Biological Tissue Movement

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Introduction

The mitral valve, also known as the bicuspid valve or left atrioventricular valve, is a valve with two flaps in the heart, that lies between the left atrium and the left ventricle. The mitral valve and the tricuspid valve are known collectively as the atrioventricular valves because they lie between the atria and the ventricles of the heart.
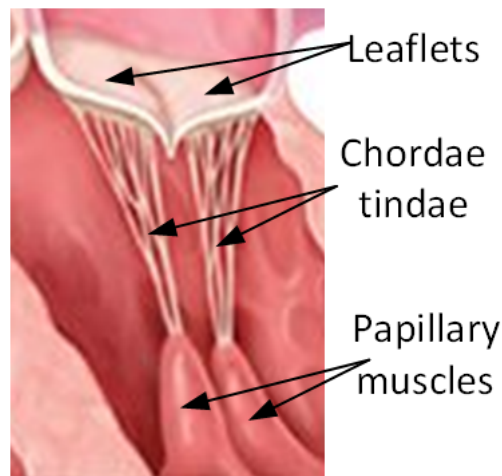

Figure 1: Mitral valve structure

Mechanical properties Chordae: L   0,025 m (length) d   0,001 m (diameter) $\rho = 1040$ kg/m3 (density) E = 2000 N/m (stiffness) Poisson's ratio of 0.49

Leaflets: E = 2.0E6 MPa (Anterior leaflet) E = 1.0E6 MPa (Posterior leaflet) $\rho = 1.06E3$ kg/m3 Poisson's ratio 0.49

Mitral valve has cyclic working conditions. Example of such you can see on figure 2.
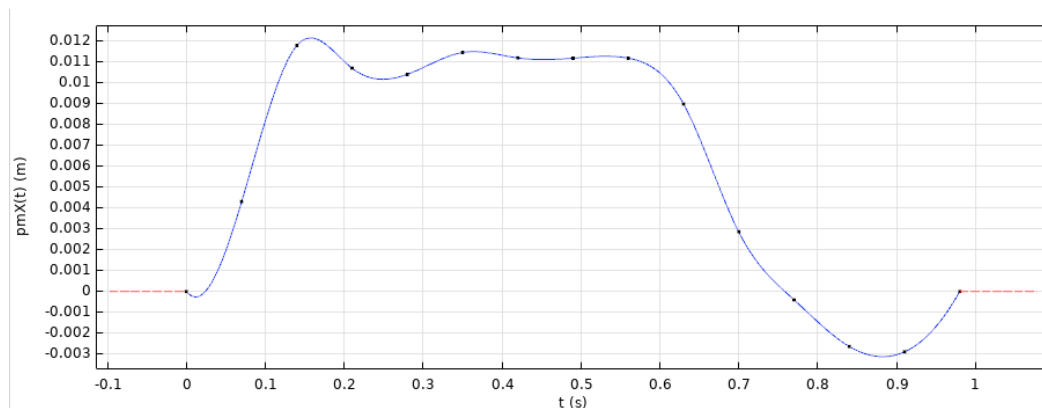

Figure 2: Displacement of papillary muscle over cardiac cycle

In normal conditions, blood flows through an open mitral valve during diastole with contraction of the left atrium, and the mitral valve closes during systole with contraction of the left ventricle. The valve opens and closes because of pressure differences, opening when there is greater pressure in the left atrium than ventricle, and closing when there is greater pressure in the ventricle than atrium. In abnormal conditions, blood may flow backwards through the valve (mitral regurgitation) or the mitral valve may be narrowed (mitral stenosis). Rheumatic heart disease often affects the mitral valve; the valve may also prolapse with age, and be affected by infective endocarditis. The mitral valve is named after the mitre of a bishop, which resembles its flaps.

