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HR-pQCT Cross-Calibration Using Standard vs. Laplace-Hamming Binarization Approach

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Running title: Standard vs. Laplace-Hamming Cross-Calibration for XCTII

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31 **Abstract**

32 High-Resolution Peripheral Quantitative Computed Tomography (HR-pQCT) has emerged as a
33 powerful imaging technique for characterizing bone microarchitecture in the human peripheral skeleton.
34 The second-generation HR-pQCT scanner provides improved spatial resolution and a shorter scan time.
35 However, the transition from the first-generation (XCTI) to second-generation HR-pQCT scanners
36 (XCTII) poses challenges for longitudinal studies, multi-center trials, and comparison to historical data.
37 Cross-calibration, an established approach for determining relationships between measurements
38 obtained from different devices, can bridge this gap and enable the utilization and comparison of legacy
39 data. The goal of this study was to establish cross-calibration equations to estimate XCTII measurements
40 from XCTI data, using both the standard and Laplace-Hamming (LH) binarization approaches. Thirty-
41 six volunteers (26–85 years) were recruited and their radii and tibiae were scanned on both XCTI and
42 XCTII scanners. XCTI images were analyzed using the manufacturer’s standard protocol. XCTII images
43 were analyzed twice: using the manufacturer’s standard protocol and the LH segmentation approach
44 previously developed and validated by our team. Linear regression analysis was used to establish cross-
45 calibration equations. Results demonstrated strong correlations between XCTI and XCTII density and
46 geometry outcomes. For most microstructural outcomes, although there were considerable differences in
47 absolute values, correlations between measurements obtained from different scanners were strong,
48 allowing for accurate cross-calibration estimations. For some microstructural outcomes with a higher
49 sensitivity to spatial resolution (e.g., trabecular thickness, cortical pore diameter), XCTII standard
50 protocol resulted in poor correlations between the scanners, while our LH approach improved these
51 correlations and decreased the difference in absolute values and the proportional bias for other
52 measurements. For these reasons and due to the improved accuracy of our LH approach compared to the
53 standard approach, as established in our previous study, we propose that investigators should use the LH
54 approach for analyzing XCTII scans, particularly when comparing to XCTI data.

55

56

57 **Keywords:** HR-pQCT, Laplace-Hamming Binarization, Gaussian Binarization, cross-calibration,
58 estimation error

59 1. Introduction

60 High-Resolution Peripheral Quantitative Computed Tomography (HR-pQCT) has emerged as a
61 powerful non-invasive imaging technique for in vivo characterization of bone microarchitecture in the
62 human peripheral skeleton. HR-pQCT quantifies geometric, densitometric, microstructural, and
63 biomechanical properties of trabecular and cortical bone ⁽¹⁻³⁾, contributing to fracture risk assessment ^(4,5).
64 Further, HR-pQCT data are used in the study of bone biology, disease progression, and treatment
65 outcomes ⁽⁶⁻¹⁰⁾.

66 The first-generation HR-pQCT scanner (XCTI) has an isotropic voxel size of 82 μm . At this resolution,
67 XCTI image analysis relies on tissue density and histomorphometric model assumptions ^(11,12). The
68 second-generation HR-pQCT scanner (XCTII) provides an improved voxel size of 61 μm . This higher
69 resolution allows for direct measurement of all trabecular parameters using distance transform methods
70 that do not rely on density and model assumptions ⁽¹³⁾. Higher resolution also provides improved
71 visualization and quantification of fine features within both the trabecular and cortical compartments.
72 However, the transition from first-generation to second-generation scanners poses challenges for
73 longitudinal studies, multi-center trials, and the comparison of XCTII-derived data to historical XCTI-
74 derived results, as these activities require ensuring compatibility and comparability of measurements
75 across different scanners.

