CardioMR User Manual

Version 0.6.70-rc19 · Nov 1, 2026 · @nasih

1. About CardioMR

CardioMR is a Windows program for reading cardiac MRI studies: LV and RV volumes and function, myocardial mass, strain, 2D flow, scar / LGE, tissue mapping and the CMR report. It opens DICOM studies straight from a folder and works offline.

Research build. Not clinically validated; not for diagnosis. Automatic and AI contours are drafts. Every result needs review by a qualified reader before it is used.

What CardioMR does:

- **LV and RV function**: EDV, ESV, SV, EF, cardiac output, LV mass and their indexed values, from short-axis cines.
- **Automatic contouring**: Auto LV, Auto RV and offline AI contours (LV endo, LV epi, RV), with a review grid that marks likely-wrong contours in red.
- **Long axis**: biplane LV volumes, MAPSE, RV FAC and TAPSE, long-axis strain.
- **Strain and wall motion**: feature-tracking strain, bullseye, regional wall motion, tagged MRI.
- **2D flow**: forward and regurgitant volumes, peak velocity, pressure gradient, mitral and tricuspid regurgitation.
- **Tissue**: LGE scar burden, T1 / T2 / T2* mapping.
- **Reports**: CMR report in Word and PDF, from the General CMR or Myocardial viability template.

CardioMR never writes into your study folders or DICOM files.

2. Installing and starting

CardioMR needs 64-bit Windows 10 or 11. Minimum hardware has not yet been measured, so the figures below are estimates from testing on one laptop.

	Minimum	Recommended
Windows	10 or 11, 64-bit	11, 64-bit
Processor	4-core Core i5 / Ryzen 5 (2017 on)	6–8 core Core i7 / Ryzen 7 (2020 on)
Memory	8 GB	16 GB

	Minimum	Recommended
Disk	1 GB for the program and AI model, plus your studies	SSD, 20 GB free
Screen	1366 × 768	1920 × 1080 or higher
Graphics card	Not used	Not used
Mouse	With a scroll wheel	With a scroll wheel

AI contours run on the processor only. On a 4-core laptop a full short-axis study takes about 20 minutes; 10 slices take about 18 seconds.

Install

1. Run the CardioMR setup program, or unzip the portable folder.
2. Start **CardioMR.exe**. Keep the program folder together: CardioMR.exe needs the **_internal** folder beside it.
3. If Windows SmartScreen warns about an unknown publisher, choose **More info → Run anyway**. CardioMR is not yet code-signed.

Licence

Each licence is for one PC and a period (3 months at first).

1. Open **Help → Licence…** and copy this PC's **machine code**.
2. Send the machine code to your CardioMR supplier and install the licence file you receive.
3. A licence normally runs for 1 year. A new PC first gets a free 30-day trial that starts by itself; the table shows what each state allows.

	Free trial (30 days)	Licence (1 year)	Viewer only (no licence or trial)
Open studies, saved work and reports	Yes	Yes	Yes
Scroll, play, zoom, brightness, measure	Yes	Yes	Yes
Saved contours and results	Yes	Yes	Read-only
Contouring, AI, LV / RV, flow, strain, mapping, scar	Yes	Yes	No

	Free trial (30 days)	Licence (1 year)	Viewer only (no licence or trial)
Save work	Yes	Yes	No
Save reports (Word, PDF, Finalize)	No: prepared on screen only	Yes	No

The title bar shows **Free trial** or **VIEWER ONLY**. A blocked button says why in the status bar. Changed program files also make CardioMR a viewer: reinstall it.

Optional AI contour model

The offline AI model (CineMA) is installed separately into `%LOCALAPPDATA%\CardioMR\CardioMR\models`. Without it, Auto LV, Auto RV and all manual tools still work.

Where your work is kept

What	Where
Settings, recent studies, report drafts, log	`%LOCALAPPDATA%\CardioMR\CardioMR`
Each study's work (contours, flows, long-axis, mapping)	The work-files folder; change it in **File → Work files folder…** (for example a department server)
Word / PDF reports	The folder you choose in the report window

CardioMR checks its own program files at start. If they were changed, saving stops until it is reinstalled. Version and data folder: **Help → About CardioMR**.

3. The screen

The main window has three workspaces, switched with the buttons under the patient details: **Editor** to draw and correct contours, **ED / ES review** to check the two key phases, and **Results** for the reviewed numbers.

