

Network meta-analysis using survival data

Nathan Green

Department of Statistic Science | University College London

Summary

- Recap part one
 - Basic NMA with binary data
- NMA with survival data
 - IPD time to event
 - Contrast-based data hazard ratios (HR)
- BUGS with R practical

References

1. **Saramago P, Chuang LH, Soares MO.** *Network meta-analysis of (individual patient) time to event data alongside (aggregate) count data.* BMC Med Res Methodol. 2014;14(1).
2. **Woods BS, Hawkins N, Scott DA.** *Network meta-analysis on the log-hazard scale, combining count and hazard ratio statistics accounting for multi-arm trials: A tutorial.* BMC Med Res Methodol. 2010;10.

Recap of part 1

- Unusual for a policy question to be informed by a single study
 - Must use all available and relevant evidence
- New treatment C: been trialled against old treatment B, but not to A
- For health economic evaluation need to compare A/B/C together
- Learn about C/A effect from C/B and B/A trial data
- Also called “mixed treatment comparisons”. Since can also “mix” direct and indirect data on same comparison...

Count data equations

Fixed effects

$$\begin{aligned}r_{st} &\sim \text{Bin}(p_{st}, n_{st}) \\ \text{logit}(p_{st}) &= \mu_s + \delta_{st} \\ \delta_{st} &\sim d_t - d_{t_{s0}}\end{aligned}$$

Random effects

$$\begin{aligned}r_{st} &\sim \text{Bin}(p_{st}, n_{st}) \\ \text{logit}(p_{st}) &= \mu_s + \delta_{st} \\ \delta_{st} &\sim N(\mu_{st}^\delta, \sigma_{st}^2) \\ \mu_{st}^\delta &\sim d_t - d_{t_{s0}}\end{aligned}$$

More realistic situation

- Different types of data we want to synthesise.

Binary data with time to event data (TTE)

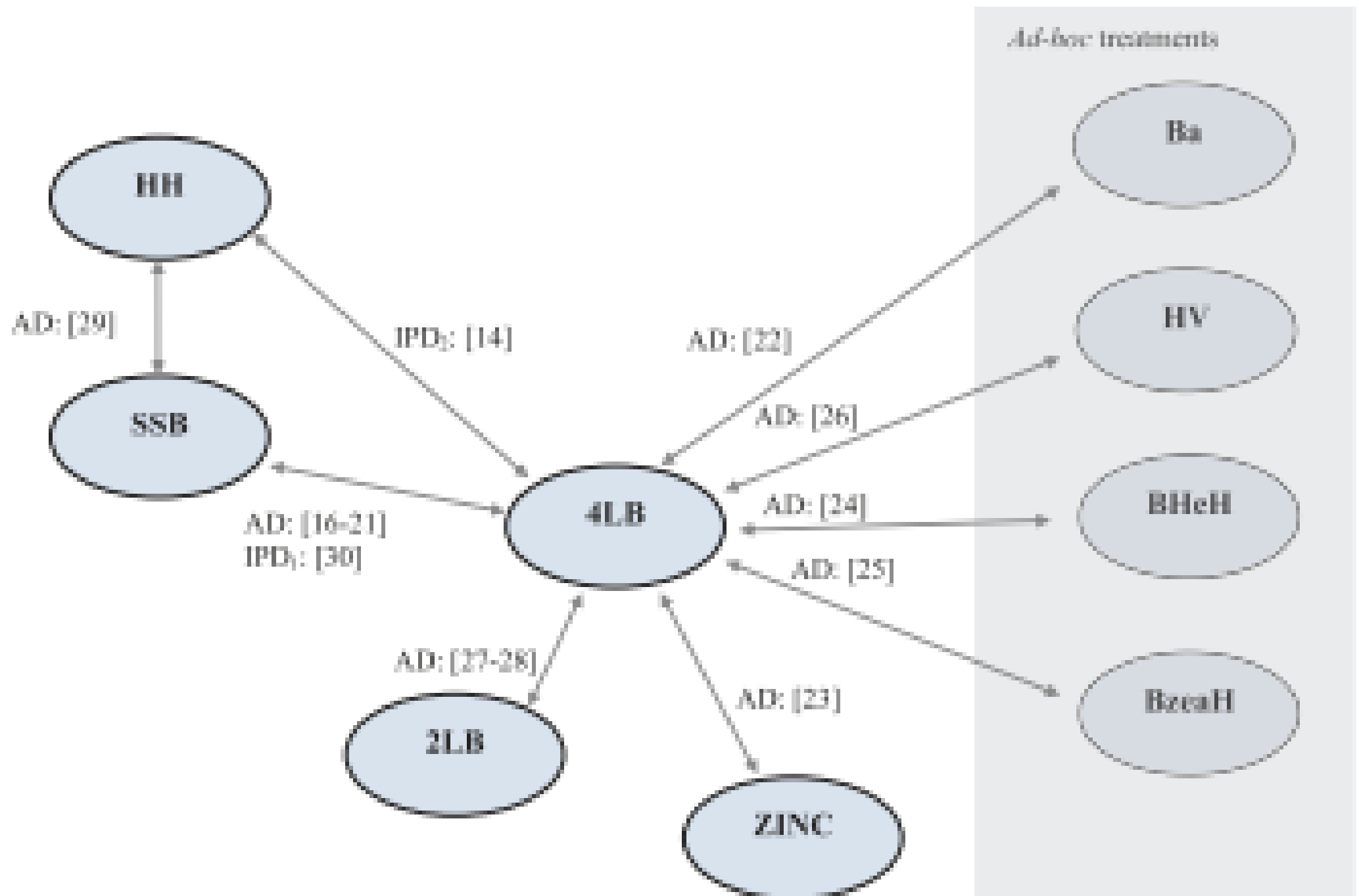
- Use example from Saramago (2014)¹
- The case study relates to compression systems aiming to deliver high compression to promote venous leg ulcer healing
- The final NMA contained data from 16 RCTs
 - 2 included RCTs had full IPD data (841 participants) which included time to healing or censoring for each participant, together with other characteristics (treatment centre, ulcer duration, size, patient mobility).
 - Remaining aggregate data only

