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## Displacement analysis of myocardial mechanical deformation (DIAMOND) reveals segmental heterogeneity of cardiac function in embryonic zebrafish

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Kyle Jewhurst, PhD  
Science Editor, *Journal of Visualized Experiments (JoVE)*

**Re: Displacement analysis of myocardial mechanical deformation (DIAMOND) reveals segmental heterogeneity of cardiac function in embryonic zebrafish (JoVE60547)**

Dear Dr. Jewhurst, JoVE editors and reviewers,

Thank you for offering us the opportunity to re-submit the above captioned manuscript for consideration in *JoVE*. We have responded to all the points raised by the editor and reviewers in a point-by-point manner. This manuscript expands on a novel technique we recently reported [Chen J. *et al.*; *JCI Insight* 2019 Apr 18;4(8)] for the measurement of segmental cardiac mechanics in zebrafish in a high-throughput manner.

Thank you for your consideration.

Sincerely,

A handwritten signature in black ink, appearing to read "René R. Sevag Packard", written over a horizontal line.

René R. Sevag Packard

**TITLE:**

**Displacement Analysis of Myocardial Mechanical Deformation (DIAMOND) Reveals Segmental Heterogeneity of Cardiac Function in Embryonic Zebrafish**

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**KEYWORDS:**

cardiac function, displacement, chemotherapy, injury, regeneration, zebrafish

**SUMMARY:**

The goal of this protocol is to detail a novel method for the assessment of segmental cardiac function in embryonic zebrafish under both physiological and pathological conditions.

**ABSTRACT:**

Zebrafish are increasingly utilized as a model organism for cardiomyopathies and regeneration. Current methods evaluating cardiac function fail to reliably detect segmental mechanics and are not readily feasible in zebrafish. Here we present a semiautomated, open-source method for the quantitative assessment of four-dimensional (4D) segmental cardiac function: displacement analysis of myocardial mechanical deformation (DIAMOND). Transgenic embryonic zebrafish were imaged in vivo using a light-sheet fluorescence microscopy system with 4D cardiac motion synchronization. Acquired 3D digital hearts were reconstructed at end-systole and end-diastole, and the ventricle was manually segmented into binary datasets. Then, the heart was reoriented and isotropically resampled along the true short axis, and the ventricle was evenly divided into eight portions (I–VIII) along the short axis. Due to the different resampling planes and matrices at end-systole and end-diastole, a transformation matrix was applied for image registration to restore the original spatial relationship between the resampled systolic and diastolic image matrices. After image registration, the displacement vector of each segment from end-systole to end-diastole was calculated based on the displacement of mass centroids in three dimensions (3D). DIAMOND shows that basal myocardial segments adjacent to the atrioventricular canal undergo the highest mechanical deformation and are the most susceptible to doxorubicin-

induced cardiac injury. Overall, DIAMOND provides novel insights into segmental cardiac mechanics in zebrafish embryos beyond traditional ejection fraction (EF) under both physiological and pathological conditions.

## INTRODUCTION:

Chemotherapy-induced cardiac toxicity and ensuing heart failure are one of the main reasons for chemotherapy discontinuation<sup>1</sup>. Therefore, cardiac functional assessment plays a crucial role in the identification of cardiac toxicity and, more importantly, in the prediction of early cardiac injury following chemotherapy<sup>2</sup>. However, current approaches for cardiac functional assessment encounter limitations. Methods such as left ventricular ejection fraction (LVEF) provide only global and often delayed cardiac mechanics after injury<sup>3,4</sup>. Tissue Doppler imaging provides segmental myocardial deformation information but suffers from significant intraobserver and interobserver variability, in part due to ultrasound beam angle dependency<sup>5</sup>. Two-dimensional (2D) speckle tracking utilizes the B-mode of echocardiography, which theoretically eliminates the angle dependency, but its accuracy is limited by out-of-plane motion<sup>6</sup>. Therefore, a rigorous approach for quantifying segmental cardiac function is lacking in both research and clinical settings.

In this context, we developed a 4D quantification method for the analysis of segmental cardiac function that we named displacement analysis of myocardial mechanical deformation (DIAMOND), to determine the displacement vectors of myocardial mass centroids in 3D space. We applied DIAMOND for the in vivo assessment of cardiac function and doxorubicin-induced cardiac toxicity with zebrafish (*Danio rerio*) as the animal model, chosen due to their regenerating myocardium and highly conserved developmental genes<sup>7</sup>. We further compared segmental DIAMOND displacement with global ejection fraction (EF) determination and 2D strain following doxorubicin treatment. By integrating DIAMOND displacement with 4D light-sheet fluorescent microscopy (LSFM) acquired rendering of embryonic zebrafish hearts, DIAMOND shows that the basal myocardial segments adjacent to the atrioventricular canal undergo the highest mechanical deformation and are the most susceptible to acute doxorubicin cardiac injury<sup>8</sup>.

## PROTOCOL:

All methods described here have been approved by the UCLA Institutional Animal Care and Use Committee (IACUC), and experiments were performed in compliance with protocols approved by the UCLA Office of Animal Research.

### 1. Breeding *Tg(cmlc2:mCherry)* zebrafish and collection of embryos

1.1. Follow the housing, breeding, and embryo collection procedures as described in previously established husbandry and breeding practices. For details, see Messerschmidt et al.<sup>9</sup>.

1.2. Treat the collected embryos with 0.003% 1-phenyl-2-thiourea (PTU) in E3 medium 18 h postfertilization to maintain the transparency of the embryos for LSFM imaging.

## 2. Doxorubicin treatment to induce cardiac injury

2.1. At 3 days postfertilization (dpf), treat the embryos with doxorubicin at a concentration of 10  $\mu$ M in E3 fish water medium. After a 24 h treatment to 4 dpf, replace the doxorubicin medium with fresh E3 medium.

CAUTION: Doxorubicin is a chemotherapy medication. Appropriate personal protective equipment (PPE) is required and the waste should be disposed of in biohazard waste containers.

## 3. Notch pathway modulation

3.1. Treat zebrafish embryos with the Notch pathway inhibitor (2S)-N-[(3,5-difluorophenyl)acetyl]-L-alanyl-2-phenylglycine 1,1-dimethylethyl ester (DAPT) at a concentration of 10  $\mu$ M in E3 fish water medium from 3–6 dpf.

3.2. Microinject the Notch downstream effectors *Notch intracellular domain (NICD)* and *Neuregulin-1 (Nrg-1)* mRNA at concentrations of 10 pg/nL and 5 pg/nL, respectively, into the 1-cell stage zebrafish embryos<sup>8,10</sup>.

NOTE: The microinjection is performed under a microscope with the support of an air pump to accurately control the volume injected. The mRNA microinjection into the cell is done when the fertilized egg is at the first cell stage. For details on the preparation and sequence of the mRNAs, see Chen et al.<sup>8</sup>. For details on the microinjection and preparation of injection needles, see Rosen et al.<sup>10</sup>.

## 4. LSFM imaging and post-imaging synchronization

4.1. For the LSFM imaging techniques and post-imaging synchronization algorithm, see details in previous publications<sup>9,11</sup>.

NOTE: Briefly, our system utilizes a continuous-wave laser as the illumination source to image all transgenic zebrafish lines. The detection module is composed of two scientific complementary metal-oxide semiconductor (sCMOS) cameras and two sets of filters for dual-channel imaging. The detection module is perpendicularly installed to the illumination plane. Each LSFM frame is acquired within a 20 msec exposure time, while the resolving power in cross section is  $\sim 0.65 \mu$ m and the step size between consecutive frames is  $\sim 2 \mu$ m. A 589 nm laser was used to excite mCherry fluorescent signals.

## 5. Reconstruction of the 3D systolic and diastolic heart

5.1. Open the folder created by the post synchronization algorithm, then open the "Output" folder. Select the middle plane of the heart and load the entire folder into ImageJ. Find the first diastolic and systolic phase and record the frame number.

5.2. Open the "Output/By State" folder and find the folders that have the same numbers as the frame numbers just recorded. Convert the images in the folder into 3D TIFF (tagged image file format) files and name them "diastole.tif" and "systole.tif".