76 Cross-calibration is an established approach for determining relationships between measurements
77 obtained from different devices, allowing for the estimation of measurements on newer devices using
78 data collected from older or different devices ⁽¹⁴⁻¹⁶⁾. The objective of this study is to estimate second-
79 generation HR-pQCT measurements from first-generation scanner data using cross-calibration. By
80 establishing reliable cross-calibration equations, we aim to bridge the gap between different generations
81 of HR-pQCT scanners and enable the utilization of the rich body of historical XCTI data in conjunction
82 with the advanced capabilities of second-generation scanners. This approach holds promise for
83 facilitating longitudinal studies, improving comparability across different research centers, and
84 enhancing the clinical application of HR-pQCT in bone health assessment. In the following sections, we
85 will describe the methodology employed for cross-calibration, present the validation results, and discuss
86 the implications of our findings. We will perform cross-calibration using both the manufacturer's

87 standard XCTII Gaussian-based binarization approach, as well as the Laplace-Hamming segmentation
88 approach we previously developed and validated for XCTII ⁽¹⁷⁾.

89 **2. Materials and Methods**

90 **2.1. Study Participants**

91 Based on the sample size in our previously published study that highlighted the effect of Laplace-
92 Hamming segmentation approach on XCTII density and structural outcome metrics, 36 volunteers (16
93 women, 20 men; 56 ± 13 years; age range 26–85; **Table 1**) were recruited to ensure sufficient eligible
94 tibia and radius scans for cross-calibration ⁽¹⁷⁾. Women known to be pregnant or breast-feeding and men
95 and women with metal implants at both scan sites (radius and tibia) were excluded. There were no other
96 health- or bone-related inclusion or exclusion criteria for enrollment. The institutional review board at
97 the University of California, San Francisco approved the study protocol, and all participants provided
98 written informed consent prior to their involvement in the study.

99 **2.2. Image Acquisition**

100 Volunteers were scanned on both first-generation (XCTI) and second-generation (XCTII) HR-pQCT
101 scanners (Scanco Medical, Brüttisellen, Switzerland) using the manufacturer’s standard in vivo
102 protocols. For XCTI, the scan settings were: source potential 60 kVp, tube current 900 mA, isotropic 82
103 μm nominal resolution. Scans were acquired 9.5 mm and 22.5 mm proximal from the joint for distal
104 radius and tibia, respectively, covering a length of 9.0 mm (110 slices). For XCTII, the scan settings
105 were: source potential 68 kVp, tube current 1460 mA, isotropic 61 μm nominal resolution. Scans were
106 acquired 9 mm and 22 mm proximal from the joint for distal radius and tibia, respectively, covering a
107 length of 10.2 mm (168 slices); compared to XCTI, XCTII captured approximately 0.5 mm more bone
108 at either end of the scan volume. The non-dominant forearm and lower leg were scanned. In the case
109 where a history of fracture or surgery was reported on the non-dominant side, the contralateral side was
110 scanned. Prior to scanning and throughout the study, the scanners were routinely calibrated using
111 scanner-specific quality control phantoms. All in vivo scans were visually inspected for motion artifacts
112 using the manufacturer’s grading scheme to ensure adequate quality for all the images included for
113 further analyses (grades 1 to 3) ⁽¹⁸⁾.

114 **2.3. Image Analysis**

115 XCTI images were analyzed using the manufacturer’s standard XCTI patient evaluation protocol, which
116 involved semi-automated contouring of the periosteal and endosteal cortical boundaries, a Laplace-
117 Hamming filter and a fixed global threshold for binarization ^(1,11). The standard microstructural
118 quantification scripts were applied, which use a combination of direct (e.g., trabecular number) and
119 indirect measurement techniques (e.g., cortical thickness).

