Bayesian analysis of coinfection with soil-transmitted helminths

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DEPARTMENT OF
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Giorgia Lepschy

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Introduction

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- Soil-transmitted helminths (STH) are three worms that share similar transmission mechanisms.
  - Ascaris (*Ascaris lumbricoides*)
  - Hookworm (*Ancylostoma duodenale* and *Necator americanus*)
  - Trichuris (*Trichuris trichiura*)

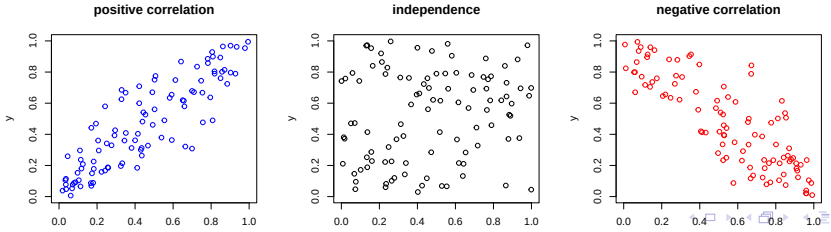
- **Coinfection with multiple species** is common and results in increased morbidity.

Aim: To be able to quantify levels of infection and coinfection from prevalence data on the three species.

The Plackett copula

Copulas

A **copula** $C(u_1, \ldots, u_d)$ is a multivariate CDF on $[0,1]^d$ with $U(0,1)$ marginals.



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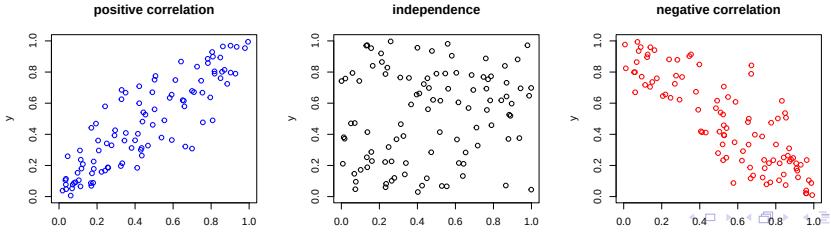
Sklar's Theorem:

$$F(x_1, \ldots, x_d) = C(F_1(x_1), \ldots, F_d(x_d))$$

for some copula $C(u_1, \ldots, u_d)$.



The bivariate Plackett copula

The bivariate **Plackett** copula describes dependence between **binary** variables U and V.

Let $u = \mathrm{P}(U = 1)$, $v = \mathrm{P}(V = 1)$ and $\phi = \dfrac{\mathrm{P}(U = 0, V = 0)\,\mathrm{P}(U = 1, V = 1)}{\mathrm{P}(U = 1, V = 0)\,\mathrm{P}(U = 0, V = 1)}$.

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$$
\begin{aligned}
P_{11} &= C(u, v|\phi) \\
P_{10} &= u - C(u, v|\phi) \\
P_{01} &= v - C(u, v|\phi) \\
P_{00} &= 1 - u - v + C(u, v|\phi)
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C(u, v|\phi) = \begin{cases} \dfrac{1 + (\phi - 1)(u + v) - \sqrt{[1 + (\phi - 1)(u + v)]^2 - 4\phi(\phi - 1)uv}}{2(\phi - 1)} & \phi \neq 1 \\ uv & \phi = 1. \end{cases}
$$

The trivariate Plackett copula

Introduce a third variable W with $w = \mathrm{P}(W = 1)$.

Let $\psi = \dfrac{P_{111}P_{100}P_{010}P_{001}}{P_{000}P_{011}P_{101}P_{110}}$.

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P_{111} &= C(u, v, w|\psi) \\
P_{110} &= C(u, v|\phi_{UV}) - C(u, v, w|\psi) \\
P_{101} &= C(u, w|\phi_{UW}) - C(u, v, w|\psi) \\
P_{011} &= C(v, w|\phi_{VW}) - C(u, v, w|\psi) \\
P_{100} &= u - C(u, v|\phi_{UV}) - C(u, w|\phi_{UW}) + C(u, v, w|\psi) \\
P_{010} &= v - C(u, v|\phi_{UV}) - C(u, w|\phi_{UW}) + C(u, v, w|\psi) \\
P_{001} &= w - C(u, w|\phi_{UW}) - C(u, w|\phi_{UW}) + C(u, v, w|\psi) \\
P_{000} &= 1 - u - v - w + C(u, v|\phi_{UV}) + C(u, w|\phi_{UW}) + C(u, w|\phi_{UW}) - C(u, v, w|\psi)
\end{aligned}
$$

Can find $C(u, v, w|\psi)$ numerically by solving the equation for ψ.