## 6. Segmentation of the ventricle

6.1. Open the image analyzing software (see **Table of Materials**). Click **File | Open data**, and load "diastole.tif" and "systole.tif". Enter the voxel size according to the imaging settings.

NOTE: For the LSM system used, the typical voxel size is  $0.65\ \mu\text{m} \times 0.65\ \mu\text{m} \times 2\ \mu\text{m}$ .

6.2. Click the "**SEGMENTATION**" panel and manually segment out the ventricle part of the heart. The built-in "**Threshold**" tool that can select all the regions above a certain intensity can facilitate this process. The ventricle is the thicker chamber with a stronger fluorescence.

NOTE: Make sure to remove the atrioventricular canal and the outflow tract in the segmented ventricle, because this affects the displacement analysis.

6.3. After the segmentation is done, click the "**Project**" panel. Right click the "**diastole.Labels.tif**" and "**systole.Labels.tif**" tabs in the console and click "**Export Data as**" to save the data as 3D TIFF files.

## 7. Creation of rectangular parallelepipeds for image registration

7.1. Run "**preplImage\_1.m**" in the programming environment (see **Table of Materials**). Open "**preplImage\_1.m**", "**ImPath**" in line 5 so the folder contains the original and segmented TIFF files, and change "**slice**" in line 4 to the number of slices of the 3D tif files.

7.2. After running the code, it will generate five new 3D TIFF files ("test.tif", "diastole\_200.tif", "systole\_200.tif", "diaLabel.tif", and "sysLabel200.tif") as well as two new folders ("resample\_dia" and "resample\_sys").

## 8. Resample systolic and diastolic 3D hearts along the short axis plane

8.1. Import all five 3D TIFF files into the image analyzing software (see **Table of Materials**).

NOTE: The voxel size is unchanged.

8.2. Go to the **MULTIPLANAR** panel. Choose "diastole\_200.tif" as the primary data. Align the X-axis (the green line in the XY plane) with the vertical long axis of the ventricle, and align the Z-axis (the red line in the YZ plane) with the horizontal long axis of the ventricle.

NOTE: The vertical long axis is determined by finding the longest axis connecting the apex and the outflow tract in the XY plane, and the horizontal long axis is determined by finding the longest

axis connecting the apex and the outflow tract in the YZ plane. Rotate the axis by placing the cursor at the end of the axis.

8.3. Choose three random points from the oblique YZ plane (the short axis plane) in a counterclockwise manner and record their 3D position coordinates.

NOTE: Make sure the points are chosen in a counterclockwise manner.

8.4. Repeat steps 8.2 and 8.3 for "systole\_200.tif".

8.5. Click the "**PROJECT**" panel. Create a "**Slice**" object for "diastole\_200.tif" by right clicking on "diastole\_200.tif" and searching for "**Slice**" object. Left click the Slice object just created, and in the **Properties panel | Options**, check "**Set Plane**" and choose three points in "**Plane Definition**". Enter the coordinates of the three points from step 7.3.

8.6. Repeat step 8.5 for "systole\_200.tif".

NOTE: The slice object created should have the name "**Slice 2**".

8.7. Right click "diastole\_200.tif" and search for "**Resample Transformed Image**" and create the object. In the **Properties** panel, choose "**Slice**" as the "**Reference**" and click **Apply**. This should generate an object named "**diastole\_200.transformed**".

8.8. Right click "**diastole\_200.transformed**" and search for "**Resample**" and create the object. Choose "**Voxel Size**" as the "**Mode**" and change "**Voxel Size**" to be  $x = 1$ ,  $y = 1$ , and  $z = 1$  in the **Properties** panel.

8.9. Click "**Apply**". This should generate an object named "**diastole\_200.resampled**". Right click "diastole\_200.resampled" and save it as a 3D TIFF file.

8.10. Repeat the same step for "diaLabel.tif" and "test.tif". Save "diaLabel.resampled" and "test.resampled" as 3D TIFF files. Repeat the same step for "systole\_200.tif", "sysLabel.tif", and "test.tif" using "**Slice 2**" as a reference, and save "systole\_200.resampled", "sysLable.resampled", and "test2.resampled" as 3D TIFF files.

NOTE: Make sure there are a total of six TIFF files saved in this step.

## 9. Division of the resampled heart

9.1. Import all six resampled files from step 8 to ImageJ. Select a slice of "systole\_200.resampled" in which the atrioventricular canal is clearly visualized. Record the number of the slice.

9.1.1. Use the "**Image | Transform | Rotate**" function of ImageJ so that the atrioventricular canal is vertical. Apply the same rotation to all files. Close all windows and save all changes.

9.1.2. Move "diastole\_200.resampled", "diaLabel.resampled", and "test.resampled" to the "resample\_dia" folder, and move "systole\_200.resampled", "sysLable.resampled", and "test2.resampled" to the "resample\_sys" folder.

9.2. Open "divider\_2\_8\_pieces.m". Change "ImPath" in line 5 and "ImPath" in line 395 to the image directory. Change the variable "Middle" in line 22 and line 411 to the slice numbers where the atrioventricular canal is clearly visualized in "systole\_200.resampled" and "diastole\_200.resampled".

9.3. Run the code, and in the prompted windows click once at the center of the ventricle and click once at the center of the atrioventricular canal. This needs to be done twice for both systole and diastole images.

## 10. Registration of systolic and diastolic image matrices

10.1. Open "register\_3.m" and change "ImPath" in line 4 to the image folder path. It might take 5–20 min to run this code depending on the computation power of the system.

NOTE: The artificially created rectangular parallelepipeds in step 7 are used for 3D rigid registration that preserves the distance between two points and angles subscribed by three points. When the end-diastole rectangular parallelepiped (red) is registered to the end-systole rectangular parallelepiped (green), the ensuing discrepant 3D location permits the derivation of a unique matrix of rigid transformation consisting of rotation and translation from the end-diastole matrix to the end-systole matrix (**Figure 1H**). We perform the registration and regularized energy minimization to denoise the matrix after the transformation using an image processing toolbox (see **Table of Materials**). For a detailed mathematical description, please see Chen et al.<sup>8</sup>.

## 11. Output of the displacement vectors

11.1. Open "displacement\_4.m" and change "ImPath" in line 4 to the image folder path.

11.2. Run "displacement\_4.m", which generates a "vector8.txt" file in the "vectors" folder. Once the "vector8.txt" file is open, there will be an 8 x 4 matrix. Each row of the matrix has four numbers, which are the magnitudes of the X component, Y component, Z component, and the SUM magnitude of the displacement vector of a specific segment of the ventricle.

NOTE: The displacement vector is obtained by calculating the displacement of the mass centroid of each segment in 3D space. We calculate the 3D mass centroid ( $P_S$  and  $P_D$ ) coordinates  $\bar{P}_k$  (where k indicates the X, Y, or Z coordinate, respectively) of each segment (I-VI) in the segmentation dataset from systole to diastole (**Figure 1J**). We define the mass centroid  $\bar{P}_k$  in 3D space as follows:



$$\bar{C}_k = \frac{1}{M_i} \sum_{j=1}^m C_{kj} \rho(x_j, y_j, z_j)$$

where  $C_x = X$ ,  $C_y = Y$ , and  $C_z = Z$ ,  $M_i$  = the mass of each segment ( $1 \leq i \leq VI$ ),  $m$  = the number of voxels of each segment, and  $\rho$  = the density function as the segmented region is 1 whereas the rest is 0. The L2-norm of the sub-displacement vectors along the X-, Y-, and Z-axes and the sum displacement vector are calculated during the cardiac cycle. There are a total of eight rows in the matrix. The first row and the eighth row contain the atrioventricular canal and are thus ignored in our analysis. Segments I to VI are represented by the second row to the seventh row.

