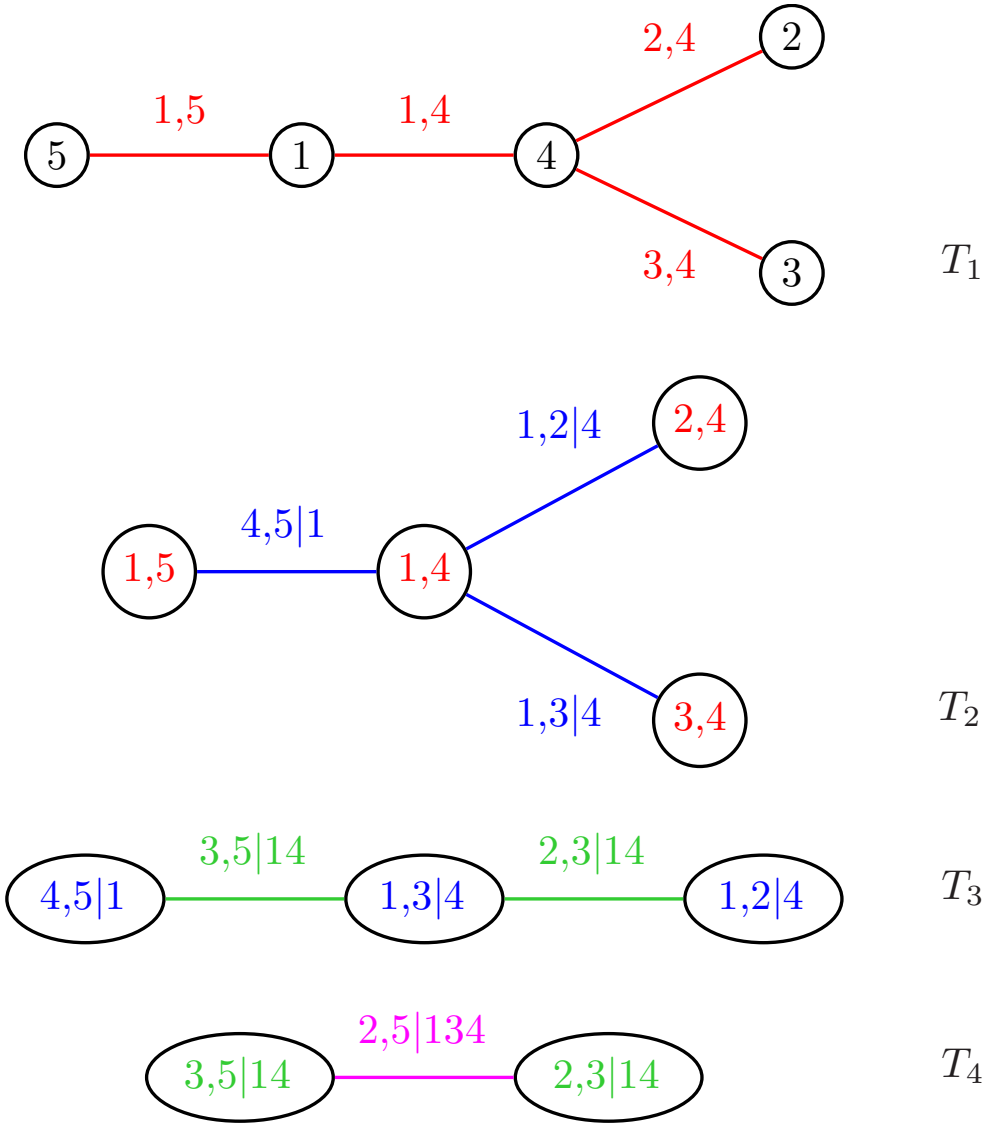

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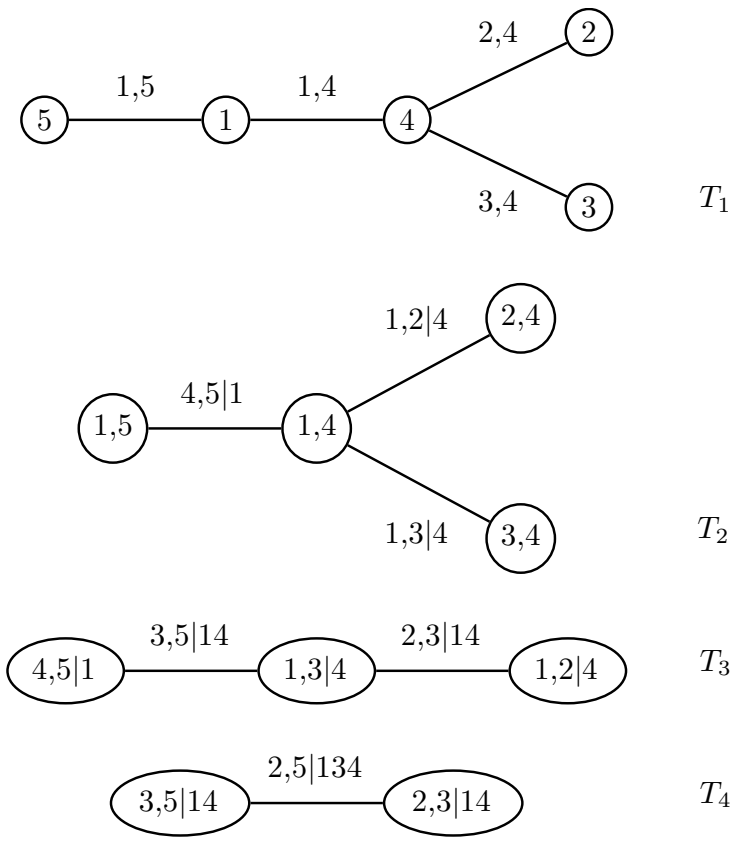
Storing R-vine copulas in matrix notation

Efficient enconding of R-vine models needed for statistical inference.

- Matrix notation by Morales-Nápoles et al. (2010) and Dißmann et al. (2013).