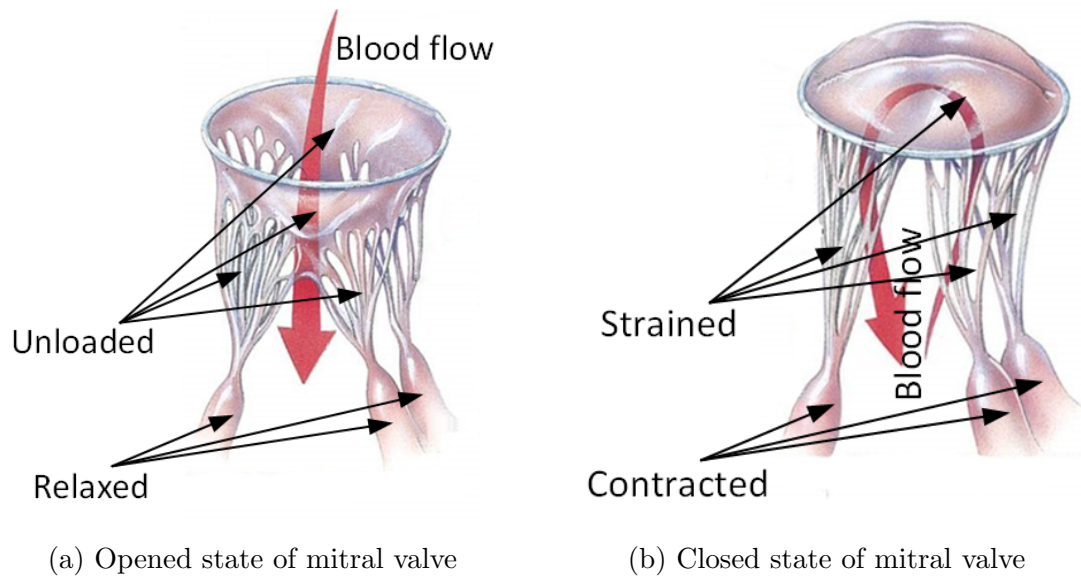(a) Opened state of mitral valve   (b) Closed state of mitral valve

Figure 3: Mitral valve working cycle

Mitral valve prolapse (MVP) is a valvular heart disease characterized by the displacement of an abnormally thickened mitral valve leaflet into the left atrium during systole. By other words, it is a condition in which the two flaps of the mitral valve doesn't close smoothly and evenly, but instead bulge (prolapse) upward into the left atrium.[1]
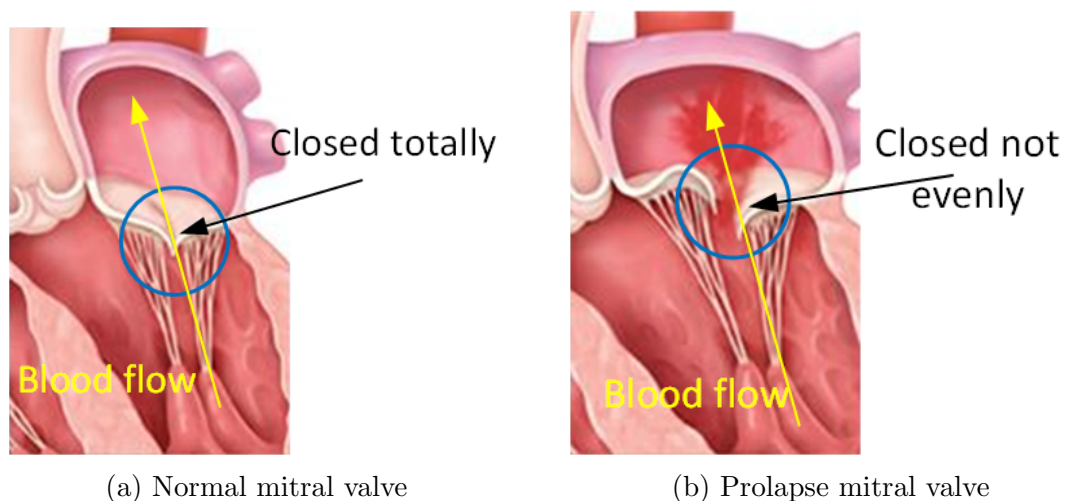

(a) Normal mitral valve   (b) Prolapse mitral valve

Figure 4: Comparison of the normal valve and prolapse

Providing the surgeon with an anatomically and biomechanically accurate computional model of a particular patient's mitral heart valve could enable preoperative surgical planning and potentially improve surgical outcome. Investigation behavior of biological tissue can be done by estimating movement of it. Tissues of biological origin, usually had a weak structure and little stiffness.

