

Bayesian meta-analysis and meta-regression for proportion studies: *The example of neurocysticercosis among people with epileptic seizures*

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Presentation objectives

- What is the **traditional methods** of meta-analysis?
- What is **Bayesian random effect model (or Bayesian hierarchical model)**?
- How have we **used** Bayesian models to conduct **meta-analysis, stratified meta-analysis and meta-regression**?

What is Neurocysticercosis (NCC)?

“Neurocysticercosis (NCC) is a zoonotic helminthic infection of the human central nervous system (CNS) caused by larval cyst of *Taenia solium*.”.....*Adapted from CDC*



Fig: *Taenia solium*

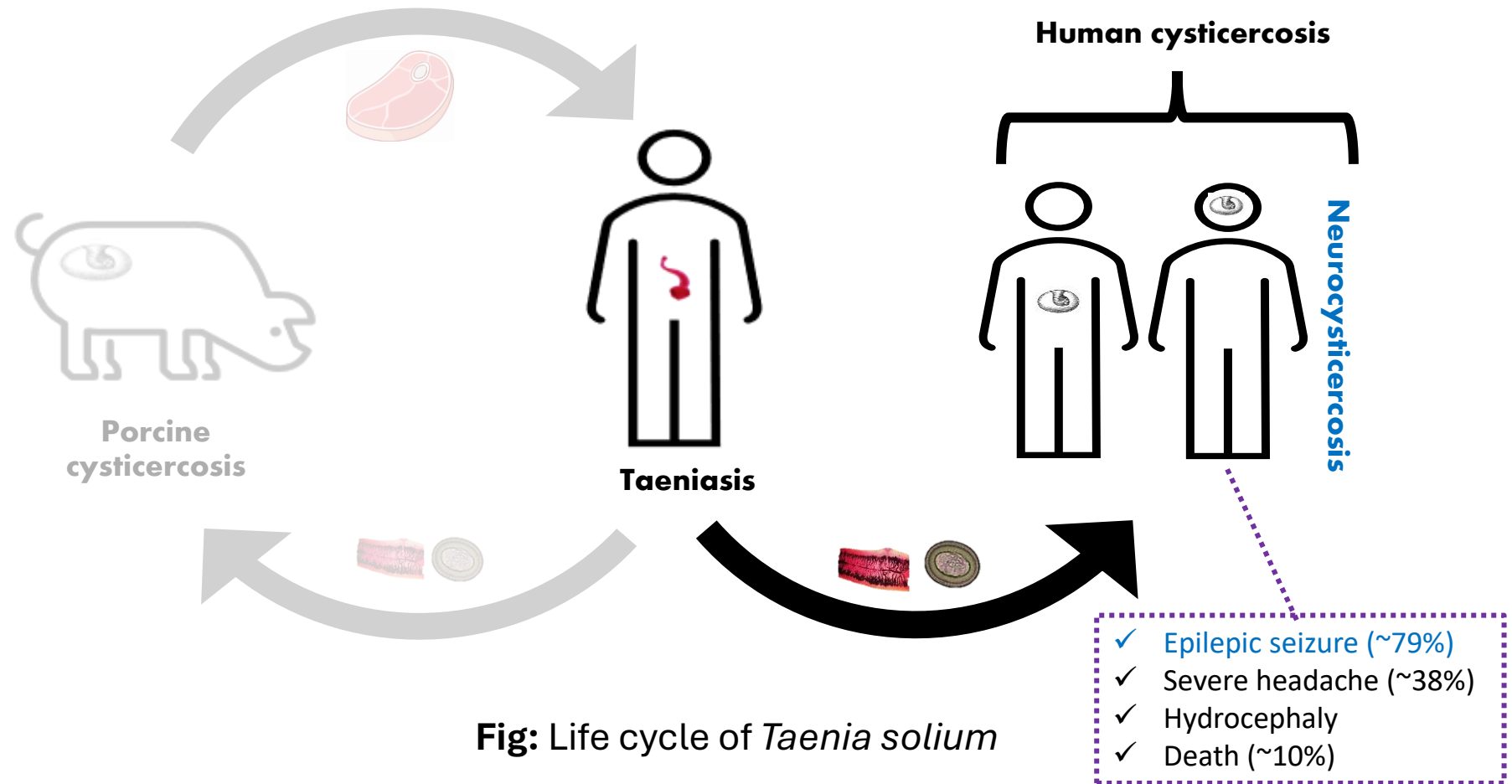
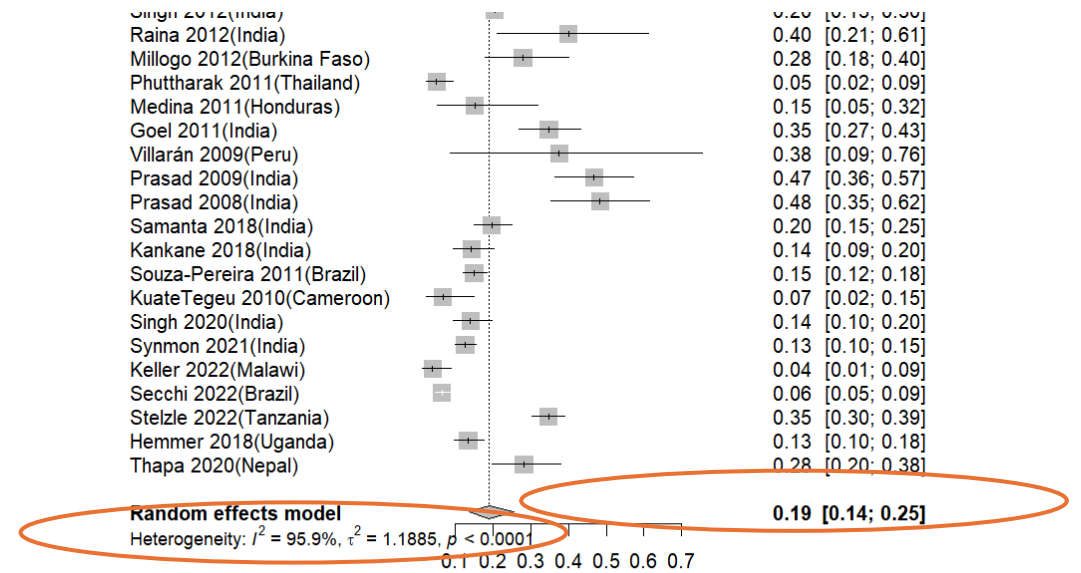
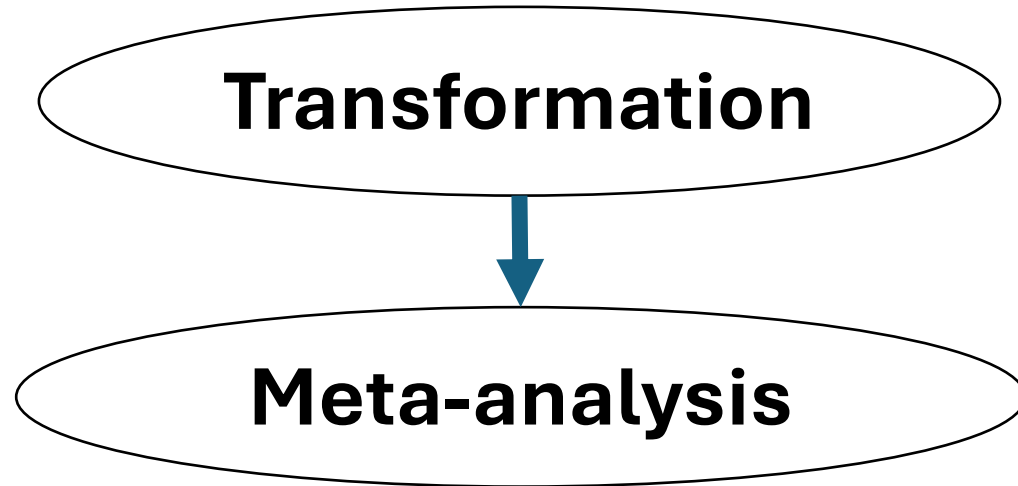


