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Appendix

Part A. Structure and Function of MARCQI

MARCQI has a central coordinating center that organizes and manages member hospitals as sites for data collection and focused quality improvement. Much of MARCQI's administrative infrastructure and data collection is organized through the participating hospitals, with local orthopaedic surgeon champions and specifically trained nurse data abstractors. MARCQI has a unique central structure that consists of a database vendor (Ortech), a data management center at the Center for Healthcare Analytics and Performance Improvement of St. Joseph Mercy Hospital, and a central coordinating center in the Department of Orthopaedic Surgery at the University of Michigan. Ortech maintains the database containing the case-level data and uses additional data from the Michigan Hospital Association's Michigan Inpatient Database (MIDB) that links patients across hospitals statewide. Ortech implements dashboards and query tools for use by the sites and the individual surgeons to monitor performance. The Ortech data are raw and not risk-standardized. The MARCQI data management center uses statistical models to produce risk-standardized collaborative reports for the sites (see Part C of this Appendix). These models were fit to MARCQI data using patient-level data that include demographics, comorbidities, laboratory values, and operative information. Weights were determined from maximum likelihood estimation methods. This takes into account the variations on patient mix across hospitals and providers, allowing for much better benchmarking. It also allows for the compilation of customized analytical de-identified data sets for quality improvement, in compliance with institutional review board data confidentiality policies for research projects. Organizationally, the coordinating center audits the sites to ensure completeness and accuracy, organizes Collaborative-wide meetings, and manages the relationship with the program sponsor (Blue Cross Blue Shield of Michigan/Blue Care Network [BCBSM/BCN]). In addition, the center is responsible for biostatistical analyses.

Data collection is done using a hybrid approach of human data abstractors and MIDB administrative billing data. Each participating hospital has a designated data abstraction staff that is trained by the MARCQI coordinating personnel. The abstractor extracts specific patient data from the hospital's electronic medical records (EMR) and enters them into the MARCQI database through a web interface or file-based upload. Even though this can be labor-intensive, it allows for case-level oversight and specific queries to answer questions and resolve inconsistencies. Implant data (manufacturer, catalog number, and lot number) for all implanted devices are captured locally through barcode scanning or manual entry, or by using the hospital's supply chain data, depending on the hospital's preference. Additional data elements (e.g., is patient readmission to a hospital different from the one where the index procedure was initially performed?) come from all participating hospitals' billing data through MIDB. Data are abstracted on all eligible cases at participating MARCQI hospitals and are audited annually by MARCQI staff, resulting in a very high-quality registry. More than 98% of qualifying cases meet our definition of a complete data set. There are 29 MARCQI sites that participate in the AJRR; they transfer their data after downloading it from the MARCQI database.

MARCQI captures data on 96% of all hip and knee arthroplasty procedures performed within the state of Michigan. Annual audits of sites include a billing audit to motivate sites to include all of their qualifying cases (primary and revision) in the registry. Submitted revisions

are associated with index primary procedures within the registry using patient and hospital identifying information. Additional revision cases are identified by linking registry data to hospital billing records that are submitted to the MIDB. The MIDB is constructed from complete billing records that hospitals submit to the Michigan Hospital Association. Therefore, MARCQI has a process to identify all qualifying primary and revision cases for which a bill was generated. However, revisions that occur outside of MARCQI sites, within or outside Michigan, are not captured. An analysis of total hip and knee replacement patients in the National Institute of Aging's Health and Retirement Study and Medicare claims showed that none of the patients in the Health and Retirement Study who had primary procedures in Michigan had revisions outside of the state, although this was based on a sample of only 1,426 patients who could be matched between the 2 data sources.

MARCQI conducts postmarket surveillance of implants. Barcode data are collected from all of the implanted devices and are stored in the database, and a device library developed and maintained by *Orthopaedic Network News* is used to convert catalog numbers to product names and device characteristics.