### REPRESENTATIVE RESULTS:

The process by which DIAMOND was developed to assess 3D segmental cardiac function is presented in **Figure 1**. Following LSM image acquisition and reconstruction in 3D of the embryonic zebrafish heart (**Figure 1A**), the true short axis plane was determined as the plane perpendicular to the vertical and horizontal long axes, both of which are determined in a multiplane viewer (**Figure 1B**). The heart was then resampled along the short axis plane (**Figure 1C**), and divided into eight equal segments constituted by even angles according to a virtual division line (red dotted line) connecting the center of the endocardial ventricular cavity to the center of the atrioventricular canal (**Figure 1E**). The 3D depictions of the identified segments are illustrated in a cross-sectional view (**Figure 1F**) and in comparison with the raw data (**Figure 2**). Segments VII and VIII were removed from the analysis because they encompass the atrioventricular canal and thus contain less myocardium compared with other segments. The different resampling planes for end-systole ( $H_s$ ) and end-diastole ( $H_D$ ) lead to distinct coordinate systems for end-systolic and end-diastolic matrixes, which need to be registered to restore their original spatial relationship (**Figure 1G**). The coordinate system of the end-systolic matrix was chosen as the reference for consistency. To determine the transformation matrix ( $T_m$ ) from the end-diastolic matrix to the end-systolic matrix, a matrix of three parallelepipeds, which is asymmetrical in 3D and has the same dimension as the original image matrix, was virtually created. The parallelepipeds were resampled twice, first in the short axis plane of the end-systole matrix, and then in the short axis plane of the end-diastole matrix, leading to different transformed parallelepipeds for end-systole (green) and end-diastole (red) (**Figure 1H**).

The green and red parallelepipeds were then registered together by a rigid body registration algorithm and  $T_m$  was calculated and applied to the end-diastole matrix to restore the coordinates (**Figure 1I**). This process permits subsequent tracking in the 3D space of the displacement vectors of mass centroids from any segment of the ventricle during the cardiac cycle (**Figure 1J**). DIAMOND displacement of ventricular segments I–VI can be tracked during multiple time points in the cardiac cycle (**Figure 1K**), which can be simplified for quantitative analysis to two time points ranging from end-systole to end-diastole (**Figure 1L**). The segments generated by DIAMOND can be visualized in **Figure 2**, where each color represent one cardiac segment.

With DIAMOND, we uncovered segmental heterogeneity of cardiac function and susceptibility to

doxorubicin-induced myocardial injury in zebrafish. Following a 24 h treatment with 10  $\mu$ M doxorubicin from 3–4 dpf (**Figure 3A**), we compared DIAMOND displacement of ventricular segments between control and chemotherapy-treated groups (**Figure 3B**) and 48 h after treatment (**Figure 3C**). All DIAMOND figures follow the same graphical pattern as the resampled ventricles along the short axis (**Figure 1E**). The data are presented as percentages by normalizing the L2-norm of the displacement vector to the inner perimeter of the heart, with the X (green), Y (blue), and Z components (orange) illustrated as their weighted contributions. At 4 dpf, the average L2-norm of the segmental displacement vectors in control fish ranged from 6.6–11.3  $\mu$ m, or 3.8–6.6% after normalization. Our results indicate that under control conditions, the basal segments I and VI undergo the largest displacements and are the ones most susceptible to doxorubicin induced cardiac injury (**Figure 3B**, 29% decrease from 6.6–4.7%,  $n = 10$  control and  $n = 8$  doxorubicin,  $p < 0.01$ ). At 6 dpf, the average L2-norm of the segmental displacement vectors in the control fish ranged from 6.8–14  $\mu$ m, or 3.9–8% after normalization. At 6 dpf, the basal segments I and VI recovered DIAMOND displacement to control levels, suggesting segmental regeneration (**Figure 3C**,  $n = 10$  control and  $n = 8$  doxorubicin). In parallel, a worsening in 2D basal strain from -53 to -38% was observed at 4 dpf following doxorubicin treatment, followed by a return to control levels at 6 dpf, corroborating the DIAMOND displacement results (**Figure 3D**, **3E**). A parallel decrease in global ejection fraction in response to doxorubicin at 4 dpf with recovery at 6 dpf was also observed (**Figure 3F**, **3G**).

We next applied DIAMOND during doxorubicin treatment and Notch pathway modulation using the Notch inhibitor DAPT and rescue using Notch downstream effectors *NICD* and *NRG1* mRNA (**Figure 4A**). *NICD* and *NRG1* mRNA microinjection rescued the decrease in DIAMOND displacement and EF after acute chemotherapy-induced injury at 4 dpf (**Figure 4B**, **4D**). Exposure to the Notch inhibitor DAPT together with doxorubicin led to a more diffuse decrease in DIAMOND displacement, in addition to the basal segments I and VI (**Figure 4B**). Moreover, inhibition of the Notch pathway after chemo-induced injury further hindered the recovery of DIAMOND displacement of the basal segments and EF at 6 dpf. The inhibition was rescued by the Notch downstream effectors *NICD* and *NRG1* (**Figure 4C**, **4E**).

#### FIGURE AND TABLE LEGENDS:

**Figure 1: 4D DIAMOND displacement development.** (A) Raw images were captured by light-sheet fluorescent microscopy. (B and C) Reconstructed 3D heart was resampled along the true short axis plane view. (D) Schematic illustration of embryonic zebrafish heart. (E and F) 2D and 3D illustrations of the division of the ventricle into eight segments excluding segments VII and VIII. (G) The different coordinate systems of end-systole and end-diastole after resampling. (H) A group of rectangular parallelepipeds was created for the generation of a transformation matrix ( $T_m$ ). (I) Registered end-systolic and end-diastolic coordinate systems by applying  $T_m$ . (J) Displacement vector of the segmental mass centroid from end-systole to end-diastole. (K) DIAMOND displacement of ventricular segments I–VI tracked during multiple time points in the cardiac cycle. (L) DIAMOND displacement of ventricular segments I–VI from end-systole to end-diastole. This figure from Chen et al.<sup>8</sup> is reproduced with permission from the American Society for Clinical Investigation (ASCI).

**Figure 2: DIAMOND segmentation of the embryonic zebrafish heart compared with raw data in 3D.** The embryonic zebrafish heart was divided into six segments (volumes) depicted here in different colors for the calculation of DIAMOND displacements (left). The displacement vector of each segment computed by DIAMOND represents its segmental cardiac function. The atrium and outflow tract were removed during segmentation. Scale bar = 50  $\mu$ m.

**Figure 3: DIAMOND unravels the segmental heterogeneity in cardiac function and susceptibility to chemotherapy-induced injury.** (A) Experimental schedule of doxorubicin treatment. (B and C) Segmental comparison of DIAMOND displacement vectors normalized to the inner myocardial perimeter between control and doxorubicin-treated groups at 4 and 6 dpf (t tests,  $**p < 0.01$ ,  $n = 8-10$  per group). (D and E) Assessment of strain in the ventricular base depicting a similar injury and regeneration pattern as the DIAMOND displacement vectors ( $*p < 0.05$ ,  $n = 6-8$  per group). (F and G) Decrease in ejection fraction in response to doxorubicin at 4 dpf with recovery at 6 dpf, following a pattern similar to segmental DIAMOND displacements at the global ventricular level (t tests,  $**p < 0.01$ , error bars SEM,  $n = 6-10$  per group). This figure from Chen et al.<sup>8</sup> is reproduced with permission from the ASCI.

**Figure 4: DIAMOND mechanics for assessment of Notch-mediated myocardial recovery following doxorubicin-induced injury.** (A) Experimental schedule. (B and C) *NICD* and *NRG1* Notch downstream effectors rescued the reduction of DIAMOND displacement in segments I and VI at 4 dpf. At 6 dpf, inhibition of Notch signaling by DAPT impaired the restoration of segmental cardiac function (ANOVA,  $**p < 0.01$  Dox vs. control;  $\dagger p < 0.05$ ,  $\dagger\dagger p < 0.01$ , Dox + DAPT vs. control,  $n = 6-10$  per group). (D and E) Ejection fraction corroborates DIAMOND mechanics at the global level (ANOVA,  $*p < 0.05$ ,  $**p < 0.01$ , error bars SEM,  $n = 5-11$  per group). This figure from Chen et al.<sup>8</sup> is reproduced with permission from the ASCI.