Such physical structure imposes restrictions on the possible tools in the measurement. Another possible problem is the limited number of measurement attempts. Such limitations of physical measurements call into question the possibility of such activities in general. An alternative to physical experiments is the numerical simulation of these experiments. There are a large number of different numerical modeling methods. All of them are derivatives of Finite Element Method(FEM) and Discrete Element Method(DEM).

While general finite-element studies are helpful for the evaluation and development of MV repair surgery, patient-specific models are required for individual therapy planning.

article 1

The patient-specific mass-spring MV model uses a segmentation of 3D TEE images for the initialization of a mass-spring model of the closed MV under systolic pressure. An iterative approach is used to adjust the spring rest-length so that the model can accurately simulate the shape of the closed MV under systolic pressure. To simulate MV annuloplasty, the model can then be deformed, according to the annuloplasty ring to be used, to create a prediction of the shape of the closed MV after surgery.

Based on the properties of the material of biological tissues and review of existing projects, the most appropriate method is Mass - Spring modeling(MSM). This method based on ideas of DEM and basic element here is very know in mechanic simple one dimensional(1D) beam.**??**

have to show so pic about MSM, with explanation what is going on

Computational complexity of MSM is much less compare to FEM-based methods, because of less number of equations to integrate on each time step. This important advantage and physics way have method describes basic element gave to MSM very wide using in computer games for calculating reality-looks hair or cloth movement in real time. Modelling by using MSM could be parallel calculated on each time step.[2] [3]
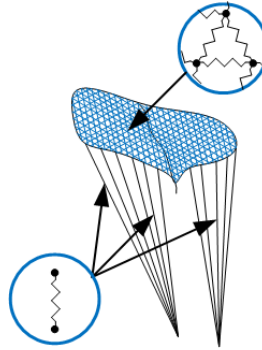

Figure 5: Displacement of papillary muscle over cardiac cycle
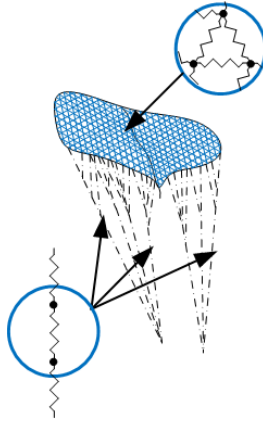
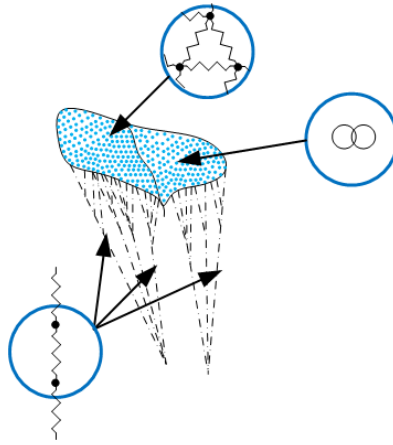Figure 6: Displacement of papillary muscle over cardiac cycle

Figure 7: Displacement of papillary muscle over cardiac cycle

Linear deformation

For investigating motion of any mechanical system need to integrate equation of motion(4). For this propose need to express all acting forces in node(1) for each node in relation to their application place.

$$F_n(X) = F_{ext}(X) + F_{elem}(x, y, z) \times [DCM] + F_{press}(x, y, z) \times [DCM] \tag{1}$$

F_{ext} is external load force, applied to node in global coordinates. Value of this force for each time step is loaded from list of loads.