120 XCTII images were analyzed twice – first with the manufacturer’s standard Gaussian segmentation
121 approach and second with the Laplace-Hamming (LH) segmentation approach we developed and
122 validated in-house ⁽¹⁷⁾. In both XCTII analysis protocols, an auto-contouring process was first used to
123 identify the periosteal and endosteal cortical boundaries; these auto-contours were checked and
124 corrected manually if necessary. In the standard protocol (i.e., the Gaussian segmentation approach), a
125 Gaussian filter and fixed BMD thresholds were then used to extract the trabecular and cortical bone. In
126 our developed LH segmentation approach, a Laplace-Hamming filter followed by a fixed global
127 threshold was used to extract the trabecular and cortical bone. In both analysis protocols, once the
128 trabecular and cortical binary masks were created, direct measurement of all parameters was performed
129 using distance transform methods ⁽¹³⁾. The LH approach affected only the microstructural parameters
130 derived from the binary masks; volumetric density and geometry measurements remain identical for
131 both the standard and LH analysis protocols ⁽¹⁷⁾. For both XCTI and XCTII, complete stacks were
132 analyzed; no registration between XCTI and XCTII volumes was performed.

133 **2.4. Cross-Calibration**

134 To compare the agreement between the measurements obtained from the two scanners, a combination of
135 cross-validation and bootstrapping approaches was utilized. For radius or tibia scans, the 36 data points
136 were first randomly divided into two sets: one set with 12 data points and another with 24 data points.
137 The 12-data points set was set aside for validation purposes (to determine the estimation error after
138 cross-calibration), while the remaining 24 data points were used for cross-calibration (using linear
139 regression analysis). During this step, 1000 sets of 12 data points were randomly selected (with
140 replacement) for establishing cross-calibration equations, resulting in 1000 sets of slopes and intercepts

141 for each output parameter (**Table 1**). The average values from these 1000 sets were recorded as the slope
142 and intercept for that specific outcome measure.

143 Next for the validation step, the cross-calibration equations were applied to the first-generation output
144 parameters to estimate the second-generation outputs, defined as XCTII*. To evaluate the accuracy of
145 these estimates, the cross-calibration error was determined by comparing XCTII* with the respective
146 actual measured values on XCTII (i.e., XCTII). This procedure was performed twice, once for the
147 XCTII standard analysis approach and a second time for the XCTII LH approach.

148 **2.5. Statistical Analysis**

149 Participant demographics were compared between the training and test sets using unpaired student's t-
150 test and Pearson's chi-squared test. Linear regression analysis was used to establish cross-calibration
151 equations. Correlation strength was defined as strong ($R^2 > 0.9$), moderate ($0.7 < R^2 < 0.9$) and weak (R^2
152 < 0.7). Bland-Altman plots were used to explore the differences between scanners. Statistical analyses
153 were performed using JMP 16 software (SAS Institute Inc., Cary, NC, USA) with significance set at $p <$
154 0.05 .

155 **3. Results**

156 **3.1. Cross-Calibration**

157 Of the total 72 scans (36 radius, 36 tibia), 2 radius scans were excluded from analyses due to motion.

158 There were strong correlations between XCTI and XCTII density outcomes (Tt.BMD, Tb.BMD,
159 Ct.BMD) at both radius and tibia ($R^2 > 0.88$; **Table 2**). Bland-Altman plots showed good agreement for
160 these outcomes between scanners at both sites although radius Ct.BMD was slightly underestimated by
161 XCTII relative to XCTI (**Supplemental Figure S1**; Note: The R^2 values in **Table 2** and the
162 **Supplementary Figures** are different because **Table 2** presents the average results from all 1000
163 bootstrapping iterations, while the **Supplementary Figures** present representative results from 1/1000
164 bootstrapping iterations).

165 Geometry outcomes Tb.Ar and Ct.Ar were strongly correlated between XCTI and XCTII at both the
166 radius and tibia ($R^2 > 0.91$; **Table 2**). Bland-Altman plots showed good agreement between scanners and
167 proportional biases were small (**Supplemental Figure S2**).

