Primary / Secondary Analysis

Analysis Plan

The primary analysis was a hospital-level analysis. All hospitals had observations on the baseline period and on the intervention period. There are two types of outcome variables:

- those for which a patient can experience once, such as *Hospital Mortality* (binary)
- those for which a patient can experience more than once, such as *Clinical Deterioration Events* (count).

For each outcome a 'numerator' and a 'denominator' was identified. For a binary outcome, the numerator was the number of events in a hospital during a particular period (baseline or intervention), and the denominator was the number of discharges. For a count outcome the numerator was the number of events in a hospital during a particular period, and the denominator was the number of patient-days. See following table for variable and macro names.

Generalized estimating equations (GEE) methods were used to account for clustering by hospital, with an exchangeable correlation structure.

Binary outcomes:

For a binary outcome, a GEE binomial model was used. There were two separate analyses, both using the number of events (x) and the number of discharges (n):

- a logit link was used, so that the log-odds of the outcome was modelled as a function of the predictors
- an identify link was used, so that the probability of the outcome was modelled as a function of the predictors

The predictor variables were:

- (1) the treatment dummy indicator and
- (2) the corresponding summary statistic (log odds or probability) for that hospital during the baseline period.

R code for GEE model of binary outcomes at the group level

```
37
```

```
# load geepack library
# n is the number of discharges at a hospital
# x is the number of events at that hospital in the post-
# randomization period
# Hospital is the categorical variable indicating which hospital
# the above numbers come from
# logitBaseline logit of baseline probability for this hospital,
```

```
45
        calculated with addition of 0.5 to numerator and 1 to
46
        denominator if x = 0
47
    # probBaseline baseline probability for this hospital,
48
49
50
51
    #model for log-odds of outcome at the group level
52
53
    GEEfit.OR <- geeglm(cbind(x, n-x)~Intervention + logitBaseline,
54
                                id = Hospital,
55
                                family = binomial,
56
                                data=EPOCH,
57
                                corstr = "exchangeable")
58
59
60
    # model for probability of outcome at the group level
61
62
    GEEfit.RD <- geeglm(cbind(x, n-x)~Intervention + probBaseline,
63
                        id = Hospital,
64
                        family =binomial(link=make.link("identity")),
65
                        data=EPOCH,
66
                        corstr = "exchangeable")
67
68
69
    # model for probability of outcome at the indovidual level
70
71
    \# y = 1 for outcome, 0 for no outcome
72
73
    GEEfit.RD <- geeglm(y~Intervention + probBaseline,</pre>
74
                         id = Hospital,
75
                        family =binomial(link=make.link("identity")),
76
                        data=EPOCH,
77
                        corstr = "exchangeable")
78
```

Count outcomes:

For a count outcome, a GEE Poisson model was used. There were two separate analyses, both using the number of events (x) and the number of patient-days (time):

- a log link was used, so that the log-rate was modelled as a function of the predictors
- an identify link was used, so that the rate was modelled as a function of the predictors

Both models included the number of patient days. With the log link, include log(patient days) as the offset. With the identity link, the code below shows how patient days were included

```
90
91
     The predictor variables were
92
           (1) the treatment dummy indicator and
93
           (2) the corresponding summary statistic (log rate or rate) for that hospital during the
94
           baseline period.
95
     See following example R code for details.
96
97
     # Modelling the log-rate
98
     # N is the number of patient days in the post-randomization
99
            period
100
     # x is the number of events in the post-randomization period
101
     # Hospital is the categorical variable indicating which hospital
102
         the above numbers come from
103
     # logBaseline is log of baseline rate for this hospital,
104
         calculated with addition of 0.5 to numerator if x = 0
105
     # Baseline is baseline rate for this hospital
106
107
108
     geefit.RR <- geeglm(x ~offset(log(N)+Intervention + logBaseline,</pre>
109
                           id = Hospital,
110
                            family = poisson,
111
                           data=EPOCH,
112
                           corstr = "exchangeable"))
113
114
     # The linear model needs this rearrangement of the data to
115
     # incorporate the time at risk
116
     # Nlin - its coefficient is the usual care intercept
117
     # NlinG - its coefficient is the rate difference
118
     # NlinB - its coefficient is the increase in the rate per unit
119
           increase of the baseline rate
120
121
     EPOCH$Nlin <- EPOCH$N/1000
122
      EPOCH$GNlin <- EPOCH$N*(d$Group=="BedsidePEWS")</pre>
      EPOCH$$BNlin <- EPOCH$N*(EPOCH$Baseline)</pre>
123
124
125
     # modelling the rate
126
127
      geefit.RD <- geeglm(x~Nlin+GNlin+BNlin-1,</pre>
128
                           id = Hospital,
129
                           family = poisson("identity"),
130
                           data=EPOCH,
131
                            corstr = "exchangeable"))
132
133
     Continuous outcomes at the individual level:
```

EPOCH SAP 3

134

The patient level continuous outcomes in Tables 2 and S4 were also modelled with a GEE, using a Gaussian model. Although the data are not normal at the individual level, the large sample size and the robustness of GEE implies that comparisons of means are largely unaffected by this non-normality.

