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Hybrid and Projective Synchronization of Multi-Scale Cancer-Invasion Model

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Abstract: The Active Control method has been employed to discuss the hybrid and projective synchronization between the two identical chaotic systems of the Tumor growth models. During the investigations analytic and computational techniques have been used. For different values of growth parameters hybrid synchronization and projective synchronization between the considered systems have been achieved. Most significantly the analytic and computational results are in an excellent agreement. This manuscript provides significant mathematical description to devise the sophisticated experimental mechanism for the treatment of tumor growth.

1. Introduction

Cancer is now becoming the leading cause of death around the world but our overall knowledge of its causes, methods of prevention and cure is still in its infancy. One strongest tool that has shown its potential in our better understanding of such a complicated biological systems is mathematical modeling [1],[2]-[5]. Mathematical models provide realistic and quantitative representations of important biological phenomena and biological interpretations of the results can give insight to make realistic predictions of the state of disease under different conditions [6]. The idea of using mathematical models for cancer was introduced in 1955 by Thomlinson and Gray(1955). After that, many mathematical models for tumor growth have been developed and the application of these models has been increased recently [7]-[11]. What makes mathematical models of tumor growth interesting is that they can be simple but indeed still indicate the complicated interactions involved[12]. The tumor growth dynamics and the anti tumor immune response dynamics in vivo are very complex[13] and not well understood mainly because in most of states, the measurements are impossible in vivo. Models are not only able to explain many phenomena observed in vivo,but they could also provide a good insight about the phenomena that are unobservable in vivo. Major causes of the complexity in the tumor systems are the diversity of levels of the tumor system(gene, molecular, cellular, tissue, organ, body and population), different time scales of each level, self-organization of the system, multitude of signaling path ways and tumor-immune and tumor-environment interactions [14]-[17]. This complexity can lead to an emergence of different types of attractors(fixed point, limit cycle,and even strange attractors)[18]-[20]. In fact,one can also experimentally demonstrate the existence of these limit cycles and strange attractors as a result of the complex dynamics of the tumor system [21], [22]. These strange behaviors of tumors can be addressed based on the inherent properties of chaos such as sensitive dependence on initial conditions[23]. Sensitive dependence on initial conditions makes the tumor growth patterns case specific, i.e.evolution of cancer for any patient is different from another patient, due to the different initial conditions for any individual. While this is a challenging issue for the oncologists, this is a very interesting topic in the field of tumor modeling. For these reasons, chaos theory could allow a

better understanding of this complex system [24]-[27].
Due to chaotic nature of tumor growth model, this could explain the unreliability of treatment and prediction of tumor evolution. More importantly, chaos in tumor growth model,could be used to adjust strategies for fighting cancer. Treatment could include some form of chaos synchronization, chaos control and/or anti-control. Since the seminal work of Pecora and Carroll [28], on the synchronization of chaotic systems. Synchronization phenomenon has formed a new body of research activities which is at the fore front of recent application topics in nonlinear dynamics [29]-[32]. As a result, enormous progress has been made in understanding various types [33]-[48] and methods [28], [49]-[61] of synchronization.
Complete synchronization is signalized by the equality of state variables evolving in time, while anti-synchronization is signalized by the disappearance of the sum of relevant variables evolving in time. In hybrid synchronization of chaotic systems ,one part of the system is synchronized and the other part is anti-synchronized so that the complete synchronization and anti-synchronization coexist in the system. Projective synchronization is interesting because of its proportionality between the synchronized dynamical states .Mainieri and Rehacek were the first to study it and they declared that two identical systems could be synchronized up to a scaling factor λ , which is a constant transformation between the synchronized variables of the driven and response systems [34]-[38]. Obviously, complete synchronization and anti phase synchronization are special cases of projective synchronization with $\lambda = 1$ and $\lambda = -1$ respectively.
In this paper we achieve hybrid and projective synchronization of the trajectory of coupled tumor growth and decay models with different initial conditions via Active control method. This study can be used as a powerful tool for adjusting strategies for fighting cancer. By synchronization, reliability of treatment and prediction of tumor evolution become possible. This paper may be a base to devise the appropriable devices for the treatment of cancer growth. Also, numerical experiments are performed to show such synchronization on tumor growth and decay models.

2. Model description

A multiscale diffusion cancer-invasion model (MDCM) was presented in [62]-[70], which considers cellular and micro environmental factors simultaneously and interactively. The model was classified as hybrid, since a continuum deterministic model (based on a system of reaction-diffusion chemotaxis equations) controls the chemical and extracellular matrix (ECM) kinetics and a discrete cellular automata-like model (based on a biased random-walk model) controls the cell migration and interaction. The interactions of the tumor cells, matrix-metalloproteinases (MMs), matrix-degradative enzymes (MDEs) and oxygen are described by the four coupled rate PDEs:

$$\frac{\partial n}{\partial t} = D_n \nabla^2 n - \chi \nabla (n \nabla f), \tag{2.1}$$

$$\frac{\partial f}{\partial t} = -\delta m f, \tag{2.2}$$

$$\frac{\partial m}{\partial t} = D_m \nabla^2 m + \mu n - \lambda m, \tag{2.3}$$

$$\frac{\partial c}{\partial t} = D_c \nabla^2 c + \beta f - \gamma n - \alpha c. \tag{2.4}$$

where n denotes the tumor cell density, f is the MM-concentration, m corresponds to the MDE-concentration and c denotes the oxygen concentration. The four variables, n, m, f, c are all functions of the 3-dimensional spatial variable x and time t. All equations represent diffusion except(2.2), which shows only temporal evolution of the MM-concentration coupled to the MDE-concentration. D_n is the tumor cell coefficient , D_m is the MDE coefficient and $D_c > 0$ is the oxygen diffusion coefficient,while $\chi, \mu, \lambda, \delta, \alpha, \gamma, \beta$ are positive constants.The other terms respectively denote:

$\chi\nabla.(n.\nabla f)$ – hapototaxis;
μN – poduction of MDE by tumor cell;
λm – decay of MDE;
δmf – degradation of MM by MDE;
αc – natural decay of oxygen;
γm – oxygen uptake and;
βf – production of oxygen by MM.

Because of its hybrid nature (cells are treated as discrete entities and micro environmental parameters are treated as continuous concentrations), the 4-dimensional (4D) model (2.1)-(2.4) can be directly linked to experimental measurements of those cellular and micro environmental parameters recognized by cancer biologists are treated as very important in cancer invasion . Furthermore, the fundamental unit of the model is the cell, and the complex collective behavior of the tumor emerges as a consequence of interactions between factors influencing the life cycle and movement of individual cells [62], [64], [65], [68], [69], [70]. In order to use realistic parameter values, the system of rate equations (2.1-2.4) was non-dimensionalised. In order to use realistic parameter values, we first of all non-dimensionalised the equations (2.1) - (2.4) in the standard way. We rescale distance with an appropriate length scale L (e.g. the maximum invasion distance of the cancer cells at this early stage of invasion, approximately 1 cm), time with τ (e.g. the average time taken for mitosis to occur, approximately 8-24 h), tumour cell density with n_0, ECM density with f_0, MDE concentration with m_0 and oxygen concentration with c_0 (where n_0, f_0, m_0 and c_0 are appropriate reference variables). Therefore, setting

$$\tilde{n} = \frac{n}{n_0}, \tilde{f} = \frac{f}{f_0}, \tilde{m} = \frac{m}{m_0}, \tilde{c} = \frac{c}{c_0}, \tilde{x} = \frac{x}{L}, \tilde{t} = \frac{t}{\tau}$$

in equations (2.1)- (2.4). After dropping the tildes notational convenience, the resulting 4D scaled system of rate PDEs [64] is given by

$$\frac{\partial n}{\partial t} = d_n \nabla^2 n - \rho \nabla (n \nabla f), \tag{2.5}$$

$$\frac{\partial f}{\partial t} = -\eta m f, \tag{2.6}$$

$$\frac{\partial m}{\partial t} = d_m \nabla^2 m + \kappa n - \sigma m, \tag{2.7}$$

$$\frac{\partial c}{\partial t} = d_c \nabla^2 c + \nu f - \omega n - \phi c. \tag{2.8}$$

The values of non-dimensional parameters were given as[64]:
$d_n = 0.0005$, $\rho = 0.01$, $\eta = 50$, $d_m = 0.0005$, $\kappa = 1$, $\sigma = 0$, $d_c = 0.5$, $\nu = 0.5$, $\omega = 0.57$, $\phi = 0.025$.

2.1. A chaotic multi-scale cancer-invasion model. [73] From the non-dimensional spatio-temporal AC model (2.5)- (2.8), discretization was formed by neglecting all the spatial derivatives which means $\nabla n, \nabla f, \nabla m, \nabla c$ all becomes zero and our coupled partial differential equations (2.5)- (2.8) reduced into ordinary coupled differential equations as all the four variable n,m,f and c now depends only on time, thus $\frac{\partial n}{\partial t} = \frac{dn}{dt}$, $\frac{\partial m}{\partial t} = \frac{dm}{dt}$, $\frac{\partial f}{\partial t} = \frac{df}{dt}$ and $\frac{\partial c}{\partial t} = \frac{dc}{dt}$.

Hence our model resulting into 4D temporal dynamical system which can de described as :

$$\dot{n} = 0, \tag{2.9}$$

$$\dot{f} = -\eta m f, \tag{2.10}$$

$$\dot{m} = \kappa n - \sigma m, \tag{2.11}$$

When simulated, the temporal system (2.9)-(2.12) with the set of parameters,

$$\rho = 0.01, \eta = 50, \kappa = 1, \sigma = 0, \nu = 0.5, \omega = 0.57, \phi = 0.025. \tag{2.13}$$

exhibits a virtually linear temporal behavior with almost no coupling between the four concentrations that have very different quantitative values (all phase plots between the four concentrations, are virtually one-dimensional). To see if a modified version of the system (2.9)-(2.12) could lead to a chaotic description of tumor growth, four new parameters α, β, γ, δ were introduced.The resulting model is:

$$\dot{n} = 0, \tag{2.14}$$

$$\dot{f} = \alpha\eta(m - f), \tag{2.15}$$

$$\dot{m} = \beta\kappa n + f(\gamma - c) - m, \tag{2.16}$$

$$\dot{c} = \nu f m - \omega n - \delta\phi c. \tag{2.17}$$

The introduction of the parameters ($\alpha, \beta, \gamma, \delta$) was motivated by the fact that tumor cell shape represents a visual manifestation of an underlying balance of forces and chemical reactions [71]. Specifically, the parameters represent the following quantities:

α = tumor cell volume (prolife ration/non − proliferation fraction),

β = glucose level,

γ = number of tumor cells,

δ = diffusion from the surface (saturation level).

For computations, the parameters were set to $\alpha = 0.06$, $\beta = 0.05$, $\gamma = 26.5$, $\delta = 40$. Small variation of these chosen values would not affect the qualitative behavior of the new temporal model (2.14)- (2.17). Simulations of (2.14)- (2.17), using the initial conditions($n(0) = .5,\ f(0) = 1.5, m(0) = c(0) = .5$) and the same non-dimensional parameters as before given in (2.13), show chaotic behavior in the form of Lorenz-like strange attractors in the 3D (f - m - c) subspace of the full 4D (n - f - m - c) phase-space.(Figure 1;(A),(B),(C) & (D))

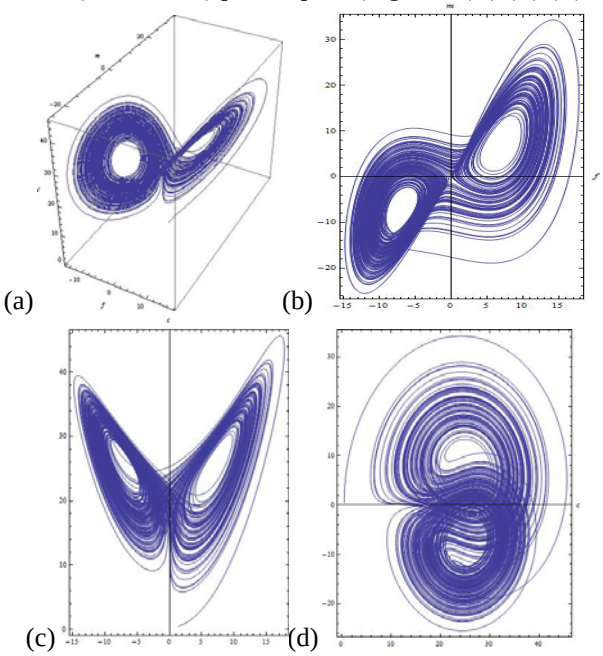


Figure 1: (a) Phase Portrait of a tumor growth system in the m-f-c space ; and projections on (b) the f-m plane, (c) the f-c plane and (d) the c-m plane.

3. Hybrid Synchronization of Two Identical Tumor Growth Model Using Active Control Method.

For a system of two identical chaotic systems to be in hybrid synchronization, we consider master/drive system with subscript 1 in Tumor growth model and slave/response system with subscript 2 in Tumor growth model with different initial conditions. Then drive and response systems are defined as follows:

$$\begin{aligned} \dot{n}_1 &= 0, \\ \dot{f}_1 &= \alpha\eta(m_1 - f_1), \\ \dot{m}_1 &= \beta\kappa n_1 + f_1(\gamma - c_1) - m_1, \\ \dot{c}_1 &= \nu f_1 m_1 - \omega n_1 - \delta\phi c_1. \end{aligned} \tag{3.1}$$

and

$$\begin{aligned}\dot{n}_2 &= 0+U_1(t),\\ \dot{f}_2 &= \alpha\eta(m_2 - f_2)+U_2(t),\\ \dot{m}_2 &= \beta\kappa n_2 + f_2(\gamma - c_2) - m_2 + U_3(t),\\ \dot{c}_2 &= \nu f_2 m_2 - \omega n_2 - \delta\phi c_2 + U_4(t).\end{aligned} \tag{3.2}$$

where $U_1(t), U_2(t), U_3(t)$ and $U_4(t)$ are the control functions in the response system. We aim to design the control functions $U_i(t)$, i=1,2,3 and 4.

To observe hybrid synchronization between the master system (3.1) and the slave system (3.2) , we firstly note that the co-existence of synchronization and anti- synchronization in a system can occur in more than one way. The master system (3.1) contains four state variables namely n_1, f_1, m_1 & c_1 Thus, various combinations of variables can be made to get synchronized while the remaining variables will then be anti-synchronized. Using the theory of combinations, it follows that there are C (4, 0)+C (4, 1)+C (4, 2)+C (4, 3)+C (4, 4) = 16 possible ways of combining the variables. Out of them, C(4,4) and C(4,0) correspond to the cases of complete synchronization and anti-synchronization respectively. Hence, there are 14 different hybrid synchronization phenomena possible.

Let us discuss two of the above mentioned cases:

Case – 1. First, we completely synchronize the state variable n_1 and m_1 ; and the state variables i.e f_1 and c_1 are anti-synchronized. The hybrid synchronization errors are defined as ;

$$e_1 = n_2 - n_1, \quad E_2 = f_2 + f_1, \quad e_3 = m_2 - m_1 \quad and \quad E_4 = c_2 + c_1. \tag{3.3}$$

using (3.1), (3.2) and (3.3) the corresponding error dynamics is given by :

$$\begin{aligned}\dot{e}_1 &= U_1(t),\\ \dot{E}_2 &= \alpha\eta(e_3 - E_2) + 2\alpha\eta m_1 + U_2(t),\\ \dot{e}_3 &= \beta\kappa e_1 + \gamma E_2 - e_3 - 2\gamma f_1 + f_1 c_1 - f_2 c_2 + U_3(t),\\ \dot{E}_4 &= \nu f_2 m_2 + \nu f_1 m_1 - \omega(e_1 + 2n_1) - \delta\phi E_4 + U_4(t).\end{aligned} \tag{3.4}$$

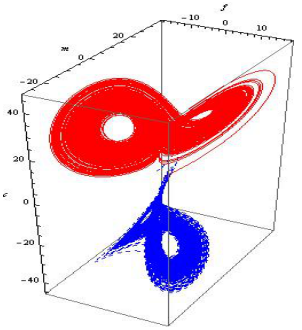


Figure 2: Phase Portrait of master (red,thick) and slave system (blue,dotted) in m-f-c space.