Fig: Life cycle of *Taenia solium*

What is the traditional method of meta-analysis? –Frequentist approach

“Two-steps method”



Generalized linear mixed model (with *logit* link)

$y_i \sim \text{Binomial}(n_i, p_i)$
 $\text{logit}(p_i) = P + u_i$
 $u_i \sim \text{Normal}(0, \tau^2)$

Here,
 y_i = # of cases
 n_i = # of samples
 p_i = study-level proportion,
 P = overall proportion
 u_i = random effect
 τ^2 = between-study variance
 (**heterogeneity**).

Major limitation:

“The frequentist approaches use **the point estimate of the heterogeneity variance as a fixed quantity**, which leads to variability underestimation” – Hackenberger (2020)

What is Bayesian random-effects model (BREM) ?

$$y_i \sim \text{Binomial}(n_i, p_i)$$

$$\text{logit}(p_i) = P + u_i \longrightarrow P \sim \text{logistic}(0,1)$$

$$u_i \sim \text{Normal}(0, \tau^2) \longrightarrow \tau \sim \text{Half_Cauchy}(0,0.5)$$



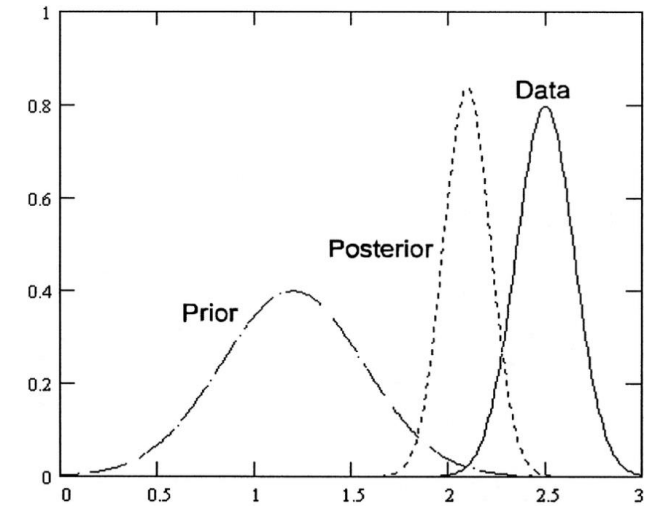
For meta-regression

$$y_i \sim \text{Binomial}(n_i, p_i)$$

$$\text{logit}(p_i) = P + \beta X_i + u_i \longrightarrow \beta \sim \text{Normal}(0,1)$$

$$u_i \sim \text{Normal}(0, \tau^2)$$

Main advantages

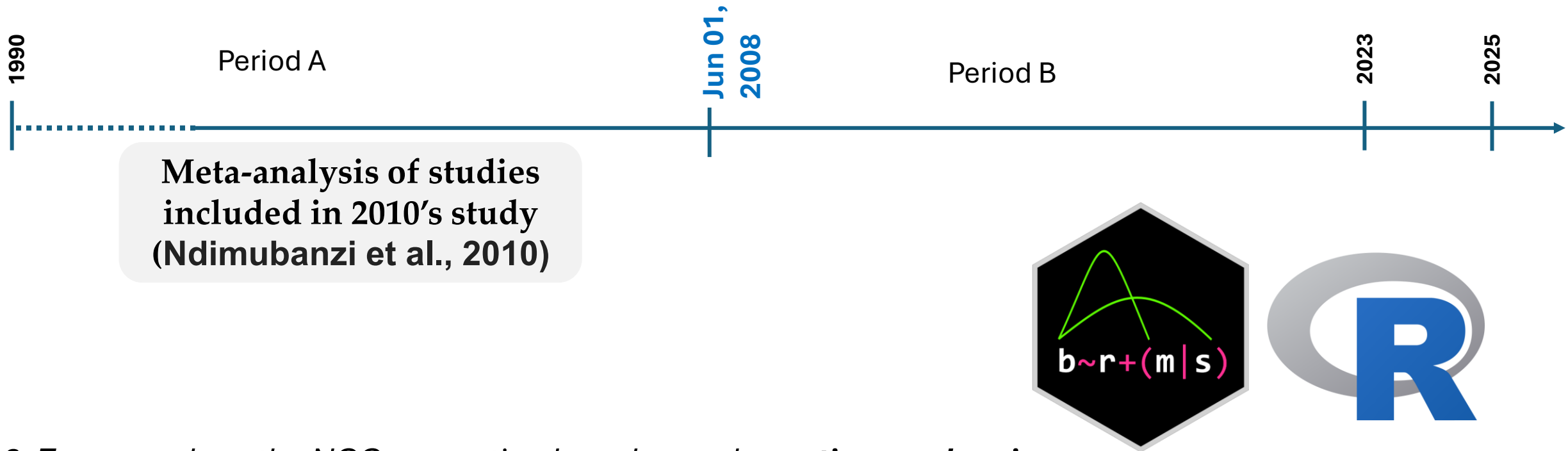


Source of Fig: LinkedIn

How have we used BREM in our study?

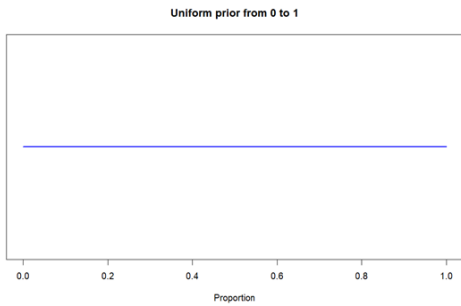
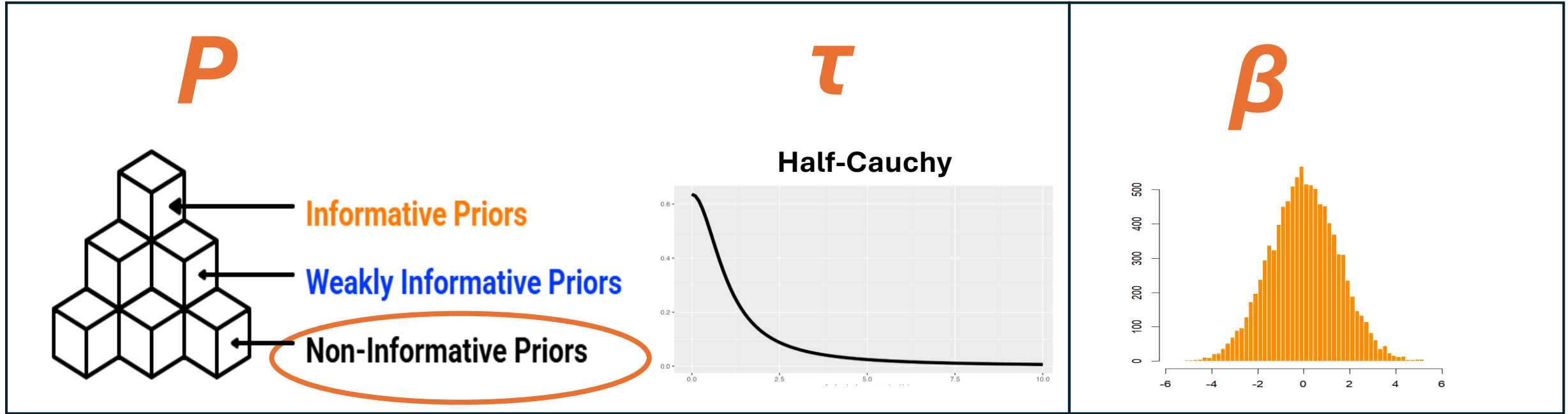
Research objectives:

