Supplementary Online Content

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This supplemental material has been provided by the authors to give readers additional information about their work.

Data Sources

We used administrative claims for Medicare Advantage and commercially insured enrollees in a research database from a single large health insurance provider in the United States.

We also used an inpatient COVID-19 dataset which included a daily updated record of COVID-19 inpatient admissions for all insurance enrollees with claims information, representing those admitted to a hospital with a primary or secondary diagnosis of COVID-19 (eTable 3), along with their current disposition (admitted, discharged, transferred, or expired).

Standardization of data entry and data structure

Medical and pharmacy claims data are captured, predominantly electronically, from sites of care seeking third-party reimbursement for both Medicare and commercial plans using the industry standard data collection forms HCFA/CMS-1500 for facility claims, UB04/CMS-1450 for professional services and outpatient claims, and NCPDP for pharmacy claims or their electronic equivalents. Structured data from these standardized forms are coded using the International Classification of Diseases, Tenth Revision, Clinical Modification (ICD-10-CM), National Drug Codes (NDC), Current Procedural Terminology (CPT) codes, and Logical Observation Identifiers Names and Codes (LOINC) codes, and Diagnosis Related Groups (DRG). This nomenclature ensures consistency of data collection across geographic regions, health systems, and payers throughout the United States.

Methods to Control for Errors in Sampling and Data Collection

Claims that do not adhere to the form or coding standards described above are rejected from reimbursement, minimizing the risk that inappropriately structured data are included in the database. Data specific to SARS-CoV-2 and COVID-19 has an additional Quality Control layer to control for errors in sampling and data collection; this is described below in the section on Quality Control.

Quality control

A COVID-19 data source-specific layer of quality control is also present, given the rapidly evolving situation. SARS-CoV-2 lab tests included in the database exclude custom local codes or codes that are not present in the LOINC organization's guidance for mapping SARS-CoV-2 and COVID-19 related LOINC terms. Test information provided via the LOINC code compliments the test type (antibody, RT-PCR, etc.) as well as the result value (detected, not detected, not given/cancelled).

Differences across groups

While the data for Medicare Advantage and commercially insured enrollees is processed in a similar manner, these groups are substantially different. First, there are systematic differences in patient characteristics, most remarkably the older age and the higher prevalence of all comorbidities. These differences are tabulated in the database. Furthermore, the commercial insurance claims that are available for analyses are a subset of the overall commercially insured population.

Data Sharing

The data are proprietary and are not available for public use but, under certain conditions, may be made available to editors and their approved auditors under a data use agreement to confirm the findings of the current study.

Technical details for Statistical Analyses

Let i denote the i^{th} hospital and j denote the j^{th} COVID patient admitted in the i^{th} hospital with $i = 1, \dots, I$ and $j = 1, \dots, n_i$. Let Y_{ij} refer to the status of the j^{th} patient which takes values either 1 if a patient is deceased or referred to hospice within 30-day from hospital admission date, and 0 if neither

death nor discharge to hospice happens within 30-day from hospital admission date. Denote by X_{ijk} the k^{th} patient-specific characteristics (e.g., gender, age, status of transfer from a nursing facility and risk factors such as indication of type-II diabetes, obesity, kidney disease, chronic obstructive pulmonary disease, heart failure, coronary artery disease, cardiomyopathy, and others that are used in calculating Elixhauser comorbidity index, see eTable 3 for the complete list of variables). In addition, we consider variables quantifying days since January 1, 2020 until a patient's admission dates to characterize hospital's effort to adapt to the changing conditions of the pandemic.

Variable selection

To screen influential variables and avoid overfitting, we fit a series of univariate generalized linear models (GLM) with a logit link function for each covariate of interest. We classify age and counts of days into discrete categories for ease of interpretability and numerical stability. We repeat the process for each covariate, test whether the corresponding effect is zero, and select the ones that are less than a level of significance threshold (i.e. 10%) based on p-value calculated from Wald-Z statistic. Comorbidity variables of alcohol abuse, liver disease, peptic ulcer, rheumatoid arthritis, and pulmonary circulation disorder are excluded as their corresponding p-values are greater than 0.10; HIV/AIDS are also excluded due to having too few cases (prevalence of exposure being less than 1%). We retain the variable referring to the number of patients admitted to a hospital in our subsequent analyses irrespective to its statistical insignificance based on univariate analysis. We use the selected covariates to conduct the subsequent regression analyses.

Calculation of hospital-specific risk standardized event rates

Hospital specific standardized risk scores are estimated using a hierarchical generalized linear model, following the methods of George, et al.[1] and Silber, et al.[2,3,4] To account for association between hospital adverse event rates and volume of patients being treated in each hospital after adjusting for other risk factors, we add a hospital attribute (i.e., logarithm of volume) in the model. Specifically, we cast the model into a generalized linear mixed model (GLMM) framework -

$$logit\ \Pr(Y_{ij} = 1) = \beta_0 + \sum_{k=1}^{K} X_{ijk}\,\beta_k\ +\ \gamma log(vol_i) +\ b_{i0};$$

where fixed effect parameters, denoted by $\theta = (\beta_0, \beta_1, \ldots, \beta_K, \gamma)$, characterize the effects of covariates on likelihood of experiencing the events and quantify the deviation from overall mean β_0. In addition, b_{i0} follows a Gaussian distribution with mean 0 and unknown variance σ_{0b}^2. Here the site-specific random effect quantifies deviation from the population mean, $\mu = \beta_0 + \sum_{k=1}^{K} X_{ijk}\,\beta_k + \gamma log(vol_i)$, and characterizes where a particular site ''*sits*" in the population. This model can be viewed as a hierarchical model where at the first level, we adjust for patient-specific demographic, comorbidities, and hospital-specific intercept; and in the second level, hospital-specific intercept is further modeled through an overall mean, fixed volume effect, and a random term.

We adopt the approach by Silber, et al.[1-3] to estimate the risk adjusted scores; in addition, we also use a variant of the model described by Drye, at al.[4] and Norman, et al.[5] by adding hospital attributes. Let $\bar{y}$ be patient-level raw event rates in the sample dataset. We fit the model with logit link function, and obtain the site-specific predicted scores as

$$p_{ij} = E(Y_{ij} = 1 \big| X_{ij}, vol_i, b_{i0}) \ = \ 1/\{1 \ + \ exp(-\beta_0 - \textstyle\sum_{k=1}^{K} X_{ijk}\,\beta_k \ - \ \gamma log(vol_i) - b_{i0})\},$$

and the corresponding expected scores as

$$e_{ij} = E(Y_{ij} = 1 | X_{ij}, vol_i) = 1/\{1 + exp(-\beta_0 - \sum_{k=1}^{K} X_{ijk}\beta_k - \gamma log(vol_i))\}.$$

Directly standardized event rates, as defined in George, et al.[1] and Silber, et al.[2,3,4], are computed by averaging the event rates for all $N = \sum_{i=1}^{I} n_i$ had each one of them been treated hypothetically in every hospital. Denote $i*$ for a different hospital from i, define $p_{i*j} = E(Y_{i*j} = 1 | X_{ij}, vol_{i*}, b_{i*0}) = 1/\{1 + exp(-\beta_0 - \sum_{k=1}^{K} X_{ijk}\beta_k - \gamma log(vol_{i*}) - b_{i*0})\}$, where for each patient j in the hospital $i*$, we have estimates for all I hospitals such that $i^* = 1, \ldots, I$. Next, directly standardized (DS) event rates for the i^{th} hospital is computed as

$$s_{i,DS} = \sum_{i*=1}^{I} \sum_{j=1}^{n_{i*}} p_{i*j} / N.$$

Since $s_{i,DS}$ is an average over all N patients, this eliminates any underlying effect arising from a different patient-mix distribution across sites. We refer the above directly standardized event rate as the score risk-standardized event rate (RSER) for a hospital in the paper.

As a sensitivity analysis, we also calculated the RSER measure using Dyre, et al.,[5] which was defined by the ratio of predicted to expected mortality or discharge to hospice, at a hospital, multiplied by the raw rate at the patient level for the entire sample. Specifically, denote by $s_{i,IS}$ the indirectly standardized (IS) hospital event rate for the i^{th} hospital.

The standardized rates based on Drye, at al.[5] and Normand, et al.[6] for each hospital are calculated as a ratio of predicted and expected deaths multiplied by patient-level observed event rate for the dataset. Specifically, predicted number of deaths for each site is computed by using the estimated regression coefficients to the corresponding patient level characteristics, adding empirical best linear unbiased predictors (EBLUP), transforming link functions into probabilities, and summing them over all patients. Similarly, the rates for the i^{th} hospital is calculated as

$$s_{i,IS} = (\sum_{j=1}^{n_i} p_{ij} / \sum_{j=1}^{n_i} e_{ij}) \times \bar{y}.$$

Note the main difference between $\boldsymbol{s_{i,DS}}$ and $\boldsymbol{s_{i,IS}}$ is that the former approach entails the probabilistic attributes and ensures ease of interpretability.

Here the estimation of fixed and random parameters are based on (restricted) maximum likelihood (RE)ML using both Laplace and adaptive Gaussian quadrature approximation techniques. While both methods provide comparable results, reported results thoughout the paper are based on the quadrature approach which entails approximating the integrals in the likelihood function and is theoretically more robust in reducing approximation error. Alternatively, a penalized quasi likelihood (PQL) method may also be adopted. Empirical best linear unbiased predictors (EBLUP) of random effects are obtained using a Bayesian formulation. We test the significance of the random effects by likelihood ratio test (LRT) that follows a mixture of Chi-squared distribution;[7,8] the corresponding p-value is <0.0001 implying the validity of using site-specific random effects. The estimated variance of the random effects is 0.19 with 95% CI (0.14, 0.24). We further investigate the marginal Akaike Information Criteria (AIC) values between GLM (25581.81) and GLMM (25414.20), and the corresponding marginal Bayesian Information Criteria (BIC) values are 25881.37 and 25589.22, respectively. To check collinearity diagnostics,

generalized variance inflation factors (< 2.00) are investigated for the fixed effects. The Spearman's rank correlation coefficient between the estimated fixed effect parameters based on GLMM and GLM is 1.00 (p-value < 0.0001) indicating high stability of regression coefficients. We check the goodness-of-fit of the model by conditional R-square (0.25), Somer's Dxy (0.48), and C-statistic (0.74). Adjusted odds ratios along with 95% confidence intervals and p-values based on Wald Z-statistic for testing the null effects are reported; see eFigure 2.

Comparing hospital specific risk standardized event rates between early and later period

We cast the GLMM into a longitudinal framework to quantify the evolution of standardized rates over early (January 1, 2020-April 30, 2020) and late (May 1, 2020-June 30, 2020) period. We turn period as a binary time variable (0 = early and 1 = late). There are 398 sites matched between early and late period that have at least 10 COVID-19 hospitalization cases along with other filters for consistency. We fit a GLMM using site-specific random intercept and slope varying over time; we assume that random terms follow a bivariate normal distribution with mean zero and unknown non-diagonal covariance matrix. Let $s_{i0,DS}$ and $s_{i1,DS}$ refer to the risk-adjusted scores associated with early ($t_{ij} = 0$) and late time-period ($t_{ij} = 1$). For brevity and notational convenience, we use t and t_{ij} interchangeably. We write the association model as below

$$logit\ \Pr(Y_{ijt} = 1) = \beta_0 + \sum_{k=1}^{K+1} X_{ijkt}\,\beta_k + \gamma log(vol_{it}) + b_{i0} + b_{i1}t_{ij};$$

where $b_i = (b_{i0}, b_{i1})$ is the set of site-specific random intercept and slope effects. Assume b_i follows multivariate Gaussian distribution mean zero and some non-diagonal covariance matrix. Note we have also added fixed effect of time. Subject-specific slope effects allow us to compute standardized risk scores at $t = 0$ and $t = 1$.

As before, we use Laplace and adaptive Gaussian quadrature approximation technique to obtain EBLUPs. Using the same method as was used to calculate the RSER earlier, we use a logit link function and obtain the predicted scores for the i-th subject at time t as $p_{ijt} = 1/\{1 + exp(-\beta_0 - \sum_{k=1}^{K+1} X_{ijkt}\,\beta_k - \gamma log(\mathrm{vol}_{it}) - b_{i0} - b_{i1}t_{ij})\}$, and the corresponding expected rates are defined by $e_{ijt} = 1/\{1 + exp(-\beta_0 - \sum_{k=1}^{K+1} X_{ijkt}\,\beta_k - \gamma log(\mathrm{vol}_{it}))\}$. We obtain risk standardized event rates p_{i*jt}, $i^* = 1, \ldots I$, and based on these rates, we can compute the RSER for each hospital at each of the early- and late-periods.

To make inference about the differences between early and late scores, we perform a paired Wilcoxon signed rank test on RSERs estimated at the early- and late-periods, and obtained a p-value <0.0001, which suggested that the medians of RSERs at the early- and late-periods are statistically significantly different. We compute Kendall rank correlation coefficient (0.4731 with p-value <0.0001) to assess the degree of similarity between rankings of hospitals with respect to RSERs associated with early and late period.

Association between hospital attributes and risk standardized event rates

Here the main objective is to quantify the association between hospital-level RSERs and hospital-attributes. We fit a linear model treating RSERs as continuous response variables while adjusting for hospital attributes (i.e., resident-to-bed ratio, number of ICU beds, number of beds, hospital settings, academic affiliation, and profit status) on 955 sites. To quantify strains of pandemic at different time points for different regions where hospitals are located, county-specific cases per 10K in the early period and relative change in cases between late- and early-period are used. We dichotomize the relative changes into a binary measure indicating 1 if cumulative cases increase in the late period, and 0

otherwise. We classify resident-to-bed ratio, number of ICU beds, number of beds, and cumulative cases per 10K during early period into discrete categories for ease of interpretability. Moreover, we add region (i.e., northeast, southeast, west, and central) as fixed effects to quantify the regional-specific variation in the associated hospital's responses. In addition, we include measures of the COVID-19 case load in the hospital's county measured as the number of cumulative cases per 10,000 residents as of May 1. We report the parameter estimates along with 95% confidence intervals and p-values based on Wald test.

As a sensitivity analysis, we also fit a hierarchical model (i.e., GLMM) as used before in computing patient-specific RSERs for all 955 hospitals. In contrast, we add both patient-specific, pandemic-strain specific, and hospital-attributes in a single model; the main objective is to quantify the extent of variation in patient-level event rates that is attributable to hospital attributes while adjusting for patient-specific risk factors. The appropriateness of using hospitals as random effects is evaluated via LRT (p-value < 0.0001). The spearman correlation coefficient between fixed-effect parameter estimates based on GLMM and an alternative model GLM (without random effect) is 1.00 (p-value < 0.0001). We check the goodness-of-fit of the GLMM by conditional R-square (0.26), Somer's Dxy (0.48), and C-statistic (0.74). We report the adjusted odds ratios along with 95% confidence intervals and p-values based on Wald test in eFigure 11.

Using the same set of hospital attributes as defined above, we fit a LM to characterize the variation in RSERs for early and late period associated with 398 sites; where we consider the differences between early and late period as our continuous response.

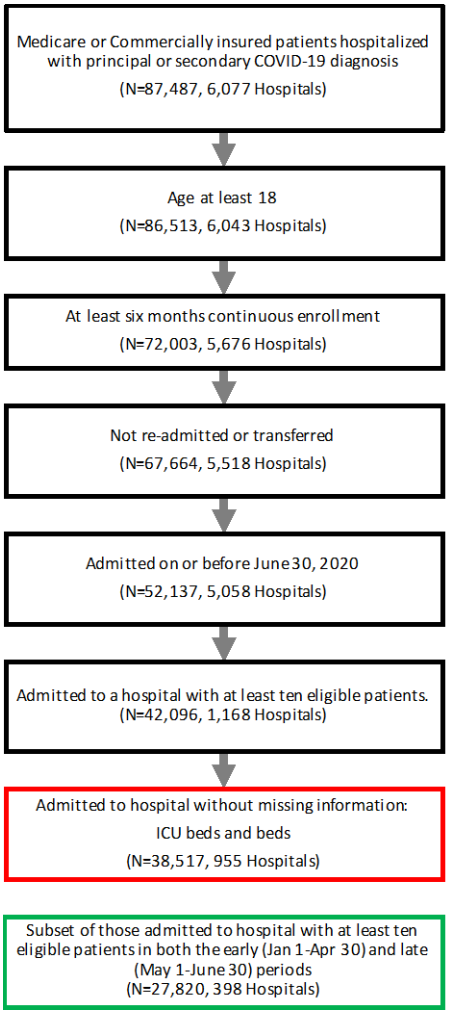
Model based comparison between quintiles

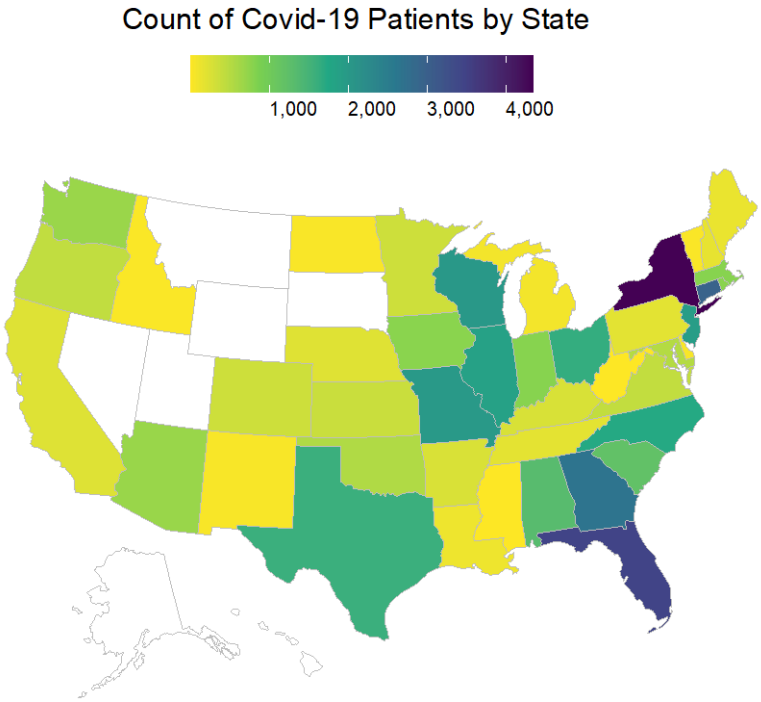
For comparison between quintiles, we fit a univariate linear regression model with the risk standardized event rates (RSERs) as outcome and quintile group indicators as covariate. We choose quntile 1 as the reference quintile, which reflects the 20% of hospitals with the best risk standardized event rates.

Illustration and codes

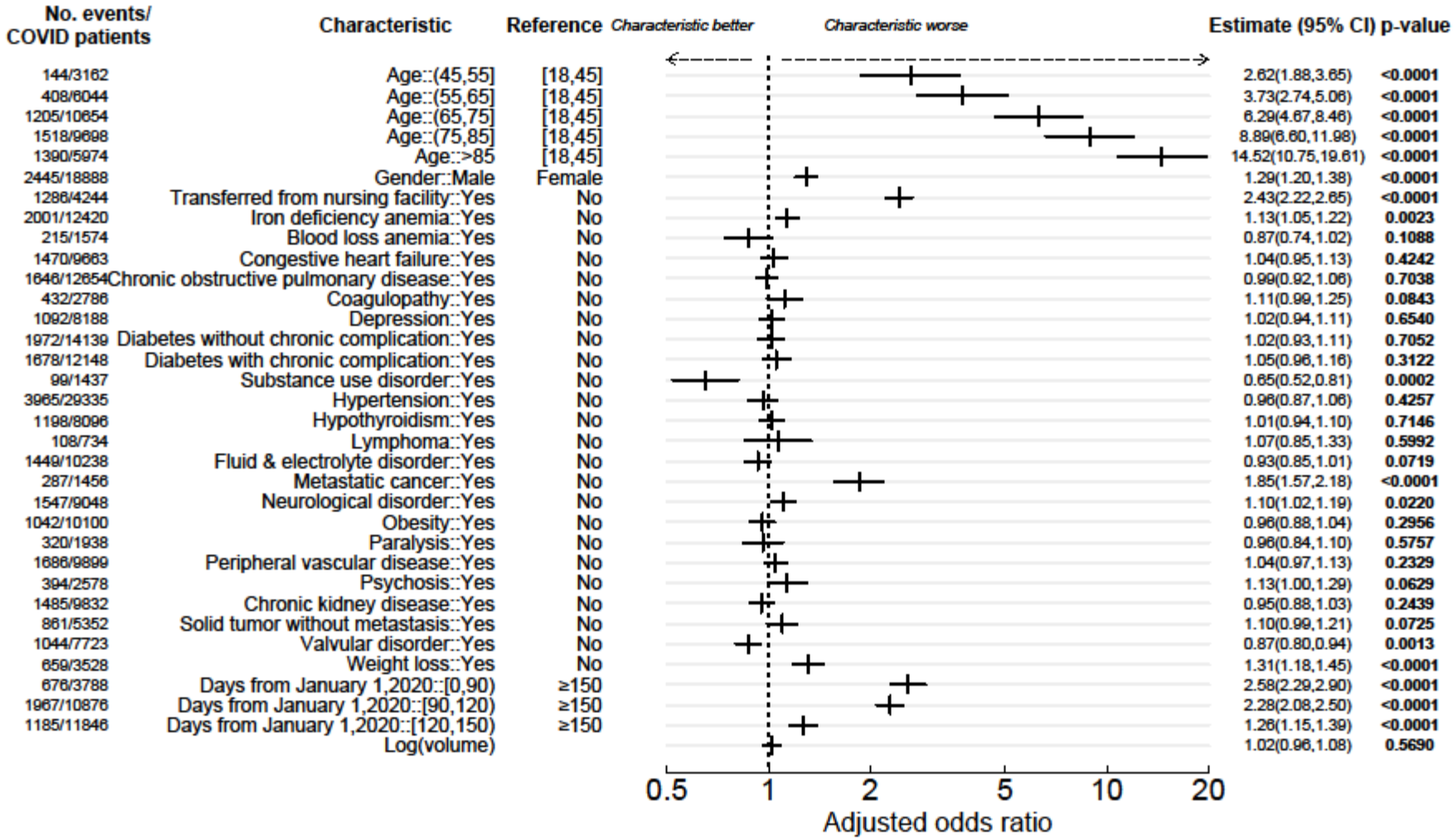
We created an artificial working dataset mimicking our analytical dataset. We illustrate the adopted methodologies for computing risk standardized event rates on this simulated data for the purpose of reproducibility and include the R-codes.

eFigure 1. Derivation and geographic distribution of the study sample.



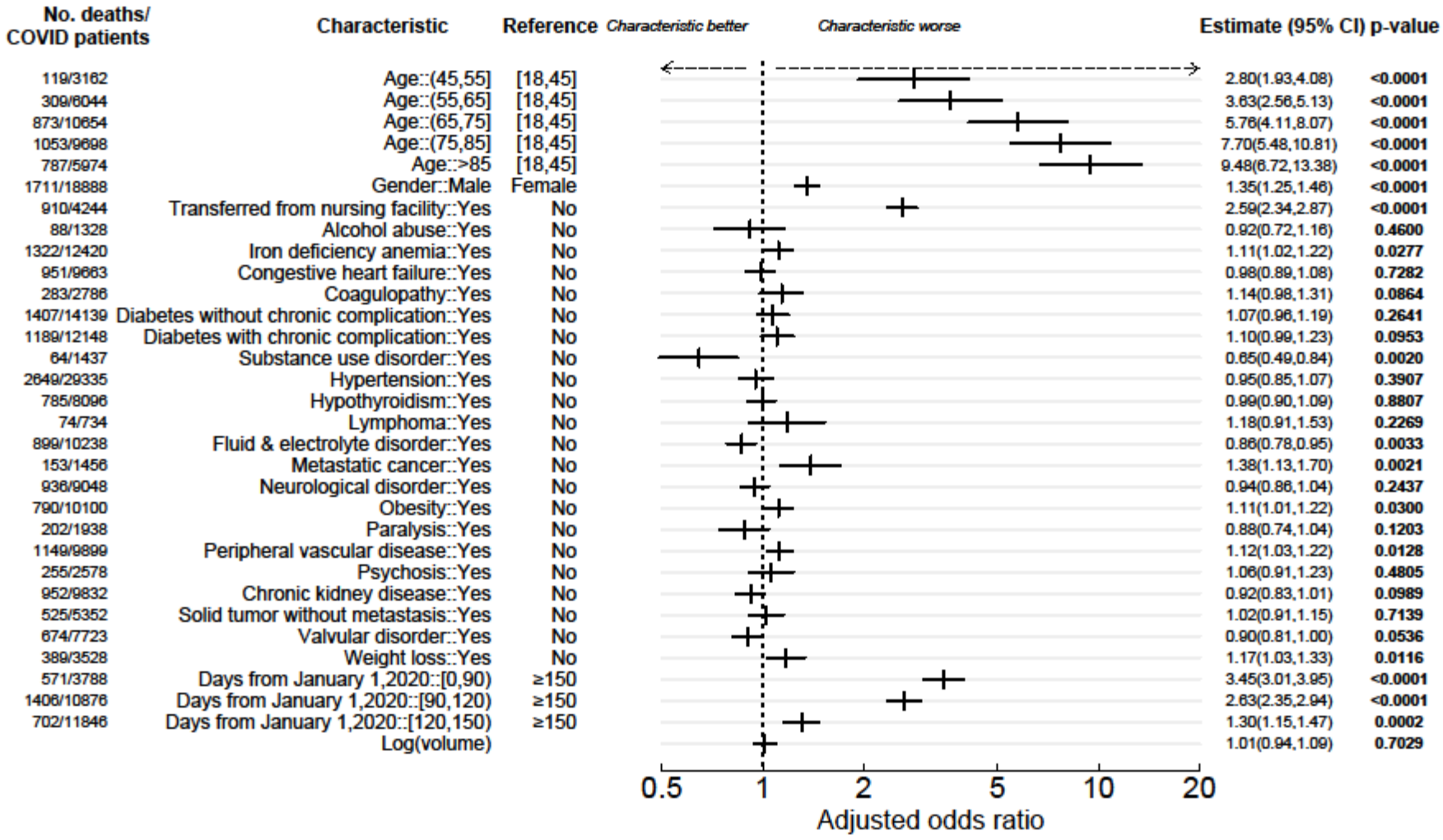


eFigure 2A. Estimated odds ratios of 30-day mortality or transfer to hospice for 955 hospitals and 38,517 patients.

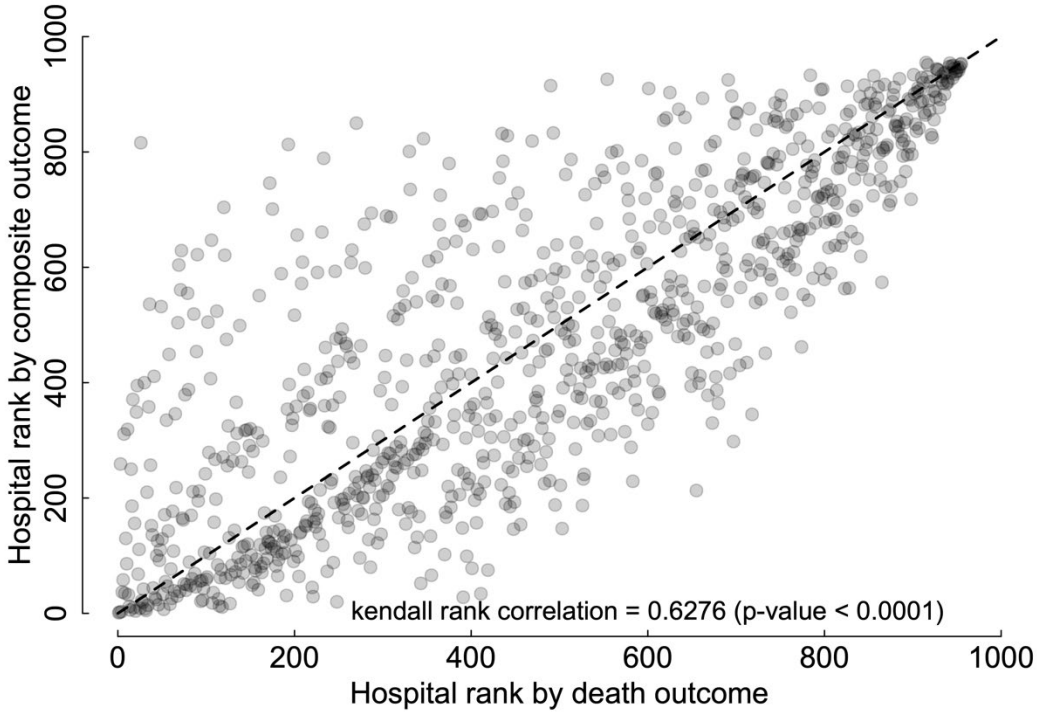


Log(volume) refers to the number of patients admitted to the hospital in our dataset. This variable is included in order to follow the model of Silber, et al[1-3] in order to compute the RSER for each hospital.

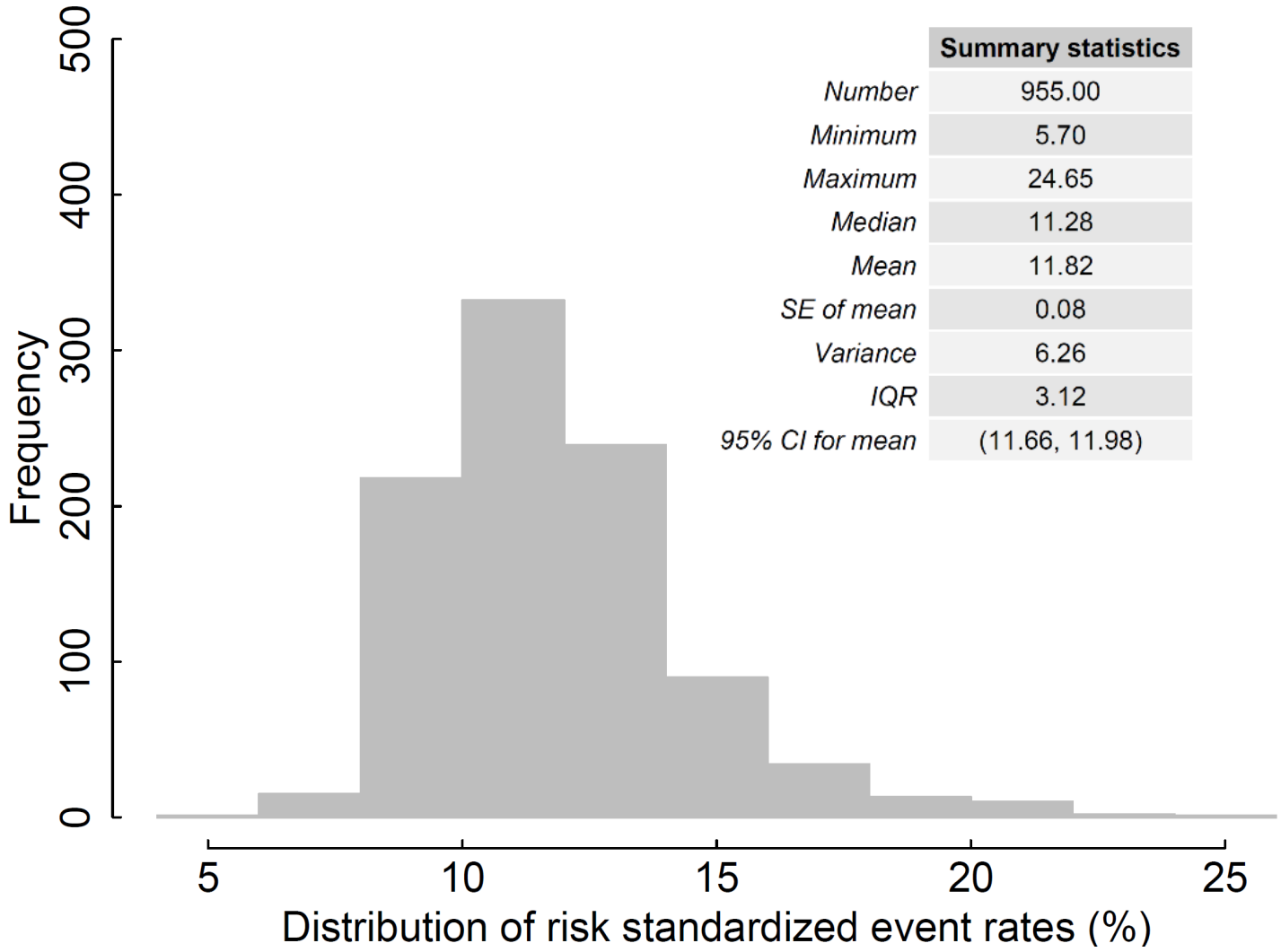
eFigure 2B. Estimated odds ratios of 30-day mortality for 955 hospitals and 38,517 patients. The analysis in eFigure 2A uses mortality or discharge to hospice as the outcome. The analysis in eFigure 2B uses only mortality.



