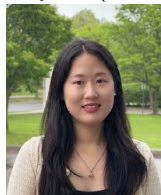


# Bayesian Copula-based Latent Variable Models

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# Copulas: The Joys

- ▶ Copulas are mathematical devices used to **model dependence between random variables** regardless of their marginals.
- ▶ If  $Y_1, Y_2, \dots, Y_K$  are continuous r.v.'s with cdfs  $F_1, F_2, \dots, F_k$ , there is an **unique copula**  $C : [0, 1]^K \rightarrow [0, 1]$  that links the joint cdf with the marginal ones (Sklar's Theorem),

$$F(t_1, \dots, t_k) = C(F_1(t_1), \dots, F_k(t_k)).$$

- ▶ Copulas are useful for **data fusion/integration** because they lead to coherent joint models, even when the marginals are in different families (e.g., Gaussian, Poisson, Student, etc) or of different types (e.g, discrete, continuous).
- ▶ Copulas **unlock information contained in the dependence part of the distribution** (second-order) that complements the information in the marginals.
- ▶ Simply put, copulas allow us to **extend statistical methods beyond the use of a multivariate Gaussian or Student**.

# Motivation

- ▶ Parametric copulas can capture a wide range of dependence patterns for lower values of  $k$ ,  $k \leq 2, 3$ .
- ▶ In higher dimensions, say  $k > 5$  a parametric family (usually indexed by a parameter of dimension  $< 3$ ) will not be able to capture complex dependencies
- ▶ Vine copulas offer additional flexibility but can be difficult to fit.
- ▶ Today: Bayesian nonparametric mixtures of copulas to extend their flexibility in higher dimensions

# Big Picture

- ▶ Bayesian estimation for copula models is desirable as the posterior incorporates uncertainty due to marginals and dependence structure (Levi and Craiu, 2018)
- ▶ We consider Bayesian nonparametric mixtures of Archimedean copulas in which the mixing distribution is the Poisson-Dirichlet process, introduced by Pitman and Yor (1997).
- ▶ It extends the range of dependence patterns that can be modeled.
- ▶ In the case of heterogeneous populations, it clusters the sample based on information contained in the marginals AND the dependence structure.

# Archimedean copulas

- ▶ An Archimedean family is characterized by a continuous, decreasing and convex **generator** function  $\phi$  such that  $\phi : [0, 1] \rightarrow \mathbb{R}^+$ ,  $\phi(0) = \infty$ ,  $\phi(1) = 0$ .
- ▶ The copula with generator  $\phi$  is defined as

$$C(u_1, \dots, u_p) = \phi^{-1}\{\phi(u_1) + \dots + \phi(u_p)\}. \quad (1)$$

- ▶ Generators  $\phi$  usually belong to families that are parameterized in terms of a single parameter  $\theta \in \Theta$
- ▶ Archimedean copulas assume that the variables are exchangeable and the mixture will preserve this.

# BNP mixtures of copulas

- ▶  $G$  has a Poisson-Dirichlet prior with scalar parameters  $a \in [0, 1)$ ,  $b > -a$  and mean parameter  $G_0$ , denoted as  $G \sim \text{PD}(a, b, G_0)$ , when

$$G(\cdot) = \sum_{k=1}^{\infty} \omega_k \delta_{\theta_k}(\cdot), \quad (2)$$

where  $\omega_1 = \nu_1$  and  $\omega_k = \nu_k \prod_{j < k} (1 - \nu_j)$  for  $k = 2, 3, \dots$ , with  $\nu_k \stackrel{\text{ind}}{\sim} \text{Be}(1 - a, b + ka)$  independent of the weights, locations  $\theta_k \stackrel{\text{iid}}{\sim} G_0$  for  $k = 1, 2, \dots$ , and  $\delta_\theta$  is the Dirac measure at  $\theta$ .

