Supplement to: Multiple imputation of missing covariates when using the Fine–Gray model

E. F. Bonneville[1], J. Beyersmann[2], R. H. Keogh[3], J. W. Bartlett[3], T. P. Morris[4], N. Polverelli[5], L. C. de Wreede[1,6,*], and H. Putter[1,7,*]

[1]Department of Biomedical Data Sciences, Leiden University Medical Center, the Netherlands
[2]Institute of Statistics, Ulm University, Germany
[3]Department of Medical Statistics, London School of Hygiene and Tropical Medicine, United Kingdom
[4]MRC Clinical Trials Unit at UCL, United Kingdom
[5]Unit of Bone Marrow Transplantation, Division of Hematology, Fondazione IRCCS Policlinico San Matteo di Pavia, Italy
[6]DKMS Clinical Trials Unit, Germany
[7]Mathematical Institute, Leiden University, the Netherlands
[*]Shared senior authorship

S1 Minimal code example

This is the minimal `R` code companion to section 3.4 of main manuscript. The parameters from the simulation study scenario with $p = 0.15$, random censoring, and correctly specified Fine–Gray were used to generate the example dataset below.

```
# Load libraries
library(data.table)
library(survival)
library(kmi)
library(mice)
library(smcfcs)

# Minimal dataset
head(dat, n = 10)
```

```
   id     time D    X      Z
1   1 0.491195 0    1  0.126
2   2 0.028680 2 <NA>  1.266
3   3 0.910797 0    0 -1.571
4   4 0.217566 2    1 -0.500
5   5 0.132420 2    0  0.781
6   6 0.800913 2    0 -0.434
7   7 0.041653 2 <NA> -0.844
8   8 0.036202 1 <NA>  1.564
9   9 0.046798 0    0 -1.653
10 10 0.997413 0 <NA> -1.196
```

```
sapply(dat, class)
```

```
       id      time         D         X         Z
"integer" "numeric"  "factor"  "factor" "numeric"
```

```
nrow(dat)
```

```
[1] 2000
```

1. Add columns $\hat{H}_1(T)$ and $\hat{H}_2(T)$ to the original data, which are the marginal cause-specific cumulative hazards for each competing risk evaluated at an individual's event or censoring time (obtained

using the Nelson–Aalen estimator).

```
# Add cause-specific event indicators + cumulative hazards
dat$D1 <- as.numeric(dat$D == 1)
dat$D2 <- as.numeric(dat$D == 2)
dat$H1 <- mice::nelsonaalen(data = dat, timevar = "time", statusvar = "D1")
dat$H2 <- mice::nelsonaalen(data = dat, timevar = "time", statusvar = "D2")
```

2. Multiply impute the potential censoring for those failing from cause 2 using {kmi}, yielding m censoring complete datasets (i.e. with "complete" V). Any completely observed covariates that are known to affect the probability of being censored should be included as predictors in the model for the censoring process. {kmi} imputes based on stratified Kaplan–Meier when Z are categorical, and based on a Cox model when at least one of Z are continuous.

```
# Multiply impute the censoring times
cens_imps <- kmi(
  formula = Surv(time, D != 0) ~ 1, # Additional predictors added here
  data = dat,
  etype = D,
  failcode = 1, # Specify event of interest
  nimp = 5
)
```

3. In each censoring complete dataset, add an additional column $\hat{\Lambda}_1(V)$. This takes the value of the marginal cumulative subdistribution hazard for cause 1 at an individual's observed or imputed subdistribution time, obtained with the Nelson–Aalen estimator based on $I(D = 1)$ and imputed V.

```
# Preparation for covariate imputation:
list_to_impute <- lapply(cens_imps$imputed.data, function(imp_dat) {

  # Adjust to new ordering from kmi (cause 2 individuals appended at bottom)
  dat_to_impute <- cbind(cens_imps$original.data, imp_dat)

  # Compute/add Lambda_1(V) in each imputed dataset
  dat_to_impute$Lambda1 <- mice::nelsonaalen(
    data = dat_to_impute,
    timevar = "newtimes", # kmi naming for V
    statusvar = "D1" # I(D=1)
  )
  return(dat_to_impute)
})

# newevent is equal to I(D=1)
head(list_to_impute[[1]])
```

```
   id     time D    X      Z D1 D2         H1         H2 newtimes newevent
1   1 0.491195 0    1  0.126  0  0 0.16736459 0.55436927 0.491195        0
3   3 0.910797 0    0 -1.571  0  0 0.25761243 0.83833716 0.910797        0
8   8 0.036202 1 <NA>  1.564  1  0 0.02028935 0.09603222 0.036202        1
9   9 0.046798 0    0 -1.653  0  0 0.02606228 0.10990397 0.046798        0
10 10 0.997413 0 <NA> -1.196  0  0 0.27549886 0.87116320 0.997413        0
12 12 0.056015 0 <NA>  0.058  0  0 0.02903112 0.12350351 0.056015        0
      Lambda1
1  0.12385222
3  0.16659793
8  0.01932257
9  0.02452308
10 0.17340532
12 0.02715245
```