This error system (3.4) to be controlled must be a linear system. To eliminate the non-linear terms

in (3.4), we redefine the control functions as :

$$U_1(t) = V_1(t),$$
$$U_2(t) = -2\alpha\eta m_1 + V_2(t),$$
$$U_3(t) = 2\gamma f_1 - f_1 c_1 + f_2 c_2 + V_3(t),$$
$$U_4(t) = -\nu f_2 m_2 - \nu f_1 m_1 + 2\omega n_1 + V_4(t). \tag{3.5}$$

Subsequently, the new error system can be expressed as:

$$\dot{e}_1 = V_1(t),$$
$$\dot{E}_2 = \alpha\eta(e_3 - E_2) + V_2(t),$$
$$\dot{e}_3 = \beta\kappa e_1 + \gamma E_2 - e_3 + V_3(t),$$
$$\dot{E}_4 = -\omega e_1 - \delta\phi E_4 + V_4(t). \tag{3.6}$$

The error system (3.6) to be controlled is a linear system with controlled inputs V_i; (i = 1, 2, 3, 4) as functions of error states e_i ; (i=1,3) and E_i ; (i=2,4). If $lim_{t\to\infty} e_i(t) = 0$, (i= 1 ,3) and $lim_{t\to\infty} E_i(t) = 0$, (i= 2, 4) ,synchronization and anti-synchronization between master and slave system is realized respectively . There are many possible choices for the controls $V_1(t), V_2(t), V_3(t)$ and $V_4(t)$ to obtain the required conditions. We choose

$$\begin{bmatrix} V_1(t) \\ V_2(t) \\ V_3(t) \\ V_4(t) \end{bmatrix} = A \begin{bmatrix} e_1 \\ E_2 \\ e_3 \\ E_4 \end{bmatrix} \tag{3.7}$$

Here A is a square matrix of order four to be determined. Choosing,

$$A = \begin{bmatrix} -1 & 0 & 0 & 0 \\ 0 & \alpha\eta - 1 & -\alpha\eta & 0 \\ -\beta\kappa & -\gamma & 0 & 0 \\ \omega & 0 & 0 & \delta\phi - 1 \end{bmatrix} \tag{3.8}$$

Using (3.7)and (3.8),we get the values for $V_1(t), V_2(t), V_3(t)$ and $V_4(t)$,then (3.4) can be rewritten as:

$$\begin{bmatrix} \dot{e}_1(t) \\ \dot{E}_2(t) \\ \dot{e}_3(t) \\ \dot{E}_4(t) \end{bmatrix} = B \begin{bmatrix} e_1(t) \\ E_2(t) \\ e_3(t) \\ E_4(t) \end{bmatrix}$$

where,

$$B = \begin{bmatrix} -1 & 0 & 0 & 0 \\ 0 & -1 & 0 & 0 \\ 0 & 0 & -1 & 0 \\ 0 & 0 & 0 & -1 \end{bmatrix} \tag{3.9}$$

Hence the error system becomes

$$\dot{e}_1 = -e_1, \quad \dot{E}_2 = -E_2, \quad \dot{e}_3 = -e_3 \quad and \quad \dot{E}_4 = -E_4 \tag{3.10}$$

Now, we consider the Lyapunov function as;

$$V(e) = 1/2e^T e = 1/2(e_1^2 + E_2^2 + e_3^2 + E_4^2) \tag{3.11}$$

which is a positive definite function on R^4. Differentiating (3.11) along the trajectories of (3.10), we get

$$\dot{V}(e) = -e_1^2 - E_2^2 - e_3^2 - E_4^2 \tag{3.12}$$

which is a negative definite function on R^4. Thus, by Lyapunov stability theory [72], the error dynamics (3.4) is globally exponentially stable. Hence, it is proved that $lim_{t\to\infty} e_i(t) = 0, \quad i = 1 \quad and \quad 3$ and $lim_{t\to\infty} E_i(t) = 0, \quad i = 2 \quad and \quad 4$ and hence, state variable n_1 and m_1 are synchronized while the state variables f_1 and c_1 are anti-synchronized. Thus, hybrid synchronization is achieved between the master and slave systems (3.1) and (3.2).

3.1. Simulation results. Numerical results are presented to demonstrate the effectiveness of the proposed technique. We select the parameters of tumor growth and decay system as $\alpha = 0.06$, $\beta = 0.05$, $\gamma = 26.5$, $\delta = 40$. So that tumor growth and decay exhibits a chaotic behavior. The initial values of the master and slave systems are $(n_1(0), f_1(0), m_1(0), c_1(0)) = (.5,1.5,.5,.5)$ and $(n_2(0), f_2(0), m_2(0), c_2(0)) = (1,-1.5,1.5,2)$ respectively, while the initial states of the error system (3.10) are $(e_1(0), E_2(0), e_3(0), E_4(0)) = (.5,0,1,2.5)$ with these initial values, the phase portrait of master and slave systems together in mfc plane display hybrid synchronization in Figure 2. The time waveform diagram of master and slave states variables are illustrated Figure 3. It is shown that the states n_1 and n_2 display a synchronization phenomenon, f_1 and f_2 shows anti synchronization behaviour, m_1 and m_2 also synchronized in complete way and c_1 and c_2 display anti synchronization behaviour. The dynamics of synchronization and anti-synchronization error functions for the drive and response systems verses time "t" is shown in (Figure 4) by trajectories $e_1(t), E_2(t), e_3(t)$ and $E_4(t)$. We can see that the synchronization error will converge to zero at $t = 6$. Thus, desired chaos synchronization is achieved between two identical tumor growth and decay systems with different initial conditions.

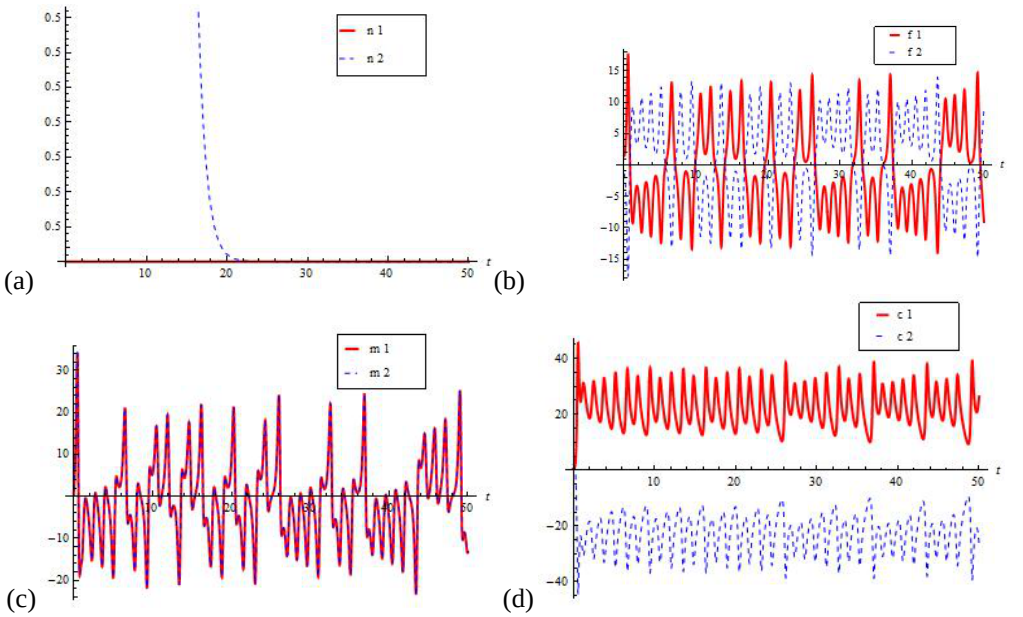


Figure 3: The time waveform diagram of the two identical tumor growth and decay systems with different initial conditions by using active control method in hybrid synchronization cases : (a) Time series signals n_1 (red,thick) and n_2 (blue,dotted) ; (b) Time series signals f_1 (red,thick) and f_2 (blue,dotted); (c) Time series signals m_1 (red,thick) and m_2 (blue,dotted) and (d) Time series signals c_1 (red,thick) and c_2 (blue,dotted).

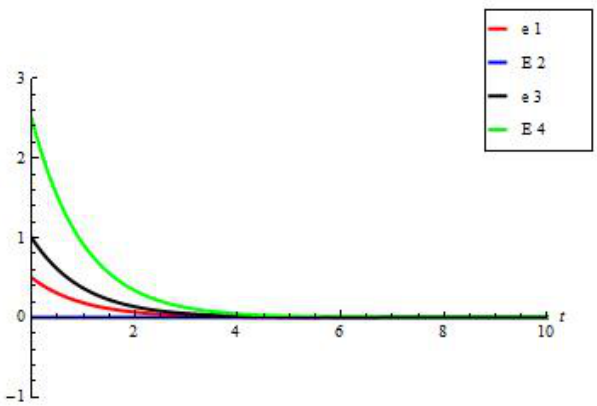


Figure 4: The synchronization error functions $e_1(t)$, $E_2(t)$, $e_3(t)$ & $E_4(t)$ of four state variable tends to 0 at t=6.

Case -2. Now consider the case where the combination is reversed i.e we anti synchronize the state variables n_1 and m_1 and completely synchronize the state variables f_1 and c_1 . The hybrid synchronization errors are defined as ;

$$E_1 = n_2 + n_1, \quad e_2 = f_2 - f_1, \quad E_3 = m_2 + m_1 \quad and \quad e_4 = c_2 - c_1. \tag{3.13}$$

using (3.1), (3.2) and (3.13), the corresponding error dynamics is given by :

$$\begin{aligned} \dot{E}_1 &= U_1(t), \\ \dot{e}_2 &= \alpha\eta(E_3 - e_2) - 2\alpha\eta m_1 + U_2(t), \\ \dot{E}_3 &= \beta\kappa E_1 + \gamma e_2 - E_3 + 2\gamma f_1 - f_1 c_1 - f_2 c_2 + U_3(t), \\ \dot{e}_4 &= \nu f_2 m_2 - \nu f_1 m_1 - \omega(E_1 - 2n_1) - \delta\phi e_4 + U_4(t). \end{aligned} \tag{3.14}$$

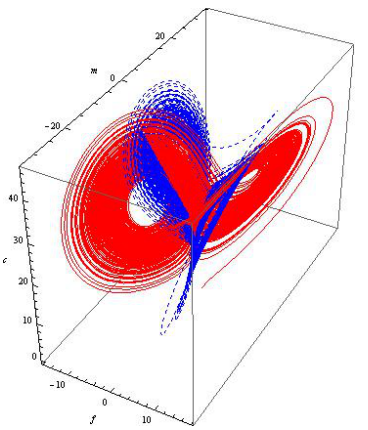


Figure 5: Phase Portrait of master system (red,thick) and slave system (blue,dotted) in m-f-c space.

Following the earlier line of arguments, we redefine the control functions as follows:

$$\begin{aligned} U_1(t) &= V_1(t), \\ U_2(t) &= 2\alpha\eta m_1 + V_2(t), \\ U_3(t) &= -2\gamma f_1 + f_1 c_1 + f_2 c_2 + V_3(t), \\ U_4(t) &= -\nu f_2 m_2 + \nu f_1 m_1 - 2\omega n_1 + V_4(t). \end{aligned} \tag{3.15}$$

Thus, the linear error system can be written as:

$$\begin{aligned} \dot{E}_1 &= V_1(t), \\ \dot{e}_2 &= \alpha\eta(E_3 - e_2) + V_2(t), \\ \dot{E}_3 &= \beta\kappa E_1 + \gamma e_2 - E_3 + V_3(t), \\ \dot{e}_4 &= -\omega E_1 - \delta\phi e_4 + V_4(t). \end{aligned} \tag{3.16}$$

This is again equivalent to the linear error dynamics as given by (3.6).Again with the same choice of matrices A and B as given in (3.8) and (3.9) respectively ,the error system becomes

$$\dot{E}_1 = -E_1, \quad \dot{e}_2 = -e_2, \quad \dot{E}_3 = -E_3 \quad and \quad \dot{e}_4 = -e_4 \tag{3.17}$$

Now we consider the Lyapunov function as;

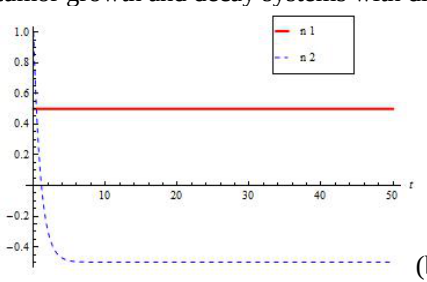
$$V(e) = 1/2e^T e = 1/2(E_1^2 + e_2^2 + E_3^2 + e_4^2) \tag{3.18}$$

which is a positive definite function on R^4. Differentiating (3.18) along the trajectories of (3.17), we get

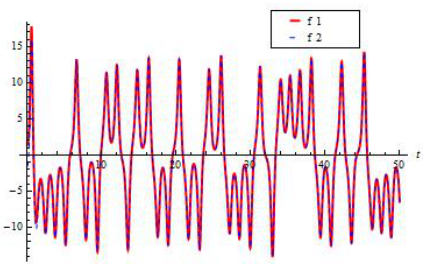
$$\dot{V}(e) = -E_1^2 - e_2^2 - E_3^2 - e_4^2 \tag{3.19}$$

which is a negative definite function on R^4. Thus, by Lyapunov stability theory [72], the error dynamics (??) is globally exponentially stable. Hence, it is proved that $lim_{t\to\infty} E_i(t) = 0, \quad i = 1 \quad and \quad 3$ and $lim_{t\to\infty} e_i(t) = 0, \quad i = 2 \quad and \quad 4$ and state variables n_1 and m_1 are anti-synchronized while the remaining state variables f_1 and c_1 are completely synchronized. Thus, hybrid synchronization is achieved between the master system (3.1) and slave system (3.2).