Part	Where	What it does
Menus	Top row	File, Flow, LV analysis, RV analysis, Strain analysis, Scar / LGE, Contours, Edit, View, Help

Part	Where	What it does
Study buttons	Top right	**Open study**, **Recent**, **Save workflow**, **CMR report**, **Patient info**
Patient line	Under the CardioMR title	Name, ID, study date and the series on screen
Workspace buttons	Under the patient line	**Editor** (Ctrl+1), **ED / ES review** (Ctrl+2), **Results** (Ctrl+3)
Panel buttons	Right of the workspace buttons	**Library**, **Analysis** and **Curve** show or hide those panels
Study library	Left	The study's series, grouped by purpose; click one to open it
Image	Centre	The current slice and phase, with contours, play controls and the slice and phase sliders
Toolbar	Above the image	Tool (Navigate, Draw, Edit, measure), contour type, Fit, zoom, Brightness, Save, Contours on/off, Propagate
Analysis panel	Right	Choose an analysis category, then a task; live results and the volume curve

The three workspaces

- **Editor**: one large image for contouring, propagation, the ball brush and cine playback. **F11** or **Maximize** enlarges the image and keeps the slice and phase controls.
- **ED / ES review**: the ED and ES phases of every slice side by side for the LV or RV. Open a tile to return to that slice and phase in the Editor.
- **Results**: the volume curve, the reviewed LV / RV measurement table, the source slices with their status, and **Measurement readiness and scope**, which lists what is still needed. A dash in the table means a value is not ready yet; the reason is listed under readiness.

Analysis categories

Category	Contains
LV analysis	LV slices, Auto LV, cavity tracing, volumes, SAX strain, long-axis function and strain, bullseye

Category	Contains
RV analysis	RV slices, Auto RV, volumes, RV long-axis function, RV stack
Tissue / LGE	Scar assessment and scar bullseye
Flow analysis	New or existing 2D flow analysis
Report	Measurements, notes, report and exports
Contour tools	Drawing, refinement, propagation and review tools

Mouse

Action	Result
Wheel	Next / previous slice
Shift + wheel	Next / previous phase
Ctrl + wheel	Zoom
Left drag	Pan (in Navigate)
Right drag	Window / level (brightness and contrast)
Right-click a contour	Contour actions

Double-click the image in Navigate to enlarge it (the same as F11); double-click again to restore it. In the long-axis windows it hides and restores the side panel.

4. Opening a study

Click **Open study**, choose the patient's DICOM folder (a CD copy or a PACS export), and CardioMR opens it on the short-axis cine. Python and internet are not needed.

1. Click **Open study** (or **File → Open DICOM folder**). The dialog starts beside your last study.
2. Choose the folder that holds the study. Subfolders are searched; a CD viewer's own files are ignored.
3. Watch the progress bar: finding files, reading them, then opening the series. **Cancel** stops loading and keeps the study already open.
4. The study opens on its short-axis cine.

To reopen one of your last 10 studies, use **Recent ▾** or **File → Recent studies**. A study whose folder has moved shows as "not found".

The study library

Series are grouped by purpose; within a group they stay in scan order.

1. **Function · LV & RV cine**: short axis, 2CH / 3CH / 4CH, LVOT, RVOT, RV and axial cines.
2. **LGE / scar**, with the TI scouts.
3. **Tissue**: T1, T2, T2*, STIR.
4. **Flow**.
5. **Perfusion**.

Localizers, surveys, HASTE and planning images are kept aside; **Show localizers and other** lists them. Documents in the study folder (PDF, Word, pictures) are listed under the library; double-click one to open it.

- **Click a series** to open it.
- **Short axis saved as one series per slice** (one breath-hold each) is combined into one stack automatically, named "… · N slices combined".
- **To combine series yourself**, Ctrl-click two or more and choose **Combine selected cine slices**.

Patient details

Height, weight and heart rate are read from the DICOM. If any is missing from the whole study, CardioMR asks for it once when the study opens; Later leaves it empty, and nothing is assumed. Check and correct them in **Patient info** (or **Report → Measurements and notes**): every indexed value and the cardiac output depend on them.

Saving and resuming work

- **Save workflow** (Ctrl+S) saves all work on this study: contours, measurement settings, scar, flow, long-axis and mapping work, and the current view. It goes to the work-files folder, never into the study folder.
- Opening the same study again resumes the saved work. It is matched by Study Instance UID and Patient ID, so a copied or moved study folder keeps its work.
- **File → Save analysis as…** (Ctrl+Shift+S) saves an extra, separately named analysis file.

5. LV function, step by step

A reportable LV result takes six steps: choose the slices, contour automatically, fix the contours flagged red, accept the ED and ES contours, confirm coverage, then read the Results. Automatic contours are proposals until you accept them, and the reviewed table stays empty (dashes) until then.

Step 1. Choose the LV slices

1. Open the short-axis cine in the **Editor**.
2. Click **Slices…** beside **Auto LV** (or **LV analysis → LV slices…**). Thumbnails of every slice are shown, zoomed on the heart.
3. Untick slices above the mitral valve and beyond the apex, then click **Apply**. At least 3 slices must stay included. Unticked slices are not contoured and not counted, but stay viewable.

