Seminar in
Taida Inst. of Mathematical Sciences

Copula modeling for dependent truncation

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Outlines

Part I: Copula: Review

- Copula - definition
- Copula - examples

Part II: Truncation data

- Truncation data
- Semi-survival copula
- Existing procedures   - moment method -

Part III: Proposed method

- Reverse-time hazard model
- Proposed method - nonparametric likelihood method –
- Simulation & data analysis
- Comparison with existing methods
- Conclusion & future work

Part I

Copula: Review

Copula

- *Definition*

The function $C: [0,1]\times[0,1]\mapsto[0,1]$ is said to be Copula when it is a bivariate distribution function having the uniform [0, 1] marginals

$$C[u,1]=u, \quad C[1,v]=v$$

- *Any bivariate distribution function* $F(x,y)$ *has a representation*

$$F(x,y)=C[F_X(x),F_Y(y)], \quad \text{where} \begin{cases} F_X(x)=F(x,\infty) \\ F_Y(y)=F(\infty,y) \end{cases}$$

Sklar's theorem (Sklar, 1959)

Copula

$$\Pr(X \le x, Y \le y) = C[\Pr(X \le x), \Pr(Y \le y)]$$

- Example 1: Independence copula

$$C[u,v] = uv$$

- Example 2: Frank copula (Genest, 1986; Frank, 1979)

$$C_\alpha[u,v] = \log_{\alpha^{-1}}\left\{1 + \frac{(\alpha^{-u}-1)(\alpha^{-v}-1)}{(\alpha^{-1}-1)}\right\}, \quad \alpha > 0$$

$$\lim_{\alpha \to 1} C_\alpha[u,v] = uv$$

- Example 3: Normal copula

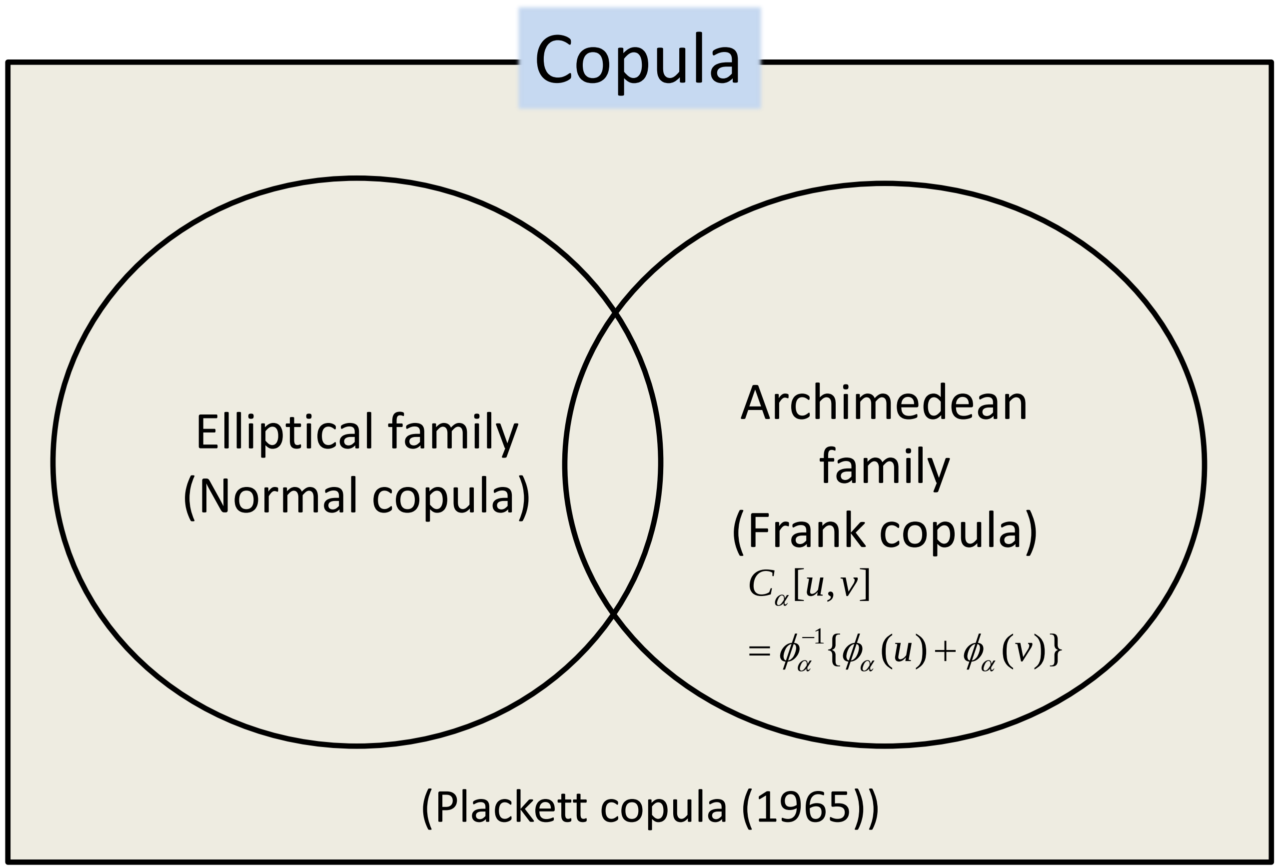
$$C_\rho[u,v] = \Phi_\rho[\Phi^{-1}(u), \Phi^{-1}(v)], \quad -1 < \rho < 1$$

Φ_ρ : Joint CDF of standard bivariate normal

$$\lim_{\rho \to 0} C_\rho[u,v] = uv$$

Copula

$$C[u, v]$$


Copula
Elliptical family
(Normal copula)
Archimedean
family
(Frank copula)
$C_\alpha[u,v]$
$= \phi_\alpha^{-1}\{\phi_\alpha(u) + \phi_\alpha(v)\}$
(Plackett copula (1965))

Copula

Copula in parametric setting

$$\Pr(X \le x, Y \le y) = C[F_X(x), F_Y(y)]$$

- Example 1: Election in UK (Smith, 2004)

  X : election time : Weibull
  Y : the number of votes: Normal
  } Joint?

  * Ali-Mikhail-Haq copula (Fukumoto, 2009) based on AIC

- Example 2: Insurance payment

  X : Indemnity payment: Parete
  Y : expenses (termed ALAE): Parete
  } Joint?

  * Frees and Valdez (1998) fit Gumbel copula based on AIC

Copula

Copula in semi-parametric setting

$$\Pr(X \le x, Y \le y) = C[F_X(x), F_Y(y)]$$

- Example 3: Australian Twin study (Prentice & Hsu, 1997)

  X : Time to disease for child 1 : Non-parametric
  Y : Time to disease for child 2: Non-parametric
  } Joint?

  * Prentice and Hsu fit Clayton copula
  * Gumbel copula may be the best one (Emura et al., 2010)

- Example 4: Transfusion-related AIDS (Lagakos et al., 1988)

  X : Incubation time of AIDS: Non-parametric
  Y : Infection time of AIDS: Non-parametric
  } Joint?