4. In each censoring complete dataset (each with different V and $\hat{\Lambda}_1(V)$, but same $\hat{H}_1(T)$ and $\hat{H}_2(T)$), create a single imputed dataset using the desired covariate imputation method(s).

```
# Prepare predictor matrices for MICE using the first censoring complete dataset
predmat_cs_approx <- predmat_fg_approx <- mice::make.predictorMatrix(list_to_impute[[1]])
predmat_cs_approx[] <- predmat_fg_approx[] <- 0
predmat_cs_approx["X", c("Z", "D1", "D2", "H1", "H2")] <- 1
predmat_fg_approx["X", c("Z", "D1", "Lambda1")] <- 1
predmat_fg_approx
```

```
          id time D X Z D1 D2 H1 H2 newtimes newevent Lambda1
id         0    0 0 0 0  0  0  0  0        0        0       0
time       0    0 0 0 0  0  0  0  0        0        0       0
D          0    0 0 0 0  0  0  0  0        0        0       0
X          0    0 0 0 1  1  0  0  0        0        0       1
Z          0    0 0 0 0  0  0  0  0        0        0       0
D1         0    0 0 0 0  0  0  0  0        0        0       0
D2         0    0 0 0 0  0  0  0  0        0        0       0
H1         0    0 0 0 0  0  0  0  0        0        0       0
H2         0    0 0 0 0  0  0  0  0        0        0       0
newtimes   0    0 0 0 0  0  0  0  0        0        0       0
newevent   0    0 0 0 0  0  0  0  0        0        0       0
Lambda1    0    0 0 0 0  0  0  0  0        0        0       0
```

```
# Prepare the methods:
# - Approx methods: model type for X | Z, outcome
methods_approx <- mice::make.method(list_to_impute[[1]])
# - SMC methods: proposal model for X | Z (need to use {smcfcs} naming)
methods_smcfcs <- mice::make.method(
  list_to_impute[[1]],
  defaultMethod = c("norm", "logreg", "mlogit", "podds")
)
methods_smcfcs
```

```
      id     time        D        X        Z       D1       D2       H1
      ""       ""       "" "logreg"       ""       ""       ""       ""
      H2 newtimes newevent  Lambda1
      ""       ""       ""       ""
```

```
# Impute X
# (parallelize this loop for speed improvements on larger data)
list_imps <- lapply(list_to_impute, function(imp_dat) {

  m <- 1
  iters <- 10

  imps_cs_approx <- mice(
    data = imp_dat,
    m = m,
    maxit = iters,
    method = methods_approx,
    predictorMatrix = predmat_cs_approx
  )

  imps_fg_approx <- mice(
    data = imp_dat,
    m = m,
    maxit = iters,
    method = methods_approx,
    predictorMatrix = predmat_fg_approx
```

```
  )

  imps_cs_smc <- smcfcs(
    originaldata = imp_dat,
    smtype = "compet",
    smformula = list(
      "Surv(time, D == 1) ~ X + Z",
      "Surv(time, D == 2) ~ X + Z"
    ),
    method = methods_smcfcs,
    m = m,
    numit = iters
  )

  imps_fg_smc <- smcfcs(
    originaldata = imp_dat,
    smtype = "coxph",
    smformula = "Surv(newtimes, D1) ~ X + Z",
    method = methods_smcfcs,
    m = m,
    numit = iters
  )

  # Bring all the imputed datasets together
  imps <- rbind.data.frame(
    cbind(method = "CCA", imp_dat),
    cbind(method = "cs_smc", imps_cs_smc$impDatasets[[1]]),
    cbind(method = "cs_approx", complete(imps_cs_approx, action = 1L)),
    cbind(method = "fg_smc", imps_fg_smc$impDatasets[[1]]),
    cbind(method = "fg_approx", complete(imps_cs_approx, action = 1L))
  )
  return(imps)
})
```