Step 2. Contour automatically

Choose one of these:

Tool	What it contours	How to start	Time
Auto LV	LV endo and LV epi, every slice and phase	**Auto LV** button or **Ctrl+Shift+L**; no click needed	About 1 minute for 12 slices × 25 phases
AI contours (offline)	LV endo, LV epi and RV, on all phases or ED / ES only	**AI contours** button or **LV analysis** menu	About 20 minutes for a full study on a 4-core laptop
Click LV cavity	LV endo on the current slice and phase	Select **Click LV cavity**, click inside the bright blood pool; wheel to the next slice, Shift+wheel to the next phase; **Esc** to stop	Instant
Draw by hand	Any contour	Toolbar tool **Draw** (D), click around the border, **Enter** to finish	—

Auto LV finds the LV by itself, contours it from apex to base and stops at the valve plane. It includes trabeculations and papillary muscles in the cavity. To trace the bright blood pool instead, untick **LV analysis → Auto LV: include trabeculations and papillary muscles in**

the cavity; use the convention your reference values use.

All new contours are unreviewed proposals (dashed). **Ctrl+Z** removes a whole Auto LV run in one step. Locked contours and unfinished drawings are never changed.

When contours land on another organ

If the LV and RV are dimmer than a neighbouring organ, usually the stomach, the automatic tools can settle on that organ. Select the heart so they stay on it. Do this before contouring whenever you see a bright organ beside the heart.

1. Click **Select heart area** in the LV tools (also in the **LV analysis** and **RV analysis** menus).
2. Drag round the whole heart, both ventricles and their walls, and release. Leave a margin: the heart can shift between breath-holds.
3. If unreviewed contours already lie outside the area, CardioMR offers to remove them. Say **Yes**, or they still count in the volumes. **Undo** restores them.
4. Run **Auto LV**, **Auto RV** or **AI contours**.

The area shows as a white dashed line on every slice and phase of this series, and is saved with the study. It applies to Auto LV, the automatic LV epicardium, Auto RV and AI contours. Click cavity and drawing by hand are not limited by it. **Clear area** removes it and keeps the contours. The source images are not changed.

In the review grid, a contour outside the area, or one running along its edge, turns red. A contour along the edge may have been cut by the selection, so enlarge the area and run again.

Step 3. Find and fix the wrong contours

After Auto LV the **slice / phase review grid** opens. Open it any time with **Contours → Slice / phase review grid…** (**Ctrl+R**).

- **Rows** are slices, **columns** are phases; ED and ES are labelled.
- A **red** ⚠ **cell** is a contour that is probably wrong. Hover over it for the reason; double-click to open that frame.
- Choose **LV endo**, **LV epi** or **RV endo** in the drop-down at the top.
- Tick **Selected slices / phases only** to see only the frames that count.

Other symbols: **R** reviewed, **Ø** absent cavity, **D** proposal, **…** unfinished, **—** missing, **×** excluded or no image, **L** locked, **!** tracking note.

In the Editor, **Ctrl+N** jumps to the next red contour and **Ctrl+Shift+N** goes back; the reason shows in the status bar.

A contour turns red when it disagrees with **both** of its neighbours:

Check	Flagged when
Area against the phases before and after	More than 1.25× different from both
Area against the slices above and below	More than 1.6× different from both (leak into atrium, RV or LVOT, or a cut into the cavity)
Centre position	Jumped more than 5 mm from both phases, or 10 mm from both slices
End slice	More than 1.5× its only neighbour (atrium or outflow tract included?)
Wall	Endocardium crosses outside the epicardium
Border	Not on an image edge, invalid outline, little myocardium around it, or copied from a neighbour because tracing failed

Normal filling, emptying and base-to-apex tapering are not flagged. These limits were tuned on synthetic studies; check every slice before reporting.

To fix a red contour:

1. Click **Ball LV endo** (or **Ball LV epi**, **Ball RV**), or press **B** for the selected contour type.
2. Place the ball beside the wall and push with its rim: from inside the contour to move the border out, from outside to move it in. The wheel changes the ball size.
3. Or redraw it with **Click LV cavity**, or **Draw** a new one.
4. If the contour is actually right, accept it with **Ctrl+Return**. Accepted contours are no longer red.

Unlock a locked contour (**Ctrl+Return** again) before correcting it.

Step 4. Set ED and ES, and accept the contours

1. In **LV analysis → Volumes and contouring**, set the **Analysis slices** and **Analysis phases**. ED and ES can be picked automatically: **Auto ED/ES** takes the largest and smallest volume. Check them on the volume curve.
2. Open **ED / ES review** (Ctrl+2). Check every slice at ED and at ES: the basal slice (valve plane, LVOT) and the apex especially.
3. At the base or apex, where there is no LV cavity in that phase, mark it **No cavity here** or **Outside ventricle**, so it counts as reviewed.

4. Click **Accept all selected contours and lock**. This accepts every completed contour in the selected slices and phases at once; **Ctrl+Z** undoes it.
5. For LV mass, the LV epi is needed at ED only.

Step 5. Confirm coverage

Tick **Coverage confirmed: the measured slices cover the whole LV from base to apex**. Without it, the result is labelled a selected-slice result and the CMR report does not use it as the ventricle's volume.

