

CytoSolver 3.0 (CS 3.0)

FAQ: Edge Detection of 3D Culture

Frequently asked question related to the rejection of 3D culture Edge Detection data.

Why does CytoSolver 3.0 reject most/all edge detection transients from 3D cultures?

CytoSolver default criteria settings are defined using primary cardiomyocytes as the reference. However, when assessing contractility using edge detection on 3D cultures, such as organoids and spheroids, there may be instances where default criteria settings will reject all traces.

In such situations, the recommended approach is to deactivate all criteria settings in the edge detection tab. To do this, follow the stepwise guide beginning below:

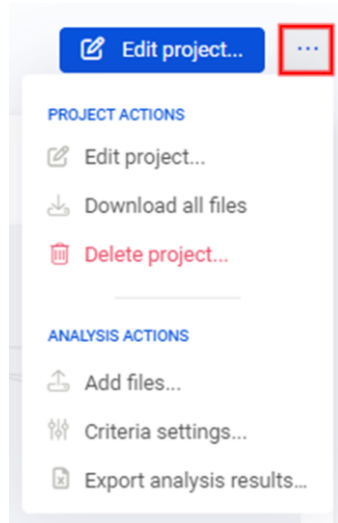
Steps:

1. Create a project.
2. Navigate to Overview page within that project.

Steps (cont.):

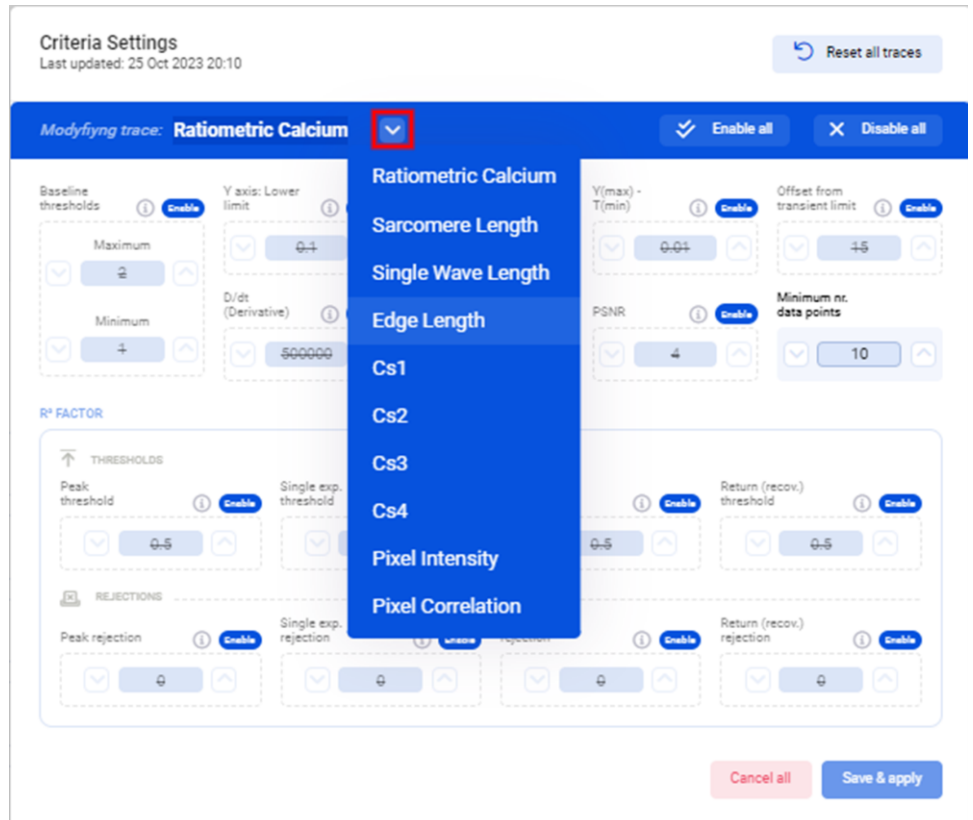
3. On the right side of the user interface, you will find three dots adjacent to the "Edit Project" option. Click on these dots, and you will see criteria settings under analysis actions (see Fig. 1.)

Figure 1: Edit project criteria selection.



4. Click on the "Criteria Settings" option; it will open the Ratiometric Calcium settings by default.
5. From there, navigate to the "Edge Length" setting using the arrow (see Fig. 2.)

Figure 2: Selecting Edge Length.



Steps (cont.):

3. Disable all > save and apply (see Fig. 3.).

Figure 3: Disabling all criteria settings within the Edge Length dialogue window.

The screenshot shows the 'Criteria Settings' dialog box for 'Edge Length'. The title bar indicates 'Modifying trace: Edge Length' and includes 'Enable all' and 'Disable all' buttons. The 'Disable all' button is highlighted with a red box. The dialog is divided into several sections:

- Baseline thresholds:** Includes 'Maximum' (set to 2) and 'Minimum' (set to 4).
- Y axis: Lower limit:** Set to 0.1.
- Y axis: Upper limit:** Set to 1000.1.
- Y(max) - T(min):** Set to 0.01.
- Offset from transient limit:** Set to 15.
- D/dt (Derivative):** Set to 5000.
- 2nd D/dt (Derivative):** Set to 5000.
- PSNR:** Set to 4.
- Minimum nr. data points:** Set to 50.

The **R² FACTOR** section is expanded to show:

- THRESHOLDS:**
 - Peak threshold: 0.85
 - Single exp. threshold: 0.85
 - Double exp. threshold: 0.85
 - Return (recov.) threshold: 0.85
- REJECTIONS:**
 - Peak rejection: 0.5
 - Single exp. rejection: 0.75
 - Double exp. rejection: 0.75
 - Return (recov.) rejection: 0.5

At the bottom right, there are 'Cancel all' and 'Save & apply' buttons. The 'Save & apply' button is highlighted with a red box.

4. Reanalyze your data files.



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