Appendix

Model

The number of cases, Y, for each observation, i, for every hospital, h, follows a Poisson distribution with mean lambda[i,h].

$$Y[i,h] \sim Poisson(lambda[i,h])$$

The log of the mean Poisson rate, with patient-days as the offset, is modelled as the sum of a random year effect, random period effect, and a hospital effect. The hierarchical modelling of the year and hospital effects allow for the year effect to vary by hospital with a variance denoted by sigma.year.

$$log(lambda[i,h]) = log(patient - days[i,h]) + mean[i,h]$$

$$mean[i,h] = year.hospital[s,h] + period.effect[p]$$

$$year.hospital[s,h] \sim Normal(year.effect[s] + hospital.effect[h], sigma.year)$$

The mean of the hospital effect is modelled as a function of an overall intercept, the type of hospital (A; non-teaching without ICU, B; non-teaching with ICU, and C; teaching with ICU) and the number of beds in the hospital, as well as a random effect relating the calendar year the hospital entered BACTOT, where g is a pointer to hospital h's first year in the BACTOT.

$$hospital.effect[h] = intercept + beta.typeB * typeB[h] + beta.typeC * typeC[h] + beta.beds * beds[h] + entry[g[h]]$$

Below are the prior distributions for the random effects.

$$entry[g] \sim Normal(0, sigma.entry)$$

$$period.effect[p] \sim Normal(0, sigma.period)$$

$$year.effect[s] \sim Normal(0, sigma2.year)$$

R code

Below is the R code used to fit the model using JAGS. *nhospital* refers to the total number of hospitals. *group.hosp* refers to the year in which a hospital entered BACTOT. *n[h]* refers to the total number of observations available for each hospital. *nyear* refers to the total number of surveillance years for which a hospital has participated in BACTOT. *Togroup* refers to the number of possible years in which new hospitals entered BACTOT. *toperiod* refers to the maximum number of surveillance periods, and *toyear* refers to the maximum number of surveillance years.

```
model{

## Likelihood function
        for(h in 1:nhospital){
                level[h] <-  beta.c + b.beds*beds[h] + phi[group.hosp[h]] + b.typeB*typeB[h] + b.typeC*typeC[h]
                risk.hosp[h] <- exp(level[h])
                        for(i in 1:n[h]){
      y[i,h] ~ dpois(lambda[i,h])
      log(lambda[i,h]) <- offset[i,h] + mean[i,h]
      mean[i,h] <-  gamma[year[i,h],h] + delta.c[period[i,h]]
      y.fitted[i,h] ~ dpois(lambda[i,h])
      }
  }

 ## Prior specification
    for(h in 1:nhospital){
     for(ii in 1:nyear[h]){
      gamma[ii,h] ~ dnorm(level[h] + gamma.c[ii] , prec.gamma)
      risk.year.hosp[ii,h] <- exp(gamma[ii,h])
     }
    }
    for(i in 1:togroup){
     phi[i] ~ dnorm(0,prec.group)
     risk.group[i] <- exp(phi[i])
  }
    for(p in 1:toperiod){
     delta.c[p] ~ dnorm(0,prec.delta.c)
     risk.period[p] <- exp(delta.c[p])
    }
    for(p in 2:toperiod){
     rr.period[p] <- exp(delta.c[p])/exp(delta.c[1])
  }
  for(i in 1:toyear){
     gamma.c[i] ~ dnorm(0,prec.gamma.c)
     risk.year[i] <- exp(gamma.c[i])
  }
  for(i in 2:toyear){
     rr.year[i] <- exp(gamma.c[i])/exp(gamma.c[1])
  }
  for(i in 2:togroup){
   rr.group[i] <- exp(phi[i])/exp(phi[1])
  }

  beta.c~dnorm(0,0.1)
  prec.gamma.c ~ dgamma(2,0.01)
```

```
sigma.gamma.c <- 1/prec.gamma.c
prec.gamma ~ dgamma(2,0.01)
sigma.gamma <- 1/prec.gamma
prec.delta.c ~ dgamma(2,0.01)
sigma.delta.c <- 1/prec.delta.c
prec.group ~ dgamma(2,0.01)
sigma.group<- 1/prec.group

b.beds ~ dnorm(0,0.1)
b.typeB ~ dnorm(0,0.1)
b.typeC ~ dnorm(0,0.1)

rr.beds <- exp(b.beds)
rr.typeB <- exp(b.typeB)
rr.typeC <- exp(b.typeC)
```

Table S1. Healthcare-associated Bloodstream Infection Cases, Patient-days and Pooled Incidence Rates for Each BACTOT Surveillance Year, Including Hospitals With no Cases.