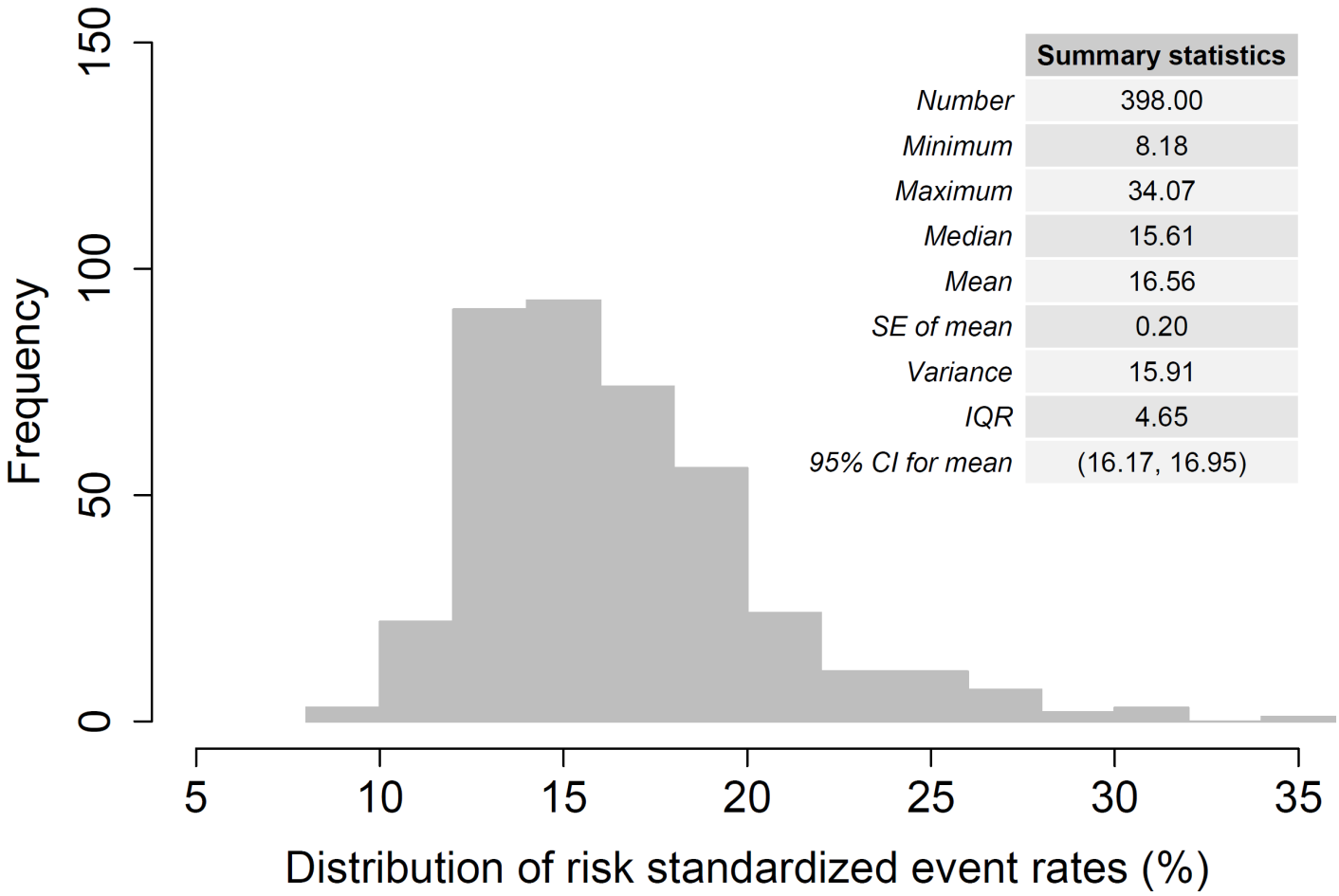
eFigure 3. Correlation of hospital rank based on the composite of mortality or hospice discharge or mortality alone.



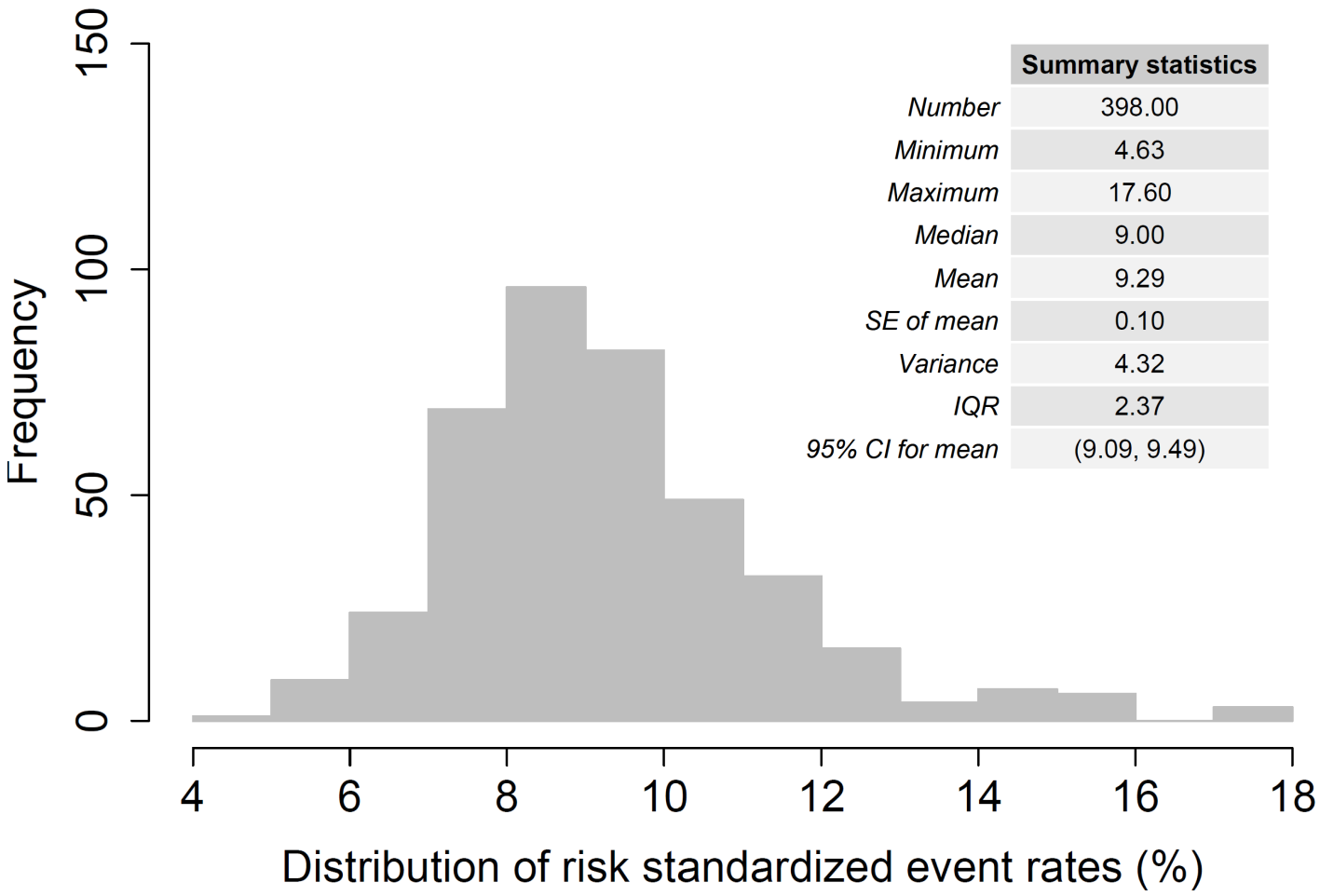
eFigure4. Distribution of risk standardized event rates for 955 hospitals and 38,517 patients



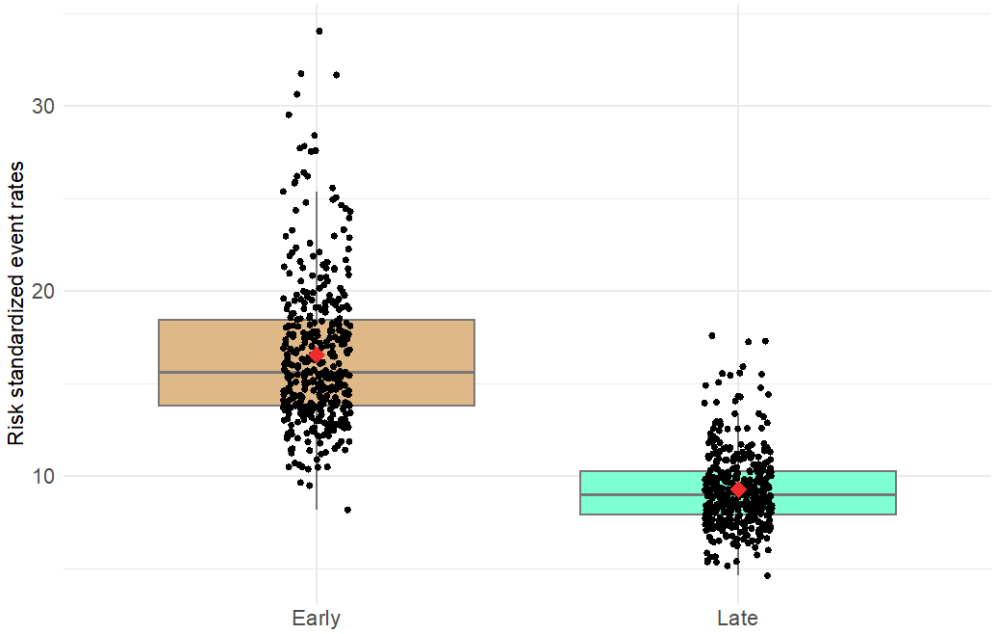
eFigure 5. Distribution of risk standardized event rates for 398 hospitals in the early period



eFigure 6. Distribution of risk standardized event rates for 398 hospitals in the later period

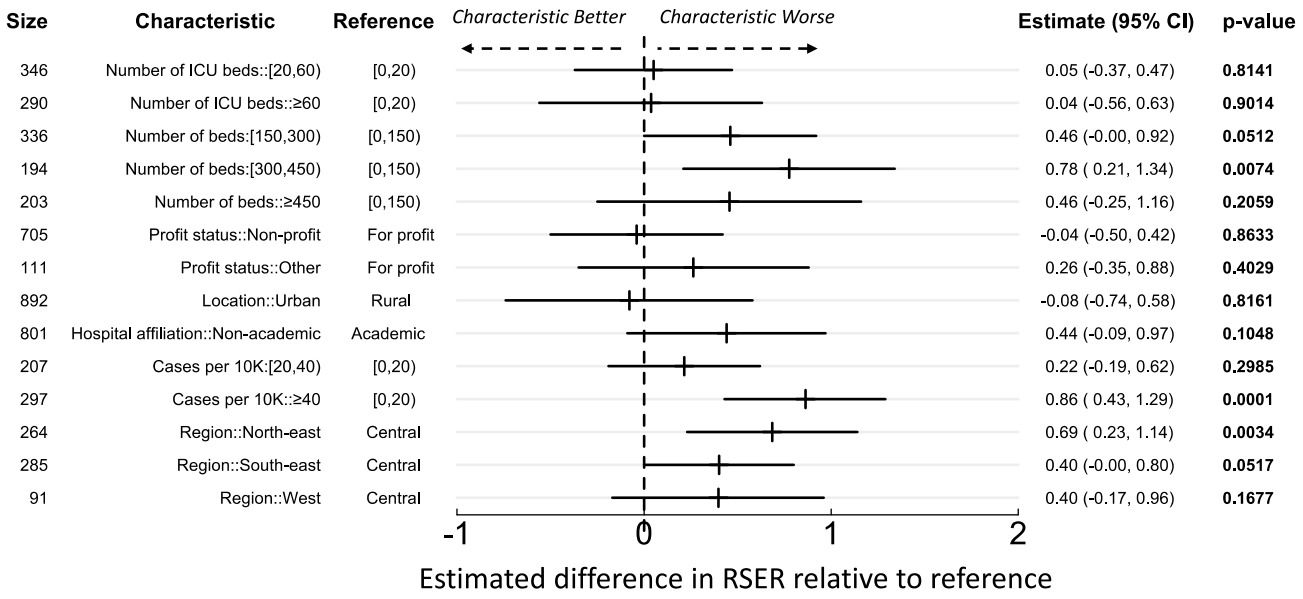


eFigure 7. Comparison of early and late period hospital-specific risk standardized rates for 30-day mortality or discharge to hospice for 398 hospitals and 27,801 patients. A higher score corresponds to worse performance.

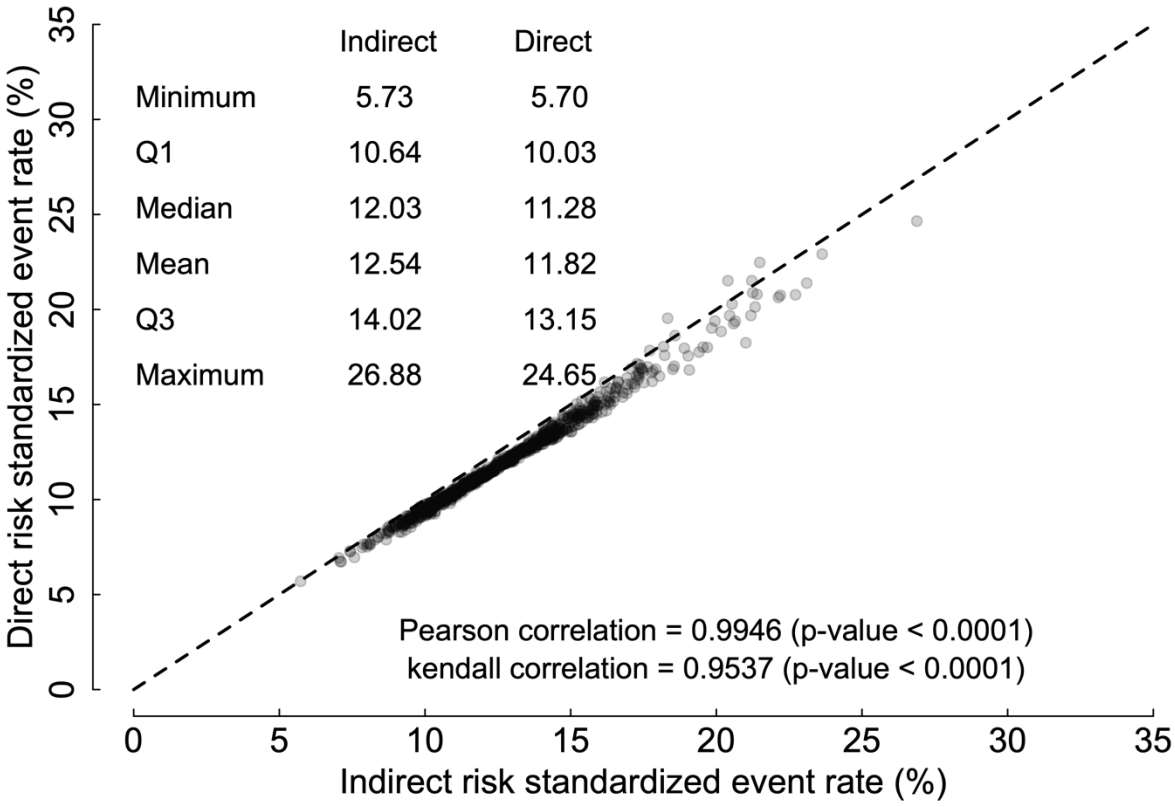


The late period (May 1-July 30, 2020) risk standardized event rates are in general lower and show a narrower range than the early period (Jan 1 to April 30, 2020) rates, suggesting both overall improvement and a reduction in variation across hospitals.

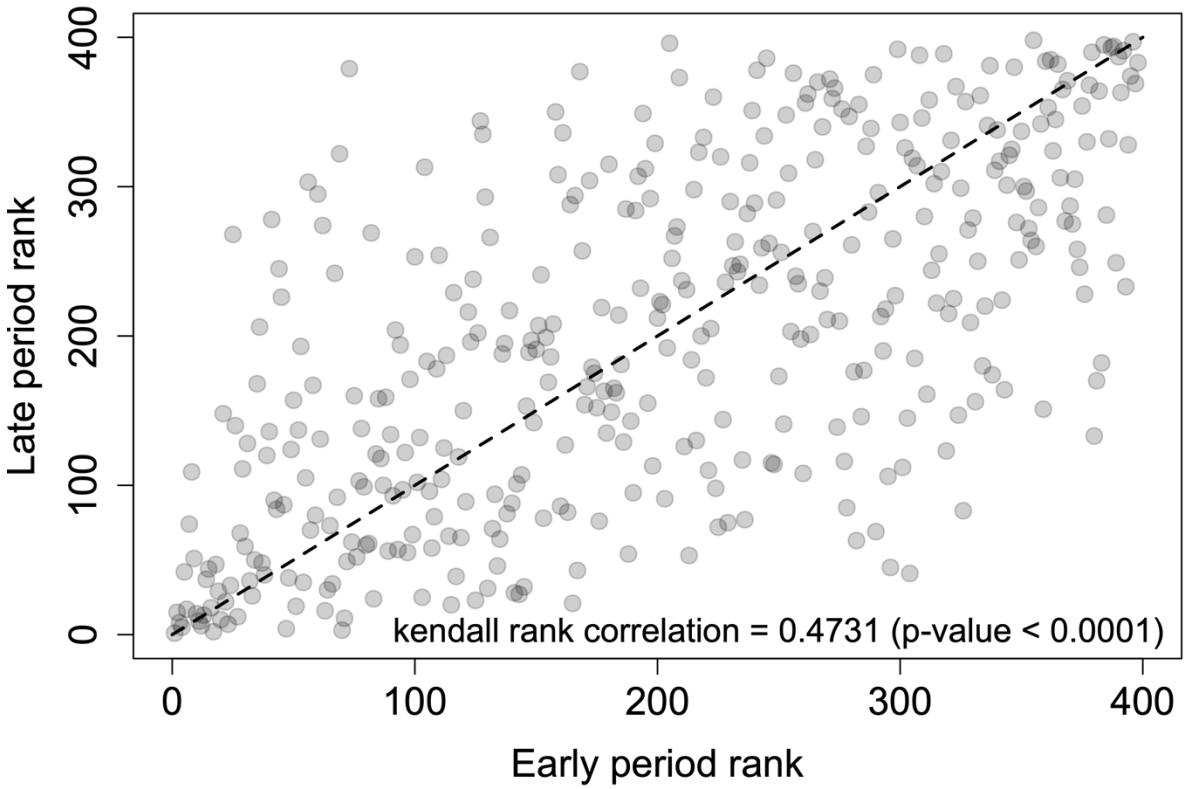
eFigure 8. Hospital characteristics associated with the risk standardized event rates of 955 hospitals.



eFigure 9. Correlation of the direct standardized event rate used in this analysis and the indirect standardized event rate

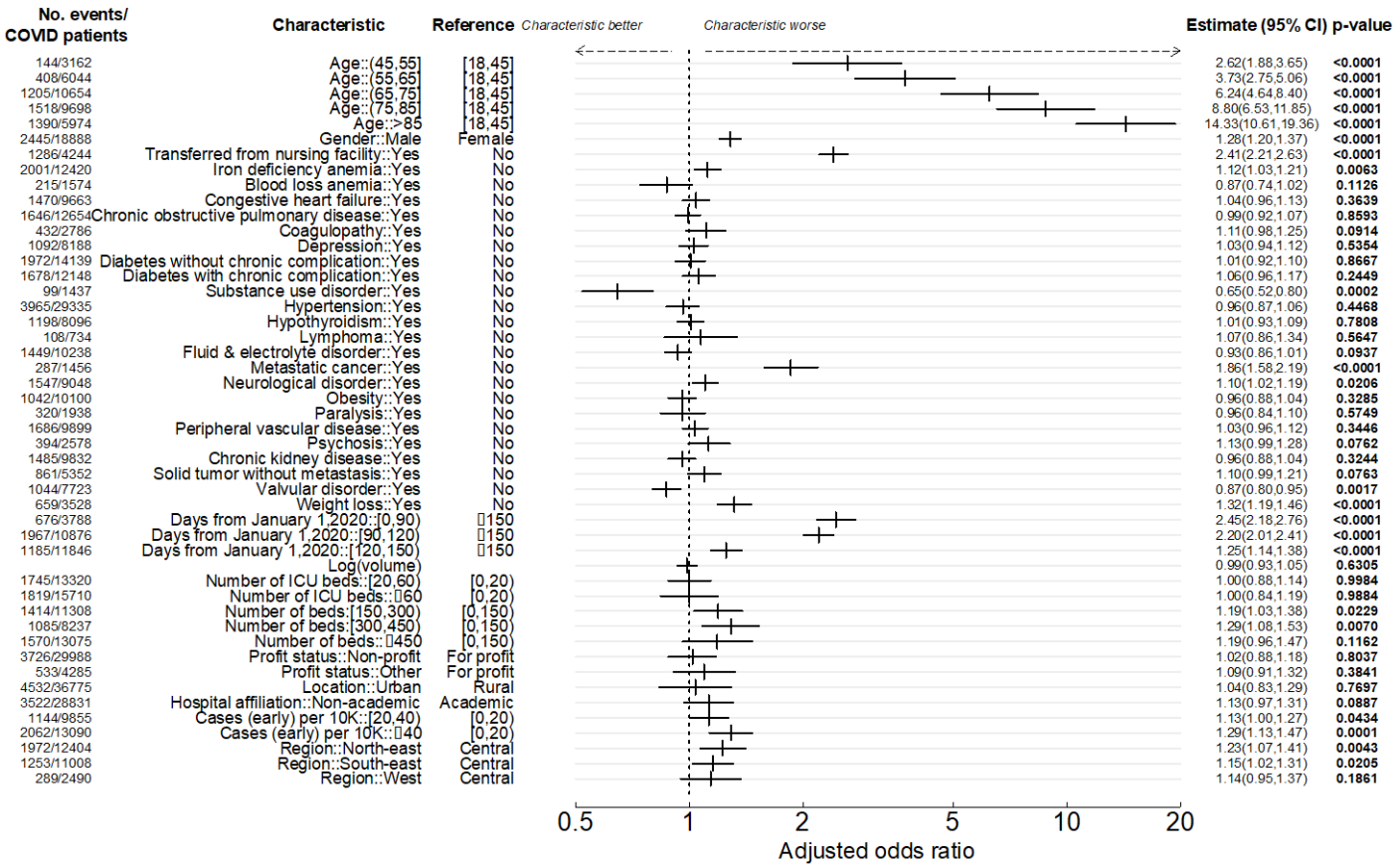


eFigure 10. Correlation of the ranking for hospitals in the early and later periods



Kendall rank correlation coefficient reflecting the similarity of each hospital's relative position in RSER between early and later periods. The coefficient value of 0.4731 reveals that hospitals with low (better) RSERs in the early period tend to have low (better) RSERs in the later period and vice versa.

eFigure 11. A hierarchical model reflecting both patient-and-hospital attributes. This analysis reveals how much variation in patient-level mortality can be explained by hospital attributes.



eTable 1A. Difference in the 30-day mortality or hospice discharge (Risk standardized event rate, RSER) compared to the best performing quintile (Q1) overall (955 hospitals) and early and late periods (398 hospitals). Q1 is the reference quintile reflecting the 20% of hospitals with the best (lowest) risk standardized event rates. For example, the bottom right cell implies that hospitals' rate of mortality or discharge to hospice in the worst performing quintile (Q5) is 5.59 percentage points greater than those in the best performing quintile (Q1).

	Overall		**Early Period**		**Late Period**	
Quintile	RSER Increase	Confidence Interval	RSER Increase	Confidence Interval	RSER Increase	Confidence Interval
Q1	Reference		Reference		Reference	
Q2	1.22	(1.01-1.43)	1.94	(1.43-2.45)	1.24	(0.97-1.50)
Q3	2.29	(2.08-2.51)	3.59	(3.07-4.10)	2.11	(1.84-2.37)
Q4	3.68	(3.47-3.89)	5.76	(5.24-6.27)	3.11	(2.85-3.38)
Q5	6.59	(6.38-6.80)	10.54	(10.03-11.05)	5.59	(5.33-5.86)

eTable 1B. Difference in the 30-day mortality (Risk standardized mortality rate, RSMR) compared to the best performing quintile (Q1) overall (955 hospitals) and early and late periods (398 hospitals). Q1 is the reference quintile reflecting the 20% of hospitals with the best (lowest) risk standardized mortality rates. For example, the bottom right cell implies that hospitals' rate of mortality in the worst performing quintile (Q5) is 5.36 percentage points greater than those in the best performing quintile (Q1).

	Overall		**Early Period**		**Late Period**	
Quintile	RSMR Increase	Confidence Interval	RSMR Increase	Confidence Interval	RSMR Increase	Confidence Interval
Q1	Reference		Reference		Reference	
Q2	0.95	(0.71-1.20)	1.94	(1.43-2.46)	0.88	(0.63-1.23)
Q3	1.91	(1.66-2.15)	3.60	(3.09-4.11)	1.80	(1.55-2.05)
Q4	3.26	(3.01-3.50)	5.84	(5.32-6.35)	2.81	(2.56-3.06)
Q5	6.71	(6.46-6.95)	11.35	(10.84-11.86)	5.36	(5.11-5.61)

eTable 2. Risk standardized 30-day mortality or discharge to hospice rates stratified by county-level cumulative reported COVID-19 case burden as of April 30, 2020 (955 hospitals)

	[0,20) Cases/ 10K people		**[20,40) Cases/ 10K people**		**≥40 Cases/ 10K people**	
Quintile	Mean RSER	Confidence Interval	Mean RSER	Confidence Interval	Mean RSER	Confidence Interval
Q1	9.15%	(9.04%-9.25%)	9.03%	(8.79%-9.28%)	8.88%	(8.59%-9.16%)
Q2	10.30%	(10.24%-10.36%)	10.24%	(10.16%-10.32%)	10.30%	(10.21%-10.39%)
Q3	11.33%	(11.27%-11.40%)	11.39%	(11.28%-11.49%)	11.39%	(11.28%-11.50%)
Q4	12.74%	(12.65%-12.84%)	12.81%	(12.66%-12.97%)	12.70%	(12.59%-12.81%)
Q5	15.23%	(14.74%-15.72%)	15.60%	(14.97%-16.23%)	15.99%	(15.50%-16.47%)

eTable 3. ICD10 codes used in the analyses

Inclusion Criteria

Inclusion Criteria	ICD-10-CM codes
COVID-19	U071, U072, B9729

Elixhauser Comorbidity Indices

Elixhauser Comorbidity Index	ICD-10-CM codes
Acquired immunodeficiency Syndrome	B20
Alcohol Use Disorder	F1010, F1011, F10120, F10121, F10129, F1014, F10150, F10151, F10159, F10180, F10181, F10182, F10188, F1019, F1020, F1021, F10220, F10221, F10229, F10230, F10231, F10232, F10239, F1024, F10250, F10251, F10259, F1026, F1027, F10280, F10281, F10282, F10288, F1029, F10921, F1094, F10950, F10951, F10959, F1096, F1097, F10980, F10981, F10982, F10988, F1099
Iron Deficiency Anemia	D501, D508, D509, D510, D511, D512, D513, D518, D519, D520, D521, D528, D529, D530, D531, D532, D538, D539, D630, D631, D638, D649
Rheumatoid Arthritis	L900, L940, L941, L943, M0500, M05011, M05012, M05019, M05021, M05022, M05029, M05031, M05032, M05039, M05041, M05042, M05049, M05051, M05052, M05059, M05061, M05062, M05069, M05071, M05072, M05079, M0509, M0510, M05111, M05112, M05119, M05121, M05122, M05129, M05131, M05132, M05139, M05141, M05142, M05149, M05151, M05152, M05159, M05161, M05162, M05169, M05171, M05172, M05179, M0519, M0520, M05211, M05212, M05219, M05221, M05222, M05229, M05231, M05232, M05239, M05241, M05242, M05249, M05251, M05252, M05259, M05261, M05262, M05269, M05271, M05272, M05279, M0529, M0530, M05311, M05312, M05319, M05321, M05322, M05329, M05331, M05332, M05339, M05341, M05342, M05349, M05351, M05352, M05359, M05361, M05362, M05369, M05371, M05372, M05379, M0539, M0540, M05411, M05412, M05419, M05421, M05422, M05429, M05431, M05432, M05439, M05441, M05442, M05449, M05451, M05452, M05459, M05461, M05462, M05469, M05471, M05472, M05479, M0549, M0550, M05511, M05512, M05519, M05521, M05522, M05529, M05531, M05532, M05539, M05541, M05542, M05549, M05551, M05552, M05559, M05561, M05562, M05569, M05571, M05572, M05579, M0559, M0560, M05611, M05612, M05619, M05621, M05622, M05629, M05631, M05632, M05639, M05641, M05642, M05649, M05651, M05652, M05659, M05661, M05662, M05669, M05671, M05672, M05679, M0569, M0570, M05711, M05712, M05719, M05721, M05722, M05729, M05731, M05732, M05739, M05741, M05742, M05749, M05751, M05752, M05759, M05761, M05762, M05769, M05771, M05772, M05779, M0579, M0580, M05811, M05812, M05819, M05821, M05822, M05829, M05831, M05832, M05839, M05841, M05842, M05849, M05851, M05852, M05859, M05861, M05862, M05869, M05871, M05872, M05879, M0589, M059, M0600, M06011, M06012, M06019, M06021, M06022, M06029, M06031, M06032, M06039, M06041, M06042, M06049, M06051, M06052, M06059, M06061, M06062, M06069, M06071, M06072, M06079, M0608, M0609, M061, M0620, M06211, M06212, M06219, M06221, M06222, M06229, M06231, M06232, M06239, M06241, M06242, M06249, M06251, M06252, M06259, M06261, M06262, M06269, M06271, M06272, M06279, M0628, M0629, M0630, M06311, M06312, M06319, M06321, M06322, M06329, M06331, M06332, M06339, M06341, M06342, M06349, M06351, M06352, M06359, M06361, M06362, M06369, M06371, M06372, M06379, M0638, M0639, M064, M0680, M06811, M06812, M06819, M06821, M06822, M06829, M06831, M06832, M06839, M06841, M06842, M06849, M06851, M06852, M06859, M06861, M06862, M06869, M06871, M06872, M06879, M0688, M0689, M069, M0800, M08011, M08012, M08019, M08021, M08022, M08029, M08031, M08032, M08039, M08041, M08042, M08049, M08051, M08052, M08059, M08061, M08062, M08069, M08071,

