

## OVERVIEW

Discrete data fields are output from 4DM in XML format, facilitating a range of integration options with our partners and health system customers. Beginning with the v2023 release of 4DM, much of the XML strings were updated, to facilitate understanding and improve readability.

Changes in both Elements and Type occurred. The table below, organized by report section, equates the v2018 and prior XML with the updated ones, and indicates where no change has been made. Our partners will have to update their API's to become compatible with 4DM's new XML export schema for reporting data.

## 10. 4DM-CVIS REPORTING Difference between Corridor4DM v2018 to 2023

Differences highlighted in **Yellow**

### 10.1.1. Injection Parameters

```
nm_base_findings = { NM_STRESS_FINDINGS, NM_REST_FINDINGS, NM_FDG_FINDINGS, NM_DELAY_FUNCTIONS }
```

ELEMENTS	v2018	v2023
Radiopharmaceutical	<code>/PATIENT_DATA/{nm_base_findings}/ INJECTION_DATA/@radioPharm</code>	<code>/PATIENT_DATA/{nm_base_findings}/ INJECTION_DATA/@radiopharmaceutical</code>
Injected Radiotracer Activity	<code>/PATIENT_DATA/{nm_base_findings}/ INJECTION_DATA/@injectionDose</code>	<code>/PATIENT_DATA/{nm_base_findings}/ INJECTION_DATA/@injectedActivity</code>

ELEMENTS	v2018 TYPE	v2023 TYPE	ATTRIBUTE CHANGES
Radiopharmaceutical	xs:string	pharmaTypes	[+] use="required"
Injected Radiotracer Activity	c4dm:floatORstring	NonNegativeDoubleOrEmpty	[+] use="required"

## 10.1.2. Imaging Elements

```
nm_findings = { NM_STRESS_FINDINGS, NM_REST_FINDINGS, NM_FDG_FINDINGS, NM_DELAY_FUNCTIONS, NM_ISCHEMIA_FINDINGS,
NM_VIABILITY_FINDINGS }
type = { FUNCTION, PERFUSION, FLOW }
```

ELEMENTS	v2018	v2023
Patient Position	<code>/PATIENT_DATA/{nm_findings}/{type}/DATASET_INFO/@imagingPosition</code>	<b>No Change</b>
Reconstruction Algorithm	<code>/PATIENT_DATA/{nm_findings}/{type}/DATASET_INFO/@corrRecon</code>	<code>/PATIENT_DATA/{nm_findings}/{type}/DATASET_INFO/@reconAlgorithm</code>
Scatter Correction Type	<code>/PATIENT_DATA/{nm_findings}/{type}/DATASET_INFO/@corrSc</code>	<code>/PATIENT_DATA/{nm_findings}/{type}/DATASET_INFO/@scatterCorrectionType</code>
Attenuation Correction Type	<code>/PATIENT_DATA/{nm_findings}/{type}/DATASET_INFO/@corrAc</code>	<code>/PATIENT_DATA/{nm_findings}/{type}/DATASET_INFO/@attenuationCorrectionType</code>

ELEMENTS	v2018 TYPE	v2023 TYPE	ATTRIBUTE CHANGES
Patient Position	xs:string	positionTypes	[+] use="required"
Reconstruction Algorithm	xs:string	reconAlgorithmTypes	[+] use="required"
Scatter Correction Type	xs:string	scatterCorrectionTypes	[+] use="required"
Attenuation Correction Type	xs:string	attenuationCorrectionTypes	[+] use="required"

### 10.1.3. LV Function – Systolic, TID and Diastolic

```
nm_base_findings = { NM_STRESS_FINDINGS, NM_REST_FINDINGS, NM_FDG_FINDINGS, NM_DELAY_FUNCTIONS }
nm_dataset = { STRESS_DATASET, REST_DATASET, FDG_DATASET, DELAY_DATASET }
```