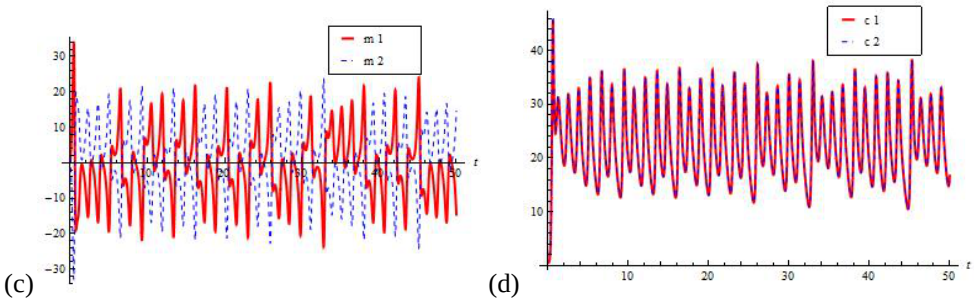
3.2. Simulation results. Numerical results are presented to demonstrate the effectiveness of the proposed technique. We select the parameters of tumor growth systems as $\alpha = 0.06$, $\beta = 0.05$, $\gamma = 26.5$, $\delta = 40$ so that tumor growth systems exhibits a chaotic behavior. The initial values of the master and slave systems are $(n_1(0), f_1(0), m_1(0), c_1(0))$ = (.5,1.5,.5,.5) and $(n_2(0), f_2(0), m_2(0), c_2(0))$ = (1,–1.5,1.5,2) respectively, while the initial states of the error system (3.17) are $(E_1(0), e_2(0), E_3(0), e_4(0))$ = (1.5,–3,2,1.5) with these initial values the phase portrait of master and slave systems together in mfc plane display hybrid synchronization (Figure 5). The time waveform diagram of master and slave states variables are illustrated in (Figure 6). It is shown that the states n_1 and n_2 display anti synchronization phenomenon, f_1 and f_2 shows complete synchronization behaviour, m_1 and m_2 also synchronized in anti way and c_1 and c_2 display complete synchronization behaviour. The dynamics of synchronization error functions for the drive and response systems verses time "t" is shown in Figure 7 by trajectories $E_1(t), e_2(t), E_3(t)$ and $e_4(t)$. These figures display that synchronization error will converge to zero at $t = 8$ and we achieve desired hybrid projective synchronization between two identical tumor growth and decay systems with different initial conditions.



(a)



(b)



(c) (d)

Figure 6: The time waveform diagram of the two identical tumor growth system with different initial condition by using active control method in hybrid synchronization cases) : (a) Time series signals n_1 (red,thick) and n_2 (blue,dotted) ; (b) Time series signals f_1 (red,thick) and f_2 (blue,dotted); (c) Time series signals m_1 (red,thick) and m_2 (blue,dotted) and (d) Time series signals c_1 (red,thick) and c_2 (blue,dotted).

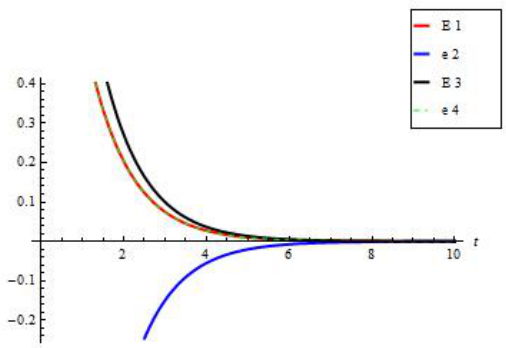


Figure 7: The synchronization error functions $E_1(t)$, $e_2(t)$, $E_3(t)$ & $e_4(t)$ of four state variable tends to 0 at t=8.

4. Projective Synchronization Between Two Identical Tumor Growth Model.

To observe the projective synchronization between master and slave systems given in (3.1)and (3.2)respectively. Lets us define the projective synchronization error as :

$$e_1 = n_2 - \lambda n_1, \quad e_2 = f_2 - \lambda f_1, \quad e_3 = m_2 - \lambda m_1 \quad and \quad e_4 = c_2 - \lambda c_1. \qquad (4.1)$$

where λ is a constant parameter. Now, the error dynamics is given as :-

$$\begin{aligned} \dot{e}_1 &= U_1(t), \\ \dot{e}_2 &= \alpha\eta(e_3 - e_2) + U_2(t), \\ \dot{e}_3 &= \beta\kappa e_1 + \gamma e_2 - e_3 + \lambda f_1 c_1 - f_2 c_2 + U_3(t), \\ \dot{e}_4 &= \nu f_2 m_2 - \lambda \nu f_1 m_1 - \omega e_1 - \delta\phi e_4 + U_4(t). \end{aligned} \qquad (4.2)$$

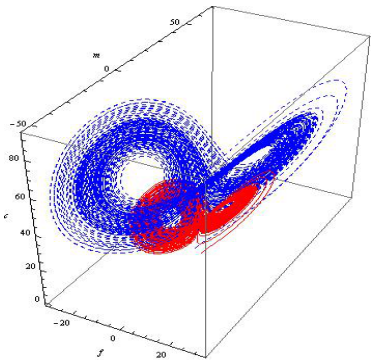


Figure 8: Phase Portrait of master system (red,thick) and slave system (blue,dotted) in m-f-c space.

This error system (4.2) to be controlled must be a linear system with control functions. Thus, let us redefine the control functions so that the terms in (4.2) which cannot be expressed as linear terms in $e_i's$ are eliminated.

$$\begin{aligned} U_1(t) &= V_1(t), \\ U_2(t) &= V_2(t), \\ U_3(t) &= -\lambda f_1 c_1 + f_2 c_2 + V_3(t), \\ U_4(t) &= -\nu f_2 m_2 + \lambda \nu f_1 m_1 + V_4(t). \end{aligned} \tag{4.3}$$

The new error system is expressed as:

$$\begin{aligned} \dot{e}_1 &= V_1(t), \\ \dot{e}_2 &= \alpha\eta(e_3 - e_2) + V_2(t), \\ \dot{e}_3 &= \beta\kappa e_1 + \gamma e_2 - e_3 + V_3(t), \\ \dot{e}_4 &= -\omega e_1 - \delta\phi e_4 + V_4(t). \end{aligned} \tag{4.4}$$

Again, (4.4) is the identical system as given in (3.6). Hence, following the same steps, the error system becomes

$$\dot{e}_1 = -e_1, \quad \dot{e}_2 = -e_2, \quad \dot{e}_3 = -e_3 \quad and \quad \dot{e}_4 = -e_4. \tag{4.5}$$

Now we consider the Lyapunov function as;

$$V(e) = 1/2 e^T e = 1/2(e_1^2 + e_2^2 + e_3^2 + e_4^2.) \tag{4.6}$$

which is a positive definite function on R^4. Differentiating (4.6) along the trajectories of (4.5), we get

$$\dot{V}(e) = -e_1^2 - e_2^2 - e_3^2 - e_4^2, \tag{4.7}$$

which is a negative definite function on R^4. Thus, by Lyapunov stability theory [72], the error dynamics (??) is globally exponentially stable. Hence, $lim_{t\to\infty} e_i(t) = 0, \quad i = 1,2,3 \quad and \quad 4.$ This ascertains the projective synchronization between the master system (3.1) and slave system (3.2).

4.1. Simulation results. Numerical results are presented to demonstrate the effectiveness of the

proposed technique. We select the parameters of tumor growth system as $\alpha = 0.06$, $\beta = 0.05$, $\gamma = 26.5$, $\delta = 40$ for these values tumor growth model exhibits a chaotic behavior. The initial values of the master and slave systems are $(n_1(0), f_1(0), m_1(0), c_1(0)) = (.5, 1.5, .5, .5)$ and $(n_2(0), f_2(0), m_2(0), c_2(0)) = (1, -1.5, 1.5, 2)$ respectively. On choosing parameter $\lambda = 2$ for projective synchronization, the initial states of the error system (4.5) becomes $(e_1(0), e_2(0), e_3(0), e_4(0)) = (0, -4.5, .5, 1)$. With these initial values the phase portraits of master and slave systems together in mfc plane display projective synchronization in Figure 8. The time waveform diagram of master and slave systems states variables are illustrated in Figure 9. It is observed that the states of slaves system converges two times the values of the states of master. The dynamics of synchronization error functions for the drive and response systems verses time "t" is shown (Figure 10) by trajectories $e_1(t), e_2(t), e_3(t)$ and $e_4(t)$. We can see that the synchronization error will converge to zero at $t = 10$ and two identical tumor growth chaotic systems are indeed achieving projective synchronization.

Also,it is easy to see that complete and anti synchronization are the special cases of projective synchronization with parameter $\lambda = 1$ and $\lambda = -1$ respectively.

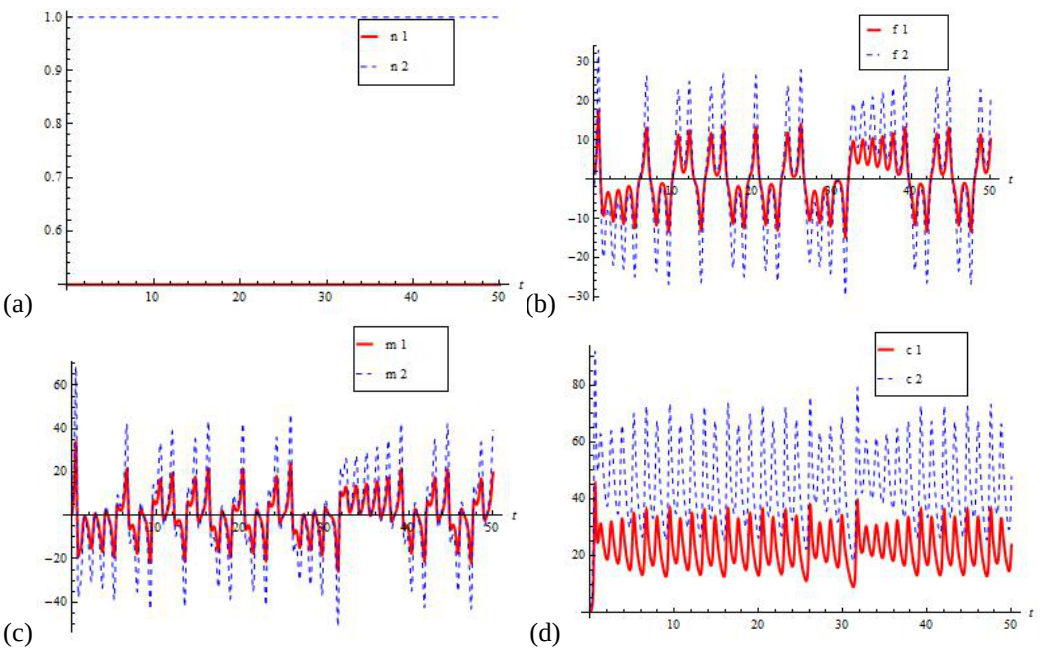


Figure 9: The time waveform diagram of the two identical tumor growth systems with different initial conditions by using active control method in projective synchronization with $\lambda = 2$: (a) Time series signals n_1 (red,thick) and n_2 (blue,dotted) ; (b) Time series signals f_1 (red,thick) and f_2 (blue,dotted); (c) Time series signals m_1 (red,thick) and m_2 (blue,dotted) and (d) Time series

signals c_1 (red,thick) and c_2 (blue,dotted).

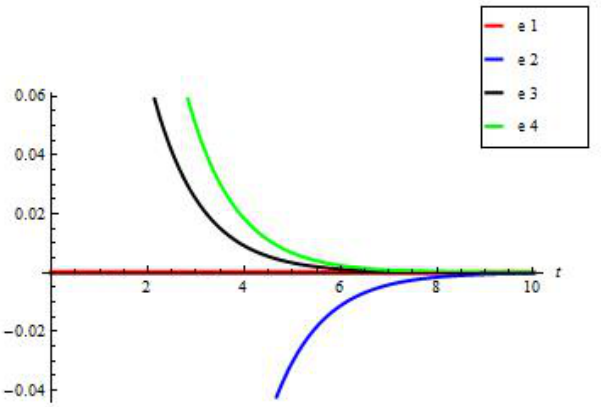


Figure 10: The synchronization error functions $e_1(t)$, $e_2(t)$, $e_3(t)$ & $e_4(t)$ of four state variable tends to 0 at t=10.

5. Conclusion

In this manuscript, we presented two kind of synchronization i.e hybrid synchronization and projective synchronization between two Tumor growth models evolving from different initial conditions using the Active Control Technique which is based on Lyapunov Stability Theory. The effectiveness and feasibility of results are validated in numerical simulations which are performed by using Mathematica software. Remarkably, our analytic and computational results are in an excellent agreement. It is a significant mathematical description to devise the sophisticated experimental mechanism for the treatment of tumor growth.

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Some new convergence theorems for a hybrid pair of nonexpansive mappings in CAT(0) spaces

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Abstract: In 2010, Sokhuma and Kaewkhao introduced a modified Ishikawa iteration scheme for a pair of single valued and multivalued nonexpansive mappings in Banach spaces and proved some convergence theorems. In this paper, we study about the convergence of modified Ishikawa iteration process for a pair of single valued and multivalued generalized nonexpansive mappings in CAT(0) spaces. In this process, we generalize many existing results in literature.

Keywords: CAT(0) spaces, Fixed point, Δ-convergence, and Opial property.
AMS Subject Classification: 47H10, 54H25.

1. Introduction

A self-mapping T defined on a bounded, closed and convex subset K of a Banach space X is said to be nonexpansive if (for all $x, y \in K$)

$$\| Tx - Ty \| \leq \| x - y \|.$$

It is well known that sequence of Picard iteration [1] defined as (for any $x_1 \in K$)

$$x_{n+1} = T^n x, \quad n \in \mathbb{N} \tag{1.1}$$

need not be convergent in respect of a nonexpansive mapping. E.g., the sequence of iterates $x_{n+1} = Tx_n$ for the mapping $T : [-1,1] \to [-1,1]$ defined by $Tx = -x$ does not converges to 0 which is indeed the fixed point of T. In an attempt to construct a convergent sequence of iterates in respect of a nonexpansive mapping, Mann [2] defined an iteration method as: (for any $x_1 \in K$)

$$x_{n+1} = (1-\alpha_n)x_n + \alpha_n Tx_n, \quad n \in \mathbb{N} \tag{1.2}$$

where $\alpha_n \in (0,1)$.

With a view to have a better rate of convergence, Ishikawa [3] introduced a new iteration procedure as follows: (for $x_1 \in K$)

$$y_n = (1-\alpha_n)x_n + \alpha_n Tx_n, x_{n+1} = (1-\beta_n)x_n + \beta_n Ty_n, \quad n \in \mathbb{N} \tag{1.3}$$

where $\alpha_n, \beta_n \in (0,1)$.

Iterative techniques for approximating fixed points of nonexpansive single-valued mappings have

been investigated by various authors (see; e.g., [4, 5, 6]) using the Mann iteration scheme or the Ishikawa iteration scheme. By now, there exists an extensive literature on the iterative fixed points for various classes of mappings. For an upto date account of literature on this theme, we refer the readers to Berinde [7].

Let X be a Banach space and K be a nonempty subset of X. Let $CB(K)$ be the family of nonempty closed bounded subsets of K while $KC(K)$ be the family of nonempty compact convex subsets of K. A subset K of X is called proximinal if for each $x \in X$, there exists an element $k \in K$ such that

$$d(x,k) = dist(x,K) = \inf\{\| x - y \| : y \in K\}.$$

It is well known that every closed convex subset of a uniformly convex Banach space is proximinal. We shall denote by $PB(K)$, the family of nonempty bounded proximinal subsets of K. The Hausdorff metric H on $CB(K)$ is defined as

$$H(A,B) = max\{\sup_{x\in A} d(x,B), \sup_{y\in B} d(y,A)\} \ \ for \ A, B \in CB(K).$$

A multivalued mapping $T : K \to CB(K)$ is said to be nonexpansive if

$$H(T(x),T(y)) \leq \| x - y \|, \ \ for \ \ all \ x, y \in K.$$

We use the notation $F(T)$ for the set of fixed points of the mapping T while $F(t,T)$ denotes the set of common fixed points of t and T, i.e. a point x is said to be a common fixed point of t and T if $x = tx \in Tx$.

In 2010, Sokhuma and Kaewkhao [8] introduced a modified Ishikawa iterative process involving a pair of single valued and multivalued nonexpansive mappings in Banach spaces and proved strong convergence theorems. This scheme has been studied by several authors [8, 9, 10, 11] with respect to different class of mappings in Banach Spaces. The purpose of this paper is to study modified Ishikawa iterative method for a hybrid pair of nonexpansive mappings in CAT(0) spaces.