1. To estimate **proportion of neurocysticercosis (NCC)** among people with **epileptic seizure**

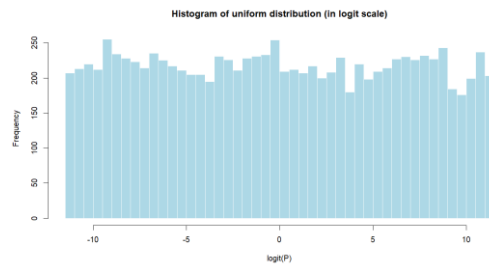


2. To assess how the NCC proportion has changed over **time and regions**.

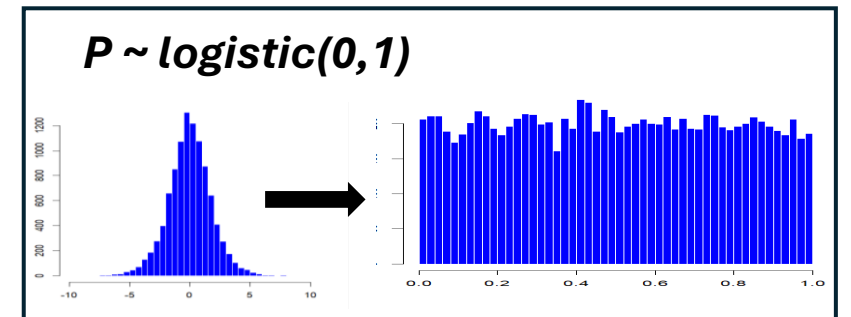
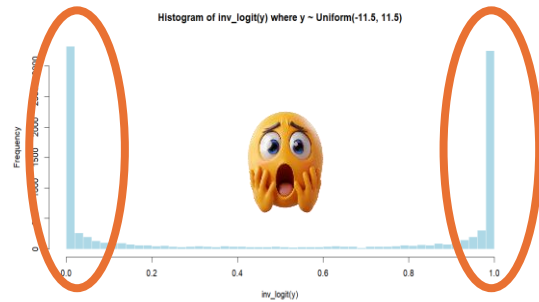
How we selected priors?