$$\begin{pmatrix} 2 & & & & \\ 5 & 3 & & & \\ 3 & 5 & 4 & & \\ 1 & 1 & 5 & 5 & \\ 4 & 4 & 1 & 1 & 1 \end{pmatrix}$$

1. $\{2,4\}, \{3,4\}, \{4,1\}, \{5,1\}$
2. $\{2,1|4\}, \{3,1|4\}, \{4,5|1\}$
3. $\{2,3|14\}, \{3,5|14\}$
4. $\{2,5|314\}$



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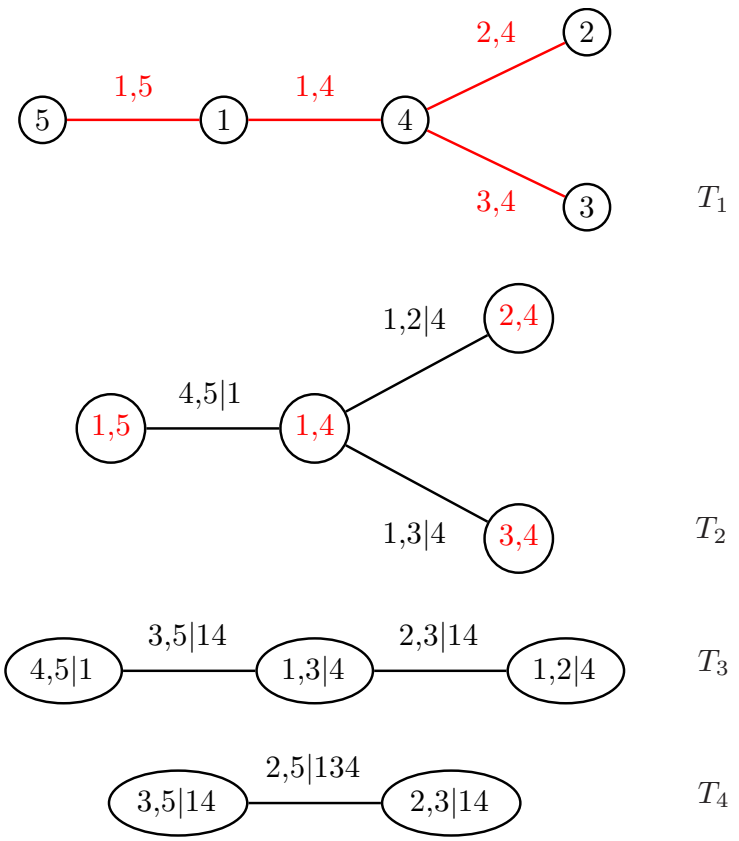

