Modeling and Simulation of Human Temporomandibular Joint Using Bond Graphs—A One-Dimensional Model

Mehak Sharma, Vikas Rastogi, and Manoj Soni

Abstract This study is proposed to devise the behavior of temporomandibular joint (TMJ) while jaw opening and closing movements in human beings using bond graph. TMJ is the most active and extensively used biomechanical joint. To diagnose TMJ disorders and provide correct medical care by exploring jaw behavior, accurate dynamic modeling of TMJ is a necessity. This study is limited to in vitro analysis and modeling techniques because it is challenging to study the actual dynamic functioning of TMJ, being an inner body joint. The primary focus of this work is to model TMJ through bond graph considering its physical resonance with a mechanical system. For this study, the human masticatory system is devised into mathematical one-dimensional model. It included morphology, the behavior of the muscle as well as its dynamic properties. The simulation has been carried out for different force patterns replicating proportional jaw activities like mouth opening and closing. The functional role of TMJ muscles has been represented by assigning nonlinear stiffness values through available literature. The muscle strength has been attributed as a damping characteristic of the jaw. The various elements of jaw, i.e., bite force, jaw mass, reaction force and velocity, have been attributed into the model, which accounts for symmetrical jaw motions.

Keywords Stiffness · Damping · Dynamics · TMJ · Bond graph · Modeling · Simulation

1 Introduction

The dynamic modeling of joints of human limbs is very complex, and the temporomandibular joint is extremely intricate in the human body. It controls mastication and

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speech. The nerves and muscles in the human jaw and face are intricately connected to the brain. It is a reciprocal synovial hinge between the mandible and temporal bone with articular disk and various muscles intertwined to perform basic jaw functions like speaking, eating, yawning, drinking, opening and closing of the mouth. Mechanically speaking, since TMJ is both ginglymus (hinging joint) and arthrodial (sliding joint), it is often labeled as a ginglymoarthrodial joint.

The unique prospect of this research work is that though there is expansive literature available on the dynamic or kinematic study of the human jaw, masticatory system and jaw muscles but this is the first attempt at studying the dynamic behavior of human jaw using bond graph technique. The dynamic behavior and movements of the jaw have been studied for decades [1–4]. The muscle activation during various jaw movements has been studied with the help of EMG data or mathematical modeling [5–9]. Three-dimensional static mathematical calculations have been also performed for jaw opening movements [10]. Muscle models, stiffness and damping characteristics have been studied and modeled in the later years [10, 11], and most recently, nonlinearity and 3D finite models for muscles are also being focused for dynamic behavior [12–14]. The present work has taken inspiration from the works of Vaz [9] who has presented bond graph modeling for a human joint with soft articular cartilage and also from Tyagi [15] who has worked on bond graph modeling of lumbar vertebrae of the spine. This paper intends to model the temporomandibular joint by using bond graphs [15] and validate the model with the available literature on TMJ biomechanics.

1.1 Biological Model–TMJ

The human skull has three main structural elements which primarily help in mastication: the mandible, the maxilla and temporal shown in Fig. 1. The maxilla remains fixed at the upper side and the mandible pivots to TMJ. The TMJ is controlled actively by the following mastication muscles: the masseter, medial Pterygoid, lateral Pterygoid and the temporalis. This allows mastication, swallowing, chewing, social interaction and speech in humans.

Due to such complex structure and intertwined connections between muscles and bone elements, it is often difficult to model TMJ accurately. We aim to model TMJ with the perspective of studying system dynamics as being an inner body joint, it is difficult to precisely understand its dynamic characteristics and functioning with experimental techniques. Hence, researchers are keen to apply in vitro techniques for studying human TMJ. The application of bond graph modeling technique to TMJ is expected to be useful for simulation and control of biomechanical prostheses, robotic equipment, and virtual reality devices. The vital focus of this research work is to study the dynamic performance of TMJ for various jaw motions like biting, chewing, eating, speaking, opening and closing of the mouth, etc.

