Supplementary Material for “Meta-analysis of Censored Adverse Events”

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A. `JAGS` model specification

Here we provide the `JAGS` model specification for the application in Section 4.

```
# application: study, cancer, drug effect included
model{
    for (j in 1:J1){
        Y[j] ~ dbin(theta[j], N[j])
        logit(theta[j]) <- theta.s[study[j]] + theta.d[drug[j]] + theta.c[cancer[j]]
    }
    for (j in 1:J2){
        Z[j] ~ dbern(p[j])
        p[j] <- pbin(cut[j], theta[j+J1], N[j+J1])  #Y<=cut
        logit(theta[j+J1]) <- theta.s[study[j+J1]] + theta.d[drug[j+J1]] + theta.c[cancer[j+J1]]
    }
    for (i1 in 1:n.study){
        theta.s[i1] <- mu.study + sigma.study*sn.study[i1]
        sn.study[i1] ~ dnorm(0,1)
    }
    mu.study ~ dnorm(0, .0001)
    sigma.study ~ dt(0, a, 1)T(0,) # a=1/A^2
    for (i2 in 1:n.drug){
        theta.d[i2] <- mu + sigma.drug*sn.drug[i2]
        sn.drug[i2] ~ dnorm(0,1)
    }
    mu ~ dnorm(0, .0001)
    sigma.drug ~ dt(0, a, 1)T(0,)
    for (i5 in 1:n.cancer){
        theta.c[i5] <- mu.cancer+sigma.cancer*sn.cancer[i5]
        sn.cancer[i5] ~ dnorm(0, 1)
    }
    mu.cancer ~ dnorm(0, .0001)
    sigma.cancer ~ dt(0, a, 1)T(0,)
}
```

B. Supplementary Simulation Results for Section 3.2

Study Sample Size	Scenario	True Value	% of LC	% of RC	Mean Absolute Deviation				Root-mean-squared Error			
					MAGEC	PEM	LRM	NAM/RVE	MAGEC	PEM	LRM	NAM/RVE
10	S5	0.2	0%	20%	**0.014**	0.020	0.020	0.014	**0.018**	0.023	0.023	0.017
		0.05	0%	20%	**0.006**	0.007	0.007	0.008	**0.008**	**0.008**	**0.008**	0.010
		0.01	0%	20%	**0.003**	0.003	0.003	0.007	0.004	**0.003**	**0.003**	0.008
	S6	0.2	40%	20%	0.020	0.015	0.015	**0.014**	0.024	0.019	0.019	**0.018**
		0.05	40%	20%	0.008	**0.007**	**0.007**	0.013	**0.009**	**0.009**	**0.009**	0.015
		0.01	40%	20%	**0.003**	**0.003**	**0.003**	0.010	**0.004**	**0.004**	**0.004**	0.011
25	S5	0.2	0%	20%	**0.009**	0.018	0.018	**0.009**	**0.011**	0.020	0.020	**0.011**
		0.05	0%	20%	**0.004**	0.005	0.005	0.007	**0.005**	0.006	0.006	0.008
		0.01	0%	20%	**0.002**	**0.002**	**0.002**	0.008	**0.002**	**0.002**	**0.002**	0.008
	S6	0.2	40%	20%	0.011	**0.010**	**0.010**	**0.010**	0.014	**0.012**	**0.012**	0.013
		0.05	40%	20%	**0.004**	0.005	0.005	0.013	**0.005**	0.006	0.006	0.014
		0.01	40%	20%	**0.002**	0.003	0.003	0.010	**0.003**	0.004	0.004	0.011
50	S5	0.2	0%	20%	**0.006**	0.018	0.018	0.007	**0.008**	0.019	0.019	0.009
		0.05	0%	20%	**0.003**	0.004	0.004	0.007	**0.004**	0.005	0.005	0.007
		0.01	0%	20%	**0.001**	**0.001**	**0.001**	0.008	**0.002**	**0.002**	**0.002**	0.008
	S6	0.2	40%	20%	**0.007**	0.008	0.008	0.009	**0.009**	0.010	0.010	0.011
		0.05	40%	20%	**0.003**	0.004	0.004	0.013	**0.004**	0.005	0.005	0.014
		0.01	40%	20%	**0.002**	0.003	0.003	0.010	**0.002**	0.003	0.003	0.011

Table B.1: Mean absolute deviations (MADs) and root mean square errors (RMSEs) of drug incidence probabilities for five methods. We compared the proposed Bayesian model (MAGEC), pooled estimation method after continuity correction (PEM), normal approximate method (NAM), logistic regression model (LRM), as well as normal approximate method with robust variance estimation (RVE) under different study sample sizes ($J = 10,\ 25,\ 50$) and two scenarios: (S5) 20% right censoring; and (S6) 40% left censoring & 20% right censoring. LC = left censoring; RC = right censoring.