MARCQI is structured to provide opportunities for face-to-face interactions through Collaborative meetings, bringing together representatives from each hospital to review data, share best practices, and prioritize future activities. Each hospital is expected to send a quality administrator, an orthopaedic surgeon clinical champion, and a data abstractor(s) to the Collaborative meetings. The Collaborative meetings are generally 4 to 5 hours long. Continuing Medical Education credits are provided, and locations rotate around the state of Michigan. The meeting format includes presentations of risk-standardized performance of each hospital (with hospital identifiers included), best practices, committee updates (device, quality, abstractor, data and publications, standardization, and patient-reported outcomes), and talks by invited speakers (experts who present on topics related to ongoing or proposed quality initiatives). The meetings are confidential (confidentiality agreements are signed by participants at each meeting), and only MARCQI participants are invited. Conflicts of interest are displayed concurrently during presentations. On-site committee meetings take place before and after the Collaborative meeting. Topics for each meeting are determined by the coordinating center, with input from MARCQI sites, surgeons, and committees.

Funding for MARCQI is provided by BCBSM/BCN through its Value Partnerships program. Although BCBSM/BCN supports the Collaborative and its associated data collection, it does not have access to data at the hospital, provider, or patient levels. The coordinating center provides Collaborative-wide metrics on performance.

Part B. Definition of Infection Used by MARCQI

The definition of infection is taken from the *MARCQI Specifications Manual for Data Abstractors*. An infection event is coded when the patient has a documented infection that meets National Healthcare Safety Network (NHSN) criteria for prosthetic joint infection. This definition requires that:

1. Infection occurs within 90 days after the associated operative procedure, AND
2. Infection involves the joint space, any part of the body deeper than the fascial/muscle layers, that is opened or manipulated during the operative procedure, AND

3. The patient has ≥1 of the following:
    a. Purulent drainage from a drain that is placed into the organ/space (e.g., closed suction drainage system, open drain, T-tube drain, computed tomography [CT]-guided drainage), OR
    b. Organisms that are identified from fluid or tissue in the organ/space by a culture or nonculture-based microbiologic testing method that is performed for purposes of clinical diagnosis or treatment (e.g., not active surveillance culture/testing (ASC/AST), OR
    c. An abscess or other evidence of infection involving the organ/space that is detected on gross anatomic or histopathologic examination, or imaging-test evidence suggestive of infection
4. AND joint infections must meet ≥1 of the following criteria:
    a. 2 positive periprosthetic specimens (tissue or fluid) with ≥1 matching organism, identified by a culture or nonculture-based microbiologic testing method that is performed for purposes of clinical diagnosis and treatment (e.g., not ASC/AST), OR
    b. A sinus tract communicating with the joint on gross anatomic examination (a sinus tract is defined as a narrow opening or passageway that can extend in any direction through soft tissue and results in dead space with the potential for abscess formation), OR
    c. Have 3 of the following minor criteria:
        i. Elevated serum C-reactive protein (CRP) level of >100 mg/L and erythrocyte sedimentation rate (ESR) of >30 mm/hr.
        ii. Elevated synovial fluid white blood-cell (WBC) count (>10,000 cells/μL) OR a "++" (or greater) change on a leukocyte esterase strip test of synovial fluid.
        iii. Elevated synovial fluid polymorphonuclear neutrophil percentage (PMN%) of >90%.
        iv. Positive histological analysis of periprosthetic tissue (>5 neutrophils [PMNs] per high power field).
        v. Organism(s) identified from a single positive periprosthetic specimen (tissue or fluid) by a culture or nonculture-based microbiologic testing method that is performed for purposes of clinical diagnosis and treatment.