168 For trabecular microstructure outcomes, there were strong correlations between scanners for BV/TV at
169 both the radius and tibia ($R^2 = 0.97$ and 0.99 , respectively; **Table 2**) and Tb.1/N.SD at radius ($R^2 = 0.92$;
170 **Table 2**). There were moderate correlations between scanners at both the radius and tibia for Tb.N ($R^2 =$
171 0.76 and 0.82 , respectively; **Table 2**) and Tb.Sp ($R^2 = 0.88$ and 0.79 , respectively; **Table 2**). Among all
172 the outcomes, Tb.Th showed the weakest correlation between scanners at both the radius and tibia ($R^2 =$
173 0.69 and 0.31 , respectively; **Table 2**). Relative to XCTI, BV/TV, Tb.Th, Tb.Sp, and Tb.1/N.SD were
174 overestimated by XCTII at both the radius and tibia, while Tb.N was underestimated by XCTII at both
175 sites. Bland-Altman plots showed a strong proportional bias for BV/TV at both the radius and tibia, for
176 Tb.Sp at the radius, and for Tb.N at the tibia (**Supplemental Figures S3 and S4**). The analysis of XCTII
177 data using our developed LH approach greatly reduced the observed proportionality bias (**Supplemental**
178 **Figures S3 and S4**).

179 For cortical microstructure outcomes, there was a strong correlation for Ct.Th at both radius and tibia
180 between scanners ($R^2 > 0.92$; **Table 2**). There was a moderate correlation for Ct.Po at both the radius and
181 tibia between scanners ($R^2 = 0.83$ at both sites; **Table 2**). Ct.Po.Dm showed the weakest correlations at
182 both the radius and tibia ($R^2 = 0.21$ and 0.38 , respectively; **Table 2**). Relative to XCTI, Ct.Po was
183 underestimated by XCTII at both the radius and tibia, while Ct.Po.Dm was overestimated by XCTII at
184 both sites (**Supplemental Figures S5 and S6**). There was a strong proportional bias in Ct.Po at both the
185 radius and tibia, which was eliminated using our LH approach (**Supplemental Figures S5 and S6**).

186 **3.2. Validation**

187 Applying the established cross-calibration equations to our test set XCTI data, the estimated values for
188 XCTII outcomes were calculated and compared against the measured values to compute percent error.
189 Linear regression and Bland-Altman plots that compare measured XCTII vs estimated XCTII* outcomes
190 using both standard and LH approaches are presented in **Figure 1** to **Figure 3**.

191 For trabecular outcomes, the mean percent error was between 0.80% and 4.65% for density and
192 geometry outcomes (Tt.BMD, Tb.BMD, Tb.Ar), and between 1.68% and 7.58% for microstructural

193 outcomes (BV/TV, Tb.N, Tb.Th, Tb.Sp, Tb.1/N.SD). For cortical outcomes, the mean percent error was
194 between 0.61% and 10.71% for density and geometry outcomes (Ct.BMD, Ct.Ar, Ct.Pm, Ct.Th), and
195 between 6.81% and 21.98% for microstructural outcomes (Ct.Po, Ct.Po.Dm). Using the LH approach for
196 cross-calibration resulted in smaller percent errors for BV/TV, Tb.Th, and Ct.Po.Dm, but larger percent
197 errors for Tb.N, Tb.Sp, and Ct.Po (**Table 3**). More specifically, percent errors for Tb.Th from LH were
198 significantly smaller at both the radius and tibia ($p = 0.04$ and < 0.001 , respectively; **Table 3**); percent
199 error for Ct.Po.Dm was significantly smaller at the radius ($p = 0.006$; **Table 3**).

200 **4. Discussion**

201 The goal of this study was to explore the feasibility and accuracy of estimating second-generation HR-
202 pQCT measurements from the first-generation scanner with cross-calibration using linear regression
203 equations. For most density, geometry, and microstructural outcomes, cross-calibration accurately
204 estimated and eliminated the differences between scanners. However, there were large estimation errors
205 for some microstructural outcomes, notably cortical porosity.