138 139 140

135

136

137

For an individual-level outcome, these models all had the same structure

141

```
142
     # y is a continuous outcome for a patient
143
     # Hospital is the hospital the patient is in
144
     # x0 is the mean value at baseline for the hospital a
145
     # patient is in
146
147
     geefit.RR <- geeglm(x ~Intervention + x0,</pre>
148
                           id = Hospital,
149
                           data=EPOCH,
150
                           corstr = "exchangeable")
151
```

151

Sensitivity to model choice

153154155

As the results of the analysis of cluster RCTs can vary somewhat with the method of analysis, models for odds ratios, probabilities, and rate ratios were also run using several other approaches

156157158

159

160

161

162

163

164

165166

167168

169

170

171

Logit and log-rate models

- GEE on only post-intervention values
- Generalized linear mixed effects regression model (GLMER) on only post-intervention values
- GEE with both pre and post values as outcomes, estimating interaction between time and intervention
- GLMER with both pre and post values as outcomes, estimating interaction between time and intervention
- GEE on post-intervention values with baseline value as a covariate
- Generalized linear mixed effects regression model (GLMER) on post-intervention values with baseline value as a covariate
- Weighted linear model (weight = 1/(variance of logit) or weight = 1/variance (log-rate))) for logits (or log-rates), with baseline logit (or log-rate)as covariate.
- Quasibinomial logistic or Poisson regression (which allows for more variance than the binomial or Poisson) on post-data, with baseline logit (or log rate) as covariate

172173174

175

176

177

Models for probability or rate

- GEE on only post-intervention values (binomial or Poisson variance, identity link)
- GEE with both pre and post values as outcomes, estimating interaction between time and intervention (binomial or Poisson variance, identity link)

- GEE on post-intervention values with baseline value as a covariate (binomial or Poisson variance, identity link)
 - Weighted linear model for post-probabilities (weight=1/(variance probability) or 1/(variance weight)), with baseline probability or rate as covariate
 - Quasibinomial regression (which allows for more variance than the binomial or Poisson) on post-data, with baseline probability as covariate (binomial or Poisson variance, identity link)

Shell Tables

Continuous outcomes

Resuscitation Team Calls	B_rt/B_PatientDays	P_rt/P_PatientDays	Poisson
Stat Calls	B_sc/B_PatientDays	P_sc/P_PatientDays	Poisson
Urgent ICU Consultations	B_rr/B_PatientDays	P_rr/P_PatientDays	Poisson
Urgent ICU Admissions	B_uicu/B_PatientDays	P_uicu/P_PatientDays	Poisson
Unplanned ICU Readmissions	B_icur/ B_PatientDischargesICU	P_icur/ P_PatientDischargesICU	Poisson
Unplanned Hospital Readmission	B_hr/ B_PatientDischarges	P_hr/ P_PatientDischarges	Poisson

191	
192	Subgroup Analysis Plan
193	
194	Two subgroup analyses are planned using the same methodology described in the previous
195	section. In the first, ECMO, the hospitals will be divided into two groups: those that have ECMO
196	service and those who do not. In the second, MET, the hospitals will be divided into two groups:
197	those that have MET service and those who do not.
198	
199	For each subgroup analysis, the treatment effect (BedsidePEWS vs. usual care) will be estimated
200	in each group of hospitals and the presence of a subgroup effect will be assessed in a single GEE

model with a one-term treatment by subgroup interaction term.

190

201

202

ICU Analysis

203204205

Analysis Plan

206207208

209

210211

This was a patient-level analysis that followed the same general procedures as outlined above. However, the data has a record for each admission to the ICU, and a patient may have more than one admission; the table below shows how these were handled. Furthermore, a few patients had admissions to the same ICU in both study periods; these patients were eliminated from this analysis. The analysis was done with one record per patient as described in the table below.

212213

Outcome	Description of the per patient outcome variable	
Total length of stay	The sum over admissions of the lengths of stay	
Average length of stay	The average over admissions of the lengths of stay	
PIM at admission	The average over admissions of the PIM at admission	
PIM II Prediction Mortality (/1000 urgent ICU discharges) (inverse-logit of <i>PIM</i>)	The average probability over admissions of the PIM II predicted mortality	
Ventilation Free Days	The days free of ventilation for the first admission	
Days of technology use	Sum of all days over all admissions of mechanical ventilation days, nitric oxide days, ECMO days and dialysis days	
Use of a technology (HFOV, ECMO, NO. Dialysis, MV)	Binary indicator of whether the technology was used on any of the days in the ICU.	
24-hour PELOD	The average over admissions of the PELOD score for the first 24 hours	
PELOD ICU Stay	The average over admissions of the PELOD score for the entire admission	

214