$P \sim \text{Uniform}(0, 1)$

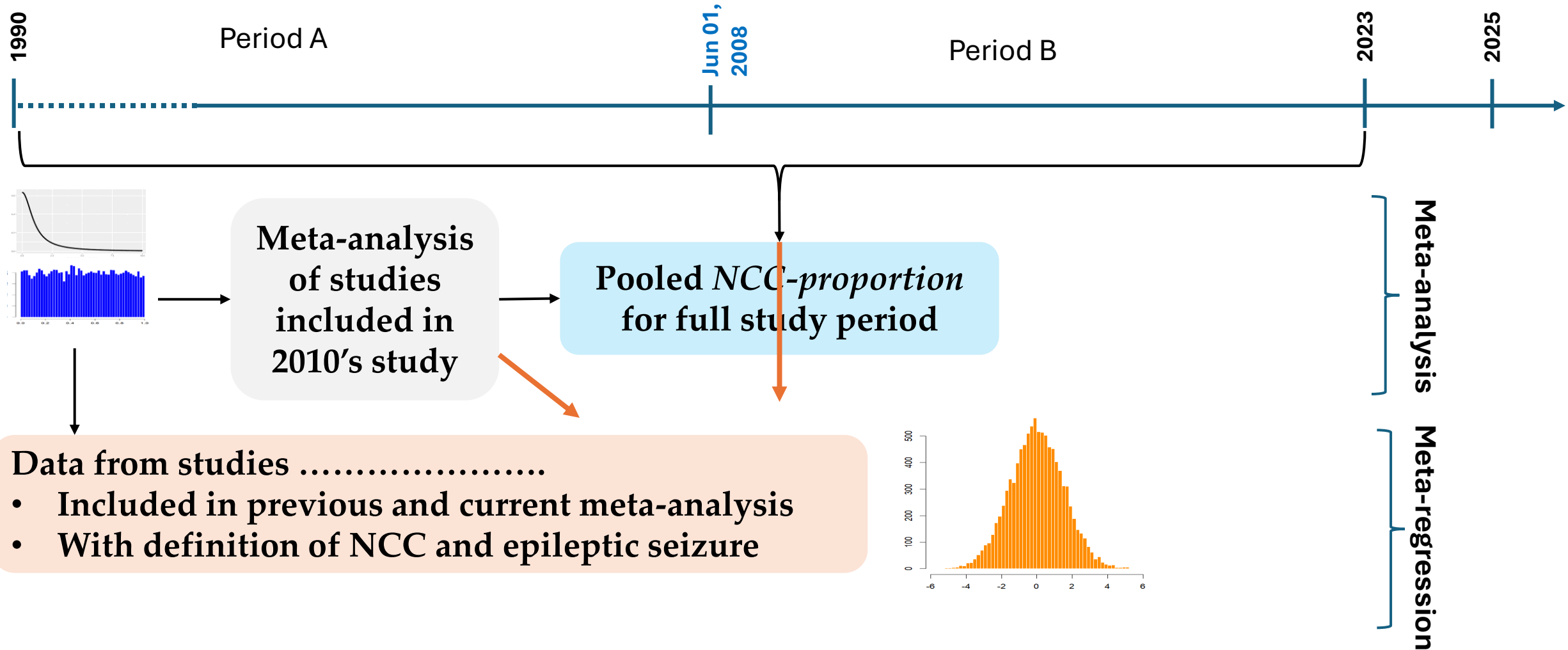


$P \sim \text{Uniform}(\text{logit}(0), \text{logit}(1))$

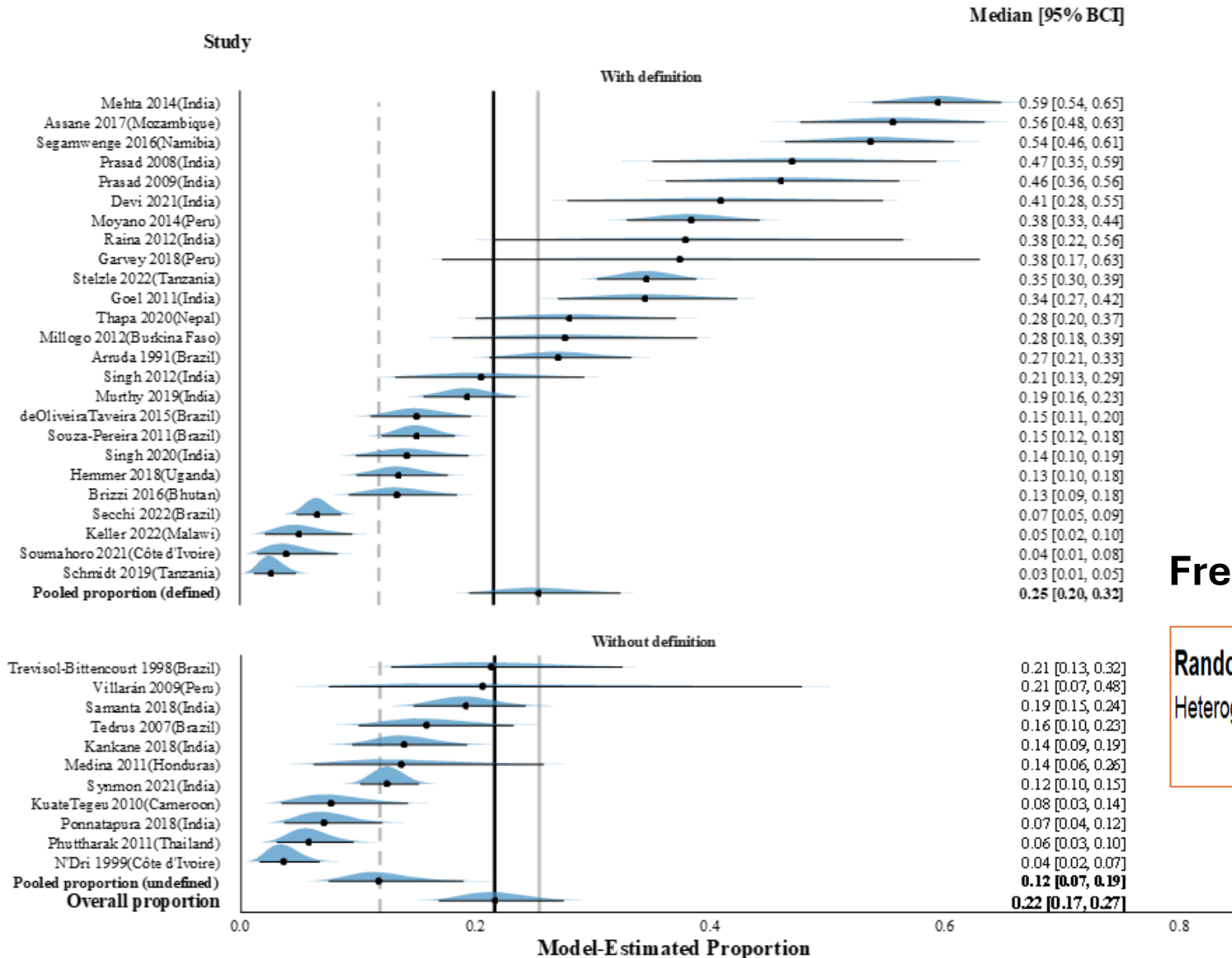


Credit: Some visual created in <https://www.napkin.ai/>
Ref: Reis, et al (2023).

How we used priors & data from a meta-analysis published in 2010? – Informative prior



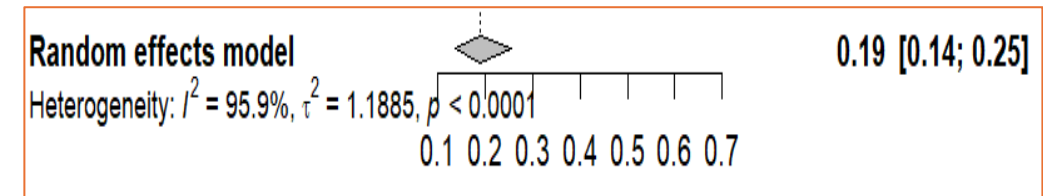
What have we found? – Bayesian meta-analysis



- **The overall median proportion:**
22% (95%BCI: 17 – 27%)
- **Between-study heterogeneity (τ):**
1.1 (95%BCI: 0.9 – 1.5)



Frequentist meta-analysis results



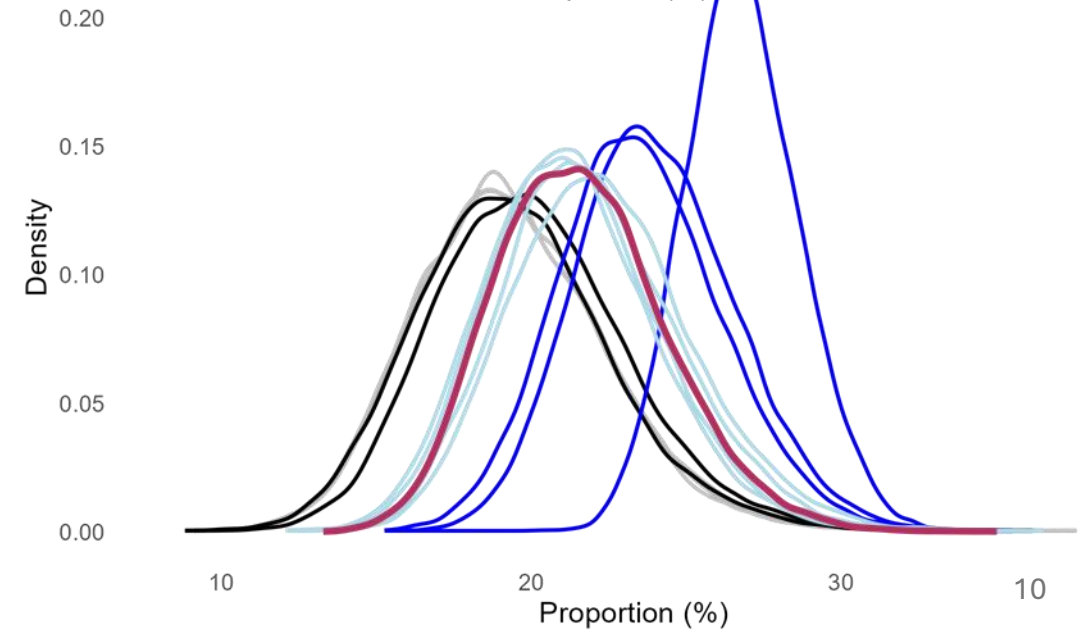
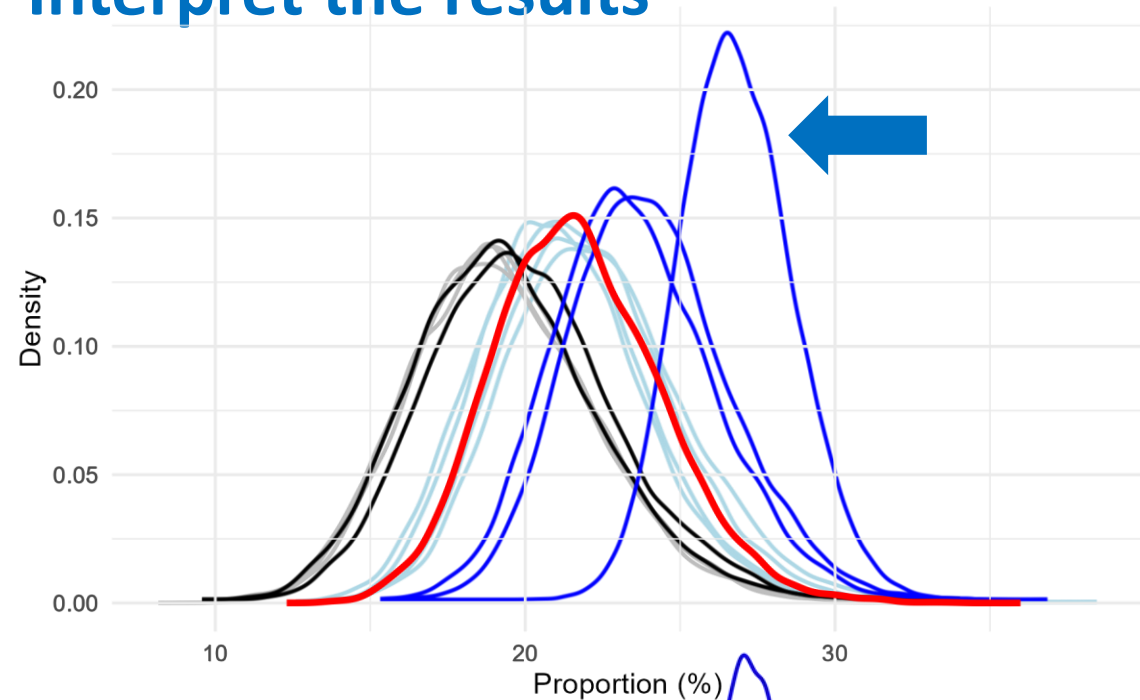
How sensitive the data to the prior? – Interpret the results