ELEMENTS	v2018	v2023
EF	<code>/PATIENT_DATA/{nm_base_findings}/FUNCTION/LV_FUNCTION_DATA/@ef</code>	<code>/PATIENT_DATA/{nm_base_findings}/{nm_dataset}/FUNCTION/LV_FUNCTION_DATA/@ef</code>
ESV	<code>/PATIENT_DATA/{nm_base_findings}/FUNCTION/LV_FUNCTION_DATA/@esv</code>	<code>/PATIENT_DATA/{nm_base_findings}/{nm_dataset}/FUNCTION/LV_FUNCTION_DATA/@esv</code>
EDV	<code>/PATIENT_DATA/{nm_base_findings}/FUNCTION/LV_FUNCTION_DATA/@edv</code>	<code>/PATIENT_DATA/{nm_base_findings}/{nm_dataset}/FUNCTION/LV_FUNCTION_DATA/@edv</code>
TID	<code>/PATIENT_DATA/{nm_base_findings}/FUNCTION/LV_FUNCTION_DATA/@dilation</code>	<code>/PATIENT_DATA/{nm_base_findings}/{nm_dataset}/FUNCTION/LV_FUNCTION_DATA/@dilation</code>
PFR	<code>/PATIENT_DATA/{nm_base_findings}/FUNCTION/LV_FUNCTION_DATA/@peakFillingRate</code>	<code>/PATIENT_DATA/{nm_base_findings}/{nm_dataset}/FUNCTION/LV_FUNCTION_DATA/@peakFillingRate</code>
PER	<code>/PATIENT_DATA/{nm_base_findings}/FUNCTION/LV_FUNCTION_DATA/@peakEmptyingRate</code>	<code>/PATIENT_DATA/{nm_base_findings}/{nm_dataset}/FUNCTION/LV_FUNCTION_DATA/@peakEmptyingRate</code>
TPFR	<code>/PATIENT_DATA/{nm_base_findings}/FUNCTION/LV_FUNCTION_DATA/@timePeakFilling</code>	<code>/PATIENT_DATA/{nm_base_findings}/{nm_dataset}/FUNCTION/LV_FUNCTION_DATA/@timePeakFilling</code>
TPER	<code>/PATIENT_DATA/{nm_base_findings}/FUNCTION/LV_FUNCTION_DATA/@timePeakEmptying</code>	<code>/PATIENT_DATA/{nm_base_findings}/{nm_dataset}/FUNCTION/LV_FUNCTION_DATA/@timePeakEmptying</code>

ELEMENTS	v2018 TYPE	v2023 TYPE	ATTRIBUTE CHANGES
EF	c4dm:integerORstring	NonNegativeIntegerOrEmpty	[+] use="required"
ESV	c4dm:integerORstring	NonNegativeIntegerOrEmpty	[+] use="required"
EDV	c4dm:integerORstring	NonNegativeIntegerOrEmpty	[+] use="required"
TID	c4dm:integerORstring	NonNegativeDoubleOrEmpty	[+] use="optional"
PFR	c4dm:floatORstring	NonNegativeDoubleOrEmpty	[+] use="optional"
PER	c4dm:floatORstring	NonNegativeDoubleOrEmpty	[+] use="optional"
TPFR	c4dm:floatORstring	NonNegativeDoubleOrEmpty	[+] use="optional"
TPER	c4dm:floatORstring	NonNegativeDoubleOrEmpty	[+] use="optional"

## 10.1.4. LV Perfusion – Polarmap Quantification

ELEMENTS	v2018	v2023
Stress Quantification (defect extent)	/PATIENT_DATA/NM_STRESS_FINDINGS/PERFUSION/LV_PERFUSION_DATA	/PATIENT_DATA/NM_STRESS_FINDINGS/STRESS_DATASET/PERFUSION/LV_PERFUSION_DATA
Rest Quantification (defect extent)	/PATIENT_DATA/NM_REST_FINDINGS/PERFUSION/LV_PERFUSION_DATA	/PATIENT_DATA/NM_REST_FINDINGS/REST_DATASET/PERFUSION/LV_PERFUSION_DATA
Reversibility (Ischemia) Quantification (extent)	/PATIENT_DATA/NM_ISCHEMIA_FINDINGS/PERFUSION/LV_PERFUSION_DATA	<b>No Change</b>

ELEMENTS	v2018 TYPE	v2023 TYPE	ATTRIBUTE CHANGES
Stress Quantification (defect extent)	c4dm:vascular_integer_data	vascular_extent_data	
Rest Quantification (defect extent)	c4dm:vascular_integer_data	vascular_extent_data	
Reversibility (Ischemia) Quantification (extent)	c4dm:vascular_integer_data	vascular_extent_data	

**Notes:**

- [ALL] Type changed from a sequence of c4dm:region\_integer\_data called “REGION” [0, 4] to sequence of four distinct vascular\_extent\_type called {LAD, LCX, RCA, GLOBAL}
- [ALL] Type removed Attribute “<attribute name=“overlay type=“xs:string”/>”

**Example**

v2018	v2023
<pre>&lt;LV_PERFUSION_DATA segmenta8on="vascular"&gt; &lt;PERF_REGION segment="lad" extent="46.3" /&gt; &lt;PERF_REGION segment="lcx" extent="0.0" /&gt; &lt;PERF_REGION segment="rca" extent="5.6" /&gt; &lt;PERF_REGION segment="tot" extent="24.6" /&gt; &lt;/LV_PERFUSION_DATA&gt;</pre>	<pre>&lt;LV_PERFUSION_DATA&gt; &lt;LAD value="46" /&gt; &lt;LCX value="0" /&gt; &lt;RCA value="6" /&gt; &lt;GLOBAL value="25" /&gt; &lt;/LV_PERFUSION_DATA&gt;</pre>