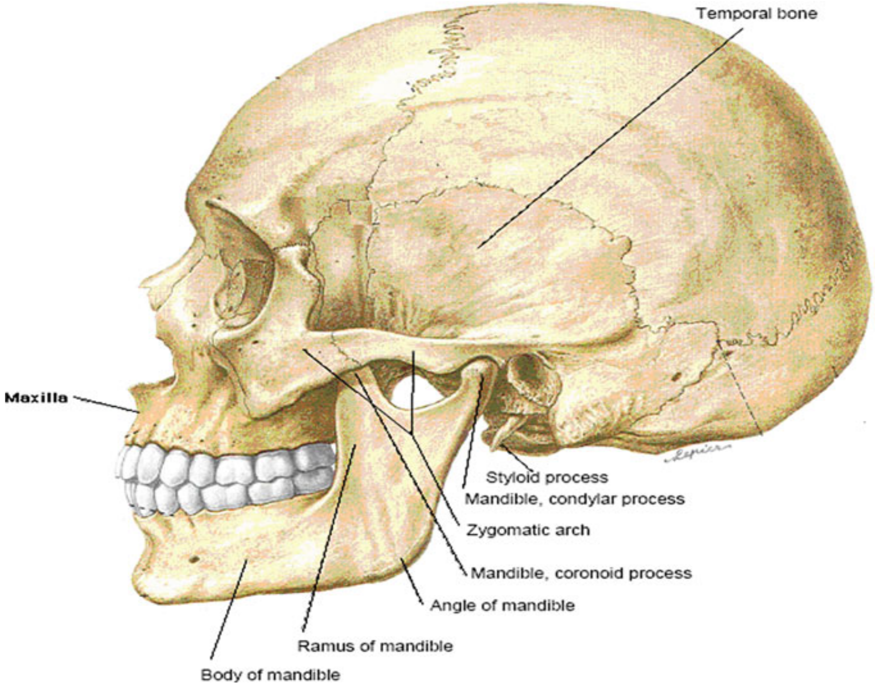


Fig. 1 Human skull (side view, [10] showing TMJ anatomy

2 Materials and Methods

2.1 Physical System

To model a bond graph for TMJ, its anatomy is studied which helps in determining the cross-sectional area of muscles, activation points and point of application of various forces. The anatomical data is evaluated and converted into a free body diagram. The schematic free body diagram of human TMJ is presented in Fig. 2.

The present work has used the schematic model of TMJ based on various forces involved from the literature [10]. The forces calculated in this model by static analysis are used for modeling of human TMJ. The muscle forces involved in this system are the temporal muscle (F_T), masseter muscle (F_M) and Pterygoid muscle (F_P). F_N is the normal force. By using three muscles and constraining the maxilla's articulating portion, the system is deemed to be statically indeterminate due to the presence of four variables: F_T, F_M, F_P, and F_N. To completely define the force system, four non-redundant equations are established. The model is calculated for all equation variables. Considering,

$$\sum F_x = 0$$

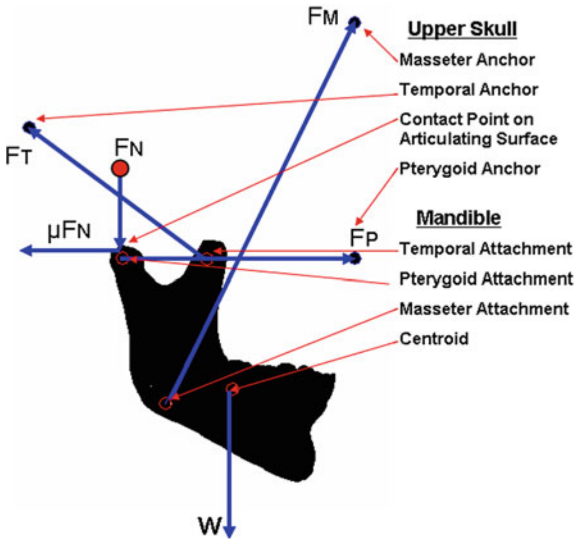


Fig. 2 Schematic of TMJ free body diagram [10]