Step 6. Read the results

Open **Results** (Ctrl+3). When **Measurement readiness and scope** reads **LV · Included-stack function ready**, the table shows EF, EDV, ESV, SV, the indexed values, cardiac output, cardiac index and LV mass.

Quick values before review. The **★ Quick LV** panel shows EF, volumes and mass live while you contour, from unaccepted contours too. They are preliminary: report only the reviewed values from **Results**.

How the numbers are calculated

Value	Method
Volume	Disc summation: sum of (area × slice spacing)
SV, EF	SV = EDV − ESV; EF = 100 × SV / EDV
LV mass	(epicardial volume − cavity volume) × 1.05 g/mL, at ED
BSA	√(height cm × weight kg / 3600)
Cardiac output	SV × heart rate

Papillary muscles and trabeculations are in the blood pool and excluded from LV mass. With fewer than 6 short-axis slices, or slices more than 12 mm apart, the report notes the volumes are approximate; compare them with the biplane long-axis volumes.

6. RV analysis

The RV has its own workflow in the **RV analysis** panel, separate from Auto LV. It follows the same pattern: choose slices, contour, fix, accept, confirm coverage.

RV volumes from the short axis

1. **RV slices…**: tick the slices that contain RV cavity. Include the RV outflow tract above the LV base and apical slices where the RV still shows. Leave out slices that show only right atrium. Without a choice, Auto RV finds the RV slices itself.
2. **Auto RV** (**Ctrl+Shift+R**) contours the RV endocardium on those slices through all phases. Or use **AI contours**, which contour the RV with the LV.
3. **Review RV frames** opens the slice × phase grid for the RV; red cells need checking. Correct with **Ball RV**. **Ctrl+Z** removes a whole Auto RV run.
4. Accept the contours and tick **Coverage confirmed**, as for the LV (section 5, steps 4–5).

The panel shows RV EF, EDV, ESV, SV, the indexed values and the RV volume curve. RV ED and ES are the RV's own largest and smallest total volume. **Copy RV results** copies a text summary.

Each RV frame ends in one of four states:

State	Meaning	Counted as
Contour	RV outline drawn	Its area
RV cavity absent	No RV blood beside the septum	Zero
Manual review required	A candidate is kept for you to check	Not counted until resolved
Segmentation failed	RV blood visible, outline not reliable	Not counted until resolved

RV volumes need every chosen RV slice resolved on at least 70% of phases.

AI "RV absent" marks. Where the AI finds no RV (often the apex or base in systole), it marks the frame RV absent. An orange line under the RV EF names those slices. Click **Go to slice …**, check the frames, then **Confirm RV absence on this slice**.

Rounded candidates. A rounded RV outline is not drawn automatically; it is marked *Manual review required: rounded candidate*. If the section really is rounded (often at the base), click **Use candidate (this slice)**.

RV checks before reporting

- **Basal slice in systole**: as the tricuspid valve descends, a basal slice may show right atrium. Leave it out or correct those frames.
- **Outflow tract**: include it up to the pulmonary valve; exclude the pulmonary artery beyond it.
- **Apex**: thin, trabeculated apical cavities can be under-contoured; correct with Ball RV.

- **Stroke volumes**: RV and LV stroke volumes should be within a few mL of each other without shunt or regurgitation.

RV long-axis function (FAC, TAPSE)

1. Open **RV analysis → RV long-axis function (4CH / RV view: FAC, TAPSE)…**.
2. On an end-diastolic phase click **★ Mark tricuspid annulus + RV apex → Auto RV**, then click three points: the **septal** tricuspid hinge, the **lateral** tricuspid hinge, and the **RV apex**.
3. The points are tracked and the RV is traced on every phase. Check ED and ES; correct with **Ball RV** or **Edit**.
4. TAPSE comes from the lateral end of the ED and ES borders. A TAPSE under 5 mm is flagged: drag the lateral end onto the hinge.
5. Click **Accept RV ED / ES**.

Results: RV ED and ES area, **FAC**, **TAPSE**, tricuspid annulus diameter, RV length and RV basal diameter. Values beyond the echo reference limits (TAPSE < 17 mm, FAC < 35%, basal diameter > 41 mm) are marked "echo ref."; CMR values differ from echo.

RV volumes in this window are an area-length estimate: EDV, ESV, SV and EF. With **Height** and **Weight** (taken from the study when known), it also shows BSA and the EDV, ESV and SV indexes, plus the cardiac index when the heart rate is known. The short-axis or RV stack volumes remain the reference.

To remove a contour, right-click it, or use **Remove contour ▾**: this phase, or all phases of this view. **Undo** restores it; a locked contour stays.

RV or axial stack

If the study has a dedicated RV stack or a transaxial cine stack, open it with **RV analysis → Open the RV stack / transaxial stack for RV volumes…**. Contour the RV on its slices; Quick RV gives the volumes. Check any Auto RV proposal on an axial stack carefully, because Auto RV is designed for the short axis.