5. Fit the Fine–Gray substantive model in each imputed dataset (using standard Cox software with $I(D = 1)$ and imputed V as outcome variables), and pool the estimates using Rubin's rules.

```
# Bind everything together
dat_imps <- rbindlist(list_imps, idcol = ".imp")
dat_imps
```

```
       .imp    method   id     time D    X       Z D1 D2         H1         H2
    1:    1       CCA    1 0.491195 0    1   0.126  0  0 0.16736459 0.55436927
    2:    1       CCA    3 0.910797 0    0 -1.571  0  0 0.25761243 0.83833716
    3:    1       CCA    8 0.036202 1 <NA>  1.564  1  0 0.02028935 0.09603222
    4:    1       CCA    9 0.046798 0    0 -1.653  0  0 0.02606228 0.10990397
    5:    1       CCA   10 0.997413 0 <NA> -1.196  0  0 0.27549886 0.87116320
   ---
49996:    5 fg_approx 1992 0.319702 2    0 -2.670  0  1 0.12370372 0.43826433
49997:    5 fg_approx 1993 0.229071 2    0 -0.243  0  1 0.09740419 0.35023923
49998:    5 fg_approx 1994 1.836303 2    1 -0.366  0  1 0.47538639 1.23075745
49999:    5 fg_approx 1997 0.702380 2    0  0.283  0  1 0.21877205 0.71087168
50000:    5 fg_approx 1999 0.023554 2    1  1.377  0  1 0.01356742 0.06584427
       newtimes newevent    Lambda1
    1: 0.491195        0 0.12385222
    2: 0.910797        0 0.16659793
    3: 0.036202        1 0.01932257
    4: 0.046798        0 0.02452308
    5: 0.997413        0 0.17340532
```

```
   ---
49996: 0.957205        0 0.17116627
49997: 0.453168        0 0.12098105
49998: 2.841599        0 0.25988878
49999: 1.170590        0 0.19454317
50000: 2.997529        0 0.26284736
```

```
# To use the usual workflow: subset one of the methods first
imps_fg_smc <- dat_imps[method == "fg_smc"]

# Fit model in each imputed dataset
mods_fg_smc <- lapply(
  X = split(x = imps_fg_smc, f = imps_fg_smc$.imp),
  FUN = function(imp_dat) coxph(Surv(newtimes, D1) ~ X + Z, data = imp_dat)
)

# Pool results
summary(pool(mods_fg_smc))
```

```
  term  estimate  std.error statistic         df      p.value
1   X1 0.7768682 0.21722362  3.576352   9.883541 5.136286e-03
2    Z 0.4920664 0.06519244  7.547906 105.385333 1.659276e-11
```

```
# Otherwise: use (nested) data.table workflow to pool for all methods simultaneously
dat_mods <- dat_imps[, .(
  mod = list(coxph(Surv(newtimes, D1) ~ X + Z, data = .SD))
), by = c("method", ".imp")]
dat_mods
```

```
       method .imp         mod
 1:       CCA    1 <coxph[22]>
 2:    cs_smc    1 <coxph[21]>
 3: cs_approx    1 <coxph[21]>
 4:    fg_smc    1 <coxph[21]>
 5: fg_approx    1 <coxph[21]>
 6:       CCA    2 <coxph[22]>
 7:    cs_smc    2 <coxph[21]>
 8: cs_approx    2 <coxph[21]>
 9:    fg_smc    2 <coxph[21]>
10: fg_approx    2 <coxph[21]>
11:       CCA    3 <coxph[22]>
12:    cs_smc    3 <coxph[21]>
13: cs_approx    3 <coxph[21]>
14:    fg_smc    3 <coxph[21]>
15: fg_approx    3 <coxph[21]>
16:       CCA    4 <coxph[22]>
17:    cs_smc    4 <coxph[21]>
18: cs_approx    4 <coxph[21]>
19:    fg_smc    4 <coxph[21]>
20: fg_approx    4 <coxph[21]>
21:       CCA    5 <coxph[22]>
22:    cs_smc    5 <coxph[21]>
23: cs_approx    5 <coxph[21]>
24:    fg_smc    5 <coxph[21]>
25: fg_approx    5 <coxph[21]>
       method .imp         mod
```

```
dat_mods[, summary(pool(as.list(mod))), by = "method"]
```

```
       method term  estimate  std.error statistic         df      p.value
```

```
 1:       CCA   X1 0.7781281 0.17916465  4.343089 152.067624 2.554742e-05
 2:       CCA    Z 0.4003856 0.10186017  3.930737 145.744472 1.304356e-04
 3:    cs_smc   X1 0.6980657 0.18538543  3.765483  14.973349 1.875994e-03
 4:    cs_smc    Z 0.5079436 0.06538007  7.769090  93.531830 9.965454e-12
 5: cs_approx   X1 0.6092265 0.19461615  3.130400  12.205414 8.525728e-03
 6: cs_approx    Z 0.5225790 0.06779656  7.708046  58.618467 1.775328e-10
 7:    fg_smc   X1 0.7768682 0.21722362  3.576352   9.883541 5.136286e-03
 8:    fg_smc    Z 0.4920664 0.06519244  7.547906 105.385333 1.659276e-11
 9: fg_approx   X1 0.6092265 0.19461615  3.130400  12.205414 8.525728e-03
10: fg_approx    Z 0.5225790 0.06779656  7.708046  58.618467 1.775328e-10
```

