

Online Material for *Bayes Factors For Choosing Among Six Common Survival Models*

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Appendix A Derivation of the Bayes Factors

Here we show how to derive the Bayes factor BF_h for testing the PH model ($H_h : \beta_q = 0, \beta_o - \beta_h = 0$) relative to the super model ($H_s : \beta_q \neq 0, \beta_o - \beta_h \neq 0$) given in Section 3.4; other Bayes factors can be derived similarly. Let $\Upsilon_1 = (\beta'_q, \beta'_o - \beta'_h)'$ and $\Upsilon_2 = \beta'_o$. Note that $(\Upsilon'_1, \Upsilon'_2)'$ is a reparametrization of β . Then the likelihood $L(\xi_J, \theta, \beta)$ can be denoted as $L(\Upsilon_1, \psi)$, where $\psi = (\xi_J, \theta, \Upsilon_2)$ are the remaining likelihood parameters under the super model. The Bayes factor for testing the PH model (now $H_h : \Upsilon_1 = 0$) relative to the super model is defined as

$$BF_h = \frac{\int L(\Upsilon_1 = 0, \psi) p_0(\psi) d\psi}{\int \mathcal{L}(\Upsilon_1, \psi) p(\Upsilon_1, \psi) d(\Upsilon_1, \psi)}, \quad (\text{A.1})$$

$p_0(\psi)$ and $p(\Upsilon_1, \psi)$ are the prior probability densities under H_h and H_s , respectively. According to the Savage-Dickey density ratio expression, if

$$p(\psi | \Upsilon_j = \mathbf{0}) = p_0(\psi), \quad (\text{A.2})$$

then BF_h can be written as

$$BF_h = \frac{p(\Upsilon_1 = \mathbf{0} | \mathcal{D})}{p(\Upsilon_1 = \mathbf{0})}, \quad (\text{A.3})$$

where $p(\Upsilon_1) = \int p(\Upsilon_1, \psi) d\psi$ and $p(\Upsilon_1 | \mathcal{D}) = \int p(\Upsilon_1, \psi | \mathcal{D}) d\psi$ are the marginal prior and posterior density of Υ_1 respectively under H_s . Following (Zhou et al., 2017, Proposition 1) it is easy to show that the assumption (A.2) holds and $p(\Upsilon_1 = \mathbf{0})$ is given by

$$p(\Upsilon_1 = \mathbf{0}) = N_p(\mathbf{0}; \mathbf{0}, \mathbf{S}_0^*) N_p(\mathbf{0}; \mathbf{0}, 2\mathbf{S}_0^*),$$

where $\mathbf{S}_0^* = \frac{3.228n}{p} (\mathbf{X}^*{}' \mathbf{X}^*)^{-1}$. Also the $p(\Upsilon_1 = \mathbf{0} | \mathcal{D})$ can be approximated by $N_{2p}(\mathbf{0}; \mathbf{m}_h, \mathbf{V}_h)$ where \mathbf{m}_h and \mathbf{V}_h are the posterior sample mean and variance of Υ_1 , respectively.

Appendix B R Code for the Two Real Data Analyses

B.1 Veterans Administration Lung Cancer Trial

The following R commands are used to fit the super model with $J = 15$, a Weibull baseline, and the hyperparameter settings in Section 3.3 of the main paper.

```

#needed packages
library(spBayesSurv)
library(survival)
library(MASS)

#data management
data(VA)
VAsub<-subset(VA, prior==0)

#fitting super model
nburn=20000; nsave=20000; nskip=9; niter=nburn+nsave
mcmc=list(nburn=nburn,nsave=nsave,nskip=nskip,ndisplay=1000)
prior=list(maxL=15,a0=1,b0=1); state=list(cpar=1)
fit=SuperSurvRegBayes(formula=Surv(stime,status)~Karn+cell,
data=VAsub,prior=prior,mcmc=mcmc, state=state,dist="weibull")

#output from summary
summary(fit) # most output removed to save space
Bayes factors relative to the super model:
AFT          PH          PO          AH          EH          YP
115.1500    26.6631    97.4011    0.2502    123.0400    10.9357

Log pseudo marginal likelihood: LPML=-509.7744
Deviance Information Criterion: DIC=1010.84

```

The following code produces the plots in Figure 1 of the main paper.

```

tgrid=seq(0.1,501.1,5);
xpred=data.frame(Karn=c(40, 60, 80), cell=c("4", "4", "4"));
estimates=plot(fit,xnewdata=xpred,tgrid=tgrid);
plot(estimates$tgrid, estimates$fhat[,1],type="l", ylim=c(0,0.01),
xlab="days", ylab="density")
lines(estimates$tgrid,estimates$fhat[,2],lty=2)
lines(estimates$tgrid,estimates$fhat[,3],lty=3)
text(30,0.0087,"PS=40"); text(50,0.0052,"PS=60"); text(100,0.0032,"PS=80")