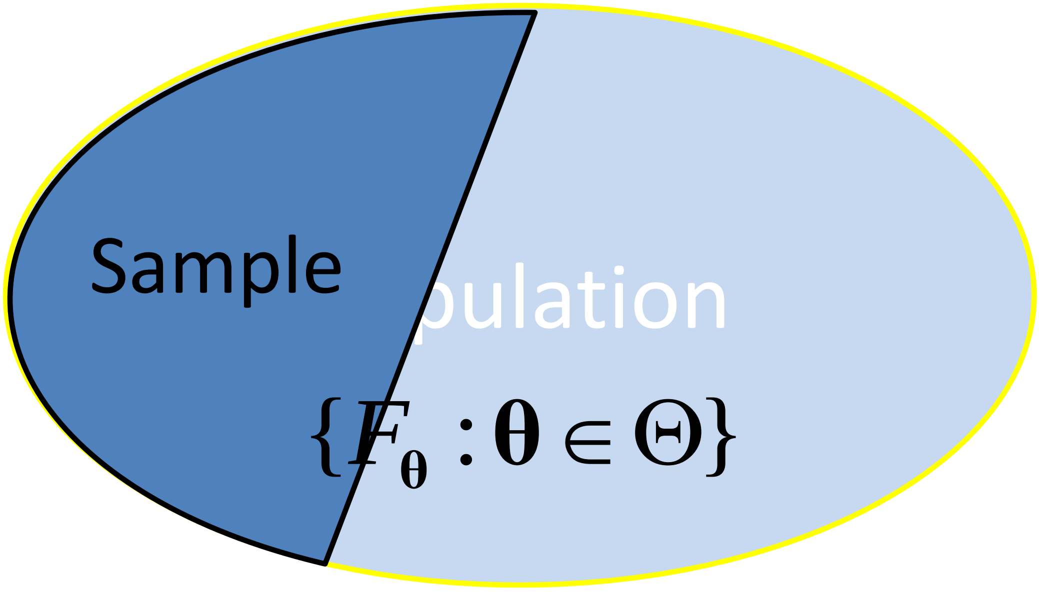
  * Chaieb et al. (2006) fit Frank copula
  * Beaudoin & Lakhal-Chaieb (2008) shows Clayton is better
  * We will argue that Clayton copula is the best one

Part II

Truncation data: Review

Truncation data

- *Truncated samples are those from which certain population values are entirely excluded* (Truncated and censored sample by Cohen, 1991)



Industry & Reliability (Book of Cohen, 1991; Navaro & Ruiz, 1996)

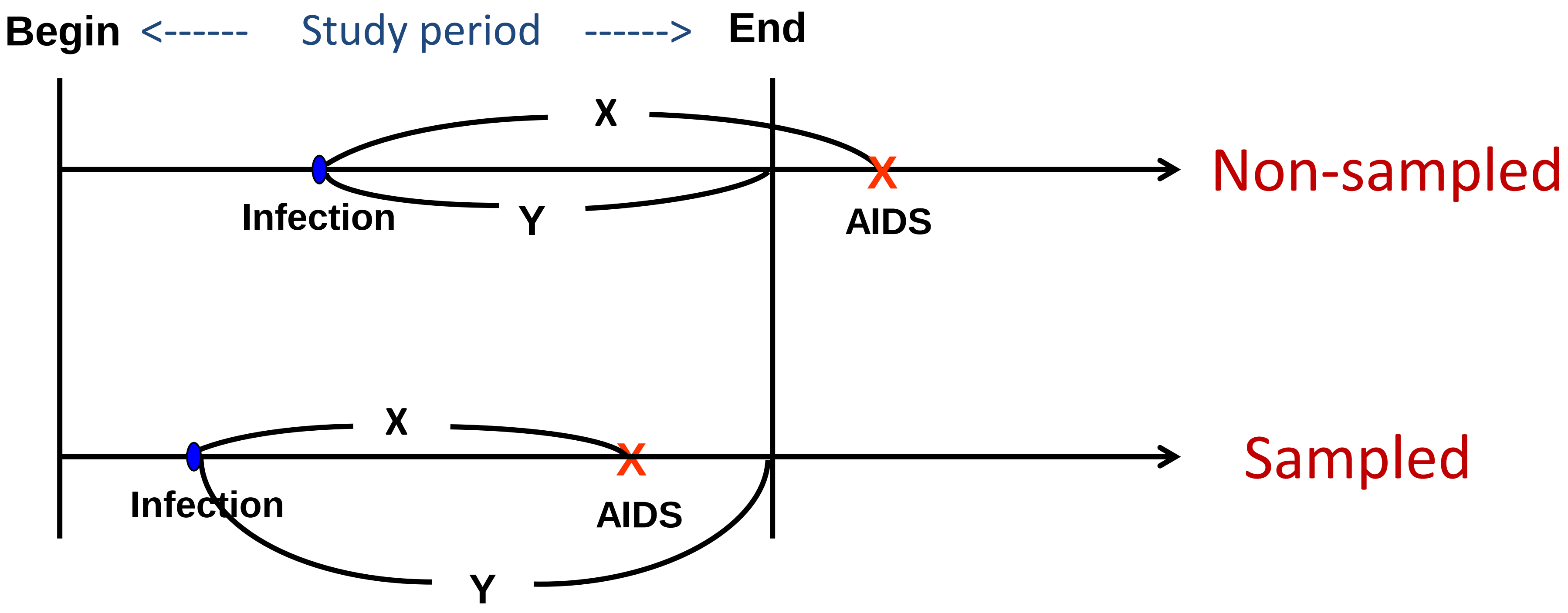
Biomedical studies (Book of Klein & Moeschberger, 2003)

Econometrics (Book of Amemiya, 1994, Chap 13)

Truncation data

- Transfusion-related AIDS

  (Lagakos et al., 1988; Kalbfleisch & Lawless, 1989)



Truncation criteria : $X \leq Y$

Truncation data

- Truncation data:

$\{(X_j, Y_j);\ j = 1, \ldots, n\}$

subject to $X_j \le Y_j$

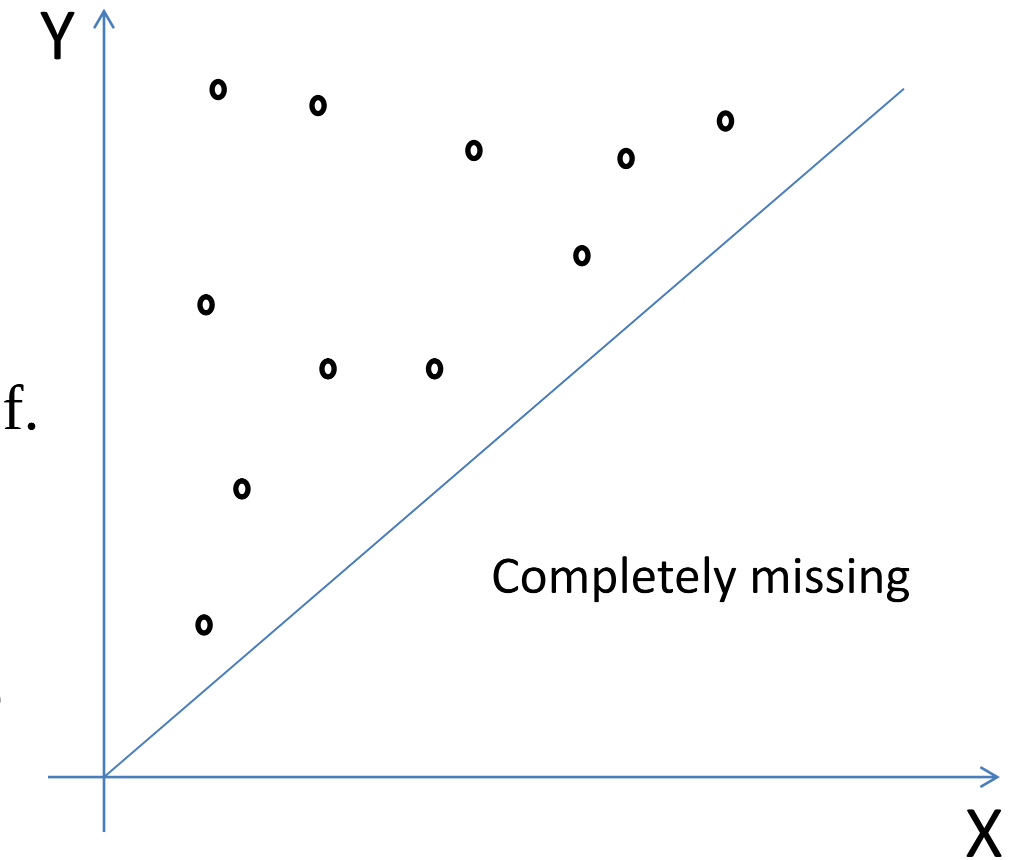
$\Downarrow$

i.i.d. from the conditional c.d.f.

$\Pr(X \le x, Y \le y \mid X \le Y)$,

where (X, Y) is

the population random variable



$$\frac{1}{n}\sum_{j=1}^{n} I(X_j \le x) \rightarrow_{Bias} \Pr(X \le x)$$

Truncation data

Traditional analysis

- Estimation of $F_X(x) = \Pr(X \le x)$

$$\hat{F}_X(x) = \prod_{u>x} \left\{ 1 - \frac{\sum_{j=1}^{n} I(X_j = u)}{\sum_{j=1}^{n} I(X_j \le u, Y_j \ge u)} \right\}$$

(Lynden-Bell, 1971; Lagakos et al., 1988)

- Quasi-independence assumption (Tsai, 1991):

$$\Pr(X \le x, Y \le y \mid X \le Y) \propto \iint_{\substack{u \le x, v \le y \\ u \le v}} dF_X(u) dF_Y(v)$$

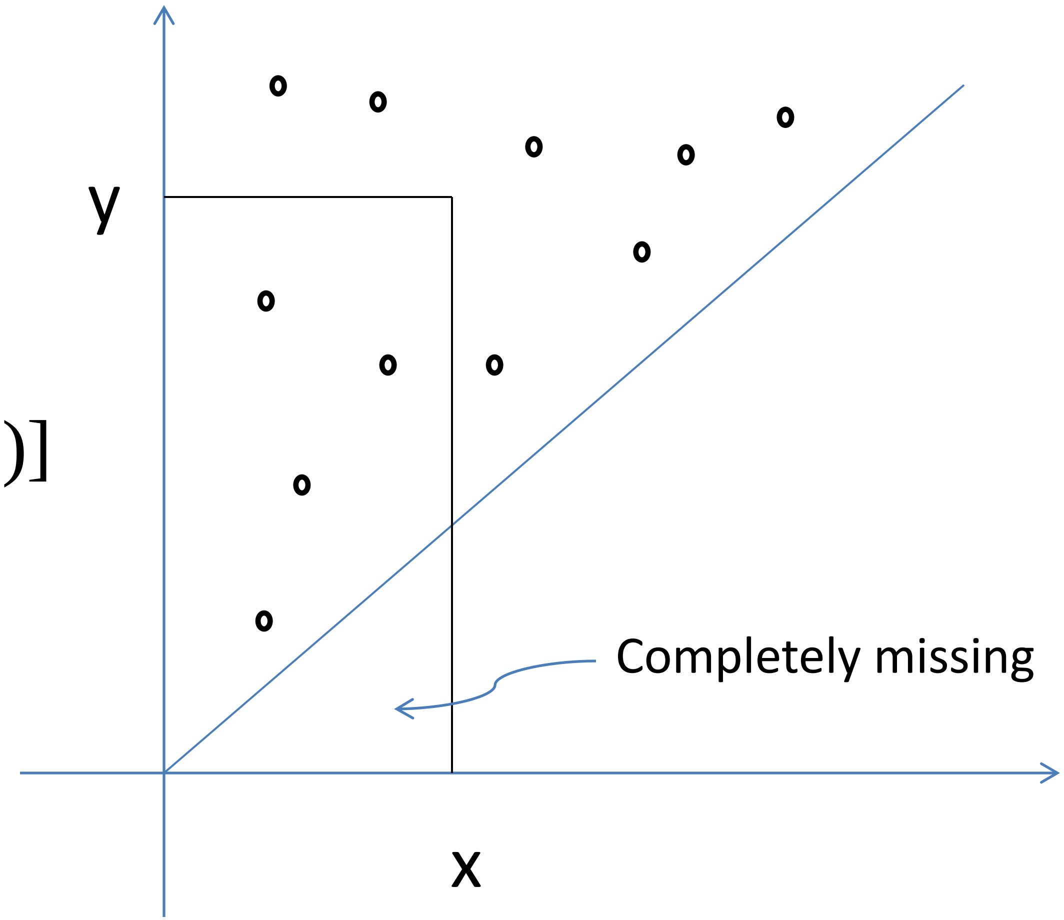
*Quasi-independence assumption is testable

(Chen et al., 1996; Martin & Betensky, 2005; Emura & Wang; 2010)