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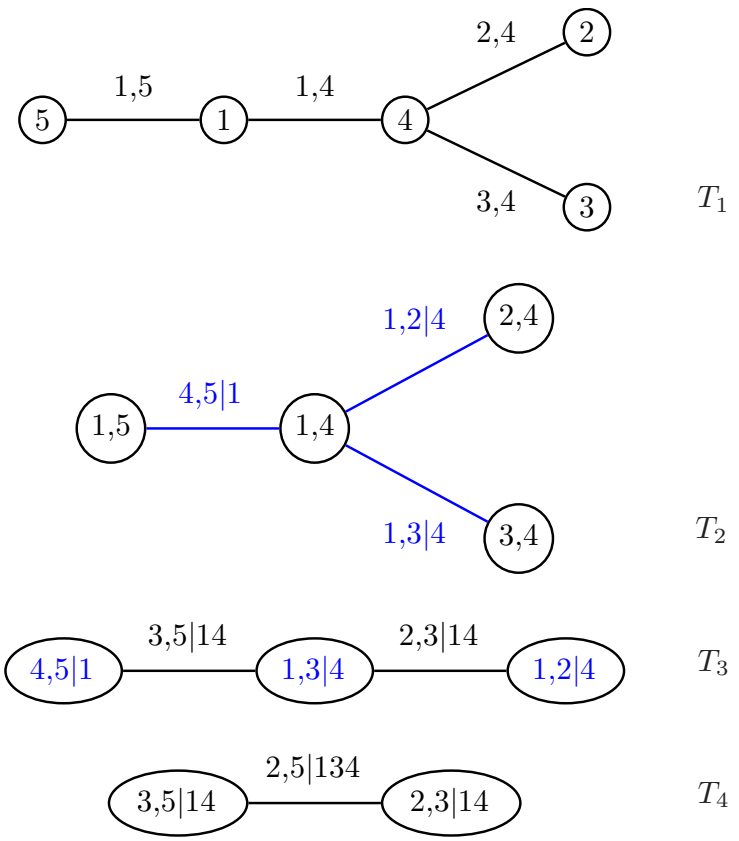

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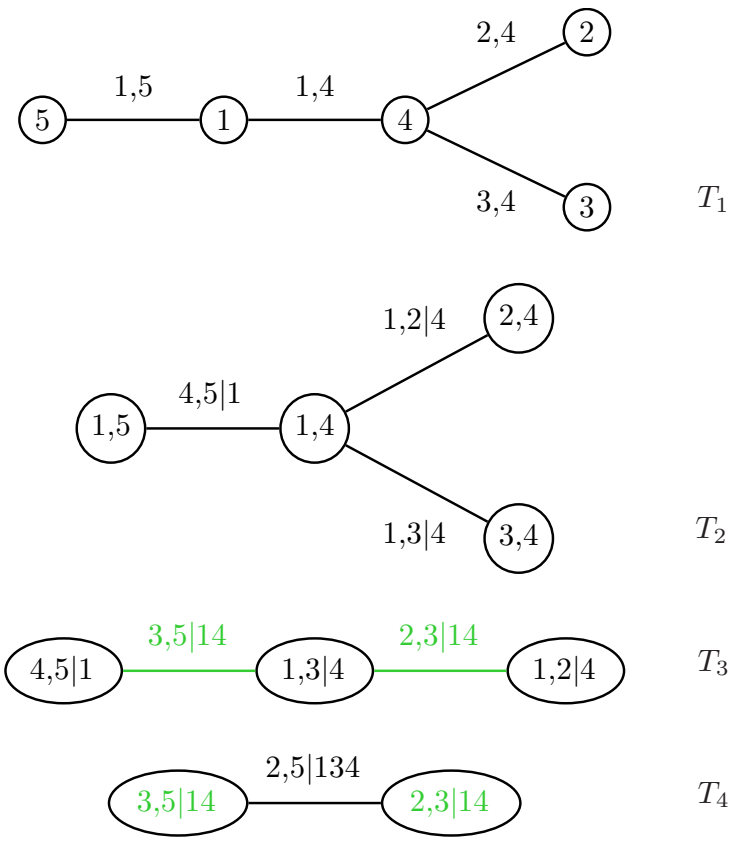

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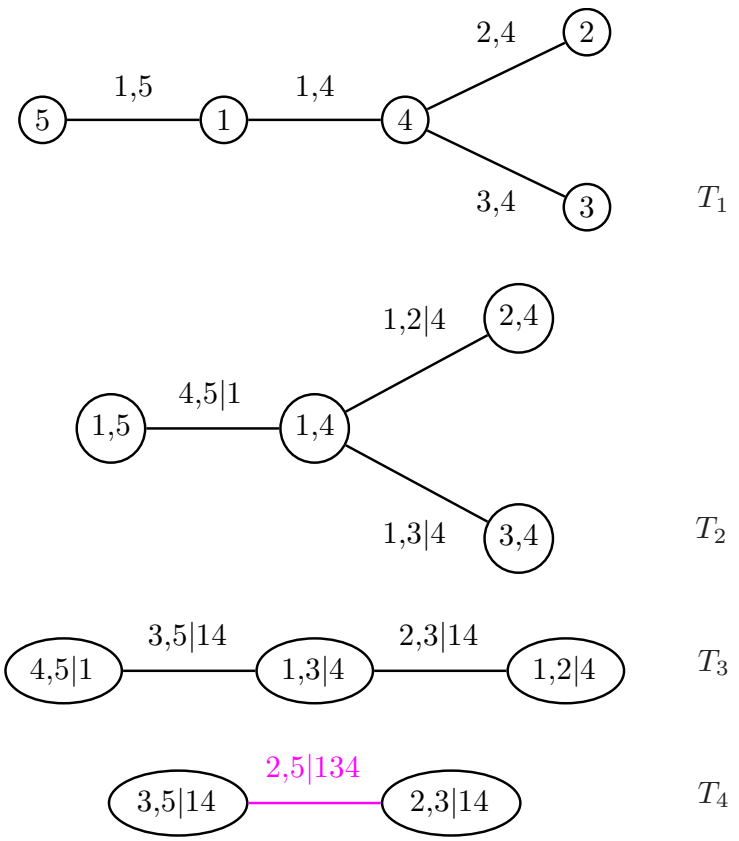