7. Long axis, strain and wall motion

These tools build on the short-axis contours from section 5, so contour the short axis first. All are research measurements; values differ between methods and vendors.

Tool	Open it from	Needs	Gives
LV long-axis (Auto LAX)	**LV long-axis** button, LV analysis menu	2CH and 4CH cines	Biplane EDV, ESV, SV, EF; MAPSE per view

Tool	Open it from	Needs	Gives
Long-axis strain	**Strain analysis → Long-axis strain…**	2CH / 3CH / 4CH cines	GLS per view and averaged; 6 segments per view
SAX strain	**Strain analysis → SAX strain**	LV endo (and epi) on all phases	GCS, GRS, strain curve
Strain dashboard	**Strain analysis → Strain dashboard…**	SAX strain and long-axis views	17-segment bullseye of LS / CS / RS, curves, apical sparing ratio, mechanical dispersion
Bullseye (17 segments)	★ **Bullseye** tab, **Wall motion / thickness (bullseye)** in Quick LV	LV endo and epi	Wall motion score, thickening, thickness at ED and ES, strain, scar per segment
Quantitative wall motion	**LV analysis → Quantitative regional wall motion…**	LV endo and epi on every phase	Thickness and thickening per segment, displacement, feature-tracking strain, suggested wall-motion class
Tagged MRI	**Strain analysis → Tagged MRI…**	SPAMM grid or line-tag series	Tissue strain, rotation, LV twist and torsion

LV long axis (Auto LAX)

1. Click **LV long-axis**. The 2CH, 3CH and 4CH cines are assigned from their names; **Assign to this view** changes them.
2. Click ★ **Auto LAX (2CH + 4CH)**. The LV is contoured on every phase of both views and cut at the mitral annulus.
3. Results appear in amber as **AUTO · not reviewed**.
4. Check every ED and ES contour, especially the mitral line. Correct with Edit or the ball; **Move apex** moves the apex point.
5. Accept the ED and ES contours and tick the review box to get the reviewed result.

MAPSE is trusted up to 20 mm; a jump of the mitral line shows "MAPSE not measurable". Hypertrophied ventricles with little bright blood are the weak point.

To remove a contour, right-click it, or use **Remove contour ▾**: this phase, or all phases of this view. **Undo** restores it; a locked contour stays.

Long-axis strain (GLS)

When the window opens, ★ **Auto strain** finds the 2CH, 3CH and 4CH cines, draws the LV border at ED and tracks it through every phase. Play each view to check the tracking and correct with Edit or redraw. To draw yourself: at ED choose **Draw**, click from one mitral annulus point around the apex to the other, press **Enter**, then **Track through all phases**.

Bullseye and wall motion score

The suggested score per segment comes from systolic thickening: ⩾ 35% normal (1), 10–35% hypokinetic (2), < 10% akinetic (3), dyskinetic (4) when the wall also moves outward.

- **Click** a segment of the wall-motion map to set your own score (cycles 1 → 4; marked •).
- **Right-click** returns it to the suggestion.
- Set segment 17 (apex) on the long-axis cines.
- **Set RV insertions**: click the anterior, then the inferior RV insertion on one slice, if the automatic septum position is wrong.

Quantitative wall motion

1. Click **Analyse wall motion**.
2. Check the tracking quality per slice; POOR or FAILED slices give no strain.
3. Per segment, accept, change, mark indeterminate or exclude the suggested class.
4. **Approve classification** writes the confirmed classes into the bullseye and the report. **Add to CMR report** adds the regional function paragraph.

8. 2D flow

Flow volumes need a **through-plane** phase-contrast series and a verified velocity calibration. An in-plane series gives peak velocity only, never flow volumes.

Measure a flow

1. Open the **Flow** menu (or the flow button in the study library) and choose the flow series. The velocity (phase) series and its magnitude series are paired automatically.
2. Check the **calibration**: VENC, velocity scaling and vessel label are read from the DICOM or the sequence name. Verify them, then tick the review boxes.
3. Outline the vessel:
    - ★ **Auto vessel** finds the vessel with the most flow and outlines it on every phase. In a pulmonary plane it can pick the aorta: check it.

- ★ **One-click vessel**: click inside the vessel on a systolic phase, then **Propagate → all phases**.
- ✥ **Move contour** drags the outline into place; tick **all phases** to move every phase.

4. Review the outline on every phase, accept it, and tick the four review boxes. ★ **Quick flow** stays amber (**AUTO · not reviewed**) until then.
5. Check the **artefact check** list (it runs after Auto vessel, or with **Check artefacts**).

Zoom: **−** / **+** zoom both images; **Zoom to vessel** centres on the outline.

Double-click an image (Navigate) to enlarge the flow window and its images; the side panel and the curve make way. Double-click again to restore.