## 10.1.5. LV Perfusion – Segmental Scoring

ELEMENTS	v2018	v2023
Stress Regional Scores	/PATIENT_DATA/NM_STRESS_FINDINGS/PERFUSION/REGIONAL_PERFUSION_SCORES	/PATIENT_DATA/NM_STRESS_FINDINGS/STRESS_DATASET/PERFUSION/REGIONAL_PERFUSION_SCORES
Stress Summed Score	/PATIENT_DATA/NM_STRESS_FINDINGS/PERFUSION/REGIONAL_PERFUSION_SCORES/@summedScore	/PATIENT_DATA/NM_STRESS_FINDINGS/STRESS_DATASET/PERFUSION/REGIONAL_PERFUSION_SCORES/@summedScore
Rest Regional Scores	/PATIENT_DATA/NM_REST_FINDINGS/PERFUSION/REGIONAL_PERFUSION_SCORES	/PATIENT_DATA/NM_REST_FINDINGS/REST_DATASET/PERFUSION/REGIONAL_PERFUSION_SCORES
Rest Summed Score	/PATIENT_DATA/NM_REST_FINDINGS/PERFUSION/REGIONAL_PERFUSION_SCORES/@summedScore	/PATIENT_DATA/NM_REST_FINDINGS/REST_DATASET/PERFUSION/REGIONAL_PERFUSION_SCORES/@summedScore
Reversibility Regional Scores	/PATIENT_DATA/NM_ISCHEMIA_FINDINGS/PERFUSION/REGIONAL_REVERSIBILITY_SCORES	No Change
Reversibility Summed Score	/PATIENT_DATA/NM_ISCHEMIA_FINDINGS/PERFUSION/REGIONAL_REVERSIBILITY_SCORES/@summedScore	No Change

ELEMENTS	v2018 TYPE	v2023 TYPE	ATTRIBUTE CHANGES
Stress Regional Scores	c4dm:regional_integer_data	regional_integer_data	
Stress Summed Score	c4dm:integerORstring	NonNegativeIntegerOrEmpty	[+] use="required"
Rest Regional Scores	c4dm:regional_integer_data	regional_integer_data	
Rest Summed Score	c4dm:integerORstring	NonNegativeIntegerOrEmpty	[+] use="required"
Reversibility Regional Scores	c4dm:regional_integer_data	regional_integer_data	
Reversibility Summed Score	c4dm:integerORstring	NonNegativeIntegerOrEmpty	[+] use="required"

**Notes:**

- [ALL REGIONAL] Type changed from a sequence of c4dm:region\_integer\_data called “REGION” [0, 17] to sequence of seventeen distinct region\_score\_data called {ProximalAnterior, ProximalAnteroseptal, ProximalInferoseptal, ProximalInferior, ProximalInferolateral, ProximalAnterolateral, MidAnterior, MidAnteroseptal, MidInferoseptal, MidInferior, MidInferolateral, MidAnterolateral, DistalAnterior, DistalSeptal, DistalInferior, DistalLateral, Apical}
- [ALL REGIONAL] Type added attribute “<xs:attribute name=“segments” type=“segmentTypes” use=“required”/>”
- [ALL REGIONAL] Type added attribute “<xs:attribute name=“summedScore” type=“NonNegativeIntegerOrEmpty” use=“required”/>”
- [ALL REGIONAL] Type removed attribute “<xs:attribute name=“overlay” type=“xs:string”/>”
- [ALL REGIONAL] Type removed attribute “<xs:attribute name=“summedScore” type=“c4dm:integerORstring”/>”

**Example**

v2018	v2023
<pre>&lt;REGIONAL_PERFUSION_SCORES summedScore="5" overlay="Zones17"&gt;   &lt;REGION segment="ProximalAnterior" value="0" /&gt;   &lt;REGION segment="ProximalAnteroseptal" value="0" /&gt;   &lt;REGION segment="ProximalInferoseptal" value="0" /&gt;   &lt;REGION segment="ProximalInferior" value="0" /&gt;   &lt;REGION segment="ProximalInferolateral" value="2" /&gt;   &lt;REGION segment="ProximalAnterolateral" value="0" /&gt;   &lt;REGION segment="MidAnterior" value="0" /&gt;   &lt;REGION segment="MidAnteroseptal" value="0" /&gt;   &lt;REGION segment="MidInferoseptal" value="0" /&gt;   &lt;REGION segment="MidInferior" value="0" /&gt;   &lt;REGION segment="MidInferolateral" value="1" /&gt;   &lt;REGION segment="MidAnterolateral" value="2" /&gt;   &lt;REGION segment="DistalAnterior" value="0" /&gt;   &lt;REGION segment="DistalSeptal" value="0" /&gt;   &lt;REGION segment="DistalInferior" value="0" /&gt;   &lt;REGION segment="DistalLateral" value="0" /&gt;   &lt;REGION segment="Apical" value="0" /&gt; &lt;/REGIONAL_PERFUSION_SCORES&gt;</pre>	<pre>&lt;REGIONAL_PERFUSION_SCORES summedScore="5" segments="17"&gt;   &lt;ProximalAnterior value="0" /&gt;   &lt;ProximalAnteroseptal value="0" /&gt;   &lt;ProximalInferoseptal value="0" /&gt;   &lt;ProximalInferior value="0" /&gt;   &lt;ProximalInferolateral value="2" /&gt;   &lt;ProximalAnterolateral value="0" /&gt;   &lt;MidAnterior value="0" /&gt;   &lt;MidAnteroseptal value="0" /&gt;   &lt;MidInferoseptal value="0" /&gt;   &lt;MidInferior value="0" /&gt;   &lt;MidInferolateral value="1" /&gt;   &lt;MidAnterolateral value="2" /&gt;   &lt;DistalAnterior value="0" /&gt;   &lt;DistalSeptal value="0" /&gt;   &lt;DistalInferior value="0" /&gt;   &lt;DistalLateral value="0" /&gt;   &lt;Apical value="0" /&gt; &lt;/REGIONAL_PERFUSION_SCORES&gt;</pre>