Truncation data

$$\Pr(X \le x, Y \le y)$$
$$= C[\Pr(X \le x), \Pr(Y \le y)]$$

The model is unidentifiable

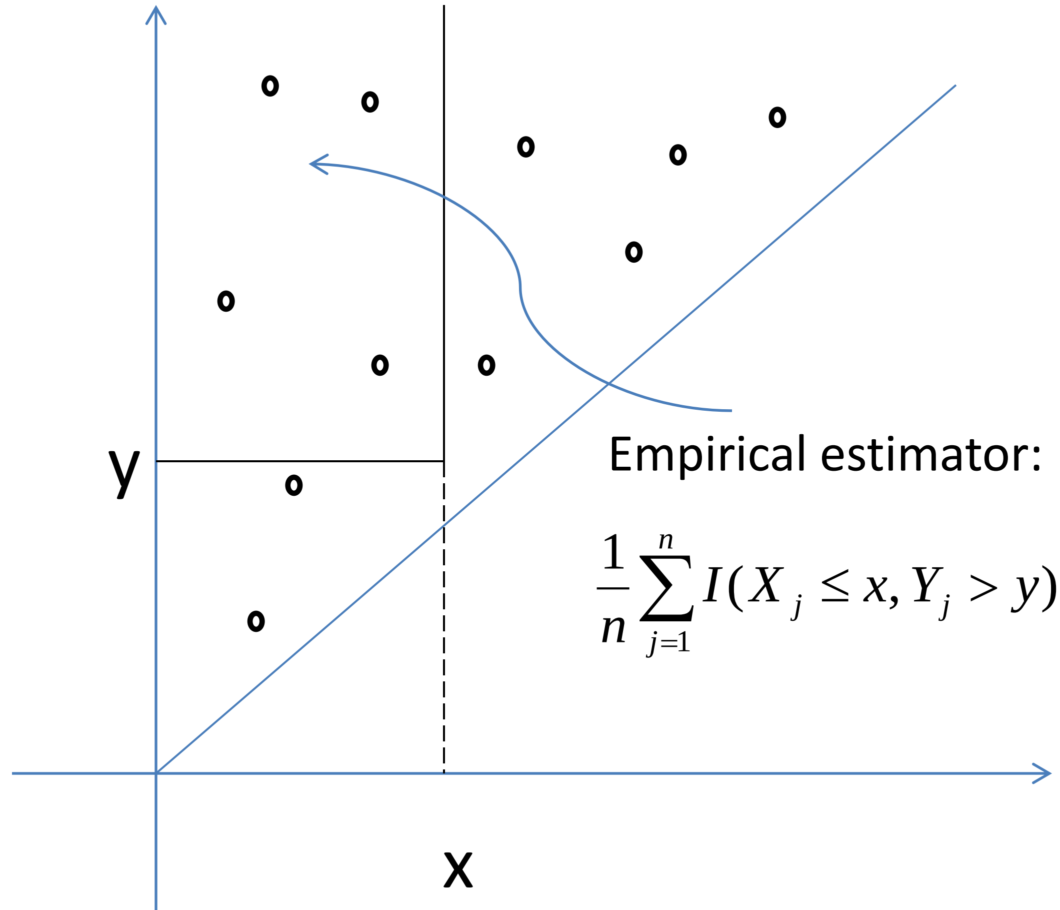


Truncation data

$$\Pr(X \le x, Y > y \mid X \le Y) = \frac{C_\alpha[F_X(x), S_Y(y)]}{c(\alpha, F_X, S_Y)}$$

where

$$c(\alpha, F_X, S_Y) = \iint_{x \le y} \frac{\partial^2}{\partial x \partial y} C_\alpha[F_X(x), S_Y(y)]dxdy$$



Empirical estimator:

$$\frac{1}{n}\sum_{j=1}^{n} I(X_j \le x, Y_j > y)$$

- Semi-survival copula

(Chaieb et al., 2006, *Biometrika*)

- Quasi-independence: $C_\alpha[u, v] = uv$

Truncation data

- Estimator for (F_X, S_Y)

$$\frac{1}{n}\sum_{j=1}^{n} I(X_j \le t, Y_j > t) = \frac{C_\alpha[F_X(t), S_Y(t)]}{c(\alpha, F_X, S_Y)},$$

where $t \in (X_1, \ldots X_n, Y_1, \ldots, Y_n)$

(Chaieb et al., 2006)

- Estimator for α

1. Conditional Kendall's tau (Chaieb et al, 2006)
2. Conditional likelihood (Emura, Wang & Hung, 2011, Sinica)

* Conditional likelihood achieves higher efficiency

Drawbacks of existing procedures

- Chaieb et al. (2006) and Emura et al. (2011) are restricted to Archimedean family

$$C_\alpha[u,v]=\phi_\alpha^{-1}\{\phi_\alpha(u)+\phi_\alpha(v)\}$$

$$\because)\ \frac{1}{n}\sum_{j=1}^{n} I(X_j \le t, Y_j > t) = \frac{C_\alpha[F_X(t), S_Y(t)]}{c(\alpha, F_X, S_Y)},$$

$$\Leftrightarrow \phi_\alpha\left(\frac{c(\alpha, F_X, S_Y)}{n}\sum_{j=1}^{n} I(X_j \le t, Y_j > t)\right) = \phi_\alpha(F_X(t)) + \phi_\alpha(S_Y(t))$$

$$\Leftrightarrow F_X(t) = \phi_\alpha^{-1}\left\{\phi_\alpha\left(\frac{c(\alpha, F_X, S_Y)}{n}\sum_{j=1}^{n} I(X_j \le t, Y_j > t)\right) - \phi_\alpha(S_Y(t))\right\}$$

- The assumption of no ties: $t \in (X_1, \ldots X_n, Y_1, \ldots, Y_n)$
- Efficiency concern

- Part III: Proposed method

Proposed method

- The preceding two methods use moment-based estimating equations for (F_X, S_Y)

- In this talk, we propose to get $(\hat{\alpha}, \hat{F}_X, \hat{S}_Y)$ by the nonparametric maximum likelihood estimator (NPMLE)

* Motivation: Higher efficiency of the NPMLE

Proposed method

- Re-parameterize (F_X, S_Y)

$$F_X(x) = e^{-H_X(x)}, \quad S_Y(y) = e^{-\Lambda_Y(y)}$$

$* H_X(x)$: Reverse - time cumulative hazard

(Lagakos et al., 1988; Navaro & Ruiz, 1996)

$* \Lambda_Y(y)$: Cumulative hazard

- Copula model:

$$\Pr(X \le x, Y > y \mid X \le Y) = \frac{C_\alpha[e^{-H_X(x)}, e^{-\Lambda_Y(y-)}]}{c(\alpha, H_X, \Lambda_Y)},$$

$$\text{where} \quad c(\alpha, H_X, \Lambda_Y) = \iint_{x \le y} -\frac{\partial^2}{\partial x \partial y} C_\alpha[e^{-H_X(x)}, e^{-\Lambda_Y(y-)}]dxdy$$

Proposed method

- Density

$$\Pr(X = x, Y = y \mid X \le Y) = \frac{\eta_\alpha[H_X(x), \Lambda_Y(y-)]}{c(\alpha, H_X, \Lambda_Y)}\{-dH_X(x)\}d\Lambda_Y(y),$$

where $\eta_\alpha[x, y] = e^{-x}e^{-y}\frac{\partial^2}{\partial u \partial u}C_\alpha[u, u]\Big|_{u=e^{-x}, v=e^{-y}}$

- Log-likelihood

$$l_n(\alpha, H_X, \Lambda_Y) =$$

$$\sum_{j=1}^{n}\log\eta_\alpha[H_X(X_j), \Lambda_Y(Y_j-)] + \log\{-dH_X(X_j)\} + \log d\Lambda_Y(Y_j) - \log c(\alpha, H_X, \Lambda_Y)$$

- Maximization for (*2n+1*) parameters

$$(\alpha, -dH_X(X_1), \dots, -dH_X(X_n), d\Lambda_Y(Y_1), \dots, d\Lambda_Y(Y_n))$$

Proposed method

- Identifiability problem

  We found that the maximum of $l_n(\alpha, H_X, \Lambda_Y)$ is not unique

  (# of parameters =2n+1 > # of observed points = 2n)

- Reduces to 2n-1 parameters

$$(\alpha, -dH_X(X_1), \ldots, -dH_X(X_n), d\Lambda_Y(Y_1), \ldots, d\Lambda_Y(Y_n))$$

$$\Downarrow$$

$$(\alpha, \underbrace{-dH_X(X_{(1)})}_{\equiv 1}, \ldots, -dH_X(X_{(n)}), d\Lambda_Y(Y_{(1)}), \ldots, \underbrace{d\Lambda_Y(Y_{(n)})}_{\equiv 1})$$

