

Tung Hai University,
Department of Statistics
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**Copula-based inference for truncation models
based on copulas**

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Outlines

Review & Motivation

- Truncation data:
- Traditional approaches
- Copula-based approaches

Proposed method

- Proposed method
- Simulation, Data analysis
- Conclusion

Part I: Review & Motivation

Truncation:

- A pair of (X, Y) is observed only when $X \leq Y$ holds.
- If $X > Y$, nothing is observed ! (truncated)

Today's focus

A special case of doubly truncated data

- X is observed only when $Z \leq X \leq Y$, where (Z, Y) is random
- If $Z=0$, this reduces to truncation

See

Efron & Petrosian (1992 *JASA*), Wang & Stovring (2007, *BMC Medical Res.*)

Shen (2010 *AISM*), Moreira & Una-Alvares (2010 *J. of Nonpar.*)

Shen (2012 *J. of App. Stat.*), but name a few.

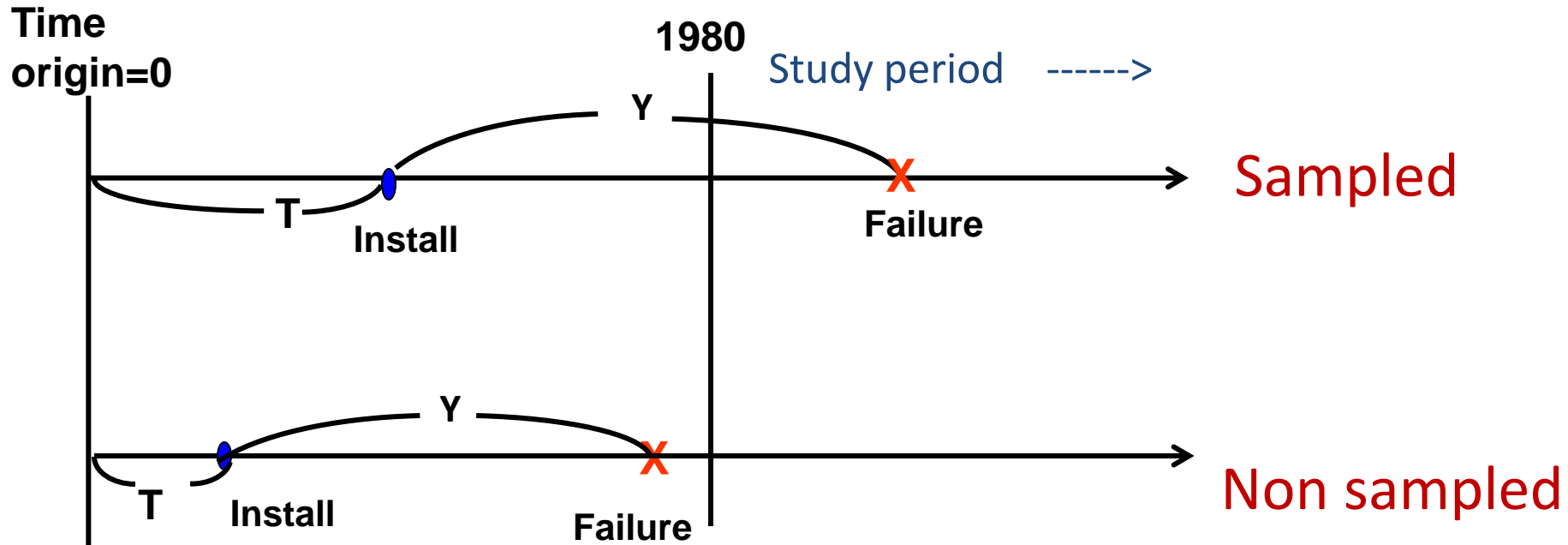
Truncation occurs in
Survival analysis of Power Transformer
(電力變壓器)



Fig. from Toshiba Corporation

What is Truncation?

- Power Transformer (電力變壓器) data
(Hong et al., 2009 *Ann. Applied Statistics*)

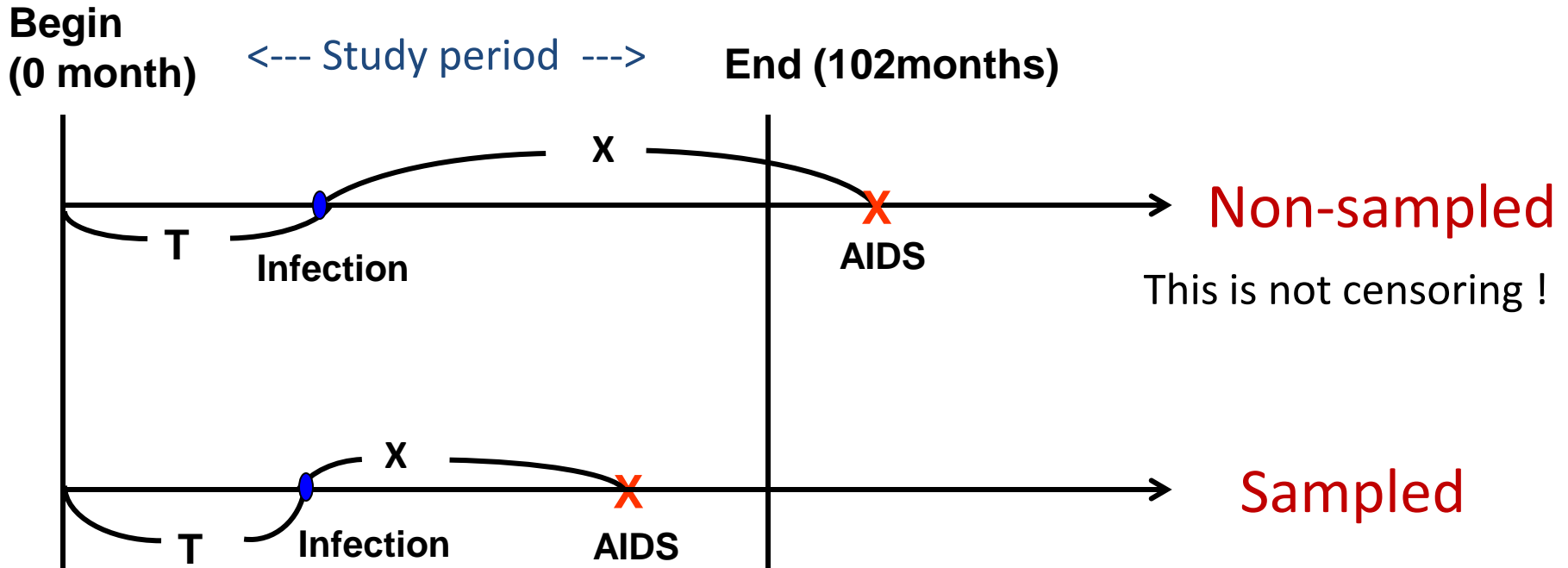


Inclusion criterion: $1980 \leq T+Y$, i.e., $1980-T = X \leq Y$

What is Truncation?