## DISCUSSION:

A rigorous strategy for quantification of segmental myocardial function is critical to assess cardiac mechanics beyond traditional EF, known to be an insensitive and delayed indicator of myocardial injury<sup>1,4,12</sup>. Hence, there has been a growing interest in markers of early myocardial changes, and a growing body of literature supports myocardial deformation parameters as an early indicator to forecast ventricular dysfunction<sup>4,13</sup>. Echocardiographic measurement of left ventricular (LV) strain provides an established method of myocardial deformation measurement<sup>13</sup>. However, tissue Doppler-based strain imaging suffers from a number of shortcomings due to angle dependency and intraobserver and interobserver variability<sup>14</sup>. Speckle tracking echocardiography (STE) can resolve angle-independent 2D and 3D tissue deformation, but the accuracy of 2D speckle tracking is affected by through-plane motion<sup>6</sup>, while 3D speckle tracking requires superior spatial resolution to resolve the positive ultrasound interference patterns (speckles) in 3D and high temporal resolution to track the speckles between frames<sup>15</sup>. In the present protocol, we describe DIAMOND displacement as a novel myocardial deformation parameter for in vivo quantification of 4D segmental cardiac function in zebrafish. Compared with EF and 2D strain as reference standards, DIAMOND provides additional segmental deformation information without being affected by through-plane motion. By integrating DIAMOND with 4D LSM, our technique can assess the displacement vector of a heart segment

20–30  $\mu\text{m}$  in width, which is currently impossible for even the most advanced 3D STE system, which has millimeter-range resolution<sup>16</sup>.

To apply DIAMOND, it is critical to have a comprehensive understanding of the anatomical structure of the embryonic zebrafish heart. During image segmentation, it is essential that the atrioventricular canal and the outflow tract are correctly identified and segmented out from the rest of the myocardium when the user is performing step 6 in the protocol. Furthermore, the horizontal and the vertical long axes of the ventricle must be accurately determined in order to derive the true short axis plane for image resampling in step 8.

The major rate limiting factor of applying DIAMOND is the manual segmentation of the ventricle, which becomes time-consuming when multiple phases during the cardiac cycle may need to be evaluated. With the advancement of machine learning and neural networks, an automated cardiac segmentation method<sup>17,18,19,20</sup> could be integrated with DIAMOND to provide monitoring of segmental cardiac function throughout the entire cardiac cycle. Further applications of DIAMOND also include the integration with echocardiography, micro-CT, or micro-MRI, suitable in larger animal models for the multiscale assessment of cardiac injury and regeneration<sup>21</sup>. However, the method will first require adaptation to the presence of myocardial fibers leading to more complex cardiac deformation including torsion in mammals<sup>22,23</sup>.

Overall, DIAMOND provides a novel method to evaluate segmental cardiac function in embryonic zebrafish under both physiological and pathological conditions and may be used as a platform for high-throughput in vivo screening of pathways associated with chemotherapy-induced cardiac toxicity.

#### ACKNOWLEDGMENTS:

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#### DISCLOSURES:

The authors have declared that no conflict of interest exists.

