GE Healthcare
VividClub

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Application News

GE imagination at work

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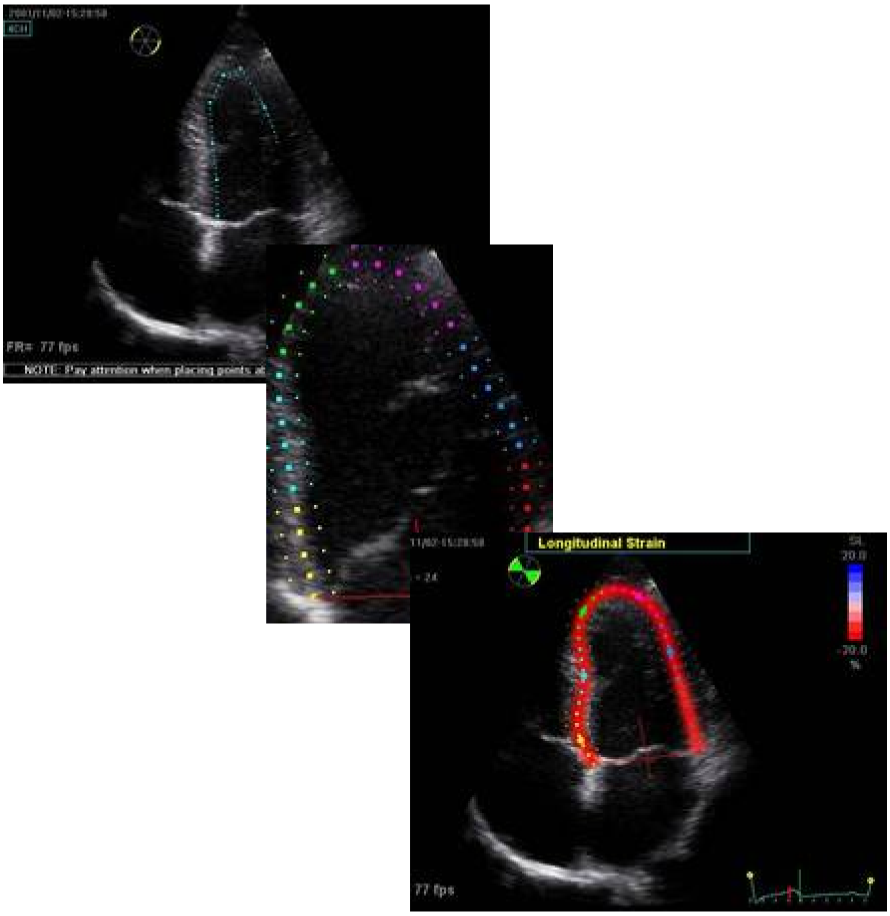
How to work with the 2D Strain Analysis package on the EchoPAC workstation



Content

NOTE

This hand out is additional training material.
For more information please refer to the user manual and/or reference manual.

Getting started

1. Create an exam
2. Connect the ECG
    a. Press Physio and change ECG Lead to get the best signal
    b. Obtain a stable ECG trace

Optimizing images

1. Sector width
    - Not too small, the myocardium must be visible during the entire cardiac cycle.
    - Not too big, this lowers the frame rate

2. Frame rate
    - Optimal between 40-90 fps
    - Optimize the frame rate with the rotary knob

3. Use the dual focus if the image quality in the apex is not acceptable
    - Check the frame rate and increase it accordingly with the rotary.

4. Store loops from all apical views
    - Apical 4 CH
    - Apical 2 CH
    - Apical LAX
    - It is recommend to acquire all three apical views sequentially in order to get comparable heart rates in all views.

Start the analysis

Press the Advanced button on the right side menu to get all options.
Then you will get the button for the Q-Analysis to click on.

On the bottom you will find the button for 2D Strain.

Define your view

A new window opens where you have to define the view you want to analyze.