## 10.1.6. LV Regional Function – Segmental Scoring

Complete the Xpath for Stress

ELEMENTS	v2018	v2023
Wall Motion Regional Scores	<code>/PATIENT_DATA/NM_STRESS_FINDINGS/FUNCTION/REGIONAL_MOTION_SCORES</code>	<code>/PATIENT_DATA/NM_STRESS_FINDINGS/STRESS_DATASET/FUNCTION/REGIONAL_MOTION_SCORES</code>
Wall Motion Summed Score	<code>/PATIENT_DATA/NM_STRESS_FINDINGS/FUNCTION/REGIONAL_MOTION_SCORES/@summedScore</code>	<code>/PATIENT_DATA/NM_STRESS_FINDINGS/STRESS_DATASET/FUNCTION/REGIONAL_MOTION_SCORES/@summedScore</code>
Wall Thickening Regional Scores	<code>/PATIENT_DATA/NM_STRESS_FINDINGS/FUNCTION/REGIONAL_THICKENING_SCORES</code>	<code>/PATIENT_DATA/NM_STRESS_FINDINGS/STRESS_DATASET/FUNCTION/REGIONAL_THICKENING_SCORES</code>
Wall Thickening Summed Score	<code>/PATIENT_DATA/NM_STRESS_FINDINGS/FUNCTION/REGIONAL_THICKENING_SCORES/@summedScore</code>	<code>/PATIENT_DATA/NM_STRESS_FINDINGS/STRESS_DATASET/FUNCTION/REGIONAL_THICKENING_SCORES/@summedScore</code>
Reversibility Regional Scores	<code>/PATIENT_DATA/NM_ISCHEMIA_FINDINGS/PERFUSION/REGIONAL_REVERSIBILITY_SCORES</code>	<b>No Change</b>
Reversibility Summed Score	<code>/PATIENT_DATA/NM_ISCHEMIA_FINDINGS/PERFUSION/REGIONAL_REVERSIBILITY_SCORES/@summedScore</code>	<b>No Change</b>

ELEMENTS	v2018 TYPE	v2023 TYPE	ATTRIBUTE CHANGES
Wall Motion Regional Scores	<code>c4dm:regional_integer_data</code>	<code>regional_integer_data</code>	
Wall Motion Summed Score	<code>c4dm:integerORstring</code>	<code>NonNegativeIntegerOrEmpty</code>	[+] use="required"
Wall Thickening Regional Scores	<code>c4dm:regional_integer_data</code>	<code>regional_integer_data</code>	
Wall Thickening Summed Score	<code>c4dm:integerORstring</code>	<code>NonNegativeIntegerOrEmpty</code>	[+] use="required"
Reversibility Regional Scores	<code>c4dm:regional_integer_data</code>	<code>regional_integer_data</code>	
Reversibility Summed Score	<code>c4dm:integerORstring</code>	<code>NonNegativeIntegerOrEmpty</code>	[+] use="required"

**Notes:**

- [ALL REGIONAL] Type changed from a sequence of c4dm:region\_integer\_data called "REGION" [0, 17] to sequence of seventeen distinct region\_score\_data called {ProximalAnterior, ProximalAnteroseptal, ProximalInferoseptal, ProximalInferior, ProximalInferolateral, ProximalAnterolateral, MidAnterior, MidAnteroseptal, MidInferoseptal, MidInferior, MidInferolateral, MidAnterolateral, DistalAnterior, DistalSeptal, DistalInferior, DistalLateral, Apical}
- [ALL REGIONAL] Type added attribute "<xs:attribute name="segments" type="segmentTypes" use="required"/>"
- [ALL REGIONAL] Type added attribute "<xs:attribute name="summedScore" type="NonNegativeIntegerOrEmpty" use="required"/>"
- [ALL REGIONAL] Type removed attribute "<xs:attribute name="overlay" type="xs:string"/>"
- [ALL REGIONAL] Type removed attribute "<xs:attribute name="summedScore" type="c4dm:integerORstring"/>"