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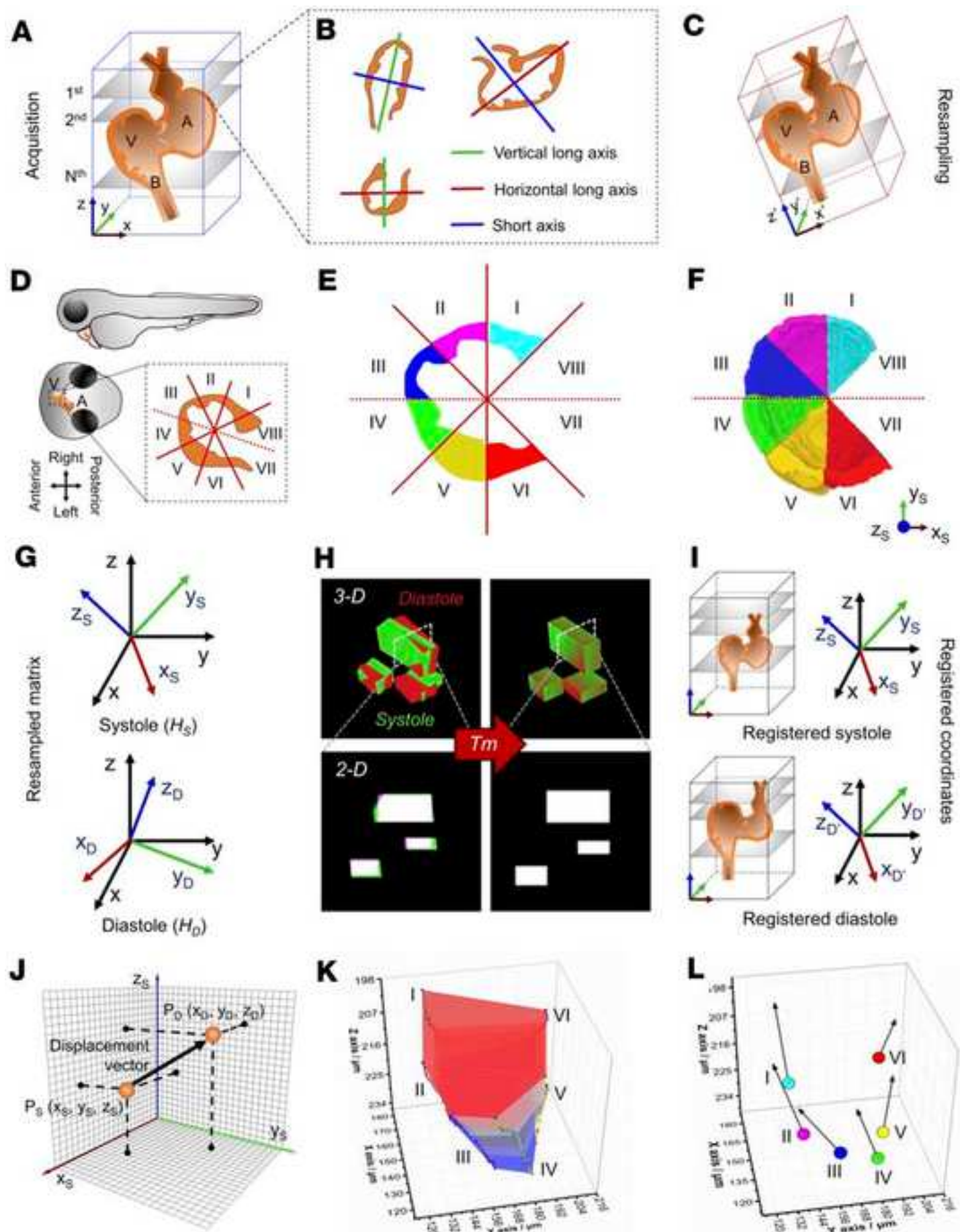
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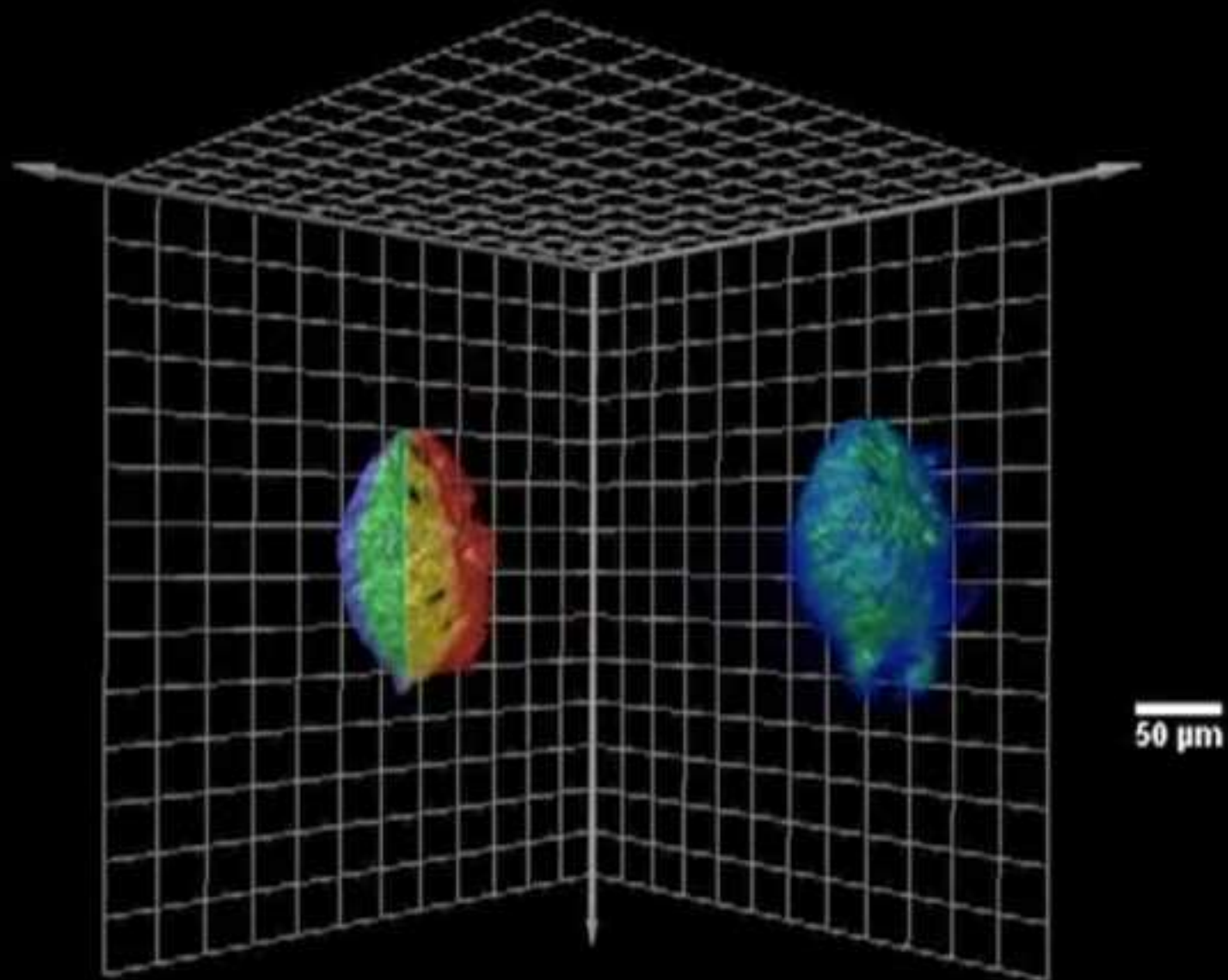
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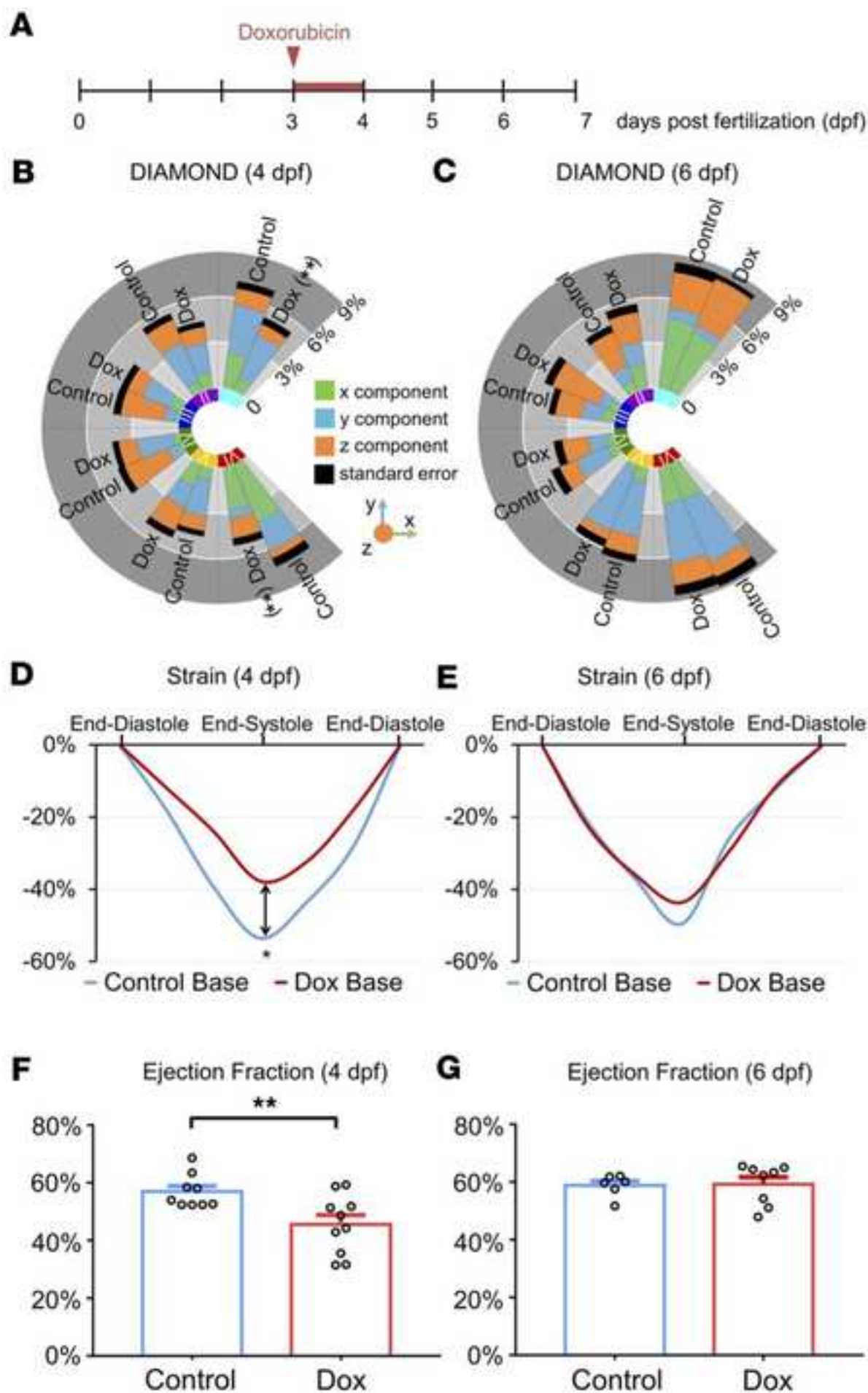
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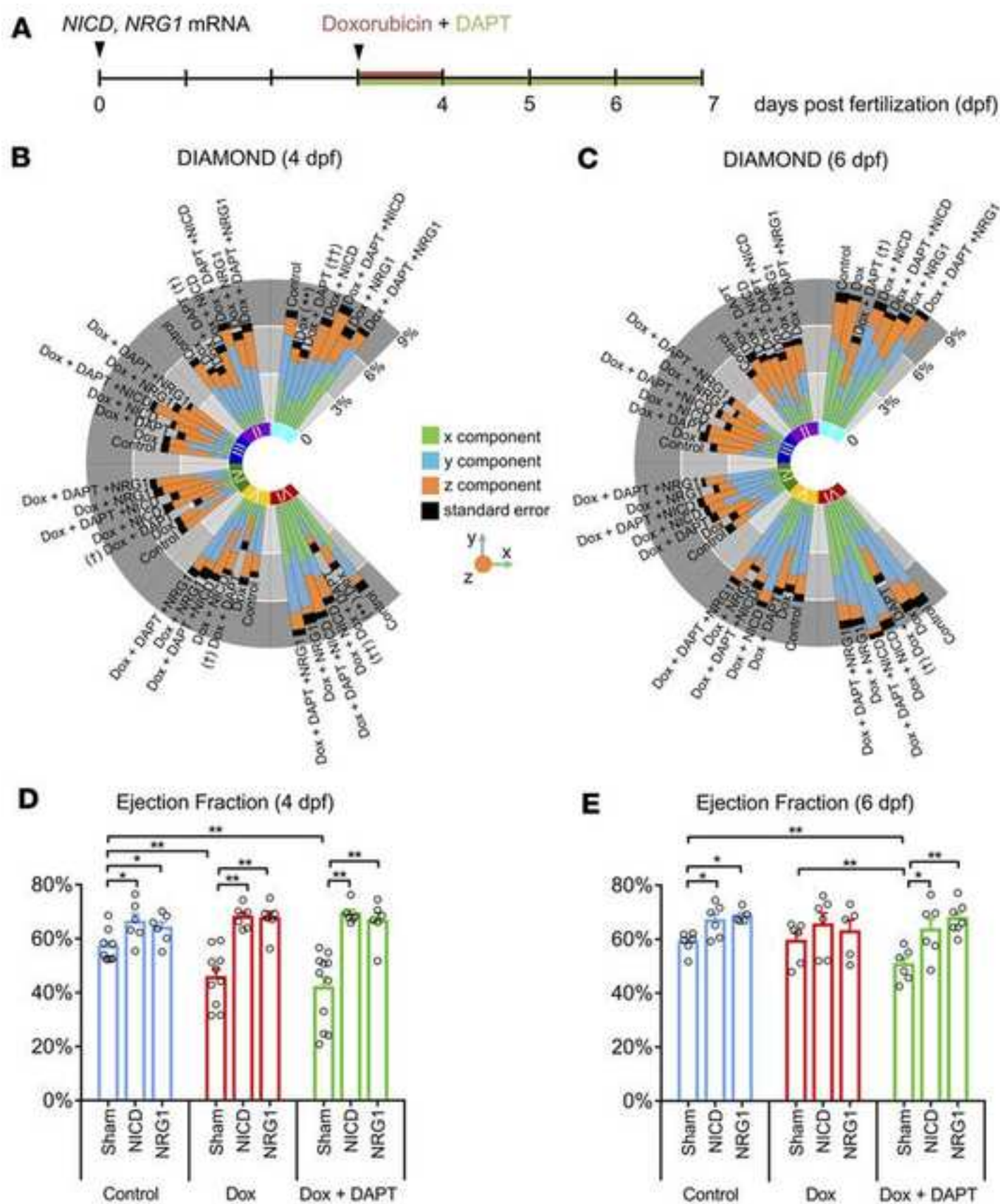