S2 Applied data example

S2.1 Data dictionary

Table 1: Data dictionary. CMV: cytomegalovirus; HLA: human leukocyte antigen; HCT-CI: Hematopoietic stem cell transplantation-comorbidity index; MF: myelofibrosis.

Characteristic	N = 3,982
Patient age (years)	58 (52, 64)
Patient/donor CMV match	
Patient negative/Donor negative	1,142 (30%)
Other	2,715 (70%)
(Missing)	125
Donor type	
HLA identical sibling	1,183 (30%)
Other	2,795 (70%)
(Missing)	4
Hemoglobin (g/dL)	9.10 (8.10, 10.40)
(Missing)	1,873
HCT-CI risk category	
Low risk (0)	1,674 (54%)
Intermediate risk $(1-2)$	743 (24%)
High risk (≥ 3)	674 (22%)
(Missing)	891
Interval diagnosis-transplantation (years)	3 (1, 9)
Karnosfky performance score	
≥ 90	2,475 (66%)
80	986 (26%)
≤ 70	267 (7.2%)
(Missing)	254
Patient sex	
Female	1,484 (37%)
Male	2,498 (63%)
Peripheral blood (PB) blasts (%)	1.0 (0.0, 3.0)
(Missing)	2,323
Conditioning	
Standard	1,373 (35%)
Reduced	2,553 (65%)
(Missing)	56
Ruxolitinib given	
No	1,832 (66%)
Yes	931 (34%)
(Missing)	1,219
Disease subclassification	
Primary MF	2,912 (73%)
Secondary MF	1,070 (27%)
Night sweats	
No	1,256 (70%)
Yes	529 (30%)
(Missing)	2,197
T-cell depletion (in- or ev-vivo)	
No	1,012 (26%)
Yes	2,905 (74%)
(Missing)	65
Cytogenetics	
Normal	1,318 (59%)
Abnormal	910 (41%)
(Missing)	1,754

White blood cell count (WBC, x10^9/L)	7 (4, 14)
(Missing)	1,884
>10% Weight loss prior to transplantation	
No	1,329 (73%)
Yes	492 (27%)
(Missing)	2,161
Year of transplantation	2,015.0 (2,012.0, 2,018.0)

[1] Median (IQR); n (%)