- ▶ The functional parameter  $G_0$  is known as the centering measure

# BNP mixtures of copulas

- ▶ Bayesian nonparametric mixture model for Archimedean copulas  
 $C(\mathbf{u} \mid \theta)$  is obtained when using the Poisson-Dirichlet process as the mixing distribution for the parameter  $\theta$

$$C(\mathbf{u}) = \int C(\mathbf{u} \mid \theta) G(d\theta) = \sum_{k=1}^{\infty} \omega_k C(\mathbf{u} \mid \theta_k), \quad (3)$$

- ▶ The Bayesian nonparametric mixture copula model can also be defined hierarchically
- ▶ For  $i = 1, \dots, n$ :

$$\begin{aligned} (U_{1i}, \dots, U_{pi}) \mid \theta_i &\sim f_C(\mathbf{u}_i \mid \theta_i) \\ \theta_i \mid G &\stackrel{\text{iid}}{\sim} G \\ G &\sim \text{PD}(a, b, G_0), \end{aligned} \quad (4)$$

where  $f_C$  is the copula density.

# BNP mixtures of copulas

- ▶ The centering measure  $G_0$  has density,  $g_0$ , with support in the parameter space  $\Theta$ .
- ▶ Pitman (1995) showed

$$f(\theta_i \mid \boldsymbol{\theta}_{-i}) = \frac{b + am_i}{b + n - 1} g_0(\theta_i) + \sum_{j=1}^{m_i} \frac{n_{i,j}^* - a}{b + n - 1} \delta_{\theta_{i,j}^*}(\theta_i), \quad (5)$$

with  $\boldsymbol{\theta}_{-i}$  being the set of all  $\theta_i$ 's excluding the  $i$ th element and  $(\theta_{i,1}^*, \dots, \theta_{i,m_i}^*)$  denoting the distinct values in  $\boldsymbol{\theta}_{-i}$ , each with frequencies  $n_{i,j}^*$ , for  $i = 1, \dots, n$ ,  $j = 1, \dots, m_i$ .



# Posterior sampling - brief discussion

- ▶ The posterior conditional distributions for each  $\theta_i$  are given by

$$f(\theta_i \mid \mathbf{u}, \boldsymbol{\theta}_{-i}) \propto (b + am_i) f(\mathbf{u}_i \mid \theta_i) g_0(\theta_i) + \sum_{j=1}^{m_i} (n_{i,j}^* - a) f_C(\mathbf{u}_i \mid \theta_i) \delta_{\theta_{i,j}^*}(\theta_i)$$

- ▶ We initialize the sampler using random draws  $\theta_i$  from the prior  $g_0$ , for  $i = 1, \dots, n$ .
- ▶ Given the chain's state at time  $t$ ,  $\boldsymbol{\theta}^{(t)} = (\theta_1^{(t)}, \dots, \theta_n^{(t)})$ , compute the unique values  $(\theta_1^*, \dots, \theta_m^*)$  in  $\boldsymbol{\theta}^{(t)}$  and re-sample each  $\theta_j^*$ ,  $j = 1, \dots, m$  from

$$f(\theta_j \mid c.c.) \propto g_0(\theta_j) \prod_{\{i: \theta_i = \theta_j^*\}} f_C(\mathbf{u}_i \mid \theta_j),$$

where c.c. stands for clustering configuration.

# Posterior sampling - brief discussion

- Draw  $\theta_i^{(t+1)}$ ,  $i = 1, \dots, n$ , from

$$f(\theta_i \mid \mathbf{u}, \mathbf{v}, \boldsymbol{\theta}_{-i}, \boldsymbol{\theta}^*) = \frac{1}{k_i} \left[ \sum_{j=1}^{m_i} (n_{i,j}^* - a) f_C(\mathbf{u}_i \mid \theta_{i,j}^*) \delta_{\theta_{i,j}^*}(\theta_i) + \sum_{j=m_i+1}^{m_i+r} \{(b + am_i)/r\} f_C(\mathbf{u}_i \mid \theta_j^*) \delta_{\theta_j^*}(\theta_i) \right],$$