Proposed method

Geometrical understanding of $-dH_X(X_{(1)})=1$

$$\Pr(X \le x_{(1)}, Y > x_{(1)} \mid X \le Y)$$

$$= \frac{C_\alpha[F_X(x_{(1)}), S_Y(x_{(1)})]}{c(\alpha, F_X, S_Y)}$$

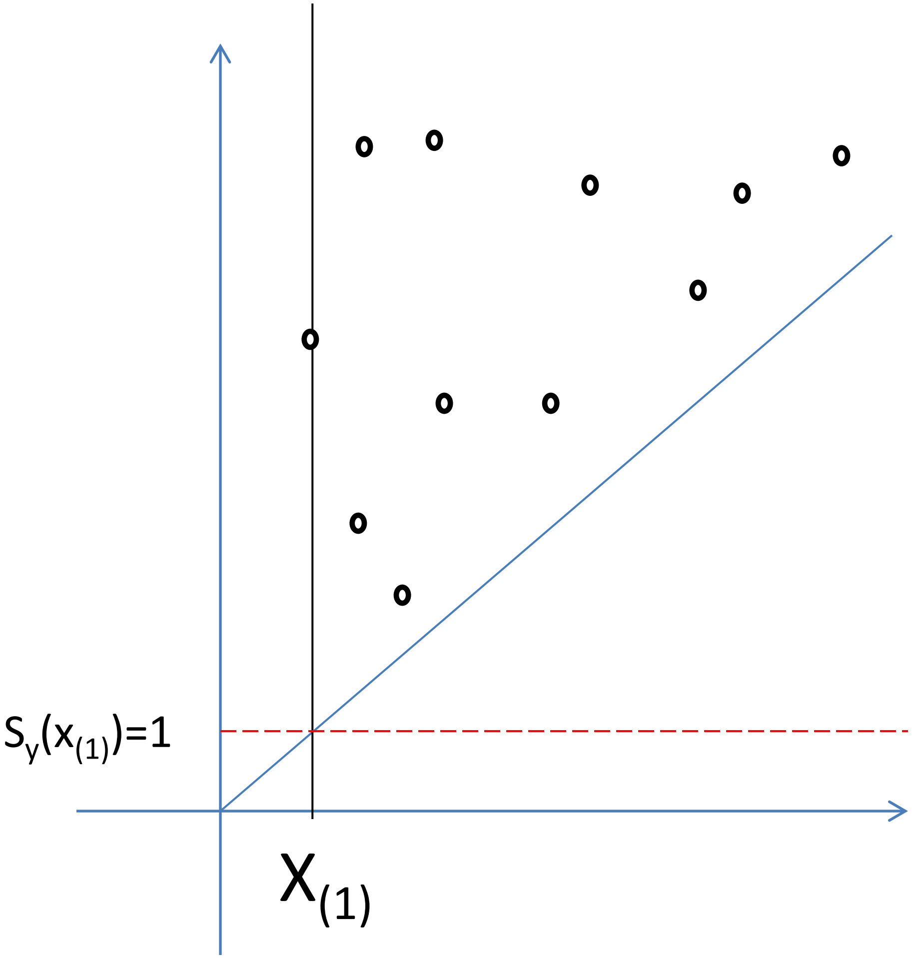
$$= \frac{F_X(x_{(1)})}{c(\alpha, F_X, S_Y)} \qquad (1)$$

$$\therefore) -dH_X(x_{(1)})$$

$$= \frac{dF_X(x_{(1)})}{F_X(x_{(1)})} \qquad \because F_X = e^{-H_X}$$

$$= \frac{\Pr(X = x_{(1)} \mid X \le Y)}{\Pr(X \le x_{(1)} \mid X \le Y)} \qquad \text{by (1)}$$

$$\leftarrow \frac{1/n}{1/n} = 1 \qquad \text{see the plot}$$



Proposed method

- *2n-1* score equations

$$0 = \partial l_n(\alpha, H_X, \Lambda_Y)/\partial\alpha$$

$$0 = \partial l_n(\alpha, H_X, \Lambda_Y)/\partial\{-dH_X(X_{(j)})\}, \quad j = 2,..,n$$

$$0 = \partial l_n(\alpha, H_X, \Lambda_Y)/\partial d\Lambda_Y(Y_{(j)}), \quad j = 1,..,n-1$$

- Breslow-Aalen type expression

$$H_X(x) = \int_x^\infty \frac{\sum_{j=1}^n I(X_j = u)}{\sum_{j=1}^n \Psi_j^{(1,0)}(u;\alpha, H_X, \Lambda_Y)}$$

$$\Lambda_Y(x) = \int_0^y \frac{\sum_{j=1}^n I(Y_j = u)}{\sum_{j=1}^n \Psi_j^{(0,1)}(u;\alpha, H_X, \Lambda_Y)}$$

Proposed method

- To get the NPMLE $(\hat{\alpha}, \hat{H}_X, \hat{\Lambda}_Y)$

  we apply a numerical maximization to

$$l_n(\alpha, H_X, \Lambda_Y) =$$

$$\sum_{j=1}^{n} \log \eta_\alpha[H_X(X_j), \Lambda_Y(Y_j-)] + \log\{-dH_X(X_j)\} + \log d\Lambda_Y(Y_j) - \log c(\alpha, H_X, \Lambda_Y)$$

  for parameter $(\alpha, -dH_X(X_1), \ldots, -dH_X(X_n), d\Lambda_Y(Y_1), \ldots, d\Lambda_Y(Y_n))$

  subject to $-dH_X(X_{(1)}) = d\Lambda_Y(Y_{(n)}) = 1$

(e.g. use “nlm” program in R)

- $l_n(\alpha, H_X, \Lambda_Y)$: twice differentiable & convex

Proposed method

- The NPMLE $(\hat{\alpha}, \hat{H}_X, \hat{\Lambda}_Y)$ is consistent & asymptotic normal
- Observed Fisher information

  = minus of the Hessian of $l_n(\alpha, H_X, \Lambda_Y)$

$$\hat{i}_n(\hat{\alpha}, \hat{H}_X, \hat{\Lambda}_Y) = \begin{bmatrix} \hat{i}_{n,11} & \hat{i}'_{n,12} \\ \hat{i}_{n,12} & \hat{i}_{n,22} \end{bmatrix}$$

- Consistent variance estimator

$$\hat{V}_n(\hat{\alpha}) \approx (\hat{i}_{n,11} - \hat{i}'_{n,12}\hat{i}^{-1}_{n,22}\hat{i}_{n,12})^{-1}$$

Proposed method

Simulation setting (I):

- Plackett copula (not Archimedean family)

$$C_\alpha[u,v] = \frac{1}{2(\alpha-1)} + \frac{u+v}{2} - \frac{[\{1+(\alpha-1)(u+v)\}^2 - 4uv\alpha(\alpha-1)]^{1/2}}{2(\alpha-1)}$$

$\alpha = 1/2.51,\ 1/5.11,\ 2.51,\ 5.11$

(s.t. Spearmen's rho $= 0.25,\ 0.5, -0.25, -0.5$)

- Exponential margins

$$H_X(x) = -\log(1-e^{-1.5x})$$

$$\Lambda_Y(y) = 0.5y$$

- Data generation

If $X_j \le Y_j$ then included in the sample. Otherwise truncated.