S2.2 Non-parametric cumulative incidence curves

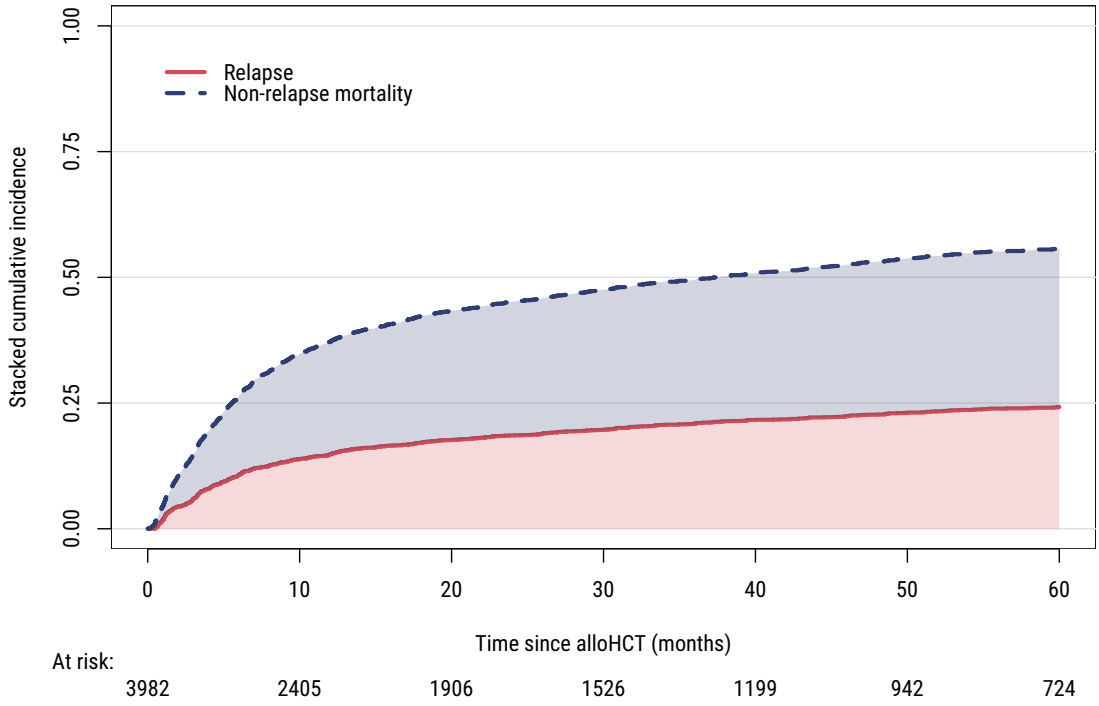

Figure 1: Stacked non-parametric cumulative incidence curves for competing relapse and non-relapse mortality, in dataset of 3982 primary and secondary myelofibrosis patients.

S2.3 Pooled regression coefficeints

Table 2: Pooled log hazard ratios [log HR, 95% confidence interval] for Fine–Gray model for relapse, cause-specific Cox model relapse, and cause-specific Cox model for non-relapse mortality (NRM).

Term + method	Relapse subdist. log HR	Relapse cause-spec. log HR	NRM cause-spec. log HR
Conditioning: reduced			
CCA	0.02 [-0.33, 0.36]	0.01 [-0.33, 0.35]	0 [-0.29, 0.28]
CS-SMC	0.13 [-0.02, 0.28]	0.1 [-0.05, 0.25]	-0.05 [-0.18, 0.07]
CS-Approx	0.13 [-0.02, 0.28]	0.1 [-0.05, 0.25]	-0.05 [-0.18, 0.07]
FG-SMC	0.13 [-0.02, 0.28]	0.1 [-0.05, 0.25]	-0.06 [-0.18, 0.07]

(continued ...)