where  $\boldsymbol{\theta}^* = \{\theta_{m_i+1}^*, \dots, \theta_{m_i+r}^*\} \stackrel{iid}{\sim} g_0$ ,

$$k_i = \sum_{j=1}^{m_i} (n_{i,j}^* - a) f_C(\mathbf{u}_i \mid \theta_{i,j}^*) + \sum_{j=m_i+1}^{m_i+r} \{(b + am_i)/r\} f_C(\mathbf{u}_i \mid \theta_j^*).$$

# Posterior sampling - brief discussion

- ▶ The hyperparameters  $(a, b)$  are important in determining the number of components in the mixture
- ▶ We assign hyperpriors instead of keeping them fixed
- ▶ Since  $a \in [0, 1)$  and  $b \in (-a, \infty)$ , the joint hyperprior is factorized as  $f(a, b) = f(b | a)f(a)$
- ▶  $f(a, b) = \text{Gamma}(b + a | c_b, d_b)\text{Beta}(a | c_a, d_a)$

# Additional considerations

- ▶ Goodness-of-fit is evaluated using the logarithm of the pseudo-marginal likelihood  $LPML = \sum_{i=1}^n \log(CPO_i)$  where  $CPO_i = f(\mathbf{u}_i | \mathbf{u}_{-i})$  and can be estimated using

$$\widehat{CPO}_i = \left[ \frac{1}{L} \sum_{l=1}^L \frac{1}{f_C(\mathbf{u}_i | \theta_i^{(l)})} \right]^{-1}.$$

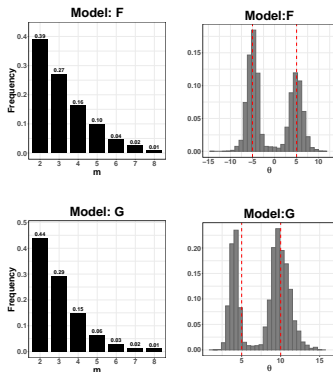
- ▶ The uncertainty about the number of mixture components is quantified by the posterior distribution but... there are multiple cluster configurations with the same number of components  $\tilde{m}$ .
- ▶ In order to select a single clustering configuration and produce further inferences, we used the search algorithm presented in Dahl et al (2022) and implemented in the R package `salso`.

# Simulation experiment - Sanity check

Data / Model	AMH	CLA	FRA	GUM	JOE	BSA
AMH	0.34	-0.08	0.02	-1.07	<b>2.48</b>	-4.32
CLA	14.75	<b>147.42</b>	74.91	78.37	53.23	7.4
FRA	0.13	7.11	<b>10.00</b>	1.62	3.09	-3.01
GUM	77.85	199.23	238.08	<b>276.27</b>	270.27	110.14
JOE	37.76	75.85	98.33	118.10	<b>120.91</b>	55.33

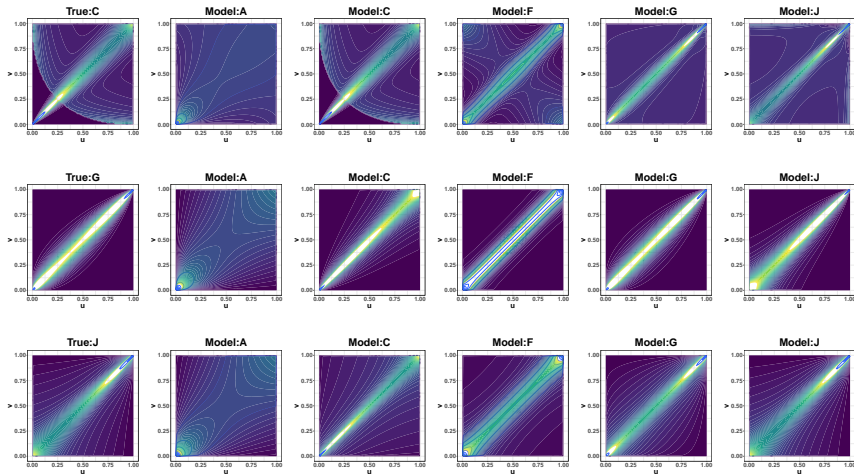
**Table:** Simulation study: Bivariate data from a mixture of Archimedean copulas. LPML statistics when taking a sample of size  $n = 200$  and fitting the five models. Bayesian semiparametric Archimedean copula competing model in the last column.