R-vine copula and parameter matrices

Copula families and parameters can be stored in associated matrices.

$$\begin{pmatrix} 2 & & & & \\ 5 & 3 & & & \\ 3 & 5 & 4 & & \\ 1 & 1 & 5 & 5 & \\ 4 & 4 & 1 & 1 & 1 \end{pmatrix} \longrightarrow \begin{pmatrix} C_{25;314} & & & \\ C_{23;14} & C_{35;14} & & \\ C_{21;4} & C_{31;4} & C_{45;1} & \\ C_{24} & C_{34} & C_{41} & C_{51} \end{pmatrix}$$

R-vine matrix objects

An RVineMatrix object contains all required matrices:

```
> Matrix = c(2,5,3,1,4,0,3,5,1,4,0,0,4,5,1,
+            0,0,0,5,1,0,0,0,0,1)
> Matrix = matrix(Matrix,5,5)
>
> family = c(0,1,3,4,4,0,0,3,4,1,0,0,0,4,1,
+            0,0,0,0,3,0,0,0,0,0)
> family = matrix(family,5,5)
>
> par = c(0,0.2,0.9,1.5,3.9,0,0,1.1,1.6,0.9,0,0,0,1.9,0.5,
+         0,0,0,0,4.8,0,0,0,0,0)
> par = matrix(par,5,5)
>
> par2 = matrix(0,5,5)
>
> RVM = RVineMatrix(Matrix=Matrix, family=family, par=par,
+                   par2=par2, names=c("V1","V2","V3","V4","V5"))
```

Simulation

```
> simdat = RVineSim(500, RVM)
```

```
> head(simdat)
       V1   V2   V3   V4   V5
[1,] 0.51 0.24 0.42 0.33 0.45
[2,] 0.23 0.14 0.16 0.12 0.20
[3,] 0.65 0.38 0.46 0.29 0.70
[4,] 0.43 0.18 0.08 0.08 0.26
[5,] 0.86 0.86 0.85 0.86 0.87
[6,] 0.71 0.71 0.80 0.68 0.88
```

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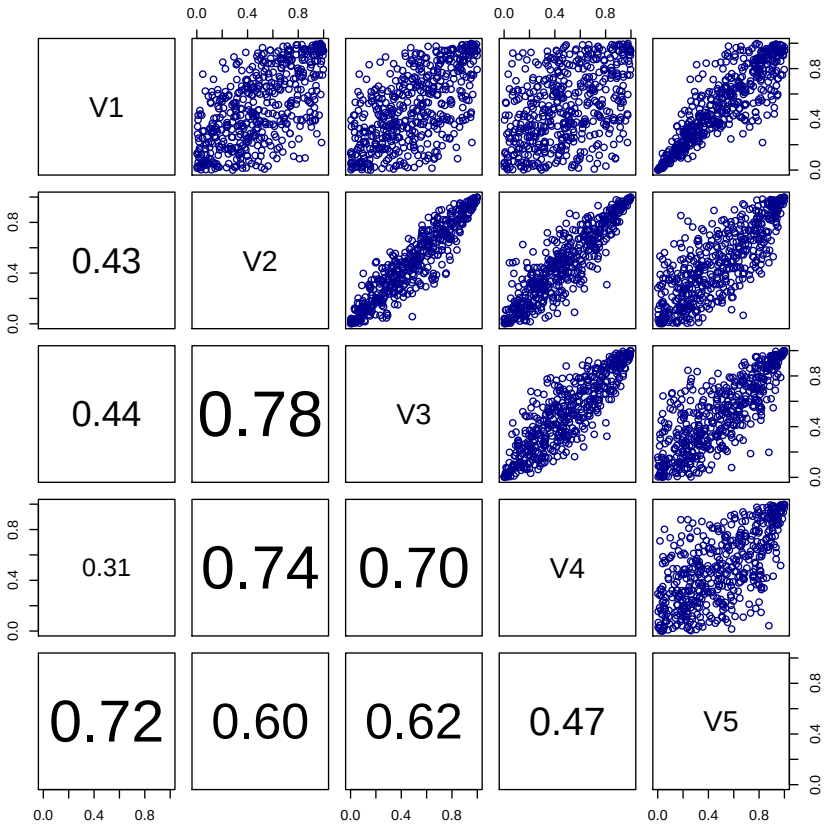