- Transfusion-related AIDS

(Lagakos et al., 1988 *Biometrika*)



Inclusion criterion: $T+X \leq 102$ i.e., $X \leq Y \equiv 102-T$

Truncation data

- Truncation data :

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

$$\text{subject to } X_j \leq Y_j$$



i.i.d. from

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

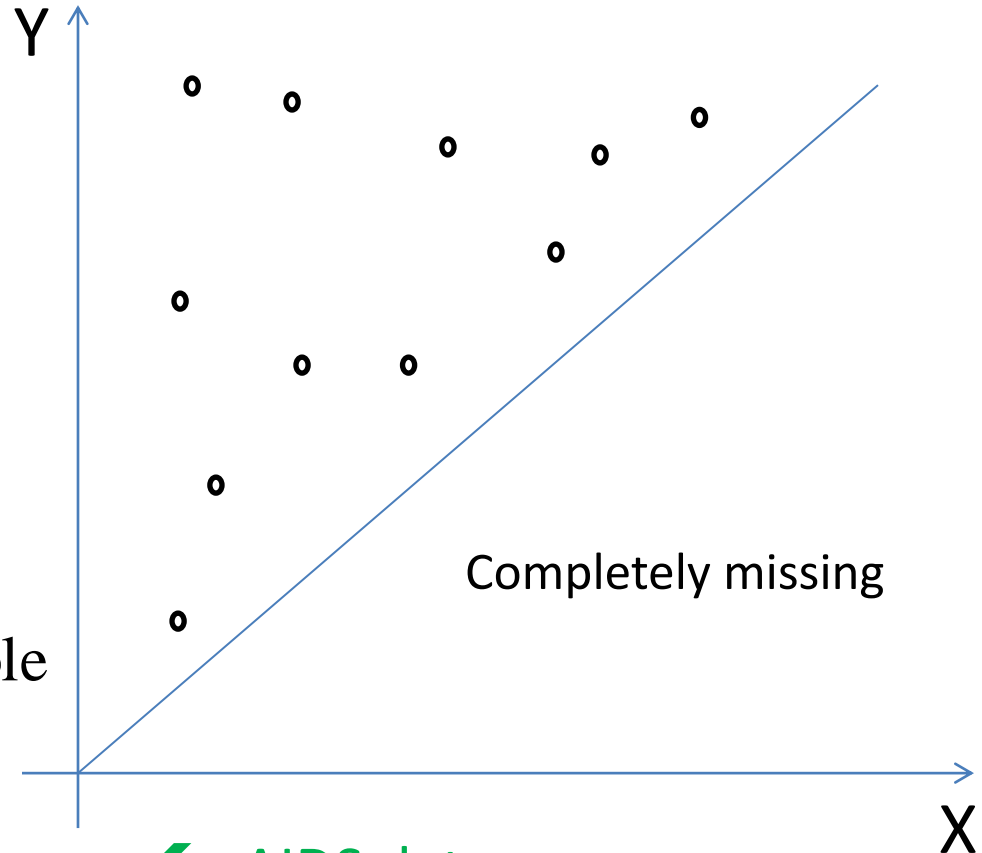
where (X, Y) is

the "*population*" random variable

Target : Estimation of

$$F_X(x) = \Pr(X \leq x)$$

$$F_Y(y) = \Pr(Y \leq y)$$



← AIDS data

← Power transformer data

Traditional analysis

- Nonparametric estimator

$$\hat{F}_X(x) = \prod_{u>x} \left\{ 1 - \frac{\sum_{j=1}^n I(X_j = u)}{\sum_{j=1}^n I(X_j \leq u, Y_j \geq u)} \right\}, \quad \hat{F}_Y(y) = 1 - \prod_{u \leq y} \left\{ 1 - \frac{\sum_{j=1}^n I(Y_j = u)}{\sum_{j=1}^n I(X_j \leq u, Y_j \geq u)} \right\}$$

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

- **Key assumption: Quasi-independence (Tsai, 1990):**

$$X \perp_Q Y : \Pr(X \leq x, Y \leq y | X \leq Y) = \frac{\int \int_{\substack{u \leq x, v \leq y \\ u \leq v}} dF_X(u) dF_Y(v)}{\int \int_{u \leq v} dF_X(u) dF_Y(v)}$$

*Quasi-independence assumption is testable

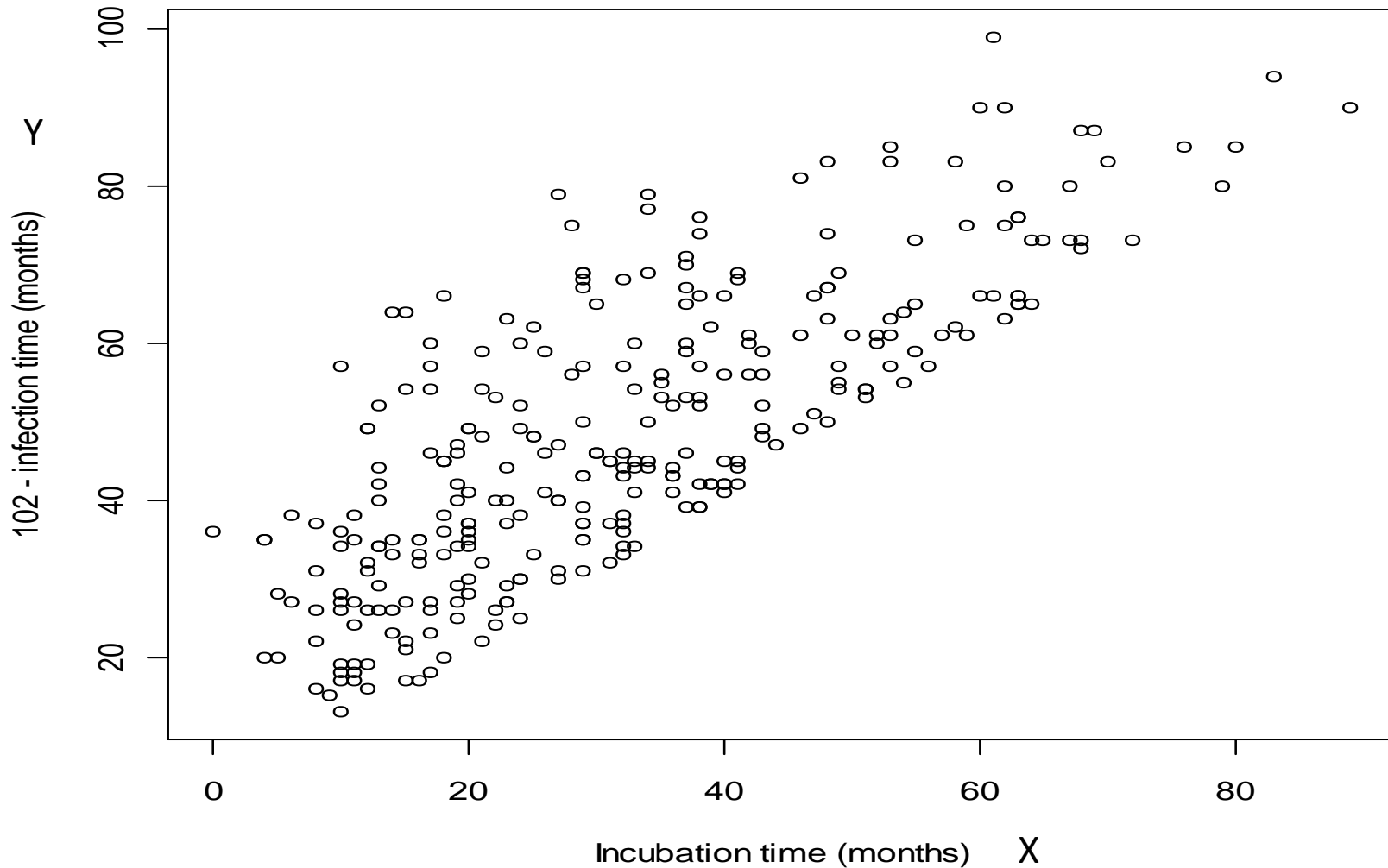
(Tsai, 1990; Chen et al., 1996; Martin & Betensky, 2005; Emura & Wang, 2010)

Quasi-independence is rejected at

P-value = 0.040 (Marting & Betensky 2005 *JASA*)

= 0.048 (Emura & Wang 2010 *JMVA*)

Transfusion-related AIDS data



- Chaieb et al. (2006 *Biometrika*) relax the quasi-independence by using “Copulas”