A Bayesian model for coinfection

Survey s has count data $n_{000}^{(s)}, \ldots, n_{111}^{(s)}$ on the number of individuals in each state.

Let $\boldsymbol{\theta}_s = (u_s, v_s, w_s, \phi_{UV}, \phi_{UW}, \phi_{VW}, \psi)$.

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Priors:

$$u_s, v_s, w_s \sim \mathrm{Beta}\left(\frac{1}{2}, \frac{1}{2}\right)$$

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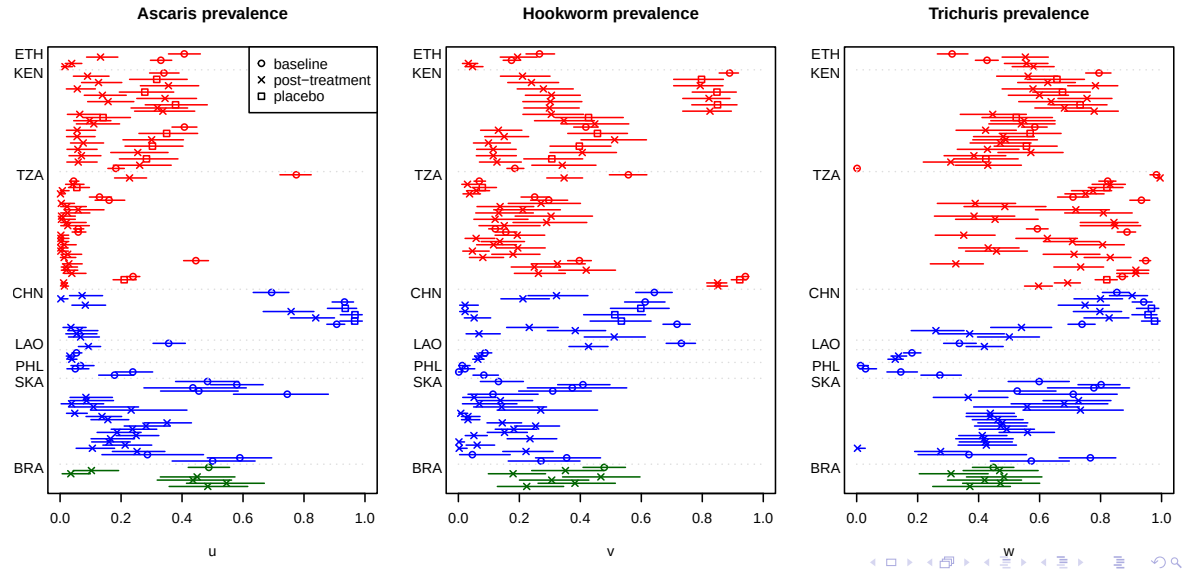
Priors:

$$u_s, v_s, w_s \sim \mathrm{Beta}\left(\frac{1}{2}, \frac{1}{2}\right) \quad \rightarrow \quad \text{Independence sampler}$$