P

$\tau_{0.5}$

τ_1

Prior distribution of NCC-proportion (P)	Half-Cauch(0, 0.5)	Half-Cauchy(0, 1)
	Posterior P	Posterior P
Non-informative priors		
Student_t(3, 0, 2.5)	19 (14 – 26)	19 (14 – 26)
Prior for SD only	19 (14 – 26)	19 (14 – 26)
Logistic (0,1)	19 (14 – 26)	19 (14 – 26)
Weakly-informative priors		
Normal (0, 1.8)	19 (14 – 26)	19 (14 – 26)
Normal (0,1)	20 (14 – 26)	20 (15 – 27)
Informative priors		
Normal (logit(0.29),0.1)	27 (23 – 31)	27 (23 – 31)
Normal (logit(0.29),0.183)	24 (19 – 29)	24 (19 – 29)
Normal (logit(0.29),0.2)	23 (19 – 29)	23 (19 – 29)
Normal (logit(0.29),0.3)	22 (17 – 27)	21 (17 – 28)
Normal (logit(0.28),0.3)	21 (17 – 27)	21 (16 – 27)
Normal (logit(0.30),0.3)	22 (17 – 28)	22 (17 – 28)
.....



How sensitive the data to the prior? – Interpret the results

τ :
 1.1 (95%BCI: 0.9 – 1.5)

τ	Heterogeneity
0.1 – 0.5	“reasonable”
0.5 - 1.0	“fairly high”
1.0 <	“fairly extreme”

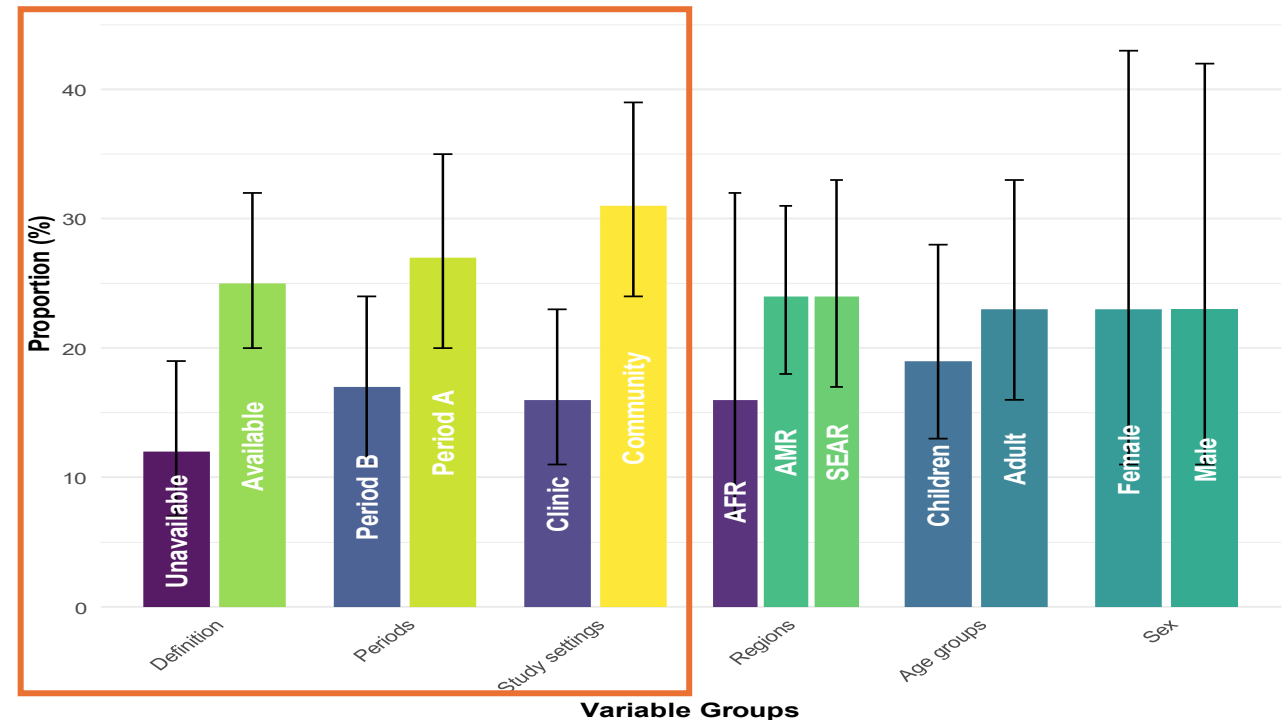
P	Posterior τ	Posterior τ
t(3, 0, 2.5)	1.1 (0.9 – 1.5)	1.1 (0.9 – 1.5)
L(0,1)	1.1 (0.9 – 1.5)	1.1 (0.9 – 1.5)
N (0, 1.8)	1.1 (0.9 – 1.5)	1.1 (0.9 – 1.5)
N(0,1)	1.1 (0.9 – 1.5)	1.1 (0.9 – 1.5)
N (logit(0.29),0.1)	1.2 (0.9 – 1.5)	1.2 (0.9 – 1.6)
N (logit(0.29),0.183)	1.1 (0.9 – 1.5)	1.2 (0.9 – 1.5)
N (logit(0.29),0.2)	1.1 (0.9 – 1.5)	1.1 (0.9 – 1.5)
N (logit(0.29),0.3)	1.1 (0.9 – 1.5)	1.1 (0.9 – 1.5)
N (logit(0.28),0.3)	1.1 (0.9 – 1.5)	1.1 (0.9 – 1.5)
N (logit(0.30),0.3)	1.1 (0.9 – 1.5)	1.1 (0.9 – 1.5)

What are the sources of BS heterogeneity?