Copula

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

- **Example 1:** Independence copula

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

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

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

- **Example 3:** Normal copula

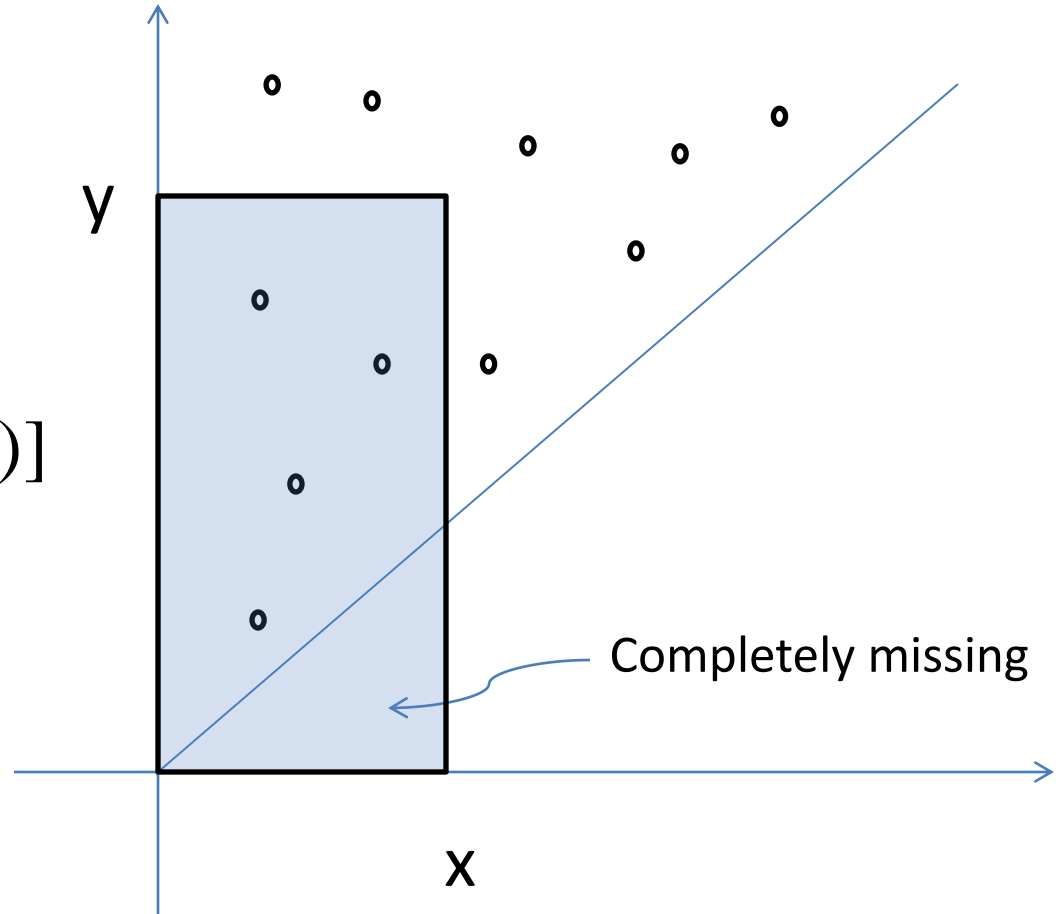
$$C_\rho[u, v] = \Phi_\rho[\Phi^{-1}(u), \Phi^{-1}(v)], \quad -1 < \rho < 1$$

Φ_ρ : Joint CDF of standard bivariate normal

Copula model

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

The model is
unidentifiable



Copula model

$$\Pr(X \leq x, Y > y | X \leq Y)$$

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

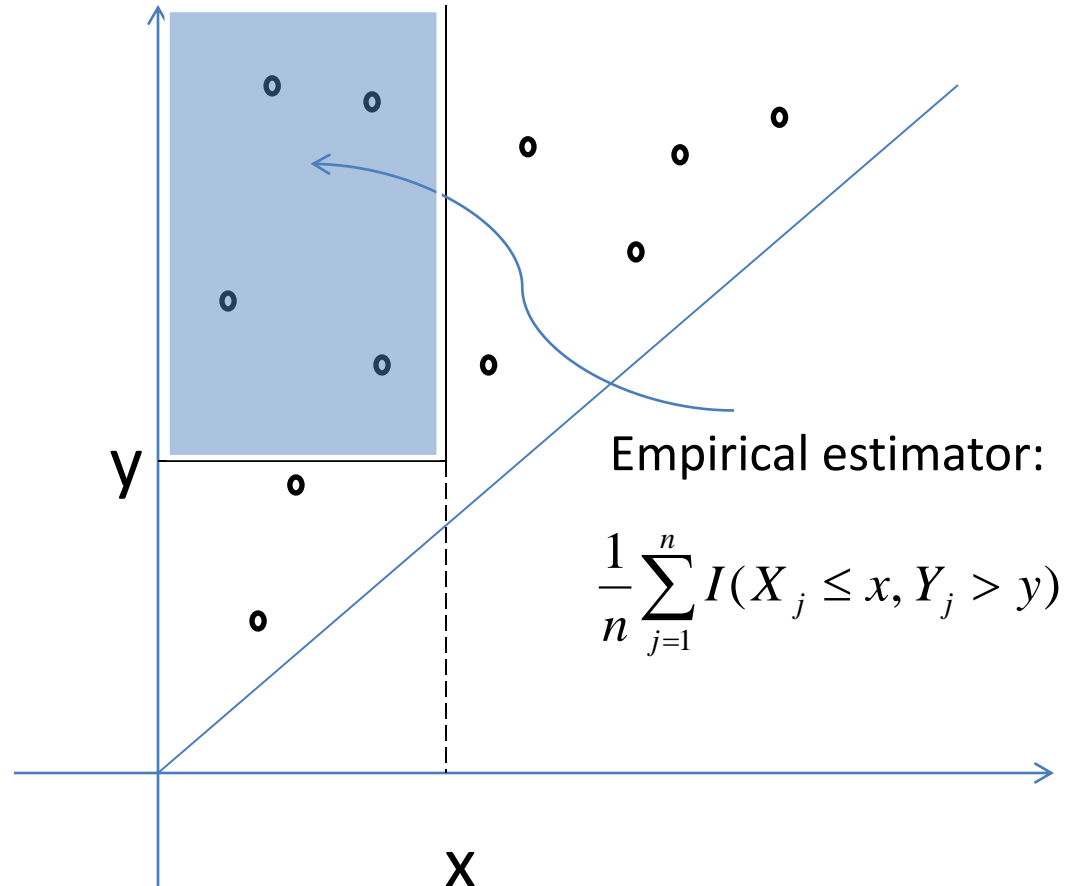
where

$$c(\alpha, F_X, S_Y) =$$

$$\iint_{x \leq y} \frac{\partial^2}{\partial x \partial y} C_\alpha[F_X(x), S_Y(y)] dx dy$$

- **Semi-survival copula**
(Chaieb et al., 2006, *Biometrika*)

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



Existing procedures

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

Useful for solving moment equations:

[Chaieb et al. (2006) and Emura et al. (2011 *Stat. Sinica*)]