**Example:**

v2018	v2023
<pre>&lt;REGIONAL_MOTION_SCORES summedScore="14" overlay="Zones17"&gt;   &lt;REGION segment="ProximalAnterior" value="0" /&gt;   &lt;REGION segment="ProximalAnteroseptal" value="0"/&gt;   &lt;REGION segment="ProximalInferoseptal" value="0"/&gt;   &lt;REGION segment="ProximalInferior" value="0" /&gt;   &lt;REGION segment="ProximalInferolateral" value="3" /&gt;   &lt;REGION segment="ProximalAnterolateral" value="3" /&gt;   &lt;REGION segment="MidAnterior" value="0" /&gt;   &lt;REGION segment="MidAnteroseptal" value="0" /&gt;   &lt;REGION segment="MidInferoseptal" value="0" /&gt;   &lt;REGION segment="MidInferior" value="0" /&gt;   &lt;REGION segment="MidInferolateral" value="3" /&gt;   &lt;REGION segment="MidAnterolateral" value="3" /&gt;   &lt;REGION segment="DistalAnterior" value="0" /&gt;   &lt;REGION segment="DistalSeptal" value="0" /&gt;   &lt;REGION segment="DistalInferior" value="0" /&gt;   &lt;REGION segment="DistalLateral" value="2" /&gt;   &lt;REGION segment="Apical" value="0" /&gt; &lt;/REGIONAL_MOTION_SCORES&gt;</pre>	<pre>&lt;REGIONAL_MOTION_SCORES summedScore="14" segments="17"&gt;   &lt;ProximalAnterior value="0" /&gt;   &lt;ProximalAnteroseptal value="0" /&gt;   &lt;ProximalInferoseptal value="0" /&gt;   &lt;ProximalInferior value="0" /&gt;   &lt;ProximalInferolateral value="3" /&gt;   &lt;ProximalAnterolateral value="3" /&gt;   &lt;MidAnterior value="0" /&gt;   &lt;MidAnteroseptal value="0" /&gt;   &lt;MidInferoseptal value="0" /&gt;   &lt;MidInferior value="0" /&gt;   &lt;MidInferolateral value="3" /&gt;   &lt;MidAnterolateral value="3" /&gt;   &lt;DistalAnterior value="0" /&gt;   &lt;DistalSeptal value="0" /&gt;   &lt;DistalInferior value="0" /&gt;   &lt;DistalLateral value="2" /&gt;   &lt;Apical value="0" /&gt; &lt;/REGIONAL_MOTION_SCORES&gt;</pre>

## 10.1.7. LV Blood Flow

ELEMENTS	v2018	v2023
Stress Blood Flow	<code>/PATIENT_DATA/NM_STRESS_FINDINGS/FLOW/MBF_DATA</code>	<code>/PATIENT_DATA/NM_STRESS_FINDINGS/STRESS_DATASET/FLOW/MBF_DATA</code>
Rest Blood Flow	<code>/PATIENT_DATA/NM_REST_FINDINGS/FLOW/MBF_DATA</code>	<code>/PATIENT_DATA/NM_REST_FINDINGS/REST_DATASET/FLOW/MBF_DATA</code>
Coronary Flow Reserve	<code>/PATIENT_DATA/NM_ISCHEMIA_FINDINGS/FLOW/CFR_DATA</code>	<b>No Change</b>

ELEMENTS	v2018 TYPE	v2022 TYPE	ATTRIBUTE CHANGES
Stress Blood Flow	<code>c4dm:vascular_float_data</code>	<code>vascular_flow_data</code>	
Rest Blood Flow	<code>c4dm:vascular_float_data</code>	<code>vascular_flow_data</code>	
Coronary Flow Reserve	<code>c4dm:vascular_float_data</code>	<code>vascular_flow_data</code>	

**Notes:**

- [ALL] Type changed from a sequence of `c4dm:region_float_data` called "REGION" [0, 4] to sequence of four distinct `vascular_flow_type` called {LAD, LCX, RCA, GLOBAL}
- [ALL] Type removed attribute "`<xs:attribute name="overlay" type="xs:string"/>`"