Bayesian meta-regression

Variables	OR (95%BCI)
Definition (yes)	2.4 (1.2 – 4.6)
Period B	0.5 (0.3 – 0.9)
S. Setting (Com.)	1.7 (1.0 – 3.0)
AMR	1.3 (0.7 – 2.7)
SEAR	2.0 (0.9 – 4.4)
MRI	0.8 (0.3 – 1.9)
CT/MRI	1.3 (0.6 – 2.6)

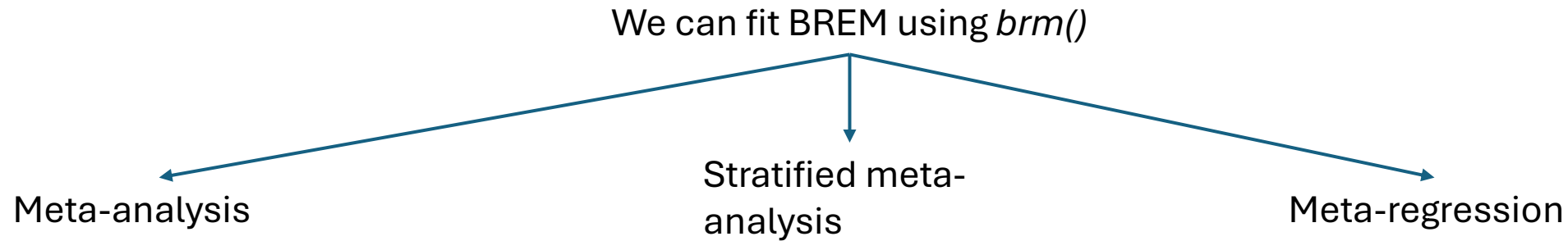
Stratified Bayesian meta-analysis



How has the NCC-proportion changed over time and across regions? – Bayesian meta-regression

Region	Proportion of NCC among PWES			OR (95%BCI)	% of OR less than 1.0
	Period A % (95%BCI)	Period B % (95%BCI)	Period A & B % (95%BCI)		
AFR	35 (18 – 57)	14 (4 – 44)	20 (8 – 40)	0.3 (0.1 – 1.9)	91
AMR	30 (22 – 40)	16 (8 – 36)	25 (18 – 34)	0.4 (0.2 – 0.9)	98
SEAR	39 (26 – 54)	26 (17 – 39)	32 (24 – 41)	0.5 (0.3 – 1.2)	95

In a nutshell.....



Major challenges

- ✓ **Assigning prior** is not straight forward
- ✓ No standard for interpreting between-study heterogeneity for proportion studies

Still, we can

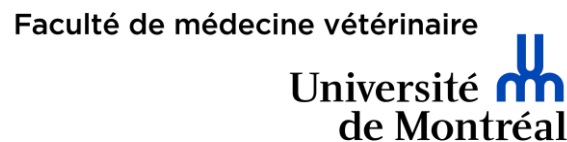
- ✓ **Combine *priori*** with recent data
- ✓ **Quantify the uncertainty** around the estimates, specially between heterogeneity estimate (τ)

References

- **Hackenberger, B.K., 2020.** Bayesian meta-analysis now—let's do it. *Croatian Medical Journal*, 61(6), p.564.
- **Ndimubanzi, et al (2010).** A systematic review of the frequency of neurocysticercosis with a focus on people with epilepsy. *PLoS neglected tropical diseases*, 4(11), p.e870.
- **Reis, et al (2023).** A practical guide to random-effects Bayesian meta-analyses with application to the psychological trauma and suicide literature. *Psychological trauma: theory, research, practice, and policy*, 15(1), p.121.
- **Lin, L. and Chu, H., 2020.** Meta-analysis of proportions using generalized linear mixed models. *Epidemiology*, 31(5), pp.713-717.
- **Wang, N., 2023.** Conducting meta-analyses of proportions in R. *Journal of Behavioral Data Science*, 3(2), pp.64-126.

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**Fond de
Lucie Besner**



Thank
you



Protocol



**To know more
about me and
my work**

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What are the challenges related to NCC?

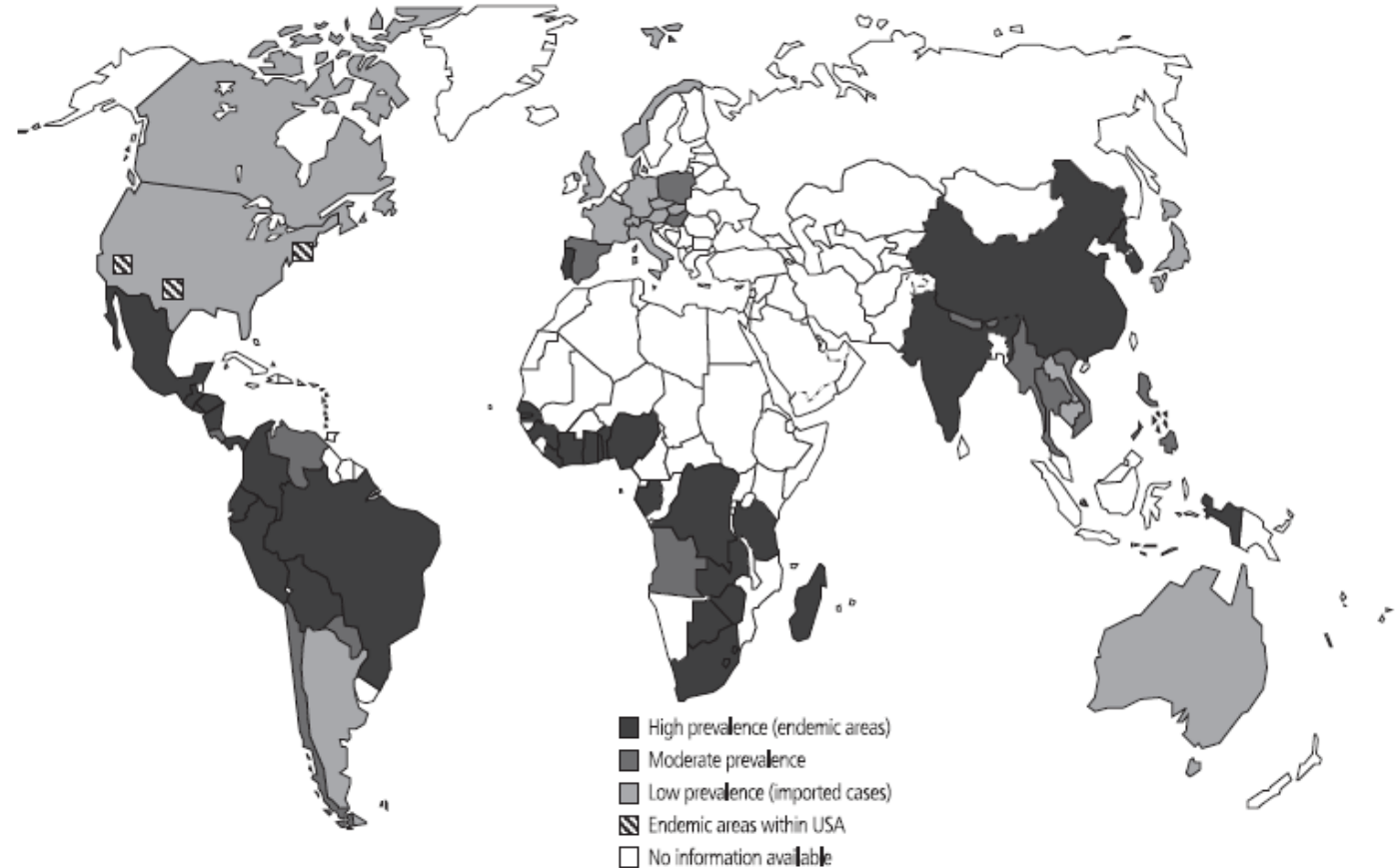
- Reported in 70+ countries
- 1.24 to 2.8 million DALYs