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

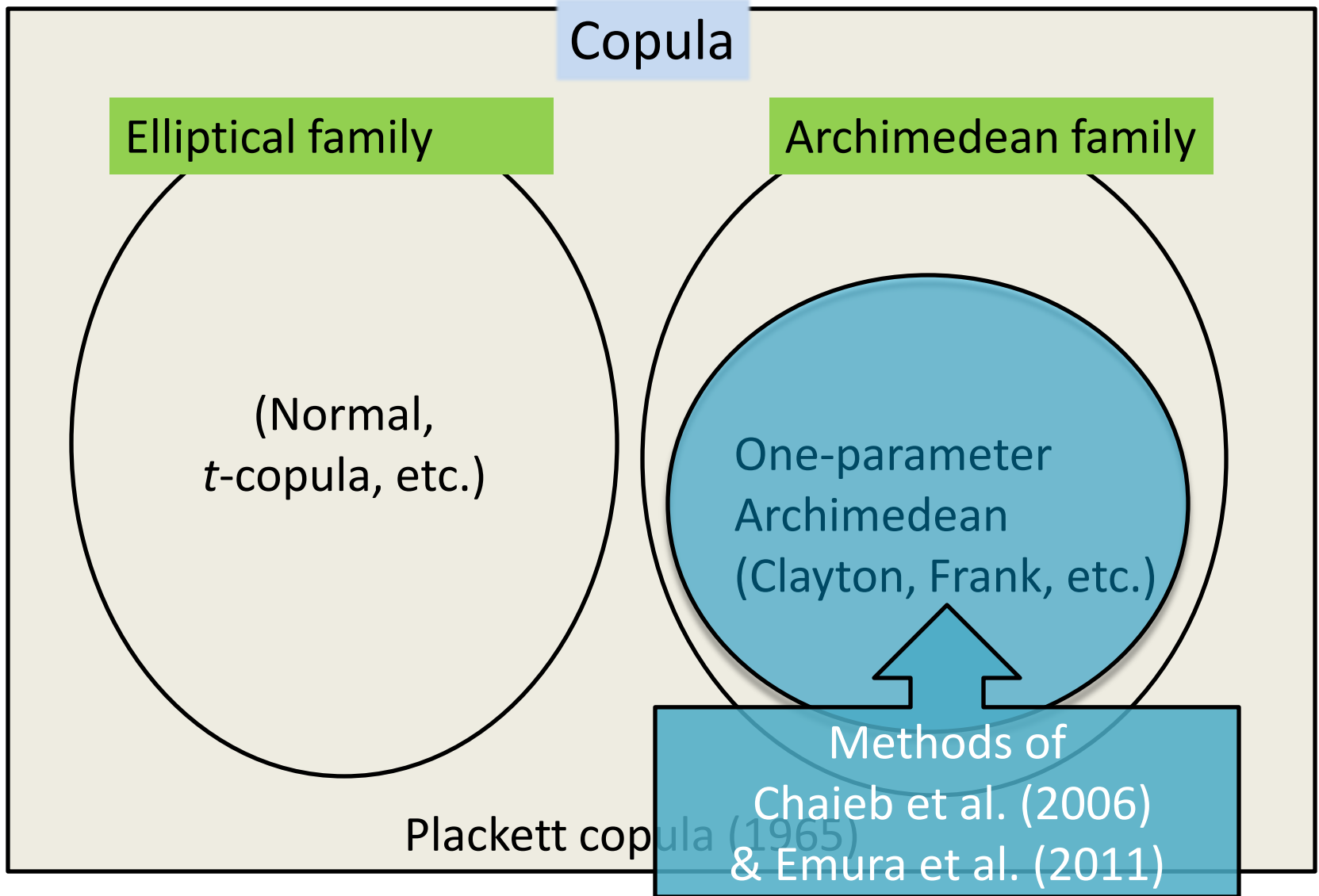
$$\Leftrightarrow \phi_\alpha \left(\frac{c(\alpha, F_X, S_Y)}{n} \sum_{j=1}^n I(X_j \leq t, Y_j > t) \right) = \phi_\alpha(F_X(t)) + \phi_\alpha(S_Y(t))$$

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

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

Sequentially solve: $S_X(X_1) \equiv 1 \rightarrow F_X(X_1) \rightarrow S_X(X_2) \rightarrow \dots$

Existing procedures



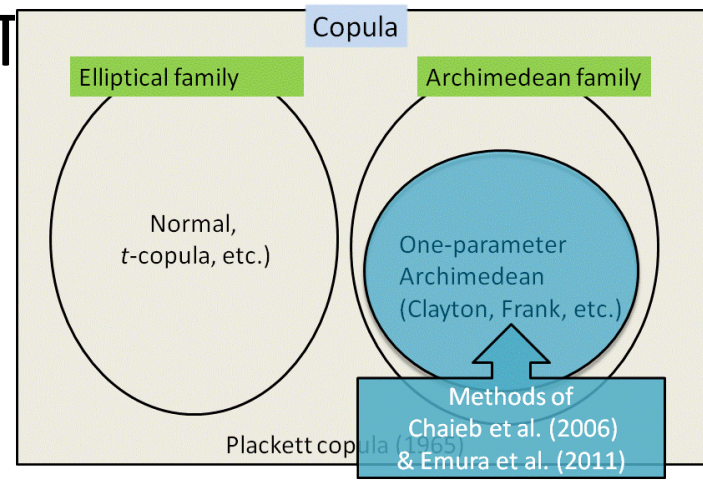
Part II: Proposed method

Proposed method

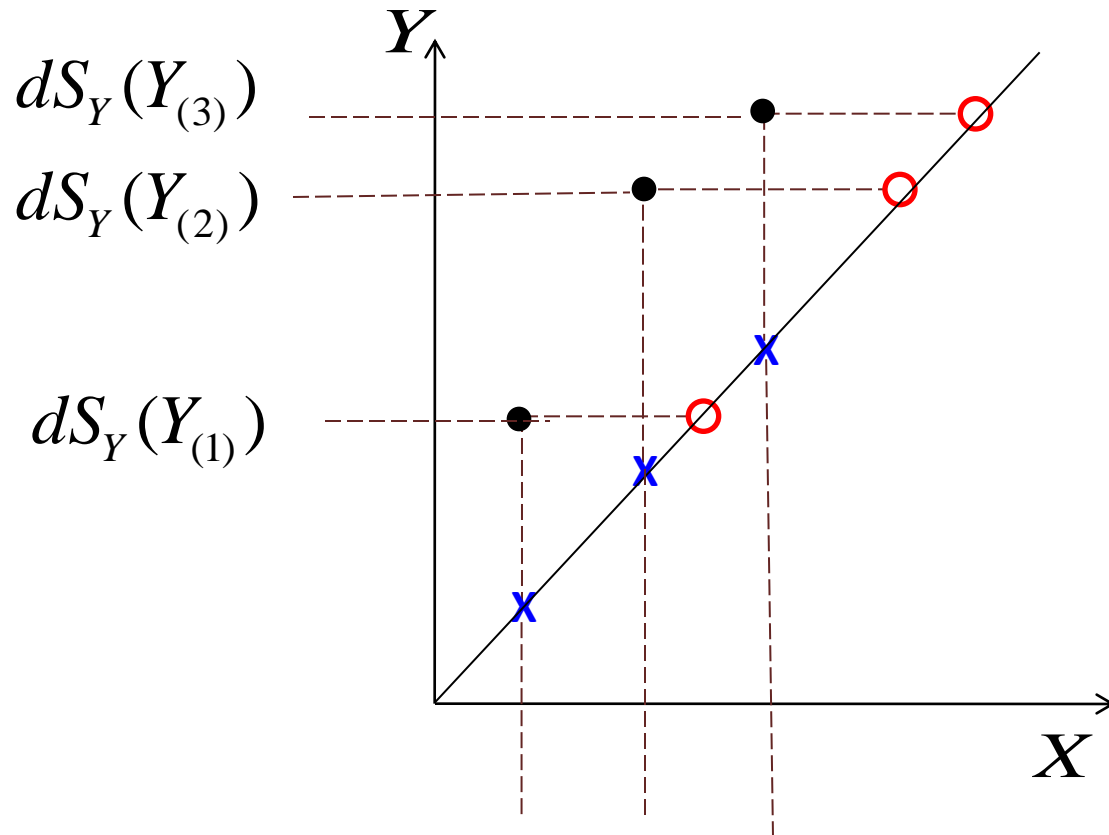
- The preceding two methods use moment-based estimating equations for (F_X, S_Y) under Archimedean copula family
- In this talk, we propose to get (\hat{F}_X, \hat{S}_Y) by the nonparametric maximum likelihood estimator (NPMLE; due to T

Advantage:

Potentially applicable for a broader class of copulas



NPMLE: due to Turnbull (1976)