Example

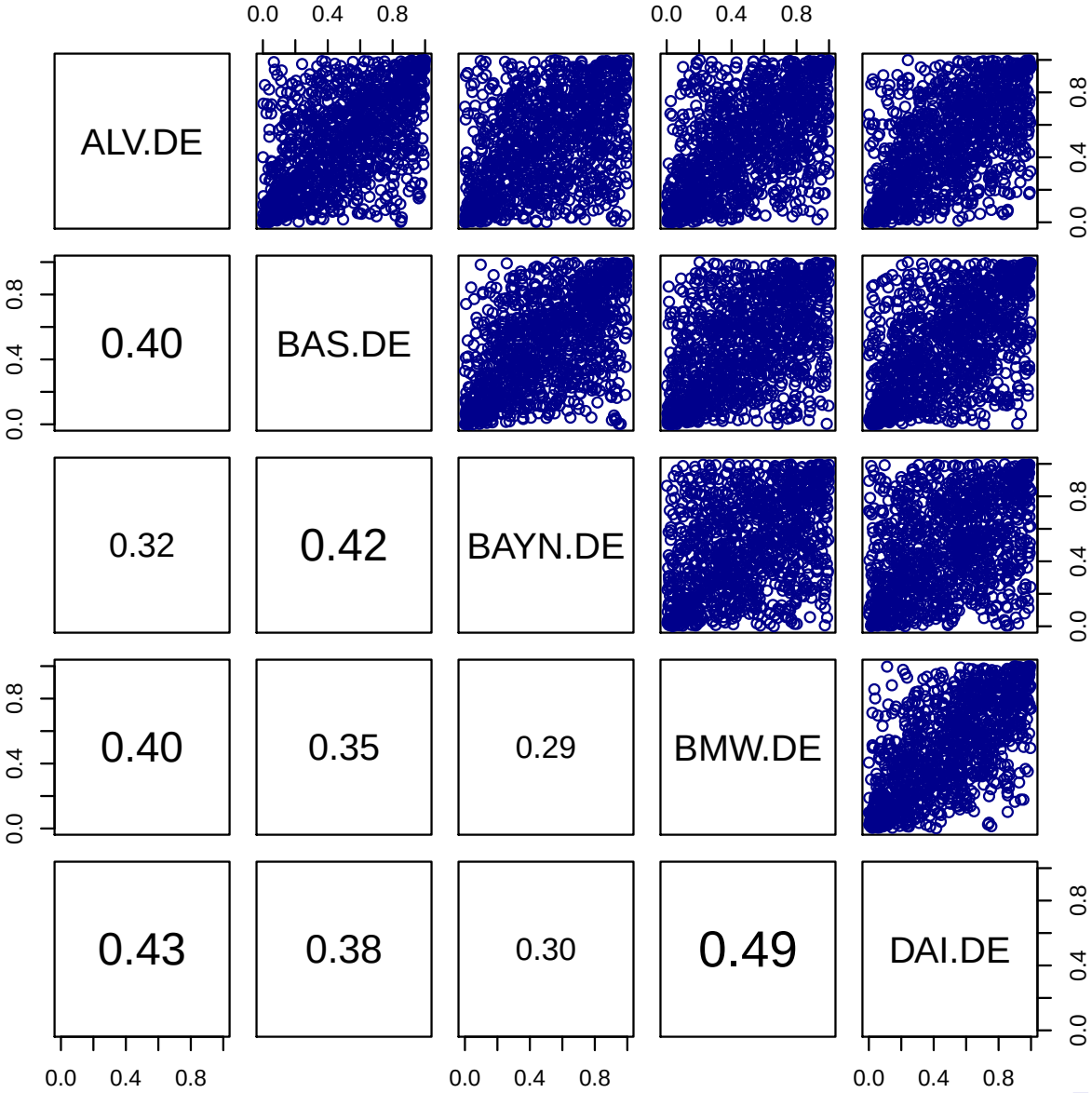
- Daily log returns of 15 major German stocks.
- Observed from January 2005 to August 2009 (1158 observations).
- Time series are filtered using GARCH(1,1) with Student's t innovations.
- Data set of standardized residuals transformed to [0,1].

Load into workspace:

```
> data(daxreturns)
```

Now: selection of trees, pair copulas and parameters in inverse order.