Distribution Unknown



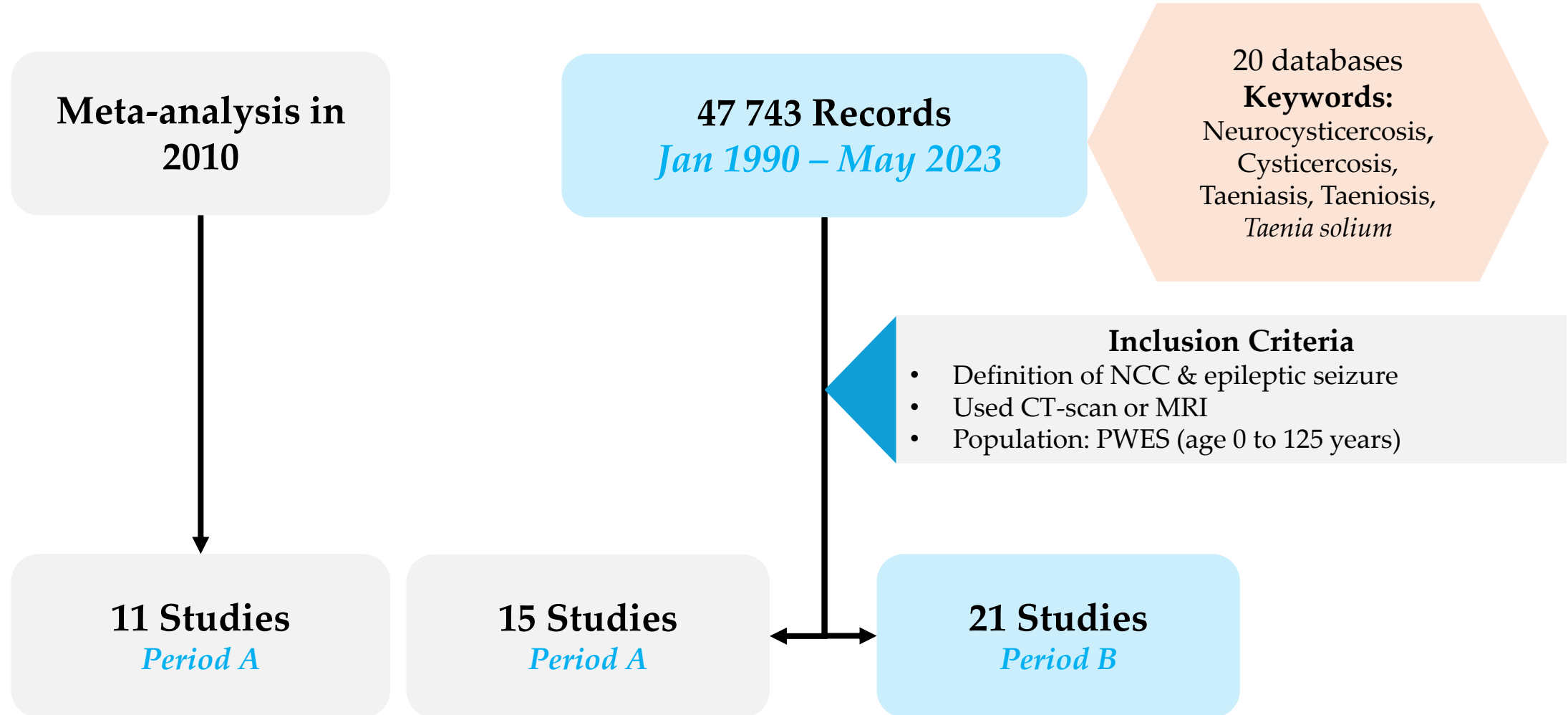
- ✓ Pleomorphic disease
- ✓ No rapid test, require CT/MRI



WHO 0081

Fig. Map showing areas where cysticercosis is endemic (black) or reported (grey) (Román, et al., 2000).

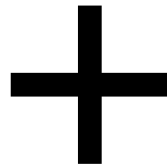
What have we found? –Systematic review



Why we use GLMM with logit link?

- Directly models binomial data without transformation, avoids bias from approximate methods.
- Proportions are constrained between 0 and 1
- Stabilizes variance

Why we use Bayesian model?



- Combine *priori* with data
- Assume random parameter
- Interpretation of 95% credible interval

Why not Bernoulli?

- No individual level data

Why need transformation if the proportion?

- Approximate study-specific proportion with normal distribution
- Stabilizing their variance