2. Some iteration procedure for multi-valued mapping

In 2005, Sastry and Babu [12] defined Ishikawa iteration scheme for multivalued mappings. Let $T : K \to PB(K)$ a multivalued mapping and fix $p \in F(T)$. Then the sequence of Ishikawa iteration is defined as follows:

Choose $x_0 \in K$,

$$y_n = \beta_n z_n + (1-\beta_n)x_n, \quad \beta_n \in [0,1], \ n \geq 0,$$

where $z_n \in T(x_n)$ such that $\| z_n - p \| = d(p,T(x_n))$ and

$$x_{n+1} = \alpha_n z_n' + (1-\alpha_n)x_n, \ \alpha_n \in [0,1], n \geq 0,$$

where $z_n' \in T(y_n)$ such that $\| z_n' - p \| = d(p,T(y_n))$.

Sastry and Babu [12] proved that Ishikawa iteration scheme for a multivalued nonexpansive mapping T converges to a fixed point of T under certain conditions. In 2007, Panyanak [13] extended the results of Sastry and Babu to uniformly convex Banach space for multivalued nonexpansive mappings. Panyanak also modified the iteration scheme of Sastry and Babu and imposed the question of convergence of this scheme. He introduced the following modified

Ishikawa iteration method,

Choose $x_0 \in K$, then

$$y_n = \beta_n z_n + (1-\beta_n)x_n, \quad \beta_n \in [a,b], 0 < a < b < 1, n \geq 0,$$

where $z_n \in Tx_n$ is such that $\| z_n - u_n \| = dist(u_n, Tx_n)$, and $u_n \in F(T)$ such that $\| x_n - u_n \| = dist(x_n, F(T))$, and

$$x_{n+1} = \alpha_n z'_n + (1-\alpha_n)x_n \quad \alpha_n \in [a,b],$$

where $z'_n \in T(y_n)$ such that $\| z'_n - v_n \| = dist(v_n, Ty_n)$, and $v_n \in F(T)$ such that $\| y_n - v_n \| = dist(y_n, F(T))$.

In 2009, Song and Wang [14] pointed out the gap in the result of Panyanak [13]. They solved/revised the gap and gave the partial answer to the question raised by Panyanak by using the following iteration scheme.

Let $\alpha_n, \beta_n \in [0,1]$ and $\gamma_n \in (0,\infty)$ such that $\lim_{n\to\infty} \gamma_n = 0$. Choose $x_0 \in K$, then

$$\begin{aligned} y_n &= \beta_n z_n + (1-\beta_n)x_n, \\ x_{n+1} &= \alpha_n z'_n + (1-\alpha_n)x_n, \end{aligned}$$

where $\| z_n - z'_n \| \leq H(Tx_n, Ty_n) + \gamma_n$ and $\| z_{n+1} - z'_n \| \leq H(Tx_{n+1}, Ty_n) + \gamma_n$ for $z_n \in Tx_n$ and $z'_n \in Ty_n$.

Simultaneously, Shahzad and Zegeye [15] extended the results of Sastry and Babu, Panyanak, and Song and Wang to quasi nonexpansive multivalued mappings and also relaxed the end point condition and compactness of the domain by using the following modified iteration scheme and gave the affirmative answer to the Panyanak question in a more general setting.

$$\begin{aligned} y_n &= \beta_n z_n + (1-\beta_n)x_n, \ \beta_n \in [0,1], \ n \geq 0, \\ x_{n+1} &= \alpha_n z'_n + (1-\alpha_n)x_n, \ \alpha_n \in [0,1], \ n \geq 0, \end{aligned}$$

where $z_n \in Tx_n$ and $z'_n \in Ty_n$.

Recently, Sokhuma and Kaewkhao [8] introduced the following modified Ishikawa iteration scheme for a pair of single valued and multivalued mapping.

Let K be a nonempty closed and bounded convex subset of Banach space X, let $t : K \to K$ be a single valued nonexpansive mapping and let $T : K \to CB(K)$ be a multivalued nonexpansive mapping. The sequence $\{x_n\}$ of the modified Ishikawa iteration is defined by

$$y_n = \beta_n z_n + (1-\beta_n)x_n, x_{n+1} = \alpha_n t y_n + (1-\alpha_n)x_n, \tag{1.4}$$

where $x_0 \in K$, $z_n \in Tx_n$ and $0 < a \leq \alpha_n, \beta_n \leq b < 1$.

Furthermore, they proved the following strong convergence theorem:

Theorem 2.1. *Let K be a nonempty compact convex subset of a uniformly convex Banach space X, and let $t : K \to K$ and $T : K \to CB(K)$ be a single valued and a multivalued nonexpansive mapping, respectively, and $F(t,T) \neq \varnothing$ satisfying $Tw = \{w\}$ for all*

$w \in F(t,T)$. *Let* $\{x_n\}$ *be the sequence of the modified Ishikawa iteration defined by (1) with* $0 < a \le \alpha_n, \beta_n \le b < 1$. *Then* $\{x_n\}$ *converges strongly to a common fixed point of* t *and* T.

3. The CAT(0) space setting

To make our presentation self contained, we collect relevant definitions and relevant results. In a metric space (X,d), a geodesic path joining $x \in X$ and $y \in X$ is a map c from a closed interval $[0,r] \subset R$ to X such that $c(0) = x, c(r) = y$ and $d(c(t), c(s)) = |s-t|$ for all $s,t \in [0,r]$. In particular, the mapping c is an isometry and $d(x,y) = r$. The image of c is called a geodesic segment joining x and y which is denoted by $[x,y]$ whenever such a segment exists uniquely. For any $x, y \in X$, we denote the point $z \in [x,y]$ by $z = (1-\alpha)x \oplus \alpha y$, where $0 \le \alpha \le 1$ if $d(x,z) = \alpha d(x,y)$ and $d(z,y) = (1-\alpha)d(x,y)$. The space (X,d) is called a geodesic space if any two points of X are joined by a geodesic and X is said to be uniquely geodesic if there is exactly one geodesic joining x and y for each $x, y \in X$. A subset K of X is called convex if K contains every geodesic segment joining any two points in K.

A geodesic triangle $\Delta(x_1, x_2, x_3)$ in a geodesic metric space (X,d) is consisted of three points of X (as the vertices of Δ) and a geodesic segment between each pair of points (as the edges of Δ). A comparison triangle for $\Delta(x_1, x_2, x_3)$ in (X,d) is a triangle $\bar{\Delta}(x_1, x_2, x_3) := \Delta(\bar{x}_1, \bar{x}_2, \bar{x}_3)$ in the Euclidean plane R^2 such that $d_{\mathsf{R}^2}(\bar{x}_i, \bar{x}_j) = d(x_i, x_j)$ for $i, j \in \{1,2,3\}$. A point $\bar{x} \in [\bar{x}_1, \bar{x}_2]$ is said to be comparison point for $x \in [x_1, x_2]$ if $d(x_1, x) = d(\bar{x}_1, \bar{x})$. Comparison points on $[\bar{x}_2, \bar{x}_3]$ and $[\bar{x}_3, \bar{x}_1]$ are defined in the same way.

A geodesic metric space X is called a CAT(0) space if all geodesic triangles satisfy the following comparison axiom namely: CAT(0) inequality

Let Δ be a geodesic triangle in X and let $\bar{\Delta}$ be its comparison triangle in R^2. Then Δ is said to satisfy the CAT(0) inequality if for all $x, y \in \Delta$ and all comparison points $\bar{x}, \bar{y} \in \bar{\Delta}$,

$$d(x,y) \le d_{\mathsf{R}^2}(\bar{x}, \bar{y}).$$

If x, y_1 and y_2 are points of CAT(0) space and y_0 is the midpoint of the segment $[y_1, y_2]$, then the CAT(0) inequality implies

$$d(x, y_0)^2 \le \frac{1}{2} d(x, y_1)^2 + \frac{1}{2} d(x, y_2)^2 - \frac{1}{4} d(y_1, y_2)^2.$$

The above inequality is known as (CN) inequality and was given by Bruhat and Tits [16]. A geodesic space is a CAT(0) space if and only if it satisfies (CN) inequality.

Towards certain classes of examples, one may recall that every convex subset of Euclidean space R^n endowed with the induced metric is a CAT(0) space. Also, the class of Hilbert spaces are

examples of CAT(0) space. Moreover, if any real normed space X is CAT(0) space, then it is a pre-Hilbert space. Furthermore, if X_1 and X_2 are CAT(0) spaces, then so is $X_1 \times X_2$. For further details on CAT(0) spaces, one can consult [16, 17, 18, 19].

Now, we collect some basic geometric properties which are instrumental throughout the discussions. Let X be a complete CAT(0) space and $\{x_n\}$ be a bounded sequence in X. For $x \in X$, set:

$$r(x, \{x_n\}) = \limsup_{n\to\infty} d(x, x_n).$$

The asymptotic radius $r(\{x_n\})$ is given by

$$r(\{x_n\}) = \inf\{r(x, x_n) : x \in X\},$$

and the asymptotic center $A(\{x_n\})$ of $\{x_n\}$ is defined as:

$$A(\{x_n\}) = \{x \in X : r(x, x_n) = r(\{x_n\})\}.$$

It is well known that in a CAT(0) space, $A(\{x_n\})$ consists of exactly one point (see Proposition 5 of [20]).

In 2008, Kirk and Panyanak [21] gave a concept of convergence in CAT(0) spaces which is analogue of weak convergence in Banach spaces and restriction of Lim's concept of convergence [22] to CAT(0) spaces.

Definition 3.1. ([21]). A sequence $\{x_n\}$ in X is said to Δ-converge to $x \in X$ if x is the unique asymptotic center of u_n for every subsequence $\{u_n\}$ of $\{x_n\}$. In this case we write $\Delta - \lim_n x_n = x$ and read as x is the Δ-limit of $\{x_n\}$.

Notice that for a given $\{x_n\} \subset X$ which Δ-converges to x and for any $y \in X$ with $y \neq x$ (owing to uniqueness of asymptotic center), we have

$$\limsup_{n\to\infty} d(x_n, x) < \limsup_{n\to\infty} d(x_n, y).$$

Thus every CAT(0) space satisfies the Opial property. Now, we collect some basic facts about CAT(0) spaces which will be frequently used throughout the text.

Lemma 3.1. ([21]). Every bounded sequence in a complete CAT(0) space admits a Δ-convergent subsequence.

Lemma 3.2. ([23]). If K is closed convex subset of a complete CAT(0) space and if (x_n) is a bounded sequence in K, then the asymptotic center of $\{x_n\}$ is in K.

Lemma 3.3. ([24]). Let (X, d) be a CAT(0) space. For $x, y \in X$ and $t \in [0,1]$, there exists a unique $z \in [x, y]$ such that

$$d(x, z) = td(x, y) \quad and \quad d(y, z) = (1-t)d(x, y).$$

Notice that we use the notation $(1-t)x \oplus ty$ for the unique point z of the above lemma.

Lemma 3.4. ([24]). For $x, y, z \in X$ and $t \in [0,1]$ we have

$$d((1-t)x \oplus ty, z) \leq (1-t)d(x, z) + td(y, z).$$

Lemma 3.5. ([24]). Let X be a CAT (0) space. Then

$$d((1-t)x \oplus ty, z)^2 \le (1-t)d(x,z)^2 + td(y,z)^2 - t(1-t)d(x,y)^2$$

for all $x, y, z \in X$ and $t \in [0,1]$.

In 2008, Shahzad and Markin [25] proved the common fixed point theorem for a hybrid pair of nonexpansive mappings.

Lemma 3.6. Let X be a complete bounded CAT(0)space and assume that $t : X \to X$ and $T : X \to 2^X$ are nonexpansive mappings with $T(x)$ a compact convex subset of X for each $x \in X$. If the mappings t and T commute then there is $z \in X$ such that $z = t(z) \in T(z)$.

The following lemma is a consequence of Lemma 2.9 of [26] which will be used to prove our main results.

Lemma 3.7. Let X be a complete $CAT(0)$ space and let $x \in X$. Suppose $\{t_n\}$ is a sequence in $[b,c]$ for some $b,c \in (0,1)$ and $\{x_n\}$, $\{y_n\}$ are sequences in X such that $\limsup_{n\to\infty} d(x_n, x) \le r$, $\limsup_{n\to\infty} d(y_n, x) \le r$, and $\lim_{n\to\infty} d((1-t_n)x_n \oplus t_n y_n, x) = r$ for some $r \ge 0$. Then

$$\lim_{n\to\infty} d(x_n, y_n) = 0.$$

Lemma 3.8. Let X be a CAT(0) space, and let K be a nonempty closed convex subset of X Then,

$$dist(y, Ty) \le d(y, x) + dist(x, Tx) + H(Tx, Ty),$$

where $x, y \in K$ and T is a multivalued mapping from K to $CB(K)$.

Now, we present the iteration scheme of Sokhuma and Kaewkhao [8] in CAT(0) spaces setting which is described as follows:

Let K be a nonempty closed and bounded convex subset of a CAT(0) space X, let $t : K \to K$ be a single valued nonexpansive mapping and let $T : K \to CB(K)$ be a multivalued nonexpansive mapping. The sequence $\{x_n\}$ of the modified Ishikawa iteration is defined by

$$y_n = \alpha_n z_n \oplus (1-\alpha_n)x_n, x_{n+1} = \beta_n t y_n \oplus (1-\beta_n)x_n \tag{3.1}$$

where $x_0 \in K$, $z_n \in Tx_n$ and $0 < a \le \alpha_n, \beta_n \le b < 1$.

The purpose of this paper is to study the convergence of iteration scheme (3.1) for nonexpansive mapping in CAT(0) spaces which enable us to enlarge the class of spaces. Our results generalize and extend the corresponding relevant results in Sokhuma and Kaewkhao [8].

4. Main Results

We first prove the following lemmas which play very important roles in this section.

Lemma 4.1. Let K be a nonempty closed convex subset of a CAT(0) space X. Let $t : K \to K$ and $T : K \to CB(K)$ be a single-valued and a multivalued nonexpansive mappings, respectively, and $F(t,T) \ne \varnothing$ satisfying $Tw = \{w\}$ for all $w \in F(t,T)$. Let

$\{x_n\}$ be the sequence of the modified Ishikawa iteration defined by (3.1). Then, $\lim_{n\to\infty} d(x_n, w)$ exists for all $w \in F(t,T)$.

Proof. Let $x_0 \in K$ and $w \in F(t,T)$, we have

$$\begin{aligned} d(x_{n+1}, w) &= d((1-\beta_n)x_n \oplus \beta_n t y_n, w) \\ &\le (1-\beta_n)d(x_n, w) + \beta_n d(ty_n, w) \\ &\le (1-\beta_n)d(x_n, w) + \beta_n d(y_n, w) \\ &= (1-\beta_n)d(x_n, w) + \beta_n d((1-\alpha_n)x_n \oplus \alpha_n z_n, w) \\ &\le (1-\beta_n)d(x_n, w) + \beta_n(1-\alpha_n)d(x_n, w) + \alpha_n\beta_n d(z_n, w) \\ &= (1-\beta_n)d(x_n, w) + \beta_n(1-\alpha_n)d(x_n, w) + \alpha_n\beta_n dist(z_n, Tw) \\ &\le (1-\beta_n)d(x_n, w) + \beta_n(1-\alpha_n)d(x_n, w) + \alpha_n\beta_n H(Tx_n, Tw) \\ &\le (1-\beta_n)d(x_n, w) + \beta_n(1-\alpha_n)d(x_n, w) + \alpha_n\beta_n d(x_n, w) \\ &= d(x_n, w) \end{aligned}$$

which implies that $\{d(x_n, w)\}$ is a decreasing and bounded below sequence i.e. convergent sequence. Thus, we conclude that the limit of $\{d(x_n, w)\}$ exists.