A first look at the data



Parameter estimation I

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

    ```
    > RVineSeqEst(data, RVM, method="itau")
    ```
  - or bivariate maximum likelihood estimation:

    ```
    > RVineSeqEst(data, RVM, method="mle")
    ```
- Very fast, since only bivariate estimation.
- Provides good starting values for joint maximum likelihood estimation.

Parameter estimation II

- Maximum likelihood estimation of all parameters jointly (log-likelihood computation: `RVineLogLik`).

```
> RVineMLE(data, RVM, start, start2, maxit,
+          grad, hessian, se)
```

- Starting values can be calculated using sequential estimation.
- Analytical gradient can be used for numerical optimization (see `RVineGrad`).
- Standard errors can be computed based on the analytical Hessian (see `RVineStdError` and `RVineHessian`).

Parameter estimation II

- Maximum likelihood estimation of all parameters jointly (log-likelihood computation: `RVineLogLik`).

```
> RVineMLE(data, RVM, start=0, start2=0, maxit,
+          grad, hessian, se)
```

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Parameter estimation III

```
> mle = RVineMLE(data=daxreturns[,1:5], RVM, start=0, start2=0,
+                grad=TRUE, hessian=TRUE, se=TRUE)
```

```
> mle$RVM$par
     [,1]  [,2] [,3] [,4] [,5]
[1,] 0.00 0.000 0.00 0.00    0
[2,] 0.14 0.000 0.00 0.00    0
[3,] 0.70 0.079 0.00 0.00    0
[4,] 1.30 1.206 1.42 0.00    0
[5,] 1.42 0.366 0.52 0.99    0
```

```
> mle$se
      [,1]  [,2]  [,3]  [,4] [,5]
[1,] 0.000 0.000 0.000 0.000    0
[2,] 0.029 0.000 0.000 0.000    0
[3,] 0.059 0.037 0.000 0.000    0
[4,] 0.031 0.028 0.036 0.000    0
[5,] 0.032 0.024 0.020 0.059    0
```

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```

Pair copula selection

- Manually using tools for bivariate analysis (e.g., contour plots or goodness-of-fit tests: `BiCopMetaContour`, `BiCopGofTest`,...).
- Automatically using AIC or BIC from a set of copula families: `BiCopSelect` (bivariate) or `RVineCopSelect` (multivariate).

```
> cops = RVineCopSelect(data=daxreturns[,1:5], familyset=NA,
+                       Matrix=Matrix, selectioncrit="AIC",
+                       indeptest=FALSE, level=0.05)
```

```
> cops$family
     [,1] [,2] [,3] [,4] [,5]
[1,]    0    0    0    0    0
[2,]    5    0    0    0    0
[3,]    2    5    0    0    0
[4,]    2   20    2    0    0
[5,]   17    2   14   20    0
```

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```

Vine tree selection I

- Sequential tree-by-tree selection according to Dißmann et al. (2013):
  1. Select maximum spanning tree (respecting the proximity condition) in terms of the absolute empirical pairwise Kendall's τ values.
  2. Select and estimate pair copulas of the tree.
  3. Compute transformed observations using *h*-functions and go back to Step 1.

- R- and C-vine copulas can be selected.
- The vine copula can be truncated to reduce the model complexity.

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```
> RVineStructureSelect(data, familyset, type,
+                      selectioncrit, indeptest,
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```

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```
> RVineStructureSelect(data, familyset, type="RVine",
+                      selectioncrit, indeptest,
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```
> RVineStructureSelect(data, familyset, type,
+                      selectioncrit, indeptest,
+                      level, trunclevel=2)
```

- R- and C-vine copulas can be selected.
- The vine copula can be truncated to reduce the model complexity.

Vine tree selection II

```
> rvm = RVineStructureSelect(data=daxreturns)
```

```
> rvm$Matrix
      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14] [,15]
 [1,]   15    0    0    0    0    0    0    0    0     0     0     0     0     0     0
 [2,]   11    4    0    0    0    0    0    0    0     0     0     0     0     0     0
 [3,]    9   11    3    0    0    0    0    0    0     0     0     0     0     0     0
 [4,]    7    9   11   11    0    0    0    0    0     0     0     0     0     0     0
 [5,]   13    7    9   12    9    0    0    0    0     0     0     0     0     0     0
 [6,]    3   13    7    8   12    7    0    0    0     0     0     0     0     0     0
 [7,]   12    3   13   10    8   12   13    0    0     0     0     0     0     0     0
 [8,]    8   12    5    5   10    8   12    5    0     0     0     0     0     0     0
 [9,]   10    8    1    2    5   10    8   12    1     0     0     0     0     0     0
[10,]    2   10   12   13    2    5   10    8   12    12     0     0     0     0     0
[11,]    1    2    8    9   13    2    5   10    8    10     8     0     0     0     0
[12,]   14    1    6    7    1   13    2    2   10     6    10    10     0     0     0
[13,]    6   14   14   14   14    1   14    1    2    14     6     6     2     0     0
[14,]    4    6   10    6    6   14    6   14   14     2    14    14     6    14     0
[15,]    5    5    2    1    7    6    1    6    6     8     2     2    14     6     6
```

Vine tree selection II