Results

Value	Unit
Net, forward and reverse volume	mL/beat
Regurgitant fraction	%
Flow	L/min
Peak velocity (fastest pixel) and peak mean velocity	cm/s
Peak and mean pressure gradient ($4v^2$)	mmHg
Vessel area	cm^2
Qp/Qs	When the study has an aortic and a pulmonary flow

Phase contrast tends to underestimate peak velocity, so peak gradients may read low.

Artefact check

Warning	What to do
Velocity encoded in-plane	No flow volumes possible. Next time set "through plane" on the scanner (sequence name ending in "in", e.g. fl2d1_v150in)
Aliasing, or peak velocity close to VENC	Repeat with a higher VENC

Warning	What to do
VENC much too high	Velocity noise is large; use a lower VENC next time
Background phase offset	Check the static-tissue ROI; offset above 0.6 cm/s is reported with the mL/beat it adds
Vessel cut obliquely, too few pixels	Interpret with care
Signal loss at peak flow	Turbulent or stenotic jet, or a device
Heart-rate change, incomplete cycle	Arrhythmia or prospective gating; volumes may be off
No R-R interval in the DICOM	The cycle is derived from the phases; verify it, then tick **cycle verified**

Valve regurgitation (MR, TR)

On the Flow page, **Valve regurgitation profile (MV / TV)** uses the volumetric method:

Valve	Regurgitant volume	Grade by
Mitral	LV stroke volume − aortic forward flow	ACC/AHA 2020: mild < 30 mL / < 30%, moderate 30–59 mL / 30–49%, severe ≥ 60 mL / ≥ 50%
Tricuspid	RV stroke volume − pulmonary forward flow	Echo thresholds (no CMR guideline): mild < 30, moderate 30–44, severe ≥ 45, massive 60–74, torrential ≥ 75 mL

Nothing is calculated when the vessel's net flow is reversed (fix the flow direction) or when forward flow exceeds the stroke volume by more than 10 mL. A difference within 10 mL reads "no measurable regurgitation".

9. Scar / LGE and tissue mapping

Scar and mapping take their LV outline from the short-axis cine, so contour the cine LV first (section 5). Both are image-processing aids: check every slice.

LGE scar burden

1. In the study library, click the short-axis **LGE** series (PSIR or magnitude) and open ★ **Scar (LGE)** (**Scar / LGE → Scar assessment**).

2. Place the LV contours on every LGE slice, one of two ways:
    - **LV contours from cine**: the cine LV is cut by each LGE plane and shifted onto the dark, nulled myocardium.
    - **AI Endo + Epi** (also **AI Endo**, **AI Epi**): offline AI on the displayed slice. PSIR series are contoured on their paired magnitude series. The first click reads the whole stack (about 20–40 s).
3. In **Slices used for contouring and scar**, untick slices that are not useful: outside the LV, valve plane, apex cap, artefact.
4. Check each slice. A slice marked **Low-confidence contour — review required** needs a close look. Correct with **Ball endo / Ball epi**, **Edit endo / epi points**, **Redraw part** or **Draw endo / epi**. **Accept slice** marks it reviewed.
5. Choose the method and click **Detect scar**:
    - **n SD** (2, 3, 5 or 6): myocardium brighter than the remote mean + n × SD.
    - **FWHM**: brighter than half way between remote and the brightest enhancement.
6. Correct with **Paint scar** / **Erase scar** (wheel = brush size). **Ctrl+Z** undoes each stroke.

Contours on the stomach, or the AI finds no LV? Click **Select heart area** at the top of the Scar panel (or **Scar / LGE → Select heart area for AI contours**), drag round the whole heart with a small margin, then click **AI Endo + Epi** or **LV contours from cine** again. Both stay inside the area, and so does the AI when it reads the short-axis cine. **Clear area** removes it. A cine up to 20° from the LGE planes can carry the LV; beyond 12° every slice is marked for review.

Results: scar as % of LV myocardial mass, scar mass (g) and volume (mL), LV mass from the LGE slices, and a per-slice table. **Microvascular obstruction** (dark core inside the infarct) shows in blue, counts as part of the infarct and is also measured on its own. The 17-segment scar bullseye uses the classes 1–25, 26–50, 51–75 and 76–100%. Transmural extent and pattern are your assessments, kept apart from the measured area.

Whole-LV scar burden needs complete slice coverage. A slice without normal reference myocardium fails rather than reading as "no scar".

Tissue mapping (T1, T2, T2*, ECV)

1. Open *Scar / LGE → Tissue mapping (T1 / T2 / T2)…**.
2. Fill in **Patient & scan details**: rhythm, breath-hold ability, indication and haematocrit (needed for ECV).
3. Check the **Scan & protocol** tab: the acquired MOLLI scheme, heart rate and timing are read from the DICOM, with any problem flagged.

4. LV contours come from the cine (your contours, or the cine AI) and are fitted to each map. Correct with **Move contours**, **Draw endo**, **Draw epi**; low-confidence slices are dashed.
5. Click ★ **Analyse all slices** for native T1, post-contrast T1, T2 and T2*.