Define your region of interest

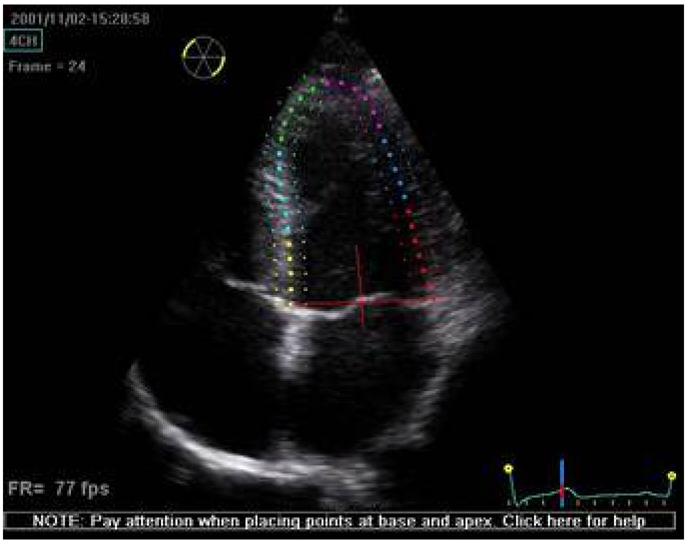
On the next screen you will get your loop focused on end-systole. It is moving a little bit back and forth (Yoyo) to better visualize the endocardial border.
The endocardial border has to be defined by the user, following the instructions on the screen where to start (i.e.4 CH view – begin on basal Septum)

NOTE: Pay attention when placing points at base and apex. Click here for help

Make a double click to define the end of the definition.
Note:
Apical views are starting from mitralvalve ring and end up at mitralvalve ring on the opposite side

Short Axis views can start everywhere but needs to be a closed circle.
For more information and examples click on the bottom of the screen on the bar with the Note.

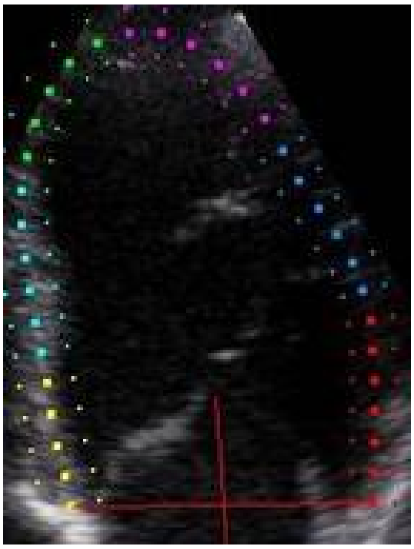
The system will detect the region of interest now automatically.



NOTE: Pay attention when placing points at base and apex. Click here for help

Verify the tracking quality

On the next screen the whole loop is analyzed.
Each wall is separated into 3 segments.



For each wall there is a scoring displayed form the system. This scoring indicates the quality of tracking.

Segment	basSept	midSept	apSept	apLat	midLat	basLat
	V	V	V	V	V	X

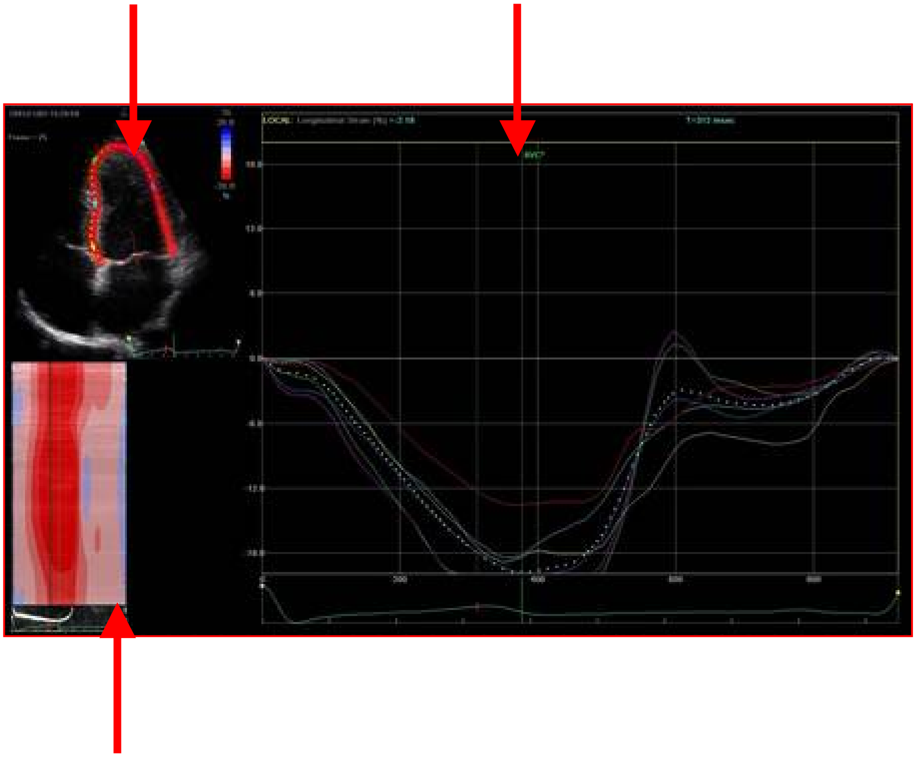
Green = good.
Red = not acceptable

You can overrule the system by clicking into the field with the V or X and change the scoring.