F_{press} is external pressure and can be described like force applied to element in local coordinates. Value of this force for each time step is loaded from list of loads.

F_{elem} is sum of internal forces of each element, which acting in node. From each element counts only half of force to node, other half going to neighbour node. In case of 1D element system, internal force of each element can be express like axial force and it is equal to integral of stress over area:

$$N(x) = \int_A \sigma dA \tag{2}$$

For 1D rod system F_{elem} can be expressed like:

$$F_{elem} = \sum_e N_e(x)/2 \tag{3}$$

The motion of nodes can be expressed by Newton's equation of motion. As 1D element was choosed as discrete element, only the normal component of the translational motion is considered, the equation reduces to

$$F(x) - m\ddot{x} = 0 \tag{4}$$

where $F(x)$ is axial force, equal to $F_n(X)$ for 1D rod system, m – mass of node and $\ddot{x}$ is acceleration, initial conditions are: $x(0) = 0$ and $\dot{x}(0) = V_0$.

Equations of motion for Euler's scheme of integration can be described like:

$$\ddot{U}(\Delta t) = Fn(X)/m \tag{5}$$

$$\dot{U}(\Delta t) = \dot{U}(t) + \ddot{U}(\Delta t)\Delta t \tag{6}$$

$$U(\Delta t) = U(t) + \dot{U}(\Delta t)\Delta t \tag{7}$$

Element force becomes from physical deformation of element. In linear case of study, deformation of element much less compare to element dimensions. It is expressed by linear geometry equation(8), which showing relation between initial length of element and length in Δt state.

$$\varepsilon = \frac{dU}{dx} = \frac{l(\Delta t) - l_0}{l_0} \tag{8}$$

According to Hook law $\sigma = \varepsilon E$ and linear geometry equation (8), inner force can be changed to:

$$N(x) = \int_A \varepsilon E dA = EA \int \varepsilon = \frac{EA}{l_0} * (l(\Delta t) - l_0) \tag{9}$$

where $l(\Delta t)$ is current length of element, l_0 length of element at $t = 0$, E – Young's modulus for element material. To be able to integrate equation of motion, need to express deformation in equation (9) by differences between displacements of nodes, to which element is connected:

$$N(x) = \frac{EA}{l_0} * (U_i - U_j) \tag{10}$$

Nonlinear deformation

Nonlinearity in main mean that element can get huge deformation compare to element demesions. Equation of F_{elem} in this case would change to nonlinear form:

$$N(x) = \int_t \int_A \sigma dA dt \tag{11}$$

From this equantion comes that cross sectional area and stiffness coefficient will get nonlinearity.

Changing of cross sectional area over time for 1D element is changing its length over time. Linear geometry equation(8), showing linear relations between length, because difference in Δt state takes according initial length of element. In case of huge deformation need to recalculate length of element on each time step and take difference of displacement according to previous time step. In end of geometry equation become to nonlinear form:

$$\varepsilon = \frac{dU}{dx} = \frac{l(\Delta t) - l(t - \Delta t)}{l(\Delta t)} \tag{12}$$

Inner force(9) also become to nonlinear form:

$$N(x) = \int_t \int_A \varepsilon E dA = EA \int_t \varepsilon = \frac{EA}{l(\Delta t)} * (l(\Delta t) - l(t - \Delta t)) \tag{13}$$

where l is current length of element, l_0 length of element at $t = 0$, E – Young's modulus for element material.