Results: segment table with ECV per segment, global, mid-septal and per-level values, and a bullseye.

- **Calibration**: map units need a stated or confirmed calibration; uncalibrated maps are for viewing only.
- **Reference ranges**: values are classified only against **your local reference ranges** (field strength, sequence, age). Adult ranges are not applied to children.
- **Post-contrast timing**: the post-contrast T1 nearest 15–20 minutes is used; outside 10–30 minutes it is flagged (ECV less reliable).

10. CMR report and export

CMR report builds the report from the analysis into a Word template. You review it, edit it, then **Finalize report**, which saves Word and PDF and locks it.

Make the report

1. Click **CMR report** (or **File → CMR report…**, **Ctrl+Alt+R**).
2. **Select template**: **General CMR** or **Myocardial viability**.
3. Click **Generate report from analysis**. It fills patient details, technique, measurements, findings, tissue, valves and flow, and the impression.
4. Edit the report. Every field is an editable box:
   - ↺ restores the automatic text.
   - Untick **in report** to leave a paragraph out.
   - **+ Add paragraph** adds your own finding under any heading.
   - ↺ **Patient from DICOM** restores the patient details.
5. Work through the **Review** panel on the right (it is never printed).
6. **Preview report** shows the pages; **Save Word** saves a draft.
7. **Finalize report** when no ⛔ item is left. It asks you to confirm your review, saves Word + PDF as a new final version, and locks the report. **Amend report** unlocks it; the next finalize is a new version.

Viability template: recovery per territory. Under **Diagnosis**, choose **Recovery · LAD**, **LCX** and **RCA**: not stated, high, intermediate or low. Each artery chosen adds one impression point, for example “The likelihood of recovery of function of LV myocardium in the

territories of LAD is high." The first point ends with "Based on the LV wall motion pattern, LV wall thickness and extent of myocardial scar." Not stated writes nothing.

During the free trial a report can be prepared and read on screen, but not saved.

After changing the analysis, click **Update from analysis**: it takes the new results, keeps your edits, and lists what changed. A conflict goes to Review with **Take new** / **Keep mine**.

What the report writes by itself

Item	Rule
LV / RV function grade	Lower normal EF (Kawel-Boehm 2020): LV 51% men / 52% women, RV 42% / 46%. Below it: mild, moderate (≥ 30%), severe (< 30%)
LV / RV size	EDV/BSA against sex-specific ranges: mildly dilated up to 3 SD, moderately up to 4 SD, severely beyond
Wall thickness	Normal < 12 mm; asymmetric septal hypertrophy if septum ≥ 13 mm and ≥ 1.3 × inferolateral wall; concentric LVH if basal and mid mean ≥ 12 mm
Wall motion	Only from wall motion scores (yours, or the bullseye when that option is on), never from the EF
"No LGE"	Only from your LGE assessment, never from a missing or automatic scar analysis
Empty fields	Left out, never written as normal

Unknown sex: the function grade uses the higher limit, and size is not graded. Enter sex, height and weight for correct grading.

Review panel

It lists what needs you before finalizing:

- Patient or examination mismatch.
- Results changed since the report was built.
- Conflicts between your edits and new results.
- Automatic (unreviewed) results, by name.
- Missing sex, height or weight; indexed values that do not match value ÷ BSA.
- LGE acquired but not assessed; a viability report without LGE.

Files

The final Word file is the record. PDF is made by Microsoft Word; without Word, CardioMR makes the PDF itself and the record says which.

AI draft (optional, online)

AI draft… in the report window asks Claude (Anthropic) to draft findings and impression from the de-identified results.

- **Never sent**: name, ID, dates, institution, physicians, DICOM headers, images.
- **Sent**: measurements, your choices, bullseye maps, sex, age, height, weight. Free text only when you tick it.
- **Show the complete request** displays exactly what will be sent.
- Nothing enters the report until you tick parts and click **Put the ticked parts into the report**.
- Needs your own Anthropic API key (**Save key**) and internet; each draft is billed to your account.

Export images, cine and DICOM

💾 **Save** above the image (or **File → Save images / cine / DICOM**):

Action	Saves
Save image as JPG…	The displayed image
Save all images of this slice as JPG…	Every phase of the slice
Save cine as video (MP4)…	The cine loop; plays on phones, PowerPoint, WhatsApp
Save cine as animated GIF…	The cine loop as GIF
Save as DICOM: this image / the cine of this slice…	Images with contours as a new DICOM series, for the PACS
Save as DICOM: the original images of this series…	Original files, unchanged or anonymised

Pictures use your window / level. Contours, scar and a label are optional; the patient name appears only when you tick it. Default folder: `Documents\CardioMR exports\<patient><date>`.

Copy results buttons in the LV, RV, flow and scar panels copy a text summary for pasting elsewhere.