Lemma 4.2. Let K be a nonempty compact convex subset of a CAT(0) space X. Let $t : K \to K$ and $T : K \to CB(K)$ be a single-valued and a multivalued nonexpansive mapping, respectively, and $F(t,T) \neq \varnothing$ satisfying $Tw = \{w\}$ for all $w \in F(t,T)$. Let $\{x_n\}$ be the sequence of the modified Ishikawa iteration defined by (3.1). If $0 < a \le \alpha_n \le b < 1$ for some $a, b \in \mathsf{R}$, then $\lim_{n\to\infty} d(ty_n, x_n) = 0$.

Proof. Let $w \in F(t,T)$. From Lemma 4.1, $\lim_{n\to\infty} d(x_n, w)$ exists and we assume that $\lim_{n\to\infty} d(x_n, w) = c$. Consider,

$$\begin{aligned} & d(ty_n, w) = d(ty_n, tw) \le d(y_n, w) \\ & = d((1-\alpha_n)x_n \oplus \alpha_n z_n, w) \\ & \le (1-\alpha_n)d(x_n, w) + \alpha_n d(z_n, w) \\ & = (1-\alpha_n)d(x_n, w) + \alpha_n dist(z_n, Tw) \\ & \le (1-\alpha_n)d(x_n, w) + \alpha_n H(Tx_n, Tw) \\ & \le (1-\alpha_n)d(x_n, w) + \alpha_n d(x_n, w) \\ & = d(x_n, w). \end{aligned}$$

Also,

$$\lim_{n\to\infty} \sup d(ty_n, w) \le \lim_{n\to\infty} \sup d(y_n, w) \le \lim_{n\to\infty} \sup d(x_n, w) = c \qquad (3)$$

Then, we have

$$c = \lim_{n\to\infty} d(x_{n+1}, w) = \lim_{n\to\infty} d((1-\alpha_n)x_n \oplus \alpha_n t y_n, w). \tag{4}$$

Owing to Lemma 3.7, we conclude from (3) and (4) that $\lim_{n\to\infty} d(ty_n, x_n) = 0$.

Lemma 4.3. Let K be a nonempty closed convex subset of a CAT(0) space X. Let $t: K \to K$ and $T: K \to CB(K)$ be a single-valued and a multivalued nonexpansive mapping, respectively, and $F(t,T) \neq \varnothing$ satisfying $Tw = \{w\}$ for all $w \in F(t,T)$. Let $\{x_n\}$ be the sequence of the modified Ishikawa iteration defined by (3.1). If $0 < a \leq \alpha_n$, $\beta_n \leq b < 1$ for some $a, b \in \mathsf{R}$, then, $\lim_{n\to\infty} d(x_n, z_n) = 0$.

Proof. Let $w \in F(t,T)$. As earlier, we put $\lim_{n\to\infty} d(x_n, w) = c$. For $n \geq 0$, we have

$$\begin{aligned} d(x_{n+1}, w) &= d((1-\beta_n)x_n \oplus \beta_n t y_n, w) \\ &\leq (1-\beta_n) d(x_n, w) \oplus \beta_n d(ty_n, w) \\ &\leq (1-\beta_n) d(x_n, w) + \beta_n d(y_n, w) \end{aligned}$$

and therefore,

$$\begin{aligned} & d(x_{n+1}, w) - d(x_n, w) \leq \beta_n (d(y_n, w) - d(x_n, w)), \\ & \frac{d(x_{n+1}, w) - d(x_n, w)}{\beta_n} + d(x_n, w) \leq d(y_n, w) \end{aligned}$$

Thus, taking limit $n \to \infty$, we obtain

$$\lim_{n\to\infty} \inf \left\{ \frac{d(x_{n+1}, w) - d(x_n, w)}{\beta_n} + d(x_n, w) \right\} \leq \lim_{n\to\infty} \inf\, d(y_n, w)$$

thereby implying

$$c \leq \lim_{n\to\infty} \inf\, d(y_n, w)$$

From (3), we have that $\lim_{n\to\infty} \sup\, d(y_n, w) \leq c$, which further implies that

$$c = \lim_{n\to\infty} d(y_n, w) = \lim_{n\to\infty} d((1-\alpha_n)x_n \oplus \alpha_n z_n, w) \tag{6}$$

Recalling that

$$\begin{aligned} d(z_n, w) &= dist(z_n, Tw) \\ &\leq H(Tx_n, Tw) \\ &\leq d(x_n, w) \end{aligned}$$

Hence, we have

$$\lim_{n\to\infty} \sup\, d(z_n, w) \leq \lim_{n\to\infty} \sup\, d(x_n, w) = c \tag{7}$$

By using Lemma 3.7 and Equations (6) and (7), we get that $\lim_{n\to\infty} d(x_n, z_n) = 0$.

Lemma 4.4. Let K be a nonempty closed convex subset of a CAT(0) space X. Let

$t : K \to K$ and $T : K \to CB(K)$ be a single-valued and a multivalued generalized nonexpansive mapping, respectively, and $F(t,T) \neq \varnothing$ satisfying $Tw = \{w\}$ for all $w \in F(t,T)$. Let $\{x_n\}$ be the sequence of the modified Ishikawa iteration defined by (3.1). If $0 < a \leq \alpha_n$, $\beta_n \leq b < 1$ for some $a, b \in \mathsf{R}$, then, $\lim_{n\to\infty} d(tx_n, x_n) = 0.$

Proof. Consider,

$$\begin{aligned} d(tx_n, x_n) &\leq d(tx_n, ty_n) + d(ty_n, x_n) \\ &\leq d(x_n, y_n) + d(ty_n, x_n) \\ &= d(x_n, (1-\alpha_n)x_n \oplus \alpha_n z_n) + d(ty_n, x_n) \\ &\leq \alpha_n d(x_n, z_n) + d(ty_n, x_n). \end{aligned}$$

Then, we have

$$\lim_{n\to\infty} d(tx_n, x_n) \leq \lim_{n\to\infty} \alpha_n d(x_n, z_n) + \lim_{n\to\infty} d(ty_n, x_n)$$

Hence, by Lemma 4.2 and 4.3, $\lim_{n\to\infty} d(tx_n, x_n) = 0$.

Theorem 4.5. *Let K be a nonempty compact convex subset of a CAT(0) space X. Let $t : K \to K$ and $T : K \to CB(K)$ be a single-valued and a multivalued nonexpansive mappings, respectively, and $F(t,T) \neq \varnothing$ satisfying $Tw = \{w\}$ for all $w \in F(t,T)$. Let $\{x_n\}$ be the sequence of the modified Ishikawa iteration defined by (3.1). If $0 < a \leq \alpha_n$, $\beta_n \leq b < 1$, then $x_{n_i} \to y$ for some subsequence $\{x_{n_i}\}$ of $\{x_n\}$ implies $y \in F(t,T)$.*

Proof. Let us suppose that $\lim_{i\to\infty} d(x_{n_i}, y) = 0$. From Lemma 4.4, we have

$$\lim_{i\to\infty} d(tx_{n_i}, x_{n_i}) = 0$$

Now, we have

$$\begin{aligned} d(x_{n_i}, ty) &\leq d(x_{n_i}, tx_{n_i}) + d(tx_{n_i}, ty) \\ &\leq d(x_{n_i}, tx_{n_i}) + d(x_{n_i}, y). \end{aligned}$$

On taking $\lim_{i\to\infty}$ both side we get,

$$\lim_{i\to\infty} d(x_{n_i}, ty) = 0.$$

Hence by uniqueness of the limit of a sequence we obtain $y = ty$, that is, $y \in F(t)$. Owing to Lemma 3.8 and by Lemma 4.4, we get that

$$\begin{aligned} dist(y, Ty) &\leq d(y, x_{n_i}) + dist(x_{n_i}, Tx_{n_i}) + H(Tx_{n_i}, Ty) \\ &\leq d(y, x_{n_i}) + d(x_{n_i}, z_{n_i}) + d(x_{n_i}, y) \to 0, as \quad 0.2cmi \to \infty. \end{aligned}$$

This implies that $y \in F(T)$. Therefore, $y \in F(t,T)$ as desired.

Theorem 4.6. *Let K be a nonempty compact convex subset of a CAT(0) space X. Let*

$t : K \to K$ and $T : K \to CB(K)$ be a single-valued and a multivalued nonexpansive mappings, respectively, and $F(t,T) \neq \varnothing$ satisfying $Tw = \{w\}$ for all $w \in F(t,T)$. Let $\{x_n\}$ be the sequence of the modified Ishikawa iteration defined by (3.1) with $0 < a \leq \alpha_n$, $\beta_n \leq b < 1$. Then x_n converges strongly to a common fixed point of t and T.

Proof. Due to the fact that K is compact and the sequence $\{x_n\}$ is contained in K, there exists a subsequence $\{x_{n_i}\}$ of $\{x_n\}$ such that $\{x_{n_i}\}$ converges strongly to some point $y \in K$, that is, $\lim_{i\to\infty} d(x_{n_i}, y) = 0$. Owing to Theorem 4.5, we have $y \in F(t,T)$, and by Lemma 4.1, we obtain that $\lim_{n\to\infty} d(x_n, y)$ exists. So, it must be the case that $\lim_{n\to\infty} d(x_n, y) = \lim_{i\to\infty} d(x_{n_i}, y)$. Therefore, $\{x_n\}$ converges strongly to a common fixed point y of t and T.

Theorem 4.7. *Let K be a nonempty compact convex subset of a CAT(0) space X. Let $t : K \to K$ and $T : K \to CB(K)$ be a single-valued and a multivalued nonexpansive mappings, respectively, and $F(t,T) \neq \varnothing$ satisfying $Tw = \{w\}$ for all $w \in F(t,T)$. Moreover, pair t and T satisfies condition (A). If sequences $\{x_n\}$, $\{\alpha_n\}$ and $\{\beta_n\}$ are defined as in (2) and (3) respectively, then $\{x_n\}$ converges strongly to some common fixed point of t and T.*

Proof. First, we show that $F(t,T)$ is closed. Let $\{x_n\}$ be a sequence in $F(t,T)$ converging to some point $z \in K$. Since

$$\begin{aligned} d(x_n, tz) &= d(tx_n, tz) \\ &\leq d(x_n, z), \end{aligned}$$

we have

$$\limsup_n d(x_n, tz) \leq \limsup d(x_n, z) = 0.$$

By uniqueness of the limit, we have $tz = z$. Also,

$$\begin{aligned} d(x_n, Tz) &\leq H(Tx_n, Tz) \\ &\leq d(x_n, z) \to 0 \text{ as } n \to \infty. \end{aligned}$$

This implies that x_n converges to some point in Tz and hence $z \in F(t,T)$. By Lemma 3.1, $\lim_{n\to\infty} d(x_n, p)$ exists for all $p \in F(T)$ and let us take to be c. If $c = 0$, then there is nothing to prove. If $c > 0$, then in view of Equation (3.3) for all $p \in F(t,T)$, we have

$$d(x_{n+1}, p) \leq d(x_n, p),$$

so that

$$\inf_{p\in F(t,T)} d(x_{n+1}, p) \leq \inf_{p\in F(T)} d(x_n, p),$$

which amounts to say that

$$d(x_{n+1}, F(T)) \leq d(x_n, F(T))$$

and hence $\lim_{n\to\infty} d(x_n, F(t,T))$ exists. Owing to Condition (A') there exists a nondecreasing function f such that

$$\lim_{n\to\infty} f(d(x_n, F(t,T))) \leq \lim_{n\to\infty} d(x_n, tx_n) = 0$$

or,

$$\lim_{n\to\infty} f(d(x_n, F(t,T))) \leq \lim_{n\to\infty} d(x_n, Tx_n) \leq \lim_{n\to\infty} d(x_n, z_n) = 0$$

so that in both the cases $\lim_{n\to\infty} f(d(x_n, F(t,T))) = 0.$ Since, f is a nondecreasing function and $f(0) = 0$, therefore $\lim_{n\to\infty} d(x_n, F(t,T)) = 0.$

This implies that there exists a subsequence $\{x_{n_k}\}$ of $\{x_n\}$ such that

$$d(x_{n_k}, p_k) \leq \frac{1}{2^k} \text{ for all k} \geq 1$$

wherein $\{p_k\}$ is in $F(t,T)$. By Lemma 3.1, we have

$$d(x_{n_{k+1}}, p_k) \leq d(x_{n_k}, p_k) \leq \frac{1}{2^k},$$

so that

$$d(p_{k+1}, p_k) \leq d(p_{k+1}, x_{n_{k+1}}) + d(x_{n_{k+1}}, p_k)$$
$$\leq \frac{1}{2^{k+1}} + \frac{1}{2^k} < \frac{1}{2^{k-1}},$$

which implies that $\{p_k\}$ is a Cauchy sequence. Since $F(t,T)$ is closed, therefore $\{p_k\}$ is a convergent sequence. Write $\lim_{k\to\infty} p_k = p.$ Now, in order to show that $\{x_n\}$ converges to p lets proceed as follows:

$$d(x_{n_k}, p) \leq d(x_{n_k}, p_k) + d(p_k, p) \to 0 \; as \; k \to \infty,$$

so that that $\lim_{k\to\infty} d(x_{n_k}, p) = 0.$ Since $\lim_{n\to\infty} d(x_n, p)$ exists, therefore $x_n \to p.$

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On the Convergence of wavelet frame operators using Calderon-Zygmund operators

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Abstract: In this paper, we define a new wavelet frame operator and investigate the convergence of wavelet frame operators via Calderon-Zygmund operators provided that the wavelet function satisfies some smoothness and decay conditions.
Keywords and Phrases: Calderon-Zygmund operators, Wavelet transforms, Wavelet frames.
AMS Subject Classification 2C40, 42C15.

1. Introduction

The continuous wavelet transform of a function $f\epsilon\ L^2(\mathbb{R}^d)$ with respect to $\psi\ \epsilon\ L^2(\mathbb{R}^d)$ is defined by

$$\big(W_\psi f\big)(s,t) = <f, T_t D_s \psi>\ , \qquad (s,t)\ \epsilon\ \Gamma := \{(s,t): s>0, t\ \epsilon\ \mathbb{R}^d\},$$

Where D_s and T_t are respectively the dilation and translation operators defined by

$$(D_s\psi)(x) = s^{-d/2}\,\psi(s^{-1}x) \quad \text{and } (T_t\psi)(x) = \psi(x-t).$$

Let $\psi_1, \psi_2\ \epsilon\ L^2(\mathbb{R}^d)$ be such that

$$C_{\psi_1,\psi_2} = \int_0^{+\infty} \overline{\widehat{\psi_1(a\omega)}}\ \widehat{\psi_2(a\omega)}\,\frac{1}{a}da$$

is a non-zero constant for $\omega \neq 0$. Therefore we have

$$f(x) = C^{-1}_{\psi_1,\psi_2} \iint_\Gamma \big(W_{\psi_1} f\big)(a,b)(T_b D_a \psi_2)(x)\,\frac{dadb}{a^{d+1}}\ , \tag{1.1}$$

Where the convergence is in $L^2(\mathbb{R}^d)$ sense. The continuous wavelet transform was extended to $L^p(\mathbb{R}^d)$ [9]. The convergence of Riemann sums of the inverse windowed Fourier transform was studied in [3, 10, 12]. The approximation of the integral (1.1) using Riemann sums was studied in [7, 11].