Surveillance year	1	2	3	4	5	6	7	8	9	10	Overall
Hospitals	79	79	79	67	56	53	51	51	46	40	79
Cases	2169	2248	2038	1942	1788	1563	1479	1356	1323	1275	17181
Patient-days	4210728	4242444	4197734	3618735	3258880	2986131	2762369	2738324	2506465	2278894	32800704
Pooled Incidence Rate (95% CI)	5.15 (4.94-5.37)	5.30 (5.08-5.52)	4.86 (4.65-5.07)	5.37 (5.13-5.61)	5.49 (5.24-5.75)	5.23 (4.98-5.5)	5.35 (5.09-5.63)	4.95 (4.7-5.22)	5.28 (5.00-5.57)	5.59 (5.30-5.91)	5.24 (5.16-5.32)

95% CI; 95% confidence interval

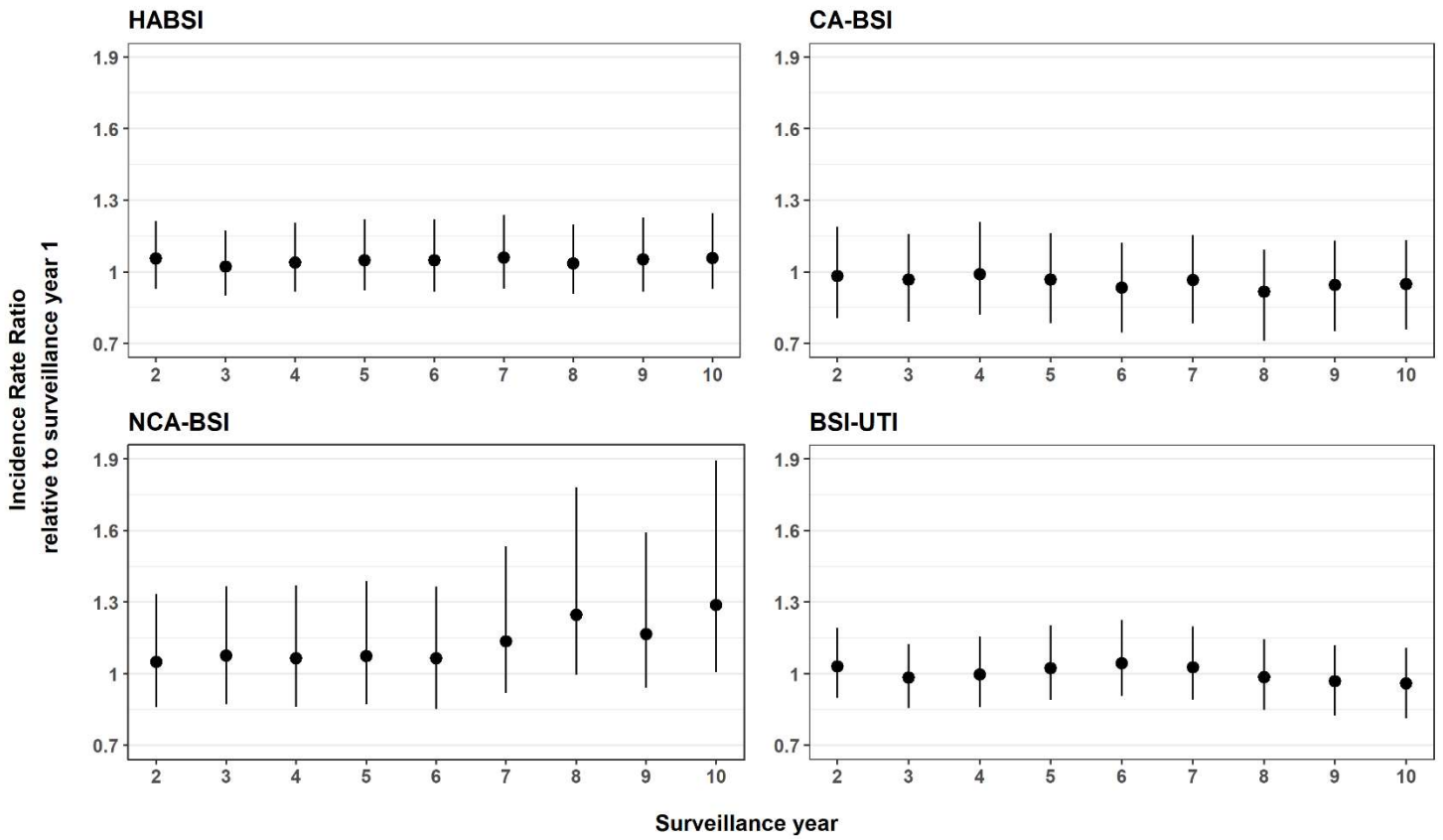

Figure S1. Posterior summaries of the incidence rate ratios of healthcare-associated bloodstream infections and its most frequent subtypes in surveillance years 2-10 relative to surveillance year 1, from all included hospitals. Dots represent the mean and the lines represent the 95% credible interval. HABSI; Healthcare-associated bloodstream infection, CA-BSI; catheter-associated bloodstream

infection, NCA-BSI; non-catheter associated primary bloodstream infection, BSI-UTI; bloodstream infection secondary to a urinary tract infection.