Notes

• A surgical site infection (SSI) will not be attributed if the following 3 criteria are ALL met: (1) during the postoperative period, the surgical site is without evidence of infection, (2) an invasive manipulation/accession of the site is performed for diagnostic or therapeutic purposes (e.g., needle aspiration, accession of ventricular shunts, or accession of breast expanders), and (3) an infection subsequently develops in a tissue level that was entered during the manipulation/accession.
• A *matching organism* is defined as 1 of the following:
    o If genus and species are identified in both specimens, they must be the same.
    o If the organism is less definitively identified in 1 culture specimen than in the other, the lesser identified organism must be identified to at least the genus level, and, at that level, the organisms must be the same (e.g., a surgical wound growing Pseudomonas species is used to meet deep incisional SSI criteria, and a blood specimen growing *Pseudomonas aeruginosa* is collected in the SSI secondary bloodstream infection [BSI] attribution period. The organisms are considered matching at the genus level; therefore, the BSI is

secondary to the SSI. Positive culture specimens of hardware from a hip or knee can be used to meet criterion 1).

• If the joint is accessed for the first time postoperatively (e.g., with a needle aspiration) or is invasively manipulated (e.g., during the process of an irrigation and debridement [I&D]) AND periprosthetic cultures that are performed AT THAT TIME return positive (indicating infection is present), this may be a reportable infection if all of the other NHSN criteria are met.

• However, if no cultures are performed or they are returned as negative at the time the joint is first accessed postoperatively and an infection subsequently develops, this cannot be captured as a periprosthetic joint infection (PJI) since the infection cannot be directly attributed to the associated joint procedure (it may be related to the invasive procedure). However, the infection may still be captured by the hospital's infection control department as an SSI.

• If an event took place at another institution and the details of the event are fully documented so the data abstractor is able to enter all data into all of the fields on the event form (Event, Date of Event, Action, and Date of Action), document the event for the arthroplasty that took place at the institution that is abstracting the case.

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Part C. Risk-Standardization Methodology Used by MARCQI

TABLE E-1 Abbreviations of Variables*

Variable Type	Variable Name	Variable Description	Data Source
Outcome (Y-variables)	Bloodtx	Blood transfusion (yes/no)	MARCQI
	SNF_Rehab	SNF rehab. (yes/no)	
	Readmission	90-day readmission (yes/no)	
	Readmission30	30-day readmission (yes/no)	
	Readmit30_Age65	30-day readmission and age ≥65 (yes/no)	
	ED_visit	90-day ED visit (yes/no)	
	Deep_Infection	90-day deep infection (yes/no)	
	Dislocation	90-day dislocation (yes/no)	
Risk factors to be considered (X-variables)	Age, age^2	Age and squared value	
	BMI, BMI^2	Body mass index and squared value	
	HGB_pre	Preop. HGB	
	Plts_pre	Preop. platelets	
	SEX	Sex/sex (male/female)	
	ASA	American Society of Anesthesiologists risk score (I~V)	
	Narcotics	Narcotics (yes/no)	
	IsHistoryOfDvtPe_ID	History of DVT/PE (yes/no)	
	Anticoagulation	Anticoagulation (yes/no)	
	SmokingStatus_ID	Smoking status (Never/past/current)	
	Steroids	Steroids (yes/no)	
	NEURO	Other neurological disorders (yes/no)	Elixhauser comorbidities derived from Michigan Inpatient Data Base (MIDB)
	COAG	Coagulopathy (yes/no)	
	WGHTLOSS	Weight loss (yes/no)	
	LYTES	Fluid and electrolyte disorders (yes/no)	
	ANEMDEF	Deficiency anemias (yes/no)	
	DRUG	Drug abuse (yes/no)	
	PSYCH	Psychoses (yes/no)	
	DEPRESS	Depression (yes/no)	
	PULMCIRC	Pulmonary circulation disease (yes/no)	
	HTN_C	Hypertension (yes/no)	
	PARA	Paralysis (yes/no)	
	CHRNLUNG	Chronic pulmonary disease (yes/no)	
	DM	Diabetes without chronic complications (yes/no)	
	DMCX	Diabetes with chronic complications (yes/no)	
	CHF	Congestive heart failure (yes/no)	
	VALVE	Valvular disease (yes/no)	
	ARTH	Rheumatoid arthritis/collagen vas (yes/no)	
	RENLFAIL	Renal failure (yes/no)	
	PERIVASC	Peripheral vascular disease (yes/no)	

	ALCOHOL	Alcohol abuse (yes/no)	
	LIVER	Liver disease (yes/no)	
	HYPOTHY	Hypothyroidism (yes/no)	

*SNF = skilled nursing facility, ED = Emergency Department, HGB = hemoglobin, DVT = deep vein thrombosis, and PE = pulmonary embolism.