	M08072, M08079, M0808, M0809, M081, M0820, M08211, M08212, M08219, M08221, M08222, M08229, M08231, M08232, M08239, M08241, M08242, M08249, M08251, M08252, M08259, M08261, M08262, M08269, M08271, M08272, M08279, M0828, M0829, M083, M0840, M08411, M08412, M08419, M08421, M08422, M08429, M08431, M08432, M08439, M08441, M08442, M08449, M08451, M08452, M08459, M08461, M08462, M08469, M08471, M08472, M08479, M0848, M0880, M08811, M08812, M08819, M08821, M08822, M08829, M08831, M08832, M08839, M08841, M08842, M08849, M08851, M08852, M08859, M08861, M08862, M08869, M08871, M08872, M08879, M0888, M0889, M0890, M08911, M08912, M08919, M08921, M08922, M08929, M08931, M08932, M08939, M08941, M08942, M08949, M08951, M08952, M08959, M08961, M08962, M08969, M08971, M08972, M08979, M0898, M0899, M1200, M12011, M12012, M12019, M12021, M12022, M12029, M12031, M12032, M12039, M12041, M12042, M12049, M12051, M12052, M12059, M12061, M12062, M12069, M12071, M12072, M12079, M1208, M1209, M320, M3210, M3211, M3212, M3213, M3214, M3215, M3219, M328, M329, M3300, M3301, M3302, M3303, M3309, M3310, M3311, M3312, M3313, M3319, M3320, M3321, M3322, M3329, M3390, M3391, M3392, M3393, M3399, M340, M341, M342, M3481, M3482, M3483, M3489, M349, M3500, M3501, M3502, M3503, M3504, M3509, M351, M353, M355, M358, M359, M360, M368, M450, M451, M452, M453, M454, M455, M456, M457, M458, M459, M4600, M4601, M4602, M4603, M4604, M4605, M4606, M4607, M4608, M4609, M461, M4650, M4651, M4652, M4653, M4654, M4655, M4656, M4657, M4658, M4659, M4680, M4681, M4682, M4683, M4684, M4685, M4686, M4687, M4688, M4689, M4690, M4691, M4692, M4693, M4694, M4695, M4696, M4697, M4698, M4699, M488X1, M488X2, M488X3, M488X4, M488X5, M488X6, M488X7, M488X8, M488X9, M4980, M4981, M4982, M4983, M4984, M4985, M4986, M4987, M4988, M4989
Blood Loss Anemia	D500, O9081, O99011, O99012, O99013, O99019, O9902, O9903
Congestive Heart Failure	I0981, I110, I130, I132, I501, I5020, I5021, I5022, I5023, I5030, I5031, I5032, I5033, I5040, I5041, I5042, I5043, I50810, I50811, I50812, I50813, I50814, I5082, I5083, I5084, I5089, I509
Chronic Obstructive Pulmonary Disease	J40, J410, J411, J418, J42, J430, J431, J432, J438, J439, J440, J441, J449, J4520, J4521, J4522, J4530, J4531, J4532, J4540, J4541, J4542, J4550, J4551, J4552, J45901, J45902, J45909, J45990, J45991, J45998, J470, J471, J479, J60, J61, J620, J628, J630, J631, J632, J633, J634, J635, J636, J64, J660, J661, J662, J668, J670, J671, J672, J673, J674, J675, J676, J677, J678, J679, J684
Coagulopathy	D65, D66, D67, D680, D681, D682, D68311, D68312, D68318, D6832, D684, D688, D689, D691, D693, D6941, D6942, D6949, D6951, D6959, D696, D7582, O99111, O99112, O99113, O99119, O9912, O9913
Depression	F320, F321, F322, F323, F328, F3281, F3289, F329, F330, F331, F332, F333, F338, F339, F341, F4321
Diabetes without Chronic Complications	E0800, E0801, E0810, E0811, E089, E0900, E0901, E0910, E0911, E099, E1010, E1011, E109, E1100, E1101, E1110, E1111, E119, E1300, E1301, E1310, E1311, E139, O24011, O24012, O24013, O24019, O2402, O2403, O24111, O24112, O24113, O24119, O2412, O2413, O24311, O24312, O24313, O24319, O2432, O2433, O24811, O24812, O24813, O24819, O2482, O2483, O24911, O24912, O24913, O24919, O2492, O2493

Diabetes with Chronic Complications	E0821, E0822, E0829, E08311, E08319, E08321, E083211, E083212, E083213, E083219, E08329, E083291, E083292, E083293, E083299, E08331, E083311, E083312, E083313, E083319, E08339, E083391, E083392, E083393, E083399, E08341, E083411, E083412, E083413, E083419, E08349, E083491, E083492, E083493, E083499, E08351, E083511, E083512, E083513, E083519, E083521, E083522, E083523, E083529, E083531, E083532, E083533, E083539, E083541, E083542, E083543, E083549, E083551, E083552, E083553, E083559, E08359, E083591, E083592, E083593, E083599, E0836, E0837X1, E0837X2, E0837X3, E0837X9, E0839, E0840, E0841, E0842, E0843, E0844, E0849, E0851, E0852, E0859, E08610, E08618, E08620, E08621, E08622, E08628, E08630, E08638, E08641, E08649, E0865, E0869, E088, E0921, E0922, E0929, E09311, E09319, E09321, E093211, E093212, E093213, E093219, E09329, E093291, E093292, E093293, E093299, E09331, E093311, E093312, E093313, E093319, E09339, E093391, E093392, E093393, E093399, E09341, E093411, E093412, E093413, E093419, E09349, E093491, E093492, E093493, E093499, E09351, E093511, E093512, E093513, E093519, E093521, E093522, E093523, E093529, E093531, E093532, E093533, E093539, E093541, E093542, E093543, E093549, E093551, E093552, E093553, E093559, E09359, E093591, E093592, E093593, E093599, E0936, E0937X1, E0937X2, E0937X3, E0937X9, E0939, E0940, E0941, E0942, E0943, E0944, E0949, E0951, E0952, E0959, E09610, E09618, E09620, E09621, E09622, E09628, E09630, E09638, E09641, E09649, E0965, E0969, E098, E1021, E1022, E1029, E10311, E10319, E10321, E103211, E103212, E103213, E103219, E10329, E103291, E103292, E103293, E103299, E10331, E103311, E103312, E103313, E103319, E10339, E103391, E103392, E103393, E103399, E10341, E103411, E103412, E103413, E103419, E10349, E103491, E103492, E103493, E103499, E10351, E103511, E103512, E103513, E103519, E103521, E103522, E103523, E103529, E103531, E103532, E103533, E103539, E103541, E103542, E103543, E103549, E103551, E103552, E103553, E103559, E10359, E103591, E103592, E103593, E103599, E1036, E1037X1, E1037X2, E1037X3, E1037X9, E1039, E1040, E1041, E1042, E1043, E1044, E1049, E1051, E1052, E1059, E10610, E10618, E10620, E10621, E10622, E10628, E10630, E10638, E10641, E10649, E1065, E1069, E108, E1121, E1122, E1129, E11311, E11319, E11321, E113211, E113212, E113213, E113219, E11329, E113291, E113292, E113293, E113299, E11331, E113311, E113312, E113313, E113319, E11339, E113391, E113392, E113393, E113399, E11341, E113411, E113412, E113413, E113419, E11349, E113491, E113492, E113493, E113499, E11351, E113511, E113512, E113513, E113519, E113521, E113522, E113523, E113529, E113531, E113532, E113533, E113539, E113541, E113542, E113543, E113549, E113551, E113552, E113553, E113559, E11359, E113591, E113592, E113593, E113599, E1136, E1137X1, E1137X2, E1137X3, E1137X9, E1139, E1140, E1141, E1142, E1143, E1144, E1149, E1151, E1152, E1159, E11610, E11618, E11620, E11621, E11622, E11628, E11630, E11638, E11641, E11649, E1165, E1169, E118, E1321, E1322, E1329, E13311, E13319, E13321, E133211, E133212, E133213, E133219, E13329, E133291, E133292, E133293, E133299, E13331, E133311, E133312, E133313, E133319, E13339, E133391, E133392, E133393, E133399, E13341, E133411, E133412, E133413, E133419, E13349, E133491, E133492, E133493, E133499, E13351, E133511, E133512, E133513, E133519, E133521, E133522, E133523, E133529, E133531, E133532, E133533, E133539, E133541, E133542, E133543, E133549, E133551, E133552, E133553, E133559, E13359, E133591, E133592, E133593, E133599, E1336, E1337X1, E1337X2, E1337X3, E1337X9, E1339, E1340, E1341, E1342, E1343, E1344, E1349, E1351, E1352, E1359, E13610, E13618, E13620, E13621, E13622, E13628, E13630, E13638, E13641, E13649, E1365, E1369, E138, P702

Substance Use Disorder	F1110, F1111, F11120, F11121, F11122, F11129, F1114, F11150, F11151, F11159, F11181, F11182, F11188, F1119, F1120, F1121, F11220, F11221, F11222, F11229, F1123, F1124, F11250, F11251, F11259, F11281, F11282, F11288, F1129, F1210, F1211, F12120, F12121, F12122, F12129, F12150, F12151, F12159, F12180, F12188, F1219, F1220, F1221, F12220, F12221, F12222, F12229, F1223, F12250, F12251, F12259, F12280, F12288, F1229, F1310, F1311, F13120, F13121, F13129, F1314, F13150, F13151, F13159, F13180, F13181, F13182, F13188, F1319, F1320, F1321, F13220, F13221, F13229, F13230, F13231, F13232, F13239, F1324, F13250, F13251, F13259, F1326, F1327, F13280, F13281, F13282, F13288, F1329, F1410, F1411, F14120, F14121, F14122, F14129, F1414, F14150, F14151, F14159, F14180, F14181, F14182, F14188, F1419, F1420, F1421, F14220, F14221, F14222, F14229, F1423, F1424, F14250, F14251, F14259, F14280, F14281, F14282, F14288, F1429, F1510, F1511, F15120, F15121, F15122, F15129, F1514, F15150, F15151, F15159, F15180, F15181, F15182, F15188, F1519, F1520, F1521, F15220, F15221, F15222, F15229, F1523, F1524, F15250, F15251, F15259, F15280, F15281, F15282, F15288, F1529, F1610, F1611, F16120, F16121, F16122, F16129, F1614, F16150, F16151, F16159, F16180, F16183, F16188, F1619, F1620, F1621, F16220, F16221, F16229, F1624, F16250, F16251, F16259, F16280, F16283, F16288, F1629, F1810, F1811, F18120, F18121, F18129, F1814, F18150, F18151, F18159, F1817, F18180, F18188, F1819, F1820, F1821, F18220, F18221, F18229, F1824, F18250, F18251, F18259, F1827, F18280, F18288, F1829, F1910, F1911, F19120, F19121, F19122, F19129, F1914, F19150, F19151, F19159, F1916, F1917, F19180, F19181, F19182, F19188, F1919, F1920, F1921, F19220, F19221, F19222, F19229, F19230, F19231, F19232, F19239, F1924, F19250, F19251, F19259, F1926, F1927, F19280, F19281, F19282, F19288, F1929, F550, F551, F552, F553, F554, F558, O99320, O99321, O99322, O99323, O99324, O99325
Hypertension	I10, I110, I119, I120, I129, I130, I1310, I1311, I132, I150, I151, I152, I158, I159, I160, I161, I169, I674, O10011, O10012, O10013, O10019, O1002, O1003, O10111, O10112, O10113, O10119, O1012, O1013, O10211, O10212, O10213, O10219, O1022, O1023, O10311, O10312, O10313, O10319, O1032, O1033, O10411, O10412, O10413, O10419, O1042, O1043, O10911, O10912, O10913, O10919, O1092, O1093, O111, O112, O113, O114, O115, O119, O161, O162, O163, O164, O165, O169
Hypothyrodism	E000, E001, E002, E009, E018, E02, E030, E031, E032, E033, E038, E039, E890
Liver Disease	B180, B181, B182, I8500, I8501, I8510, I8511, K700, K702, K7030, K7031, K7040, K7041, K709, K7210, K7211, K7290, K7291, K730, K731, K732, K738, K739, K740, K741, K742, K743, K744, K745, K7460, K7469, K754, K7581, K760, K766, K7689, K769, Z944

Lymphoma	C8100, C8101, C8102, C8103, C8104, C8105, C8106, C8107, C8108, C8109, C8110, C8111, C8112, C8113, C8114, C8115, C8116, C8117, C8118, C8119, C8120, C8121, C8122, C8123, C8124, C8125, C8126, C8127, C8128, C8129, C8130, C8131, C8132, C8133, C8134, C8135, C8136, C8137, C8138, C8139, C8140, C8141, C8142, C8143, C8144, C8145, C8146, C8147, C8148, C8149, C8170, C8171, C8172, C8173, C8174, C8175, C8176, C8177, C8178, C8179, C8190, C8191, C8192, C8193, C8194, C8195, C8196, C8197, C8198, C8199, C8200, C8201, C8202, C8203, C8204, C8205, C8206, C8207, C8208, C8209, C8210, C8211, C8212, C8213, C8214, C8215, C8216, C8217, C8218, C8219, C8220, C8221, C8222, C8223, C8224, C8225, C8226, C8227, C8228, C8229, C8230, C8231, C8232, C8233, C8234, C8235, C8236, C8237, C8238, C8239, C8240, C8241, C8242, C8243, C8244, C8245, C8246, C8247, C8248, C8249, C8250, C8251, C8252, C8253, C8254, C8255, C8256, C8257, C8258, C8259, C8260, C8261, C8262, C8263, C8264, C8265, C8266, C8267, C8268, C8269, C8280, C8281, C8282, C8283, C8284, C8285, C8286, C8287, C8288, C8289, C8290, C8291, C8292, C8293, C8294, C8295, C8296, C8297, C8298, C8299, C8300, C8301, C8302, C8303, C8304, C8305, C8306, C8307, C8308, C8309, C8310, C8311, C8312, C8313, C8314, C8315, C8316, C8317, C8318, C8319, C8330, C8331, C8332, C8333, C8334, C8335, C8336, C8337, C8338, C8339, C8350, C8351, C8352, C8353, C8354, C8355, C8356, C8357, C8358, C8359, C8370, C8371, C8372, C8373, C8374, C8375, C8376, C8377, C8378, C8379, C8380, C8381, C8382, C8383, C8384, C8385, C8386, C8387, C8388, C8389, C8390, C8391, C8392, C8393, C8394, C8395, C8396, C8397, C8398, C8399, C8400, C8401, C8402, C8403, C8404, C8405, C8406, C8407, C8408, C8409, C8410, C8411, C8412, C8413, C8414, C8415, C8416, C8417, C8418, C8419, C8440, C8441, C8442, C8443, C8444, C8445, C8446, C8447, C8448, C8449, C8460, C8461, C8462, C8463, C8464, C8465, C8466, C8467, C8468, C8469, C8470, C8471, C8472, C8473, C8474, C8475, C8476, C8477, C8478, C8479, C8490, C8491, C8492, C8493, C8494, C8495, C8496, C8497, C8498, C8499, C84A0, C84A1, C84A2, C84A3, C84A4, C84A5, C84A6, C84A7, C84A8, C84A9, C84Z0, C84Z1, C84Z2, C84Z3, C84Z4, C84Z5, C84Z6, C84Z7, C84Z8, C84Z9, C8510, C8511, C8512, C8513, C8514, C8515, C8516, C8517, C8518, C8519, C8520, C8521, C8522, C8523, C8524, C8525, C8526, C8527, C8528, C8529, C8580, C8581, C8582, C8583, C8584, C8585, C8586, C8587, C8588, C8589, C8590, C8591, C8592, C8593, C8594, C8595, C8596, C8597, C8598, C8599, C860, C861, C862, C863, C864, C865, C866, C880, C882, C883, C884, C888, C889, C9000, C9001, C9002, C9010, C9011, C9012, C9020, C9021, C9022, C9030, C9031, C9032, C960, C962, C9620, C9621, C9622, C9629, C964, C969, C96A, C96Z, D47Z9
Fluid and Electrolyte Disorder	E860, E861, E869, E870, E871, E872, E873, E874, E875, E876, E8770, E8771, E8779, E878
Metastatic Cancer	C770, C771, C772, C773, C774, C775, C778, C779, C7800, C7801, C7802, C781, C782, C7830, C7839, C784, C785, C786, C787, C7880, C7889, C7900, C7901, C7902, C7910, C7911, C7919, C792, C7931, C7932, C7940, C7949, C7951, C7952, C7960, C7961, C7962, C7970, C7971, C7972, C7981, C7982, C7989, C799, C7B00, C7B01, C7B02, C7B03, C7B04, C7B09, C7B1, C7B8, C800, C801, R180
Neurological Disorder	E7500, E7501, E7502, E7509, E7510, E7511, E7519, E7523, E7525, E7526, E7529, E754, F842, G10, G110, G111, G112, G113, G114, G118, G119, G120, G121, G1220, G1221, G1222, G1223, G1224, G1225, G1229, G128, G129, G132, G138, G20, G214, G2401, G2402, G2409, G242, G248, G254, G255, G2581, G300, G301, G308, G309, G3101, G3109, G311, G312, G3181, G3182, G3183, G3184, G3185, G3189, G319, G3281, G35, G361, G368, G369, G370, G371, G372, G373, G374, G375, G378, G379, G40001, G40009, G40011, G40019, G40101, G40109, G40111, G40119, G40201, G40209, G40211, G40219, G40301, G40309, G40311, G40319, G40401, G40409, G40411, G40419, G40501, G40509, G40801, G40802, G40803, G40804, G40811, G40812, G40813, G40814, G40821, G40822, G40823, G40824, G4089, G40901, G40909, G40911, G40919, G40A01, G40A09, G40A11, G40A19, G40B01, G40B09, G40B11, G40B19, G47411, G47419, G47421, G47429, G803, G890, G910, G911, G912, G913, G914, G918, G919, G937, G9389, G939, G94, O99350, O99351, O99352, O99353, O99354, O99355, P9160, P9161, P9162, P9163, R410, R4182, R4701, R5600, R5601, R561, R569
Obesity	E6601, E6609, E661, E662, E668, E669, O99210, O99211, O99212, O99213, O99214, O99215, R939, Z6830, Z6831, Z6832, Z6833, Z6834, Z6835, Z6836, Z6837, Z6838, Z6839, Z6841, Z6842, Z6843, Z6844, Z6845, Z6854

Paralysis	G041, G800, G801, G802, G804, G808, G809, G8100, G8101, G8102, G8103, G8104, G8110, G8111, G8112, G8113, G8114, G8190, G8191, G8192, G8193, G8194, G8220, G8221, G8222, G8250, G8251, G8252, G8253, G8254, G830, G8310, G8311, G8312, G8313, G8314, G8320, G8321, G8322, G8323, G8324, G8330, G8331, G8332, G8333, G8334, G834, G835, G8381, G8382, G8383, G8384, G8389, G839, I69031, I69032, I69033, I69034, I69039, I69041, I69042, I69043, I69044, I69049, I69051, I69052, I69053, I69054, I69059, I69061, I69062, I69063, I69064, I69065, I69069, I69131, I69132, I69133, I69134, I69139, I69141, I69142, I69143, I69144, I69149, I69151, I69152, I69153, I69154, I69159, I69161, I69162, I69163, I69164, I69165, I69169, I69231, I69232, I69233, I69234, I69239, I69241, I69242, I69243, I69244, I69249, I69251, I69252, I69253, I69254, I69259, I69261, I69262, I69263, I69264, I69265, I69269, I69331, I69332, I69333, I69334, I69339, I69341, I69342, I69343, I69344, I69349, I69351, I69352, I69353, I69354, I69359, I69361, I69362, I69363, I69364, I69365, I69369, I69831, I69832, I69833, I69834, I69839, I69841, I69842, I69843, I69844, I69849, I69851, I69852, I69853, I69854, I69859, I69861, I69862, I69863, I69864, I69865, I69869, I69931, I69932, I69933, I69934, I69939, I69941, I69942, I69943, I69944, I69949, I69951, I69952, I69953, I69954, I69959, I69961, I69962, I69963, I69964, I69965, I69969, R532
Peripheral Vascular Disease	I700, I701, I70201, I70202, I70203, I70208, I70209, I70211, I70212, I70213, I70218, I70219, I70221, I70222, I70223, I70228, I70229, I70231, I70232, I70233, I70234, I70235, I70238, I70239, I70241, I70242, I70243, I70244, I70245, I70248, I70249, I7025, I70261, I70262, I70263, I70268, I70269, I70291, I70292, I70293, I70298, I70299, I70301, I70302, I70303, I70308, I70309, I70311, I70312, I70313, I70318, I70319, I70321, I70322, I70323, I70328, I70329, I70331, I70332, I70333, I70334, I70335, I70338, I70339, I70341, I70342, I70343, I70344, I70345, I70348, I70349, I7035, I70361, I70362, I70363, I70368, I70369, I70391, I70392, I70393, I70398, I70399, I70401, I70402, I70403, I70408, I70409, I70411, I70412, I70413, I70418, I70419, I70421, I70422, I70423, I70428, I70429, I70431, I70432, I70433, I70434, I70435, I70438, I70439, I70441, I70442, I70443, I70444, I70445, I70448, I70449, I7045, I70461, I70462, I70463, I70468, I70469, I70491, I70492, I70493, I70498, I70499, I70501, I70502, I70503, I70508, I70509, I70511, I70512, I70513, I70518, I70519, I70521, I70522, I70523, I70528, I70529, I70531, I70532, I70533, I70534, I70535, I70538, I70539, I70541, I70542, I70543, I70544, I70545, I70548, I70549, I7055, I70561, I70562, I70563, I70568, I70569, I70591, I70592, I70593, I70598, I70599, I70601, I70602, I70603, I70608, I70609, I70611, I70612, I70613, I70618, I70619, I70621, I70622, I70623, I70628, I70629, I70631, I70632, I70633, I70634, I70635, I70638, I70639, I70641, I70642, I70643, I70644, I70645, I70648, I70649, I7065, I70661, I70662, I70663, I70668, I70669, I70691, I70692, I70693, I70698, I70699, I70701, I70702, I70703, I70708, I70709, I70711, I70712, I70713, I70718, I70719, I70721, I70722, I70723, I70728, I70729, I70731, I70732, I70733, I70734, I70735, I70738, I70739, I70741, I70742, I70743, I70744, I70745, I70748, I70749, I7075, I70761, I70762, I70763, I70768, I70769, I70791, I70792, I70793, I70798, I70799, I708, I7090, I7091, I7092, I7100, I7101, I7102, I7103, I711, I712, I713, I714, I715, I716, I718, I719, I720, I721, I722, I723, I724, I725, I726, I728, I729, I731, I7381, I7389, I739, I742, I743, I744, I76, I771, I7770, I7771, I7772, I7773, I7774, I7775, I7776, I7777, I7779, I790, I791, I798, K551, K558, K559, Z95820, Z95828
Psychosis	F200, F201, F202, F203, F205, F2081, F2089, F209, F22, F23, F24, F250, F251, F258, F259, F28, F29, F3010, F3011, F3012, F3013, F302, F303, F304, F308, F309, F310, F3110, F3111, F3112, F3113, F312, F3130, F3131, F3132, F314, F315, F3160, F3161, F3162, F3163, F3164, F3170, F3171, F3172, F3173, F3174, F3175, F3176, F3177, F3178, F3181, F3189, F319, F324, F325, F3340, F3341, F3342, F348, F3481, F3489, F349, F39, F4489, F843
Pulmonary Circulation	I2601, I2602, I2609, I2690, I2692, I2699, I270, I271, I2781, I2782, I2783, I2789, I279, I289, T800XXA, T82817A, T82818A
Chronic Kidney Disease	I120, I1311, I132, N183, N184, N185, N186, N189, N19, Z4901, Z4902, Z4931, Z4932, Z9115, Z940, Z992

Solid Tumor without Metastasis	C000, C001, C002, C003, C004, C005, C006, C008, C009, C01, C020, C021, C022, C023, C024, C028, C029, C030, C031, C039, C040, C041, C048, C049, C050, C051, C052, C058, C059, C060, C061, C062, C0680, C0689, C069, C07, C080, C081, C089, C090, C091, C098, C099, C100, C101, C102, C103, C104, C108, C109, C110, C111, C112, C113, C118, C119, C12, C130, C131, C132, C138, C139, C140, C142, C148, C153, C154, C155, C158, C159, C160, C161, C162, C163, C164, C165, C166, C168, C169, C170, C171, C172, C173, C178, C179, C180, C181, C182, C183, C184, C185, C186, C187, C188, C189, C19, C20, C210, C211, C212, C218, C220, C221, C222, C223, C224, C227, C228, C229, C23, C240, C241, C248, C249, C250, C251, C252, C253, C254, C257, C258, C259, C260, C261, C269, C300, C301, C310, C311, C312, C313, C318, C319, C320, C321, C322, C323, C328, C329, C33, C3400, C3401, C3402, C3410, C3411, C3412, C342, C3430, C3431, C3432, C3480, C3481, C3482, C3490, C3491, C3492, C37, C380, C381, C382, C383, C384, C388, C390, C399, C4000, C4001, C4002, C4010, C4011, C4012, C4020, C4021, C4022, C4030, C4031, C4032, C4080, C4081, C4082, C4090, C4091, C4092, C410, C411, C412, C413, C414, C419, C430, C4310, C4311, C43111, C43112, C4312, C43121, C43122, C4320, C4321, C4322, C4330, C4331, C4339, C434, C4351, C4352, C4359, C4360, C4361, C4362, C4370, C4371, C4372, C438, C439, C450, C451, C452, C457, C470, C4710, C4711, C4712, C4720, C4721, C4722, C473, C474, C475, C476, C478, C479, C480, C481, C482, C488, C490, C4910, C4911, C4912, C4920, C4921, C4922, C493, C494, C495, C496, C498, C499, C49A0, C49A1, C49A2, C49A3, C49A4, C49A5, C49A9, C4A0, C4A10, C4A11, C4A111, C4A112, C4A12, C4A121, C4A122, C4A20, C4A21, C4A22, C4A30, C4A31, C4A39, C4A4, C4A51, C4A52, C4A59, C4A60, C4A61, C4A62, C4A70, C4A71, C4A72, C4A8, C4A9, C50011, C50012, C50019, C50021, C50022, C50029, C50111, C50112, C50119, C50121, C50122, C50129, C50211, C50212, C50219, C50221, C50222, C50229, C50311, C50312, C50319, C50321, C50322, C50329, C50411, C50412, C50419, C50421, C50422, C50429, C50511, C50512, C50519, C50521, C50522, C50529, C50611, C50612, C50619, C50621, C50622, C50629, C50811, C50812, C50819, C50821, C50822, C50829, C50911, C50912, C50919, C50921, C50922, C50929, C510, C511, C512, C518, C519, C52, C530, C531, C538, C539, C540, C541, C542, C543, C548, C549, C55, C561, C562, C569, C5700, C5701, C5702, C5710, C5711, C5712, C5720, C5721, C5722, C573, C574, C577, C578, C579, C58, C600, C601, C602, C608, C609, C61, C6200, C6201, C6202, C6210, C6211, C6212, C6290, C6291, C6292, C6300, C6301, C6302, C6310, C6311, C6312, C632, C637, C638, C639, C641, C642, C649, C651, C652, C659, C661, C662, C669, C670, C671, C672, C673, C674, C675, C676, C677, C678, C679, C680, C681, C688, C689, C6900, C6901, C6902, C6910, C6911, C6912, C6920, C6921, C6922, C6930, C6931, C6932, C6940, C6941, C6942, C6950, C6951, C6952, C6960, C6961, C6962, C6980, C6981, C6982, C6990, C6991, C6992, C700, C701, C709, C710, C711, C712, C713, C714, C715, C716, C717, C718, C719, C720, C721, C7220, C7221, C7222, C7230, C7231, C7232, C7240, C7241, C7242, C7250, C7259, C729, C73, C7400, C7401, C7402, C7410, C7411, C7412, C7490, C7491, C7492, C750, C751, C752, C753, C754, C755, C758, C759, C760, C761, C762, C763, C7640, C7641, C7642, C7650, C7651, C7652, C768, C7A00, C7A010, C7A011, C7A012, C7A019, C7A020, C7A021, C7A022, C7A023, C7A024, C7A025, C7A026, C7A029, C7A090, C7A091, C7A092, C7A093, C7A094, C7A095, C7A096, C7A098, D030, D0310, D0311, D03111, D03112, D0312, D03121, D03122, D0320, D0321, D0322, D0330, D0339, D034, D0351, D0352, D0359, D0360, D0361, D0362, D0370, D0371, D0372, D038, D039, E3121, E3122, E3123
Peptic Ulcer	K254, K255, K256, K257, K259, K264, K265, K266, K267, K269, K274, K275, K276, K277, K279, K284, K285, K286, K287, K289
Valvular Disorder	A5203, I050, I051, I052, I058, I059, I060, I061, I062, I068, I069, I070, I071, I072, I078, I079, I080, I081, I082, I083, I088, I089, I091, I0989, I340, I341, I342, I348, I349, I350, I351, I352, I358, I359, I360, I361, I362, I368, I369, I370, I371, I372, I378, I379, I38, I39, Q230, Q231, Q232, Q233, Z952, Z953, Z954
Weight Loss	E40, E41, E42, E43, E440, E441, E45, E46, E640, R634, R636

References for Appendix

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eMethods.

An illustration of estimating risk standardized event rates to measure variation in hospital outcomes based on simulated data

Md Nazmul Islam

11/16/2020

Necessary functions

We load the necessary packages and define the inputs and outputs associated with the main functions

used in the illustration. Next we spell out the analytical functions used in the manuscript;

we define them in three sections - (A) data arrangment, (B) model fitting, and (C) visualization respectively.

```{r}

# R version 3.6.3

library(MuMIn); library(glmmTMB); library(MASS); library(dplyr); library(lme4);

library(DescTools); library(psych); library(GLMMadaptive); library(performance); library(fastDummies)


## Definitions (input)

# ylist = Response variable name; "mbr_death_flag"
```

XXX_adj = vector of all covariates; c("age", "gender", "cancer",...)

ranlist = Random effect; "(`1 | hosp_name)"

reml = TRUE; Boolean for REML, otherwise ML

Dataf_original = Original unarranged raw data (Variable names should be exactly as same as defined within this function)

Dataf = Dataframe containing reponse & covariates after arranging in appropriate category

Dataf_el = Dataframe containing response and covariates for early and late period with at-least 10 patients in each period

Data_score = Dataframe with scores having hospital names

Data_score_earlylate = Dataframe with scores having hospital names with period specifying early and late time

Data_analytical = Analytical dataframe used in computing standardized scores

hosp_id = Hospital attributes name (e.g., bed_size; see below for example)

apnd2 = Extra hospital data (as needed) to add in the dataframe

comorb_nm = Comorbidity names in details (see below for example)

addsize = TRUE; Boolean whether size is added in computing scores in hierarchical model

laplace = TRUE; Boolean if TRUE laplace approximation is adopted; otherwise

approximation of integrand is considered via Gaussian quadrature

AA/BB/CC/DD/EE/FF = Different filtering options to extract data from the Dataf_original

s1 = Difference in scores used in Bland-Altman (BA) plot

s2 = Average of scores used in BA plot

score_early2j, score_later2j = Scores for early and late period for each site used in BA plot

Definitions (Output)

fom3 = glmm object

hospital_fit_object = Hospital model fit

LRT_re = LRT of random effects

aic_null = Akaike information criteria for GLM model

aic_alt = Akaike information criteria for GLMM model

SS = Marginal & conditional R-squared (goodness of fit) for GLMM

Summary = Summary of GLMM fit

cor_lme_lmer = Correlation of fixed effects between GLM and GLMM

rank_cor = Correlation between predicted probabilities and observed responses (C and Dxy statistic) for GLMM

nY = Response

ybar = Observed death rate

orp = Coefficients estimates (fixed effects) for GLMM

RANFOM = BLUPs

or = Odds ratio based on GLMM

lb = Lower bound of 95% CI for OR

ub = Upper bound of 95% CI for OR

pred = Predicted probabilities for Dyre et al. (Numerator)

estm = Expected probabilities for Dyre et al. (Denominator)

uid = Site names

score = Score based on Dyre et al.

Score_DS_mean = Score based on Silber et al.

