

INTRODUCTION

- Network meta-analysis (NMA) is increasingly employed to compare multiple treatments simultaneously in healthcare research [1]
- **Synthesizing safety outcomes often involves sparse networks**, with limited direct evidence and/or few studies per comparison [2]
- These networks pose significant challenges in robustly estimating effects, particularly for rare event outcomes [2]

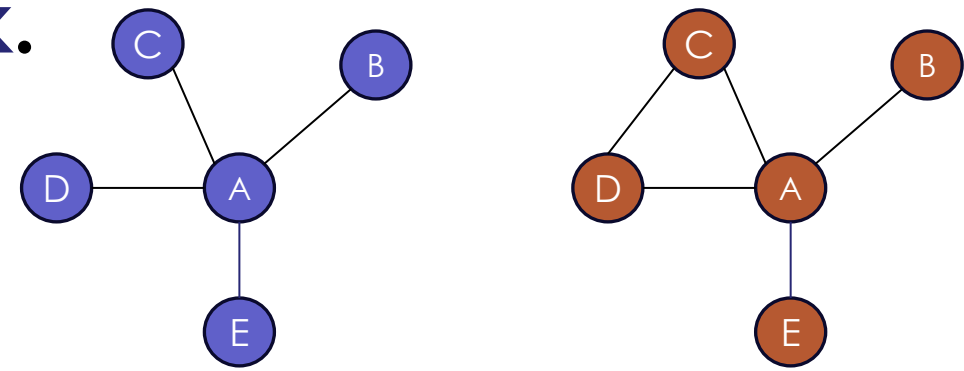
OBJECTIVES

- This study aimed to **identify and compare robust methodological approaches for analyzing binary rare event data**, to provide recommendations on model choice and implications in regulatory submissions.

METHODS

Simulations

- This **simulation study** followed the methodology outlined by Evrenoglou *et al.* [2] to generate data for **two distinct NMA structures: a star-shaped network and a network with a closed loop**. Only **two-arm studies** (each comparing a treatment against the reference) were constructed. The simulations were conducted under conditions of **no heterogeneity**, with **consistency maintained across treatment comparisons within the closed-loop network**.



- A total of **16 scenarios per network** were explored, varying baseline event risk, sample size per study arm, number of treatments in the network and number of studies per treatment comparison:

Table 1. Overview of scenarios. For each scenario 100 datasets were generated.

Scenario	Sample size (N)	Treatments	Studies per comparison	Mean Events Reference Arm	Mean Events Treatment Arms	% Studies with 0 events Reference Arm	% Studies with 0 events Treatment Arm
Baseline event risk (%): 1%-5%							
1	20-60	5	1	1.21	2.23	33.98%	18.28%
2	20-60	8	1	1.20	2.13	34.66%	19.01%
3	20-60	5	4	1.20	2.25	34.93%	17.66%
4	20-60	8	4	1.20	2.14	34.43%	19.08%
5	100-200	5	1	4.53	8.42	4.20%	0.93%
6	100-200	8	1	4.50	8.01	4.06%	1.30%
7	100-200	5	4	4.49	8.41	3.99%	1.02%
8	100-200	8	4	4.51	8.04	3.83%	1.10%
Baseline event risk (%): 0.5%-10%							
9	20-60	5	1	2.12	3.79	21.55%	11.03%
10	20-60	8	1	2.10	3.62	22.20%	12.10%
11	20-60	5	4	2.10	3.81	22.32%	11.26%
12	20-60	8	4	2.10	3.64	22.19%	12.06%
13	100-200	5	1	7.91	14.30	3.40%	1.15%
14	100-200	8	1	7.94	13.89	3.31%	1.26%
15	100-200	5	4	7.87	14.27	3.55%	1.09%
16	100-200	8	4	7.89	13.72	3.38%	1.33%

Evaluated models

Model **performance** was assessed by calculating **the mean difference between estimated and true log odds ratios averaged over 100 simulated datasets**.