```
> rvm = RVineStructureSelect(data=daxreturns)
```

```
> rvm$Matrix
      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14] [,15]
 [1,]   15    0    0    0    0    0    0    0    0     0     0     0     0     0     0
 [2,]   11    4    0    0    0    0    0    0    0     0     0     0     0     0     0
 [3,]    9   11    3    0    0    0    0    0    0     0     0     0     0     0     0
 [4,]    7    9   11   11    0    0    0    0    0     0     0     0     0     0     0
 [5,]   13    7    9   12    9    0    0    0    0     0     0     0     0     0     0
 [6,]    3   13    7    8   12    7    0    0    0     0     0     0     0     0     0
 [7,]   12    3   13   10    8   12   13    0    0     0     0     0     0     0     0
 [8,]    8   12    5    5   10    8   12    5    0     0     0     0     0     0     0
 [9,]   10    8    1    2    5   10    8   12    1     0     0     0     0     0     0
[10,]    2   10   12   13    2    5   10    8   12    12     0     0     0     0     0
[11,]    1    2    8    9   13    2    5   10    8    10     8     0     0     0     0
[12,]   14    1    6    7    1   13    2    2   10     6    10    10     0     0     0
[13,]    6   14   14   14   14    1   14    1    2    14     6     6     2     0     0
[14,]    4    6   10    6    6   14    6   14   14     2    14    14     6    14     0
[15,]    5    5    2    1    7    6    1    6    6     8     2     2    14     6     6
```

Illustrating R-vine copula models

Selected R-vine trees:

```
> RVineTreePlot(data=NULL, RVM=rvm, tree=1,
+               edge.labels=c("family","theotau"))
```

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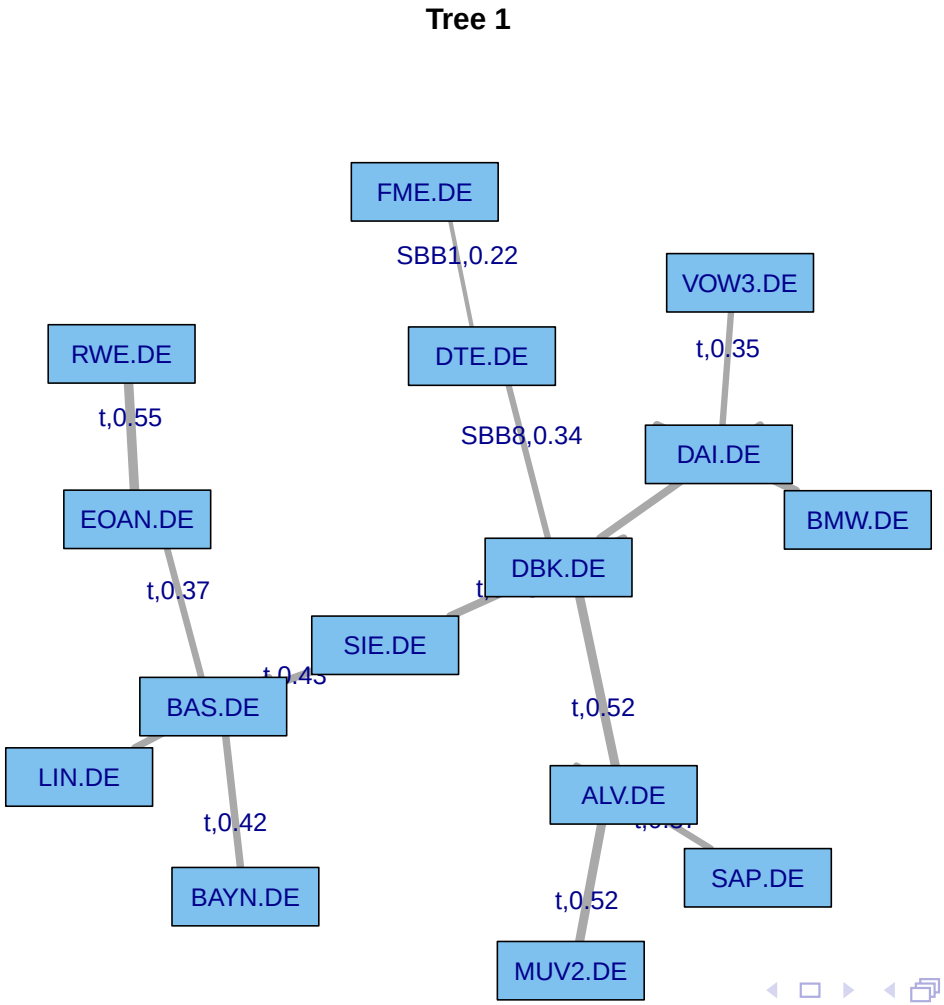
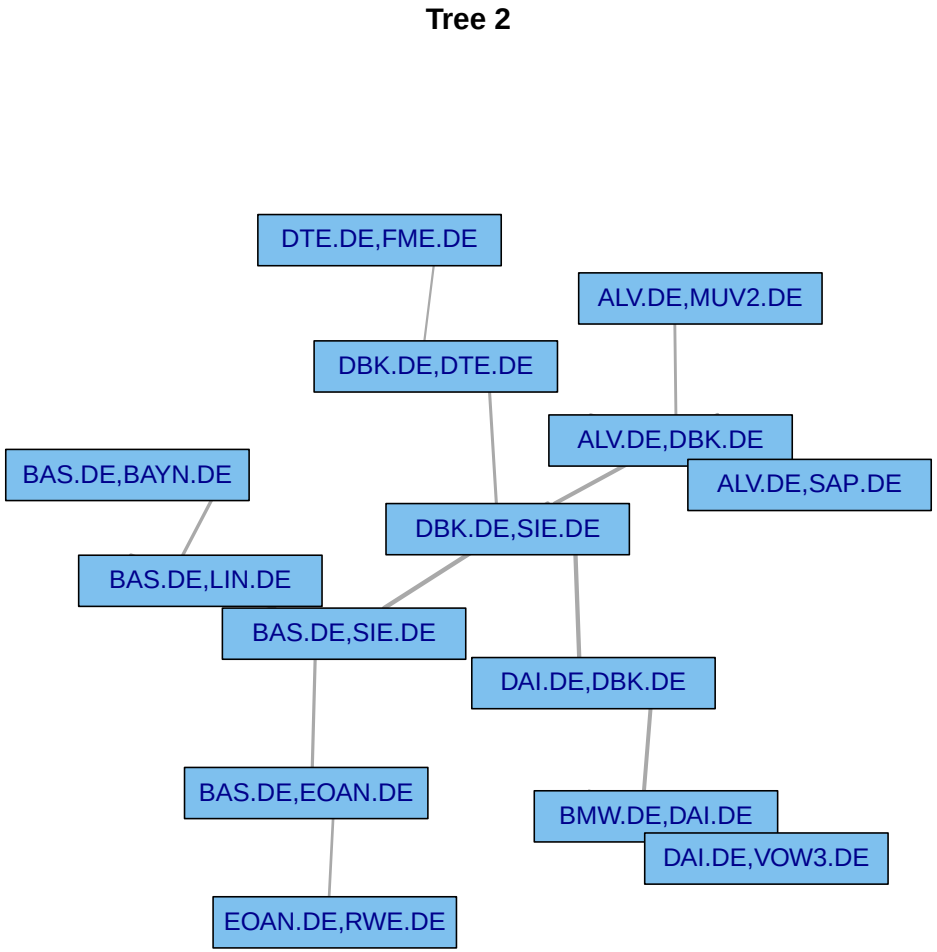


Illustrating R-vine copula models

Selected R-vine trees:

```
> RVineTreePlot(data=NULL, RVM=rvm, tree=2,
+                edge.labels=FALSE)
```



Discrimination among vine copula models I

- AIC and BIC: `RVineAIC` and `RVineBIC`.
- Tests by Vuong (1989) and by Clarke (2007) for non-nested comparisons of two R-vine models RVM1 and RVM2:

```
> RVineVuongTest(data, RVM1, RVM2)
> RVineClarkeTest(data, RVM1, RVM2)
```

Discrimination among vine copula models II

- Select a C-vine copula for comparison:

```
> cvm = RVineStructureSelect(daxreturns, type="CVine")
```

- Compare the models in terms of AIC values and the Vuong test:

```
> c(RVineAIC(daxreturns,rvm)$AIC, RVineAIC(daxreturns,cvm)$AIC)
[1] -9808.44 -9804.42

> RVineVuongTest(daxreturns, rvm, cvm)
$statistic
[1] 0.27

$statistic.Akaike
[1] 0.068

$statistic.Schwarz
[1] -0.44
...
```

- The models are essentially indistinguishable.

Discrimination among vine copula models II

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Outlook

Current projects and plans:

- Move code from `C` to `C++`.
- Parallelize numerical maximum likelihood estimation.
- Implement asymmetric copulas (Tawn).
- Bayesian estimation and model selection.

Thank you to my package coauthors: Ulf Schepsmeier & Jakob Stöber

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Thank you very much for your attention!

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