Score_DS = N X K matrix of scores (each patients (total N) probability for each one of the K hospitals)

unadj_score = Observed (raw) rate for each hospital

hosp_orig_vol = Volume for each hospital

Type of functions used

A1. arrange_dataf_race()

A2. arrange_dataf_hospital

A3. '%!in%'

A4. filtering_function()

A5. firstup()

A6. function_character()

B1. glmmfit()

B2. glmmfit_intslope()

B3. hospital_outcome_regression()

B4. qunitile_compare()

B5. glmmfit_patient_hospital()

C1. plotOR_paper()

C2. plotScore_paper_single_rotate()

```
# C3. bland_altman_all()

# C4. summary_statistics_table()

# C5. Compare_numeric_boxplot_ggplot()

# C6. plotOR_paper_hospital()

# C7. quintile_descriptive()


# A1. Create categorical Dataf_original (Multiple rows per site)

arrange_dataf_race <- function(Dataf_original){



 Dataf_original$academic_flag <- ifelse(Dataf_original$academic_flag == 1, "Academic",

                        ifelse(is.na(Dataf_original$academic_flag) == TRUE, NA, "Non-academic"))


 Dataf_original$non_profit_flag <- ifelse(Dataf_original$non_profit_flag == 1, "Non-profit",

                         ifelse(is.na(Dataf_original$non_profit_flag) == TRUE, NA, "Profit"))



 Dataf_original$icu_beds_class <- ifelse(Dataf_original$icu_beds < 10, "0 <= ICU < 10",

                        ifelse(Dataf_original$icu_beds >= 10 & Dataf_original$icu_beds < 20, "10 <= ICU < 20",

                            ifelse(Dataf_original$icu_beds >= 20 & Dataf_original$icu_beds < 30, "20 <= ICU < 30",

                                ifelse(Dataf_original$icu_beds >= 30 & Dataf_original$icu_beds < 40, "30 <= ICU < 40",

                                    ifelse(Dataf_original$icu_beds >= 40 & Dataf_original$icu_beds < 50, "40 <= ICU < 50",

                                        ifelse(Dataf_original$icu_beds >= 50 & Dataf_original$icu_beds < 70, "50 <= ICU < 70",

                                            ifelse(is.na(Dataf_original$icu_beds) == TRUE, NA, "70 <= ICU")))))))


 table(Dataf_original$icu_beds_class)


 summary(Dataf_original$resident_to_bed_ratio)

 Dataf_original$resident_to_bed_ratio_class <- ifelse(Dataf_original$resident_to_bed_ratio < 0.001, "0 <= Ratio <
0.001",
```

```
                        ifelse(Dataf_original$resident_to_bed_ratio >= 0.001 & Dataf_original$resident_to_bed_ratio <
0.01, "0.001 <= Ratio < 0.01",
                               ifelse(Dataf_original$resident_to_bed_ratio >= 0.01 &
Dataf_original$resident_to_bed_ratio < 0.05, "0.01 <= Ratio < 0.05",
                                      ifelse(Dataf_original$resident_to_bed_ratio >= 0.05 &
Dataf_original$resident_to_bed_ratio < 0.10, "0.05 <= Ratio < 0.10",
                                             ifelse(Dataf_original$resident_to_bed_ratio >= 0.10 &
Dataf_original$resident_to_bed_ratio < 0.15, "0.10 <= Ratio < 0.15",
                                                    ifelse(Dataf_original$resident_to_bed_ratio >= 0.15 &
Dataf_original$resident_to_bed_ratio < 0.25, "0.15 <= Ratio < 0.25",
                                                           ifelse(Dataf_original$resident_to_bed_ratio >= 0.25 &
Dataf_original$resident_to_bed_ratio < 0.50, "0.25 <= Ratio < 0.50",
                                                                  ifelse(is.na(Dataf_original$resident_to_bed_ratio) == TRUE, NA, "0.50
<= Ratio"))))))))

 table(Dataf_original$resident_to_bed_ratio_class)




 summary(Dataf_original$beds)

 Dataf_original$beds_class <- ifelse(Dataf_original$beds < 200, "0 <= Beds < 200",
                  ifelse(Dataf_original$beds >= 200 & Dataf_original$beds < 400, "200 <= Beds < 400",
                      ifelse(Dataf_original$beds >= 400 & Dataf_original$beds < 600, "400 <= Beds < 600",
                          ifelse(is.na(Dataf_original$beds) == TRUE, NA, "600 <= Beds"))))


 table(Dataf_original$beds_class)


 ## Counts of days since Feb1

 count_day <- as.numeric(c(Dataf_original$mbr_admit_dt - as.Date("2020-01-01"))) # year-month-day

 count_day_class <- ifelse(count_day <= 90, "1 < Count <= 90",
                  ifelse(count_day > 90 & count_day <= 120, "90 < Count <= 120",
                      ifelse(count_day > 120 & count_day <= 150, "120 < Count <= 150",
                          "150 < Count")))
```

```
Dataf_original$count_day  <- count_day
Dataf_original$count_day2 <- count_day^2

Dataf_original$count_day_class <- factor(count_day_class, levels = c("1 < Count <= 90", "90 < Count <= 120",
                                                                     "120 < Count <= 150", "150 < Count"))

#table(Dataf_original$count_day_class)
#table(Dataf_original$count_day_class, Dataf_original$mbr_death_flag)
#tb[, 2]/ rowSums(tb)

Dataf_original$gender <- ifelse(Dataf_original$gender == "m", "Male",
                                ifelse(Dataf_original$gender == "f", "Female", NA))

ixf <- grep("aeci_", colnames(Dataf_original),  value  = F)

QQ <- paste0("Dataf_original$", colnames(Dataf_original)[ixf]," <- Dataf_original %>% select(",
colnames(Dataf_original)[ixf],") %>%
            replace(is.na(.), 0) %>%
            mutate(", colnames(Dataf_original)[ixf]," = ifelse(", colnames(Dataf_original)[ixf]," > 0, 'Yes', 'No')) %>%
            unlist()",
            collapse = ";")
QQ <- eval(parse(text = QQ))



comorb_id <- grep("aeci_", colnames(Dataf_original),  value  = T)
```

```
Dataf_original$mapd_comm_flag <- ifelse(Dataf_original$lob == "medicare", "Medicare", "Commercial")

# age class
Dataf_original$age_class <- ifelse(Dataf_original$age <= 45, "18 < age <= 45",
                    #ifelse(Dataf_original$age > 35 & Dataf_original$age <= 45, "35 < age <= 45",
                    ifelse(Dataf_original$age > 45 & Dataf_original$age <= 55, "45 < age <= 55",
                        ifelse(Dataf_original$age > 55 & Dataf_original$age <= 65, "55 < age <= 65",
                            ifelse(Dataf_original$age > 65 & Dataf_original$age <= 75, "65 < age <= 75",
                                ifelse(Dataf_original$age > 75 & Dataf_original$age <= 85, "75 < age <= 85",

                                    "85 < age")))))



Dataf_original$elix <- ifelse(Dataf_original$elix < 0, 0, Dataf_original$elix); summary(Dataf_original$elix)
Dataf_original$elix[which(is.na(Dataf_original$elix) == TRUE)] <- 0

Dataf_original$elix_class <- ifelse(Dataf_original$elix >= 0 & Dataf_original$elix < 1, "[0, 1)",
                    ifelse(Dataf_original$elix >= 1 & Dataf_original$elix < 10, "[1, 10)",
                        ifelse(Dataf_original$elix >= 10 & Dataf_original$elix < 20, "[10, 20)",
                            ">=20")))


 Dataf_original$race_cd[which(is.na(Dataf_original$race_cd) == TRUE | Dataf_original$race_cd %in% c("hispanic",
"native american",
                                                "other", "asian"))] <- "unknown"

 Dataf_original$race_cd_class <- ifelse(Dataf_original$race_cd %!in% c("african-american", "caucasian"),
"other/unknown",
                        Dataf_original$race_cd)
```

```
Dataf_original$mbr_death_flag <- ifelse(Dataf_original$mbr_death_flag == 1, "Event", "Alive")
Dataf_original$mbr_death_flag  <- Dataf_original$mbr_death_flag %>% replace(is.na(.), "Alive")

Dataf_original$mbr_mortality_flag <- ifelse(Dataf_original$mbr_mortality_flag == 1, "Event", "Alive")
Dataf_original$mbr_mortality_flag  <- Dataf_original$mbr_mortality_flag %>% replace(is.na(.), "Alive")

Dataf_original$snf_nursing_flag <- ifelse(Dataf_original$snf_nursing_flag == 1, "Yes", "No")
Dataf_original$snf_nursing_flag  <- Dataf_original$snf_nursing_flag %>% replace(is.na(.), "No")

Dataf_original$hosp_region <- ifelse(Dataf_original$hosp_region == "ct", "Central",
                      ifelse(Dataf_original$hosp_region == "ne", "North-east",
                          ifelse(Dataf_original$hosp_region == "se", "South-east",
                              ifelse(Dataf_original$hosp_region == "we", "West", "Other"))))

Dataf_original$hosp_usr_class <- ifelse(Dataf_original$hosp_usr_class == "U", "Urban",
                        ifelse(Dataf_original$hosp_usr_class == "R", "Rural",
                            ifelse(Dataf_original$hosp_usr_class == "S", "Semi-urban",
                                "Other")))

Dataf_original$hosp_income_class <- ifelse(Dataf_original$hosp_avg_income <= 50000, "50K >= income",
                                ifelse(Dataf_original$hosp_avg_income > 50000 & Dataf_original$hosp_avg_income <= 65000, "50K
< income <= 65K",
                                    ifelse(Dataf_original$hosp_avg_income > 65000 & Dataf_original$hosp_avg_income <= 80000,
"65K < income <= 80K",
                                        "80K < income")))
```

```
 Dataf_original$mbr_income_class <- ifelse(Dataf_original$mbr_income <= 50000, "50K >= income", #"60K < income")
                        ifelse(Dataf_original$mbr_income > 50000 & Dataf_original$mbr_income <= 65000, "50K < income
<= 65K",
                               ifelse(Dataf_original$mbr_income > 65000 & Dataf_original$mbr_income <= 100000, "65K <
income <= 100K",
                                      "100K < income")))


 output = list(Dataf_original = Dataf_original, comorb_id = comorb_id)
}


# A2. Create data for hospital regression and turn one row per site data
arrange_dataf_hospital <- function(Data_score, Data_analytical, hosp_id, apnd2,
                        period = FALSE, allsite = "Yes-Median", name2add, name2add_num){

 symbol <- "\u2265"; symbol2 <- intToUtf8(8804)
 mid <- (Data_score$reference)
 Data7 <- do.call(rbind, lapply(seq_len(length(mid)), function(uu)
  Data_analytical[which(Data_analytical$hosp_name == mid[uu])[1], # same for all subjects
       colnames(Data_analytical) %in% c(hosp_id, "resident_to_bed_ratio","hosp_name", "icu_beds", "beds")]
 ))

 ## Redefining ICU
 mt <- match(Data7$hosp_name, apnd2$hosp_name)
 sum(is.na(mt))
 Data7$icu_beds <- apnd2$ICU_beds[mt]


 ## Redefining profit
```

```
Data7$non_profit_flag <- apnd2$Profit_flag[mt]
Data7$non_profit_flag <- ifelse(Data7$non_profit_flag == "For Profit", "Profit",
                        ifelse(Data7$non_profit_flag == "Not for profit", "Non-profit", "Other"))
table(Data7$non_profit_flag)

## Cases
Data7$cases_per_10k <- apnd2$cases_per_10k[mt]
Data7$`Early.Period.1/1-4/30` <- apnd2$`Early.Period.1/1-4/30`[mt]
Data7$`Late.Period:.5/1-6/30` <- apnd2$`Late.Period:.5/1-6/30`[mt]
Data7$`%.change` <- apnd2$`%.change`[mt]


## Deaths
Data7$deaths_per_10k <- apnd2$deaths_per_10k[mt]

## Redefining user class
Data7$hosp_usr_class <- apnd2$Rural_urban[mt]
Data7$hosp_usr_class <- ifelse(Data7$hosp_usr_class == "R", "Rural", "Urban")




if(period == FALSE){
  Data7$score <- unlist(lapply(seq_len(length(mid)), function(uu)
    Data_score$score[which(Data_score$reference == mid[uu])]))

  Data7$unadj_score <- unlist(lapply(seq_len(length(mid)), function(uu)
    Data_score$unadjusted_score[which(Data_score$reference == mid[uu])]))
```

```
  if(allsite == "Yes-Median") {
    grp1 <- which(Data7$score <= median(Data7$score))
    Data7$event <- rep("Worse", nrow(Data7))
    Data7$event[grp1] <- "Better"
  }

} else if(period == "Early"){

  Data7$score <- unlist(lapply(seq_len(length(mid)), function(uu)
    Data_score$early_score[which(Data_score$reference == mid[uu])]))

  Data7$unadj_score <- unlist(lapply(seq_len(length(mid)), function(uu)
    Data_score$early_unadj_score[which(Data_score$reference == mid[uu])]))

} else if(period == "Later"){

  Data7$score <- unlist(lapply(seq_len(length(mid)), function(uu)
    Data_score$later_score[which(Data_score$reference == mid[uu])]))

  Data7$unadj_score <- unlist(lapply(seq_len(length(mid)), function(uu)
    Data_score$later_unadj_score[which(Data_score$reference == mid[uu])]))
} else if(period == "Both"){
  ## Defining response %increment
  Data7$early_score <- unlist(lapply(seq_len(length(mid)), function(uu)
    Data_score$early_score[which(Data_score$reference == mid[uu])]))

  Data7$later_score <- unlist(lapply(seq_len(length(mid)), function(uu)
    Data_score$later_score[which(Data_score$reference == mid[uu])]))

  incr <- (Data7$later_score - Data7$early_score) / Data7$early_score * 100
  grp1 <- which(incr <= -50)
```

```
  length(grp1)

  Data7$event <- rep("Worse", nrow(Data7))
  Data7$event[grp1] <- "Better"
  table(Data7$event)

  Data7$difference <- Data7$later_score - Data7$early_score
}

dim(Data7)



# icu
Data7$icu_beds_class <- ifelse(Data7$icu_beds < 20, "0 <= ICU < 20",
                        ifelse(Data7$icu_beds >= 20 & Data7$icu_beds < 60, "20 <= ICU < 60",
                            #ifelse(Data7$icu_beds >= 60 & Data7$icu_beds < 100, "60 <= ICU < 100",
                            # ifelse(Data7$icu_beds >= 90 & Data7$icu_beds < 120, "90 <= ICU < 120",
                            ifelse(is.na(Data7$icu_beds) == TRUE, NA, "60 <= ICU")))
table(Data7$icu_beds_class); sum(is.na(Data7$icu_beds_class))
t1 <- table(Data7$icu_beds_class, Data7$event)
t1[, 2] / rowSums(t1)

# beds
Data7$beds_class <- ifelse(Data7$beds < 150, "0 <= Beds < 150",
                    ifelse(Data7$beds >= 150 & Data7$beds < 300, "150 <= Beds < 300",
                        ifelse(Data7$beds >= 300 & Data7$beds < 450, "300 <= Beds < 450",
                            #ifelse(Data7$beds >= 450 & Data7$beds < 600, "450 <= Beds < 600",
                            ifelse(is.na(Data7$beds) == TRUE, NA, "450 <= Beds"))))
table(Data7$beds_class); sum(is.na(Data7$beds_class))
t1 <- table(Data7$beds_class, Data7$event)
t1[, 2] / rowSums(t1)
```

```
# ratio
Data7$resident_to_bed_ratio_class <- ifelse(Data7$resident_to_bed_ratio < 0.05, "0 <= Ratio < 0.05",
                                    ifelse(Data7$resident_to_bed_ratio >= 0.05 & Data7$resident_to_bed_ratio < 0.25, "0.05 <=
Ratio < 0.25",
                                           ifelse(is.na(Data7$resident_to_bed_ratio) == TRUE, NA, "0.25 <= Ratio")))
table(Data7$resident_to_bed_ratio_class); sum(is.na(Data7$resident_to_bed_ratio_class))

table(Data7$hosp_usr_class)

# cases
summary(Data7$cases_per_10k)
summary(Data7$deaths_per_10k)

Data7$cases_class <- ifelse(Data7$cases_per_10k < 20, "0 <= Cases < 20",
                            ifelse(Data7$cases_per_10k >= 20 & Data7$cases_per_10k < 40, "20 <= Cases < 40",
                                   ifelse(is.na(Data7$cases_per_10k) == TRUE, NA, "40 <= Cases")))

Data7$cases_class_early <- ifelse(Data7$`Early.Period.1/1-4/30` < 20, "0 <= Cases < 20",
                                  ifelse(Data7$`Early.Period.1/1-4/30` >= 20 & Data7$`Early.Period.1/1-4/30` < 40, "20 <= Cases < 40",

                                         ifelse(is.na(Data7$`Early.Period.1/1-4/30`) == TRUE, NA, "40 <= Cases")))

Data7$cases_class_late <- ifelse(Data7$`Late.Period:.5/1-6/30` < 20, "0 <= Cases < 20",
                                 ifelse(Data7$`Late.Period:.5/1-6/30` >= 20 & Data7$`Late.Period:.5/1-6/30` < 40, "20 <= Cases < 40",

                                        ifelse(is.na(Data7$`Late.Period:.5/1-6/30`) == TRUE, NA, "40 <= Cases")))


Data7$cases_class_late_diff <- ifelse(Data7$`Late.Period:.5/1-6/30` < 30, "0 <= Cases < 30",
```

```
                        ifelse(Data7$`Late.Period:.5/1-6/30` >= 30 & Data7$`Late.Period:.5/1-6/30` < 60, "30 <= Cases <
60",
                               ifelse(Data7$`Late.Period:.5/1-6/30` >= 60 & Data7$`Late.Period:.5/1-6/30` < 90, "60 <= Cases
< 90",
                                      ifelse(is.na(Data7$`Late.Period:.5/1-6/30`) == TRUE, NA, "90 <= Cases"))))


 Data7$cases_change_binary <- ifelse(Data7$`%.change` < 0, "Decrease",
                        ifelse(is.na(Data7$`%.change`) == TRUE, NA, "Increase"))



 Data7$cases_interaction <- ifelse(Data7$cases_change_binary == "Increase" & Data7$cases_class_early == "20 <=
Cases < 40", "20 <= Cases < 40 & Increase",
                          ifelse(Data7$cases_change_binary == "Increase" & Data7$cases_class_early == "40 <= Cases", "40
<= Cases & Increase", "otherwise"))




 Data7$`%.change` <- Data7$`%.change` * 100
 Data7$cases_change <- ifelse(Data7$`%.change` < 0, "<0%",
                       ifelse(Data7$`%.change` >= 0 & Data7$`%.change` < 100, "[0,100)%",
                           ifelse(Data7$`%.change` >= 100 & Data7$`%.change` < 250, "[100,250)%",
                               ifelse(is.na(Data7$`%.change`) == TRUE, NA, ">=250%"))))



 table(Data7$cases_class_late); sum(is.na(Data7$cases_class))
 table(Data7$cases_change)
 t1 <- table(Data7$cases_class, Data7$event)
 t1[, 2] / rowSums(t1)


 # deaths
```

```
Data7$deaths_class <- ifelse(Data7$deaths_per_10k < 1, "0 <= Deaths < 1",
                      ifelse(Data7$deaths_per_10k >= 1 & Data7$deaths_per_10k < 3, "1 <= Deaths < 3",
                        ifelse(Data7$deaths_per_10k >= 3 & Data7$deaths_per_10k < 5, "3 <= Deaths < 5",
                          ifelse(is.na(Data7$deaths_per_10k) == TRUE, NA, "5 <= Deaths"))))
table(Data7$deaths_class); sum(is.na(Data7$deaths_class))
t1 <- table(Data7$deaths_class, Data7$event)
t1[, 2] / rowSums(t1)



# Combination
Data7$combination1_flag <- ifelse(Data7$resident_to_bed_ratio <= 0.25 & Data7$academic_flag == "Academic",
                          "Academic|<=0.25", ifelse(Data7$resident_to_bed_ratio > 0.25 & Data7$academic_flag ==
"Academic",
                                                    "Academic|>0.25", "Non"))

Data7$combination2_flag <- ifelse(Data7$resident_to_bed_ratio <= 0.25 & Data7$academic_flag == "Academic",
"Academic|<=0.25",
                          ifelse(Data7$resident_to_bed_ratio > 0.25 & Data7$academic_flag == "Academic",
"Academic|>0.25",
                            ifelse(Data7$resident_to_bed_ratio <= 0.25 & Data7$academic_flag == "Non-academic",
"Non|<=0.25",
                              ifelse(Data7$resident_to_bed_ratio > 0.25 & Data7$academic_flag == "Non-academic",
"Non|>0.25", NA))))

table(Data7$combination2_flag)



Data7 <- Data7 %>% mutate_if(is.character, as.factor)
Data7 <- within(Data7, event <- relevel(event, ref = "Better"))
Data7 <- within(Data7, icu_beds_class <- relevel(icu_beds_class, ref = "0 <= ICU < 20"))
Data7 <- within(Data7, resident_to_bed_ratio_class <- relevel(resident_to_bed_ratio_class, ref = "0 <= Ratio < 0.05"))
Data7 <- within(Data7, beds_class <- relevel(beds_class, ref = "0 <= Beds < 150"))
Data7 <- within(Data7, academic_flag <- relevel(academic_flag, ref = "Academic"))
```

```
Data7 <- within(Data7, hosp_usr_class  <- relevel(hosp_usr_class, ref = "Rural"))

Data7 <- within(Data7, non_profit_flag  <- relevel(non_profit_flag, ref = "Profit"))

Data7 <- within(Data7, hosp_region  <- relevel(hosp_region, ref = "Central"))

Data7 <- within(Data7, deaths_class  <- relevel(deaths_class, ref = "0 <= Deaths < 1"))

Data7 <- within(Data7, cases_class  <- relevel(cases_class, ref = "0 <= Cases < 20"))

Data7 <- within(Data7, cases_class_early  <- relevel(cases_class_early, ref = "0 <= Cases < 20"))

Data7 <- within(Data7, cases_class_late  <- relevel(cases_class_late, ref = "0 <= Cases < 20"))

Data7 <- within(Data7, cases_class_late_diff  <- relevel(cases_class_late_diff, ref = "0 <= Cases < 30"))

Data7 <- within(Data7, cases_change  <- relevel(cases_change, ref = "<0%"))

Data7 <- within(Data7, cases_interaction  <- relevel(cases_interaction, ref = "otherwise"))

Data7 <- within(Data7, cases_change_binary  <- relevel(cases_change_binary, ref = "Decrease"))

Data7 <- within(Data7, combination1_flag  <- relevel(combination1_flag, ref = "Non"))

Data7 <- within(Data7, combination2_flag  <- relevel(combination2_flag, ref = "Non|>0.25"))



## Hospital levels variables

# user

mlist_user <- c("hosp_usr_class"); varlist_user <- c("Location::Urban");

reflist_user <- rep("Rural", length(varlist_user)); mlist0_user <- rep("hosp_usr_class", length(varlist_user))


# ratio

mlist_ratio <- c("resident_to_bed_ratio_class"); varlist_ratio <- c("Resident to bed ratio::[0.05,0.25)", paste0("Resident to bed ratio::", symbol,"0.25"));

reflist_ratio <- rep("[0,0.05)", length(varlist_ratio)); mlist0_ratio <- rep("resident_to_bed_ratio_class", length(varlist_ratio))


# ICU

mlist_icu <- c("icu_beds_class"); varlist_icu <- c("Number of ICU beds::[20,60)",

                                    #"Number of ICU beds::[60,100)",
```

```
                                    paste0("Number of ICU beds::", symbol,"60"));
reflist_icu <- rep("[0,20)", length(varlist_icu)); mlist0_icu <- rep("icu_beds_class", length(varlist_icu))



# Combination1
mlist_combination1 <- c("combination1_flag"); varlist_combination1 <- c(paste0("Academic|",symbol2,"0.25",
"Academic|>0.25"));
reflist_combination1 <- rep("Non", length(varlist_combination1));
mlist0_combination1 <- rep("combination1_flag", length(varlist_combination1))

# Combination2
mlist_combination2 <- c("combination2_flag"); varlist_combination2 <- c(paste0("Academic|",symbol2,"0.25"),
                                        "Academic|>0.25", paste0("Non|",symbol2,"0.25"));
reflist_combination2 <- rep("Non|>0.25", length(varlist_combination2));
mlist0_combination2 <- rep("combination2_flag", length(varlist_combination2))



# region
mlist_region <- c("hosp_region"); varlist_region <- c("Region::North-east",
                                    "Region::South-east",
                                    "Region::West");
reflist_region <- rep("Central", length(varlist_region)); mlist0_region <- rep("hosp_region", length(varlist_region))

# beds
mlist_beds <- c("beds_class"); varlist_beds <- c("Number of beds::[150,300)",
                                "Number of beds::[300,450)",
                                paste0("Number of beds::", symbol,"450"));
reflist_beds <- rep("[0,150)", length(varlist_beds)); mlist0_beds <- rep("beds_class", length(varlist_beds))

# academic
```

```
mlist_academic <- c("academic_flag"); varlist_academic <- c("Hospital affiliation::Non-academic");

reflist_academic <- rep("Academic", length(varlist_academic)); mlist0_academic <- rep("academic_flag", length(varlist_academic))


# profit

mlist_profit <- c("non_profit_flag"); varlist_profit <- c("Profit status::Non-profit", "Profit status::Other");

reflist_profit <- rep("For profit", length(varlist_profit)); mlist0_profit <- rep("non_profit_flag", length(varlist_profit))



# cases

mlist_cases <- c("cases_class"); varlist_cases <- c("Cases per 10K::[20,40)",

                                    paste0("Cases per 10K::", symbol,"40"));

reflist_cases <- rep("[0,20)", length(varlist_cases)); mlist0_cases <- rep("cases_class", length(varlist_cases))



# cases early

mlist_casesearly <- c("cases_class_early"); varlist_casesearly <- c("Cases (early) per 10K::[20,40)",

                                        paste0("Cases (early) per 10K::", symbol,"40"));

reflist_casesearly <- rep("[0,20)", length(varlist_casesearly)); mlist0_casesearly <- rep("cases_class_early", length(varlist_casesearly))


# cases late

mlist_caseslate <- c("cases_class_late"); varlist_caseslate <- c("Cases (late) per 10K::[20,40)",

                                      paste0("Cases (late) per 10K::", symbol,"40"));

reflist_caseslate <- rep("[0,20)", length(varlist_caseslate)); mlist0_caseslate <- rep("cases_class_late", length(varlist_caseslate))


# cases change

mlist_caseschange <- c("cases_change"); varlist_caseschange <- c("Cases change %::[0,100)", "Cases change %::[100,250)",

                                      paste0("Cases change %::", symbol,"250"));

reflist_caseschange <- rep("<0%", length(varlist_caseschange)); mlist0_caseschange <- rep("cases_change", length(varlist_caseschange))
```

```
# cases change binary

mlist_caseschangebinary <- c("cases_change_binary"); varlist_caseschangebinary <- c("Cases change::Increase");

reflist_caseschangebinary <- rep("Decrease", length(varlist_caseschangebinary));

mlist0_caseschangebinary <- rep("cases_change_binary", length(varlist_caseschangebinary))



# cases interaction (MATCH HOW MANY CASE BUCKETS YOU HAVE)

mlist_casesinteraction <- c("cases_interaction"); varlist_casesinteraction <- c("Cases::[20,40) & Increase",
paste0("Cases::", symbol,"40 & Increase"));

reflist_casesinteraction <- rep("otherwise", length(varlist_casesinteraction)); mlist0_casesinteraction <-
rep("cases_interaction",

                                                    length(varlist_casesinteraction))



# cases late

mlist_caseslatediff <- c("cases_class_late_diff"); varlist_caseslatediff <- c("Cases (late) per 10K::[30,60)", "Cases (late)
per 10K::[60,90)",

                                                paste0("Cases (late) per 10K::", symbol,"90"));

reflist_caseslatediff <- rep("[0,30)", length(varlist_caseslatediff)); mlist0_caseslatediff <- rep("cases_class_late_diff",
length(varlist_caseslatediff))



# deaths

mlist_deaths <- c("cases_class"); varlist_deaths <- c("Deaths per 10K::[1,3)", "Deaths per 10K::[3,5)",

                                        paste0("Deaths per 10K::", symbol,"5"));

reflist_deaths <- rep("[0,1)", length(varlist_deaths)); mlist0_deaths <- rep("deaths_class", length(varlist_deaths))



name2add <- name2add;
```

```
name2add_num <- name2add_num


## This to use for descriptive statistics
Data73 <- Data7[, colnames(Data7) %in% c("score", "cases_class", "cases_class_early",
                                         "cases_class_late", "cases_class_late_diff",
                                         "cases_change", "cases_interaction", "cases_change_binary", "deaths_class",
                                         "academic_flag", "non_profit_flag",
                                         "beds_class", "hosp_usr_class",
                                         "combination1_flag", "combination2_flag",
                                         "icu_beds_class", "resident_to_bed_ratio_class",
                                         "hosp_name", "event",
                                         "hosp_state", "hosp_region", name2add)]
if(period == "Both"){
  Data73 <- Data7[, colnames(Data7) %in% c("score", "difference", "cases_class", "cases_class_early",
                                           "cases_class_late", "cases_interaction", "cases_class_late_diff",
                                           "cases_change", "cases_change_binary", "deaths_class",
                                           "academic_flag", "non_profit_flag",
                                           "beds_class", "hosp_usr_class",
                                           "combination1_flag", "combination2_flag",
                                           "icu_beds_class", "resident_to_bed_ratio_class",
                                           "hosp_name", "event",
                                           "hosp_state", "hosp_region", name2add)]
}

Data73 <- Data73[complete.cases(Data73), ] # for descriptive statistics


Data72 <- Data7[, colnames(Data7) %in% c("score", name2add, "cases_class", "cases_class_early",
                                         "cases_class_late", "cases_interaction", "cases_class_late_diff",
                                         "cases_change", "cases_change_binary", "hosp_name", "event",
                                         "hosp_state", "hosp_region")]
dim(Data72)
```

```
 if(period == "Both"){
  Data72 <- Data7[, colnames(Data7) %in% c("score", "cases_class", "cases_class_early",
                                           "cases_class_late", "cases_interaction", "cases_class_late_diff",
                                           "cases_change", "cases_change_binary",
                                           "difference", name2add, "hosp_name", "event",
                                           "hosp_state", "hosp_region")]
 }

 Data72 <- Data72[complete.cases(Data72), ]


 output = list(Data7 = Data7, Data72 = Data72, Data73 = Data73,

          name2add = name2add, name2add_num = name2add_num,

          mlist_combination2 = mlist_combination2,  reflist_combination2 =  reflist_combination2,
          varlist_combination2 = varlist_combination2, mlist0_combination2 = mlist0_combination2,

          mlist_combination1 = mlist_combination1,  reflist_combination1 =  reflist_combination1,
          varlist_combination1 = varlist_combination1, mlist0_combination1 = mlist0_combination1,

          mlist_user =  mlist_user, varlist_user = varlist_user, reflist_user = reflist_user, mlist0_user  = mlist0_user,

          mlist_region = mlist_region, mlist0_region = mlist0_region, varlist_region = varlist_region, reflist_region =
reflist_region,

          mlist_profit = mlist_profit, mlist0_profit = mlist0_profit, varlist_profit = varlist_profit, reflist_profit =
reflist_profit,

          mlist_beds = mlist_beds,  reflist_beds =  reflist_beds,
```

mlist0_beds = mlist0_beds, varlist_beds = varlist_beds,

mlist_academic = mlist_academic, reflist_academic = reflist_academic,
varlist_academic = varlist_academic, mlist0_academic = mlist0_academic,

mlist_icu = mlist_icu, reflist_icu = reflist_icu,
mlist0_icu = mlist0_icu, varlist_icu = varlist_icu,

mlist_deaths = mlist_deaths, varlist_deaths = varlist_deaths,
reflist_deaths = reflist_deaths, mlist0_deaths = mlist0_deaths,

mlist_cases = mlist_cases, varlist_cases = varlist_cases,
reflist_cases = reflist_cases, mlist0_cases = mlist0_cases,

mlist_caseschange = mlist_caseschange, varlist_caseschange = varlist_caseschange,
reflist_caseschange = reflist_caseschange, mlist0_caseschange = mlist0_caseschange,

mlist_caseschangebinary = mlist_caseschangebinary, varlist_caseschangebinary = varlist_caseschangebinary,
reflist_caseschangebinary = reflist_caseschangebinary, mlist0_caseschangebinary = mlist0_caseschangebinary,

mlist_casesearly = mlist_casesearly, varlist_casesearly = varlist_casesearly,
reflist_casesearly = reflist_casesearly, mlist0_casesearly = mlist0_casesearly,

mlist_caseslate = mlist_caseslate, varlist_caseslate = varlist_caseslate,
reflist_caseslate = reflist_caseslate, mlist0_caseslate = mlist0_caseslate,