## 4-D Cardiac Cycle with DIAMOND and Raw Data









Name of Material/Equipment	Company	Catalog Number	Comments/Description
Amira6	FEI		Image analyzing software
DAPT	Millipore Sigma	D5942-5MG	
Doxorubicin hydrochloride	Millipore Sigma	D1515-10MG	
Ethyl 3-aminobenzoate methanesulfonate	Millipore Sigma	E10521-10G	Tricaine
MATLAB	MathWorks		Programming environment
MATLAB Image Processing Toolbox	MathWorks		Image processing toolbox





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 Author(s): HETEROGENEITY OF CARDIAC FUNCTION IN EMBRYONIC ZEBRA- FISH  
JUNJIE CHEN, RENE R SEVAG PACKARD

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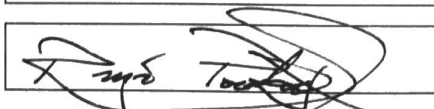
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We thank the Editor and the Reviewers for their time and expert comments. We have addressed all the points raised in a systematic manner.

### Editor's comments:

#### Comment 1

Protocol Language: Please re-write ALL text in the protocol in the imperative voice/tense as if you are telling someone how to do the technique (i.e. "Do this", "Measure that" etc.) Any text that cannot be written in the imperative tense may be added as a "Note", however, notes should be used sparingly and actions should be described in the imperative tense wherever possible.

1) For example: 1.2: Treat the collected embryos with 0.003% 1-phenyl-2-thiourea (PTU, Sigma-Aldrich) in E3 medium 18 hours post fertilization to maintain the transparency of the embryos for LSFM imaging.

#### Response 1

We have fixed the imperative voice/tense in the manuscript based on the editor's comments.

#### Comment 2

Protocol Detail: Please note that your protocol will be used to generate the script for the video, and must contain everything that you would like shown in the video. Please add more specific details (e.g. button clicks for software actions, numerical values for settings, etc) to your protocol steps. There should be enough detail in each step to supplement the actions seen in the video so that viewers can easily replicate the protocol. Some examples:

- 1) 3.1: define DAPT.
- 2) 3.2: How exactly was microinjection performed? Was this done under a microscope? Was the injection manual or was a syringe pump used? Where in the body do you inject? Mention needle gauge. Are the zebra fish anesthetized? If so, how?
- 3) Section 4: Given the goals laid out in the summary "to detail a novel method for the assessment of segmental cardiac function in embryonic zebrafish under both physiological and pathological conditions"; the protocol is incomplete without a more detailed description of the LSFM imaging technique. This can be brief, however, the current description is insufficient.

#### Response 2

1) DAPT is a  $\gamma$ -secretase inhibitor, and its full name is (2S)-N-[(3,5-Difluorophenyl)acetyl]-L-alanyl-2-phenylglycine 1,1-dimethylethyl ester. We have defined its full name in the manuscript.

2) We have added the following text into the manuscript Protocol Section 3.2:

'The microinjection is performed under a microscope with the support of an air pump to accurately control the volume injected. The microinjection is done when the fertilized egg is at the first cell stage, at which time the mRNA is injected into the cell. [...] For details on the microinjection and preparation of injection needles, see Rosen *et al.*'

3) We have added a more detailed description of the LSFM imaging technique in Protocol Section 4.1:

'Briefly, our system utilizes a continuous-wave laser as the illumination source to image all transgenic zebrafish lines. The detection module is composed of two scientific complementary metal-oxide semiconductor (sMOS) cameras and two sets of filters for dual-channel imaging. The detection module is perpendicularly installed to the illumination plane. Each LSFM frame is acquired within a 20 msec exposure time, while the resolving power in cross-section is  $\sim 0.65 \mu\text{m}$  and the step size between consecutive frames is  $\sim 2 \mu\text{m}$ .'

#### Reference

Rosen, J. N., *et al.* Microinjection of Zebrafish Embryos to Analyze Gene Function. *JoVE*. doi:10.3791/1115 (25), e1115, (2009).

#### Comment 3

Protocol Highlight: After you have made all of the recommended changes to your protocol (listed above), please re-evaluate the length of your protocol section. There is a 10-page limit for the protocol text, and a 3- page limit for filmable content. If your protocol is longer than 3 pages, please highlight  $\sim 2.5$  pages or less of text (which includes headings and spaces) in yellow, to identify which steps should be visualized to tell the most cohesive story of your protocol steps.

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- 3) Please highlight complete sentences (not parts of sentences). Include sub-headings and spaces when calculating the final highlighted length.
- 4) Notes cannot be filmed and should be excluded from highlighting.
- 5) Please bear in mind that software steps without a graphical user interface/calculations/ command line scripting cannot be filmed.
- 6) Please edit the title to focus on the highlighted portions of the protocol.

#### Response 3

We have re-evaluated the length of the protocol section and made sure that it does not exceed the page limit. We have revised the protocol based on the editor's suggestions.

#### Comment 4

Discussion: JoVE articles are focused on the methods and the protocol, thus the discussion should be similarly focused. Please ensure that the discussion covers the following in detail and in paragraph form (3-6 paragraphs): 1) modifications and troubleshooting, 2) limitations of the technique, 3) significance with respect to existing methods, 4) future applications and 5) critical steps within the protocol.

#### Response 4

We have revised the discussion based on the editor's suggestions.

#### Comment 5

Figures: define all error bars.

#### Response 5

All error bars have been defined in the figure legends.

#### Comment 6

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#### Response 6

We have removed all commercial sounding languages and the products have been referred to in the Table of Materials.