11. Keyboard shortcuts

The shortcuts used most are **Ctrl+Shift+L** (Auto LV), **Ctrl+R** (review grid), **Ctrl+N** (next red contour), **B** (ball brush) and **Ctrl+Return** (accept).

Keys	Action	Group
Ctrl+O	Open DICOM folder	Study
Ctrl+Shift+O	Open a saved analysis	Study
Ctrl+S	Save this study's workflow	Study
Ctrl+Shift+S	Export a copy of this analysis to a file	Study
Ctrl+Alt+R	CMR report	Study
Ctrl+1 / Ctrl+2 / Ctrl+3	Editor / ED / ES review / Results	Workspace
F11	Maximize image (again to restore)	Workspace
Ctrl+Shift+L	Auto LV: all slices and phases	Contouring
Ctrl+Shift+E	Auto LV epicardium from existing LV endo	Contouring
Ctrl+Shift+R	Auto RV	Contouring
Ctrl+P	Propagate to all slices	Contouring
Ctrl+Shift+A	Refine selected short-axis outline	Contouring
Ctrl+R	Slice / phase review grid	Review
Ctrl+N / Ctrl+Shift+N	Next / previous flagged (red) contour	Review
Ctrl+J	Next unfinished measurement frame	Review
Ctrl+Return	Accept / unlock selected contour	Review
Ctrl+Z / Ctrl+Y	Undo / redo	Editing
N	Navigate tool	Tools
D	Draw contour	Tools
E	Edit contour	Tools
B	Ball brush for the selected contour	Tools
M / Shift+M	Measure distance (mm) / area (cm²)	Tools
Enter	Finish a drawn contour	Drawing

Keys	Action	Group
Backspace	Remove the last point of a drawing	Drawing
Esc	Cancel a drawing or stroke; leave a tool	Drawing
Space	Play / pause cine	Viewing
← / →	Previous / next phase	Viewing
F	Fit and auto window	Viewing
I	Invert greyscale	Viewing
O	Show / hide contours	Viewing
Ctrl+= / Ctrl+−	Zoom in / out	Viewing

Mouse: wheel = slice, Shift+wheel = phase, Ctrl+wheel = zoom, right-drag = window / level, right-click a contour = contour actions. Double-click in Navigate = enlarge / restore. With the ball brush, the wheel changes the ball size.

12. Troubleshooting

Most problems are answered by a message on screen: read the status bar, the orange or amber line under a result, or **Measurement readiness and scope** in Results.

Problem	Cause	What to do
Results show dashes (—)	Contours not yet accepted, or coverage not confirmed	Follow section 5, steps 4–5; the readiness box lists what is missing
Quick LV and Results values differ	Quick LV uses unaccepted contours	Report the Results values
Auto LV: "Slice propagation needs at least two slice locations"	The short axis was saved one series per slice	Ctrl-click the slice series and choose **Combine selected cine slices**
A short-axis cine opens as 1 slice × hundreds of images	Older version on a Philips study	Open the study again in this version
Auto LV contours the atrium or LVOT at the base	Basal slice in systole is above the valve	Untick it in **Slices…**, or mark **Outside ventricle** in those phases

Problem	Cause	What to do
Many red cells at the apex in systole	Small cavity, tangential cut	Check them; mark **No cavity here** where the cavity has gone
RV EF withheld or shown with an orange line	AI "RV absent" marks not confirmed, or RV slices not resolved	**Go to slice …**, check, then **Confirm RV absence on this slice**
Flow gives no volumes	The series is in-plane encoded	Only peak velocity is possible; acquire through-plane next time
Flow: net volume negative	Flow direction reversed	Set the forward direction in the flow window
"MAPSE not measurable"	The ES mitral line jumped	Move the mitral line onto the annulus with **Move mitral line**
AI contours missing from the menu or do nothing	AI model not installed	Install the CineMA model through the AI contours window
AI contours very slow	Runs on the processor only	Expect about 20 min for a full study on a 4-core laptop; use **ED and ES only** for speed
Saving work and reports stopped	Licence expired or missing	**Help → Licence…**; send the machine code for a new licence
Saving stopped: "program files changed"	A program file was altered or removed	Reinstall CardioMR
Windows SmartScreen blocks the program	CardioMR is not code-signed	**More info → Run anyway**, or ask IT to allow it
PDF not made	Microsoft Word not available	CardioMR makes the PDF itself; the Word file stays the record
A study's saved work does not come back	It was saved under another Study Instance UID or Patient ID	Use **File → Open analysis…** (Ctrl+Shift+O) on the saved analysis file

Contours on the stomach or another bright organ: select the heart area, remove the stray contours when asked, and run the contouring again (section 5, When contours land on another organ).

Getting help

- **Help → About CardioMR** shows the version, the data folder and the notices.
- The log and settings are in `%LOCALAPPDATA%\CardioMR\CardioMR`. Send the log with a description and a screenshot when reporting a problem.
- **Help → Workflow, methods and limitations** shows a short in-program guide. Help → User manual (F1) opens this manual.