Repeat until we get *n* (=125 or 250) pair of (X_j, Y_j)

Simulation results (positive dependence)

Parameter		*Mean* (*Bias*)	*SE*	*SEE*	95%*Cov*
Spearman's ρ = 0.25 (α =1/2.15, $\Pr(X \leq Y) = 0.79$)					
$\log(\alpha)$=-0.765	n =125	-0.778 (-0.013)	0.407	0.407	0.945
	n =250	-0.697 (0.068)	0.311	0.296	0.965
$H_X(t) = 0.693$	n =125	0.736 (0.043)	0.123	0.121	0.955
	n =250	0.733 (0.040)	0.090	0.086	0.970
$\Lambda_Y(t) = 0.693$	n =125	0.710 (0.017)	0.144	0.139	0.960
	n =250	0.725 (0.032)	0.104	0.102	0.970
Spearman's ρ = 0.50 (α =1/5.11, $\Pr(X \leq Y) = 0.84$)					
$\log(\alpha)$=-1.631	n =125	-1.642 (-0.011)	0.323	0.319	0.965
	n =250	-1.652 (-0.021)	0.231	0.222	0.940
$H_X(t) = 0.693$	n =125	0.726 (0.033)	0.101	0.092	0.910
	n =250	0.716 (0.023)	0.067	0.064	0.920
$\Lambda_Y(t) = 0.693$	n =125	0.704 (0.011)	0.110	0.102	0.960
	n =250	0.701 (0.008)	0.068	0.069	0.950

Simulation results (negative dependence)

Parameter		*Mean* (*Bias*)	*SE*	*SEE*	95%*Cov*
Spearman's ρ = -0.25 (α =2.15, $\Pr(X \le Y) = 0.72$)					
$\log(\alpha)$=0.765	n=125	0.859 (0.094)	0.598	0.554	0.960
	n=250	0.717 (-0.048)	0.342	0.359	0.930
$H_X(t) = 0.693$	n=125	0.809 (0.116)	0.313	0.244	0.960
	n=250	0.717 (0.024)	0.139	0.138	0.935
$\Lambda_Y(t) = 0.693$	n=125	0.793 (0.100)	0.363	0.267	0.960
	n=250	0.699 (0.006)	0.139	0.137	0.930
Spearman's ρ = -0.50 (α =5.11, $\Pr(X \le Y) = 0.70$)					
$\log(\alpha)$= 1.631	n=125	1.758 (0.127)	0.818	0.598	0.915
	n=250	1.708 (0.077)	0.534	0.386	0.955
$H_X(t) = 0.693$	n=125	0.883 (0.190)	0.582	0.343	0.925
	n=250	0.787 (0.094)	0.374	0.196	0.960
$\Lambda_Y(t) = 0.693$	n=125	0.862 (0.169)	0.624	0.354	0.885
	n=250	0.775 (0.082)	0.404	0.207	0.955

Proposed method

Simulation setting (II):

- Frank copula (Archimedean family)

$$C_\alpha[u, v] = \log_{\alpha^{-1}}\left\{1 + \frac{(\alpha^{-u} - 1)(\alpha^{-v} - 1)}{(\alpha^{-1} - 1)}\right\},$$

$$\log(\alpha) = 2.38,\ 5.746,\ -2.38,\ -5.746$$

$$(\text{s.t. Kendall's tau} = 0.25,\ 0.5,\ -0.25,\ -0.5)$$

- Exponential margins

$$H_X(x) = -\log(1 - e^{-1.5x})$$

$$\Lambda_Y(y) = 0.5y$$

- Compare with estimator of Chaieb et al. (2006) and Emura et al. (2011)

Simulation results (positive dependence)

Parameter	*n*	*NPMLE*	*Emura et al.*	*Chaeib et al.*
		Kendall's τ =0.25		
$\log(\alpha)$ =2.38	125	0.0661 (0.8767)	-0.0075 (0.8546)	-0.0051 (0.8569)
	250	-0.1113 (0.5707)	-0.1326 (0.5636)	-0.1325 (0.5650)
$F_X(t) = 0.50$	125	-0.0067 (0.0509)	-0.0034 (0.0518)	-0.0034 (0.0518)
	250	-0.0115 (0.0409)	-0.0097 (0.0412)	-0.0098 (0.0413)
$S_Y(t) = 0.50$	125	-0.0033 (0.0585)	-0.0045 (0.0594)	-0.0045 (0.0595)
	250	-0.0057 (0.0437)	-0.0057 (0.0440)	-0.0057 (0.0441)
		Kendall's τ =0.5		
$\log(\alpha)$ =5.746	125	-0.0008 (1.1621)	-0.2696 (0.9674)	-0.2673 (0.9735)
	250	0.0580 (0.7594)	-0.0684 (0.6817)	-0.0675 (0.6835)
$F_X(t) = 0.50$	125	-0.0122 (0.0460)	-0.0092 (0.0426)	-0.0092 (0.0426)
	250	-0.0028 (0.0347)	-0.0022 (0.0325)	-0.0022 (0.0325)
$S_Y(t) = 0.50$	125	0.0006 (0.0470)	-0.0005 (0.0443)	-0.0005 (0.0443)
	250	-0.0029 (0.0386)	-0.0029 (0.0364)	-0.0028 (0.0364)

Each cell contains the average bias ($\times 10^{-2}$) and standard deviation ($\times 10^{-2}$) (in parenthesis) based on 200 runs.

Simulation results (negative dependence)

Parameter	*n*	*NPMLE*	*Emura et al.*	*Chaeib et al.*
		Kendall's τ =-0.25		
$\log(\alpha)$=-2.38	125	-0.1158 (1.1836)	0.3508 (1.0770)	0.3501 (1.0670)
	250	-0.0225 (1.0129)	0.0540 (1.0019)	0.0187 (1.0668)
$F_X(t) = 0.50$	125	-0.0175 (0.1063)	0.0404 (0.1142)	0.0403 (0.1140)
	250	-0.0207 (0.0831)	0.0141 (0.0939)	0.0114 (0.0944)
$S_Y(t) = 0.50$	125	-0.0161 (0.1112)	0.0421 (0.1132)	0.0419 (0.1129)
	250	-0.0136 (0.0918)	0.0211 (0.0948)	0.0183 (0.0953)
		Kendall's τ =-0.5		
$\log(\alpha)$=-5.746	125	0.6819 (0.9779)	2.4216 (2.0641)	2.3795 (2.1017)
	250	0.5088 (0.9816)	2.0827 (2.1311)	2.0571 (2.1160)
$F_X(t) = 0.50$	125	0.0485 (0.0882)	0.2099 (0.1676)	0.2070 (0.1695)
	250	0.0303 (0.0752)	0.1728 (0.1758)	0.1704 (0.1755)
$S_Y(t) = 0.50$	125	0.0508 (0.0862)	0.2090 (0.1695)	0.2061 (0.1715)
	250	0.0338 (0.0800)	0.1757 (0.1728)	0.1732 (0.1728)

Each cell contains the average bias ($\times 10^{-2}$) and standard deviation ($\times 10^{-2}$) (in parenthesis) based on 200 runs.