Table 2: *(continued)*

Term + method	Relapse subdist. log HR	Relapse cause-spec. log HR	NRM cause-spec. log HR
FG-Approx	0.13 [-0.03, 0.28]	0.1 [-0.06, 0.25]	-0.05 [-0.18, 0.07]
CMV match: other			
CCA	0.04 [-0.31, 0.4]	0.05 [-0.3, 0.41]	0.09 [-0.19, 0.37]
CS-SMC	-0.1 [-0.26, 0.05]	-0.05 [-0.2, 0.11]	0.22 [0.08, 0.36]
CS-Approx	-0.1 [-0.26, 0.05]	-0.05 [-0.2, 0.11]	0.22 [0.08, 0.36]
FG-SMC	-0.1 [-0.26, 0.05]	-0.04 [-0.2, 0.11]	0.22 [0.08, 0.36]
FG-Approx	-0.11 [-0.26, 0.05]	-0.05 [-0.2, 0.11]	0.22 [0.08, 0.35]
Cytogenetics: abnormal			
CCA	0.36 [0.04, 0.68]	0.37 [0.05, 0.68]	-0.08 [-0.35, 0.19]
CS-SMC	0.35 [0.15, 0.54]	0.35 [0.16, 0.54]	-0.07 [-0.23, 0.1]
CS-Approx	0.36 [0.17, 0.55]	0.35 [0.16, 0.54]	-0.08 [-0.25, 0.08]
FG-SMC	0.36 [0.17, 0.55]	0.36 [0.17, 0.54]	-0.06 [-0.21, 0.08]
FG-Approx	0.34 [0.17, 0.52]	0.34 [0.17, 0.51]	-0.07 [-0.22, 0.08]
Donor relation: other			
CCA	0.12 [-0.28, 0.52]	0.2 [-0.2, 0.6]	0.53 [0.18, 0.88]
CS-SMC	-0.26 [-0.41, -0.1]	-0.19 [-0.34, -0.03]	0.35 [0.21, 0.5]
CS-Approx	-0.25 [-0.41, -0.1]	-0.18 [-0.34, -0.02]	0.36 [0.21, 0.5]
FG-SMC	-0.26 [-0.41, -0.1]	-0.19 [-0.34, -0.03]	0.35 [0.2, 0.49]
FG-Approx	-0.26 [-0.41, -0.1]	-0.19 [-0.34, -0.03]	0.35 [0.2, 0.49]
Hemoglobin (per 5 g/dL)			
CCA	-0.38 [-0.85, 0.09]	-0.39 [-0.85, 0.08]	-0.12 [-0.49, 0.25]
CS-SMC	-0.24 [-0.51, 0.03]	-0.3 [-0.58, -0.03]	-0.19 [-0.42, 0.04]
CS-Approx	-0.25 [-0.53, 0.02]	-0.32 [-0.59, -0.06]	-0.19 [-0.41, 0.02]
FG-SMC	-0.25 [-0.51, 0.02]	-0.29 [-0.56, -0.02]	-0.08 [-0.28, 0.11]
FG-Approx	-0.23 [-0.5, 0.04]	-0.27 [-0.54, 0]	-0.09 [-0.29, 0.11]
HCT-CI $(1-2)$			
CCA	-0.15 [-0.53, 0.22]	-0.04 [-0.42, 0.33]	0.38 [0.08, 0.69]
CS-SMC	-0.22 [-0.42, -0.01]	-0.17 [-0.37, 0.03]	0.15 [-0.02, 0.31]
CS-Approx	-0.19 [-0.38, 0.01]	-0.14 [-0.34, 0.06]	0.15 [-0.01, 0.31]
FG-SMC	-0.22 [-0.42, -0.01]	-0.18 [-0.38, 0.02]	0.12 [-0.04, 0.28]
FG-Approx	-0.19 [-0.38, 0.01]	-0.15 [-0.35, 0.04]	0.11 [-0.05, 0.27]
HCT-CI (≥ 3)			
CCA	-0.27 [-0.7, 0.16]	-0.19 [-0.62, 0.23]	0.4 [0.07, 0.73]
CS-SMC	-0.07 [-0.28, 0.14]	-0.01 [-0.21, 0.2]	0.27 [0.1, 0.44]
CS-Approx	-0.08 [-0.28, 0.13]	-0.02 [-0.22, 0.18]	0.26 [0.1, 0.43]
FG-SMC	-0.06 [-0.27, 0.14]	-0.02 [-0.22, 0.19]	0.21 [0.05, 0.37]
FG-Approx	-0.08 [-0.28, 0.11]	-0.04 [-0.23, 0.16]	0.21 [0.05, 0.38]
Interval diagnosis to alloHCT (decades)			
CCA	0.01 [-0.24, 0.26]	0 [-0.25, 0.26]	-0.03 [-0.25, 0.19]
CS-SMC	-0.02 [-0.14, 0.09]	-0.02 [-0.14, 0.1]	0.05 [-0.05, 0.15]
CS-Approx	-0.03 [-0.14, 0.09]	-0.02 [-0.14, 0.1]	0.05 [-0.05, 0.15]
FG-SMC	-0.02 [-0.14, 0.09]	-0.02 [-0.13, 0.1]	0.05 [-0.05, 0.15]
FG-Approx	-0.02 [-0.14, 0.09]	-0.02 [-0.14, 0.1]	0.05 [-0.05, 0.15]
Karnofsky (80)			
CCA	-0.09 [-0.48, 0.31]	-0.08 [-0.48, 0.31]	0.04 [-0.27, 0.34]
CS-SMC	0.07 [-0.1, 0.24]	0.12 [-0.05, 0.28]	0.17 [0.03, 0.31]
CS-Approx	0.06 [-0.1, 0.23]	0.1 [-0.06, 0.27]	0.15 [0.01, 0.29]
FG-SMC	0.07 [-0.09, 0.24]	0.12 [-0.05, 0.29]	0.17 [0.03, 0.31]
FG-Approx	0.07 [-0.1, 0.24]	0.12 [-0.06, 0.29]	0.17 [0.03, 0.31]
Karnofsky (≤ 70)			
CCA	0.63 [0.15, 1.11]	0.79 [0.3, 1.28]	0.33 [-0.13, 0.79]
CS-SMC	0.44 [0.19, 0.69]	0.55 [0.3, 0.81]	0.31 [0.08, 0.53]
CS-Approx	0.42 [0.17, 0.67]	0.51 [0.26, 0.76]	0.26 [0.04, 0.49]
FG-SMC	0.44 [0.19, 0.7]	0.55 [0.29, 0.81]	0.32 [0.09, 0.54]
FG-Approx	0.43 [0.17, 0.68]	0.53 [0.28, 0.78]	0.31 [0.08, 0.53]
Disease subclassification: secondary MF			