Once you can agree on this press approve to come to the next step.

The curves

Once approved the system will show a screen with three main components.
The analyzed loop with the color-coded parametric information.
An anatomical M-Mode that displays the color over the whole myocardium.
The curves extracted from a sample volume visible in the middle of each segment as a solid dot.



The scale for the analyzed modes is automatically set to the normal value for the respective mode.

To adjust the scale to your needs there is a slider in the middle of the menu.

The different modes

The different modes can be changed in the menu.

Depending on the view there are different possible directions and there are different modes.

Directions of analysis depending on the analysed view.

Longitudinal	all apical views
Transverse	all apical views
Circumferential	Parasternal short axis
Radial	Parasternal short axis

Analysis modes

V	velocity
SR	strain rate
S	strain
D	displacement
Rot	rotation
Rot R	rotation rate

The different screens

There are different analysis screens available:

The Trace screen

That's the first screen that comes up in the analysis.

Upper left	color-coded parametric information in the loop
Lower left	anatomical M-Mode
Right side	local trace curves

The single screen

Only the color-coded loop is displayed here.

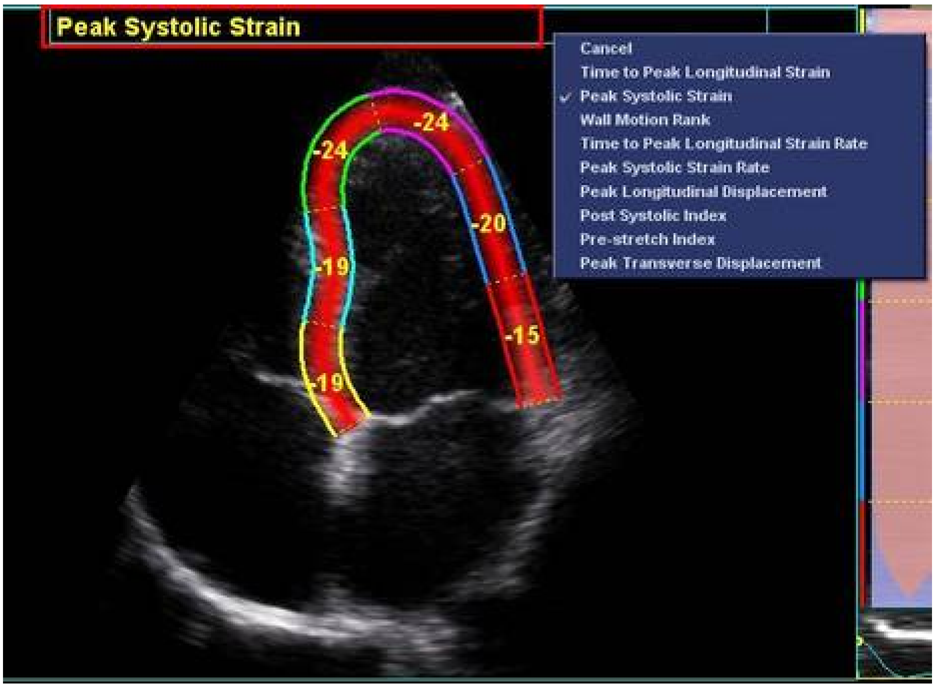
The quad screen

The quad screen is subdivided into the following portions.

Upper left	color-coded loop
Upper right	the traces
Upper right	anatomical M-Mode

Upper left	a still frame where you can change between different options

Click on the title i.e. Peak Systolic Strain. A list will open where you can make your selection.



For each segment the system detects the values and displays them with numbers inside the segment and the according color.