#### Comment 7

Table of Materials: Please revise the table of the essential supplies, reagents, and equipment. The table should include the name, company, and catalog number of all relevant materials/software in separate columns in an xls/xlsx file. Please include items such as software, instruments, zebrafish rearing reagents, etc

#### Response 7

The Table of Materials has been revised based on the editor's comments.

#### Comment 8

Please define all abbreviations at first use.

#### Response 8

All abbreviations have been properly defined at first use.

### **Reviewers' comments:**

#### **Reviewer #1:**

##### General Comments

The manuscript describes a procedure to analyze mechanical deformation from images of zebrafish hearts. As such, this is an important endeavor, and a useful tool for people analyzing the biomechanics of heart development, especially those using zebrafish - although it is likely adaptable to other species and images (future work). However, the manuscript falls short in explaining even in general terms the assumptions behind the algorithms employed: a better description of intended registration and simplifications is required. As it stands the paper is merely a manual for a very specific software and a VERY specific example - if someone wants to deviate from this example, it is not clear he/she will have the tools to properly use the software as no guidance is provided.

##### Response

We thank the reviewer for the supportive comments. To address the reviewer's concerns regarding the details of the algorithms, we have revised and added multiple sections of the manuscript (Protocol sections 8.3, 8.6, 10.1, 11.2). These provide the reader with further details and explanations regarding the algorithms, and thus more freedom to deviate from them as appropriate for a different set of experiments.



### Major Comments

The paper does not really describe the main idea behind the program/algorithm. The paper should state the main principles use to calculate/estimate deformation. Instead, the paper goes into excruciating details of how to upload the data into the program, how to rotate the heart, etc. It never describes how the registration is performed, and how corresponding points/regions are determined by the algorithm. This is probably mathematically complex, and does not need to be specified in detail, but at least give an idea of how these steps are done internally. This will be valuable for the user as well, who will be able to focus on important issues for instance during the initial manual alignment, which is probably crucial for the analysis.

### Response

We thank the reviewer for the opportunity for clarification. We have added the following description into the manuscript Protocol Section step 10.1:

'The artificially created rectangular parallelepipeds in step 7 are used for 3-D rigid registration which preserves the distance between two points and angles subscribed by three points. When the end-diastole rectangular parallelepiped (red) is registered to the end-systole rectangular parallelepiped (green), the ensuing discrepant 3-D location permits the derivation of a unique matrix of rigid transformation consisting of rotation and translation from the end-diastole matrix to the end-systole matrix (Figure 1H). We performed the registration and regularized energy minimization (to denoise the matrix after the transformation) using the image processing toolbox (see Table of Materials). For a detailed mathematical description of the above process, please see Chen *et al.*'

### Reference

Chen, J. *et al.* Displacement analysis of myocardial mechanical deformation (DIAMOND) reveals segmental susceptibility to doxorubicin-induced injury and regeneration. *JCI Insight*. 4 (8), (2019).

### Minor Comment 1

What do you mean by 'focal cardiac mechanics'? I do not think the algorithm is doing that - but perhaps adding an explanation will help clarify.

### Response 1

We thank the reviewer for the opportunity for clarification. To this end, we have removed 'focal' and 'local' from the manuscript and use only 'segmental'.

### Minor Comment 2

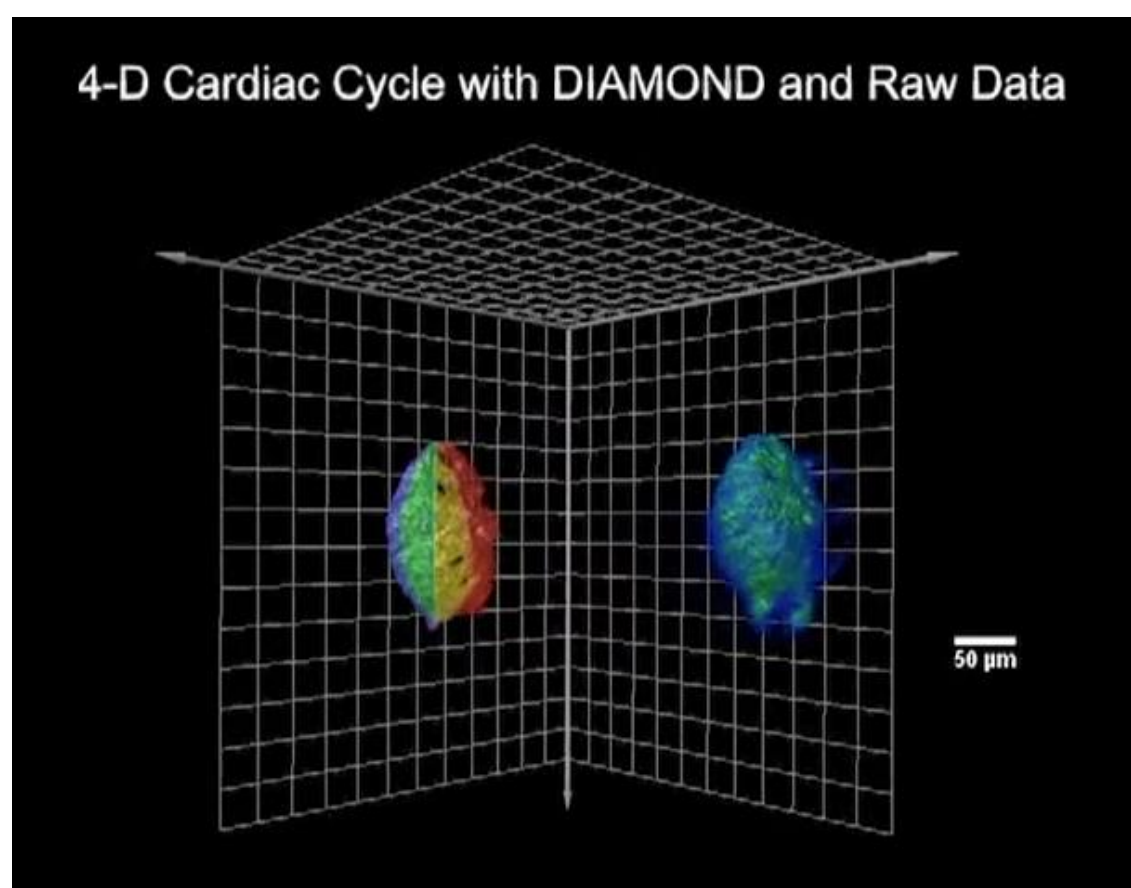
What is 'segmental cardiac function'?

### Response 2

We thank the reviewer for the opportunity to further expand this concept. Given Figure 2 provides the best visualization to address this question, we have revised the Figure 2 legend for further clarification:

'The embryonic zebrafish heart was divided into six segments (volumes) depicted here with different colors for the calculation of DIAMOND displacements (left). The displacement vector of each segment computed by DIAMOND represents its segmental cardiac function.'

We also present Figure 2 below for visual depiction.



### Minor Comment 3

Sections 4 to 11. I understand that the algorithms are described in previous publications, however, a very brief description of them is necessary here. This is kind of a user manual, that does not give you any clue of what you are doing or why. The steps specify opening of folders and the such, it would be beneficial to know what the folders contain exactly, for example, "image stacks containing a 3D reconstruction of the heart at diastole". Not in excruciating detail, but briefly.

### Response 3

We appreciate the reviewer's comment. We have added the following description of the algorithm into Protocol Section step 10.1:

'The artificially created rectangular parallelepipeds in step 7 are used for 3-D rigid registration which preserves the distance between two points and angles subscribed by three points. When the end-diastole rectangular parallelepiped (red) is registered to the end-systole rectangular parallelepiped (green), the ensuing discrepant 3-D location permits the derivation of a unique matrix of rigid transformation consisting of rotation and translation from the end-diastole matrix to the end-systole matrix (Figure 1H). We perform the registration and regularized energy minimization (to denoise the matrix after the transformation) using the image processing toolbox (see Table of Materials). For a detailed mathematical description, please see Chen *et al.*'

This description is also used to address reviewer 1's major comment.