Data

ID	Study	Treatment	Follow up (weeks)	Number patients	Mean duration (months)	Mean size (cm ²)	Number healed	Evidence format available
16	Duby <i>et al.</i> 1993 [18]	4LB	12	25	20.5	11.9	11	AD
		SSB	12	25	26.7	13.1	10	
17	Scriven <i>et al.</i> 1998 [19]	4LB	52	32	13	13.3	17.6	AD
		SSB	52	32	21	8.3	18.24	
18	Partsch <i>et al.</i> 2001 [20]	4LB	16	53	1.25	1.5	33	AD
		SSB	16	59	1	1.9	43	
19	Ukat <i>et al.</i> 2003 [21]	4LB	12	44	–	17.7	13	AD
		SSB	12	45	–	12.2	10	
20	Franks <i>et al.</i> 2004 [22]	4LB	24	74	2	5	59	AD
		SSB	24	82	2	3.5	62	
21	Junger <i>et al.</i> 2004b [23]	SSB	12	60	5.57	5.95	19	AD
		HH	12	61	4.14	5.62	29	
22	Kralj <i>et al.</i> 1996 [24]	4LB	24	20	7.9	18.6	7	AD
		<i>Ad hoc</i> : Ba	24	20	6.9	17.2	8	
23	Polignano <i>et al.</i> 2004b [25]	4LB	24	39	–	10.1	29	AD
		ZINC	24	29	–	9.3	19	
24	Wilkinson <i>et al.</i> 1997 [26]	4LB	12	17	–	11.2	8	AD
		<i>Ad hoc</i> : BHeH	12	18	–	8.6	8	
25	Colgan <i>et al.</i> 1995 [27]	4LB	12	10	9.3	27.5	6	AD
		<i>Ad hoc</i> : Bzeah	12	10	66.5	48.5	7	
26	Blecken <i>et al.</i> 2005 [28]	4LB	12	12	–	50.08	4	AD
		<i>Ad hoc</i> : HV	12	12	–	48.98	4	
27	Moffatt <i>et al.</i> 2008 [29]	4LB	4	42	48.8	5.7	3	AD
		2LB	4	39	46.6	11.8	6	
28	Szewczyk <i>et al.</i> 2010 [30]	4LB	12	15	–	6	9	AD
		2LB	12	16	–	5.3	10	
29	Wong <i>et al.</i> 2012 [31]	4LB	24	107	–	–	72	AD
		SSB	24	107	–	–	77	
30	Iglesias <i>et al.</i> 2004 [32]	4LB	52	195	3	3.81	107	IPD
		SSB	52	192	3	3.82	86	
14	Ashby <i>et al.</i> 2013 [17]	4LB	52	224	12.29	9.30	157	IPD
		HH	52	230	10.82	9.41	163	

AD – aggregate-level data; IPD – individual patient data; 4LB, SSB, HH, Zinc paste, 2LB and the *ad hoc* systems Ba, BHeH, Bzeah, HV as described in Additional file 1.