```

B.2 Breast Cancer Study

The following R commands are used to fit the super model with $J = 15$, a Weibull baseline, and the hyperparameter settings in Section 3.3 of the main paper.

```

library(spBayesSurv)
library(KMsurv)
library(survival)

data(bcdeter)
bcdeter$status=(1-as.numeric(is.na(bcdeter$upper)))*3
bcdeter$status[bcdeter$lower==0]=2;

```

```

bcdeter$status[which(bcdeter$lower==bcdeter$upper)]=1;
bcdeter$lower[bcdeter$lower==0]=bcdeter$upper[bcdeter$lower==0]

#fitting super model
nburn=10000; nsave=5000; nskip=9; niter=nburn+nsave
mcmc=list(nburn=nburn,nsave=nsave,nskip=nskip,ndisplay=500)
prior=list(maxL=15,a0=1,b0=1)
state=list(cpar=1)
fit=SuperSurvRegBayes(formula=Surv(lower,upper,status, type="interval")~treat,
data=bcdeter,prior=prior,mcmc=mcmc,state=state,dist="weibull");
summary(fit)

```

Bayes factors relative to the super model:

AFT	PH	PO	AH	EH	YP
17.556	32.443	4.065	24.474	7.880	7.826

Log pseudo marginal likelihood: LPML=-150.6149

Deviance Information Criterion: DIC=299.4162

Number of subjects: n=95

The following code produces the plots in Figure 2 of the main paper.

```

tgrid = seq(1e-10,70,.5);
xpred = data.frame(treat = c(1, 2));
estimates=plot(fit, xnewdata=xpred, tgrid=tgrid);

plot(survfit(Surv(lower,upper,status, type="interval")~treat, data=bcdeter), lty=
1:2, xlab="Time in Month", ylab="Survival Probability", cex.axis=1.5, cex.lab=1.5)
lines(estimates$tgrid, estimates$Shat[,1], "l");
lines(estimates$tgrid, estimates$Shat[,2], lty=2);
legend(2,0.2,c("Radiotherapy alone","Radiation plus chemotherapy"),
lty=c(1:2),cex=1.2)

```

Appendix C Additional Simulation Results

C.1 Sensitivity Analysis for the g -Prior

To study the impact of information g -prior, we consider two cases $M = 10$ and $M = 50$ for testing AFT, PH and PO in Table S1. The two different M values yield almost identical results, indicating that our method is not very sensitive to the choice of g -prior.

Table S1: Proportion of times Bayes factor selects each model when truth is known out of 500 replicated data sets.

Baseline	n	g -prior with $M = 10$			g -prior with $M = 50$		
		Model picked			Model picked		
		AFT	PH	PO	AFT	PH	PO
True AFT model							
Lognormal	200	0.948	0.040	0.012	0.964	0.028	0.008
	500	0.968	0.000	0.032	0.980	0.002	0.018
	1000	0.982	0.000	0.018	0.976	0.000	0.024
Mixture	200	1.000	0.000	0.000	0.998	0.002	0.000
	500	1.000	0.000	0.000	1.000	0.000	0.000
	1000	1.000	0.000	0.000	1.000	0.000	0.000
Weibull	200	0.444	0.554	0.002	0.482	0.514	0.004
	500	0.370	0.630	0.000	0.374	0.626	0.000
	1000	0.364	0.634	0.002	0.356	0.644	0.000
True PH model							
Lognormal	200	0.036	0.962	0.002	0.026	0.974	0.000
	500	0.000	0.998	0.002	0.000	1.000	0.000
	1000	0.000	1.000	0.000	0.000	1.000	0.000
Mixture	200	0.008	0.930	0.062	0.004	0.930	0.066
	500	0.002	0.986	0.012	0.002	0.986	0.012
	1000	0.000	1.000	0.000	0.000	0.996	0.004
Weibull	200	0.376	0.618	0.006	0.482	0.518	0.000
	500	0.372	0.624	0.004	0.436	0.564	0.000
	1000	0.414	0.586	0.000	0.434	0.566	0.000
True PO model							
Lognormal	200	0.852	0.094	0.054	0.878	0.108	0.014
	500	0.722	0.024	0.254	0.848	0.018	0.134
	1000	0.456	0.000	0.544	0.554	0.004	0.442
Mixture	200	0.002	0.120	0.878	0.006	0.122	0.872
	500	0.000	0.008	0.992	0.000	0.018	0.982
	1000	0.000	0.000	1.000	0.000	0.000	1.000
Weibull	200	0.814	0.036	0.150	0.930	0.020	0.050
	500	0.342	0.008	0.650	0.586	0.006	0.408
	1000	0.090	0.000	0.910	0.126	0.000	0.874

References

- Zhou, H., Hanson, T., and Zhang, J. (2017). Generalized accelerated failure time spatial frailty model for arbitrarily censored data. *Lifetime Data Analysis*, 23(3):495–515.