Proposed method

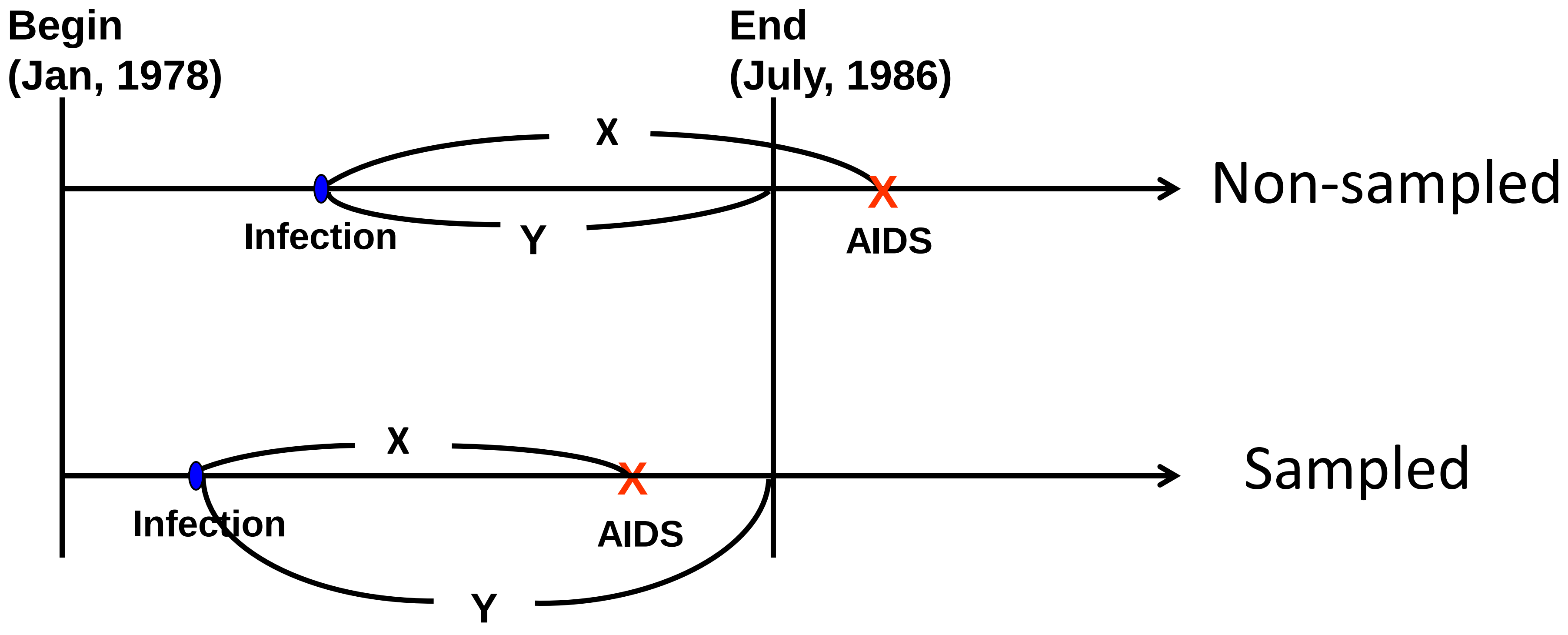
Data analysis

- Transfusion-related AIDS (Kalbfleisch & Lawless, 1989, JASA)

  X : Time from infection to AIDS (month)

  Y : 102 - time of infection (month)

  n : sample size = 293



Proposed method

Proposed method

- Model selection with (*K+1*) different copulas

$$\begin{cases} C^{(0)}[u,v] = uv \\ C_\alpha^{(k)}[u,v], \quad k = 1,\ldots,K \end{cases}$$

where $\lim_{\alpha \to 1} C_\alpha^{(k)}[u,v] = uv$

- Deviance

$$2\{l_n(\hat{\alpha}, \hat{H}_X, \hat{\Lambda}_Y) - l_n(1, \hat{H}_X^{\alpha=1}, \hat{\Lambda}_Y^{\alpha=1})\} \quad \sim \quad \chi^2_{df=1}$$

Step 1: Calculate deviances for *K* copulas

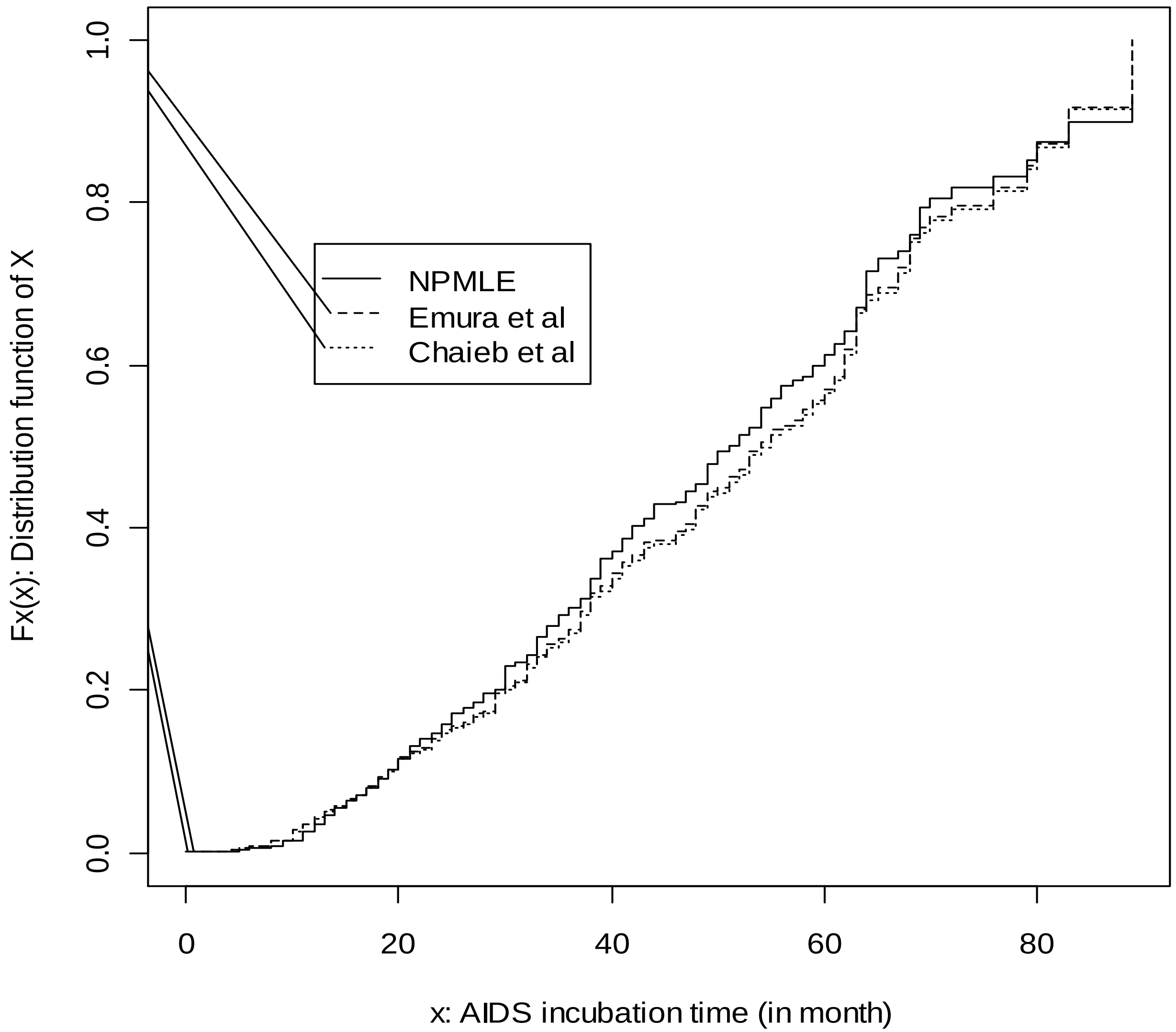
Step 2: Choose the copula with largest deviance & p-value <0.05