Network diagram



IPD model

- i th participant in j th study in k th treatment arm

$$t_{ijk} \sim Weibull(s, \lambda_{ijk}) I(t_{ijk}^c)$$

$$\log(\lambda_{ijk}) = \begin{cases} \mu_j^{IPD} + \gamma_j^c + \beta_{0j}x_{ijk}, & \text{if } k = b \\ \mu_j^{IPD} + d_{bk} + \gamma_j^c + \beta_{0j}x_{ijk}, & \text{if } k > b \end{cases}$$

$$x_{ijk} \sim N(m, p) \quad \gamma_j^c \sim N(0, \pi)$$

AD model

- The linear predictor, $\log(\lambda_{jk}^{AD})$ was a function of the baseline log-hazard of an event for treatment b in study j , μ_j^{AD} , and by the log-hazard ratio for treatment k and baseline treatment b , d_{bk} ($= d_{1k} - d_{1b}$). Note that there are parameters common to both model parts, namely the log-hazard ratios and the shape parameter of the time to healing distribution.

$$r_{jk} \sim \text{Bin}(p_{jk}, n_{nk})$$

$$p_{jk} = 1 - \exp(-\lambda_{jk}^{AD} (t_{jk}^{AD})^s)$$

$$\log(\lambda_{jk}^{AD}) = \begin{cases} \mu_j^{AD}, & \text{if } k = b \\ \mu_j^{AD} + d_{bk}, & \text{if } k > b \end{cases}$$

Data format

- `treat`: treatment arm (coded 1,2)
- `baseline`: reference treatment code,
- `t.obs`: time to event in months (under censoring)
- `t.cens`: time of censoring in months,
- `n.subjects`: Number of participants in IPD
- `n.treat`: Number of treatments
- `a.id`: study number
- `a.treat`: treatment arm code (coded from 1 to number of treatments),
- `r`: number of events in trial arm
- `n`: number of patients in trial arm
- `a.base`: reference treatment code
- `a.time`: follow-up time of trial
- `n.agg.trials`: Number of AD studies
- `n.agg.arms`: Number of AD study arms

Data format

```
1 load(here::here("part 2/practical/tte_counts_input_data.RData"))
2
3 input_dat
```

```
$n.subjects
```

```
[1] 3
```

```
$n.treat
```

```
[1] 2
```

```
$n.agg.trials
```

```
[1] 2
```

```
$n.agg.arms
```

```
[1] 2
```

```
$treat
```

```
[1] 1 1 2
```

```
$baseline
```

```
[1] 1 1 1
```

```
$t.obs
```

```
[1] 3.50 2.33 NA
```

```
$t.cens
```

```
[1] 0.0 0.0 11.9
```

Coding in BUGS

- **Part 1:** Model for IPD

```
1 model {
2   ### Part 1: Model for IPD
3
4   for(i in 1:n.subjects) {
5     # Weibull likelihood for IPD
6     t.obs[i] ~ dexp(zu[i])I(t.cens[i], )
7
8     # Model for IPD
9     log(zu[i]) <- mu + d[treat[i]] - d[baseline[i]]
10  }
11
12  # Vague prior for IPD
13  mu ~ dnorm(0, 1.0E-6)
```

Coding in BUGS

- **Part 2:** Model for aggregate data

```
1  ### Part 2: Model for aggregate data
2
3  for (i in 1:n.agg.arms) {
4    # Binomial likelihood for AD
5    r[i] ~ dbin(pa[i], n[i])
6
7    # Model for AD
8    pa[i] <- 1 - exp(-zu.a[i] * a.time[i])
9    log(zu.a[i]) <- mu.a[a.id[i]] + d[a.treat[i]] - d[a.base[i]]
10 }
11
12 # Vague priors for AD
13 for(j in 1:n.agg.trials) {
14   mu.a[j] ~ dnorm(0, 1.0E-6)
15 }
```

Coding in BUGS

- **Part 3:** Model for combining all estimates of treatment effect

```
1   ### Model for combining all estimates of treatment effect
2
3   # Vague prior for basic parameters
4   d[1] <- 0
5
6   for (k in 2:n.treat) {
7     d[k] ~ dnorm(0, 1.0E-6)
8   }
9 }
```

Binary data with contrast-based survival data

- Use example from Woods (2010)¹
- Data on survival endpoints are usually summarised using either *hazard ratio*, *cumulative number of events*, or *median* survival statistics
- NMA of survival endpoints can combine count and hazard ratio statistics in a single analysis on the hazard ratio scale
- A worked example of an analysis of mortality data in chronic obstructive pulmonary disease (COPD)