mlist_caseslatediff = mlist_caseslatediff, varlist_caseslatediff = varlist_caseslatediff,
reflist_caseslatediff = reflist_caseslatediff, mlist0_caseslatediff = mlist0_caseslatediff,

```
        mlist_casesinteraction = mlist_casesinteraction, varlist_casesinteraction = varlist_casesinteraction,
        reflist_casesinteraction = reflist_casesinteraction, mlist0_casesinteraction = mlist0_casesinteraction,

        mlist_ratio  = mlist_ratio, varlist_ratio  = varlist_ratio, reflist_ratio = reflist_ratio, mlist0_ratio  = mlist0_ratio)
}



# A3. Not exist
'%!in%' <- function(x, y) !('%in%'(x, y))

# A4. Filtering function
filtering_function <- function(AA, BB, CC, DD, EE, FF, Main){

 Main2G <- Main
 dim(Main2G)

 if(AA != "none"){
  mystring <- AA #input$filter_desc1
  splt <- unlist(strsplit(mystring, "::"))
  AA1 <- splt[1]
  AA2 <- ifelse(splt[2] == "Yes", 'Yes', ifelse(splt[2] == "No", 'No', splt[2]))
  filter <- paste0("which(Main2G$", AA1, " == '", AA2, "')", sep = "")
  filter <- eval(parse(text = filter))
  if(length(filter) > 0){
   Main2G <- Main2G[filter, ] # creating subset by filters
  } else{
   Main2G <- Main2G
  }
 }
 dim(Main2G)
```

```
if(BB != "none"){

 mystring <- BB #input$filter_desc2 # then do it for second filter

 if(mystring == ">= 1mo in 2019"){
  filter2 <- which(Main2G$mm_2019 >= 1)
 } else if(mystring == ">= 2mo in 2019"){
  filter2 <- which(Main2G$mm_2019 >= 2)
 } else if(mystring == ">= 3mo in 2019"){
  filter2 <- which(Main2G$mm_2019 >= 3)
 } else if(mystring == ">= 4mo in 2019"){
  filter2 <- which(Main2G$mm_2019 >= 4)
 } else if(mystring == ">= 5mo in 2019"){
  filter2 <- which(Main2G$mm_2019 >= 5)
 } else if(mystring == ">= 6mo in 2019"){
  filter2 <- which(Main2G$mm_2019 >= 6)
 } else if(mystring == ">= 7mo in 2019"){
  filter2 <- which(Main2G$mm_2019 >= 7)
 } else if(mystring == ">= 8mo in 2019"){
  filter2 <- which(Main2G$mm_2019 >= 8)
 } else if(mystring == ">= 9mo in 2019"){
  filter2 <- which(Main2G$mm_2019 >= 9)
 } else if(mystring == ">= 10mo in 2019"){
  filter2 <- which(Main2G$mm_2019 >= 10)
 } else if(mystring == ">= 11mo in 2019"){
  filter2 <- which(Main2G$mm_2019 >= 11)
 } else if(mystring == "12mo in 2019"){
  filter2 <- which(Main2G$mm_2019 >= 12)
 }
 length(filter2)
```

```
  if(length(filter2) > 0){
    Main2G <- Main2G[filter2, ] # creating subset by filters
  } else{
    Main2G <- Main2G
  }

  #Main2G <- Main2G[filter2, ]

}
dim(Main2G)

CC_num <- 1
if(CC != "none"){ ## Counts

  #CC <- "Patient counts >= 10"
  CC_num <- as.numeric(strsplit(CC, ">=")[[1]][2])

  filter3 <- which(Main2G$hosp_patient_cnts >= CC_num)

  if(length(filter3) > 0){
    Main2G <- Main2G[filter3, ] # creating subset by filters
    #Main2G <- Main2G[Main2G$hosp_name %in% select_hosp, ]
  } else{
    Main2G <- Main2G
  }
}
dim(Main2G)

if(DD != "none"){# lob
  filter4 <- which(Main2G$mapd_comm_flag == DD)
```

```
  if(length(filter4) > 0){
    Main2G <- Main2G[filter4, ] # creating subset by filters
  } else{
    Main2G <- Main2G
  }

  #Main2G <- Main2G[which(Main2G$mapd_comm_flag == DD), ]
}
dim(Main2G)

if(EE != "none"){ #EE

  filter5 <- which(Main2G$age >=
                     as.numeric(strsplit(EE, ">=")[[1]][2]))

  if(length(filter5) > 0){
    Main2G <- Main2G[filter5, ] # creating subset by filters
  } else{
    Main2G <- Main2G
  }

}
dim(Main2G)


if(FF != "none"){ # readmitted/transferred

  filter6 <- which(Main2G$diff_hosp_flag == ifelse(FF == "Excluding readmission/transfer patients", 0, 1))

  if(length(filter6) > 0){
    Main2G <- Main2G[filter6, ] # creating subset by filters
```

```
  } else{
    Main2G <- Main2G
  }

  #Main2G <- Main2G[which(Main2G$diff_hosp_flag == ifelse(FF == "Excluding readmission/transfer patients", 0, 1)), ]
 }
 dim(Main2G)

 output = list(Main2G = Main2G, CC_num = CC_num)
}

# A5. Upper case
firstup <- function(x) {
 substr(x, 1, 1) <- toupper(substr(x, 1, 1))
 x
}

# A6. Set reference group in categorical data
function_character <- function(Data22, variable_list_BAR, count_variable = TRUE){

 symbol <- "\u2265"; symbol2 <- intToUtf8(8804)

 Data22 <- Data22 %>% mutate_if(is.character, as.factor)

 if(length(grep(variable_list_BAR, "Income", value = TRUE)) > 0){
  Data22 <- within(Data22, hosp_income_class <- relevel(hosp_income_class, ref = "80K < income"))
 }
 if(length(grep(variable_list_BAR, "ICU", value = TRUE)) > 0){
  Data22 <- within(Data22, icu_beds_class <- relevel(icu_beds_class, ref = "70 <= ICU"))
 }
 if(length(grep(variable_list_BAR, "Ratio", value = TRUE)) > 0){
```

```
  Data22 <- within(Data22, resident_to_bed_ratio_class <- relevel(resident_to_bed_ratio_class, ref = "0.50 <= Ratio"))
}
if(length(grep(variable_list_BAR, "Beds", value = TRUE)) > 0){
  Data22 <- within(Data22, beds_class <- relevel(beds_class, ref = "600 <= Beds"))
}
if(length(grep(variable_list_BAR, "Academic", value = TRUE)) > 0){
  Data22 <- within(Data22, academic_flag <- relevel(academic_flag, ref = "Academic"))
}
if(length(grep(variable_list_BAR, "Profit", value = TRUE)) > 0){
  Data22 <- within(Data22, non_profit_flag <- relevel(non_profit_flag, ref = "Non-profit"))
}
if(length(grep(variable_list_BAR, "User", value = TRUE)) > 0){
  Data22 <- within(Data22, hosp_usr_class  <- relevel(hosp_usr_class, ref = "Rural"))
}



if(length(grep(variable_list_BAR, "Race", value = TRUE)) > 0){
  Data22 <- within(Data22, race_cd_class <- relevel(race_cd_class, ref = "caucasian"))
}
if(length(grep(variable_list_BAR, "Age", value = TRUE)) > 0){
  Data22 <- within(Data22, age_class <- relevel(age_class, ref = "18 < age <= 45"))
}
if(length(grep(variable_list_BAR, "Gender", value = TRUE)) > 0){
  Data22 <- within(Data22, gender <- relevel(gender, ref = "Female"))
}
if(length(grep(variable_list_BAR, "Elix", value = TRUE)) > 0){
  Data22 <- within(Data22, elix_class <- relevel(elix_class, ref = "[0, 1)"))
}
if(count_variable  == TRUE){
  if(length(grep(variable_list_BAR, "Count", value = TRUE)) > 0){
    Data22 <- within(Data22, count_day_class <- relevel(count_day_class, ref = "150 < Count"))
```

```
  }
 }

 if(length(grep(variable_list_BAR, "Comorbidity", value = TRUE)) > 0){
  QQ <- paste0("Data22 <- within(Data22, ", comorb_id, " <- relevel(",comorb_id, ", ref = 'No'))", collapse = "; ")
  QQ <- eval(parse(text = QQ))
 }
 if(length(grep(variable_list_BAR, "Nurse", value = TRUE)) > 0){
  Data22 <- within(Data22, snf_nursing_flag  <- relevel(snf_nursing_flag, ref = "No"))
 }

 if(length(grep(variable_list_BAR, "LOB", value = TRUE)) > 0){
  Data22 <- within(Data22, lob  <- relevel(lob, ref = "commercial"))
 }
 if(length(grep(variable_list_BAR, "Numeric", value = TRUE)) > 0){
  Data22$count_day <- scale(Data22$count_day)
  Data22$count_day2 <- scale(Data22$count_day2)
 }

 try(Data22 <- within(Data22, mbr_death_flag <- relevel(mbr_death_flag, ref = "Alive")))

 try(Data22 <- within(Data22, mbr_mortality_flag <- relevel(mbr_mortality_flag, ref = "Alive")))


 Data22 <- Data22[order(Data22$hosp_name), ] # order by hosp name

 output = list(Data22 = Data22)
}


# B1. Single GLMM fit
```

```
glmmfit <- function(ylist, XXX_adj, ranlist, reml, Dataf, addsize = FALSE, laplace = TRUE){

 ## Base model (GLM) ##
 a1 <- paste0("glm(", ylist," ~ ")
 a2 <- paste0("", XXX_adj, "", collapse = " + ")
 QQ <- paste0("", a1, "", a2, ", data = Dataf, family = binomial(link = 'logit'))") # remove NAs by default
 fom <- try(eval(parse(text = QQ)))



 ## glmm
 if(laplace == TRUE){
  a1 <- paste0("glmmTMB(", ylist," ~ ", ranlist, " + ")
  a2 <- paste0("", XXX_adj, "", collapse = " + ")
  QQ <- paste0("", a1, "", a2, ", REML = reml, data = Dataf, family = binomial)") # remove NAs by default
  system.time(fom3 <- try(eval(parse(text = QQ))))
  summary(fom3)
 } else if(laplace == FALSE){
  # Get the parenthesis and what is inside
  # Remove parenthesis
  ranlist <- substring(ranlist, 2, nchar(ranlist) - 1) # extract within parenthesis
  a1 <- paste0("", ylist," ~ ")
  a2 <- paste0("", XXX_adj, "", collapse = " + ")
  QQ <- paste0("GLMMadaptive::mixed_model(fixed = ", a1, "", a2, ", random = ~", ranlist, ",
               data = Dataf, family = binomial(), control = list(nAGQ = 11))")
  system.time(fom3 <- try(eval(parse(text = QQ))))
  summary(fom3)
 }

 ## Testing variance (RE)
 x2 <- as.numeric(-2 * logLik(fom) + 2 * logLik(fom3))
 LRT_re <- 0.5 * (1 - pchisq(x2, df = 1))
```

```
## AIC
aic_null <- AIC(logLik(fom))
aic_alt <- AIC(logLik(fom3))

bic_null <- BIC(fom)
bic_alt <- BIC(fom3)



if(laplace == TRUE){
  ## Correlation test
  cor_lme_lmer <- cor.test(coef(fom), fixef(fom3)$cond) ## Assessing model performance (conditional/marginal R2)
  SS <- MuMIn::r.squaredGLMM(fom3) ## confidence intervals for the variances of the random intercepts
  varint <- confint(fom3)[-c(1 : length(fixef(fom3)$cond)), ]
  VIFfx <- NULL
} else if(laplace == FALSE){
  ## Correlation test
  cor_lme_lmer <- cor.test(coef(fom), fixef(fom3)) ## Assessing model performance (conditional/marginal R2)
  SS <- r2_nakagawa(fom3, by_group = FALSE)
  varint <- confint(fom3, parm = "var-cov", level = 0.95) ## confidence intervals for the variances of the random
intercepts
  VIFfx <- VIF(fom3, type = "fixed") ## Variance inflation
}

## C and Dxy: correlation between predicted probabilities and observed responses
if(ylist == "mbr_death_flag"){
  nY <- ifelse(Dataf$mbr_death_flag == "Event", 1, 0)
} else if(ylist == "mbr_mortality_flag"){
  nY <- ifelse(Dataf$mbr_mortality_flag == "Event", 1, 0)
}
probs <- binomial()$linkinv(predict(fom3))
```

```
rank_cor <- .somers2(probs, as.numeric(nY))



## Generating scores
sm <- summary(fom3)
if(laplace == TRUE){
  orp <- sm$coefficients$cond[-1, 1] #$coefficients[-1, 1]
  or <- exp(orp)
  VCV <- vcov(fom3, sandwich = TRUE)
  sdorp <- sqrt(diag(VCV$cond)[-1])
  BN <- exp(confint(fom3, level = 0.95))
  BN <- BN[-c(1, nrow(BN)), ] # taking-out intercept and variance
} else if(laplace == FALSE){
  orp <- sm$coef_table[-1, 1]
  or <- exp(orp)
  VCV <- vcov(fom3, sandwich = TRUE)
  sdorp <- sqrt(diag(VCV)[-c(1, length(diag(VCV)))])
  BN <- exp(confint(fom3, parm = "fixed-effects", level = 0.95))[-1, ]
}
lb <- BN[, 1]
ub <- BN[, 3]



## Estimating scores
if(laplace == TRUE){
  XFOM <- getME(fom3, "X")
  ZFOM <- getME(fom3, "Z")
  FIXFOM <- fixef(fom3)$cond
  RANFOM <- ranef(fom3)$cond$hosp_name

  LP <- XFOM %*% FIXFOM + ZFOM %*% RANFOM$`(Intercept)`
```

```
  FLP <- XFOM %*% FIXFOM

} else if(laplace == FALSE){
  XFOM <- model.matrix(fom3, type = "fixed")
  ZFOM  <- fastDummies::dummy_cols(Dataf$hosp_name)[, -1];
  FIXFOM <- fixef(fom3)
  RANFOM <- ranef(fom3)
  LP <- XFOM %*% FIXFOM + as.matrix(ZFOM) %*% RANFOM
  FLP <- XFOM %*% FIXFOM
}
pred <- as.vector(exp(LP) / (1 + exp(LP)))
estm <- as.vector(exp(FLP) / (1 + exp(FLP)))



if(ylist == "mbr_death_flag"){
  tb <- table(Dataf$mbr_death_flag)
  ybar <- as.numeric(tb[names(tb) %in% "Event"]) /
    length(Dataf$mbr_death_flag)
} else if(ylist == "mbr_mortality_flag"){
  tb <- table(Dataf$mbr_mortality_flag)
  ybar <- as.numeric(tb[names(tb) %in% "Event"]) /
    length(Dataf$mbr_mortality_flag)
}



### Method 1: Drye et al.
uid <- rownames(RANFOM) #rownames(ranef(fom3)$hosp_name)
score <- list()
for(ll in 1 : length(uid)){
  num <- pred[which(Dataf$hosp_name == uid[ll])]
```

```
  den <- estm[which(Dataf$hosp_name == uid[ll])]
  score[[ll]] <- sum(num) / sum(den) * ybar # 1/ni got cancelled out in numer and denom
 }
 score <- unlist(score)

 ### Method 2: Jeff et al.
 bigMat <- do.call(cbind, lapply(seq_len(length(uid)), function(ll){

  if(addsize == FALSE){
   # first part is specific-to-patient and second part (hypothetically) for each one of H hospitals
   if(laplace == TRUE){
    XFOM %*% FIXFOM +  # RE if subject belongs to this hospital
     RANFOM$`(Intercept)`[which(rownames(RANFOM) == uid[ll])] # logit()
   } else if(laplace == FALSE){
    XFOM %*% FIXFOM +  # RE if subject belongs to this hospital
     RANFOM[which(rownames(RANFOM) == uid[ll])] # logit()
   }

  } else if(addsize == TRUE){
   if(laplace == TRUE){
    XFOM[, colnames(XFOM) %!in% "size"] %*% FIXFOM[names(FIXFOM) %!in% "size"] + # size changes for different h
     RANFOM$`(Intercept)`[which(rownames(RANFOM) == uid[ll])] +          # RE if subject belongs to this hospital
     Dataf$size[which(Dataf$hosp_name == uid[ll])][1] * FIXFOM[names(FIXFOM) %in% "size"] # size if subject belongs
to this hospital
   } else if(laplace == FALSE){
    XFOM[, colnames(XFOM) %!in% "size"] %*% FIXFOM[names(FIXFOM) %!in% "size"] + # size changes for different h
     RANFOM[which(rownames(RANFOM) == uid[ll])] +          # RE if subject belongs to this hospital
     Dataf$size[which(Dataf$hosp_name == uid[ll])][1] * FIXFOM[names(FIXFOM) %in% "size"] # size if subject belongs
to this hospital
   }
  }
```

```
}))

logitinv <- function(ff) {exp(ff) / (1 + exp(ff))}
score_DS <- apply(bigMat, 2, logitinv)
score_DS_mean <- apply(score_DS, 2, mean)

## Unadjusted score
if(ylist == "mbr_death_flag"){
  unadj_score <- unlist(lapply(seq_len(length(uid)),
                               function(uu) {
                                 tr <- table(Dataf$mbr_death_flag[Dataf$hosp_name == uid[uu]])

                                 if(length(which(names(tr) %in% "Event")) > 0){
                                   tr[names(tr) %in% "Event"] / sum(tr)
                                 } else if(length(which(names(tr) %in% "Event")) == 0){
                                   0
                                 }

                               }))
  length(unadj_score)

  ## Volume
  I <- length(uid)
  hosp_orig_vol <- unlist(lapply(seq_len(I), function(ii) {
    ir1 <- which(as.numeric(Dataf$hosp_name) == ii)
    ir2 <- table(Dataf$mbr_death_flag[ir1])
    paste0("", ir2[which(names(ir2) %in% "Event")], "/", sum(ir2), "")
  }))
} else if(ylist == "mbr_mortality_flag"){
  unadj_score <- unlist(lapply(seq_len(length(uid)),
                               function(uu) {
```

```
                    tr <- table(Dataf$mbr_mortality_flag[Dataf$hosp_name == uid[uu]])

                    if(length(which(names(tr) %in% "Event")) > 0){
                      tr[names(tr) %in% "Event"] / sum(tr)
                    } else if(length(which(names(tr) %in% "Event")) == 0){
                      0
                    }

                  }))
  length(unadj_score)

  ## Volume
  I <- length(uid)
  hosp_orig_vol <- unlist(lapply(seq_len(I), function(ii) {
    ir1 <- which(as.numeric(Dataf$hosp_name) == ii)
    ir2 <- table(Dataf$mbr_mortality_flag[ir1])
    paste0("", ir2[which(names(ir2) %in% "Event")], "/", sum(ir2), "")
  }))


}

output = list(fom3 = fom3, LRT_re = LRT_re, aic_null = aic_null,
              aic_alt  = aic_alt, bic_null =  bic_null, bic_alt = bic_alt,
              SS = SS, cor_lme_lmer = cor_lme_lmer,
              probs = probs, rank_cor = rank_cor, varint = varint, VIFfx = VIFfx,
              nY = nY, lb = lb,
              ub = ub, sdorp = sdorp, or = or, orp = orp, pred = pred,
              estm = estm, ybar = ybar, uid = uid,
              score = score, score_DS = score_DS,
              score_DS_mean = score_DS_mean, summary = sm,
```

```
        unadj_score = unadj_score, hosp_orig_vol = hosp_orig_vol)
}



# B2. Single GLMM with random intercept/slope effects
glmmfit_intslope <- function(ylist, XXX_adj,
                             ranlist = "(1 + period|hosp_name)",
                             reml, Dataf_el, addsize = TRUE, sizedef = "Dynamic",
                             method = "Silber", laplace = TRUE){

 ## Volume calculation
 unm <- unique(Dataf_el$hosp_name)
 # Total (early +  late)
 Dataf_el$size_tt <- rep(NA, nrow(Dataf_el))
 for(uu in 1 : length(unm)){
  iz <- which(Dataf_el$hosp_name == unm[uu])
  Dataf_el$size_tt[iz] <- rep(length(iz), length(iz))
 }
 sum(is.na(Dataf_el$size_tt))
 summary(Dataf_el$size_tt)

 # Total (early & early+late)
 Dataf_el$size_el <- Dataf_el$size_tt #rep(NA, nrow(Dataf_el))
 for(uu in 1 : length(unm)){
  iz <- which(Dataf_el$hosp_name == unm[uu] & Dataf_el$period == 0)
  Dataf_el$size_el[iz] <- rep(length(iz), length(iz))
 }

 # Total (early & late)
 Dataf_el$size_eln <- rep(NA, nrow(Dataf_el))
 for(uu in 1 : length(unm)){
```

```
  iz <- which(Dataf_el$hosp_name == unm[uu] & Dataf_el$period == 0)
  Dataf_el$size_eln[iz] <- rep(length(iz), length(iz))
}
for(uu in 1 : length(unm)){
  iz <- which(Dataf_el$hosp_name == unm[uu] & Dataf_el$period == 1)
  Dataf_el$size_eln[iz] <- rep(length(iz), length(iz))
}
if(sum(is.na(Dataf_el$size_eln) > 0)){
  stop("check here")
}

if(sizedef == "Dynamic"){
  Dataf_el$size <- Dataf_el$size_el
} else if(sizedef == "Together"){
  Dataf_el$size <- Dataf_el$size_tt
} else if(sizedef == "Dynamic-non"){
  Dataf_el$size <- Dataf_el$size_eln
}
Dataf_el$size <- log(Dataf_el$size)



if("period" %!in% XXX_adj){
  XXX_adj <- c(XXX_adj, "period")
}
XXX_adj



## Base model (GLM)
a1 <- paste0("glm(", ylist," ~ 1 + period + ")
a2 <- paste0("", XXX_adj, "", collapse = " + ")
QQ <- paste0("", a1, "", a2, ", data = Dataf_el, family = binomial(link = 'logit'))") # remove NAs by default
```

```
fom <- try(eval(parse(text = QQ)))



## GLMM
if(laplace == TRUE){
  a1 <- paste0("glmmTMB(", ylist," ~ 1 + period + ", ranlist, " + ")
  a2 <- paste0("", XXX_adj, "", collapse = " + ")
  QQ <- paste0("", a1, "", a2, ", REML = reml, data = Dataf_el, family = binomial)") # remove NAs by default
  system.time(fom30 <- try(eval(parse(text = QQ))))

}else if(laplace == FALSE){
  # Get the parenthesis and what is inside
  # Remove parenthesis
  ranlist0 <- substring(ranlist, 2, nchar(ranlist) - 1) # extract within parenthesis
  ranlist <- strsplit(ranlist0, "+ ")[[1]][3]

  a1 <- paste0("", ylist," ~ ")
  a2 <- paste0("", XXX_adj, "", collapse = " + ")
  QQ <- paste0("GLMMadaptive::mixed_model(fixed = ", a1, "", a2, " + period, random = ~", ranlist, ",
               data = Dataf_el, family = binomial(), control = list(nAGQ = 11))")
  system.time(fom3 <- try(eval(parse(text = QQ))))
  summary(fom3)
}



## Testing variance (RE)
x2 <- as.numeric(-2 * logLik(fom) + 2 * logLik(fom3))
LRT_re <- 0.5 * (1 - pchisq(x2, df = 1))

## AIC
aic_null <- AIC(logLik(fom))
```

```
  aic_alt <- AIC(logLik(fom3))


  bic_null <- BIC(fom)
  bic_alt <- BIC(fom3)


  if(laplace == TRUE){
    ## Correlation test
    cor_lme_lmer <- cor.test(coef(fom), fixef(fom3)$cond) ## Assessing model performance (conditional/marginal R2)
    SS <- MuMIn::r.squaredGLMM(fom3) ## confidence intervals for the variances of the random intercepts
    varint <- confint(fom3)[-c(1 : length(fixef(fom3)$cond)), ]
    VIFfx <- NULL
  } else if(laplace == FALSE){
    ## Correlation test
    cor_lme_lmer <- cor.test(coef(fom), fixef(fom3)) ## Assessing model performance (conditional/marginal R2)
    SS <- r2_nakagawa(fom3, by_group = FALSE)
    varint <- confint(fom3, parm = "var-cov", level = 0.95) ## confidence intervals for the variances of the random
intercepts
    VIFfx <- VIF(fom3, type = "fixed") ## Variance inflation
  }



  ## C and Dxy: correlation between predicted probabilities and observed responses
  if(ylist == "mbr_death_flag"){
    nY <- ifelse(Dataf_el$mbr_death_flag == "Event", 1, 0)
  } else if(ylist == "mbr_mortality_flag"){
    nY <- ifelse(Dataf_el$mbr_mortality_flag == "Event", 1, 0)
  }


  probs <- binomial()$linkinv(predict(fom3))
  rank_cor <- .somers2(probs, as.numeric(nY))
```

```
## Generating scores
sm <- summary(fom3)
if(laplace == TRUE){
  orp <- sm$coefficients$cond[-1, 1]
  or <- exp(orp)
  VCV <- vcov(fom3, sandwich = TRUE)
  sdorp <- sqrt(diag(VCV$cond)[-1])
  BN <- exp(confint(fom3, level = 0.95))
  BN <- BN[-c(1, nrow(BN)), ] # taking-out intercept and variance
} else if(laplace == FALSE){
  orp <- sm$coef_table[-1, 1]
  or <- exp(orp)
  VCV <- vcov(fom3, sandwich = TRUE)
  sdorp <- sqrt(diag(VCV))
  sdorp <- sdorp[names(sdorp) %in% names(or)]
  BN <- exp(confint(fom3, parm = "fixed-effects", level = 0.95))[-1, ]
}

lb <- BN[, 1]
ub <- BN[, 3]

## Estimating scores
if(laplace == TRUE){
  XFOM <- getME(fom3, "X")
  ZFOM <- getME(fom3, "Z"); dim(ZFOM)
  FIXFOM <- fixef(fom3)$cond
  RANFOM <- c(ranef(fom3)$cond$hosp_name[,1],
              ranef(fom3)$cond$hosp_name[,2])
  LP <- XFOM %*% FIXFOM + ZFOM %*% RANFOM
  FLP <- XFOM %*% FIXFOM
```

```
  uid <- rownames(ranef(fom3)$cond$hosp_name)

} else if(laplace == FALSE){
  XFOM <- model.matrix(fom3, type = "fixed")
  QQ <- paste0("mform <- ", ylist," ~ ",ranlist,"")
  QQ <- eval(parse(text = QQ))
  bar.f <- findbars(mform) # list with 3 terms
  mf <- model.frame(subbars(mform),data = Dataf_el)
  rt <- lme4::mkReTrms(bar.f, mf)
  ZFOM <- t(rt$Zt)

  FIXFOM <- fixef(fom3)
  RANFOM <- ranef(fom3)
  LP <- XFOM %*% FIXFOM + as.matrix(ZFOM) %*% as.vector(t(RANFOM))
  FLP <- XFOM %*% FIXFOM

  uid <- rownames(ranef(fom3))
}
pred <- as.vector(exp(LP) / (1 + exp(LP)))
estm <- as.vector(exp(FLP) / (1 + exp(FLP)))



if(ylist == "mbr_death_flag"){
  tb <- table(Dataf_el$mbr_death_flag)
  ybar <- as.numeric(tb[names(tb) %in% "Event"]) /
    length(Dataf_el$mbr_death_flag)
} else if(ylist == "mbr_mortality_flag"){
  tb <- table(Dataf_el$mbr_mortality_flag)
  ybar <- as.numeric(tb[names(tb) %in% "Event"]) /
```

```
   length(Dataf_el$mbr_mortality_flag)
}




## Score caluclation based on Method 1: Drye et al.
score <- score_early2 <-  score_early2j <- score_later2 <- score_later2j <- list()
for(ll in 1 : length(uid)){
  num <- pred[which(Dataf_el$hosp_name == uid[ll])]
  den <- estm[which(Dataf_el$hosp_name == uid[ll])]
  score[[ll]] <- sum(num) / sum(den) * ybar # 1/ni got cancelled out in numer and denom
}
score <- unlist(score)

## Early score Method 1: Drye et al.
if(ylist == "mbr_death_flag"){
  tb <- table(Dataf_el$mbr_death_flag[which(Dataf_el$period == 0)])
  ybar_early <- as.numeric(tb[names(tb) %in% "Event"]) /
    length(Dataf_el$mbr_death_flag[which(Dataf_el$period == 0)])
} else if(ylist == "mbr_mortality_flag"){
  tb <- table(Dataf_el$mbr_mortality_flag[which(Dataf_el$period == 0)])
  ybar_early <- as.numeric(tb[names(tb) %in% "Event"]) /
    length(Dataf_el$mbr_mortality_flag[which(Dataf_el$period == 0)])

}



for(ll in 1 : length(uid)){
  num <- pred[which(Dataf_el$hosp_name == uid[ll] & Dataf_el$period == 0)]
  den <- estm[which(Dataf_el$hosp_name == uid[ll] & Dataf_el$period == 0)]
```

```
  score_early2[[ll]] <- sum(num) / sum(den) * ybar
  score_early2j[[ll]] <- sum(num) / sum(den) * ybar_early # 1/ni got cancelled out in numer and denom
}
score_early2 <- unlist(score_early2)
score_early2j <- unlist(score_early2j)


## Late score Method 1: Drye et al.
if(ylist == "mbr_death_flag"){
  tb <- table(Dataf_el$mbr_death_flag[which(Dataf_el$period == 1)])
  ybar_later <- as.numeric(tb[names(tb) %in% "Event"]) /
    length(Dataf_el$mbr_death_flag[which(Dataf_el$period == 1)])
} else if(ylist == "mbr_mortality_flag"){
  tb <- table(Dataf_el$mbr_mortality_flag[which(Dataf_el$period == 1)])
  ybar_later <- as.numeric(tb[names(tb) %in% "Event"]) /
    length(Dataf_el$mbr_mortality_flag[which(Dataf_el$period == 1)])
}


for(ll in 1 : length(uid)){
  num <- pred[which(Dataf_el$hosp_name == uid[ll] & Dataf_el$period == 1)]
  den <- estm[which(Dataf_el$hosp_name == uid[ll] & Dataf_el$period == 1)]
  score_later2[[ll]] <- sum(num) / sum(den) * ybar
  score_later2j[[ll]] <- sum(num) / sum(den) * ybar_later # 1/ni got cancelled out in numer and denom
}
score_later2 <- unlist(score_later2)
score_later2j <- unlist(score_later2j)
summary(score_later2)
summary(score_later2j)
```

```
 length(score_early2); length(score_later2)


 ### Score calculation based on Method 2: Silber et al.


 ## Bigmat (Overall) : NOT USED
 bigMat <- do.call(cbind, lapply(seq_len(length(uid)), function(ll){


   if(laplace == TRUE){
    if(addsize == FALSE){
     # first part is specific-to-patient and second part (hypothetically) for each one of H hospitals
     XFOM %*% FIXFOM +      # RE if subject belongs to this hospital
      Dataf_el$period * ranef(fom3)$cond$hosp_name[which(rownames(ranef(fom3)$cond$hosp_name)  == uid[ll]), 2]
+
      ranef(fom3)$cond$hosp_name[which(rownames(ranef(fom3)$cond$hosp_name)  == uid[ll]), 1]
    } else if(addsize == TRUE){
     XFOM[, colnames(XFOM) %!in% "size"] %*% FIXFOM[names(FIXFOM) %!in% "size"] +  # RE if subject belongs to this
hospital
      ranef(fom3)$cond$hosp_name[which(rownames(ranef(fom3)$cond$hosp_name)  == uid[ll]), 1] +
      Dataf_el$period * ranef(fom3)$cond$hosp_name[which(rownames(ranef(fom3)$cond$hosp_name)  == uid[ll]), 2]
+
      mean(Dataf_el$size[which(Dataf_el$hosp_name == uid[ll])]) * FIXFOM[names(FIXFOM) %in% "size"] # as size
changes
    } # taking mean(Dataf_el$size[]) as size changes between early and late for each hospital
   }else if(laplace == FALSE){
    if(addsize == FALSE){
     # first part is specific-to-patient and second part (hypothetically) for each one of H hospitals
     XFOM %*% FIXFOM +      # RE if subject belongs to this hospital
      Dataf_el$period * ranef(fom3)[which(rownames(ranef(fom3))  == uid[ll]), 2] +
      ranef(fom3)[which(rownames(ranef(fom3))  == uid[ll]), 1]
    } else if(addsize == TRUE){
     XFOM[, colnames(XFOM) %!in% "size"] %*% FIXFOM[names(FIXFOM) %!in% "size"] +  # RE if subject belongs to this
hospital
      ranef(fom3)[which(rownames(ranef(fom3))  == uid[ll]), 1] +
```

```
        Dataf_el$period * ranef(fom3)[which(rownames(ranef(fom3))  == uid[ll]), 2] +
        mean(Dataf_el$size[which(Dataf_el$hosp_name == uid[ll])]) * FIXFOM[names(FIXFOM) %in% "size"] # as size changes
     }

   }
 }))
 logitinv <- function(ff) {exp(ff) / (1 + exp(ff))}
 score_DS <- apply(bigMat, 2, logitinv)
 score_DS_mean <- apply(score_DS, 2, mean)


 ## Early Method 2: Silber (exploting BOTH periods info)
 bigMat_early <- do.call(cbind, lapply(seq_len(length(uid)), function(ll){

   if(laplace == TRUE){
    if(addsize == FALSE){
      # first part is specific-to-patient and second part (hypothetically) for each one of H hospitals
      XFOM[, colnames(XFOM) %!in% "period"] %*% FIXFOM[colnames(XFOM) %!in% "period"] +      # RE if subject belongs to this hospital
        0 * FIXFOM[colnames(XFOM) %in% "period"] + # adjusted for fixed early time-effects
        0 * ranef(fom3)$cond$hosp_name[which(rownames(ranef(fom3)$cond$hosp_name)  == uid[ll]), 2] +
        ranef(fom3)$cond$hosp_name[which(rownames(ranef(fom3)$cond$hosp_name)  == uid[ll]), 1]
    } else if(addsize == TRUE){
      XFOM[ , colnames(XFOM) %!in% c("size", "period")] %*% FIXFOM[names(FIXFOM) %!in% c("size", "period")] +  # RE if subject belongs to this hospital
        0 * FIXFOM[colnames(XFOM) %in% "period"] + # adjusted for fixed time- effects
        ranef(fom3)$cond$hosp_name[which(rownames(ranef(fom3)$cond$hosp_name)  == uid[ll]), 1] + # random intercept for hypothetical site
        0 * ranef(fom3)$cond$hosp_name[which(rownames(ranef(fom3)$cond$hosp_name)  == uid[ll]), 2] + # random slope for hypothetical site
        Dataf_el$size[which(Dataf_el$hosp_name == uid[ll] & Dataf_el$period == 0)][1] * FIXFOM[names(FIXFOM) %in% "size"] # size for hypothetical site
```

```
    }
  } else if(laplace == FALSE){
    if(addsize == FALSE){
      # first part is specific-to-patient and second part (hypothetically) for each one of H hospitals
      XFOM[, colnames(XFOM) %!in% "period"] %*% FIXFOM[colnames(XFOM) %!in% "period"] +      # RE if subject belongs to this hospital
        0 * FIXFOM[colnames(XFOM) %in% "period"] + # adjusted for fixed early time-effects
        0 * ranef(fom3)[which(rownames(ranef(fom3))  == uid[ll]), 2] +
        ranef(fom3)[which(rownames(ranef(fom3))  == uid[ll]), 1]
    } else if(addsize == TRUE){
      XFOM[ , colnames(XFOM) %!in% c("size", "period")] %*% FIXFOM[names(FIXFOM) %!in% c("size", "period")] +  # RE if subject belongs to this hospital
        0 * FIXFOM[colnames(XFOM) %in% "period"] + # adjusted for fixed time- effects
        ranef(fom3)[which(rownames(ranef(fom3))  == uid[ll]), 1] + # random intercept for hypothetical site
        0 * ranef(fom3)[which(rownames(ranef(fom3))  == uid[ll]), 2] + # random slope for hypothetical site
        Dataf_el$size[which(Dataf_el$hosp_name == uid[ll] & Dataf_el$period == 0)][1] * FIXFOM[names(FIXFOM) %in% "size"] # size for hypothetical site
    }
  }
 }))
 score_DS_early <- apply(bigMat_early, 2, logitinv)
 score_DS_mean_early <- apply(score_DS_early, 2, mean)


 ## Late Method 2: Silber et al.
 bigMat_late <- do.call(cbind, lapply(seq_len(length(uid)), function(ll){

  if(laplace == TRUE){
    if(addsize == FALSE){
      # first part is specific-to-patient and second part (hypothetically) for each one of H hospitals
      XFOM[, colnames(XFOM) %!in% "period"] %*% FIXFOM[colnames(XFOM) %!in% "period"] +      # RE if subject belongs to this hospital
```

```
        1 * FIXFOM[colnames(XFOM) %in% "period"] + #adjusted for fixed late

        1 * ranef(fom3)$cond$hosp_name[which(rownames(ranef(fom3)$cond$hosp_name)  == uid[ll]), 2] +

        ranef(fom3)$cond$hosp_name[which(rownames(ranef(fom3)$cond$hosp_name)  == uid[ll]), 1]

    } else if(addsize == TRUE){

      XFOM[, colnames(XFOM) %!in% c("size", "period")] %*% FIXFOM[names(FIXFOM) %!in% c("size", "period")] +  # RE if subject belongs to this hospital

        1 * FIXFOM[colnames(XFOM) %in% "period"] + #adjusted for fixed late effect

        ranef(fom3)$cond$hosp_name[which(rownames(ranef(fom3)$cond$hosp_name)  == uid[ll]), 1] + # random intercept for hypothetical site

        1 * ranef(fom3)$cond$hosp_name[which(rownames(ranef(fom3)$cond$hosp_name)  == uid[ll]), 2] +# random slope for hypothetical site

        Dataf_el$size[which(Dataf_el$hosp_name == uid[ll] & Dataf_el$period == 1)][1] * FIXFOM[names(FIXFOM) %in% "size"] # fixed size for hypothetical site

      # size changes in early/late. Hypothetically each patient comes from each period and each hospital

    }

  } else if(laplace == FALSE){

    if(addsize == FALSE){

      # first part is specific-to-patient and second part (hypothetically) for each one of H hospitals

      XFOM[, colnames(XFOM) %!in% "period"] %*% FIXFOM[colnames(XFOM) %!in% "period"] +      # RE if subject belongs to this hospital

        1 * FIXFOM[colnames(XFOM) %in% "period"] + #adjusted for fixed late

        1 * ranef(fom3)[which(rownames(ranef(fom3))  == uid[ll]), 2] +

        ranef(fom3)[which(rownames(ranef(fom3))  == uid[ll]), 1]

    } else if(addsize == TRUE){

      XFOM[, colnames(XFOM) %!in% c("size", "period")] %*% FIXFOM[names(FIXFOM) %!in% c("size", "period")] +  # RE if subject belongs to this hospital

        1 * FIXFOM[colnames(XFOM) %in% "period"] + #adjusted for fixed late effect

        ranef(fom3)[which(rownames(ranef(fom3))  == uid[ll]), 1] + # random intercept for hypothetical site