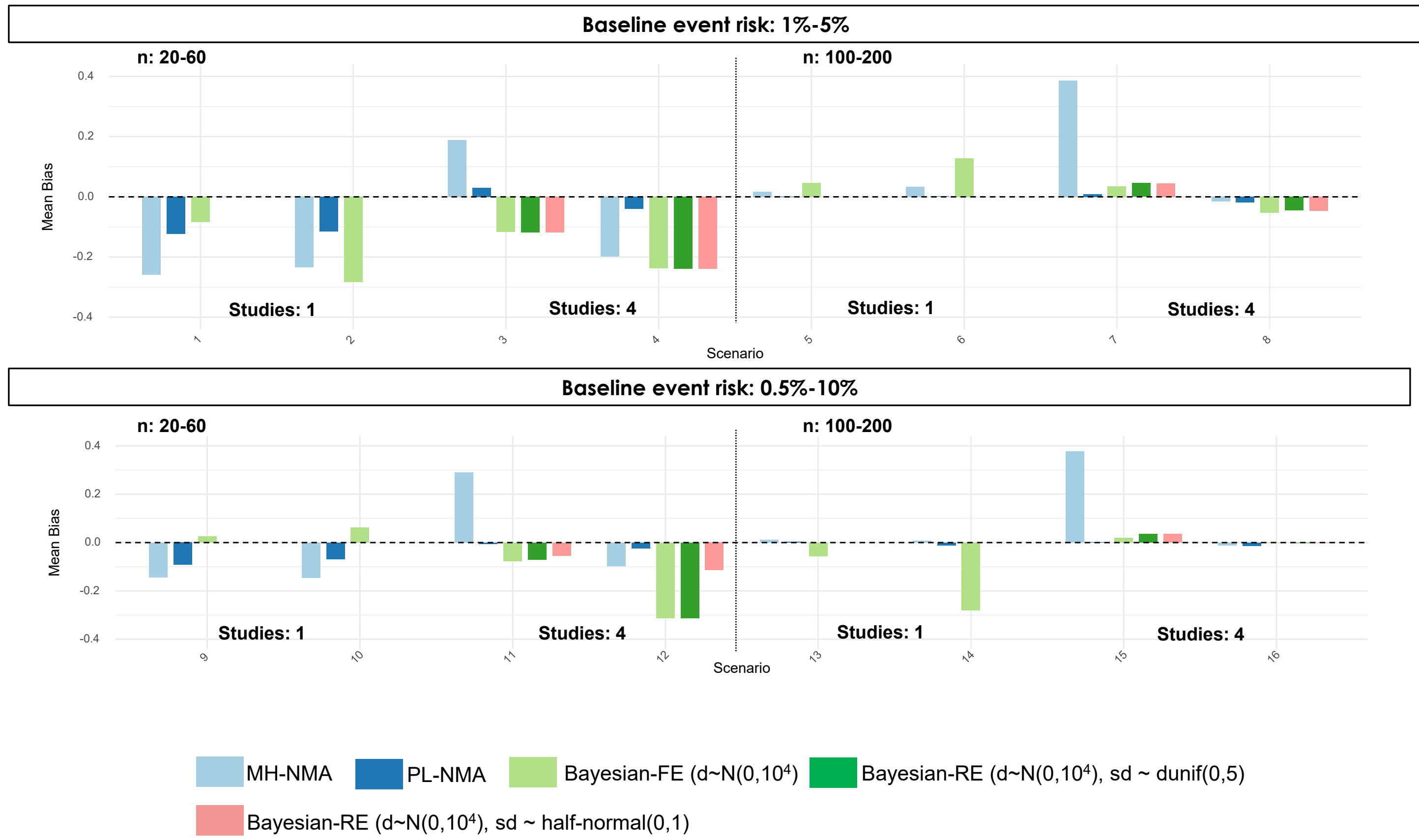
- Fixed-effect (FE) **Mantel-Haenszel (MH) NMA** with continuity correction for studies with zero event arms.[3]
- FE **Penalized Likelihood (PL) NMA** model.[2]
- **Fixed and random-effects (RE) Bayesian NMA with exact binomial likelihood with non-informative priors** and applying continuity correction for studies with zero event arms. [4]
- **RE Bayesian NMA with exact binomial likelihood model with a more informative prior** on the between study variance parameter and applying continuity correction for studies with zero event arms. [4]
- For Bayesian models, non-informative priors were used following NICE DSU TSD recommendations. [4] A half-normal (0,1) prior was chosen as the more informative prior for the between-study variance. **RE models were not run for networks with single-study treatment comparisons**. The Gelman-Rubin statistic was used to check model convergence.

RESULTS

Star-shaped network

Across **low-sample scenarios**, the **PL-NMA** model **generally provided the least biased estimates**, except in scenarios 1 and 9, where Bayesian FE models showed the lowest bias. For **higher-sample scenarios**, **PL-NMA consistently outperformed all other models**. In scenarios with **multiple studies per treatment comparison**, **heterogeneous baseline risks**, and **larger sample sizes**, **Bayesian models** also demonstrated robust performance with **least biased results**.