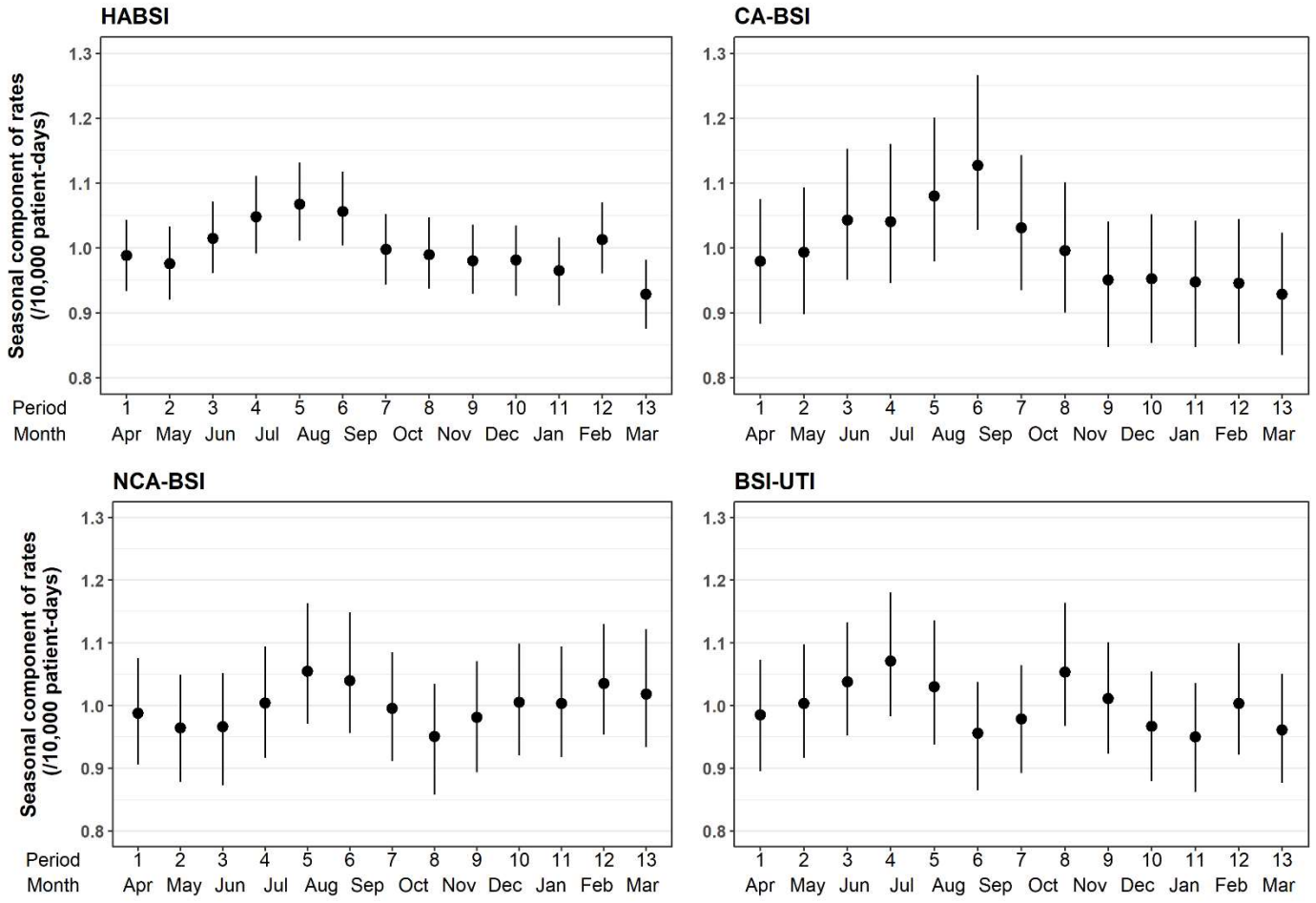

Figure S2. Posterior summaries of the period component of healthcare-associated bloodstream infections and its most frequent subtypes incidence rates from all included hospitals. Dots represent the mean and the lines represent the 95% credible interval. HABSI; Healthcare-associated bloodstream infection, CA-BSI; catheter-associated bloodstream infection, NCA-BSI; non-catheter associated primary bloodstream infection, BSI-UTI; bloodstream infection secondary to a urinary tract infection.