Maximize the NPMLE
with constraints:

$$0 \leq dF_X(X_{(1)}) \leq 1$$

$$0 \leq dF_X(X_{(2)}) \leq 1$$

$$0 \leq dF_X(X_{(3)}) \leq 1$$

$$\sum_{i=1}^3 dF_X(X_{(i)}) = 1$$

$$dF_X(X_{(1)}) \quad dF_X(X_{(2)}) \quad dF_X(X_{(3)})$$

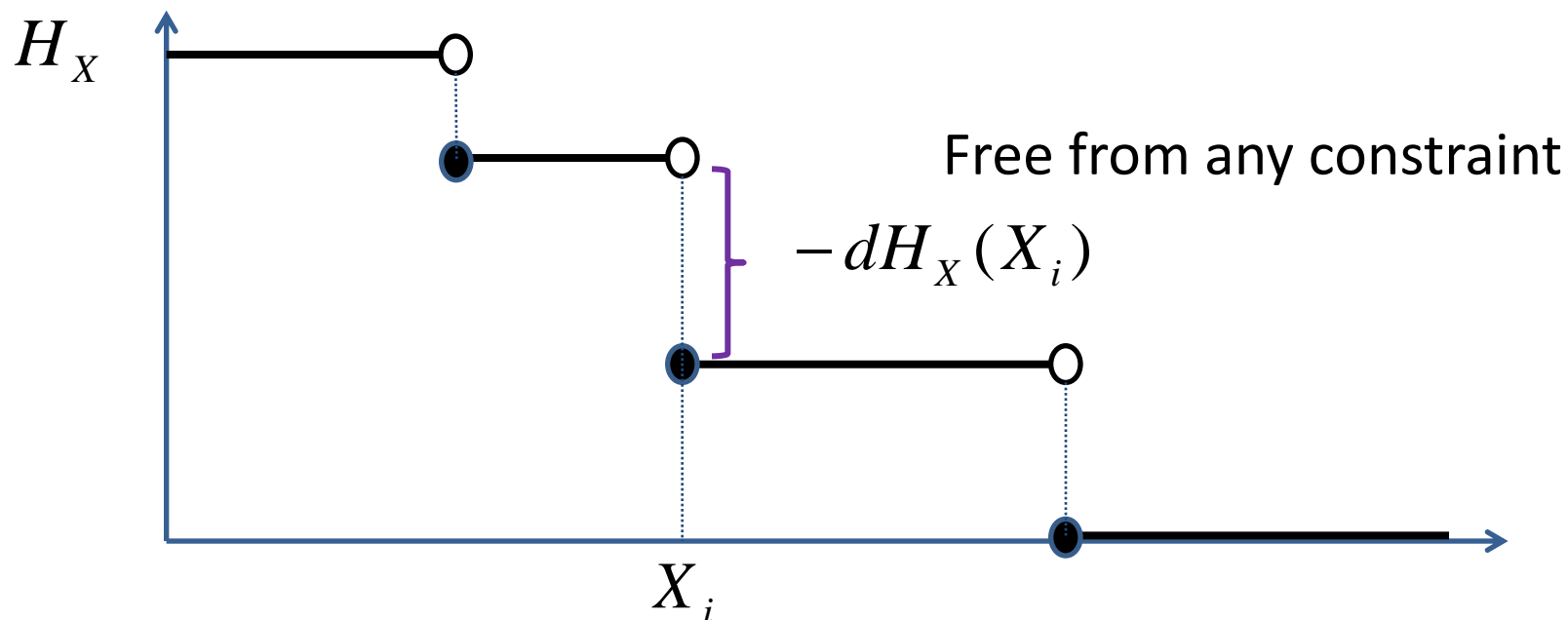
- Parameterize (F_X, S_Y) as follows:

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

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

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

- * $\Lambda_Y(y)$: Cumulative hazard



Proposed method

- Semi-survival Copula (Chaieb et al., 2006)

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

where $c(\alpha, H_X, \Lambda_Y) = \iint_{x \leq y} -\frac{\partial^2}{\partial x \partial y} C_\alpha[e^{-H_X(x)}, e^{-\Lambda_Y(y^-)}] dx dy$

leading to the density

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

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

Proposed method

- Log-likelihood

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

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

→ Maximize 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**

The maximum of $l_n(\alpha, H_X, \Lambda_Y)$ is not unique

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

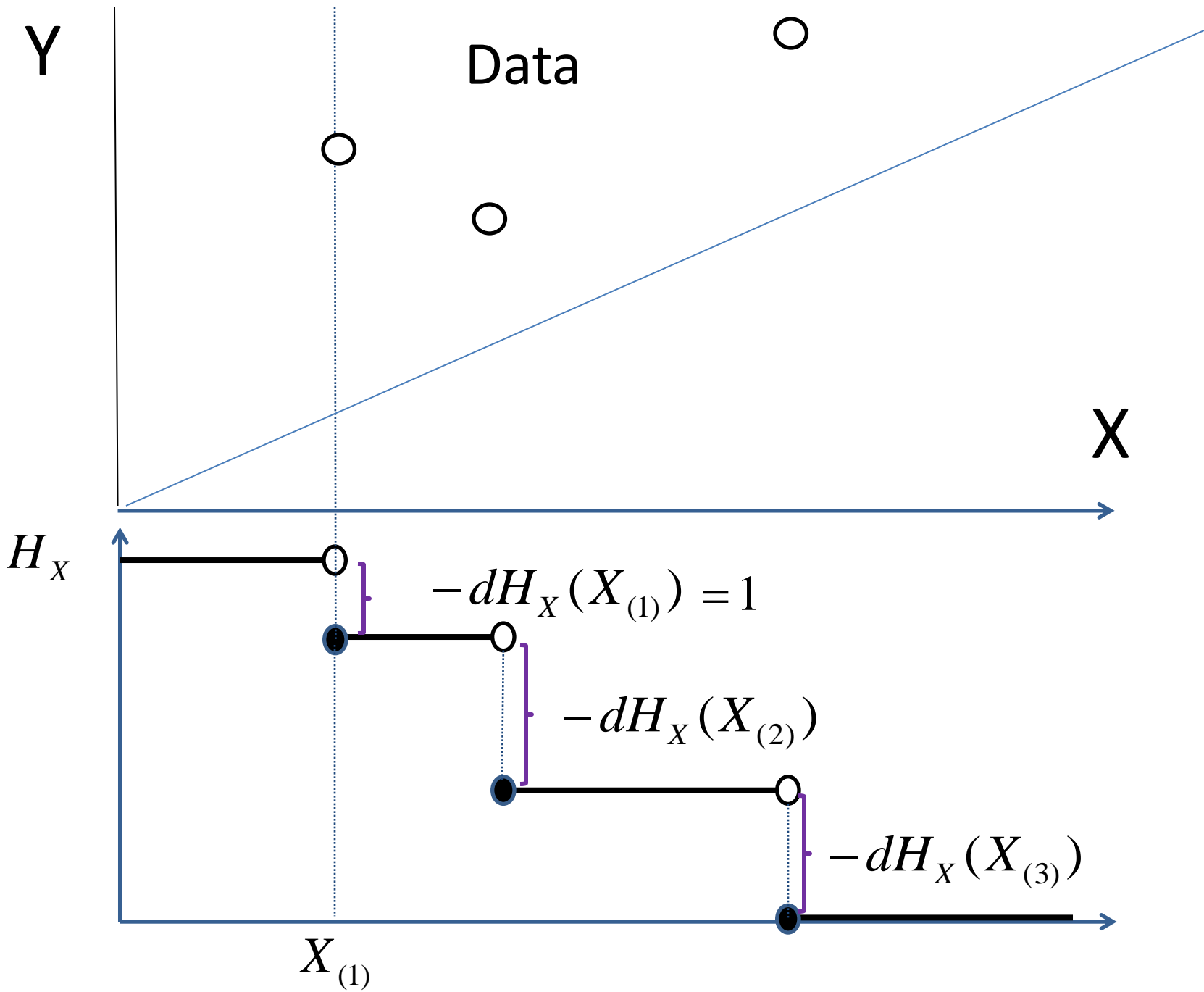
*analogy with the linear regression with $p > n$

- **Idea:** reduces to $2n-1$ parameters

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



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



Proposed method

- $2n-1$ score equations

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

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

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

leading to a self-consistency (Turnbull, 1976)
type equations

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

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

Proposed method

- Quasi-Newton algorithm to maximize

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

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

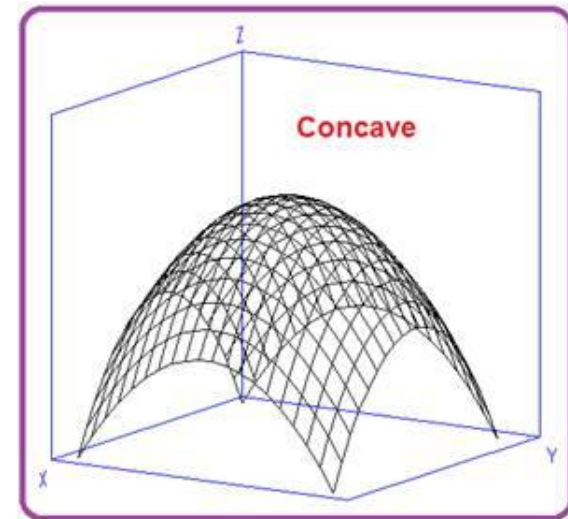
Requirements:

- twice differentiable
- Unique maximum
- No constraint in parameter space

Especially, one can apply “nlm” routine in R.