Data

- Input RCT data binary counts table

Author/Trial (Date)	Treatment	r (deaths)	N (patients)
Boyd (1997) [12]	Salmeterol	1	229
	Placebo	1	227
Calverly/TRISTAN (2003) [13]	Fluticasone	4	374
	Salmeterol	3	372
	SFC	2	358
	Placebo	7	361
Celli (2003) [14]	Salmeterol	1	554
	Placebo	2	270

- Input RCT hazard summary table

Author/Trial (Date)	Treatment	Base	HR	HR _{LCI}	HR _{UCI}	$\ln(HR)$	$se(\ln(HR))$
Burge/ISOLDE (2000) [15]	Fluticasone	Placebo	0.76	0.51	1.13	-0.276	0.203
Calverly/TORCH (2007) [16]	SFC	Placebo	0.811	0.670	0.982	-0.209	0.098
	Salmeterol	Placebo	0.857	0.710	1.035	-0.154	0.096
	Fluticasone	Placebo	1.056	0.883	1.264	0.055	0.092
	SFC	Salmeterol	0.946	0.777	1.151	-0.056	0.100
	SFC	Fluticasone	0.768	0.636	0.927	-0.264	0.096

Count statistics on log-hazard ratio scale

- For r_{sk} is the cumulative count of subject who have experienced an event in arm k of study s ; n_{sk} is total number of subjects in arm k of study s and F_{sk} is the cumulative probability of subject having an event.

$$r_{sk} \sim \text{Bin}(F_{sk}, n_{sk})$$

- The log cumulative hazard for each trial arm is then

$$\ln(H_{sk}) = \ln(-\ln(1 - F_{sk}))$$

- The log cumulative hazard is estimated as the sum of a study specific ‘baseline’ term α_s and a treatment effect coefficient β_k :

$$\ln(H_{s,k}) = \alpha_s + \beta_k - \beta_b$$

where $\beta_1 = 0$ for the reference treatment and β_b represents the treatment effect for the baseline treatment in study s .

What is β_k ?

- Under the assumption of proportional hazards, β_k is *both* log cumulative hazard ratio *and* log hazard ratio:

$$\ln\left(\frac{\exp(\beta_k)h_{sb}}{h_{sb}}\right) = \ln\left(\frac{\int_0^t \exp(\beta_k)h_{sb}}{\int_0^t h_{sb}}\right) = \beta_k$$

Combining count and hazard ratio statistics in an NMA

- x_{skb} is log hazard ratio estimate for study s comparing treatments k and b

$$x_{skb} \sim N \left(\ln \left(\frac{h_{sk}}{h_{sb}} \right), se_{skb}^2 \right)$$

then

$$\ln \left(\frac{h_{sk}}{h_{sb}} \right) = \beta_k - \beta_b$$

Coding in BUGS

- For hazard ratio reporting studies

```
1 for (ii in 1:LnObs) {  
2   Lmu[ii] <- alpha[Lstudy[ii]]*multi[ii] + beta[Ltx[ii]] - beta[Lbase[ii]]  
3   Lprec[ii] <- 1 / pow(Lse[ii], 2)  
4   Lmean[ii] ~ dnorm(Lmu[ii], Lprec[ii])  
5 }
```

- For binary data reporting studies

```
1 for (ss in 1:BnObs) {  
2   logCumHaz[ss] <- alpha[Bstudy[ss]] + beta[Btx[ss]] - beta[Bbase[ss]]  
3   cumFail[ss] <- 1 - exp(-1 * exp(logCumHaz[ss]))  
4   Br[ss] ~ dbin(cumFail[ss], Bn[ss])  
5 }
```

Going further

References

1. **Saramago P, Chuang LH, Soares MO.** *Network meta-analysis of (individual patient) time to event data alongside (aggregate) count data.* BMC Med Res Methodol. 2014;14(1).
2. **Woods BS, Hawkins N, Scott DA.** *Network meta-analysis on the log-hazard scale, combining count and hazard ratio statistics accounting for multi-arm trials: A tutorial.* BMC Med Res Methodol. 2010;10.
3. **Donegan S, Williamson P, D'Alessandro U, Garner P, Smith C:** *Combining individual patient data and aggregate data in mixed treatment comparison meta-analysis: individual patient data may be beneficial if only for a subset of trials.* Stat Med 2013, 32(6):914–930.
4. **Berlin J, Santanna J, Schmid C, Szczech L, Feldman H:** *Individual patient- versus group-level data meta-regressions for the investigation of treatment effect modifiers: ecological bias rears its ugly head.* Stat Med 2002, 21(3):371–387.
5. **Riley R, Lambert P, Staessen J, Wang J, Gueyffier F, Thijs L, Bouitrie F:** *Meta-analysis of continuous outcomes combining individual patient data and aggregate data.* Stat Med 2008, 27(11):1870–1893