206 As expected, and consistent with previous studies, cross-scanner correlations for density and geometry
207 outcomes were stronger compared to those for microstructural outcomes⁽¹⁴⁻¹⁶⁾. Density and geometry
208 metrics are less sensitive to resolution and image artifacts (including motion artifacts) due to their
209 quantification over larger scales, lending them greater stability across scanners. This is also in line with
210 previous multi-center studies reporting a smaller variability in density and geometry measures across
211 different XCTI scanners compared to microstructural measures^(19,20). Conversion of density and
212 geometry metrics from first-generation to second-generation scanners is therefore feasible.

213 We found large differences in the absolute values of some microstructural outcomes between the two
214 scanners. Consistent with the findings of Agarwal et. al. and Manske et. al.^(14,15), we found that XCTII
215 overestimated BV/TV, Tb.Th, and Tb.Sp and underestimated Tb.N and Ct.Po relative to XCTI. This can
216 be explained by the inherent differences in the acquisition and analysis approach of the two scanners,
217 including differences in resolution, image analysis (filtering and thresholding), and quantitative analysis
218 approach (XCTII direct vs XCTI indirect). The standard XCTII analysis approach also obscures some
219 fine features in both the trabecular and cortical compartments in the segmentation step and thickens
220 larger trabeculae, therefore resulting in overestimated BV/TV, Tb.Th and Tb.Sp and underestimated

221 Tb.N and Ct.Po, as established in our previous publication ⁽¹⁷⁾. Despite these differences in absolute
222 values, the correlations between the two scanners were strong for these parameters, explaining the
223 relatively small percent error in estimated values. However, for some other microstructural outputs such
224 as Tb.Th and Ct.Po.Dm, in addition to the large differences in absolute values, the correlations were
225 weak between the two scanners, resulting in relatively larger percent errors in the estimated values. This
226 could be due to the higher sensitivity of these outcomes to spatial resolution, suggesting that estimating
227 XCTII data from XCTI data for such measures may not be recommended using XCTII standard analysis
228 approach. Using our developed XCTII LH approach, which is more consistent with the analysis
229 approach of XCTI, improved the correlations and, therefore, resulted in smaller estimate errors for these
230 metrics. In addition, we found stronger cross-scanner correlations and better agreement between the
231 measured and estimated values at the tibia compared to the radius due to fewer motion artifacts in the
232 tibia scans compared to the radius scans.

233 Our study has a number of strengths. First, including both the standard and LH binarization approaches
234 provides direct comparisons and insight into the effects of different segmentation approaches on the
235 cross-calibration process and the consequent estimations. Next, combining cross-validation and
236 bootstrapping takes advantage of the benefits of both two methods – bootstrapping provides estimates
237 for the parameters, and cross-validation provides estimates of the test error.

238 Our study also has a number of important limitations. First, despite the proven improved accuracy and
239 reproducibility of the LH binarization approach compared to the standard approach for XCTII for the
240 cohort studied here, the effect of LH on HR-pQCT outcome metrics has not been examined for disease
241 cohorts with pathology-specific bone microarchitecture (e.g., great cortical bone loss with chronic
242 kidney disease). Thus, the effect of LH should be evaluated on a cohort-by-cohort basis before any
243 generalization can be made upon further validation. Additionally, although bootstrapping was deployed
244 to minimize the cross-calibration bias, sex was not matched between the tibia training and test sets,
245 potentially contributing to the proportional biases and limiting the robustness of the cross-calibration
246 results when extrapolated to larger and more diverse cohorts. However, this bootstrapping approach can
247 be readily adapted to produce additional cross-calibration equations in diverse cohorts, which can
248 potentially be integrated with our cross-calibration equations with improved generalizability. Last, it's
249 worth mentioning that since we chose to perform our analysis on full scan regions for both XCTI and

250 XCTII, reference line placement inconsistency may be a potential contributor to our reported error
251 values. However, all our scans were acquired by one skilled operator to minimize such errors.