We also added the following description to Protocol section 11.2:

'The displacement vector is obtained by calculating the displacement of the mass centroid of each segment in 3D space. We calculate the 3-D mass centroid ( $P_s$  and  $P_D$ ) coordinates  $\overline{C}_k$  (where  $k$  indicates the x, y, or z coordinate, respectively) of each segment (I-VI) in the segmentation dataset from systole to diastole (Figure 1J). We define the mass centroid  $\overline{C}_k$  in 3-D space as follows:

$$\overline{C}_k = \frac{1}{M_i} \sum_{j=1}^m C_{kj} \rho(x_j, y_j, z_j)$$

where  $C_x = x$ ,  $C_y = y$ , and  $C_z = z$ ,  $M_i$  is the mass of each segment ( $1 \leq i \leq VI$ ),  $m$  is interpreted as the number of voxels of each segment, and  $\rho$  denotes the density function as the segmented region is 1 whereas the rest is 0. The L2-norm of the sub-displacement vectors along the x-, y-, z-axis and the sum displacement vector are calculated during the cardiac cycle.'

### Reference

Chen, J. *et al.* Displacement analysis of myocardial mechanical deformation (DIAMOND) reveals segmental susceptibility to doxorubicin-induced injury and regeneration. *JCI Insight*. 4 (8), (2019).

### Minor Comments 4 and 5

Section 8. This step is likely critical. The reader should be reminded of important issues to take into account. "Make sure to...." Also, what exactly needs to be accomplished here? Some guidance will be beneficial.

Same as above for Sections 9 to 11.

### Responses 4 and 5

We thank the reviewer for this valuable comment. This step is to correctly find the true short axis planes for both systolic and diastolic hearts and to resample the hearts along the short axis planes. We have added several important notes for this step into the manuscript as follows:

- In step 8.3: 'Make sure the points are chosen in a counterclockwise manner'.
- In step 8.8: 'Make sure there are total 6 TIFF files saved in this step'.

### Minor Comment 6

Results. I do not understand what are the 'segments' and what they represent. Are they volumetric regions? How exactly are they defined?

### Response 6

This description is also used to address reviewer 1's minor comment 2. Given Figure 2 provides the best visualization to address this question, we have revised the Figure 2 legend for further clarification:

'The embryonic zebrafish heart was divided into six segments (volumes) depicted here with different colors for the calculation of DIAMOND displacements (left). The displacement vector of each segment computed by DIAMOND represents its segmental cardiac function.'

### Minor Comment 7

How is the registration performed? How are the mass centroids determined and why?

### Response 7

The below description is also used to address reviewer 1's minor comment 3. We have added the following description into the manuscript step 11.2:

'The displacement vector is obtained by calculating the displacement of the mass centroid of each segment in 3D space. We calculated the 3-D mass centroid ( $P_s$  and  $P_D$ ) coordinates  $\overline{C_k}$  (where  $k$  indicates the x, y, or z coordinate, respectively) of each segment (I-VI) in the segmentation dataset from systole to diastole (Figure 1J). We define the mass centroid  $\overline{C_k}$  in 3-D space as follows:

$$\overline{C_k} = \frac{1}{M_i} \sum_{j=1}^m C_{kj} \rho(x_j, y_j, z_j)$$

where  $C_x = x$ ,  $C_y = y$ , and  $C_z = z$ ,  $M_i$  is the mass of each segment ( $1 \leq i \leq VI$ ),  $m$  is interpreted as the number of voxels of each segment, and  $\rho$  denotes the density function as the segmented region is 1 whereas the rest is 0. The L2-norm of the sub-displacement vectors along the x-, y-, z-axis and the sum displacement vector are calculated during the cardiac cycle'.

## Reviewer #2:

### General Comments

DIAMOND is interesting method to uncover cardiac functions from optical technique. Authors have used light-sheet microscopy and zebrafish animal model to demonstrate the cardiac mechanics after treating Doxorubicine which is commonly used for chemotherapy. Using DIAMOND method, the authors have compared cardiac mechanics such as displacement vectors of segmented areas. It has been well-tested with sham model, Doxo-treated model, DAPT treated model, and rescued models. However, I do have some minor concerned before publication.

### Response

We thank the Reviewer for the supportive comments.

### Minor Concern 1

Authors mentioned they adjust threshold to make fluorescent signal strong from weak fluorescent signal. This process possibly includes noise around stronger fluorescent signal. I was wondering if this affects the accuracy of DIAMOND analysis?

### Response 1

We thank the reviewer for this valuable comment. We did not use the 'Threshold' tool mentioned in Protocol Section 6.2 to make 'weak' fluorescent signals 'strong'. Based on our experience, the fluorescent signal from *Tg(cmlc2:mCherry)* is sufficiently strong to clearly visualize the heart. The 'Threshold' tool was used to select all the regions above a certain intensity threshold in order to facilitate manual segmentation. Noise is removed afterwards manually, thus it should not affect the accuracy of DIAMOND. We have added the following description of the 'Threshold' tool to Protocol section 6.2: 'The built-in "Threshold" tool that can select all the regions above a certain intensity can facilitate this process'.

### Minor Concern 2

It is clear how they determines short axis plane. However, it is not clear how to determine vertical and horizontal long axis. It is important to clarify because short axis plane is perpendicular to two planes.

### Response 2

We thank the reviewer for this valuable comment. We have added this description into the manuscript section 8.2" 'The vertical long axis is determined by finding the longest axis connecting the apex and the outflow tract in the XY plane, and the horizontal long axis is determined by finding the longest axis connecting the apex and the outflow tract in the YZ plane'.

## Reviewer #3:

### General Comments

The authors set out to create an automatic method to calculate displacement strain from light sheet fluorescence microscopy images. The method (DIAMOND) is easy to use and clearly spelled out in the abstract. The program also calculates conventional cardiac function parameters such as volumes and ejection fraction. DIAMOND is robust and takes 4D data as input.

### Response

We thank the Reviewer for the supportive comments.

### Major Comment 1

Are there any issues or dependence of DIAMOND on light-sheet fluorescence microscopy parameters such as power, laser angle, or emission wavelength? If so, please recommend some optimal settings so that others can reproduce the robustness of the method.

#### Response 1

We thank the reviewer for this valuable comment. There is no dependence on the power of the LSFM system, as long as the laser intensity is sufficient enough to excite the fluorescent signal. The angle of the laser is always perpendicular to the camera. Emission wavelength should be determined by the fluorescent protein expressed by the sample, and the proper filter should be chosen to eliminate the background noise generated by the source laser. However, there is dependence on the resolution and image quality of the microscope, because a good image quality is essential for image segmentation and anatomical structure visualization. We recommend the lateral resolution to be at least 1  $\mu\text{m}$ . We have added the description of the angle and wavelength to Protocol section 4.1.

#### Major comment 2

How do you deal with non-cyclical motion (i.e. arrhythmia)? It seems that the authors use a model that depends on cyclical repetitive motion to reconstruct different cardiac phases in 3D. My concern is when users apply DIAMOND to either early embryonic stages with pulsatile motion or mutation cases with arrhythmic heart rate.

#### Response 2

We agree with the reviewer that there might be concerns when DIAMOND is applied to those studies. During early embryonic stages, it is difficult to acquire high quality images given the heart is blocked by the yolk sac. We have tried to image 1 and 2 dpf zebrafish hearts with LSFM, but the image quality was subpar.

Most post-imaging reconstruction algorithms are based on the assumption that the heart is undergoing a cyclical repetitive motion. Because our current post-imaging processing algorithm also relies on this assumption, DIAMOND cannot be applied to arrhythmic hearts. If the reader would want to study arrhythmia in zebrafish using optical methods, the best currently available options are Electrically Tunable Lens-SPIM (ETL-SPIM) or light field microscopy. However, the ETL-SPIM system is technically challenging (Mickoleit *et al.*) and light field microscopy currently suffers from low spatial resolution. This should be an area of future research.

#### Reference

Mickoleit, M. *et al.* High-resolution reconstruction of the beating zebrafish heart. *Nat Methods*. **11** 919,(2014).