TABLE E-2 List of Models, Outcomes, Risk Factors, and for Each Model*

GLMM Models	Joint	Measure/ Outcome (Y-Variable)	Risk Factors to Be Considered (X-Variables)
1	Hip	Bloodtx	Age, age^2, BMI, BMI^2, HGB_pre, Plts_pre, SEX, ASA, Narcotics, (NEURO, COAG, WGHTLOSS, LYTES, ANEMDEF, DRUG, PSYCH, DEPRESS)†
2	Hip	SNF_Rehab	Age, age^2, BMI, BMI^2, HGB_pre, SEX, ASA, Narcotics, (PULMCIRC, HTN_C, PARA, NEURO, CHRNLUNG, DM, DMCX, COAG, WGHTLOSS, DRUG, PSYCH, DEPRESS)†
3	Hip	Readmission	Age, age^2, BMI, HGB_pre, Plts_pre, ASA, Narcotics, (CHF, VALVE, NEURO, CHRNLUNG, DRUG, DEPRESS)†
4	Hip	Readmission30	Age, age^2, BMI, BMI^2, HGB_pre, ASA, Narcotics, (VALVE, NEURO, CHRNLUNG, COAG, DEPRESS)†
5	Hip	Readmit30_Age65	Age, BMI, HGB_pre, ASA, Steroids, Narcotics, (VALVE, NEURO)†
6	Hip	ED_visit	Age, age^2, ASA, Steroids, Narcotics, (CHRNLUNG, DMCX, PSYCH, DEPRESS, PSYCH, DEPRESS)†
7	Hip	Deep_Infection	Age, age^2, BMI, Plts_pre, SEX, SmokingStatus_ID, Narcotics, (CHF, DMCX, ARTH, DEPRESS)†
8	Hip	Dislocation	Age, age^2, BMI, HGB_pre, Plts_pre, ASA, IsHistoryOfDvtPe_ID, Anticoagulation, SmokingStatus_ID
9	Knee	Bloodtx	Age, age^2, BMI, BMI^2, HGB_pre, Plts_pre, SEX, ASA, Narcotics, (PULMCIRC, NEURO, RENLFAIL, COAG, WGHTLOSS, LYTES, PSYCH, DEPRESS)†
10	Knee	SNF_Rehab	Age, age^2, BMI, BMI^2, HGB_pre, SEX, ASA, Steroids, Narcotics, (CHF, PULMCIRC, PARA, NEURO, CHRNLUNG, DM, DMCX, RENLFAIL, COAG, WGHTLOSS, LYTES, ANEMDEF, DRUG, PSYCH, DEPRESS)†
11	Knee	Readmission	Age, age^2, BMI, BMI^2, HGB_pre, SEX, ASA, Smokingstatus_ID, Steroids, Narcotics, (CHF, PULMCIRC, PERIVASC, HTN_C, NEURO, CHRNLUNG, DMCX, RENLFAIL, COAG, ALCOHOL, PSYCH, DEPRESS)†
12	Knee	Readmission30	Age, age^2, HGB_pre, SEX, ASA, Smokingstatus_ID, Narcotics, (PULMCIRC, HTN_C, CHRNLUNG, DMCX, RENLFAIL, COAG, BLDLOSS, ALCOHOL, PSYCH, DEPRESS)†
13	Knee	Readmit30_Age65	Age, HGB_pre, SEX, ASA, Smokingstatus_ID, Narcotics, (CHF CHRNLUNG)†
14	Knee	ED_visit	Age, age^2, BMI, HGB_pre, Plts_pre, ASA, Smokingstatus_ID, Narcotics, (CHF, PULMCIRC, NEURO, CHRNLUNG, DMCX, HYPOTHY, LIVER, DRUG, PSYCH, DEPRESS)†
15	Knee	Deep_Infection	BMI, BMI^2, SEX, Smokingstatus_ID, (CHF, HTN_C, NEURO, DMCX, ANEMDEF, PSYCH)†