Table 1: Analysis of the Transfusion-related AIDS data

opula Type	Form*	Association parameter $\hat{\alpha}$ (SE)	Kendall's $\tau(\hat{\alpha})$	95% CI for α	Deviance (p-value)
Clayton	R	1.521 (0.172)	0.207	(1.218, 1.898)	8.568 (0.003)
ppendix C.1)	S	1.645 (0.233)	0.244	(1.246, 2.171)	5.228 (0.022)
	SS	0.763 (0.033)	0.134	(0.701, 0.831)	19.028 (0.000)
Frank	R, S	55.725 (42.704)	0.390	(12.41, 250.24)	10.828 (0.001)
ppendix C.2)	SS	0.018 (0.014)	0.390	(0.004, 0.081)	10.828 (0.001)
Plackett	R, S	5.293 (1.390)	0.356	(3.164, 8.856)	8.068 (0.005)
ppendix C.4)	SS	0.189 (0.050)	0.356	(0.113, 0.316)	8.068 (0.005)
Gumbel	R	1.459 (0.136)	0.315	(1.257, 1.821)	7.868 (0.005)
ppendix C.3)	S	1.340 (0.120)	0.254	(1.170, 1.678)	6.368 (0.012)
vo-parameter	R	$\hat{\alpha}$:1.521 (0.400) $\hat{\beta}$:1.000 (**)	0.207	α :(1.116, 3.348) β : (**)	8.588 (0.003)
ppendix C.5)	S	$\hat{\alpha}$:1.344 (0.264) $\hat{\beta}$:1.235 (0.140)	0.309	α :(1.076, 2.551) β :(1.073, 1.756)	7.928 (0.005)

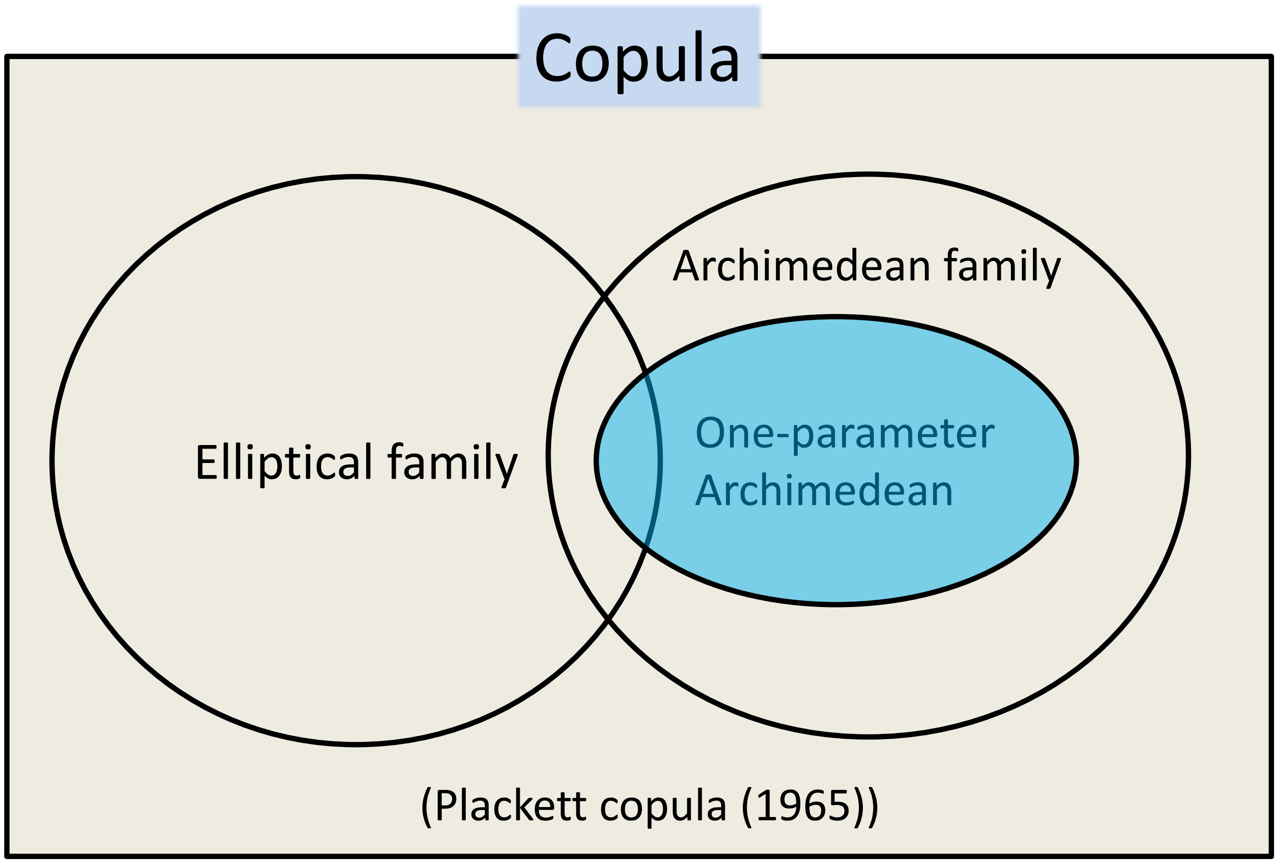
Under Clayton copula

$\hat{F}_X(x) = e^{-\hat{H}_X(x)}$: Time from infection to AIDS (month)



Proposed method

Major advantage: NPMLE can fit more copulas not restricted within one-parameter Aarchimedean family; Model selection among broader copulas



Summary: Proposed method

- We proposed NPMLE for dependent truncation data
- The application of the reverse-time hazard function and semi-survival copula is the key to have a Breslow-Aalen type formula
- The NPMLE can fit broad class of copula and easily adjust for ties
- SD can be estimated by the inverse Fisher information, which is confirmed by simulations
- Under negative correlation, NPMLE worked better than the Emura et al. (2011) and Chaieb et al. (2006)
- NPMLE is computationally demanding (drawback)

Further research

- Theory & simulations for the proposed model selection

$$2\{l_n(\hat{\alpha}, \hat{H}_X, \hat{\Lambda}_Y) - l_n(1, \hat{H}_X^{\alpha=1}, \hat{\Lambda}_Y^{\alpha=1})\} \quad \sim \quad \chi^2_{df=1}$$

1. Proof
2. Numerical comparison with the model selection proposed by Beaudoin & Lakhal-Chaieb (2008, stat. in med.)

- Computational demands for elliptical copulas

Numerical techniques to non-closed form copulas ?

- Regression under dependent truncation

I am currently working on the accelerated failure time regression of the form

$$Y = \beta' Z + \gamma X + \varepsilon$$

Thank you for your kind attention