# Simulation experiment - Sanity check



**Figure:** Simulation: Bivariate data from a mixture of Archimedean copulas with  $n = 500$ . Posterior distributions when using the same kernel used to sample the data. Vertical dotted lines correspond to the true values.

# Simulation experiment - Sanity check



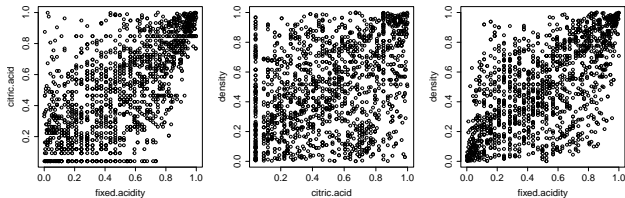
# Wine analysis

- ▶ We consider the red wine data of ? which consists of several physicochemical tests of the red variants of 1,599 Portuguese wines (*Vinho verde*)
- ▶ We concentrate on three variables: fixed acidity ( $X_1$ ), citric acid ( $X_2$ ) and density ( $X_3$ )
- ▶ The MCMC was run for 15,000 iterations with a burn-in of 5,000
- ▶ The LPML scores are:

Copula	AMH	Clayton	Frank	Gumbel	Joe
LPML	279	604	685	711	413

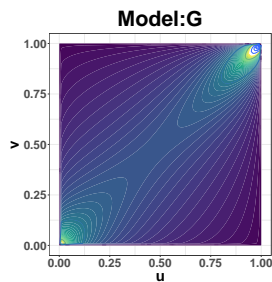
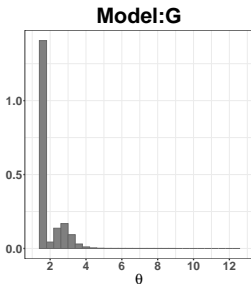
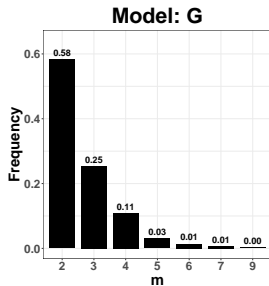


# Wine analysis



**Figure:** Red wine data: fixed acidity, citric acid, and density. Pairwise scatterplots of the three variables.

# Wine analysis



# Wine analysis

- ▶ The posterior estimation of Kendall tau for the best-fitting model, Gumbel, is 0.361 with a 95% CI of (0.24, 0.70).
- ▶ The CI contains the three empirical Kendall tau values that correspond to pairwise association parameters among the three characteristics of the wine.
- ▶ Implementing our clustering selection procedure, we obtain two groups with copula parameters estimated at: 1.52 with a 95% CI (1.48, 1.56) and weight 0.98; and at 6.08 with 95% CI (4.94, 7.41) and weight 0.02.

# What I would like to see

- ▶ A mixture model where the symmetry is not required  
 $Dep(x_i, x_j) \neq Dep(x_{i'}, x_{j'})$ .
- ▶ Integration of asymmetric Archimedean copulas in the current framework.
- ▶ Can we identify copula families whose mixtures are dense in the space of copulas of dimension  $d$ ?
- ▶ Papers available here:  
<https://www.utstat.toronto.edu/craiu/Papers/index.html>