How we specified the model? – using *brm()* function

Bayesian random-effect logistic model

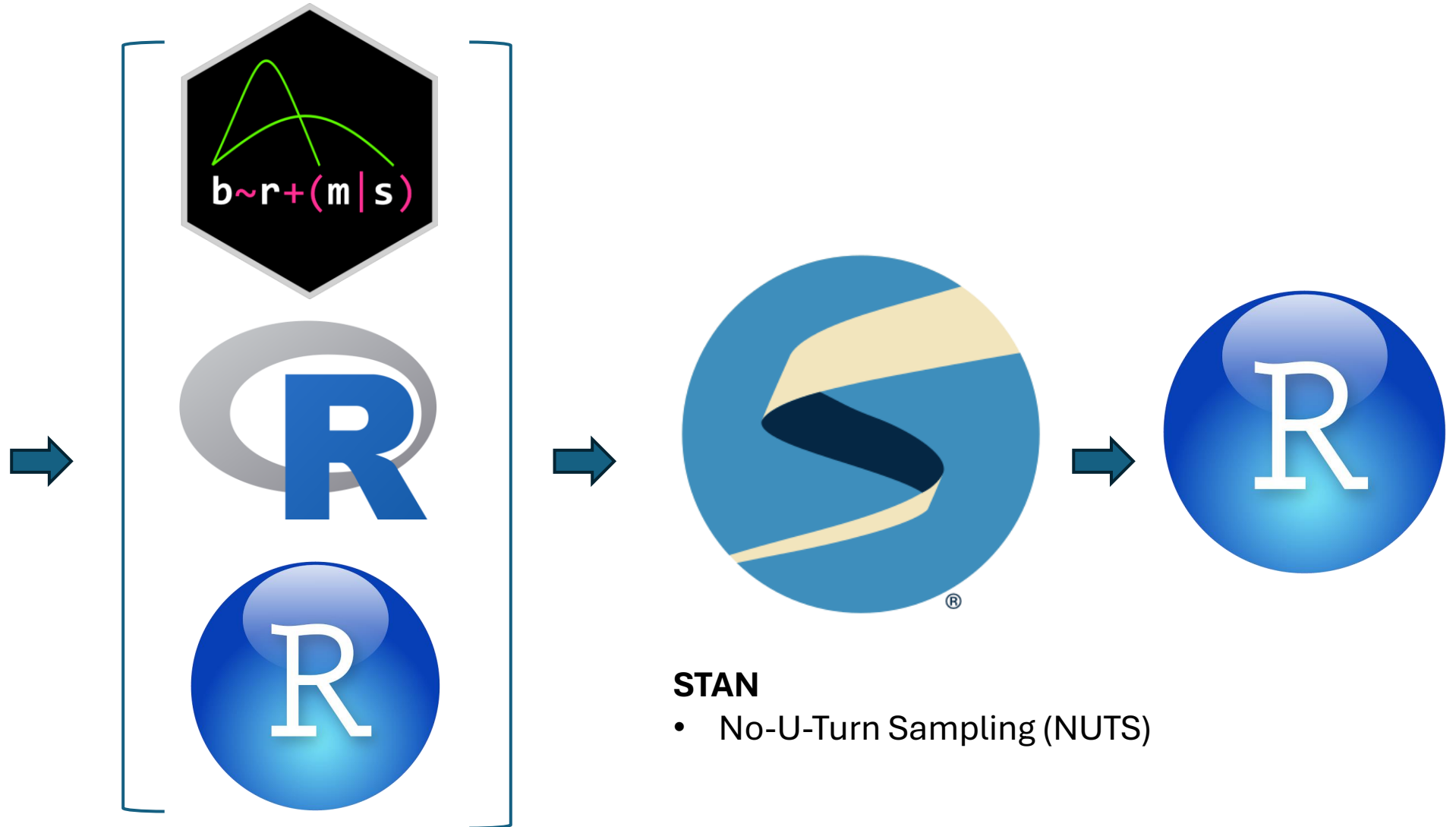
$$y_i = \text{Binomial}(n_i, p_i)$$

$$\text{logit}(p_i) = P + u_i$$

$$P = \text{Normal}(0, 1)$$

$$u_i = \text{Normal}(0, \tau^2)$$

$$\tau = \text{Half_Cauchy}(0, 0, 5)$$



STAN

- No-U-Turn Sampling (NUTS)

Model convergence?

```
> summary(mod_ip_1)
Family: binomial
Links: mu = logit
Formula: y | trials(n) ~ (1 | Study)
Data: dat_meta (Number of observations: 36)
Draws: 4 chains, each with iter = 10000; warmup = 5000; thin = 1;
total post-warmup draws = 20000
```

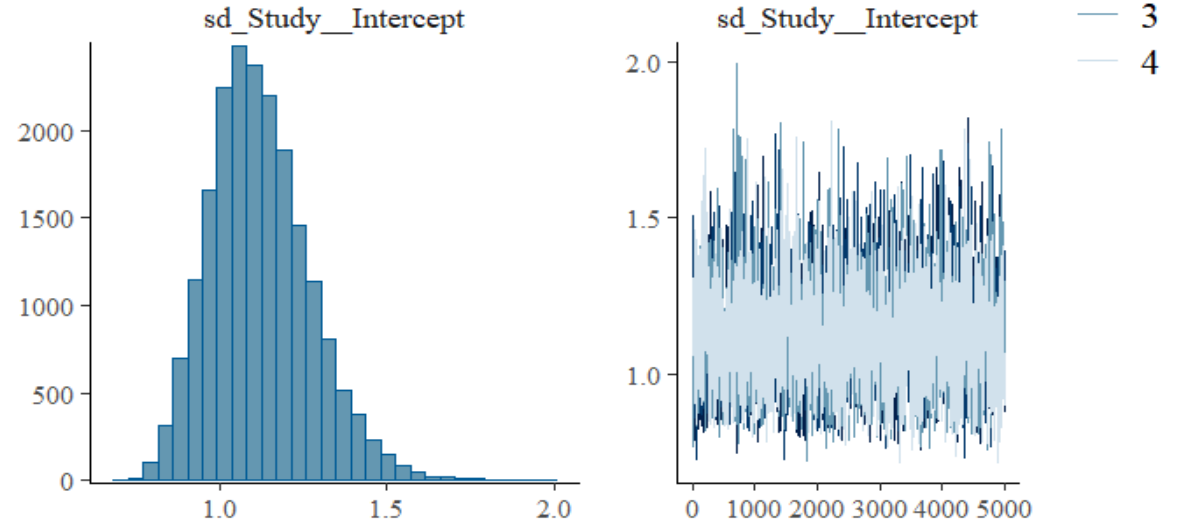
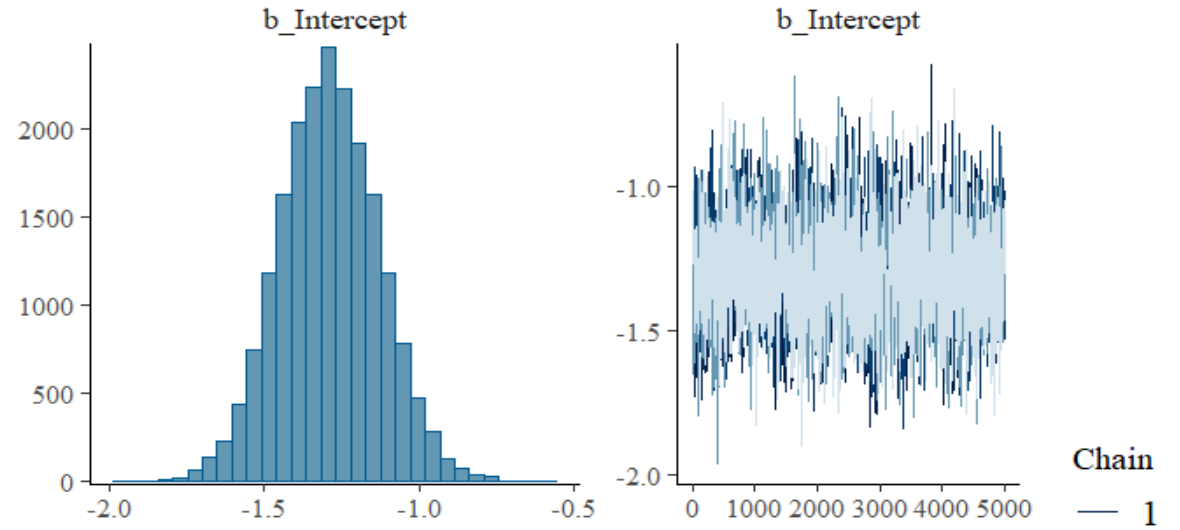
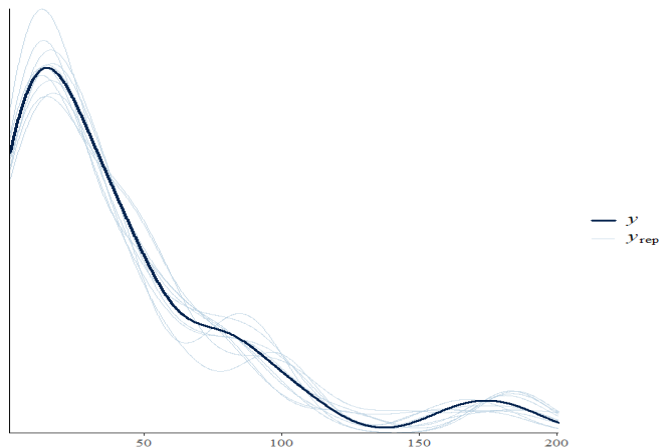
Multilevel Hyperparameters:
~Study (Number of levels: 36)

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sd(Intercept)	1.12	0.15	0.87	1.45	1.00	2394	4571

Regression Coefficients:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	-1.29	0.16	-1.60	-0.97	1.00	1911	3541

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS and Tail_ESS are effective sample size measures, and Rhat is the potential scale reduction factor on split chains (at convergence, Rhat = 1).



More References

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2. **Carabin, H., Ndimubanzi, P.C., Budke, C.M., Nguyen, H., Qian, Y., Cowan, L.D., Stoner, J.A., Rainwater, E. and Dickey, M., 2011.** Clinical manifestations associated with neurocysticercosis: a systematic review. *PLoS neglected tropical diseases*, 5(5), p.e1152.
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 - <https://www.cdc.gov/parasites/cysticercosis/biology.html>
 - <https://www.napkin.ai/>