**Example:**

v2018	v2023
<pre>&lt;MBF_DATA overlay="Vascular"&gt;   &lt;REGION segment="LAD" value="1.14" /&gt;   &lt;REGION segment="LCX" value="0.88" /&gt;   &lt;REGION segment="RCA" value="1.05" /&gt;   &lt;REGION segment="Global" value="1.02" /&gt; &lt;/MBF_DATA&gt;</pre>	<pre>&lt;MBF_DATA&gt;   &lt;LAD value="1.14" /&gt;   &lt;LCX value="0.88" /&gt;   &lt;RCA value="1.05" /&gt;   &lt;GLOBAL value="1.02" /&gt; &lt;/MBF_DATA&gt;</pre>

## 10.1.8. LV Metabolism Quantification (FDG for assessment of Hibernating, Scar)

ELEMENTS	v2018	v2023
FDG Quantification (defect extent)	<code>/PATIENT_DATA/NM_FDG_FINDINGS/PERFUSION/LV_PERFUSION_DATA</code>	<code>/PATIENT_DATA/NM_FDG_FINDINGS/FDG_DATASET/PERFUSION/LV_PERFUSION_DATA</code>
Hibernating/Viability Quantification (extent)	<code>/PATIENT_DATA/NM_VIABILITY_FINDINGS/PERFUSION/LV_VIABILITY_DATA</code>	No Change
Scar Quantification (extent)	<code>/PATIENT_DATA/NM_VIABILITY_FINDINGS/PERFUSION/LV_SCAR_DATA</code>	No Change

ELEMENTS	v2018 TYPE	v2023 TYPE	ATTRIBUTE CHANGES
FDG Quantification (defect extent)	<code>c4dm:vascular_integer_data</code>	<code>vascular_extent_data</code>	
Hibernating/Viability Quantification (extent)	<code>c4dm:vascular_integer_data</code>	<code>vascular_extent_double_data</code>	
Scar Quantification (extent)	<code>c4dm:vascular_integer_data</code>	<code>vascular_extent_double_data</code>	

**Notes:**

- [ALL] Type changed from a sequence of `c4dm:region_integer_data` called "REGION" [0, 4] to sequence of four distinct `vascular_extent_type` or `vascular_extent_double_type` called {LAD, LCX, RCA, GLOBAL}
- [ALL] Type removed Attribute "`<attribute name="overlay" type="xs:string"/>`"

**Example:**

v2018	v2023
<pre>&lt;LV_PERFUSION_DATA overlay="Vascular"&gt;   &lt;REGION segment="LAD" value="3" /&gt;   &lt;REGION segment="LCX" value="100" /&gt;   &lt;REGION segment="RCA" value="1" /&gt;   &lt;REGION segment="Global" value="28" /&gt; &lt;/LV_PERFUSION_DATA&gt;</pre>	<pre>&lt;LV_PERFUSION_DATA&gt;   &lt;LAD value="3" /&gt;   &lt;LCX value="100" /&gt;   &lt;RCA value="1" /&gt;   &lt;GLOBAL value="28" /&gt; &lt;/LV_PERFUSION_DATA&gt;</pre>

## 10.1.9. LV Metabolism Scoring (FDG for assessment of Hibernating, Scar)

ELEMENTS	v2018	v2023
FDG Regional Scores	<code>/PATIENT_DATA/NM_FDG_FINDINGS/PERFUSION/REGIONAL_PERFUSION_SCORES</code>	<code>/PATIENT_DATA/NM_FDG_FINDINGS/FDG_DATASET/PERFUSION/REGIONAL_PERFUSION_SCORES</code>
FDG Summed Score	<code>/PATIENT_DATA/NM_FDG_FINDINGS/PERFUSION/REGIONAL_PERFUSION_SCORES/@summedScore</code>	<code>/PATIENT_DATA/NM_FDG_FINDINGS/FDG_DATASET/PERFUSION/REGIONAL_PERFUSION_SCORES/@summedScore</code>
Hibernating Regional Scores	<code>/PATIENT_DATA/NM_VIABILITY_FINDINGS/PERFUSION/REGIONAL_VIABILITY_SCORES</code>	No Change
Hibernating Summed Score	<code>/PATIENT_DATA/NM_VIABILITY_FINDINGS/PERFUSION/REGIONAL_VIABILITY_SCORES/@summedScore</code>	No Change
Scar Regional Scores	<code>/PATIENT_DATA/NM_VIABILITY_FINDINGS/PERFUSION/REGIONAL_SCAR_SCORES</code>	No Change
Scar Summed Score	<code>/PATIENT_DATA/NM_VIABILITY_FINDINGS/PERFUSION/REGIONAL_SCAR_SCORES/@summedScore</code>	No Change

ELEMENTS	v2018 TYPE	v2023 TYPE	ATTRIBUTE CHANGES
FDG Regional Scores	<code>c4dm:regional_integer_data</code>	<code>regional_integer_data</code>	
FDG Summed Score	<code>c4dm:integerORstring</code>	<code>NonNegativeIntegerOrEmpty</code>	[+] use="required"
Hibernating Regional Scores	<code>c4dm:regional_integer_data</code>	<code>regional_integer_data</code>	
Hibernating Summed Score	<code>c4dm:integerORstring</code>	<code>NonNegativeIntegerOrEmpty</code>	[+] use="required"
Scar Regional Scores	<code>c4dm:regional_integer_data</code>	<code>regional_integer_data</code>	
Scar Summed Score	<code>c4dm:integerORstring</code>	<code>NonNegativeIntegerOrEmpty</code>	[+] use="required"