        1 * ranef(fom3)[which(rownames(ranef(fom3))  == uid[ll]), 2] + # random slope for hypothetical site

        Dataf_el$size[which(Dataf_el$hosp_name == uid[ll] & Dataf_el$period == 1)][1] * FIXFOM[names(FIXFOM) %in% "size"] # fixed size for hypothetical site

      # size changes in early/late. Hypothetically each patient comes from each period and each hospital

    }
```

```
  }
 }))
 score_DS_late <- apply(bigMat_late, 2, logitinv)
 score_DS_mean_late <- apply(score_DS_late, 2, mean)




 ## Early Method 2: Silber et al. (early and late separate 10K for early and 17K for late kind of)
 bigMat_early2 <- do.call(cbind, lapply(seq_len(length(uid)), function(ll){


  if(laplace == TRUE){
   if(addsize == FALSE){
    # first part is specific-to-patient and second part (hypothetically) for each one of H hospitals
    XFOM[which(Dataf_el$period == 0), ] %*% FIXFOM +      # RE if subject belongs to this hospital
     Dataf_el$period[which(Dataf_el$period == 0)] *
ranef(fom3)$cond$hosp_name[which(rownames(ranef(fom3)$cond$hosp_name)  == uid[ll]), 2] +
     ranef(fom3)$cond$hosp_name[which(rownames(ranef(fom3)$cond$hosp_name)  == uid[ll]), 1]
   } else if(addsize == TRUE){
    XFOM[which(Dataf_el$period == 0), colnames(XFOM) %!in% "size"] %*% FIXFOM[names(FIXFOM) %!in% "size"] +  #
RE if subject belongs to this hospital
     ranef(fom3)$cond$hosp_name[which(rownames(ranef(fom3)$cond$hosp_name)  == uid[ll]), 1] + #
     Dataf_el$period[which(Dataf_el$period == 0)] *
ranef(fom3)$cond$hosp_name[which(rownames(ranef(fom3)$cond$hosp_name)  == uid[ll]), 2] +
     Dataf_el$size[which(Dataf_el$hosp_name == uid[ll] & Dataf_el$period == 0)][1] * FIXFOM[names(FIXFOM) %in%
"size"]
   }
  } else if(laplace == FALSE){
   if(addsize == FALSE){
    # first part is specific-to-patient and second part (hypothetically) for each one of H hospitals
    XFOM[which(Dataf_el$period == 0), ] %*% FIXFOM +      # RE if subject belongs to this hospital
     Dataf_el$period[which(Dataf_el$period == 0)] * ranef(fom3)[which(rownames(ranef(fom3))  == uid[ll]), 2] +
```

```
        ranef(fom3)[which(rownames(ranef(fom3))  == uid[ll]), 1]
    } else if(addsize == TRUE){
      XFOM[which(Dataf_el$period == 0), colnames(XFOM) %!in% "size"] %*% FIXFOM[names(FIXFOM) %!in% "size"] +  # RE if subject belongs to this hospital
        ranef(fom3)[which(rownames(ranef(fom3))  == uid[ll]), 1] + #
        Dataf_el$period[which(Dataf_el$period == 0)] * ranef(fom3)[which(rownames(ranef(fom3))  == uid[ll]), 2] +
        Dataf_el$size[which(Dataf_el$hosp_name == uid[ll] & Dataf_el$period == 0)][1] * FIXFOM[names(FIXFOM) %in% "size"]
    }
  }
 }))
 score_DS_early2 <- apply(bigMat_early2, 2, logitinv)
 score_DS_mean_early2 <- apply(score_DS_early2, 2, mean)



 ## Late Method 2: Silber et al.
 bigMat_late2 <- do.call(cbind, lapply(seq_len(length(uid)), function(ll){
  if(laplace == TRUE){
    if(addsize == FALSE){
      # first part is specific-to-patient and second part (hypothetically) for each one of H hospitals
      XFOM[which(Dataf_el$period == 1), ] %*% FIXFOM +      # RE if subject belongs to this hospital
        Dataf_el$period[which(Dataf_el$period == 1)] * ranef(fom3)$cond$hosp_name[which(rownames(ranef(fom3)$cond$hosp_name)  == uid[ll]), 2] +
        ranef(fom3)$cond$hosp_name[which(rownames(ranef(fom3)$cond$hosp_name)  == uid[ll]), 1]
    } else if(addsize == TRUE){
      XFOM[which(Dataf_el$period == 1), colnames(XFOM) %!in% "size"] %*% FIXFOM[names(FIXFOM) %!in% "size"] +  # RE if subject belongs to this hospital
        ranef(fom3)$cond$hosp_name[which(rownames(ranef(fom3)$cond$hosp_name)  == uid[ll]), 1] + #
        Dataf_el$period[which(Dataf_el$period == 1)] * ranef(fom3)$cond$hosp_name[which(rownames(ranef(fom3)$cond$hosp_name)  == uid[ll]), 2] +
        Dataf_el$size[which(Dataf_el$hosp_name == uid[ll] & Dataf_el$period == 1)][1] * FIXFOM[names(FIXFOM) %in% "size"]
    }
```

```
  } else if(laplace == FALSE){
    if(addsize == FALSE){
      # first part is specific-to-patient and second part (hypothetically) for each one of H hospitals
      XFOM[which(Dataf_el$period == 1), ] %*% FIXFOM +      # RE if subject belongs to this hospital
        Dataf_el$period[which(Dataf_el$period == 1)] * ranef(fom3)[which(rownames(ranef(fom3))  == uid[ll]), 2] +
        ranef(fom3)[which(rownames(ranef(fom3))  == uid[ll]), 1]
    } else if(addsize == TRUE){
      XFOM[which(Dataf_el$period == 1), colnames(XFOM) %!in% "size"] %*% FIXFOM[names(FIXFOM) %!in% "size"] +  # RE if subject belongs to this hospital
        ranef(fom3)[which(rownames(ranef(fom3))  == uid[ll]), 1] + #
        Dataf_el$period[which(Dataf_el$period == 1)] * ranef(fom3)[which(rownames(ranef(fom3))  == uid[ll]), 2] +
        Dataf_el$size[which(Dataf_el$hosp_name == uid[ll] & Dataf_el$period == 1)][1] * FIXFOM[names(FIXFOM) %in% "size"]
    }
  }
 }))
 score_DS_late2 <- apply(bigMat_late2, 2, logitinv)
 score_DS_mean_late2 <- apply(score_DS_late2, 2, mean)


 me_early <- 1.96 * apply(score_DS_early, 2, sd) / sqrt(nrow(score_DS_early))
 score_boot_q1_early <- apply(score_DS_early, 2, summary_25l)
 score_boot_q3_early <- apply(score_DS_early, 2, summary_75l)
 score_boot_025_early <- apply(score_DS_early, 2, summary_025l)
 score_boot_975_early <- apply(score_DS_early, 2, summary_975l)

 me_late <- 1.96 * apply(score_DS_late, 2, sd) / sqrt(nrow(score_DS_late))
 score_boot_q1_late <- apply(score_DS_late, 2, summary_25l)
 score_boot_q3_late <- apply(score_DS_late, 2, summary_75l)
 score_boot_025_late <- apply(score_DS_late, 2, summary_025l)
 score_boot_975_late <- apply(score_DS_late, 2, summary_975l)
```

```
## Bland-altman plot
if(method == "Drye"){
  s1 <- score_later2j - score_early2j
  s2 <- (score_later2j + score_early2j) / 2
} else if(method == "Silber"){
  s1 <- score_DS_mean_late - score_DS_mean_early
  s2 <- (score_DS_mean_late + score_DS_mean_early) / 2
}

## Volume
I <- length(uid)

## Unadjusted score
if(ylist == "mbr_death_flag"){
  hosp_orig_vol_early <- unlist(lapply(seq_len(I),
                                       function(ii) {
                                         ir1 <- which(Dataf_el$hosp_name == uid[ii] & Dataf_el$period == 0)
                                         ir2 <- table(Dataf_el$mbr_death_flag[ir1])
                                         paste0("", ir2[which(names(ir2) %in% "Event")], "/", sum(ir2), "")
                                       }))

  hosp_orig_vol_later <- unlist(lapply(seq_len(I), function(ii) {
    ir1 <- which(Dataf_el$hosp_name == uid[ii] & Dataf_el$period == 1)
    ir2 <- table(Dataf_el$mbr_death_flag[ir1])
    paste0("", ir2[which(names(ir2) %in% "Event")], "/", sum(ir2), "")
  }))

  unadj_score <- unlist(lapply(seq_len(length(uid)),
```

```
                    function(uu) {
                     tr <- table(Dataf_el$mbr_death_flag[Dataf_el$hosp_name == uid[uu]])

                     if(length(which(names(tr) %in% "Event")) > 0){
                      tr[names(tr) %in% "Event"] / sum(tr)
                     } else if(length(which(names(tr) %in% "Event")) == 0){
                      0
                     }

                    }))
  hosp_orig_vol <- unlist(lapply(seq_len(l), function(ii) {
   ir1 <- which(as.numeric(Dataf_el$hosp_name) == ii)
   ir2 <- table(Dataf_el$mbr_death_flag[ir1])
   paste0("", ir2[which(names(ir2) %in% "Event")], "/", sum(ir2), "")
  }))

} else if(ylist == "mbr_mortality_flag"){

  hosp_orig_vol_early <- unlist(lapply(seq_len(l),
                                function(ii) {
                                 ir1 <- which(Dataf_el$hosp_name == uid[ii] & Dataf_el$period == 0)
                                 ir2 <- table(Dataf_el$mbr_mortality_flag[ir1])
                                 paste0("", ir2[which(names(ir2) %in% "Event")], "/", sum(ir2), "")
                                }))

  hosp_orig_vol_later <- unlist(lapply(seq_len(l), function(ii) {
   ir1 <- which(Dataf_el$hosp_name == uid[ii] & Dataf_el$period == 1)
   ir2 <- table(Dataf_el$mbr_mortality_flag[ir1])
   paste0("", ir2[which(names(ir2) %in% "Event")], "/", sum(ir2), "")
  }))
```

```
 unadj_score <- unlist(lapply(seq_len(length(uid)),
                        function(uu) {
                         tr <- table(Dataf_el$mbr_mortality_flag[Dataf_el$hosp_name == uid[uu]])

                         if(length(which(names(tr) %in% "Event")) > 0){
                          tr[names(tr) %in% "Event"] / sum(tr)
                         } else if(length(which(names(tr) %in% "Event")) == 0){
                          0
                         }

                        }))

 hosp_orig_vol <- unlist(lapply(seq_len(l), function(ii) {
  ir1 <- which(as.numeric(Dataf_el$hosp_name) == ii)
  ir2 <- table(Dataf_el$mbr_mortality_flag[ir1])
  paste0("", ir2[which(names(ir2) %in% "Event")], "/", sum(ir2), "")
 }))

}



hosp_orig_vol_early[1]; hosp_orig_vol_later[1]
length(unadj_score)


output = list(fom3 = fom3, LRT_re = LRT_re, aic_null = aic_null, aic_alt  = aic_alt,
           varint = varint, VIFfx = VIFfx, bic_null = bic_null, bic_alt = bic_alt,
           score_early2 = score_early2, score_later2 = score_later2,
           SS = SS, cor_lme_lmer = cor_lme_lmer,
           probs = probs, rank_cor = rank_cor, nY = nY, lb = lb,
```

```
        ub = ub, sdorp = sdorp, or = or, orp = orp, pred = pred,
        estm = estm, ybar = ybar, uid = uid, score = score, summary = sm,
        unadj_score = unadj_score, hosp_orig_vol_later = hosp_orig_vol_later,
        hosp_orig_vol_early = hosp_orig_vol_early,
        hosp_orig_vol = hosp_orig_vol,
        s1 = s1, s2 = s2,  score_later2j =  score_later2j,
        score_later2 =  score_later2j,  score_early2j =  score_early2j,
        score_early2 =  score_early2, ybar_early = ybar_early,
        ybar_later = ybar_later,

        ## Results for Silber
        score_DS_late = score_DS_late, score_DS_late2 = score_DS_late2,
        score_DS_mean_late = score_DS_mean_late, score_DS_mean_late2 = score_DS_mean_late2,

        me_late = me_late,  score_boot_q1_late =  score_boot_q1_late, score_boot_q3_late = score_boot_q3_late,
        score_boot_025_late = score_boot_025_late, score_boot_975_late  = score_boot_975_late,

        score_DS_early = score_DS_early, score_DS_early2 = score_DS_early2,
        score_DS_mean_early  = score_DS_mean_early, score_DS_mean_early2  = score_DS_mean_early2,

        me_early =  me_early, score_boot_q1_early = score_boot_q1_early, score_boot_q3_early =
score_boot_q3_early,
        score_boot_025_early = score_boot_025_early, score_boot_975_early = score_boot_975_early
  )
}



# B3. Hospital outcome regression
hospital_outcome_regression <- function(Data_analytical, Data_score,
                                        hosp_id = c("hosp_usr_class", "hosp_income_class", "hosp_region", "hosp_state",
"snf_nursing_flag", "beds_class", "icu_beds_class", "resident_to_bed_ratio_class", "non_profit_flag","academic_flag"),
```

```
                    apnd2,
                    reml = FALSE,
                    period = FALSE,
                    transformation = "scale",
                    glmlog = FALSE,
                    allsite = "No",
                    ranlist = "(1 | hosp_state)",
                    addregion = TRUE,
                    name2add = c("icu_beds_class", "resident_to_bed_ratio_class", "beds_class",
                            "non_profit_flag", "hosp_usr_class", "deaths_class"),
                    name2add_num  = c("icu_beds", "resident_to_bed_ratio", "beds", "non_profit_flag",
                                "hosp_usr_class", "deaths_class"),
                    varlist_bar = "ICU:Ratio:Beds:Profit:User:Deaths"){

symbol <- "\u2265"; symbol2 <- intToUtf8(8804)

length(unique(Data_analytical$hosp_name))
am3 <- arrange_dataf_hospital(Data_score, Data_analytical, hosp_id, apnd2, period = period,
                        allsite = allsite, name2add = name2add, name2add_num = name2add_num)
Data7 <- am3$Data7; Data72 <- am3$Data72; Data73 <- am3$Data73

mlist_combination1 <- am3$mlist_combination1; varlist_combination1 <- am3$varlist_combination1;
reflist_combination1 <- am3$reflist_combination1; mlist0_combination1 <- am3$mlist0_combination1

mlist_casesinteraction <- am3$mlist_casesinteraction; varlist_casesinteraction <- am3$varlist_casesinteraction;
reflist_casesinteraction <- am3$reflist_casesinteraction; mlist0_casesinteraction <- am3$mlist0_casesinteraction


mlist_combination2 <- am3$mlist_combination2; varlist_combination2 <- am3$varlist_combination2;
reflist_combination2 <- am3$reflist_combination2; mlist0_combination2 <- am3$mlist0_combination2
```

```
mlist_beds <- am3$mlist_beds; try(mlist_academic <- am3$mlist_academic);
mlist_icu <- am3$mlist_icu; mlist_ratio <- am3$mlist_ratio;
mlist_user <- am3$mlist_user; try(mlist_profit <- am3$mlist_profit);
mlist_region <- am3$mlist_region; mlist_cases <- am3$mlist_cases; mlist_deaths <- am3$mlist_deaths
mlist_casesearly <- am3$mlist_casesearly; mlist_caseslate <- am3$mlist_caseslate;
mlist_caseslatediff <- am3$mlist_caseslatediff; mlist_caseschange <- am3$mlist_caseschange;
mlist_caseschangebinary <- am3$mlist_caseschangebinary

reflist_beds <- am3$reflist_beds; try(reflist_academic <- am3$reflist_academic);
reflist_icu <- am3$reflist_icu; reflist_ratio <- am3$reflist_ratio;
reflist_user <- am3$reflist_user; try(reflist_profit <- am3$reflist_profit);
reflist_region <- am3$reflist_region; reflist_cases <- am3$reflist_cases; reflist_deaths <- am3$reflist_deaths
reflist_casesearly <- am3$reflist_casesearly; reflist_caseslate <- am3$reflist_caseslate;
reflist_caseslatediff <- am3$reflist_caseslatediff; reflist_caseschange <- am3$reflist_caseschange
reflist_caseschangebinary <- am3$reflist_caseschangebinary

mlist0_beds <- am3$mlist0_beds; try(mlist0_academic <- am3$mlist0_academic);
mlist0_icu <- am3$mlist0_icu; mlist0_ratio <- am3$mlist0_ratio
mlist0_user <- am3$mlist0_user; try(mlist0_profit <- am3$mlist0_profit);
mlist0_region <- am3$mlist0_region;  mlist0_cases <- am3$mlist0_cases; mlist0_deaths <- am3$mlist0_deaths
mlist0_casesearly <- am3$mlist0_casesearly; mlist0_caseslate <- am3$mlist0_caseslate;
mlist0_caseslatediff <- am3$mlist0_caseslatediff; mlist0_caseschange <- am3$mlist0_caseschange
mlist0_caseschangebinary <- am3$mlist0_caseschangebinary

varlist_beds <- am3$varlist_beds; varlist_academic <- am3$varlist_academic;
varlist_icu <- am3$varlist_icu; varlist_ratio <- am3$varlist_ratio;
varlist_user <- am3$varlist_user; try(varlist_profit <- am3$varlist_profit);
varlist_region <- am3$varlist_region; varlist_cases <- am3$varlist_cases; varlist_deaths <- am3$varlist_deaths
varlist_casesearly <- am3$varlist_casesearly; varlist_caseslate <- am3$varlist_caseslate;
varlist_caseslatediff <- am3$varlist_caseslatediff; varlist_caseschange <- am3$varlist_caseschange
varlist_caseschangebinary <- am3$varlist_caseschangebinary
```

```
if(addregion == TRUE){
  name2add <- c(am3$name2add, "hosp_region")
} else{
  name2add <- am3$name2add
}



## Numeric scores
if(period != "Both"){
  Data72$scoreScale <- scale(Data72$score) # - mean(Data72$score)
  Data72$scoreLog <- log(Data72$score)
  Data72$scoreSqrt <- sqrt(Data72$score)

  if(transformation == "scale"){
    Data72$scoreme <- as.numeric(Data72$scoreScale)
  } else if(transformation == "log"){
    Data72$scoreme <- as.numeric(log(Data72$score))
  } else if(transformation == "sqrt"){
    Data72$scoreme <- as.numeric(sqrt(Data72$score))
  } else if(transformation == "min-max"){
    Data72$scoreme <- (Data72$score - min(Data72$score)) /
      (max(Data72$score) - min(Data72$score))
  } else if(transformation == "original"){
    Data72$scoreme <- as.numeric(Data72$score)
  }
} else if(period == "Both"){
  Data72$scoreme <- Data72$difference
}

## LRT for each variables GLM with random effects
```

```
if(glmlog == FALSE){
  a1 <- paste0("lm(scoreme ~ ")
  a2 <- paste0("", name2add, "", collapse = " + ")
  QQ <- paste0("", a1, "", a2, ", singular.ok = TRUE, data = Data72)")
  fit11<- eval(parse(text = QQ))
} else if(glmlog == TRUE){
  a1 <- paste0("glm(scoreme ~ ") #
  a2 <- paste0("", name2add, "", collapse = " + ")
  QQ <- paste0("", a1, "", a2, " , singular.ok = TRUE,
               family = gaussian(link = 'log'),
               data = Data72)")
  fit11 <- eval(parse(text = QQ))
}
summary(fit11)
dim(Data72)
length(Data72$hosp_name)

vif <- DescTools::VIF(fit11)
vif

# Full model mixed
if(is.null(ranlist) == FALSE){
  fit1 <- lmer(as.formula(paste0('scoreme ~ ', paste0(name2add, collapse = '+' ), '+', ranlist,'')),
               data = Data72, REML = reml)
  try(aic_alt <- AIC(logLik(fit1)))
} else{
  fit1 <- aic_alt <- NULL
}

test_table1 <- test_table2 <- list(); fit0 <- NULL
for(ii in 1 : length(name2add)){
```

```
  ## Null Hypothesis
  if(glmlog == FALSE){
    a1 <- paste0("lm(scoreme ~ ")
    a2 <- paste0("", name2add[name2add %!in% name2add[ii]], "", collapse = " + ")
    QQ <- paste0("", a1, "", a2, ", singular.ok = TRUE, data = Data72)")
    fit00 <- eval(parse(text = QQ))

    if(is.null(ranlist) == FALSE){
      fit0 <- lmer(as.formula(paste0('scoreme ~ ', paste0(name2add[name2add %!in% name2add[ii]],
                                          collapse = '+' ), '+', ranlist,'')), data = Data72, REML = reml)
      test_table2[[ii]] <- stats::anova(fit0, fit1, test = "LRT")
    } else{
      fit0 <- NULL
    }
  } else if(glmlog == TRUE){

    a1 <- paste0("glm(scoreme ~ ")
    a2 <- paste0("", name2add[name2add %!in% name2add[ii]], "", collapse = " + ")
    QQ <- paste0("", a1, "", a2, ", singular.ok = TRUE, family = gaussian(link = 'log'),
                 data = Data72)")
    fit00 <- eval(parse(text = QQ))
  }
  test_table1[[ii]] <- stats::anova(fit00, fit11, test = "LRT")
}


if(is.null(ranlist) == FALSE) {
  if(isSingular(fit1) == TRUE){
    fit_final <- fit11 # LM
  } else{
```

```
   fit_final <- fit1 # Mixed
  }
} else{
  fit_final <- fit11 # LM
}


## Test of random effects
if(is.null(ranlist) == FALSE){
  ## Testing variance (RE)
  x2 <- as.numeric(-2 * logLik(fit11) + 2 * logLik(fit1))
  LRT_re <- 0.5 * (1 - pchisq(x2, df = 1))
  LRT_re
  if(LRT_re > 0.05){
    print("Random effect is not needed. Drop random term and refit")
  }
}

## AIC
aic_null <- AIC(logLik(fit11))


## Not systematic pattern implying assumption of homoscedaticity
pred <- predict(fit_final)
resd <- Data72$scoreme - pred


# fixed-effect
b.lme4 <- summary(fit_final)$coef[, 1]
b.sd.lme4 <- summary(fit_final)$coef[, 2]
```

```
dataplot_CM <- data.frame("Effect" = b.lme4,
                          "lb" = b.lme4 - 1.96 * b.sd.lme4,
                          "ub" = b.lme4 + 1.96 * b.sd.lme4,
                          "SE" = b.sd.lme4,
                          "Variable" = names(b.lme4),
                          "pv" = 2 * (1 - pnorm(abs(b.lme4/b.sd.lme4))))

dataplot_CM


vv <- varlist_bar
txt <- strsplit(vv, ":")[[1]]
## final name
txt2 <- paste0("mlist0_", tolower(txt), "", sep = "", collapse = ", ")
QQ <- paste0("c(", txt2,")")
QQ <-  eval(parse(text = QQ))



dataplot_CM$finalname <- c("Intercept", QQ)


## ylab_name
txt2 <- paste0("varlist_", tolower(txt), "", sep = "", collapse = ", ")
QQ <- paste0("c(", txt2,")")
QQ <- eval(parse(text = QQ))
dataplot_CM$ylab_name <- c("Intercept", QQ)


## reference
txt2 <- paste0("reflist_", tolower(txt), "", sep = "", collapse = ", ")
QQ <- paste0("c(", txt2,")")
QQ <- eval(parse(text = QQ))
dataplot_CM$reference <- c(NA, QQ)
```

```
 dataplot_CM$allpoint <- unlist(lapply(seq_len(nrow(dataplot_CM)), function(hh)

  paste0("",sprintf("%5.2f",round(dataplot_CM$Effect[hh], 2))," (",sprintf("%5.2f",round(dataplot_CM$lb[hh],
2)),",",sprintf("%5.2f",round(dataplot_CM$ub[hh], 2)), ")")))


 dataplot_CM$pv <- sprintf("%0.4f", as.numeric(dataplot_CM$pv))

 dataplot_CM$pv[which(dataplot_CM$pv == "0.0000")] <- "<0.0001"


 dataplot_CM <- dataplot_CM[-1, ]


 ## Obtain cases

 dataplot_CM$ylab_name_numb <- t(do.call(cbind, lapply(seq_len(nrow(dataplot_CM)), function(uu) {


  where <- dataplot_CM$finalname[uu]

  where

  numb <- table(Data72[, colnames(Data72) %in% where])


  snumb <- sum(numb)


  if("1" %!in% names(numb)){ # RUN IFF VALUES 1/0 IS NOT USED FOR CATEGORY

   what <- strsplit(as.character(dataplot_CM$Variable[uu]), where)[[1]][2]

   numb <- numb[which(names(numb) == what)]

  } else{

   what <- as.character(1)

   numb <- numb[which(names(numb) == what)]

  }


  GG <- paste0("median(Data72$score[which(Data72$", where," == '", what,"')])")

  GG <- eval(parse(text = GG))
```

```
  as.vector(c(numb, round(((numb/snumb) * 100), 2), GG))
 }))))



 output = list(vif = vif, pred = pred, resd = resd,
               Data72 = Data72, fit1 = fit1, fit11 = fit11, fit0 = fit0, fit00 = fit00,
               test_table1 = test_table1, test_table2 = test_table2, dataplot_CM = dataplot_CM,
               aic_alt = aic_alt, aic_null = aic_null)
}



# B4. Quintile comparison (model-based)
qunitile_compare <- function(Data_score, take_log = FALSE, glmlog = FALSE){

 q1 <- quantile(Data_score$score, 0.20)
 q2 <- quantile(Data_score$score, 0.40)
 q3 <- quantile(Data_score$score, 0.60)
 q4 <- quantile(Data_score$score, 0.80)

 iq1 <- which(Data_score$score <= q1)
 for(jj in 2 : 4){
  QQ <- paste0("iq",jj," <- which(Data_score$score > q",(jj-1), " & Data_score$score <= q",jj,")")
  QQ <- eval(parse(text = QQ))
 }
 iq5 <- which(Data_score$score > q4)

 id_q <- unlist(lapply(seq_len(5), function(kk){
  QQ <- paste0("rep(as.character('Q",kk,"'), length(iq", kk,"))")
  QQ <- eval(parse(text = QQ))
 }))
```

```
if(take_log == FALSE){
  dataq <- data.frame("score" = Data_score$score,
                      "group" = id_q,
                      "reference" = Data_score$reference)
} else if(take_log == TRUE){
  dataq <- data.frame("score" = log(Data_score$score),
                      "group" = id_q,
                      "reference" = Data_score$reference)
}

dataq$group <- relevel(dataq$group, ref = "Q1")

if(glmlog == FALSE){
  fit_expl <- lm(score ~ group, singular.ok = TRUE, data = dataq)
} else if(glmlog ==  TRUE){
  fit_expl <- glm(score ~ group, singular.ok = TRUE,
                  family = gaussian(link = "log"),
                  data = dataq)
}
summary(fit_expl)

# fixed-effect
b.lm <- summary(fit_expl)$coef[-1, 1]
b.sd.lm <- summary(fit_expl)$coef[-1, 2]

if(take_log == TRUE | glmlog == TRUE){
  datq <- data.frame("Effect" = exp(b.lm),
                     "lb" = exp(b.lm - 1.96 * b.sd.lm),
                     "ub" = exp(b.lm + 1.96 * b.sd.lm),
                     "SE" = b.sd.lm,
                     "Variable" = names(b.lm),
```

```
                "pv" = 2 * (1 - pnorm(abs(b.lm/b.sd.lm))))
  } else if(take_log == FALSE & glmlog == FALSE){
    datq <- data.frame("Effect" = b.lm,
                "lb" = b.lm - 1.96 * b.sd.lm,
                "ub" = b.lm + 1.96 * b.sd.lm,
                "SE" = b.sd.lm,
                "Variable" = names(b.lm),
                "pv" = 2 * (1 - pnorm(abs(b.lm/b.sd.lm))))
  }

  output = list(datq = datq, id_q = id_q)
}



# B5. Single GLMM for patient + hospital attributes
glmmfit_patient_hospital <- function(Data_analytical, hospital_fit_object, XXX_adj, add2, ranlist = paste0("(1 |
hosp_name)"),
                        ylist = "mbr_death_flag", variable_list = "Age:Gender:Nurse", comorb_nm, comorb_id){

  ## Getting data for hosp attributes
  XXX_adj2 <- c(XXX_adj, add2)

  Data23 <- Data_analytical; dim(Data23)
  uid2 <- unique(Data23$hosp_name); L <- length(uid2)

  Data23$beds_class <- Data23$icu_beds_class <- Data23$non_profit_flag <-
    Data23$hosp_usr_class <- Data23$academic_flag <- Data23$cases_class <-
    Data23$cases_class_early <- Data23$cases_class_late <-
    Data23$cases_class_late_diff <- Data23$cases_change <-
    Data23$cases_change_binary <- Data23$cases_interaction <-
```

```
 Data23$hosp_region <- rep(NA, nrow(Data23))

for(ll in 1 : L){
 rep_id <- which(Data23$hosp_name == uid2[ll])
 take_id <- which(hospital_fit_object$Data72$hosp_name == uid2[ll])
 Li <- length(rep_id)

 val_bed  <- hospital_fit_object$Data72$beds_class[take_id]
 val_icu <- hospital_fit_object$Data72$icu_beds_class[take_id]

 val_case <- hospital_fit_object$Data72$cases_class[take_id]
 val_case_early <- hospital_fit_object$Data72$cases_class_early[take_id]
 val_case_late <- hospital_fit_object$Data72$cases_class_late[take_id]
 val_case_late_diff <- hospital_fit_object$Data72$cases_class_late_diff[take_id]
 val_case_change <- hospital_fit_object$Data72$cases_change[take_id]
 val_case_change_binary <- hospital_fit_object$Data72$cases_change_binary[take_id]
 val_case_interaction <- hospital_fit_object$Data72$cases_interaction[take_id]

 val_pro <- hospital_fit_object$Data72$non_profit_flag[take_id]
 val_usr <- hospital_fit_object$Data72$hosp_usr_class[take_id]
 val_aca <- hospital_fit_object$Data72$academic_flag[take_id]
 val_reg <- hospital_fit_object$Data72$hosp_region[take_id]

 Data23$beds_class[rep_id] <- rep(as.character(val_bed), Li)
 Data23$icu_beds_class[rep_id] <- rep(as.character(val_icu), Li)
 Data23$non_profit_flag[rep_id] <- rep(as.character(val_pro), Li)
 Data23$hosp_usr_class[rep_id] <- rep(as.character(val_usr), Li)
 Data23$academic_flag[rep_id] <- rep(as.character(val_aca), Li)

 Data23$cases_class[rep_id] <- rep(as.character(val_case), Li)
 Data23$cases_class_early[rep_id] <- rep(as.character(val_case_early), Li)
```

```
  Data23$cases_class_late[rep_id] <- rep(as.character(val_case_late), Li)
  Data23$cases_class_late_diff[rep_id] <- rep(as.character(val_case_late_diff), Li)

  Data23$cases_change[rep_id] <- rep(as.character(val_case_change), Li)
  Data23$cases_change_binary[rep_id] <- rep(as.character(val_case_change_binary), Li)
  Data23$cases_interaction[rep_id] <- rep(as.character(val_case_interaction), Li)

  Data23$hosp_region[rep_id] <- rep(as.character(val_reg), Li)
 }

 ## setting reference category
 Data23 <- Data23 %>% mutate_if(is.character, as.factor)
 Data23 <- within(Data23, icu_beds_class <- relevel(icu_beds_class, ref = "0 <= ICU < 20"))
 Data23 <- within(Data23, beds_class <- relevel(beds_class, ref = "0 <= Beds < 150"))
 Data23 <- within(Data23, academic_flag <- relevel(academic_flag, ref = "Academic"))
 Data23 <- within(Data23, hosp_usr_class  <- relevel(hosp_usr_class, ref = "Rural"))
 Data23 <- within(Data23, non_profit_flag  <- relevel(non_profit_flag, ref = "Profit"))
 Data23 <- within(Data23, hosp_region  <- relevel(hosp_region, ref = "Central"))
 Data23 <- within(Data23, cases_class_early  <- relevel(cases_class_early, ref = "0 <= Cases < 20"))
 Data23 <- within(Data23, cases_interaction  <- relevel(cases_interaction, ref = "otherwise"))
 Data23 <- within(Data23, cases_change_binary  <- relevel(cases_change_binary, ref = "Decrease"))
 Data23 <- within(Data23, cases_class  <- relevel(cases_class, ref = "0 <= Cases < 20"))
 Data23 <- within(Data23, cases_class_early  <- relevel(cases_class_early, ref = "0 <= Cases < 20"))
 Data23 <- within(Data23, cases_class_late  <- relevel(cases_class_late, ref = "0 <= Cases < 20"))
 Data23 <- within(Data23, cases_class_late_diff  <- relevel(cases_class_late_diff, ref = "0 <= Cases < 30"))
 Data23 <- within(Data23, cases_change  <- relevel(cases_change, ref = "<0%"))

 ## Model fitting
 gmft_hosp <- glmmfit(ylist, XXX_adj = XXX_adj2, ranlist, reml = TRUE, Data_analytical = Data23, addsize = TRUE, laplace
= FALSE)
 summary(gmft_hosp$fom3)
```

```
lb_hosp <- gmft_hosp$lb; ub_hosp <- gmft_hosp$ub; sdorp_hosp <- gmft_hosp$sdorp;
or_hosp <- gmft_hosp$or; orp_hosp <- gmft_hosp$orp;
dat_hosp <- data.frame("Variable" = names(or_hosp),
                       "bOR" =  or_hosp,
                       "lb" =  lb_hosp,
                       "ub" = ub_hosp,
                       "pval" = 2 * (1 - pnorm(abs(orp_hosp/sdorp_hosp))))
symbol <- "\u2265"; symbol2 <- intToUtf8(8804)

mlist_age <- c("age_class"); varlist_age <- c("Age::[45,55)", "Age::[55,65)",
                                    "Age::[65,75)", "Age::[75,85)", paste0("Age::", symbol,"85"));
reflist_age <- rep("[18,45)", length(varlist_age)); mlist0_age <- rep("age_class", length(varlist_age))

mlist_gender <- c("gender"); varlist_gender <- c("Gender::Male"); reflist_gender <- rep("Female",
length(varlist_gender));
mlist0_gender <- rep("gender", length(varlist_gender))
mlist_elix <- c("elix_class"); varlist_elix <- c("Elixhauser::[1,10)", "Elixhauser::[10,20)",
                                      paste0("Elixhauser::", symbol,"20"));
reflist_elix <- rep("[0,1)", length(varlist_elix)); mlist0_elix <- rep("elix_class", length(varlist_elix))

mlist_comorbidity <- c(comorb_id); varlist_comorbidity <- paste0("", comorb_nm, "::Yes", sep = "");
reflist_comorbidity <- rep("No", length(varlist_comorbidity)); mlist0_comorbidity <- comorb_id
mlist_race <- c("race_cd_class"); varlist_race <- c("Race::African-american", "Race::Other");
reflist_race <- rep("Caucasian", length(varlist_race)); mlist0_race <- rep("race_cd_class", length(varlist_race))


mlist_nurse <- c("snf_nursing_flag"); varlist_nurse <- c("Transferred from nursing facility::Yes");
reflist_nurse <- rep("No", length(varlist_nurse)); mlist0_nurse <- rep("snf_nursing_flag", length(varlist_nurse))
mlist_lob <- c("lob"); varlist_lob <- c("LOB::Medicare"); reflist_lob <- "Commercial"; mlist0_lob <- "lob"

mlist_count <- c("count_day_class"); varlist_count <- c("Days from January 1,2020::[0,90)",
```

```
                                        "Days from January 1,2020::[90,120)", "Days from January 1,2020::[120,150)")
reflist_count <- rep(paste0("", symbol,"150"), length(varlist_count));
mlist0_count <- rep("count_day_class", length(varlist_count))

mlist_numeric <- c("count_day", "count_day2"); varlist_numeric <- c("Days", "Days^2");
reflist_numeric <- rep(NA, length(mlist_numeric)); mlist0_numeric <- c("count_day", "count_day2")

mlist_size <- c("size"); varlist_size <- c("Log(volume)"); reflist_size <- NA; mlist0_size <- c("size")

## Hospital levels variables
# user
mlist_user <- c("hosp_usr_class"); varlist_user <- c("Location::Urban");
reflist_user <- rep("Rural", length(varlist_user)); mlist0_user <- rep("hosp_usr_class", length(varlist_user))

# ratio
mlist_ratio <- c("resident_to_bed_ratio_class"); varlist_ratio <- c("Resident to bed ratio::[0.05,0.25)",
                                                    paste0("Resident to bed ratio::", symbol,"0.25"));
reflist_ratio <- rep("[0,0.05)", length(varlist_ratio)); mlist0_ratio <- rep("resident_to_bed_ratio_class",
                                                    length(varlist_ratio))

# ICU
mlist_icu <- c("icu_beds_class"); varlist_icu <- c("Number of ICU beds::[20,60)",
                                    paste0("Number of ICU beds::", symbol,"60"));
reflist_icu <- rep("[0,20)", length(varlist_icu)); mlist0_icu <- rep("icu_beds_class", length(varlist_icu))