Convergence criteriat:

1. $2n-1$ scores are zero at $(\hat{\alpha}, \hat{H}_X, \hat{\Lambda}_Y)$
2. Hessian matrix at $(\hat{\alpha}, \hat{H}_X, \hat{\Lambda}_Y)$ is positive definite
(Hessian matrix are concave, it should be a global maxima)



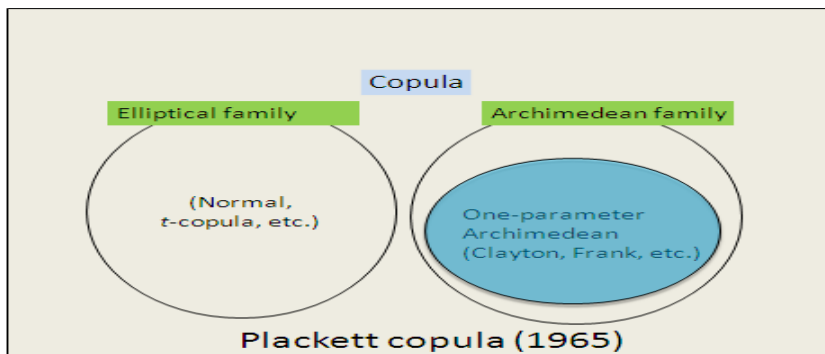
Proposed method

- The NPMLE $(\hat{\alpha}, \hat{H}_X, \hat{\Lambda}_Y)$ is **consistent & asymptotic normal** (Emura & Wang 2012 *JMVA*)
- 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, e.g.,

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



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. Spearman'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:** $\Pr(X \leq x, Y > y) = C_{\alpha}[e^{-H_X(x)}, e^{-\Lambda_Y(y^-)}]$

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

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

Positive dependence, 200 repetitions

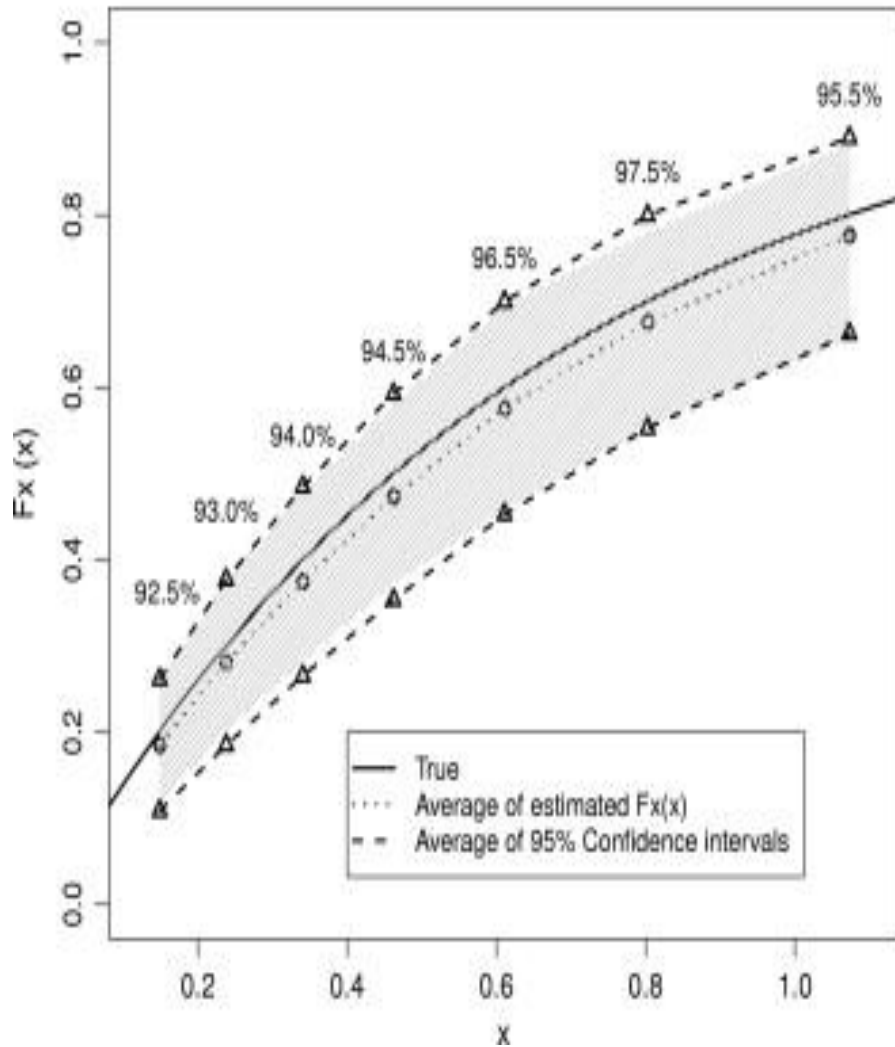
<i>Parameter</i>		<i>Mean(Bias)</i>	<i>SE</i>	<i>SEE</i>	<i>95%Cov</i>
Spearman's $\rho = 0.25$ ($\alpha = 1/2.15$, $\Pr(X \leq Y) = 0.79$)					
$\log(\alpha) = -0.765$	$n = 125$	-0.778 (-0.013)	0.407	0.407	0.945
	$n = 250$	-0.697 (0.068)	0.311	0.296	0.965
$H_X(t) = 0.693$	$n = 125$	0.736 (0.043)	0.123	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 $\rho = 0.50$ ($\alpha = 1/5.11$, $\Pr(X \leq Y) = 0.84$)					
$\log(\alpha) = -1.631$	$n = 125$	-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