$$\sum F_y = 0$$
$$\sum M_o = 0$$
$$F_N = \text{Constant}$$

Hence, the equations of motion of the temporomandibular joint of a human skull in a static equilibrium are written as:

$$\sum F_x = F_{Tx} - F_{Mx} - F_{Px} + F_{Nx} + \mu F_{Nx} = 0 \tag{1}$$

$$\sum F_y = F_{Ty} + F_{Py} + F_{My} - F_{Ny} + \mu F_{Ny} \cdot W = 0 \tag{2}$$

$$\sum M_o = F^*_{Tx}(T_{yp}) - F^*_{Ty}(T_{xp}) - F^*_{My}(M_{yp}) - F^*_{Nx}(N_{yp}) + F^*_{Ny}(N_{xp}) - \mu F^*_{Nx}(N_{yp}) - \mu F^*_{Ny}(N_{xp}) + W^*(C_{xp}) = 0 \tag{3}$$

$$\Delta PE_C = F_T * D_T + F_M * D_M + F_P * D_P + \mu F_N * D_N \tag{4}$$

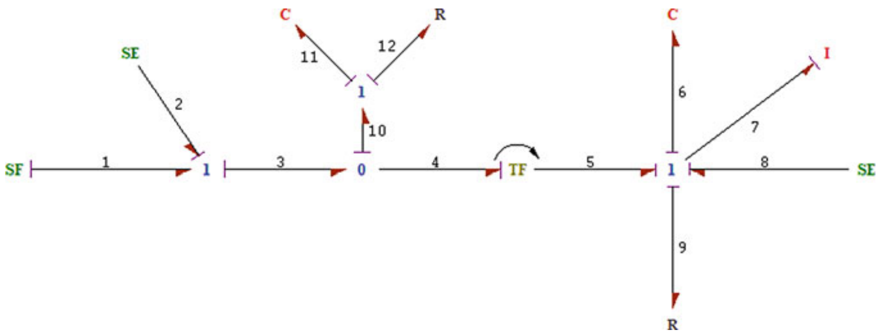


Fig. 3 Bond graph model TMJ in one-dimensional system

2.2 TMJ: One-Dimensional Computational Bond Graph Model

To obtain a simplified model, consider the free body diagram shown in Fig. 2. All forces are considered to be in static equilibrium. The dynamic behavior of TMJ is simulated by appropriating a one-dimensional rigid element of TMJ with material damping and synovial viscous damping as a case study. In this model at Fig. 3, SE at link 2 represents reaction force and SF at 1 depicts the initial velocity of the model. SE at 8 is the bite force that can be assigned values to simulate the model. Linear muscle stiffness of the model is represented by C, capacitance at 6 and damping of the muscle is depicted by R, resistance at 9. Nonlinear stiffness and damping are modeled at C (link 11) and R (link 12) respectively. Inertia I at link 7 represents the mass of jaw. TF is the transfer function with modulus as x/y representing a fraction of distances between bite point to reaction point and muscle action point.

2.3 Simulation for a One-Dimensional System

The bond graph of the temporomandibular joint is simulated on SYMBOLS—Shakti software using Runge–Kutta fourth-order method. While simulating, the relative motion of the muscles and bones is modeled using a minimal and frictionless coefficient of friction. The average mass of the human jaw (internal body) is taken as 0.30 kg [9]. The table below represents the parameters for simulation: (Table 1).