252 In summary, we found good agreement between density and geometry outcomes measured by XCTI and
253 XCTII; there were large differences in the absolute values for some of the microstructural outcomes,
254 suggesting that they should be directly compared between the two scanners. However, we found
255 moderate to strong correlations for these microstructural outcomes between scanners despite the large
256 differences in absolute values, showing that XCTII outcomes can be estimated from XCTI
257 measurements using the established cross-calibration equations. For microstructural outputs such as
258 Tb.Th and Ct.Po.Dm that have a higher sensitivity to spatial resolution, the standard segmentation
259 approach on XCTII resulted in weak correlations between the scanners, while the LH approach we
260 developed and validated in-house resulted in stronger correlations between the two scanners for these
261 outcomes. These stronger correlations were accompanied by reduced percent errors in these outcomes,
262 as well decreased differences in absolute values and the proportional bias in Bland-Altman plots for
263 other measurements. For these reasons, and considering the improved accuracy of our LH approach
264 compared to the standard approach established in our previous publication ⁽¹⁷⁾, we propose that
265 investigators should use the LH approach for analyzing scans on XCTII, particularly when comparing to
266 XCTI data.

267 **5. Disclosures**

268 Saghi Sadoughi – None

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280 **7. Data Availability Statement**

281 The data that support the findings of this study are available on request from the corresponding author.
282 The data are not publicly available due to privacy or ethical restrictions.

283 **8. References**

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351

352

353 9. Figures and Tables

354

355 **Figure 1:** Regression and Bland-Altman plots for Tt.vBMD (A-D), Tb.vBMD (E-H), Ct.vBMD (I-L)
356 Tb.Ar (M-P), and Ct.Ar (Q-T) assessed using measured XCTII values and the estimated XCTII* values
357 from XCTI at the radius (left) and tibia (right). On regression plots, the dashed line indicates the line of
358 unity. On Bland-Altman plots, the solid black line indicates the mean difference, the dashed lines
359 indicate the 95% limits of agreement, and the gray line indicates zero.

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362 **Figure 2.** Regression and Bland-Altman plots for BV/TV (**A-D**), Tb.N (**E-H**), Tb.Th (**I-L**), Tb.Sp (**M-**
363 **P**), Tb.1/N.SD (**Q-T**), Ct.Po (**U-X**), and Ct.Po.Dm (**Y-AB**) assessed using the measured XCTII values
364 and the estimated XCTII* values from XCTI at the radius using the standard (left) and LH (right)
365 approach. On regression plots, the dashed line indicates the line of unity. On Bland-Altman plots, the
366 solid black line indicates the mean difference, the dashed lines indicate the 95% limits of agreement, and
367 the gray line indicates zero.

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370 **Figure 3.** Regression and Bland-Altman plots for BV/TV (**A-D**), Tb.N (**E-H**), Tb.Th (**I-L**), Tb.Sp (**M-**
371 **P**), Tb.1/N.SD (**Q-T**), Ct.Po (**U-X**), and Ct.Po.Dm (**Y-AB**) assessed using measured the XCTII values
372 and the estimated XCTII* values from XCTI at the tibia using the standard (left) and LH (right)
373 approach. On regression plots, the dashed line indicates the line of unity. On Bland-Altman plots, the
374 solid black line indicates the mean difference, the dashed lines indicate the 95% limits of agreement, and
375 the gray line indicates zero.

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377 **Table 1.** Participant characteristics categorized by Training and Test sets for bootstrapping. Values are
378 shown as mean \pm SD, or count (percentage). Unpaired student's t-test and Pearson's chi-squared test
379 were performed between the Training and Test sets when applicable.

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382 **Table 2.** Regression analysis results for trabecular and cortical outcomes reported for both the standard
383 and LH approach. All values represent averages derived from the cross-calibration procedure.

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385 **Table 3.** Mean absolute percent error between measured XCTII and estimated XCTII* outcomes by
386 cross-calibration for trabecular and cortical outcomes, reported for both the standard and developed LH
387 approach. The *p*-values are obtained from the paired student's t-test performed between the percent
388 errors from the standard and LH approach.

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