Setting $a > e \geq 1$ and $b > 0$, we define the operator $S_{a,b,e;\psi_1,\psi_2}$ as

$$S_{a,b,e;\psi_1,\psi_2} f = \frac{b^d(a^d - e)}{da^{d/2} C_{\psi_1,\psi_2}} \sum_{j\epsilon Z, k\epsilon \mathbb{Z}^d} <f, T_{t_{j,k}} D_{s_j} \psi_1> T_{t_{j,k}} D_{s_j} \psi_2\ , \tag{1.2}$$

Where $\big(s_j, t_{j,k}\big)\ \epsilon\ E_{j,k} := \Big[a^{j-1/2}, a^{j+1/2}\Big) \times a^j b\,\Big(k + \big[-1/2, 1/2\big)^d\Big)$.

It can be easily seen that $S_{a,b,e;\psi_1,\psi_2} f$ can be viewed as a Riemann sum of the integral in (1.1) with respect to the Haar measure $\frac{dadb}{a^{d+1}}$ on Γ.

In this paper, we study the convergence of $S_{a,b,e;\psi_1,\psi_2}$ in $\mathcal{B}\big(L^p(\mathbb{R}^d)\big)$ by using Calderón–Zygmund operators, where $\mathcal{B}\big(L^p(\mathbb{R}^d)\big)$ is the space of all bounded linear operators on $L^p(\mathbb{R}^d), 1 < p < \infty$. We show that it tends to the identity operator for all $1 < p < \infty$ provided ψ_1 and ψ_2 satisfies certain smoothness and decay conditions. We also investigate the

convergence of $S_{a,b,e;\psi_1,\psi_2}$ as operators from Hardy space $H^1(\mathbb{R}^d)$ to $L^1(\mathbb{R}^d)$ and also from their respective duals
$L^\infty(\mathbb{R}^d)$ to $BMO(\mathbb{R}^d)$ respectively

.

2. Definitions, Notations and preliminary results

Notation 2.1. We use the following set of multi index:

$$\alpha = (\alpha_1, \alpha_2, \dots, \alpha_d), \qquad |\alpha| = \alpha_1 + \alpha_2 + \cdots + \alpha_d, \qquad \alpha! = \alpha_1!\ \alpha_2!\ \dots \alpha_d!,$$

$$x^\alpha = {x_1}^{\alpha_1}\ \dots\ {x_d}^{\alpha_d}, \quad (X^\alpha f)(x) = x^\alpha f(x), \qquad (\partial^\alpha f)(x) = \frac{\partial^{|\alpha|}}{\partial {x_1}^{\alpha_1}\ \dots\ \partial {x_d}^{\alpha_d}} f(x)$$

Also, for $a \in \mathbb{R}$, $\lfloor a \rfloor$ denotes the greatest integer less than or equal to a.

Definition 2.2. [2] The Banach space $\mathcal{F}_1(\mathbb{R}^d)$ defined by

$$\mathcal{F}_1(\mathbb{R}^d) = \{f \in L^2(\mathbb{R}^d) : W_\varphi f, W_f \varphi \in L^1(\Gamma)\},$$

Where $\varphi(x) = \left(\partial^2_{x_1} + \dots + \partial^2_{x_d}\right)^d e^{-\pi x^2}$ is a fixed function and

$$L^p(\Gamma) = \left\{\phi : ||\phi|| = \left(\iint_\Gamma |\phi(u,v)|^p \frac{dudv}{u^{d+1}}\right)^{1/p} < \infty\right\}.$$

Definition 2.3.[9]We call $K(x,y)$ a Calderon – Zygmund Kernel if there exists constants $C_k > 0$ and $0 < \delta \leq 1$ such that for any $(x,y) \in \mathbb{R}^d \times \mathbb{R}^d$ with $x \neq y$, we have

$$|K(x,y)| \leq \frac{C_k}{|x-y|^d}, \tag{2.3.1}$$

$$\left|K(x,y) - K(x,y')\right| \leq \frac{C_k |y-y'|^\delta}{|x-y|^{d+\delta}}, \quad |y-y'| \leq \frac{1}{2}|x-y|, \tag{2.3.2}$$

$$\left|K(x,y) - K(x,y')\right| \leq \frac{C_k |x-x'|^\delta}{|x-y|^{d+\delta}}, \quad |x-x'| \leq \frac{1}{2}|x-y|, \tag{2.3.3}$$

Definition 2.4. We call T a Calderon –Zygmund operator if
(i) T is a bounded operator on $L^2(\mathbb{R}^d)$,
(ii) there exists a Calderon- Zygmund kernel $K(x,y)$ such that for any compactly supported $f \in L^2(\mathbb{R}^d)$,

$$(Tf)(x) = \int_{\mathbb{R}^d} K(x,y) f(y) dy, \qquad x \in \mathbb{R}^d \backslash supp(f).$$

It is well known fact that a Calderon –Zygmund operator is bounded from $L^1(\mathbb{R}^d)$ to the weak $L^1(\mathbb{R}^d)$. Here, we state the following result which can be proved by standard method.

Proposition 2.5. [5, Theorem 8.2.1] Let T be a Calderon- Zygmund operator with kernel satisfying (2.3.1), (2.3.2) and (2.3.3).Then T is a bounded operator from $L^1(\mathbb{R}^d)$ to $L^1{}_{weak}(\mathbb{R}^d)$ and

$||T||_{L^1 \to L^1{}_{weak}} \leq \theta^{d/2} ||T||_{L^2 \to L^2} + \theta^{-\delta} C_k C_\delta$, for all $\theta > 2d^{1/2} + 1$,

where $C_\delta = d^{\delta/2}(3/2)^{d+\delta} \int_{\mathbb{R}^d \backslash [-1,1]^d} |u|^{-d-\delta} du$.

The property of Calderon – Zygmund operators which is used in this paper is that they are bounded from $H^1(\mathbb{R}^d)$ to $L^1(\mathbb{R}^d)$. We state the result without proof.

Proposition 2.6. Let T be a Calderon- Zygmund operator with kernel satisfying (2.3.1), (2.3.2) and (2.3.3).Then T is a bounded operator from $H^1(\mathbb{R}^d)$ to $L^1(\mathbb{R}^d)$ and

$$||T||_{H_1\to L^1} \le \theta^{d/2}||T||_{L^2\to L^2} + \theta^{-\delta}C_kC_\delta, \qquad for\ all\ \theta > 2d^{1/2} + 1,$$

where $C_\delta = d^{\delta/2}(3/2)^{d+\delta}\int_{\mathbb{R}^d\setminus[-1,1]^d}|u|^{-d-\delta}du.$

The following result is also useful which is known as Marcinkiewicz interpolation theorem. Here we state it with an explicit estimation on the operator bound.

Proposition 2.7. [4, Theorem 1.3.2]. If an operator T satisfies the following two conditions,

$$||Tf||_{L^{p_1}{}_{weak}} \le C_1||f||_{L^{p_1}},\ \ ||Tf||_{L^{p_2}{}_{weak}} \le C_2||f||_{L^{p_2}},$$

Where $1 \le p_1 \le p_2$, then for $0 < t < 1, 1/p = (1-t)/p_1 + t/p_2$, we have

$||Tf||_{L^p} \le MC_1{}^{1-t}C_2{}^t||f||_{L^p}$, where $M = 2(p/(p-p_1) + p/(p_2-p))^{1/p}$.

The following result shows that for wavelet functions from $\mathcal{F}_1(\mathbb{R}^d)$, the operators $S_{a,b,e;\psi_1,\psi_2}$ converge to the the identity operator in $\mathcal{B}(L^2(\mathbb{R}^d))$.

Proposition 2.8. [7, Theorem 4.2]. Let $\psi_1, \psi_2 \in \mathcal{F}_1(\mathbb{R}^d)$ be such that $C_{\psi_1,\psi_2} \neq 0$. Then $S_{a,b,e;\psi_1,\psi_2}$ is well defined on $\mathbb{R}^d$ and

$$\lim_{(a,b)\to(1,0)} ||\, S_{a,b,e;\psi_1,\psi_2} - I\,||_{L^2\to L^2} = 0.$$

Now the following auxiliary result gives the sufficient condition for $f \in \mathcal{F}_1(\mathbb{R}^d)$.

Proposition 2.9. [13, Theorem 3.5] Set $n_0 = \lfloor d/2 \rfloor + 1$. Let β and γ are positive constants such that $d/2 < \gamma \le d$ and $1/\beta + 1/(2\gamma) < 1/d$. Suppose f satisfy the following conditions,

(i) $|(\partial^\alpha f)(x)| \le C/(1+|x|)^\beta,\ \ |\alpha| \le n_0 - 1,$

(ii) $|f - \sum_{|\alpha|\le n_0-1}(\partial^\alpha f)(t)(x-t)^\alpha/\alpha!\,| \le C|x-t|^\gamma$, $\gamma > d/2$,

(iii) $\int_{\mathbb{R}^d} x^\alpha f(x)dx = 0, whenever\ |\alpha| \le n_0 - 1,$

Then $f \in \mathcal{F}_1(\mathbb{R}^d)$.

2. Main Result

Theorem 3.1. *Let $S_{a,b,e;\psi_1,\psi_2}$ be defined as in (1.2). If ψ_1 and ψ_2 are functions on $\mathbb{R}^d$ satistying the following conditions,*

(i) $|(\partial^\alpha\psi_i)(x)| \le C/(1+|x|)^\beta,\ \ |\alpha| \le n_0 - 1,$

(ii) $|\psi_i - \sum_{|\alpha|\le n_0-1}(\partial^\alpha\psi_i)(t)(x-t)^\alpha/\alpha!\,| \le C|x-t|^\gamma$, and

(iii) $\int_{\mathbb{R}^d} x^\alpha\psi_i(x)dx = 0, whenever\ |\alpha| \le n_0 - 1$, where $n_0 = \lfloor d/2 \rfloor + 1, \beta$ and γ are positive constants such that $d/2 < \gamma \le d$ and $1/\beta + 1/(2\gamma) < 1/d$.

Then we have

$$\lim_{(a,b)\to(1,0)} ||\, S_{a,b,e;\psi_1,\psi_2} - I\,||_{L^p\to L^p} = 0, \quad 1 < p < \infty, \qquad 3.1.1$$

$$\lim_{(a,b)\to(1,0)} ||\, S_{a,b,e;\psi_1,\psi_2} - I\,||_{L^1\to L^1{}_{weak}} = 0, \qquad 3.1.2$$

$$\lim_{(a,b)\to(1,0)} ||\, S_{a,b,e;\psi_1,\psi_2} - I\,||_{H^1\to L^1} = 0, \qquad 3.1.3$$

$$\lim_{(a,b)\to(1,0)} ||\, S_{a,b,e;\psi_1,\psi_2} - I\,||_{L^\infty\to BMO} = 0, \qquad 3.1.4$$

Where I stands for corresponding embedding mapping.

Proof of theorem 3.1. We first show that $S_{a,b,e;\psi_1,\psi_2}$ is well defined on $L^p(\mathbb{R}^d)$. For that, a standard method is to prove that it is a bounded linear operator on $L^2(\mathbb{R}^d)$ and related to some Calderon – Zygmund kernel. For $S_{a,b,e;\psi_1,\psi_2}$, it is sufficient to show that

$$K(x,y)=\frac{b^d(a^d-e)}{da^{d/2}C_{\psi_1,\psi_2}}\sum_{j\epsilon Z,k\epsilon\mathbb{Z}^d}(T_{t_{j,k}}D_{s_j}\psi_2(x))\overline{\left(T_{t_{j,k}}D_{s_j}\psi_1\right)(y)} \qquad 3.1.5$$

Is a Calderon- Zygmund kernel.

We need some lemmas for the proof of main result.

Lemma 3.2. Let ψ_1 and ψ_2 are functions on $\mathbb{R}^d$ such that $|\psi_i(x)|\le\frac{C}{(1+|x|)^{d+\varepsilon}}$ and $|\psi_i(x)-\psi_i(y)|\le C|x-y|^{\upsilon}$, $i=1,2$, where γ and ε are constants, $0<\upsilon\le 1$ and $\varepsilon>0$. Define

$$K(x,y)=\frac{b^d(a^d-e)}{da^{d/2}C_{\psi_1,\psi_2}}\sum_{j\epsilon Z,k\epsilon\mathbb{Z}^d}\omega_{j,k}(T_{t_{j,k}}D_{s_j}\psi_2)(x)\overline{\left(T_{t_{j,k}}D_{s_j}\psi_1\right)(y)}, \qquad 3.1.6$$

Where $\omega_{j,k}$ assumes values -1, 0, 1. Then $K(x,y)$ is a Calderon-Zygmund kernel with constant

$$C_k=\frac{b^d(a^d-e)}{da^{d/2}|C_{\psi_1,\psi_2}|}\left(\begin{array}{c}\left(2+a^{1/2}\right)^d C^2C_\varepsilon\left(\frac{a^{5d/2}}{a^d-e}+\frac{2^{d+1+\varepsilon}a^{d+\varepsilon/2}}{a^\varepsilon-e}\right)\\ +(1+2^{d+\upsilon\eta})C_{\gamma,\varepsilon,\eta}\left(\frac{a^{5(d+\upsilon\eta)/2}}{a^{d+\upsilon\eta}-e}+\frac{a^{(d+\upsilon\eta)/2+(d+\varepsilon)(1-\eta)/2}}{a^{(d+\varepsilon)(1-\eta)-(d+\upsilon\eta)}-e}\right)\end{array}\right) \qquad 3.1.7$$

and $\delta=\upsilon\eta$, where $\eta=\varepsilon/\big(2(d+\upsilon+\varepsilon)\big)$.

The above result can be proved with the standard method for convergence and basic properties of orthonormal wavelets (see[1,6]).

For the boundedness of the above operator, we have the following lemma.

Lemma 3.3. Let ψ_1 and ψ_2 are functions on $\mathbb{R}^d$ such that $|\psi_i(x)|\le\frac{C}{(1+|x|)^{d+\varepsilon}}$ and $|\psi_i(x)-\psi_i(y)|\le C|x-y|^{\upsilon}$, $i=1,2$, where υ and ε are constants, $0<\upsilon\le 1$ and $\varepsilon>0$. Let

$S_{a,b,e;\psi_1,\psi_2}$ be defined as in (1.2). If $S_{a,b,e;\psi_1,\psi_2}$ is well defined on $L^2(\mathbb{R}^d)$ and $\lim_{(a,b)\to(1,0)}||S_{a,b,e;\psi_1,\psi_2}-I||_{L^2\to L^2}=0$, then $S_{a,b,e;\psi_1,\psi_2}$ is well defined on $L^p(\mathbb{R}^d)$ and

$$\lim_{(a,b)\to(1,0)}||S_{a,b,e;\psi_1,\psi_2}-I||_{L^p\to L^p}=0,\quad 1<p<\infty,$$

Proof of Lemma 3.3. Let $K(x,y)$ be defined by (3.1.5). By lemma (3.2), $K(x,y)$ is a Calderon- Zygmund kernel i.e; $K(x,y)$ satisfies (2.3.1), (2.3.2) and (2.3.3), where C_k is given by (3.1.7), $\delta=\upsilon\eta$, and $\eta=\varepsilon/\big(2(d+\upsilon+\varepsilon)\big)$. It is clear that $C_k<\infty$. Consequently $S_{a,b,e;\psi_1,\psi_2}$, and therefore $S_{a,b,e;\psi_1,\psi_2}-I$, are Calderon – Zygmund operators with the same kernel.