3 Results and Interpretations for One Dimensional Model

In this simulation, results are produced for average values of bite force. The simulation results are validated from the other mathematical studies, and 40–50 mm of

Table 1 Parameters used for one-dimensional model simulation

Type of properties (Jaw)	Range
Joint reaction force (jaw opening)	2.71-48.61 N
Joint reaction force (jaw closing)	7.7–64.9 N
Velocity during mastication	28–98 mm/s
Distance b/w premolar and joint	105.6 ± 0.05 mm
Distance b/w molar and joint	111.2 ± 0.3 mm
Distance between incisor and joint	100.6 ± 0.1 mm
Mass of mandible	3.1 ± 0.3 N
Bite force	200–1000 N
Muscle stiffness	10–15 N/mm
Damping muscle	1.2 Ns/mm
Muscle stiffness nonlinear	10.9 N/mm
Damping muscle nonlinear	2 Ns/mm

the jaw opening (displacement) for a bite force of 600 N has been obtained from the simulation results. The results analyzed for 600 N bite force through FFT analyzer tool of SYMBOLS—Shakti are shown in Figs. 4, 5 and 6.

- Figure 4 represents the force value of 600 N (average) which has been simulated using bond graph while biting action in continuous movements (jaw opening).

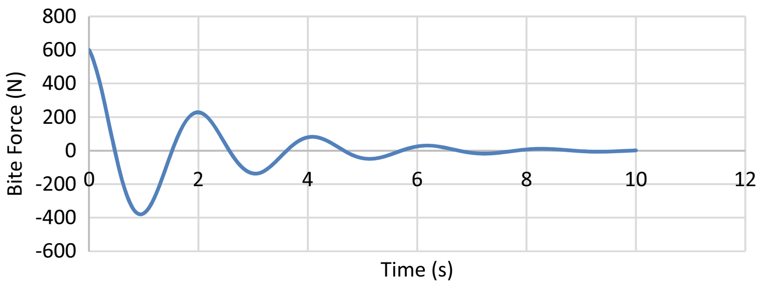
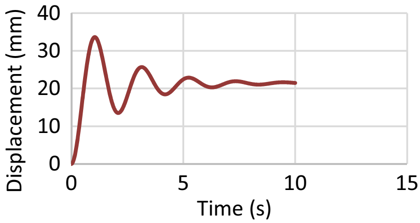


Fig. 4 Average bite force (600 N)

Fig. 5 Displacement at 600 N jaw opening



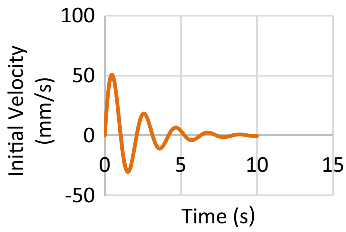


Fig. 6 Initial velocity for biting at 600 N

Table 2 Comparison of obtained results from present study with available literature

Type of parameter	Present study	Past studies (cited values)
Average biting force (N)	600 N	400–600 N [10]
Average jaw opening (mm)	35 mm	30–40 m [16]

- In Figs. 4 and 5, the graph shows the force and displacement values at its peak and trough, which represents jaw in action from bringing it in a state of motion from a state of rest.
- In Fig. 6, the maximum initial velocity due to biting action has been plotted.
- The average bite force in humans in masticatory action has been precisely modeled and simulated using bond graphs. This has been studied and reviewed previously by using experimental as well as simulation techniques (Table 2).

4 Conclusion

This paper has proposed a novel method to study the dynamic simulation of the human jaw using bond graph modeling technique. This paper represents bond graph model for TMJ dynamic simulation for the first time in the field of TMJ biomechanics. It can be further elaborated and used for biomechanical purposes like prostheses simulation, robotics and virtual reality systems. From the results of the present study, the following conclusions can be interpreted:

1. Bond graph model is a unique tool to study the biomechanics of TMJ which involves complex muscle motion and activation.
2. A biting force of 600 N produces a jaw (opening) displacement of a maximum of 35 mm which is similar to the values found in the available literature.
3. The effectiveness of the simulated bond graph model for one-dimensional model of TMJ in the present study is validated from the relevant biomechanical studies.

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