# region
mlist_region <- c("hosp_region"); varlist_region <- c(
  "Region::North-east",
  "Region::South-east",
  "Region::West");
reflist_region <- rep("Central", length(varlist_region)); mlist0_region <- rep("hosp_region", length(varlist_region))
```

```
# beds
mlist_beds <- c("beds_class"); varlist_beds <- c("Number of beds:[150,300)",
                                    "Number of beds:[300,450)",
                                    paste0("Number of beds::", symbol,"450"));
reflist_beds <- rep("[0,150)", length(varlist_beds)); mlist0_beds <- rep("beds_class", length(varlist_beds))

# academic
mlist_academic <- c("academic_flag"); varlist_academic <- c("Hospital affiliation::Non-academic");
reflist_academic <- rep("Academic", length(varlist_academic));
mlist0_academic <- rep("academic_flag", length(varlist_academic))

# profit
mlist_profit <- c("non_profit_flag"); varlist_profit <- c("Profit status::Non-profit", "Profit status::Other");
reflist_profit <- rep("For profit", length(varlist_profit));
mlist0_profit <- rep("non_profit_flag", length(varlist_profit))

# cases
mlist_cases <- c("cases_class"); varlist_cases <- c("Cases per 10K:[20,40)",
                                    paste0("Cases per 10K::", symbol,"40"));
reflist_cases <- rep("[0,20)", length(varlist_cases)); mlist0_cases <- rep("cases_class", length(varlist_cases))


# cases
mlist_cases <- c("cases_class"); varlist_cases <- c("Cases per 10K::[20,40)",
                                    paste0("Cases per 10K::", symbol,"40"));
reflist_cases <- rep("[0,20)", length(varlist_cases)); mlist0_cases <- rep("cases_class", length(varlist_cases))


# cases early
mlist_casesearly <- c("cases_class_early"); varlist_casesearly <- c("Cases (early) per 10K::[20,40)",
```

```
                                        paste0("Cases (early) per 10K::", symbol,"40"));

 reflist_casesearly <- rep("[0,20)", length(varlist_casesearly)); mlist0_casesearly <- rep("cases_class_early",
length(varlist_casesearly))


 # cases late

 mlist_caseslate <- c("cases_class_late"); varlist_caseslate <- c("Cases (late) per 10K::[20,40)",

                                        paste0("Cases (late) per 10K::", symbol,"40"));

 reflist_caseslate <- rep("[0,20)", length(varlist_caseslate)); mlist0_caseslate <- rep("cases_class_late",
length(varlist_caseslate))


 # cases change

 mlist_caseschange <- c("cases_change"); varlist_caseschange <- c("Cases change %::[0,100)", "Cases change
%::[100,250)",

                                        paste0("Cases change %::", symbol,"250"));

 reflist_caseschange <- rep("<0%", length(varlist_caseschange)); mlist0_caseschange <- rep("cases_change",
length(varlist_caseschange))



 # cases change binary

 mlist_caseschangebinary <- c("cases_change_binary"); varlist_caseschangebinary <- c("Cases change::Increase");

 reflist_caseschangebinary <- rep("Decrease", length(varlist_caseschangebinary));

 mlist0_caseschangebinary <- rep("cases_change_binary", length(varlist_caseschangebinary))



 # cases interaction

 mlist_casesinteraction <- c("cases_interaction");

 varlist_casesinteraction <- c("Cases::[20,40) & Increase", paste0("Cases::", symbol,"40 & Increase"));

 reflist_casesinteraction <- rep("otherwise", length(varlist_casesinteraction));

 mlist0_casesinteraction <- rep("cases_interaction", length(varlist_casesinteraction))


 # cases late

 mlist_caseslatediff <- c("cases_class_late_diff");
```

```
varlist_caseslatediff <- c("Cases (late) per 10K::[30,60)", "Cases (late) per 10K::[60,90)",
                           paste0("Cases (late) per 10K::", symbol,"90"));
reflist_caseslatediff <- rep("[0,30)", length(varlist_caseslatediff));
mlist0_caseslatediff <- rep("cases_class_late_diff", length(varlist_caseslatediff))

# deaths
mlist_deaths <- c("cases_class"); varlist_deaths <- c("Deaths per 10K:[1,3)", "Deaths per 10K:[3,5)",
                                        paste0("Deaths per 10K::", symbol,"5"));
reflist_deaths <- rep("[0,1)", length(varlist_deaths)); mlist0_deaths <- rep("deaths_class", length(varlist_deaths))



## Rearranging dat for coefficients
txt <- strsplit(variable_list, ":")[[1]]
## final name
txt2 <- paste0("mlist0_", tolower(txt), "", sep = "", collapse = ", ")
QQ <- paste0("c(", txt2,")")
QQ <-  eval(parse(text = QQ))



inout_ix <- unlist(lapply(seq_len(length(QQ)), function(ii) {
  inout <- grep(QQ[ii], dat_hosp$Variable, value = F)
  if(length(inout) >= 1){
    1
  } else{
    9999 # missing
  }
}))

lni <- which(inout_ix == 9999)
if(length(lni) > 0){
  dat_hosp$finalname <-  QQ[- which(inout_ix == 9999)]
```

```
} else{
  dat_hosp$finalname <- QQ
}

## ylab_name
txt2 <- paste0("varlist_", tolower(txt), "", sep = "", collapse = ", ")
QQ <- paste0("c(", txt2,")")
QQ <- eval(parse(text = QQ))

if(length(lni) > 0){
  dat_hosp$ylab_name <-  QQ[- which(inout_ix == 9999)]
} else{
  dat_hosp$ylab_name <- QQ
}
##reference
txt2 <- paste0("reflist_", tolower(txt), "", sep = "", collapse = ", ")
QQ <- paste0("c(", txt2,")")
QQ <- eval(parse(text = QQ))

if(length(lni) > 0){
  dat_hosp$reference <- QQ[- which(inout_ix == 9999)]
} else{
  dat_hosp$reference <- QQ
}
name_coef <- as.character(dat_hosp$Variable)

##Obtain cases
ylab_name_numb <- t(do.call(cbind, lapply(seq_len(nrow(dat_hosp)), function(uu) {

  where <- dat_hosp$finalname[uu]
  where
```

```
  numb <- table(Data23[, colnames(Data23) %in% where])
  what <- strsplit(name_coef[uu], where)[[1]][2]
  numb <- numb[which(names(numb) == what)]

  QQ <- subset(Data23, select = c(where, ylist))

  numb_event <- length(which(QQ[, 1] == what & QQ[, 2] == "Event"))

  as.vector(c(numb, numb_event))
 }))

 ## Merging all
 dat_hosp$ylab_name_numb <- ylab_name_numb[, 1]
 dat_hosp$ylab_name_numb_event <- ylab_name_numb[, 2]
 dat_hosp$allpoint <- unlist(lapply(seq_len(nrow(dat_hosp)), function(hh)
  paste0("",sprintf("%2.2f",round(dat_hosp$bOR[hh], 2)),"(",sprintf("%2.2f",round(dat_hosp$lb[hh],
2)),",",sprintf("%2.2f",round(dat_hosp$ub[hh], 2)), ")")))

 dat_hosp$ylab_name_numbX = paste0("", dat_hosp$ylab_name_numb_event, "/", dat_hosp$ylab_name_numb, "")

 zerome <- which(dat_hosp$ylab_name_numbX == "0/0")
 if(length(zerome) > 0){
  dat_hosp$ylab_name_numbX[zerome] <- NA
 }

 dat_hosp$pval <- sprintf("%0.4f", dat_hosp$pval)
 dat_hosp$pval[which(dat_hosp$pval == "0.0000")] <- "<0.0001"

 output = list(dat_hosp = dat_hosp, gmft_hosp = gmft_hosp)
}
```

```
# Internal function in Hmisc package for somer's C /Dxy statistic
.somers2 = function (x, y, weights = NULL, normwt = FALSE, na.rm = TRUE)
{
 if (length(y) != length(x))
  stop("y must have same length as x")
 y <- as.integer(y)
 wtpres <- length(weights)
 if (wtpres && (wtpres != length(x)))
  stop("weights must have same length as x")
 if (na.rm) {
  miss <- if (wtpres)
   is.na(x + y + weights)
  else is.na(x + y)
  nmiss <- sum(miss)
  if (nmiss > 0) {
   miss <- !miss
   x <- x[miss]
   y <- y[miss]
   if (wtpres)
    weights <- weights[miss]
  }
 }
 else nmiss <- 0
 u <- sort(unique(y))
 if (any(!(y %in% 0:1) ))
  stop("y must be binary")
 if (wtpres) {
  if (normwt)
   weights <- length(x) * weights/sum(weights)
  n <- sum(weights)
```

```
  }
  else n <- length(x)
  if (n < 2)
    stop("must have >=2 non-missing observations")
  n1 <- if (wtpres)
    sum(weights[y == 1])
  else sum(y == 1)
  if (n1 == 0 || n1 == n)
    return(c(C = NA, Dxy = NA, n = n, Missing = nmiss))
  mean.rank <- if (wtpres){
    require(Hmisc,quietly=TRUE)
    wtd.mean(wtd.rank(x, weights, na.rm = FALSE), weights *
             y)
  } else mean(rank(x)[y == 1])
  c.index <- (mean.rank - (n1 + 1)/2)/(n - n1)
  dxy <- 2 * (c.index - 0.5)
  r <- c(c.index, dxy, n, nmiss)
  names(r) <- c("C", "Dxy", "n", "Missing")
  r
}



# C1. Forest plot of odds ratio
plotOR_paper <- function(dataplot, xl = 0.2, xu = 5,
                         title = "Main title",
                         txtcol = paste0("No. events/\nCOVID patients"),
                         xlab_title = "Adjusted odd"){
  lc <- nrow(dataplot)
  revy <- seq_len(lc)
  plot(x = dataplot$bOR, y = rev(seq_len(lc)),
       xlab = xlab_title, ylab = '', xaxt = "n",
```

```
    yaxt = "n", pch = NA, log = "x",
    lwd = 2, cex.lab = 1.5, cex.main = 2,
    cex = 2, cex.axis = 2,
    xlim = c(xl, xu))

atx <- axTicks(1)
axis(1, at = atx, labels = atx, cex.axis = 1.7)
ven_tex_lb <- xl;
ven_tex_ub <- 0.9;
ven_tex_lb1 <- 1.1;
ven_tex_ub1 <- xu

ven_tex <- nrow(dataplot) + 1.5

RR <- as.character(dataplot$reference)
dataplot$reference <- RR

# Var names
mtext(side = 2, dataplot$ylab_name,
     at = rev(revy), line = 7, las = 2,
     cex = 1, font = 1)

# Reference names
mtext(side = 2, StrAlign(dataplot$reference, sep = "\\r"), at = rev(revy), las = 1, cex = 1,
     font = 1, line = ifelse(txtcol == "No. events/\nCOVID patients", 2, 3), col = "black")

# CI values
mtext(side = 4, StrAlign(dataplot$allpoint, sep = "\\r"),
     at = rev(revy),
     las = 2, cex = 0.8, font = 1)
```

```
# P values
col_pv <- ifelse(dataplot$pval <= 0.05, "orange",
                 ifelse(dataplot$pval > 0.05 & dataplot$pval <= 0.10, "purple", "black"))

mtext(side = 4, StrAlign(as.character(dataplot$pval), sep = "\\r"),
      at = rev(revy), col = "black",
      las = 2, line = 7, cex = 0.8, font = 2)

# Events
mtext(side = 2, dataplot$ylab_name_numbX, at = rev(revy), las = 2,
      line = 25, cex = 0.8, font = 1, col = "black")



# Column names
mtext(side = 2, txtcol, at = (ven_tex + 1),
      line = 23, las = 1, cex = 1,
      font = 2, col = "black")

mtext(side = 2, paste0("Characteristic better"), at = (ven_tex + 1),
      line = -5,
      las = 1, cex = 0.8, lwd = 1.2,
      font = 3,
      col = "black")

mtext(side = 2, paste0("Characteristic worse"), at = (ven_tex + 1),
      line = -15,
      las = 1, cex = 0.8, lwd = 1.2,
      font = 3, col = "black")

mtext(side = 4, title, at = (ven_tex + 2),
      line = -43,
```

```
    las = 1, cex = 1.5, lwd = 1.2,
    font = 21, col = "black")


mtext(side = 2, paste0("Reference"), at = (ven_tex + 1),
    line = 2,
    las = 1, cex = 1, lwd = 1.2,
    font = 2, col = "black")

mtext(side = 2, paste0("Characteristic"), at = (ven_tex + 1),
    line = 9,
    las = 1, cex = 1, lwd = 1.2,
    font = 2, col = "black")

mtext(side = 4, paste0("Estimate (95% CI)"),
    at = (ven_tex + 1),
    line = -1,
    las = 1, cex = 1, lwd = 1.2,
    font = 2, col = "black")

mtext(side = 4, paste0("p-value"),
    at = (ven_tex + 1),
    line = 7,
    las = 1, cex = 1, lwd = 1.2,
    font = 2, col = "black")


segments(x0 = xl, x1 = xu, y0 = revy, y1 = revy,
       col = "#EEEEEE", lty = 1, lwd = 2)
segments(x0 = 1, x1 = 1, y0 = 0, y1 = tail(revy, 1) + 1,
       col = "black", lty = 3, lwd = 2)
```

```
  segments(round(dataplot$lb, 2),
           rev(revy), round(dataplot$ub, 2),
           rev(revy),
           col = "black", lty = 1, lwd = 2)

  arrows(ven_tex_lb, (ven_tex -
                        ifelse(txtcol == "No. events/\nCOVID patients", 0.7, 1)),
         ven_tex_ub, (ven_tex -
                        ifelse(txtcol == "No. events/\nCOVID patients", 0.7, 1)), col = "black",
         lwd = 1, code = 1, lty = 5, length = 0.10)
  arrows(ven_tex_lb1, (ven_tex -
                         ifelse(txtcol == "No. events/\nCOVID patients", 0.7, 1)),
         ven_tex_ub1, (ven_tex -
                         ifelse(txtcol == "No. events/\nCOVID patients", 0.7, 1)), col = "black",
         lwd = 1, code = 2, lty = 5, length = 0.10)

  points(dataplot$bOR, rev(seq_len(lc)),
         xlab = '', lwd = 2,
         col = "black",
         cex = 1.5,
         pch = 3)
}

## C2. RSER/RSMR line plot
plotScore_paper_single_rotate <- function(dataplot,
                                          dataplot2 = NULL,
                                          xl = 0,
                                          xu = 0.30,
                                          maxX = 1000,
                                          sec_xl = -0.15,
```

```
                        sec_xu = 0.75,
                        atx1 = c(1, 200, 400, 600, 800, 960),
                        type = "early",
                        plot_unadj = TRUE,
                        ybar_early = ybar_early,
                        ybar_later = ybar_later,
                        ybar_orig,
                        confidence = FALSE,
                        title = "Hospital-specific standardized risk score",
                        ylab_title = "Standardized score",
                        xlab_title = "Hospital rank",
                        legend_title = "event"){
lc <- nrow(dataplot)
revy <- seq_len(lc)



if(is.null(type) == TRUE){
  QQ <- dataplot$score
} else if(is.null(type) == FALSE & type != "both"){
  QQ <- paste0("dataplot$", type,"_score")
  QQ <- eval(parse(text = QQ))
} else if(type == "both"){
  QQ1 <- paste0("dataplot$early_score")
  QQ1 <- eval(parse(text = QQ1))

  QQ <- QQ1
  QQ2 <- paste0("dataplot2$later_score")
  QQ2 <- eval(parse(text = QQ2))
}
```

```
plot(y = QQ,
    x = rev(seq_len(lc)),
    main = '',
    xlim = c(1, maxX),
    xlab = xlab_title,
    ylab = '', xaxt = "n",
    yaxt = "n", pch = NA, #log = "x",
    lwd = 2,
    cex.lab = 1.8,
    cex = 1.8,
    cex.axis = 1.8,
    ylim = c(xl, xu))

atx <- seq(xl, xu, length.out = 6)

# bottom
axis(2, at = atx, line = 0, col = "black",
    lwd = 2, labels = atx, cex.axis = 1.8)

axis(1, at = atx1, line = 0, col = "black",
    lwd = 2, labels = atx1, cex.axis = 1.8)

# Unadj score
mtext(side = 2, ylab_title, line = 2, font = 21,
     lwd = 1.2, cex = 1.8, las = 3)


## Orginal
segments(y0 = ybar_orig, y1 = ybar_orig,
        x0 = -1, x1 = lc,
        col = "black",
```

```
        lty = 2, lwd = 2)

if(is.null(type) == FALSE){
  if(type == "early"){
    # early
    segments(y0 = ybar_early, y1 = ybar_early,
             x0 = -1, x1 = lc,
             col = "black",
             lty = 3, lwd = 1.8)
  }
}
if(is.null(type) == FALSE){
  if(type == "later"){
    # later
    segments(y0 = ybar_later, y1 = ybar_later,
             x0 = -1, x1 = lc,
             col = "black",
             lty = 6, lwd = 1.8)
  }
}

symbol <- "\u2265"; symbol2 <- intToUtf8(8804)

compare_ybar <- ifelse(is.null(type) == TRUE,
                       ybar_orig,
                       ifelse(type == "early",
                            ybar_early, ybar_later))

if(length(type %in% c("early", "both", "later")) != 0){

  points(y = rev(QQ),
```

```
      x = rev(seq_len(lc)),
      xlab = '', lwd = 0.8,
      col = ifelse(rev(QQ > compare_ybar),
                   "red", "blue"),
      cex = 0.4, pch = ifelse(type == "early", 3, 23))

if(confidence == "SE mean"){
  polygon(x = c(seq_len(lc), rev(seq_len(lc))),
          y = c(dataplot$score_boot_mean_lb,
                rev(dataplot$score_boot_mean_ub)),
          col =  adjustcolor("black", alpha.f = 0.40),
          border = NA)
}else if(confidence == "IQR"){
  polygon(x = c(seq_len(lc), rev(seq_len(lc))),
          y = c(dataplot$score_boot_q1,
                rev(dataplot$score_boot_q3)),
          col =  adjustcolor("gray", alpha.f = 0.40),
          border = NA)
} else if(confidence == "Yale 95%"){
  polygon(x = c(seq_len(lc), rev(seq_len(lc))),
          y = c(dataplot$score_boot_025,
                rev(dataplot$score_boot_975)),
          col =  adjustcolor("orange", alpha.f = 0.20),
          border = NA)
}

points(y = rev(QQ),
      x = rev(seq_len(lc)),
      xlab = '', lwd = 0.8,
      col = ifelse(rev(QQ > compare_ybar),
                   "red", "blue"),
```

```
        cex = 0.4, pch = ifelse(type == "early", 3, 23))

}



if(is.null(type) == TRUE){


  points(y = rev(QQ),
         x = rev(seq_len(lc)),
         xlab = '', lwd = 0.8,
         col = ifelse(rev(QQ > compare_ybar),
                      "red", "blue"),
         cex = 0.4, pch = 3)
  if(confidence == "SE mean"){
    polygon(x = c(seq_len(lc), rev(seq_len(lc))),
            y = c(dataplot$score_boot_mean_lb,
                  rev(dataplot$score_boot_mean_ub)),
            col =  adjustcolor("black", alpha.f = 0.40),
            border = NA)
  }else if(confidence == "IQR"){
    polygon(x = c(seq_len(lc), rev(seq_len(lc))),
            y = c(dataplot$score_boot_q1,
                  rev(dataplot$score_boot_q3)),
            col =  adjustcolor("gray", alpha.f = 0.40),
            border = NA)
  } else if(confidence == "Yale 95%"){
    polygon(x = c(seq_len(lc), rev(seq_len(lc))),
            y = c(dataplot$score_boot_025,
                  rev(dataplot$score_boot_975)),
            col =  adjustcolor("orange", alpha.f = 0.20),
            border = NA)
```

```
  }
  points(y = rev(QQ),
         x = rev(seq_len(lc)),
         xlab = '', lwd = 0.6,
         col = ifelse(rev(QQ > compare_ybar),
                      "red", "blue"),
         cex = 0.4, pch = 3)

}



if(plot_unadj == TRUE){
  ## secondary axes
  par(new = TRUE)  # Add new plot
  ## secondary
  if(is.null(type) == TRUE){
    EE <- sprintf("%0.3f", as.numeric(dataplot$unadj_score))
    EE <- as.numeric(EE)
  } else{
    EE <- paste0("dataplot$", type,"_unadj_score")
    EE <- eval(parse(text = EE))
  }

  dataplot$diff_u <- EE - QQ
  summary(dataplot$diff_u)



  plot(y = dataplot$diff_u,
       x = rev(seq_len(lc)),
       main = '',
       xlim = c(1, maxX),
```

```
    xlab = '',
    ylab = '',
    xaxt = "n",
    yaxt = "n",
    pch = NA,
    lwd = 2,
    cex.lab = 2,
    cex = 2,
    cex.axis = 2,
    ylim = c(sec_xl, sec_xu))
atx4 <- seq(sec_xl, sec_xu, by = 0.15)



axis(4, at = atx4,
    line = 0,
    col = "black",
    lwd = 2,
    labels = atx4,
    cex.axis = 1.8)



mtext(side = 4, "Rate differences (unadjusted - standardized)",
     line = 2, font = 21,
     lwd = 1.2, cex = 2)

points(y = rev(dataplot$diff_u),
      x = rev(seq_len(lc)),
      xlab = '', lwd = 1.2,
      col = adjustcolor("gray2", alpha.f = 0.30),
      cex = 1,
      pch = 17)
```

```
} # unadj plot ends

# legend
if(plot_unadj == TRUE & is.null(type) == TRUE){

  legend('topleft', bty = "n", cex = 1.4,
         pch = c(NA, 17),
         lwd = c(3, NA),
         lty = c(2),
         col = c("gray2", "black"),
         horiz = F,
         c(paste0("Observed ", legend_title, " rate"),
           paste0("Unadjusted ", legend_title, " rate")))
} else if(plot_unadj == FALSE & is.null(type) == TRUE){


  legend('topleft', bty = "n", cex = 1.2,
         pch = c(NA),
         lwd = c(2),
         lty = c(2),
         col = c("black"),
         horiz = F,
         paste0("Observed ", legend_title, " rate"))

} else if(plot_unadj == FALSE & is.null(type) == FALSE & type != "both"){

  if(type == "early"){
    legend('topleft', bty = "n", cex = 1.2,
           pch = c(NA, NA),
           lwd = c(3, 3),
```

```
        lty = c(2, 3),
        col = c("black", "black"),
        horiz = F,
        c(paste0("Observed ", legend_title, " rate"),
          paste0("Observed ", legend_title, " rate in early period (January 1 - April 30, 2020)")))
 }
 if(type == "later"){
  legend('topleft', bty = "n", cex = 1.2,
        pch = c(NA),
        lwd = c(3),
        lty = c(6),
        col = c("black"),
        horiz = F,
        paste0("Observed ", legend_title, " rate in late period (May 1 - June 30, 2020)"))
 }



} else if(plot_unadj == FALSE & is.null(type) == FALSE & type == "both"){



  legend('topleft', bty = "n", cex = 1.2,
       pch = c(NA, NA, NA),
       lwd = c(1.5, 1.5, 1.5),
       lty = c(2, 3, 6),
       col = c("black", "black", "black"),
       horiz = F,
       c(paste0("Observed ", legend_title, " rate"),
         paste0("Observed ", legend_title, " rate in early period (January 1 - April 30, 2020)"),
         paste0("Observed ", legend_title, " rate in late period (May 1 - June 30, 2020)")))
}
```

```
}



# C3. Bland-Altman
bland_altman_all <- function(s1, s2,
                             score_early2j,
                             score_later2j,
                             ylm_l = -25, ylm_u = 10, xlm_l = 0, xlm_u = 40,
                             legend_title = "event",
                             region_com, col_region,
                             slope = c(-2/3, -2/7, 2/9),
                             N1 = c(286, 111, 1, 0)){
  par(pty = "s")
  plot(x = s2,
       y = s1,
       cex = 0.9,
       ylab = paste0('Absolute change in risk standardized\n', legend_title, ' rates (Late - Early) %'),
       xlab = paste0('\n\n\n\n\nAverage of early and late risk \nstandardized ', legend_title,' rates (%)'),
       pch = 20,
       col = adjustcolor("gray4", alpha.f = 0.10),
       lwd = 2, cex.lab = 1.3,
       type = "p", axes = FALSE,
       xlim = c(xlm_l, xlm_u),
       ylim = c(ylm_l, ylm_u))



  abline(h = 0, lwd = 2, lty = 5)
  axis(2, at = c(-25, -20, -15, -10, -5, 0, 5, 10),
       labels = sprintf("%2.0f", c(-25, -20, -15, -10, -5, 0, 5, 10)),
       lwd = 2, cex.axis = 1.4)
```

```
axis(1, at = seq(xlm_l, xlm_u, length.out = 5),
     labels = seq(xlm_l, xlm_u, length.out = 5), lwd = 2,
     cex.axis = 1.4)



if(is.null(slope) == TRUE){
  segments(x0 = xlm_l, x1 = xlm_u, y0 = 0, y1 = ylm_l,
           col = "black", lty = 5, lwd = 2)
} else{

  polygon(x = c(xlm_l, xlm_u, xlm_u, xlm_l),
          y = c(ylm_l, ylm_l, 0, 0),
          col = adjustcolor("red", alpha.f = 0.10),
          border = adjustcolor("red", alpha.f = 0.2),
          lwd = 1.5,
          lty = c("solid"))

  nr <- ifelse(slope < 0, abs(ylm_l) / abs(slope),
               ylm_u / slope)

  for(uu in 1 : length(nr)){
    if(uu == 1){
      polygon(x = c(xlm_l, xlm_l, nr[uu]),
              y = c(0, ylm_l, ylm_l),
              col = adjustcolor("green", alpha.f = 0.10),
              border = adjustcolor("green", alpha.f = 0.20),
              lwd = 1.5,
              lty = c("solid"))
    }else if(uu == 2){
      polygon(x = c(xlm_l, xlm_u, xlm_u, nr[1]),
              y = c(0, (slope[2] * nr[1]), ylm_l, ylm_l),
```

```
            col = adjustcolor("yellow", alpha.f = 0.10),
            border = adjustcolor("yellow", alpha.f = 0.20),
            lwd = 1.5,
            lty = c("solid"))
    } else if(uu == 3){
      polygon(x = c(xlm_l, xlm_u, xlm_u),
            y = c(0, 0, (xlm_u * slope[uu])),
            col = adjustcolor("purple", alpha.f = 0.10),
            border = adjustcolor("purple", alpha.f = 0.20),
            lwd = 1.5,
            lty = c("solid"))
    }
  }
}

## re-adding points
points(x = s2,
       y = s1,
       cex = 0.9,
       pch = 20,
       col = adjustcolor("gray4", alpha.f = 0.10),
       lwd = 2)



symbol <- "\u2265"; symbol2 <- intToUtf8(8804)
mtext(side = 1,
      StrAlign(paste0("n = ",N1[1],""), sep = "\\l"),
      at = 5,
      las = 1, cex = 1,
      font = 22,
```

```
      line = -5, col = "black")
  mtext(side = 1, StrAlign(paste0("n = ",N1[2],""), sep = "\\l"),
      at = 35, las = 1, cex = 1, font = 22,
      line = -7, col = "black")
  mtext(side = 1, StrAlign(paste0("n = ",N1[3],""), sep = "\\l"),
      at = 35,
      las = 1, cex = 1,
      font = 22,
      line = -12, col = "black")
  mtext(side = 1, StrAlign(paste0("n = ",N1[4],""), sep = "\\l"),
      at = 35,
      las = 1, cex = 1,
      font = 22,
      line = -17, col = "black")

  # legend
  legend("topleft", bty = "n", cex = 0.8,
       lwd = 7,
       x.intersp = 1,
       y.intersp = 1,
       col = c(adjustcolor("green", alpha.f = 0.50),
            adjustcolor("yellow", alpha.f = 0.50),
            adjustcolor("red", alpha.f = 0.50),
            adjustcolor("purple", alpha.f = 0.50)),
       horiz = F,
       c("50% or more relative reduction",
         "[25-50)% reduction",
         "[0,25)% relative reduction",
         "(0,25]% relative increment"))
}
```

```
# C4. Find summary statistics of a vector
summary_statistics_table <- function(score2find){
 stat <- stat.desc(score2find, basic = TRUE)
 stat <- c(stat, quantile(score2find, 0.75) -
           quantile(score2find, 0.25))

 result <- as.matrix(stat)

 rownames(result) <- c(head(rownames(result), (length(stat) - 1)), "IQR")#,



 result <- result[rownames(result) %in% c("nbr.val", "min", "max",
                                          "median", "mean",
                                          "SE.mean",
                                          "var",
                                          "IQR"), ]

 result <- as.matrix(result)
 rownames(result) <- c("Number", "Minimum", "Maximum", "Median", "Mean",
                       "SE of mean",
                       "Variance", "IQR")
 colnames(result) <- "Summary statistics"
 result <- as.data.frame(round(result, 3))

 cimean <- paste0("(", sprintf("%0.2f", mean(score2find) - 1.96 * sd(score2find) /
                                sqrt(length(score2find))), ", ",sprintf("%0.2f", mean(score2find) + 1.96 * sd(score2find) /
                                                                        sqrt(length(score2find))),")")

 result$`Summary statistics` <- sprintf("%0.2f", result$`Summary statistics`)
```

```
  result2 <- c(result$`Summary statistics`, cimean)
  result2 <- as.matrix(result2)
  rownames(result2) <- c(rownames(result), "95% CI for mean")
  colnames(result2) <- "Summary statistics"
  grid.table(as.data.frame(result2))
}



# c5. Generate bi-variate boxplots
Compare_numeric_boxplot_ggplot <- function(Data_score_earlylate, ylab_title = "Risk standardized event rates") {

  x_pos_cat <- c(0.75, 1.25, 1.85, 2.25)
  x_pos_num <- c(1, 2)

  # Draw plot
  p <- ggplot(data = Data_score_earlylate, aes_string(x = "Period", y = "Score")) +
    # Drawing boxplot
    geom_boxplot(colour = "gray47", fill = c("burlywood", "aquamarine"),
                 notch = FALSE, show.legend = FALSE, outlier.shape = NA) +
    # Giving title
    # Finding median and confidence band for median
    stat_summary(fun.data = f_median, geom = "crossbar",
                 colour = NA, fill = "lemonchiffon3", width = 0.8, alpha = 0.8) +
    # Jitter
    geom_jitter(position = position_jitter(width = 0.08, height = 0.01, seed = 521)) +

    theme_minimal() +

    # changing lable/axes size
    theme(
      axis.text.x = element_text(size = 14),
```

```
    axis.text.y = element_text(size = 14),
    axis.title.y = element_text(size = 14),
    axis.title.x = element_text(size = 14),
    axis.title = element_text(size = 14),
    legend.text = element_text(size = 14)) +

  labs(x = "") + labs(y = ylab_title) +
  # Displaying mean
  stat_summary(fun.y = mean, geom = "point",
               shape = 18, size = 5, color = "firebrick2")
 p
}



# C6. Forest plot of hospital attributes
plotOR_paper_hospital <- function(dataplot_CM,
                          xl = -4, xu = 14,
                          atx = c(-3, -2, -1, 0, 1, 2, 3),
                          xlab_title = "Effect of covariates on mean COVID hospitalization (in days)",
                          title = ""){

 lc <- nrow(dataplot_CM)
 revy <- seq_len(lc)

 adj_x <- dataplot_CM$Effect;
 adj_lb <- dataplot_CM$lb; adj_ub <- dataplot_CM$ub



 adj_xl <- xl
 adj_xu <- xu
 plot(x = adj_x,
```

```
    y = rev(seq_len(lc)),
    xlab = xlab_title,
    main = '', cex.axis = 2,
    ylab = '', xaxt = "n", lwd = 2,
    cex.lab = 1.5, cex.main = 2,
    cex = 2, yaxt = "n", pch = NA,
    xlim = c(adj_xl, adj_xu))



atx <- atx
axis(1, at = atx, labels = atx, cex.axis = 1.7, lwd = 1)

ven_tex <- nrow(dataplot_CM) + 1.5

RR <- as.character(dataplot_CM$reference)
dataplot_CM$reference <- RR

# Var names
mtext(side = 2, dataplot_CM$ylab_name,
     at = rev(revy),
     line = 5, las = 2, cex = 0.8,
     font = 1,
     col = "black")

# Count
mtext(side = 2, as.vector(dataplot_CM$ylab_name_numb[,1]),
     at = rev(revy),
     line = 17, las = 2, cex = 0.8,
     font = 1,
     col = "black")
```

```
# Reference names
mtext(side = 2, StrAlign(dataplot_CM$reference, sep = "\\l"),
    at = rev(revy),
    las = 1, cex = 0.8, line = 0, font = 1, col = "black")

# CI values
mtext(side = 4, StrAlign(dataplot_CM$allpoint, sep = "\\r"), at = rev(revy), las = 2,
    cex = 0.8, font = 1, col = "black")

col_pv <- "black"

# p-value
mtext(side = 4, StrAlign(dataplot_CM$pv, sep = "\\r"),
    at = rev(revy), las = 2,
    cex = 0.8, line = 8, font = 2,
    col = col_pv)



# Column names
mtext(side = 2, paste0("Reference"), at = (ven_tex),
    line = 0,
    las = 1, cex = 1, lwd = 1,
    font = 2, col = "black")

mtext(side = 2, paste0("Characteristic"), at = (ven_tex),
    line = 7,
    las = 1, cex = 1, lwd = 1, font = 2,
    col = "black")
```

```
mtext(side = 2, paste0("Size"), at = (ven_tex),
      line = 17,
      las = 1, cex = 1, lwd = 1, font = 2,
      col = "black")

mtext(side = 4, paste0("Estimate (95% CI)"),
      at = ven_tex,
      line = -1,
      las = 1, cex = 1,
      lwd = 1, font = 2,
      col = "black")

mtext(side = 4, paste0("p-value"),
      at = ven_tex,
      line = 8,
      las = 1, cex = 1,
      lwd = 1, font = 2,
      col = "black")

segments(x0 = xl, x1 = xu, y0 = revy, y1 = revy,
         col = "#EEEEEE", lty = 1, lwd = 2)

segments(round(adj_lb, 2), rev(revy),
         round(adj_ub, 2), rev(revy),
         col = "black", lty = 1, lwd = 2)

segments(x0 = 0, x1 = 0,
         y0 = 0, y1 = tail(revy, 1) + 1,
         col = "black", lty = 2,
         lwd = 2)
```

```
  points(adj_x, rev(seq_len(lc)),
         xlab = '', lwd = 2,
         col = "black", cex = 1.5, pch = 3)
}


# C7. Descriptive comparisons
quintile_descriptive <- function(Data_score, id_q){

  dataqa <- data.frame("score" = datam$score,
                       "group" = id_q,
                       "reference" = datam$reference)
  description   <- describeBy(dataqa$score, dataqa$group, digits = 4, mat = TRUE)
  a1 <- round(description[, 5] - 1.96 * description[, 6] / sqrt(description[, 4]), 4)
  a2 <- round(description[, 5] + 1.96 * description[, 6] / sqrt(description[, 4]), 4)



  ## difference from Q5
  lb_dif <- (description$mean[5] - description$mean) - 1.96 *
    sqrt((description$sd^2)/description$n +
           (description$sd[5]^2)/description$n[5])

  mean_dif <- (description$mean[5] - description$mean)

  ub_dif <- (description$mean[5] - description$mean) + 1.96 *
    sqrt((description$sd^2)/description$n +
           (description$sd[5]^2)/description$n[5])

  z_dif <- mean_dif / sqrt((description$sd^2)/description$n + (description$sd[5]^2)/description$n[5])
  p_value_dif <- 2 * (1 - pnorm(abs(z_dif)))
```

```
  mean_dif[5] <- ub_dif[5] <- lb_dif[5] <- z_dif[5] <- p_value_dif[5] <- NA

  a3 <- c(colnames(description), "lb_mean", "ub_mean",
          "mean_dif_Q5", "lb_dif_Q5", "ub_dif_Q5", "z_dif", "p_value_dif")
  description <- cbind(description, a1, a2, mean_dif, lb_dif, ub_dif, z_dif, p_value_dif)
  colnames(description) <- a3
  rownames(description) <- c("Q1", "Q2", "Q3", "Q4", "Q5")

  output = list(description = description)
}
```