And nonlinear equantion of inner force for integration:

$$N(x) = \frac{EA}{l_0} * (U_i - U_j) \tag{14}$$

Mechanic equivalent of fibrous tissue could be described as system of 1D rods. Example of such flat 2D system are shown on figure 9.
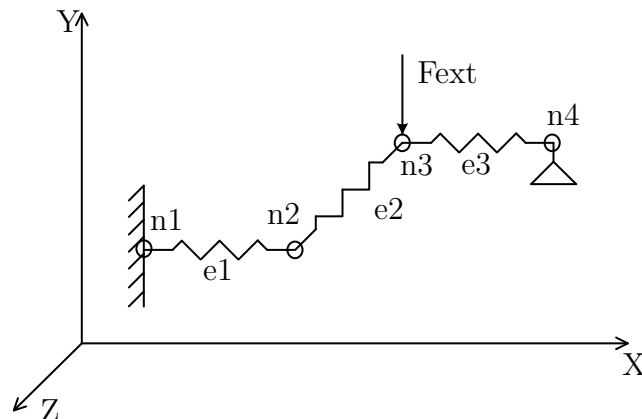

Figure 8: 1D Rod system in global coordinate system

System consists of discrete elements e_1, e_2 and e_3. All elements are connected to each other through nodes n_2, n_3 and to special points through n_1 and n_4. Each element e_n of system has own orientation in global coordinate system.

pic about loc glob coords of one element

In case that node does not have external interrupt, like pressure or other applied force, schematic represent of node can be as on figure 9.
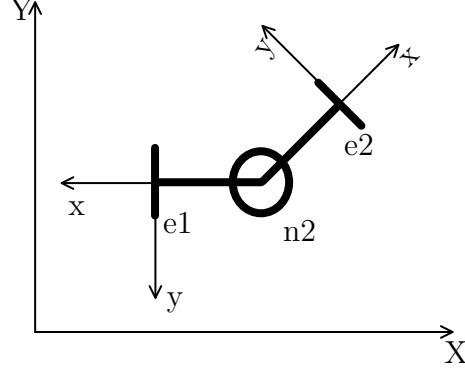

Figure 9: Extracted node from system

Mathematical model of discrete system is expressed by equations of nodes motion. As elements is 1D, nodes will be 1D as well. All system acting in global coordinate system $\{X, Y, Z\}$ and each element acting in own local coordinate system $\{x, y, z\}$.

Let's try to describe minimal possible way to get simulation of such structure as shown on figure 8. From schematic representation of node comes that all vector variables of node should be calculated in global coordinate system and element variables in own local coordinate system(figure 9). For transformation between coordinate systems direction cosine matrix (DCM)(15) can be used.

$$DCM = \begin{bmatrix} cos(X,x) & cos(X,y) & cos(X,z) \\ cos(Y,x) & cos(Y,y) & cos(Y,z) \\ cos(Z,x) & cos(Z,y) & cos(Z,z) \end{bmatrix} \tag{15}$$

where $\{X, Y, Z\}$ is global coordinate system and $\{x, y, z\}$ is local coordinate system.

According to primitive scheme of node 9, mass of each node can be calculated, like sum of half mass of each element, which acting in node. $m_n = \sum_e m_e/2$

Integration schemes

Euler first order explisit

$$(16)$$

Runge-Kutta schemes find application within discrete element simulations. While being of high accuracy they are computationally expensive.

$$kr_1 = v(t), kv_1 = a(t)$$

$$r_2 = r(t) + \frac{1}{2} * \Delta t * kr_1, v_2 = v(t) + \frac{1}{2} * \Delta t * kv_1$$

$$kr_2 = v_2, kv_2 = a(t + \Delta t)$$

$$r_3 = r(t) + \frac{1}{2} * \Delta t * kr_2, v_3 = v(t) + \frac{1}{2} * \Delta t * kv_2$$

$$kr_3 = v_3, kv_3 = a(t + 2\Delta t)$$

$$r_4 = r(t) + \frac{1}{2} * \Delta t * kr_3, v_4 = v(t) + \frac{1}{2} * \Delta t * kv_3 \qquad (17)$$

$$kr_4 = v_4, kv_3 = a(t + 3\Delta t)$$

$$r(t + \Delta t) = r(t) + \Delta t * (\frac{1}{6}kr_1 + \frac{1}{3}kr_2 + \frac{1}{3}kr_3 + \frac{1}{6}kr_4)$$

$$v(t + \Delta t) = v(t) + \Delta t * (\frac{1}{6}kv_1 + \frac{1}{3}kv_2 + \frac{1}{3}kv_3 + \frac{1}{6}kv_4)$$