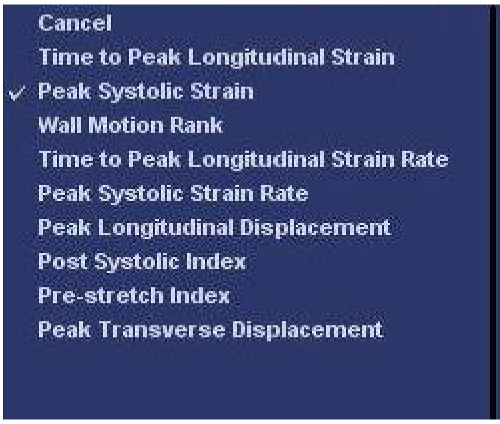
Here two example for the different options.

Peak detections:
For each segment the system is detecting the peak value doesn't matter where it is in time of the heart cycle.

Time detection:
For each segment the system is detecting the time that is needed to reach the i.e. peak longitudinal strain.

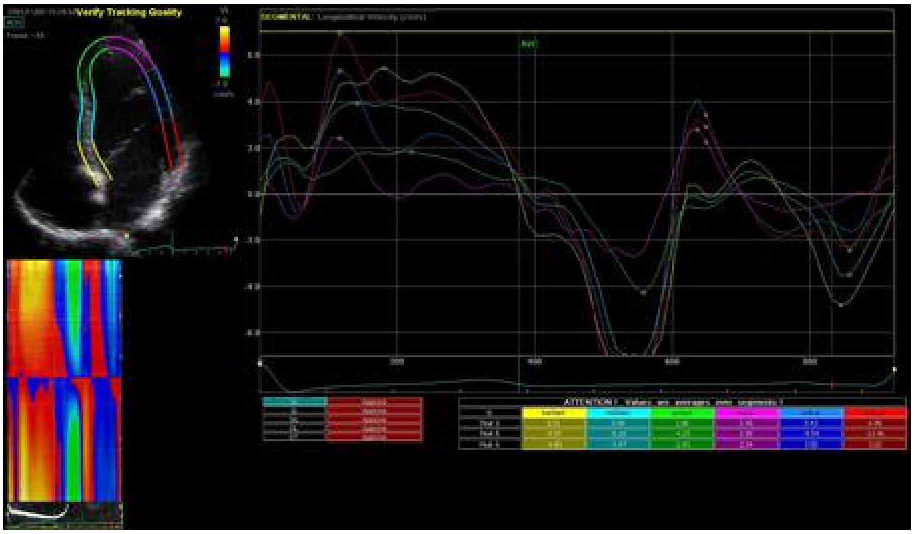
Note:
There are different modes available for apical and parasternal views.

Apical



Parasternal

The results screen



Upper left image	still frame with the ROI borders
Lower left image	anatomical M-Mode
Right side	you will see the traces for each segment that was approved with good

tracking quality in the beginning (segments with the X will be excluded here).

The table below gives some parameters with automatically detected measurements.

VL Approve
SL Approve
SrL Approve
DL Approve
DT Approve

ATTENTION ! Values are averages over segments !						
VL	basSept	midSept	apSept	apLat	midLat	basLat
Peak S	5.51	3.99	1.88	2.49	5.43	6.98
Peak E	-9.97	-8.10	-4.23	2.90	-9.54	-13.46
Peak A	-4.80	-3.47	-2.41	2.34	3.50	3.02

On the left side the different modes can be selected.
Following this nomenclature you will find the following.

Last letter direction of analysis

L = longitudinal
T = transverse
C = circumferential
R = radial

The first letters analysis mode

V = velocity
D = displacement
S = strain
Sr = strain rate
Rot = rotation

The different measurements:
Velocity Peak S = max positive velocity in systole
Peak E = detecting the peak of E-wave
Peak A = detecting the peak of A-wave
Strain Peak G = maximum negative strain in the complete heart cycle
Peak S = max. negative strain only during systole
Peak P = max positive strain value
Displacement Peak S = maximum value during systole

Adjust your measurements

It is possible to change the automatically detected measurement points in the result screen. Click on the point to change and move it to the desired position.
With the next click the measurement point is set and the new values are entered in the table.

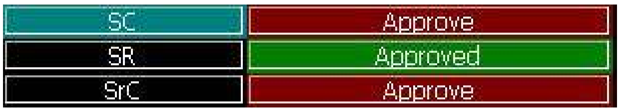
Exporting your data

There are different possibilities to store the analyzed data.
In the trace screen you have four options to store the data

By pressing one of the options the data will be stored first on the hard drive of the computer.