As ,

$\lim_{(a,b)\to(1,0)}||S_{a,b,e;\psi_1,\psi_2}-I||_{L^2\to L^2}=0$, for any $0<\lambda<1$, there exists constants a_0 and b_0 such that for any $1<a<a_0, 0<b<b_0$, we have

$$||S_{a,b,e;\psi_1,\psi_2}-I||_{L^2\to L^2}\le\lambda<1.$$

Using proposition (2.5), we have

$\lim_{(a,b)\to(1,0)}||S_{a,b,e;\psi_1,\psi_2}-I||_{L^1\to L^1_{weak}}\le M_\delta$, where $M_\delta=2^{d/2+2e}\theta^{d/2}+4\theta^{-\delta}C_kC_\delta$.

By using proposition (2.7), we have

$$||S_{a,b,e;\psi_1,\psi_2}f-f||_{L^p}\le MM_\delta^{2/p-1}\lambda^{2-2/p}||f||_{L^p},\ 1<p<2,$$

where $M=2(p/(p-p_1)+p/(p_2-p))^{1/p}$. Therefore

$$||S_{a,b,e;\psi_1,\psi_2}-I||_{L^p\to L^p}\le MM_\delta^{2/p-1}\lambda^{2-2/p},\ 1<a<a_0,\ 0<b<b_0.$$

Also for $1<a<a_0$, $0<b<b_0$, $Sup\,M_\delta<\infty$. Therefore, we have

$$\lim_{(a,b)\to(1,0)} || S_{a,b,e;\psi_1,\psi_2} - I ||_{L^p \to L^p} = 0, \ 1 < p < 2.$$

Next, we have consider the case of $2 < p < \infty$. For that, we consider the adjoint of $S_{a,b,e;\psi_1,\psi_2} - I$. It is clear that $\left(S^*_{a,b,e;\psi_1,\psi_2} h\right)(y) = \int_{\mathbb{R}^d} \overline{K(x,y)}\, h(x)dx$, where $\overline{K(x,y)}$ is also a Calderón-Zygmund kernel and hence, $S^*_{a,b,e;\psi_1,\psi_2}$ is a Calderón-Zygmund operator. By using similar arguments, we have

$$\lim_{(a,b)\to(1,0)} || S^*_{a,b,e;\psi_1,\psi_2} - I ||_{L^q \to L^q} = 0, \ 1 < p < 2.$$

On the other hand, it is known that

$$\lim_{(a,b)\to(1,0)} || S_{a,b,e;\psi_1,\psi_2} - I ||_{L^p \to L^p} = \lim_{(a,b)\to(1,0)} || S^*_{a,b,e;\psi_1,\psi_2} - I ||_{L^q \to L^q}, \qquad \frac{1}{p} + \frac{1}{q} = 1,$$

Thus we have

$$\lim_{(a,b)\to(1,0)} || S_{a,b,e;\psi_1,\psi_2} - I ||_{L^p \to L^p} = 0, \ 2 < p < \infty.$$

Now we need to show the convergence of $S_{a,b,e;\psi_1,\psi_2}$ in $\mathcal{B}\left(L^2(\mathbb{R}^d)\right)$, for which it suffices to prove that $\psi_1, \psi_2 \in \mathcal{F}_1(\mathbb{R}^d)$. By proposition (2.8), it is clear that the wavelet functions from $\mathcal{F}_1(\mathbb{R}^d)$, the operators $S_{a,b,e;\psi_1,\psi_2}$ converge to the identity operator in $\mathcal{B}\left(L^2(\mathbb{R}^d)\right)$. Also by the virtue of propostion (2.9), it is clear that $\psi_1, \psi_2 \in \mathcal{F}_1(\mathbb{R}^d)$. This completes the proof of (3.1.1).

Now we proceed to prove (3.1.2). By proposition (2.5), we have

$$||S_{a,b,e;\psi_1,\psi_2} - I||_{L^1 \to L^1_{weak}} \leq 2^{d/2+2}\theta^{d/2} ||S_{a,b,e;\psi_1,\psi_2} - I||_{L^2 \to L^2} + \frac{M_1}{\theta^\delta},$$

Where $\theta > 2d^{1/2} + 1$ is an arbitrary constant and

$$M_1 = Sup_{1<a<2,0<b<1} \frac{4C_k d^{\delta/2}\, 3^{d+\delta}}{2^{d+\delta}} \int_{\mathbb{R}^d \setminus [-1,1]^d} \frac{du}{|u|^{d+\delta}} < \infty.$$

For any $\varepsilon > 0$, we can find some $\theta_0 > 2d^{1/2} + 1$ such that $M_1 < \frac{\varepsilon\, {\theta_0}^\delta}{2}$.

On the other hand, we can see from (3.1.1) that there exists some $1 < a_0 < 2$ and $0 < b_0 < 1$ such that $|| S_{a,b,e;\psi_1,\psi_2} - I ||_{L^2 \to L^2} < \frac{\varepsilon}{2^{d/2+3}\, {\theta_0}^{d/2}}, 1 < a < a_0, 0 < b < b_0$.

Hence $||S_{a,b,e;\psi_1,\psi_2} - I||_{L^1 \to L^1_{weak}} < \varepsilon, 1 < a < a_0, 0 < b < b_0$.

This proves (3.1.2).

Now (3.1.3) can be proved similarly as that of (3.1.2) by using proposition (2.6).

Also, (3.1.4) is the immediate consequence of (3.1.3) because BMO and L^∞ are the duals of H^1 and L^1 respectively.

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Some Conditions on Concircular Curvature Tensor in Kenmotsu Manifolds

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Abstract : The object of the present paper is to study Ricci solitons in Kenmotsu manifolds when the concircular curvature tensor satisfies Ricci-semisymmetric, Ricci-pseudosymmetric, locally φ-symmetric, φ-recurrent, generalized φ-recurrent conditions.

Keywords : Ricci soliton, Locally φ-symmetric, φ-recurrent, Generalizedφ-recurrent, Kenmotsu Manifold, Einstein metric, Concircular curvature tensor.
AMS Classification : 53C05, 53C20, 53C25, 53D10.

1. Introduction

During 1982, Hamilton [12] made the fundamental observation that Ricci flow is an excellent tool for simplifying the structure of the manifold. It is a process which deforms the metric of a Riemannian manifold analogous to the diffusion of heat there by smoothing out the irregularity in the metric. It is given by

$$\frac{\partial g}{\partial t} = -2Ricg,$$

where g is a Riemannian metric. $Ricg$ is the Ricci curvature tensor, t is time.

Ricci solitons move under the Ricci flow simply by diffeomorphisms of the initial metric that is they are stationary points of the Ricci flow in space of metrics of $\varphi_t: M \to M$. Here the metric $g(t)$ is the pull back of the initial metric $g(0)$ by a 1-parameter family of diffeomorphisms (t) generated by a vector field on a manifold M.

A Ricci soliton is a generalization of an Einstein metric and is defined on a Riemannian manifold (M, g). A Ricci soliton is a triple (g, V, λ) with g a Riemannian metric, V is a vector field and λ is a real scalar such that

$$L_V g + 2S + 2\lambda g = 0, \tag{1.1}$$

Where S is a Ricci tensor of M and $L_V$denotes the Lie derivative operator along the vector field V, λ is constant. A Ricci soliton is said to be shrinking, steady and expanding when λ is negative, zero and positive respectively.

Let (M, g) be an n-dimensional differentiable manifold of class C^∞. We denote ∇ by its Levi-Civita connection. We define endomorphisms $R(X,Y)$ and $X \wedge Y$ by

$$R(X,Y)Z = \nabla_X \nabla_Y Z - \nabla_X \nabla_Y Z - \nabla_{[X,Y]} Z, \tag{1.2}$$

$$(X \wedge Y)Z = g(Y,Z)X - g(X,Z)Y, \tag{1.3}$$

respectively, where $X, Y, Z \in \chi(M)$, $\chi(M)$ being the Lie algebra of vector fields on M. The Riemannian Christoffel curvature tensor R is defined by $R(X,Y,Z,W) = g(R(X,Y)Z,W)$, $W \in \chi(M)$. Let S and r denote the Ricci tensor and scalar curvature of M respectively. The Ricci operator Q is defined by $g(QX,Y) = S(X,Y)$.

We define the tensors $R \cdot S$ and $Q(g,S)$ by

$$(R(X,Y) \cdot S)(X_1,X_2) = -S(R(X,Y)X_1, X_2) - S(X_1,R(X,Y)X_2),$$
$$Q(g,S)(X_1,X_2; X,Y) = -S((X \wedge Y)X_1, X_2) - S(X_1,(X \wedge Y)X_2),$$

respectively, where $X_1, X_2, X, Y \in \chi(M)$.

A Riemannian manifold satisfying $R \cdot S = 0$ is called Ricci-semisymmetric. Where S is the Ricci tensor. If the tensors $R \cdot S$ and $Q(g,S)$ are linearly dependent then M is called Ricci-pseudosymmetric. This is equivalent to

$$R \cdot S = L_S\, Q(g,S),$$

holding on the set $U_S = \{x \in M : S \neq \frac{r}{n}\, g \text{ at } x\}$, where L_S is some function onU_S.

The study of Ricci solitons in contact geometry were initiated by Sharma [23] and Tripathi [25]. Later the study was extended by Calinet. al. [6], Bagewadi et. al. ([16], [2]), Debnath et. al. [9], Chandra et. al. [7], Lorentzian α-Sasakian, Trans-Sasakian,$(LCS)_n$ and almost $C(\alpha)$manifolds using Eisenhart problem [10]. The authors Ashoka et. al. ([1], [4]) and Nagaraja et. al. [18] studied Ricci solitons in $(LCS)_n$, Kenmostu manifolds using semi-symmetric and Ricci-semisymmetric conditions on different curvature tensors.

The notion of local symmetry has been weakened by many authors in several ways to different extent. As a weaker version of local symmetry, Takahashi [24] introduced the notion of φ-symmetry on a Sasakian manifold. Generalizing the notion of φ -symmetry, De et. al. [8] introduced the notion of φ -recurrent Sasakian manifold. In the context of contact geometry, the notion of φ -symmetry is introduced and studied by Boeckx et. al. [5] with several examples. The study of generalized φ -recurrent Sasakian manifolds was initiated by Oubina et. al. [19] and further it has been carried out by the authors Bagewadi et. al. ([26], [27]), Jun et. al. [17], Patilet. al. [20], Prakasha et. al.([21], [22]) and many others.

Motivated by the above studies, in this paper we study Ricci soltions in Kenmotsu manifolds when concircular curvature tensor satisfies Ricci-semisymmetric, Ricci- pseudosymmetric, locally φ-symmetric, φ-recurrent, generalized φ-recurrent conditions.

2. Preliminaries

Let M be a n -dimensional almost contact Reimannaian manifold with structure tensors(φ, ξ, η, g). whereφ is a (1,1) tensor field, ξ is the structure vector field, η is a 1-form and g is a Riemannian metric. It is well known that (φ, ξ, η, g) structure satisfies the following conditions:

$$\eta(\xi) = 1, \quad \eta \circ \varphi = 0, \quad \varphi\,\xi = 0, \tag{2.1}$$
$$\varphi^2 X = -X + \eta(X)\xi, \quad g(X,\xi) = \eta(X), \tag{2.2}$$
$$g(\varphi X, \varphi Y) = g(X,Y) - \eta(X)\,\eta(Y), \tag{2.3}$$

for all vector fields X, Y on M. If moreover

$$(\nabla_X \varphi)Y = g(\varphi X, Y)\xi - \eta(Y)\,\varphi X, \tag{2.4}$$
$$\nabla_X \xi = X - \eta(X)\xi, \tag{2.5}$$

where ∇ denotes the Riemannian connection of g hold, then $(M^n, \varphi, \xi, \eta, g)$ is called Kenmotsu manifold.

In Kenmotsu manifold, the following relations hold:

$$(\nabla_X \eta)Y = g(\varphi X, \varphi Y) = g(X,Y) - \eta(X)\eta(Y). \tag{2.6}$$
$$R(X,Y)Z = \eta(Y)g(X,Z) - \eta(X)\,g(Y,Z). \tag{2.7}$$

From (2.7), it easily follows that

$$R(X,Y)\xi = \eta(X)Y - \eta(Y)X, \tag{2.8}$$

$$R(\xi, X)Y = \eta(Y)X - g(X, Y)\xi, \tag{2.9}$$
$$S(X, \xi) = -(n-1)\eta(X), \tag{2.10}$$
$$S(\varphi X, \varphi Y) = S(X, Y) + (n-1)\eta(X)\eta(Y), \tag{2.11}$$

for any vector fields X, Y, Z, where R is the Riemannian curvature tensor and S is the Ricci tensor.

Let (g, ξ, λ)be a Ricci solition in an n-dimensional Kenmotsu manifold M. From (2.5) we have

$$(L_\xi g)(X, Y) = 2[g(X, Y) - \eta(X)\eta(Y)]. \tag{2.12}$$

From (1.1) and (2.12) we have

$$S(X, Y) = \eta(X)\eta(Y) - (\lambda + 1)g(X, Y). \tag{2.13}$$

The above equation yields

$$QX = \eta(X)\xi - (\lambda + 1)X, \tag{2.14}$$
$$S(X, \xi) = -\lambda\eta(X), \tag{2.15}$$
$$r = -\lambda n - (n-1), \tag{2.16}$$

Where S is the Ricci tensor, Q is the Ricci operator and r is the scalar curvature on M.

Definition 2.1. A Kenmotsu manifold is said to be locally φ-symmatric if

$$\varphi^2((\nabla_W C)(X, Y)Z) = 0, \tag{2.17}$$

for all vector fields X, Y, Z, W orthogonal to ξ.

Definition 2.2. A Kenmotsu manifold is said to be locally concircularly φ-symmetric

$$\varphi^2((\nabla_W C)(X, Y)Z) = 0, \tag{2.18}$$

for all vector fields X, Y, Z, W orthogonal to ξ.

Definition 2.3. A Kenmotsu manifold is said to be concircularly φ-recurrent manifold if there exists a non-zero 1-form A such that

$$\varphi^2((\nabla_W C)(X, Y)Z) = A(W)C(X, Y)Z, \tag{2.19}$$

for all vector fields X, Y, Z, W orthogonal to ξ.