Simulating patient outcome data

Here we simulate patient outcome data for different hospitals. Note that data is generated without considering any clinical perspective and thus does not mean anything intuitively. This is solely for the purpose of illustrating the adopted methodologies to compute risk standardized scores. Consider response being a binary variable with 1 denoting patient-specific adverse event and 0 otherwise. The covariates consist of simulated demographic, clinical, and comorbid variables.

```{r simul}
## Simulating data
names <- c("age_class", "gender", "snf_nursing_flag",
           "aeci_aids_flag",  "aeci_alcohol_flag", "aeci_anemdef_flag",
           "aeci_arth_flag", "aeci_bldloss_flag", "aeci_chf_flag", "aeci_chrnlung_flag",
           "aeci_coag_flag", "aeci_depress_flag", "aeci_dm_flag", "aeci_dmcx_flag",
           "aeci_drug_flag", "aeci_htn_flag", "aeci_hypothy_flag", "aeci_liver_flag",
           "aeci_lymph_flag", "aeci_lytes_flag", "aeci_mets_flag", "aeci_neuro_flag",
           "aeci_obese_flag", "aeci_para_flag", "aeci_perivasc_flag", "aeci_psych_flag",
           "aeci_pulmcirc_flag", "aeci_renlfail_flag", "aeci_tumor_flag", "aeci_ulcer_flag",
           "aeci_valve_flag", "aeci_wghtloss_flag",  "count_day_class", "size",
           "mbr_death_flag", "hosp_name")
```

```
 # comorbidity names
 tow <- names[names %!in% c('gender', 'snf_nursing_flag', 'size', 'mbr_death_flag', 'hosp_name',
            'count_day_class', 'age_class')]

K <- 500 # Number of sites
dataN <- list()

set.seed(33)
beta_com <- round(rnorm(length(tow), 0, 1), 2)
beta_int <- rnorm(1, -2, 4)
beta_age <- rnorm(1, 1, 1)
beta_nurse <- rnorm(1, -0.5, 0.50)
beta_count <- rnorm(1, 0.10, 0.50)
beta_gender <- rnorm(1, -0.50, 0.50)
beta_size <- 0 #rnorm(1, 0.1, 0.2)
#mbr_death_flag <- list()
c(beta_com, beta_age, beta_count,  beta_nurse, beta_size, beta_int, beta_gender)
dataN_All <- do.call(rbind, lapply(seq_len(K), function(kk) {

  set.seed(7777 + kk)
  nh <- round(runif(1, 10, 200))  # number of patients in each hospital; minimum 10 and maximum 500
  dataN$hosp_name <- rep(paste0("Hospital_", kk,""), nh)
  dataN$size <- rep(nh, nh)
  dataN$size_scale <- log(dataN$size)

  for(jj in 1 : length(names)){
    if(names[jj] == "gender"){
      set.seed(jj + 8000)
      QQ <- paste0("dataN$", names[jj], " <- rbinom(", nh, ", 1, 0.60)")
      QQ <- eval(parse(text = QQ))
    }
```

```
  if(names[jj] == "snf_nursing_flag"){
    set.seed(jj + 1)
    QQ <- paste0("dataN$", names[jj], " <- rbinom(", nh, ", 1, 0.40)")
    QQ <- eval(parse(text = QQ))
  }
  if(names[jj] %!in% c("gender", "snf_nursing_flag", "mbr_death_flag", "hosp_name",
                       "size", "count_day_class", "age_class")){
    set.seed(jj + 1000)
    prob_c <- runif(1, 0.3, 0.7)
    QQ <- paste0("dataN$", names[jj], " <- rbinom(", nh, ", 1, prob_c)")
    QQ <- eval(parse(text = QQ))
  }
  if(names[jj] == "age_class"){
    set.seed(jj + 3000)
    dataN$age <- round(rnorm(nh, mean = 65, sd = 20)) # mean age 65 and sd 15
    dataN$age_scale <- (dataN$age - min(dataN$age)) / (max(dataN$age) - min(dataN$age))
  }
  if(names[jj] == "count_day_class"){
    set.seed(jj + 5000)
    dataN$count_day <- round(runif(nh, min = 10, max = 200)) # minimum count of day 10 and maximum 180
    dataN$count_day_scale <- (dataN$count_day - min(dataN$count_day)) / (max(dataN$count_day) -
min(dataN$count_day))
  }
 } # loop for each variable ends
 #as.data.frame(dataN)

 tow <- names[names %!in% c('gender', 'snf_nursing_flag', 'size', 'mbr_death_flag', 'hosp_name',
                            'count_day_class', 'age_class')]

 set.seed(kk + 88)
 bi <- rnorm(1, 0, 1) # 3 site-specific
```

```
  eij <- rnorm(nh, 0, 1.5) # each patient-specific



  EE <- paste0("dataN$", tow, " * ", beta_com, "", collapse = "+")
  QQ <- paste0("link_fix <- beta_int + dataN$count_day_scale * beta_count +
               dataN$age_scale * beta_age +
               dataN$snf_nursing_flag * beta_nurse + dataN$gender * beta_gender +
               dataN$size_scale * beta_size + ", EE, " + bi + eij")
  QQ <- eval(parse(text = QQ))
  QQp <- (exp(QQ)/(1 + exp(QQ)))
  QQp
  dataN$mbr_death_flag <- ifelse(QQp  >= 0.5, 1, 0)
  table(dataN$mbr_death_flag)
  as.data.frame(dataN)
} # loop for each hospital ends
))

for(jj in 1 : length(names)){
  if(names[jj] == "gender"){
    QQ <- paste0("dataN_All$", names[jj], " <- ifelse(dataN_All$", names[jj], " == 1,
                 'Male', 'Female')")
    QQ <- eval(parse(text = QQ))
  }
  if(names[jj] == "snf_nursing_flag"){
    QQ <- paste0("dataN_All$", names[jj], " <- ifelse(dataN_All$", names[jj], " == 1,
                 'Yes', 'No')")
    QQ <- eval(parse(text = QQ))
  }
  if(names[jj] %!in% c("gender", "snf_nursing_flag", "mbr_death_flag", "hosp_name",
                       "size", "count_day_class", "age_class")){
    QQ <- paste0("dataN_All$", names[jj], " <- ifelse(dataN_All$", names[jj], " == 1,
```

```
            'Yes', 'No')")
  QQ <- eval(parse(text = QQ))
 }
 if(names[jj] == "mbr_death_flag"){
  QQ <- paste0("dataN_All$", names[jj], " <- ifelse(dataN_All$", names[jj], " == 1,
            'Event', 'Alive')")
  QQ <- eval(parse(text = QQ))
 }
 if(names[jj] == "age_class"){
  dataN_All$age_class <- ifelse(dataN_All$age <= 45, "18 < age <= 45",
   ifelse(dataN_All$age > 45 & dataN_All$age <= 55, "45 < age <= 55",
    ifelse(dataN_All$age > 55 & dataN_All$age <= 65, "55 < age <= 65",
     ifelse(dataN_All$age > 65 & dataN_All$age <= 75, "65 < age <= 75",
      ifelse(dataN_All$age > 75 & dataN_All$age <= 85, "75 < age <= 85", "85 < age")))))
 }
 if(names[jj] == "count_day_class"){
  dataN_All$count_day_class <- ifelse(dataN_All$count_day <= 90, "1 < Count <= 90",
   ifelse(dataN_All$count_day > 90 & dataN_All$count_day <= 120, "90 < Count <= 120",
    ifelse(dataN_All$count_day > 120 & dataN_All$count_day <= 150, "120 < Count <= 150",
                                    "150 < Count")))
 }
}



# defining reference categories
dataN_All <- dataN_All %>% mutate_if(is.character, as.factor)
dataN_All <- within(dataN_All, age_class <- relevel(age_class, ref = "18 < age <= 45"))
dataN_All <- within(dataN_All, gender <- relevel(gender, ref = "Female"))
dataN_All <- within(dataN_All, count_day_class <- relevel(count_day_class, ref = "150 < Count"))
dataN_All <- within(dataN_All, snf_nursing_flag  <- relevel(snf_nursing_flag, ref = "No"))
dataN_All <- within(dataN_All, mbr_death_flag <- relevel(mbr_death_flag, ref = "Alive"))
```

```
dataN_All$size <- log(dataN_All$size)  # log transformation

comorb <- names[names %!in% c("gender", "snf_nursing_flag", "mbr_death_flag", "size", "hosp_name",
"count_day_class", "age_class")]

for(jj in 1 : length(comorb)){

  QQ <- paste0("dataN_All <- within(dataN_All, ", comorb, " <- relevel(",comorb, ", ref = 'No'))", collapse = "; ")

  QQ <- eval(parse(text = QQ))

}


dim(dataN_All)

table(dataN_All$mbr_death_flag)

length(unique(dataN_All$hosp_name))
```


Fitting generalized linear mixed model

Following the procedures described in Drye et al. and Silber et al., we compute hospital specific risk standardized rates (RSERs) or risk standardized mortality rates (RSMRs). In this example, we focus only on composite outcomes (i.e., RSERs).

```{r}
system.time(fit0 <- glmmfit(ylist = "mbr_death_flag",
            XXX_adj = c(names[names %!in% c("mbr_death_flag", "hosp_name")]),
            ranlist = "(1 | hosp_name)",
            reml = TRUE,
            Dataf = dataN_All,
            addsize = TRUE,
            laplace = FALSE))
```


We extract the model outputs.

```{r}
# Model outputs
```

```
fom <- fit0$fom; fom3 <- fit0$fom3; LRT_re <- fit0$LRT_re; aic_null <- fit0$aic_null;
aic_alt <- fit0$aic_alt; SS <- fit0$SS; cor_lme_lmer <- fit0$cor_lme_lmer;
probs <- fit0$probs; rank_cor <- fit0$rank_cor; nY <- fit0$nY; lb <- fit0$lb
ub <- fit0$ub; sdorp <- fit0$sdorp; or <- fit0$or; orp <- fit0$orp; pred <- fit0$pred;
estm <- fit0$estm; ybar <- fit0$ybar; uid <- fit0$uid;
score <- fit0$score; score_DS_mean <- apply(fit0$score_DS, 2, mean)
unadj_score <- fit0$unadj_score; hosp_orig_vol = fit0$hosp_orig_vol

# Score table
datScore_orig <- data.frame("score" = as.numeric(score),
                            "score_DS_mean" = as.numeric(score_DS_mean),
                            "reference" = as.character(uid),
                            "volume" = hosp_orig_vol,
                            "unadjusted_score" = unadj_score)

# Odds ratio table
dat <- data.frame("Variable" = names(or),
                  "bOR" =  or,
                  "lb" =  lb,
                  "ub" = ub,
                  "pval" = 2 * (1 - pnorm(abs(orp/sdorp))))

# Rearranging data for forest plot
symbol <- "\u2265"; symbol2 <- intToUtf8(8804)
ylist <- "mbr_death_flag"
mlist_age <- c("age_class"); varlist_age <- c("Age::[45,55)", "Age::[55,65)", "Age::[65,75)",
                "Age::[75,85)", paste0("Age::", symbol,"85"));
reflist_age <- rep("[18,45)", length(varlist_age)); mlist0_age <- rep("age_class",
                                                    length(varlist_age))
comorb_nm <- c("Acquired immune deficiency syndrome", "alcohol abuse",
               "Iron deficiency anemia", "Rheumatoid arthritis", "bloodloss anemia",
```

```
        "Congestive heart failure", "Chronic obstructive pulmonary disease",
        "Coagulopathy", "depression", "Diabetes without chronic complication",
        "Diabetes with chronic complication", "drug abuse", "hypertension",
        "hypothyroidism", "liver disease", "lymphoma", "fluid/electrolyte disorder",
        "metastatic cancer", "neurological disorders", "obesity", "paralysis",
        "peripheral vascular disease" ,"psychosis", "pulmonary circulation disorder",
        "Chronic kidney disease", "tumor w/o metastasis", "peptic ulcer disease",
        "valvular disorder", "Weight loss")

mlist_gender <- c("gender"); varlist_gender <- c("Gender::Male"); reflist_gender <- rep("Female",
length(varlist_gender)); mlist0_gender <- rep("gender", length(varlist_gender))
mlist_comorbidity <- c(tow); varlist_comorbidity <- paste0("", comorb_nm, "::Yes", sep = "");
reflist_comorbidity <- rep("No", length(varlist_comorbidity)); mlist0_comorbidity <- tow
mlist_nurse <- c("snf_nursing_flag"); varlist_nurse <- c("Transferred from nursing facility::Yes");
reflist_nurse <- rep("No", length(varlist_nurse)); mlist0_nurse <- rep("snf_nursing_flag",
                                        length(varlist_nurse))
mlist_count <- c("count_day_class"); varlist_count <- c("Days from January 1,2020::[0,90)",
          "Days from January 1,2020::[90,120)", "Days from January 1,2020::[120,150)")
reflist_count <- rep(paste0("", symbol,"150"), length(varlist_count));
mlist0_count <- rep("count_day_class", length(varlist_count))
mlist_size <- c("size"); varlist_size <- c("Log(volume)"); reflist_size <- NA;
mlist0_size <- c("size")

## Fixed effects
variable_list = "Age:Gender:Nurse:Comorbidity:Count:Size"
txt <- strsplit(variable_list, ":")[[1]]
txt2 <- paste0("mlist_", tolower(txt), "", sep = "", collapse = ", ")
XXX <- paste0("c(", txt2,")")
XXX <- eval(parse(text = XXX))
variable_list_BAR <- paste0("", txt, collapse = "|")
```

```
txt <- strsplit(variable_list, ":")[[1]]
## final name
txt2 <- paste0("mlist0_", tolower(txt), "", sep = "", collapse = ", ")
QQ <- paste0("c(", txt2,")")
QQ <-  eval(parse(text = QQ))

inout_ix <- unlist(lapply(seq_len(length(QQ)), function(ii) {
  inout <- grep(QQ[ii], dat$Variable, value = F)
  if(length(inout) >= 1){
    1
  } else{
    9999 # missing
  }
}))

lni <- which(inout_ix == 9999)
if(length(lni) > 0){
  dat$finalname <-  QQ[- which(inout_ix == 9999)]
} else{
  dat$finalname <- QQ
}

txt2 <- paste0("varlist_", tolower(txt), "", sep = "", collapse = ", ")
QQ <- paste0("c(", txt2,")")
QQ <- eval(parse(text = QQ))

if(length(lni) > 0){
  dat$ylab_name <-  QQ[- which(inout_ix == 9999)]
} else{
  dat$ylab_name <- QQ
}
```

```
txt2 <- paste0("reflist_", tolower(txt), "", sep = "", collapse = ", ")
QQ <- paste0("c(", txt2,")")
QQ <- eval(parse(text = QQ))

if(length(lni) > 0){
  dat$reference <- QQ[- which(inout_ix == 9999)]
} else{
  dat$reference <- QQ
}
name_coef <- as.character(dat$Variable)

ylab_name_numb <- t(do.call(cbind, lapply(seq_len(nrow(dat)), function(uu) {
  where <- dat$finalname[uu]
  numb <- table(dataN_All[, colnames(dataN_All) %in% where])
  what <- strsplit(name_coef[uu], where)[[1]][2]
  numb <- numb[which(names(numb) == what)]
  QQ <- subset(dataN_All, select = c(where, ylist))
  head(QQ)
  numb_event <- length(which(QQ[, 1] == what & QQ[, 2] == "Event"))
  as.vector(c(numb, numb_event))
})))
dat$ylab_name_numb <- ylab_name_numb[, 1]
dat$ylab_name_numb_event <- ylab_name_numb[, 2]
dat$allpoint <- unlist(lapply(seq_len(nrow(dat)), function(hh)
  paste0("",sprintf("%2.2f",round(dat$bOR[hh], 2)),"(",sprintf("%2.2f",round(dat$lb[hh],
2)),",",sprintf("%2.2f",round(dat$ub[hh], 2)), ")")))
dat$ylab_name_numbX = paste0("", dat$ylab_name_numb_event, "/", dat$ylab_name_numb, "")
zerome <- which(dat$ylab_name_numbX == "0/0")
if(length(zerome) > 0){
  dat$ylab_name_numbX[zerome] <- NA
```

```
}
```

Comparison between two methods

```{r}
sm1 <- summary(datScore_orig$score)   # Dyre et al.
sm2 <- summary(datScore_orig$score_DS_mean) # Silber et al.

cr <- cor(datScore_orig$score, datScore_orig$score_DS_mean)
par(bty = "n", mar = c(5, 5, 5, 5), mgp = c(2, 0.5, 0), xpd = FALSE, tcl = 0.25, cex = 0.9)
plot(x = datScore_orig$score,
    y = datScore_orig$score_DS_mean,
    xlim = c(0, 0.3), ylim = c(0, 0.3),
    xlab = "Dyre et al. (P/E * y_bar)",
    ylab = "Silber et al.",
    cex.axis = 2,
    pch = 19,
    col = adjustcolor("blue", alpha.f = 0.20),
    type = "p",
    cex = 1,
    cex.lab = 1.5)
abline(0, 1, lwd = 1)
text(0.15, 0.02, cex = 1.5, paste0("Correlation between scores = ", round(cr, 4),""))

# variable
legend(x = 0.03, y = 0.35, ncol = 1L, bty = "n",
      cex = 1.5,
      x.intersp = 2.2,
      y.intersp = 1,
      inset = c(0.01, 0),
      text.width = c(strwidth("1,000,00")),
```

```
      xjust = 1, yjust = 1,
      title = '',
      legend = c("", c("Minimum", "Q1",
                       "Median", "Mean",
                       "Q3", "Maximum")))

legend(x = 0.09, y = 0.35, ncol = 1L, bty = "n",
      cex = 1.5,
      x.intersp = 2.2,
      y.intersp = 1,
      inset = c(0.01, 0),
      text.width = c(strwidth("1,000,00")),
      xjust = 1, yjust = 1,
      title = '',
      legend = c('Dyre',
            sprintf("%6.4f", c(round(sm1, 4)))))

legend(x = 0.14, y = 0.35, ncol = 1L, bty = "n",
      cex = 1.5,
      #x.intersp = 1.8,
      #y.intersp = 1,
      x.intersp = 2.2,
      y.intersp = 1,
      inset = c(0.01, 0),
      text.width = c(strwidth("1,000,00")),
      xjust = 1, yjust = 1,
      title = '',
      legend = c('Silber',
            sprintf("%6.4f", c(round(sm2, 4)))))

```

Model performance evaluation

```{r}
validation <- data.frame("Test of random-effects" = sprintf("%0.4f", as.numeric( fit0$LRT_re)),
                         "AIC of null model (GLM)" = sprintf("%0.4f", as.numeric(fit0$aic_null)),
                         "AIC of full model (GLMM)" = sprintf("%0.4f", as.numeric(fit0$aic_alt)),
                         "Correlation of estimates" = sprintf("%0.4f", as.numeric(fit0$cor_lme_lmer$estimate)),
                         "Test of correlation" = sprintf("%0.4f", as.numeric(fit0$cor_lme_lmer$p.value)),
                         "C-statistic (random prediction)" = sprintf("%0.4f", as.numeric(fit0$rank_cor[1])),
                         "Dxy (rank-correlation)" = sprintf("%0.4f", as.numeric(fit0$rank_cor[2])),
                         "Marginal R-square" = sprintf("%0.4f", as.numeric(fit0$SS[2])),
                         "Conditional R-square" = sprintf("%0.4f", as.numeric(fit0$SS[1])))
validation
```

Estimation of adjusted odds ratio

```{r}
dat$pval <- sprintf("%0.4f", dat$pval)
dat$pval[which(dat$pval == "0.0000")] <- "<0.0001"
par(bty = "n", mar = c(2, 25, 1, 7), mgp = c(2, 0.5, 0), xpd = FALSE, tcl = 0.25, cex = 0.9)

plotOR_paper(dataplot = dat,
        xl = 0.5, xu = 15,
        title = "",
        txtcol = paste0("No. Events/\nCOVID patients"), xlab_title =
  paste0("Estimated odds ratio of death or transfer-to-hospice within 30 days post-admission"))
```

Hospital specific risk standardized event rates

```{r}
ORDER_FF <- datScore_orig[order(datScore_orig$score_DS_mean), ]
```

```
dataplotR <- data.frame("score" = as.numeric(ORDER_FF$score_DS_mean),
                        "reference" = ORDER_FF$reference,
                        "volume" = ORDER_FF$volume,
                        "unadj_score" = ORDER_FF$unadjusted_score)


plotScore_paper_single_rotate(dataplot = dataplotR,
                              dataplot2 = NULL,
                              xl = 0,
                              xu = 1,
                              maxX = 500,
                              sec_xl = -0.15,
                              sec_xu = 0.75,
                              atx1 = c(1, 100, 200, 300, 400, 500),
                              type = NULL,
                              plot_unadj = FALSE,
                              ybar_early = NULL,
                              ybar_later = NULL,
                              ybar_orig = fit0$ybar,
                              confidence = FALSE,
                              title = "Hospital-specific standardized risk score",
                              ylab_title = "Standardized score",
                              xlab_title = "Hospital rank",
                              legend_title = "event")
```