Negative dependence, 200 repetitions

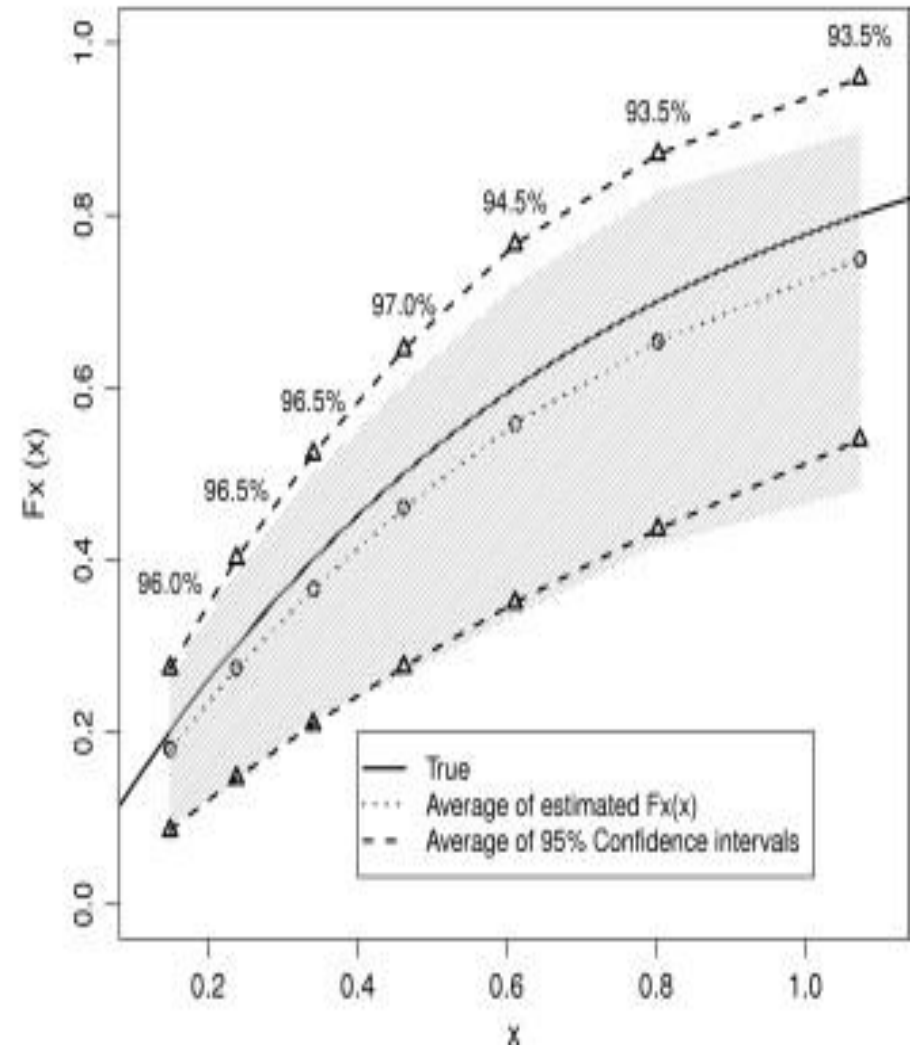
<i>Parameter</i>		<i>Mean(Bias)</i>	<i>SE</i>	<i>SEE</i>	<i>95%Cov</i>
Spearman's $\rho = -0.25$ ($\alpha = 2.15$, $\Pr(X \leq Y) = 0.72$)					
$\log(\alpha) = 0.765$	$n = 125$	0.859 (0.094)	0.598	0.554	0.960
	$n = 250$	0.717 (-0.048)	0.342	0.359	0.930
$H_X(t) = 0.693$	$n = 125$	0.809 (0.116)	0.313	0.244	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 $\rho = -0.50$ ($\alpha = 5.11$, $\Pr(X \leq Y) = 0.70$)					
$\log(\alpha) = 1.631$	$n = 125$	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

Performance of $\hat{F}_X(x) = e^{-\hat{H}_X(x)}$

Positive Association: Kendall's tau = 0.25



Negative Association: Kendall's tau = -0.25



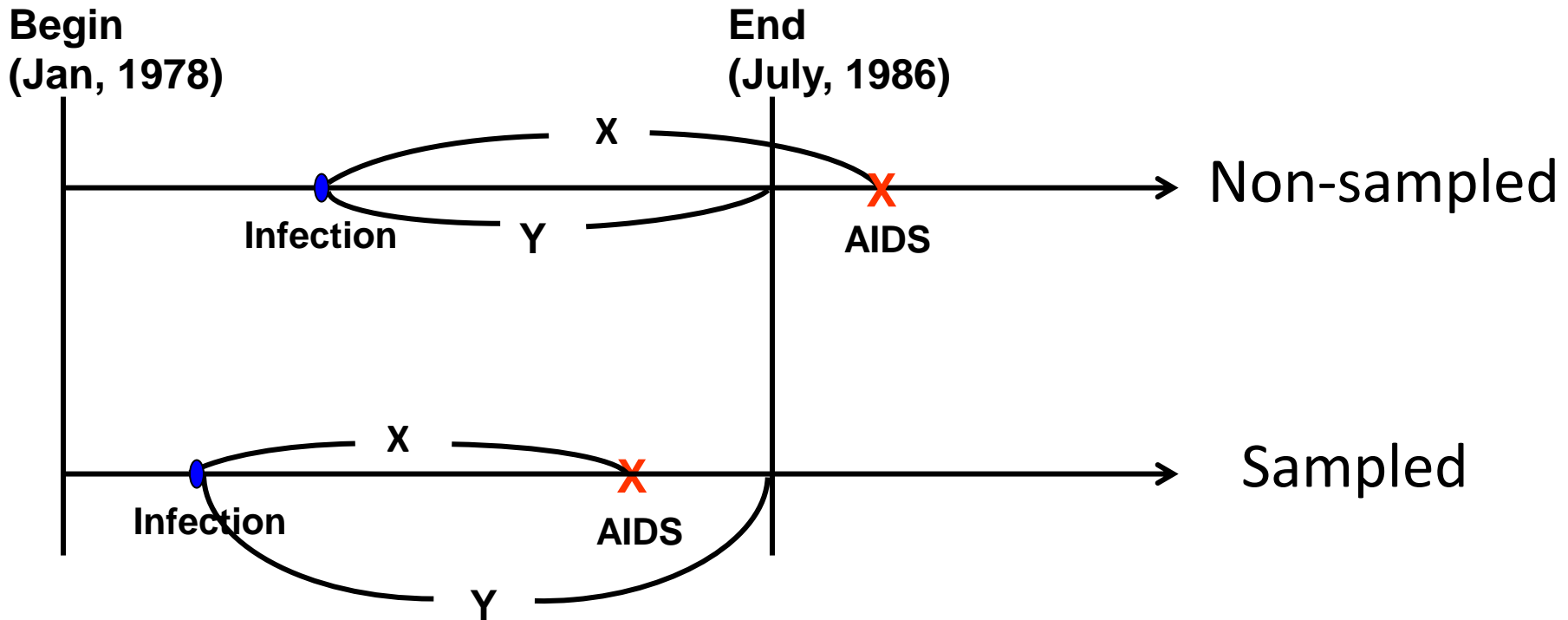
Data analysis

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

X : Time from infection to AIDS (month) ← Estimation

Y : 102 - time of infection (month)

n : sample size = 293



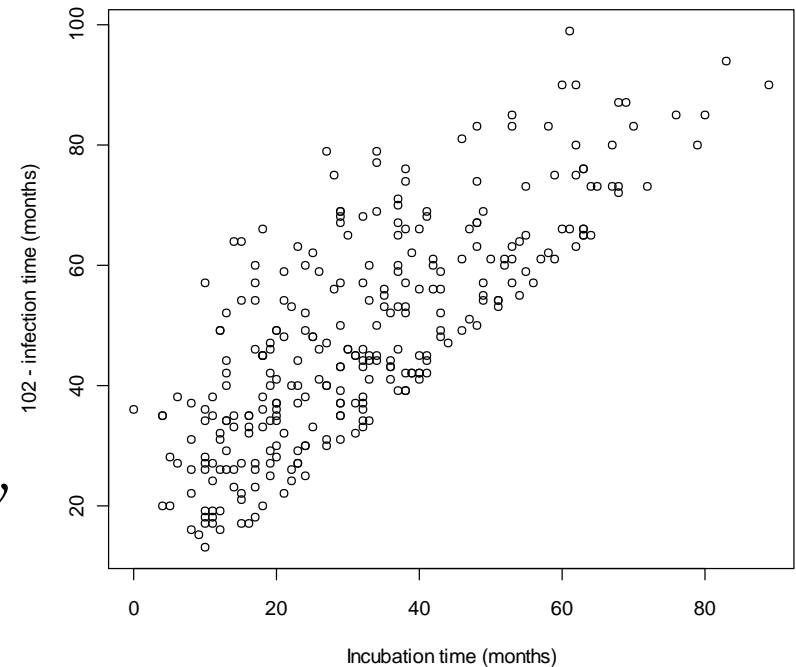
Model selection

Transfusion-related AIDS data

- $(K+1)$ candidate copulas

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

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



- Deviance: $C_{\alpha}^{(k)}$ vs. $C^{(0)}$

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

Step 1: Calculate deviances for K copulas

Step 2: Choose the copula with **smallest p-value** (<0.05)