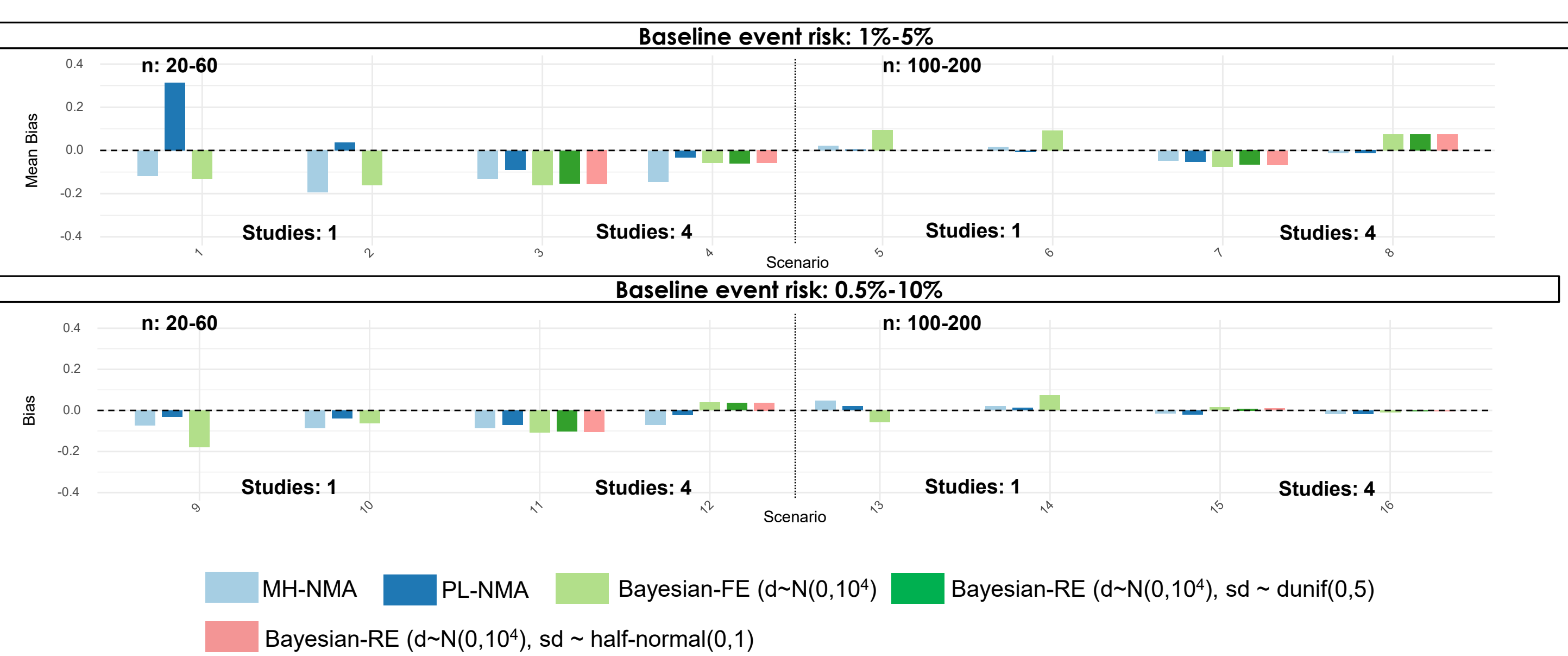
Figure 1. Mean bias across multiple treatment effects for the star-shape network.



Single-loop network

In **low-sample scenarios**, the **PL-NMA** model generally yielded the **least biased estimates**, except in scenario 1. For **higher-sample scenarios involving a single study per treatment comparison**, both **PL-NMA** and **MH-NMA** consistently resulted in low bias. In scenarios with **multiple studies per treatment comparison**, **heterogeneous baseline risks**, and **larger sample sizes**, all models showed similar performance, with **Bayesian models exhibiting** low values of mean bias, less than 0.2.

Figure 2. Mean bias across multiple treatment effects for the single-loop network.



CONCLUSIONS

- While some of the evaluated models offer reliable estimates, the **choice of approach for sparse NMAs is multi-faceted**.
- The utility of synthesising all-zero event studies need to be justified, and sensitivity analyses should always be conducted to ensure robustness of the results.

REFERENCES

1. Jaiswal N, Field R. Network meta-analysis: The way forward for evidence-based decisions. Clin Epidemiol Glob Health. 2024;26:101531. doi:10.1016/j.cegh.2024.101531. 2. Evrenoglou T, White IR, Afach S, Mavridis D, Chaimani A. Network meta-analysis of rare events using penalized likelihood regression. Stat Med. 2022;41(26):5203-5219. doi:10.1002/sim.9562. 3. Efthimiou O, Rücker G, Schwarzer G, Higgins JPT, Egger M, Salanti G. Network meta-analysis of rare events using the mantel-Haenszel method. Stat Med. 2019;38(16):2992-3012. 4. Dias S, Welton N, Sutton A. NICE DSU Technical Support Document 2: A Generalised Linear Modelling Framework for Pairwise and Network Meta-Analysis of Randomised Controlled Trials. National Institute for Health and Care Excellence (NICE). 2014.

DISCLOSURES

GF, AN, KP and AG are employees of Amaris Consulting. Authors declare no conflict of interest.