*In each model, patients were included as long as there were no missing data for the Y variable or for the X variables. Outcomes (Y-variables) and risk factors (X-variables that are not in all capital letters) are collected by MARCQI. Inclusion of risk factors in each model is determined by significance and clinical expert judgment, as well as publications in the field. Continuous risk factors (X-variables), including age, BMI, HGB_pre (preop. HGB), and Plts_pre (preop. platelets), are centered at corresponding mean values. GLMM = generalized linear mixed effect model, age^2 = squared age, and BMI^2 = squared BMI.
†Risk factors (X-variables) are retrieved from the Michigan Inpatient Data Base (MIDB).

The risk-standardization approach has been broadly applied to calculate quality measures (standardized mortality rate [SMR][28], standardized readmission ratio [SRR][29,30], etc.). The goal of risk standardization is to account for the differences in patient characteristics (or risk factors, including patient demographic and clinical characteristics, etc.) across units (patients, physicians, hospital sites, etc.) that might be related to the patient outcome; thus, the risk-adjusted quality measure is made comparable across units by multiplying a population-level scale factor[31,32].

MARCQI estimates the risk-standardized quality measures (RSQMs)[28,30] for patient outcomes using the variables described in Table E-1. Quality measures (Y-variables) include Bloodtx, SNF_Rehab, Readmission, Readmission30, Readmit30_Age65, ED_visit, Deep_Infection, and Dislocation. The risk factors, (the X-variables in Table E-2 including age, sex, BMI, and/or selected clinical covariates, laboratory tests, health conditions, etc.) are determined based on clinical relevance, publications in the field, and statistical relevance. Models are developed for hips and knees separately. Table E-2 provides the details.

A 3-step process is developed in the MARCQI to calculate and visualize RSQMs. More specifically:

Step 1: Risk Adjustment Using the Generalized Linear Mixed Effect Model

The generalized linear mixed effect model (GLMM) is an effective tool to analyze multilevel or hierarchical data to account for the correlation of the observed outcomes with risk factors (X-variables), including patient-level demographics, clinical variables, and chronic health conditions, etc. Through logistic regression[33,34], MARCQI develops a random-intercept mixed-effect model for each outcome (Y-variable)[35,36], and calculates the number of predicted and expected outcomes (Y-variables) for each unit as the inputs for the next step.

Step 2: RSQM

The RSQM is calculated as the ratio of the number of "predicted" outcomes to the number of "expected" outcomes, multiplied by the registry-wide unadjusted rate of the outcome:

$$RSQM = (predicted/expected) \times registry\text{-}wide\ raw\ average\ rate$$

where the numerator *"predicted"* is the total number of predicted outcomes and the denominator *"expected"* is the total number of expected outcomes adjusting for risk factors, which are obtained from step 1. The raw registry-wide average rate (i.e., scaling factor) is obtained from the registry patients and serves as the reference for comparison, allowing for each unit's RSQM to be compared to the observed registry-wide rate. The statistical preference using the *predicted/expected* ratio has been discussed in detail[30,37,38]. The RSQM with 80% and 95% confidence intervals (CIs) for each unit is calculated using an unrestricted random resampling (URS) method, which selects units with equal probability and with replacement, and 1,000 replicates[39,40].

Step 3: Visualization of RSQMs for Collaborative Meetings and Quarterly Reports

For performance comparison and quality improvement, RSQMs with 80% and 95% CIs that are obtained from step 2 can be visualized using forest plots[41] and scorecards with different colors, etc. The units can be categorized into performance-based subgroups (e.g., higher than the

registry average rate, lower than the registry average rate, or no difference from the registry average rate).