**Notes:**

- [ALL REGIONAL] Type changed from a sequence of c4dm:region\_integer\_data called "REGION" [0, 17] to sequence of seventeen distinct region\_score\_data called {ProximalAnterior, ProximalAnteroseptal, ProximalInferoseptal, ProximalInferior, ProximalInferolateral, ProximalAnterolateral, MidAnterior, MidAnteroseptal, MidInferoseptal, MidInferior, MidInferolateral, MidAnterolateral, DistalAnterior, DistalSeptal, DistalInferior, DistalLateral, Apical}
- [ALL REGIONAL] Type added attribute "<xs:attribute name="segments" type="segmentTypes" use="required"/>"
- [ALL REGIONAL] Type added attribute "<xs:attribute name="summedScore" type="NonNegativeIntegerOrEmpty" use="required"/>"
- [ALL REGIONAL] Type removed attribute "<xs:attribute name="overlay" type="xs:string"/>"
- [ALL REGIONAL] Type removed attribute "<xs:attribute name="summedScore" type="c4dm:integerORstring"/>"

**Example:**

v2018	v2023
<pre>&lt;REGIONAL_PERFUSION_SCORES summedScore="14" overlay="Zones17"&gt;   &lt;REGION segment="ProximalAnterior" value="0" /&gt;   &lt;REGION segment="ProximalAnteroseptal" value="0" /&gt;   &lt;REGION segment="ProximalInferoseptal" value="0" /&gt;   &lt;REGION segment="ProximalInferior" value="0" /&gt;   &lt;REGION segment="ProximalInferolateral" value="3" /&gt;   &lt;REGION segment="ProximalAnterolateral" value="3" /&gt;   &lt;REGION segment="MidAnterior" value="0" /&gt;   &lt;REGION segment="MidAnteroseptal" value="0" /&gt;   &lt;REGION segment="MidInferoseptal" value="0" /&gt;   &lt;REGION segment="MidInferior" value="0" /&gt;   &lt;REGION segment="MidInferolateral" value="3" /&gt;   &lt;REGION segment="MidAnterolateral" value="3" /&gt;   &lt;REGION segment="DistalAnterior" value="0" /&gt;   &lt;REGION segment="DistalSeptal" value="0" /&gt;   &lt;REGION segment="DistalInferior" value="0" /&gt;   &lt;REGION segment="DistalLateral" value="2" /&gt;   &lt;REGION segment="Apical" value="0" /&gt; &lt;/REGIONAL_PERFUSION_SCORES&gt;</pre>	<pre>&lt;REGIONAL_PERFUSION_SCORES summedScore="14" segments="17"&gt;   &lt;ProximalAnterior value="0" /&gt;   &lt;ProximalAnteroseptal value="0" /&gt;   &lt;ProximalInferoseptal value="0" /&gt;   &lt;ProximalInferior value="0" /&gt;   &lt;ProximalInferolateral value="3" /&gt;   &lt;ProximalAnterolateral value="3" /&gt;   &lt;MidAnterior value="0" /&gt;   &lt;MidAnteroseptal value="0" /&gt;   &lt;MidInferoseptal value="0" /&gt;   &lt;MidInferior value="0" /&gt;   &lt;MidInferolateral value="3" /&gt;   &lt;MidAnterolateral value="3" /&gt;   &lt;DistalAnterior value="0" /&gt;   &lt;DistalSeptal value="0" /&gt;   &lt;DistalInferior value="0" /&gt;   &lt;DistalLateral value="2" /&gt;   &lt;Apical value="0" /&gt; &lt;/REGIONAL_PERFUSION_SCORES&gt;</pre>

## 10.1.10. CT Calcium Scoring

ELEMENTS	v2018	v2023
Agatston Calcium Score		<code>/PATIENT_DATA/CASC_FINDINGS/CASC_TOT/@score</code>

ELEMENTS	v2018 TYPE	v2023 TYPE	ATTRIBUTE CHANGES
Agatston Calcium Score		<code>casc_region_and_percentiles</code>	

## 10.2 Changes from Corridor4DM v2023 to v2024

### 10.2.1 Calcium Scoring updates

Additional lesions scored for calcium in new elements

ELEMENTS	v2023	v2024
Calcium Score	<code>/PATIENT_DATA/CASC_FINDINGS/CASC_DATASET/</code>	<code>/PATIENT_DATA/CASC_FINDINGS/CASC_DATASET/</code>