Snapshot	complete image of the analysis screen – still frame (JPG)
Store AVI	the loop will be stored as running movie (AVI)
Store Trace	all curve details are stored in a text file and can be used for further statistical analysis (TXT)
Store Full	all curve details are stored in a type of excel format (CSV)

In the result screen a still frame of each curve analyze can be stored by pressing the approval button behind each of the parameters.



Every time you choose one of these options a new window will appear where you can add a name to your file and then store it.


d:\echopac_pc\archive\export\2ds\2007_04_24

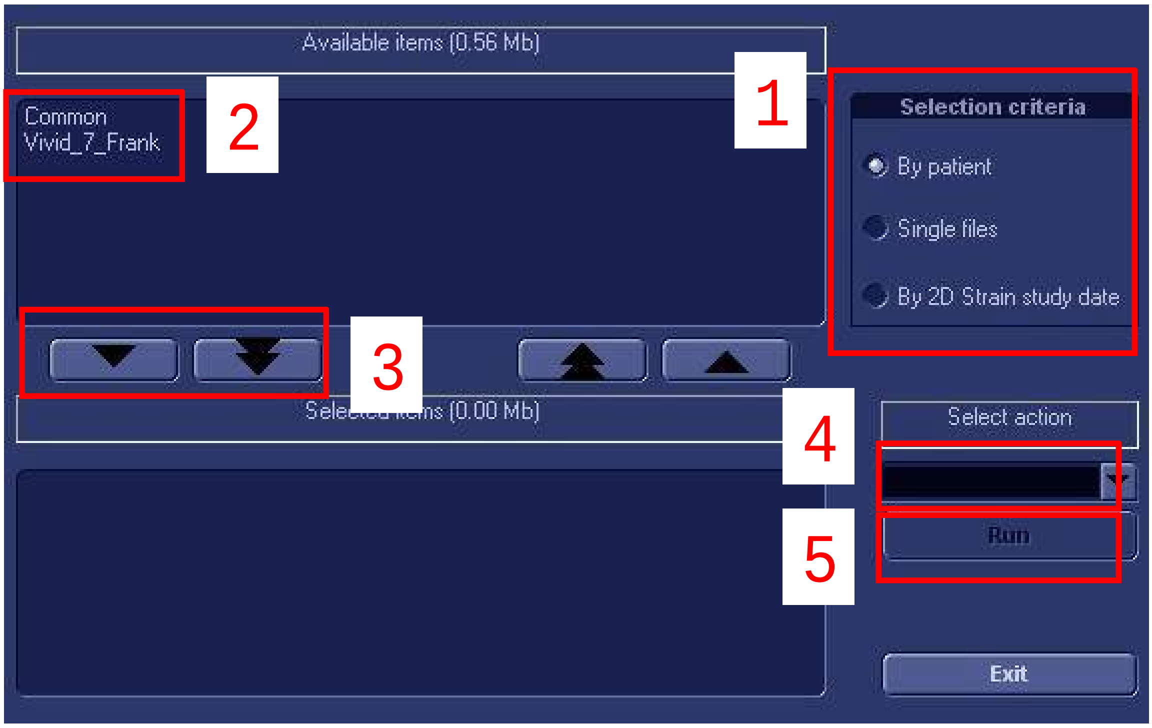
2ds61_vivid_7_frank_vivid_7_02_11_2001_sax-mv_sc_se TEST

File type JPG

Together with the image also a .CSV file is stored. This file contains the measurement results.

Once you have finished all your storage you might want to copy it to a removable media.
You can either use a CD/DVD (needs to be formatted before) or an USB memory stick.
To move the data from the hard drive to your media press the Files button.

A new window opens where are different actions to take.



Selection criteria: ● By patient ○ Single files ○ By 2D Strain study date

Step 1	Select the type of sort you want to have your files displayed in the window: *By patient* (all related files to this patient are included) *Single files* (every file will be displayed separately) *By 2D strain study date* (sort by the date of your analysis)
Step 2	Select the files you want to copy from the list
Step 3	Press the arrow keys to move the files into the lower part
Step 4	Select the place where you want to copy your data to
Step 5	Press Run to start the copy operation

Exit the analysis

Press the exit button to leave the 2D Strain analysis tool.

The system will ask you if you want to store the data.

Do you want to store the loop?

If you press yes, the system will remember your settings.

Take the loop back from the clipboard – Q-Analysis – 2D Strain. The system will run through the whole processing until the approval image. The only thing to do is to check and approve the settings.