(continued …)

Table 2: *(continued)*

Term + method	Relapse subdist. log HR	Relapse cause-spec. log HR	NRM cause-spec. log HR
CCA	-0.05 [-0.45, 0.35]	-0.02 [-0.42, 0.38]	0.07 [-0.27, 0.41]
CS-SMC	0.01 [-0.17, 0.19]	0.01 [-0.17, 0.19]	0 [-0.16, 0.15]
CS-Approx	0 [-0.18, 0.18]	0 [-0.18, 0.19]	0 [-0.16, 0.15]
FG-SMC	0 [-0.18, 0.18]	0 [-0.18, 0.18]	-0.01 [-0.16, 0.15]
FG-Approx	0 [-0.18, 0.18]	0 [-0.18, 0.18]	-0.01 [-0.16, 0.15]
Night sweats: yes			
CCA	-0.33 [-0.7, 0.04]	-0.4 [-0.77, -0.02]	-0.02 [-0.32, 0.27]
CS-SMC	-0.18 [-0.41, 0.05]	-0.2 [-0.44, 0.03]	-0.02 [-0.23, 0.19]
CS-Approx	-0.12 [-0.36, 0.13]	-0.14 [-0.38, 0.1]	0.03 [-0.19, 0.24]
FG-SMC	-0.17 [-0.4, 0.07]	-0.18 [-0.41, 0.05]	0.01 [-0.16, 0.19]
FG-Approx	-0.16 [-0.4, 0.07]	-0.18 [-0.42, 0.05]	0 [-0.17, 0.18]
Patient age (decades)			
CCA	0.1 [-0.09, 0.28]	0.13 [-0.06, 0.32]	0.13 [-0.02, 0.28]
CS-SMC	-0.03 [-0.12, 0.05]	0.01 [-0.08, 0.09]	0.21 [0.14, 0.29]
CS-Approx	-0.03 [-0.12, 0.05]	0.01 [-0.08, 0.09]	0.21 [0.14, 0.29]
FG-SMC	-0.04 [-0.12, 0.05]	0.01 [-0.08, 0.09]	0.22 [0.15, 0.3]
FG-Approx	-0.03 [-0.12, 0.05]	0.01 [-0.08, 0.09]	0.22 [0.15, 0.3]
Patient sex: male			
CCA	-0.24 [-0.56, 0.09]	-0.18 [-0.51, 0.15]	0.39 [0.11, 0.68]
CS-SMC	-0.1 [-0.24, 0.05]	-0.06 [-0.21, 0.09]	0.18 [0.05, 0.31]
CS-Approx	-0.1 [-0.24, 0.05]	-0.06 [-0.21, 0.09]	0.18 [0.05, 0.31]
FG-SMC	-0.09 [-0.24, 0.05]	-0.06 [-0.2, 0.09]	0.18 [0.05, 0.31]
FG-Approx	-0.1 [-0.24, 0.05]	-0.06 [-0.21, 0.08]	0.18 [0.05, 0.31]
PB Blasts (per 5%)			
CCA	0.16 [-0.04, 0.36]	0.17 [-0.02, 0.37]	0 [-0.18, 0.18]
CS-SMC	0.18 [0.05, 0.31]	0.18 [0.05, 0.31]	0.01 [-0.12, 0.13]
CS-Approx	0.19 [0.07, 0.31]	0.19 [0.07, 0.32]	0.01 [-0.12, 0.13]
FG-SMC	0.17 [0.04, 0.3]	0.17 [0.05, 0.3]	-0.01 [-0.12, 0.1]
FG-Approx	0.18 [0.05, 0.32]	0.18 [0.05, 0.31]	-0.02 [-0.12, 0.09]
Ruxolitinib given: yes			