New Elements	Type
CASC_AAO	<code>c4dm: casc_region</code>
CASC_DAO	<code>c4dm: casc_region</code>
CASC_AV	<code>c4dm: casc_region</code>
CASC_MV	<code>c4dm: casc_region</code>
CASC_TV	<code>c4dm: casc_region</code>
CASC_PV	<code>c4dm: casc_region</code>

**Example:**

v2023	v2024
<pre> &lt;CASC_DATASET&gt; ... &lt;CASC_LM score="0" volume="0.0" lesions="0"/&gt; &lt;CASC_LAD score="482" volume="367.0" lesions="4"/&gt; &lt;CASC_LCX score="0" volume="0.0" lesions="0"/&gt; &lt;CASC_RCA score="200" volume="185.0" lesions="5"/&gt; &lt;CASC_TOT score="682" volume="553.0" lesions="9"/&gt; &lt;/CASC_DATASET&gt; </pre>	<pre> &lt;CASC_DATASET&gt; ... &lt;CASC_LM score="0" volume="0.0" lesions="0"/&gt; &lt;CASC_LAD score="482" volume="367.0" lesions="4"/&gt; &lt;CASC_LCX score="0" volume="0.0" lesions="0"/&gt; &lt;CASC_RCA score="200" volume="185.0" lesions="5"/&gt; &lt;CASC_TOT score="682" volume="553.0" lesions="9"/&gt; &lt;CASC_AAO score="563154" volume="422365.0" lesions="1" /&gt; &lt;CASC_DAO score="0" volume="0.0" lesions="0" /&gt; &lt;CASC_AV score="0" volume="0.0" lesions="0" /&gt; &lt;CASC_MV score="52353" volume="39265.0" lesions="1" /&gt; &lt;CASC_TV score="0" volume="0.0" lesions="0" /&gt; &lt;CASC_PV score="9762" volume="7321.0" lesions="1" /&gt; &lt;/CASC_DATASET&gt; </pre>

## 10.2.2 iMFR data

ELEMENTS	v2023	v2024
CFR_DATA	/PATIENT_DATA/NM_ISCHEMIA_FINDINGS/FLOW/CFR_DATA	/PATIENT_DATA/NM_ISCHEMIA_FINDINGS/FLOW/CFR_DATA

## 10.2.2 iMFR data continued...

New Attributes	Type	Attribute Changes
iMfrNormalExtent	NonNegativeDoubleOrEmpty	use="required"
iMfrNormalMean	NonNegativeDoubleOrEmpty	use="required"
iMfrDiffuseExtent	NonNegativeDoubleOrEmpty	use="required"
iMfrDiffuseMean	NonNegativeDoubleOrEmpty	use="required"
iMfrFocalExtent	NonNegativeDoubleOrEmpty	use="required"
iMfrFocalMean	NonNegativeDoubleOrEmpty	use="required"
iMfrMismatchExtent	NonNegativeDoubleOrEmpty	use="required"
iMfrMismatchMean	NonNegativeDoubleOrEmpty	use="required"

**Example:****v2023**

```
<CFR_DATA overlay="Vascular">
  <LAD value="1.25" extent="83.75" />
  <LCX value="0.75" extent="100.00" />
  <RCA value="1.53" extent="68.89" />
  <GLOBAL value="1.17" extent="81.96" />
</CFR_DATA>
```

**v2024**

```
<CFR_DATA overlay="Vascular">
  <LAD value="1.25" extent="83.75" iMfrNormalExtent="0.48" iMfrNormalMean="2.027"
iMfrDiffuseExtent="89.90" iMfrDiffuseMean="1.309" iMfrFocalExtent="9.62"
iMfrFocalMean="0.840" iMfrMismatchExtent="0.00" iMfrMismatchMean="" />
  <LCX value="0.75" extent="100.00" iMfrNormalExtent="0.00" iMfrNormalMean=""
iMfrDiffuseExtent="10.83" iMfrDiffuseMean="0.998" iMfrFocalExtent="89.17"
iMfrFocalMean="0.736" iMfrMismatchExtent="0.00" iMfrMismatchMean="" />
  <RCA value="1.53" extent="68.89" iMfrNormalExtent="7.58" iMfrNormalMean="2.049"
iMfrDiffuseExtent="90.91" iMfrDiffuseMean="1.490" iMfrFocalExtent="1.52"
iMfrFocalMean="1.094" iMfrMismatchExtent="0.00" iMfrMismatchMean="" />
  <GLOBAL value="1.17" extent="81.96" iMfrNormalExtent="2.39" iMfrNormalMean="2.047"
iMfrDiffuseExtent="69.57" iMfrDiffuseMean="1.364" iMfrFocalExtent="28.04"
iMfrFocalMean="0.757" iMfrMismatchExtent="0.00" iMfrMismatchMean="" />
</CFR_DATA>
```