C. Comprehensive Forest Plot for Real-Data Application

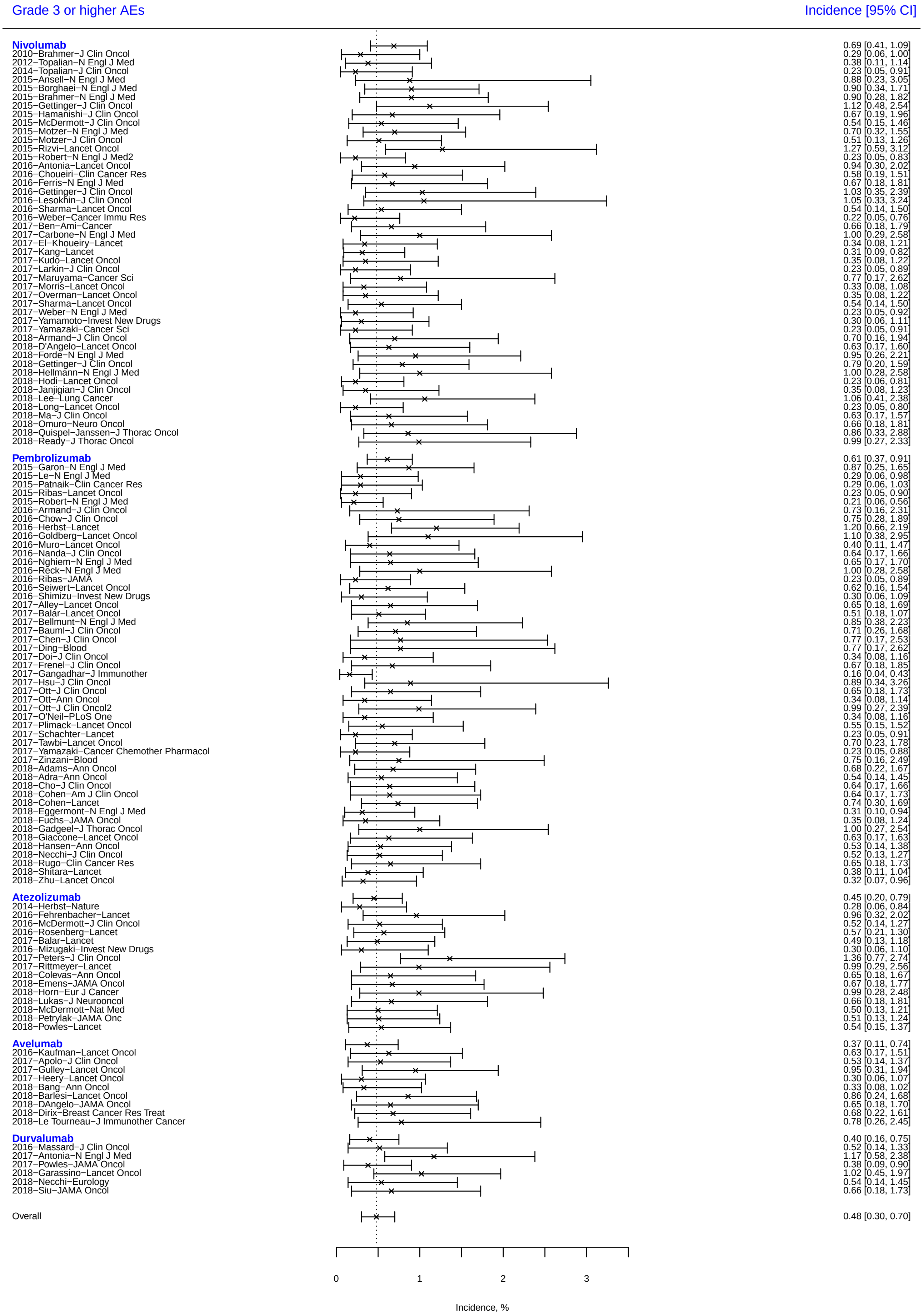

Figure C.1: Incidence of grade 3 or higher AE (Pneumonitis) by study