CCA	0.08 [-0.26, 0.43]	0.08 [-0.26, 0.43]	-0.05 [-0.33, 0.23]
CS-SMC	-0.02 [-0.2, 0.17]	-0.03 [-0.22, 0.16]	-0.06 [-0.21, 0.1]
CS-Approx	0.01 [-0.19, 0.2]	-0.01 [-0.2, 0.18]	-0.05 [-0.21, 0.11]
FG-SMC	-0.02 [-0.21, 0.17]	-0.03 [-0.22, 0.16]	-0.04 [-0.19, 0.11]
FG-Approx	0 [-0.19, 0.18]	-0.01 [-0.2, 0.17]	-0.04 [-0.19, 0.11]
T-cell depletion: yes			
CCA	0.2 [-0.21, 0.62]	0.16 [-0.25, 0.58]	-0.23 [-0.54, 0.08]
CS-SMC	0.3 [0.13, 0.48]	0.26 [0.09, 0.44]	-0.18 [-0.32, -0.04]
CS-Approx	0.3 [0.12, 0.48]	0.26 [0.08, 0.43]	-0.19 [-0.33, -0.05]
FG-SMC	0.31 [0.13, 0.48]	0.26 [0.09, 0.44]	-0.18 [-0.31, -0.04]
FG-Approx	0.31 [0.13, 0.48]	0.26 [0.09, 0.44]	-0.18 [-0.32, -0.04]
WBC count (log)			
CCA	0.17 [0.02, 0.33]	0.17 [0.01, 0.33]	0.02 [-0.12, 0.15]
CS-SMC	0.17 [0.09, 0.26]	0.18 [0.09, 0.27]	0 [-0.07, 0.07]
CS-Approx	0.17 [0.08, 0.26]	0.17 [0.09, 0.26]	0 [-0.08, 0.07]
FG-SMC	0.17 [0.09, 0.26]	0.18 [0.09, 0.26]	-0.01 [-0.07, 0.05]
FG-Approx	0.17 [0.1, 0.25]	0.18 [0.1, 0.26]	-0.01 [-0.08, 0.05]
Weight loss: yes			
CCA	0 [-0.37, 0.38]	0.05 [-0.33, 0.43]	0.17 [-0.13, 0.48]
CS-SMC	0.23 [-0.03, 0.49]	0.27 [0.01, 0.53]	0.16 [-0.05, 0.36]
CS-Approx	0.24 [0, 0.47]	0.28 [0.04, 0.51]	0.16 [-0.05, 0.36]
FG-SMC	0.23 [-0.01, 0.47]	0.24 [0.01, 0.48]	0.06 [-0.12, 0.24]
FG-Approx	0.24 [0, 0.48]	0.26 [0.02, 0.49]	0.06 [-0.14, 0.26]
Year of alloHCT (decades)			
CCA	-0.36 [-0.99, 0.26]	-0.41 [-1.04, 0.23]	-0.15 [-0.67, 0.37]
CS-SMC	-0.08 [-0.34, 0.18]	-0.11 [-0.37, 0.15]	-0.24 [-0.46, -0.02]

(continued …)

Table 2: *(continued)*

Term + method	Relapse subdist. log HR	Relapse cause-spec. log HR	NRM cause-spec. log HR
CS-Approx	-0.09 [-0.35, 0.17]	-0.12 [-0.38, 0.14]	-0.24 [-0.46, -0.02]
FG-SMC	-0.08 [-0.34, 0.17]	-0.12 [-0.37, 0.14]	-0.24 [-0.46, -0.03]
FG-Approx	-0.08 [-0.34, 0.17]	-0.11 [-0.37, 0.14]	-0.24 [-0.46, -0.03]