Table 1: Analysis of the Transfusion-related AIDS data

$C_\alpha[u, v]$	Form ^(a)	$\hat{\alpha}$ (SE)	Kendall's τ on (X, Y)	95% CI for α	Deviance (p -value ^(b))
Clayton	Semi-survival	0.763 (0.033)	0.134	(0.701, 0.831)	19.028 (0.000)
	Regular	1.521 (0.172)	0.207	(1.218, 1.898)	8.568 (0.003)
	Survival	1.645 (0.233)	0.244	(1.246, 2.171)	5.228 (0.022)
Frank	Semi-survival	0.018 (0.014)	0.390	(0.004, 0.081)	10.828 (0.001)
Plackett	Semi-survival	0.189 (0.050)	0.356	(0.113, 0.316)	8.068 (0.005)
Normal	Semi-survival	-0.516 (0.083)	0.345	(-0.201, -0.831)	14.341(0.000)
t - (df=10)	Semi-survival	-0.520 (0.076)	0.350	(-0.234, -0.806)	9.559 (0.002)
t - (df=5)	Semi-survival	-0.507 (0.073)	0.344	(-0.223, -0.790)	3.959 (0.047)
Gumbel	Regular	1.459 (0.136)	0.315	(1.257, 1.821)	7.868 (0.005)
	Survival	1.340 (0.120)	0.254	(1.170, 1.678)	6.368 (0.012)
Two- parameter	Regular	$\hat{\alpha}$:1.521 (0.400) $\hat{\beta}$:1.000 ^(c)	0.207	α :(1.116, 3.348)	8.588 (0.003)
	Survival	$\hat{\alpha}$:1.344 (0.264) $\hat{\beta}$:1.235 (0.140)	0.309	α :(1.076, 2.551) β :(1.073, 1.756)	7.928 (0.019)

Smallest
P-value

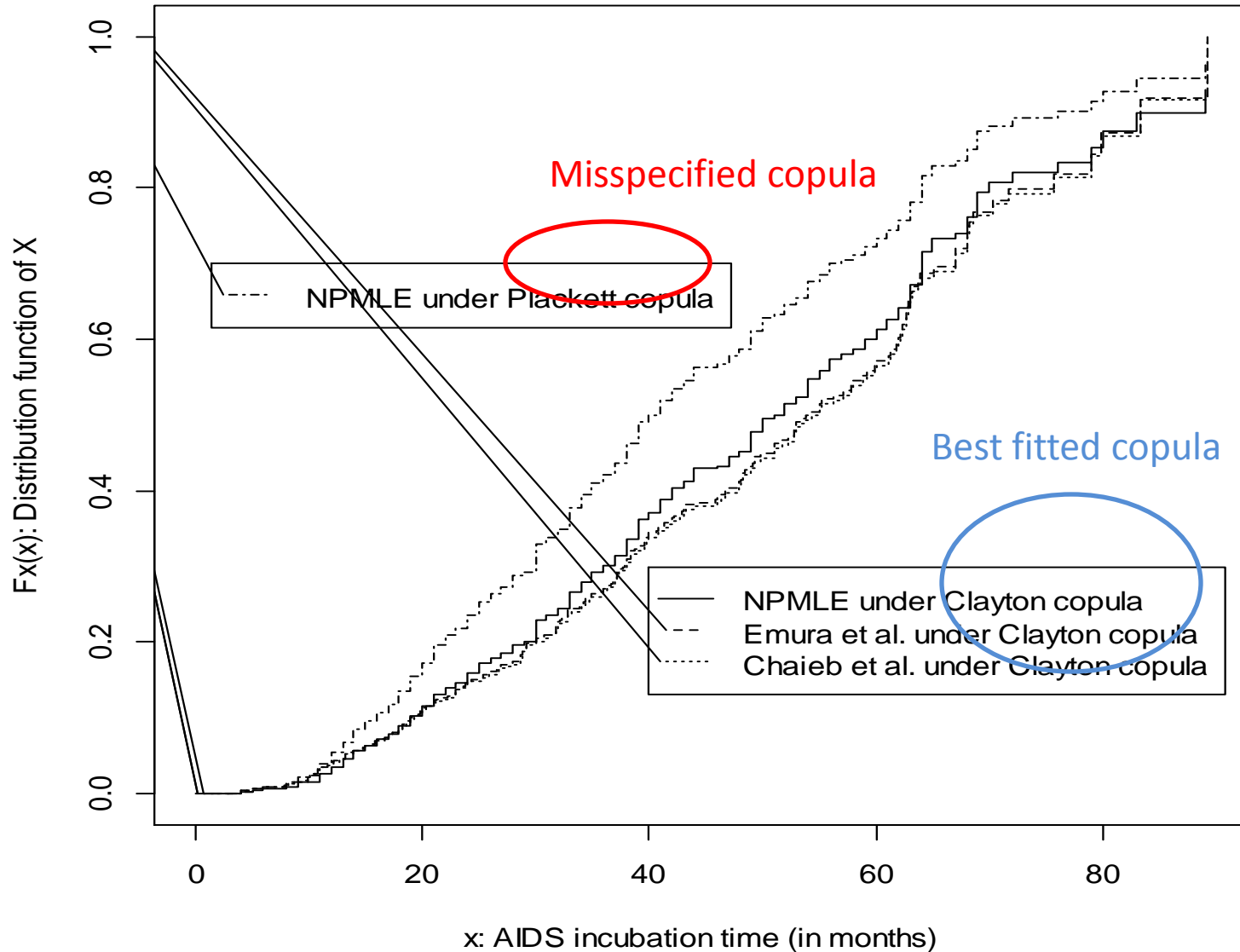
(a) A Copula $C_\alpha[u, v]$ is used to model the distribution of (X, Y) in three different forms:

i) Semi-survival form: $\Pr(X \leq x, Y > y | X \leq Y) = C_\alpha[e^{-H_X(x)}, e^{-\Lambda_Y(y)}] / c,$

ii) Regular form: $\Pr(X \leq x, Y > y | X \leq Y) = (e^{-H_X(x)} - C_\alpha[e^{-H_X(x)}, 1 - e^{-\Lambda_Y(y)}]) / c,$

iii) Survival form: $\Pr(X \leq x, Y > y | X \leq Y) = (e^{-\Lambda_Y(y)} - C_\alpha[1 - e^{-H_X(x)}, e^{-\Lambda_Y(y)}]) / c.$

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

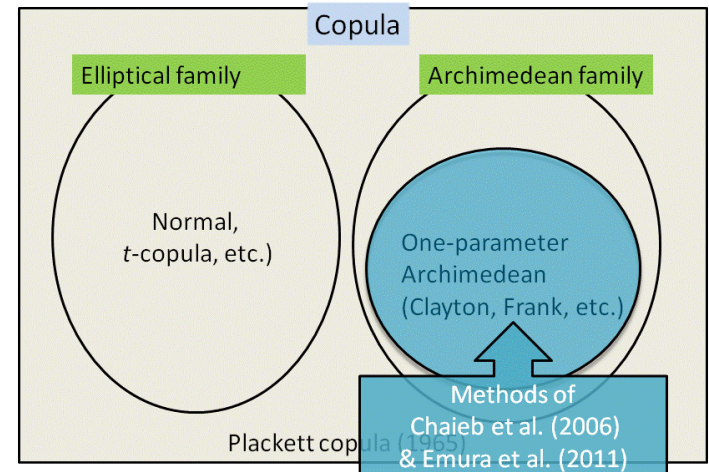


Summary

We proposed the NPMLE under semi-survival copula with reverse-time hazard modeling

Advantage of the proposed NPMLE

- Broader class of copula than existing methods
than Chaieb et al.(2006) & Emura et al. (2011)
- Equip Copula model selection via likelihood comparison



Disadvantage

- NPMLE is computationally very demanding
(numerical maximization in high-dimensional space)

Thank you for your kind attention

- Emura T & Wang W (2012)
Nonparametric maximum likelihood estimation for dependent truncation data based on copulas.
to appear in Journal of Multivariate Analysis.
- Proposed method is implemented in R depend.truncation package.
available at CRAN <http://cran.r-project.org/>