The central difference scheme, also known as velocity Verlet is a very widely used integration method of second order. This was initially proposed by Cundall and Strack (1979) and adopted by several other authors. Velocities in the upcoming time step t +

t/2 and positions at t +

t are calculated as

$$v(t + \Delta t/2) = v(t + \Delta t/2) + a(t - \Delta t/2) * \Delta t$$
$$x(t + \Delta t) = x(t) + v(t + \Delta t/2) * \Delta t \qquad (18)$$

predictor–corrector schemes very commonly used for molecular dynamics and discrete element applications are Gear's schemes. They are based on three stages, whereas in addition to the predictor and corrector step known from the Adams-method an evaluation step is added. Schemes considered here are the third order Gear's method (GPC3) and the fourth order Gear's method (GPC4). In the prediction step positions and their higher derivatives are calculated based on Taylor series expansions as

$$c(t + \Delta t, p) = c(t)$$

$$b(t + \Delta t, p) = b(t) + c(t) * \Delta t$$

$$a(t + \Delta t, p) = a(t) + b(t) * \Delta t^2 + \frac{1}{6} * c(t) * \Delta t^2 \qquad (19)$$

$$v(t + \Delta t, p) = v(t) + a(t) * \Delta t + \frac{1}{2} * b(t) * \Delta t^2 + \frac{1}{6} * c(t) * \Delta t^3$$

$$x(t + \Delta t, p) = x(t) + v(t) * \Delta t + \frac{1}{2} * a(t) * \Delta t^2 + \frac{1}{6} * b(t) * \Delta t^3 + \frac{1}{24} * c(t) * \Delta t^4$$

with the first and second derivative of the accelerations calculated as for GPC3:

$$b(t) = \frac{da(t)}{dt}$$
$$c(t) = 0 \qquad (20)$$

8

for GPC4:

$$b(t) = \frac{\mathrm{d}a(t)}{\mathrm{d}t}$$
$$c(t) = \frac{\mathrm{d}b(t)}{\mathrm{d}t}$$

(21)

In the evaluation step the difference in the accelerations calculated based on the acceleration $a(t + \Delta t, p)$ and the acceleration $a(t + \Delta t)$ calculated from positions $x(t + \Delta t, p)$ and velocities $v(t + \Delta t, p)$ is obtained by

In the following, correction step positions and their higher derivatives are calculated based on their values from the previous time step and the obtained difference in acceleration as

Gear's scheme parameters k1-k5 for GPC3: $k_1 = 1/12, k_2 = 5/12, k_3 = 1, k_4 = 1, k_5 = 0$ for GPC4: $k_1 = 19/240, k_2 = 3/8, k_3 = 1, k_4 = 3/2, k_5 = 1$

Results

List of literature

[1] Emil Hayek, Christian N Gring, and Brian P Griffin. "Mitral valve prolapse". In: *The Lancet* 365.9458 (Feb. 2005), pp. 507–518. ISSN: 0140-6736. DOI: 10.1016/S0140-6736(05)17869-6. URL: https://www.sciencedirect.com/science/article/pii/S0140673605178696?via%7B%5C%%7D5C=ihub.

[2] Allan Rasmusson, Jesper Mosegaard, and Thomas Sangild Sørensen. "Exploring parallel algorithms for volumetric Mass-Spring-Damper models in CUDA". In: *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*. 2008. ISBN: 3540705201. DOI: 10.1007/978-3-540-70521-5_6.

[3] Ronan Mendonça Amorim et al. "An electro-mechanical cardiac simulator based on cellular automata and mass-spring models". In: *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*. 2012. ISBN: 9783642333491. DOI: 10.1007/978-3-642-33350-7-45.