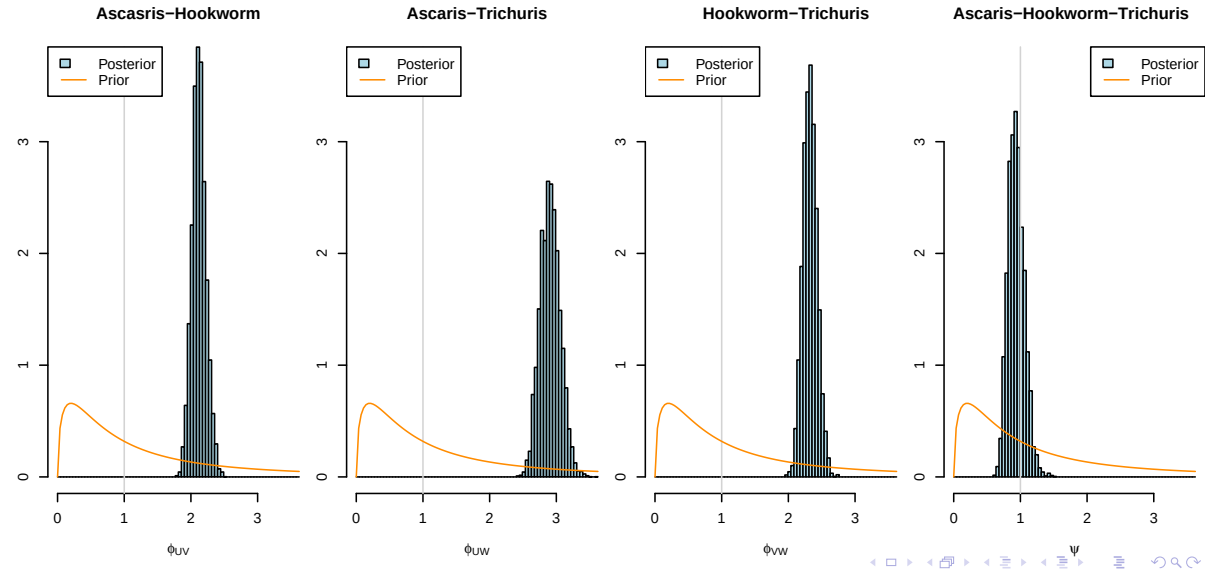
$$\phi_{UV}, \phi_{UW}, \phi_{VW}, \psi \sim F_{3,3} \quad \rightarrow \quad \text{Log-normal random walk}$$

Results

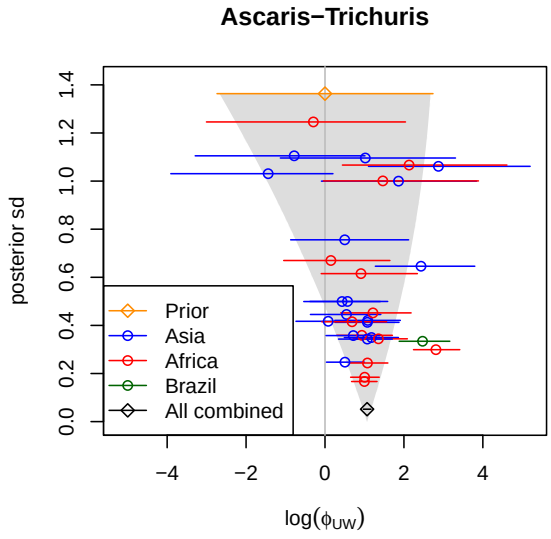
Prevalences

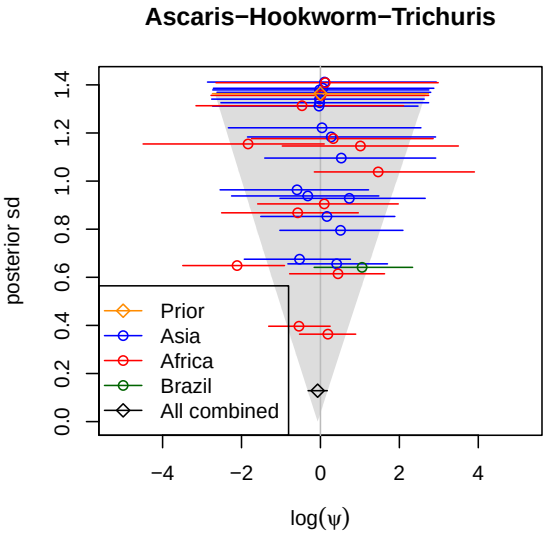


Posteriors of the copula parameters



Bayesian funnel plots





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The Plackett copula model allows us to evaluate the **any STH** goal from just **marginal prevalence data**.

Conclusion

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- Coinfection with multiple STH species is common and leads to additional morbidity and suffering.
- The Bayesian Plackett copula model describes the levels of coinfection present in survey individuals, including quantifying uncertainty.

Can evaluate progress towards the 2030 goal for STH from the available marginal prevalence data.