Definition 2.4. A Kenmotsu manifold is said to be generalized concircularly φ-recurrent manifold if its curvature tensor C satisfies the relation

$$\varphi^2((\nabla_w C)(X, Y)Z) = A(W)C(X, Y)Z + B(W)\{g(Y, Z)X - g(X, Z)Y\}, \tag{2.20}$$

Where A and B are 1-forms, B is non-zero and these are defined by

$$A(W) = g(W, \rho_1), B(W) = g(W, \rho_2),$$

and ρ_1 , ρ_2 are vector fields associated with 1-forms A, B respectively. Here C is the concircular curvature tensor given by

$$C(X, Y)Z = R(X, Y)Z - \frac{r}{n(n-1)}[g(Y, Z)X - g(X, Z)Y. \tag{2.21}$$

Taking $X = \xi$, $Y = X$, $Z = Y$ in (2.21) and using (2.2), (2.8) and (2.9), we obtain

$$C(\xi, X)Y = \left[1 - \frac{r}{n(n-1)}\right][\eta(Y)X - g(X, Y)\xi. \tag{2.22}$$

$$C(X, Y)\xi = \left[1 - \frac{r}{n(n-1)}\right][\eta(X)Y - \eta(Y)X]. \tag{2.23}$$

3. Ricci Solitons In Kenmotsu Manifold Satisfying $C \cdot S = L_S Q(g, S)$

Let us consider an n-dimensional Kenmotsu manifold which satisfies the condition $C(\xi, X) \cdot S = L_S Q(g, S)$ implies that

$$S(C(\xi, X)Y, Z) + S(Y, C(\xi, X)Z) = L_S[S((\xi \wedge X)Y, Z) + S(Y, (\xi \wedge X)Z)]. \tag{3.1}$$

Using (1.3), (2.10), (2.22) in (3.1), we get

$$\left[L_S + \frac{r}{n(n-1)}\right][S(X, Z)\eta(Y) + S(Y, X)\eta(Z) + (n-1)\eta(Z)g(X, Y) + (n-1)\eta(Y)g(X, Z)] = 0. \tag{3.2}$$

If $L_S + \left(\frac{r}{n(n-1)}\right) \neq 0$ then equation (3.2) reduces to

$$[S(X,Z)\,\eta(Y) + S(Y,X)\,\eta(Z) + (n-1)\,\eta(Z)\,g(X,Y) + (n-1)\,\eta(Y)\,g(X,Z)] = 0. \quad (3.3)$$

Let $Z = \xi$ in (3.3) we have

$$S(X,Y) = -(n-1)\,g(X,Y). \quad (3.4)$$

Taking $X = Y = e_i$ and summing over $i = 1, 2, \ldots\ldots\ldots\ldots, n$ in (3.4) we get

$$r = -n(n-1). \quad (3.5)$$

In view of (2.16) and (3.5) we obtain

$$\lambda = \frac{(n-1)^2}{n}.$$

Hence we state the following:

Theorem 3.1. *A Ricci soliton in n-dimensional Kenmotsu manifold satisfying $C \cdot S = L_S\,Q(g,S)$ is expanding provided $L_S \neq -\left(\frac{r}{n(n-1)}\right)$.*

Let (M^n, g) is a n-dimensional Kenmotsu manifold and (g, V, λ) is a Ricci soliton in (M^n, g). If V is a conformal killing vector field, then

$$L_V g = \rho g. \quad (3.6)$$

From (1.1), we have

$$S = (\lambda g + \tfrac{1}{2} L_V g). \quad (3.7)$$

From (3.6) and (3.7), we get

$$S(X, Y) = \left(\lambda + \tfrac{\rho}{2}\right) g(X,Y) \quad (3.8)$$

Let (M^n, g) be a Kenmotsu manifold. Then from (3.7), we have

$$C \cdot S = S(C(X,Y)Z,W) + S(Z, C(X,Y)W).$$

$$C \cdot S = -(\lambda + \tfrac{\rho}{2})\,[g(C(X,Y)Z,W) + g(C(X,Y)W,Z)]. \quad (3.9)$$

Using (2.21) in (3.9), we get

$$C \cdot S = -(\lambda + \tfrac{\rho}{2})\,[R(X,Y,Z,W) + R(X,Y,W,Z)] = 0. \quad (3.10)$$

i. e (M^n, g) is concircular Ricci-semisymmetric.

Conversely, suppose $C \cdot S = 0$.

$$S(C(X,Y)Z,W) + S(Z,C(X,Y)W) = 0. \quad (3.11)$$

Taking $X = W = \xi$ in (3.11) and using (2.10), (2.22) and (2.23), we get

$$S(Y,Z) = -(n-1)\,g(Y,Z).$$

Substituting this in (1.1), we obtain

$$(L_V g)(Y,Z) = \rho\, g(Y,Z).$$

where $\rho = 2((n-1) - \lambda)$ i. e V is conformal killing. Thus, we state the following:

Theorem 3.2. *Let (g, V, λ) be a Ricci soliton in Kenmotsu manifold (M^n, g). Then (M^n, g) is concircularly Ricci-semisymmetric if and only if V is conformal killing.*

4. Ricci Soliton in Generalized Concircular φ - Recurrent Kenmotsu Manifold

Let us consider a generalized concircular φ-recurrent Kenmotsu manifold. Then by virtue of (2.2) and (2.20) we have

$$-\big((\nabla_W C)(X,Y)Z\big) + \eta\big((\nabla_W C)(X,Y)Z\big)\xi = A(W)C(X,Y)Z + B(W)\{g(Y,Z)X - g(X,Z)Y\}. \quad (4.1)$$

From which follows that

$$-g\big((\nabla_W C)(X,Y)Z,U\big) + \eta\big((\nabla_W C)(X,Y)Z\big)\eta(U)$$

$$= A(W)\, g(C(X,Y)Z,U) + B(W)\{g(Y,Z)\, g(X,U) - g(X,Z)\, g(Y,U)\}. \quad (4.2)$$

Let $\{e_i\}$, $i = 1, 2, \cdots, n$ be orthonormal basis of the tangent space at any point of the manifold. Then by putting $X = Y = e_i$ in (4.2) and taking summation over i, $1 \le i \le n$, we get

$$(\nabla_W S)(Y,Z) = \frac{dr(W)}{n}\, g(Y,Z) - \frac{dr(W)}{n(n-1)}\,[g(Y,Z) - \eta(Y)\,\eta(Z)]$$
$$- A(W)\left[S(Y,Z) - \frac{r}{n}\, g(Y,Z)\right] - B(W)\,(n-1)\, g(Y,Z). \quad (4.3)$$

Replacing Z by ξ in (4.3) and using (2.2) and (2.10), we have

$$(\nabla_W S)(Y,\xi) = \left[\frac{dr(W)}{n} + A(W)\left((n-1) + \frac{r}{n}\right) - B(W)\,(n-1)\right]\eta(Y). \quad (4.4)$$

Now we have

$$(\nabla_W S)(Y,\xi) = \nabla_W S(Y,\xi) - S(\nabla_W Y,\xi) - S(Y,\nabla_W \xi).$$

Using (2.5), (2.6) and (2.10) in the above relation, it follows that

$$(\nabla_W S)(Y,\xi) = -[S(Y,W) + (n-1)\, g(Y,W)]. \quad (4.5)$$

In view of (4.4) and (4.5), we have

$$S(Y,W) = -(n-1)\, g(Y,W) - \frac{dr(W)}{n}\,\eta(Y) - A(W)\left[(n-1) + \frac{r}{n}\right]\eta(Y)$$
$$+ B(W)(n-1)g(Y,W). \quad (4.6)$$

Replacing Y by φY and W by φW in (4.6) and using (2.3), (2.11), we obtain

$$S(Y,W) = -(n-1)g(Y,W). \quad (4.7)$$

Now, by virtue of (4.7) and (2.13), we get

$$\lambda = \frac{(n-1)^2}{n}.$$

Therefore, λ is positive. Hence we state the following:

Theorem 4.1. *A Ricci soliton in n-dimensional generalized concircularly φ-recurrent Kenmotsu manifold is expanding.*

Similarly, we obtain the same results for locally concircularly φ-symmetric and concircular φ-recurrent Kenmotsu manifold. Hence we get the following corollaries:

Corollary 4.1. A Ricci soliton in n-dimensional locally concircularly φ-symmetric Kenmotsu manifold is expanding.

Corollary 4.2. A Ricci soliton in n-dimensional concircularly φ-recurrent Kenmotsu manifold is expanding.

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Properties Determining the Application of New Complex Continuous Wavelets

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Abstract: In this paper, we contrive certain properties of new complex continuous wavelets (which we proposed in a recent time) such as their time bandwidth product and relationship between scale and frequency using them and compared it with the well known existing wavelets which help in selecting of these wavelets in any application of interest.
Keywords: Complex Continuous Wavelets, Time-bandwidth product, Scale to frequency.

1. Introduction

Complex continuous wavelets over real-valued continuous wavelets give more detailed information in transient signal detection. The complex continuous wavelet transform of a real signal is plotted in modulus form and phase form, rather than in real and imaginary forms. In the complex continuous wavelet transform analysis, the modulus maxima and the phase crossings, reveals the locations of sharp signal transitions. Also, by making use of the phase information, the local maxima and inflection points, can be recognized.

It is well known fact that the choice of mother wavelet is application-dependent. So far there is no means of selecting a suitable wavelet basis, other than experience and the method of choosing an appropriate wavelet basis has primarily been that of trial and error. In the paper [1], the author discussed about the properties of wavelets which may helps mother wavelet selection in a chosen application.

So in this paper we discuss certain properties of the family of new complex continuous wavelets [2] which we proposed in a recent time, which may help in determining the choice of mother wavelet for various applications.

2. Complex Continuous Wavelets:

2.1. New complex continuous wavelet

This family is built with different order by starting from the complex function

$$\psi(x) = e^{-ix}.\frac{1}{1+x^2}$$

and taking the k^{th} derivative of $\psi(x)$ the integer k is the parameter of this family and represents the order of the wavelet of the family i.e. $\psi_k(x)$ is a Complex Continuous Wavelet for each k and

$$\psi_k(x) = C_k \frac{d^k}{dx^k}\left(\psi(x)\right)$$

In the previous formula, C_k is such that $\left\|\psi_k(x)\right\|^2 = 1, \forall k = 1,2,3.....,8$.

where $\psi_k(x)$ is the k^{th} derivative of $\psi(x)$ and $C_k = \left(\int_{-\infty}^{\infty}\left|\frac{d^k}{dx^k}(\psi(x))\right|^2 dx\right)^{-1/2}$

It has been verified that for the above functions $\psi_k(x)$,

- $\int_{-\infty}^{\infty}\left|\psi_k(x)\right|^2 dx = 1 < \infty \quad , \forall k = 1,2,3.....,8$.
- $C_{\psi_k} = \int_{-\infty}^{\infty}\frac{\left|\hat{\Psi}_k(\omega)\right|^2}{\omega}d\omega < \infty$
- $\int_{-\infty}^{\infty}\psi_k(x)dx = 0, \quad \forall k = 1,2,3.....,8$.

Moreover $\int_{-\infty}^{\infty} x\psi_k(x)dx = 0, \forall k = 2,3.....,8$.

Where $\hat{\Psi}_k(\omega)$ is the fourier transform of $\psi_k(x)$ and

$\hat{\Psi}_k(\omega) = \int_{-\infty}^{\infty}\psi_k(x)e^{-i\omega x}dx = \pi(i\omega)^k \mathrm{e}^{-|\omega+1|}$.

Hence the functions $\psi_k(x)$, $\forall k = 1,2,3.....,8$ forms a family of One dimensional complex continuous wavelets. Each member is named as crsw followed by their order.

2.2. Some existing complex continuous wavelet:

2.2.1. Complex Gaussian Wavelets (cgau)

This family is built starting from the complex Gaussian function $f(x) = C_p \mathrm{e}^{-ix}\mathrm{e}^{-x^2}$ and by taking the p^{th} derivative of $f(x)$. The integer p is the parameter of this family and in the previous formula, C_p is such that $\left\|f^p(x)\right\|^2 = 1$, where $f^p(x)$ is the p^{th} derivative of $f(x)$.

2.2.2. Complex Morlet Wavelets (cmor)

A complex Morlet wavelet is defined by $\psi(x) = \frac{1}{\sqrt{\pi f_b}}\mathrm{e}^{2i\pi f_c x}\mathrm{e}^{-\frac{x^2}{f_b}}$ where f_b is a bandwidth parameter and f_c is a wavelet center frequency. The order of the wavelet is defined by $f_c - f_b$.

3. Properties

3.1. Time-bandwidth product of the wavelets

The time width and the frequency width of the wavelet function $\psi_k(x)$ are defined as

$$\Delta_t^2 = \frac{\int_{-\infty}^{\infty} x^2 \left|\psi_k(x)\right|^2 dx}{\int_{-\infty}^{\infty} \left|\psi_k(x)\right|^2 dx} \quad \text{and} \quad \Delta_\omega^2 = \frac{\int_{-\infty}^{\infty} \omega^2 \left|\hat{\Psi}_k(\omega)\right|^2 d\omega}{\int_{-\infty}^{\infty} \left|\hat{\Psi}_k(\omega)\right|^2 d\omega}$$

Thus $\Delta_t^2.\Delta_\omega^2$ defines the time-bandwidth product of the wavelet. Lesser values of Δ_t^2 and Δ_ω^2 correspond, respectively, to higher time and frequency localizations. Among the existing complex continuous wavelets the optimum time-frequency localization (lesser time-band width product) holds only for those complex continuous wavelets containing Gaussian function e^{-x^2} [1] such as complex gaussian and complex morlet wavelets.

The values of time width and frequency width for each member of the new complex continuous wavelets along with complex morlet and complex gaussian wavelets are computed and tabulated. From the tabulated values it can be observe that the time width of these new complex wavelets has got lesser values as compared to that of complex gaussian wavelets and complex morlet wavelet and hence are more appropriate to use in those application which requires good localisation in time such as examination of QRS complex in ECG signals. The Power Spectral Density (PSD) which shows the strength of the variations(energy) as a function of frequency are also computed for each member of the family and are given in the following figure.

Complex Gaussian wavelets				New Complex wavelets				Complex Morlet wavelets			
Order	Δ_t^2	Δ_ω^2	$\Delta_t^2.\Delta_\omega^2$	Order	Δ_t^2	Δ_ω^2	$\Delta_t^2.\Delta_\omega^2$	Order	Δ_t^2	Δ_ω^2	$\Delta_t^2.\Delta_\omega^2$
1	0.50000	5	2.5	1	1	3.6667	3.6667	1-1.5	0.3750	40.1451	15.054
2	0.45000	7.6000	3.42	2	0.45455	7.6818	3.4917	1-1	0.2500	40.483	10.121
3	0.44737	10.053	4.4972	3	0.21893	14.024	3.0703	1-0.5	0.1250	41.4784	5.1848
4	0.44895	12.429	5.5802	4	0.14430	22.502	3.2471	1-0.1	0.0250	49.4784	1.2370
5	0.45114	14.759	6.6584	5	0.11118	33.000	3.6689	6-2	0.5000	36.5000	18.250
6	0.45326	17.056	7.7310	6	0.090911	45.500	4.1365				
7	0.45520	19.329	8.7988	7	0.076923	60.000	4.6154				
8	0.45694	21.584	9.8624	8	0.066667	76.500	5.1				

Table 1: Time-width, Frequency-width and timeband-width product of the wavelets

3.2 Conversion of scale to frequency:

The continuous wavelet transform (CWT) converts the signal from time domain (one dimension) to scale-time domain (two dimension) which is not very easy to understand compared with the Fast

Fourier Transform (FFT) result [3]. The scale value can be converted into frequency (pseudo-frequency), the value of which depends on the central frequency of the applied wavelets and the scale value a and is given by

$$f_a = \frac{f_c}{a.\Delta}$$

where

- a is a scale.
- Δ is the sampling period.
- f_c is the center frequency of a wavelet in Hz.
- f_a is the pseudo-frequency corresponding to the scale a, in Hz.

The idea is to associate with a given wavelet a purely periodic signal of frequency f_c and $f_c = \frac{1}{\lambda}$ where λ is the Fourier wavelength (frequency Fourier factor) and the relationship between the equivalent Fourier period and the wavelet scale can be derived analytically for a particular wavelet function by substituting a cosine wave of a known frequency into wavelet transform definition [4] and computing the scale a at which the wavelet power spectrum reaches its maximum and it is found to be $\lambda_k = \frac{4\pi}{2k+1}$ where $k = 1, 2, 3...., 8.$

The following table shows the values of f_c for various members of the wavelets.

k	f_c
1	$\frac{3}{4\pi}$
2	$\frac{5}{4\pi}$
3	$\frac{7}{4\pi}$
4	$\frac{9}{4\pi}$
5	$\frac{11}{4\pi}$
6	$\frac{13}{4\pi}$
7	$\frac{15}{4\pi}$
8	$\frac{17}{4\pi}$

Table 2: Central frequency f_c

The following figures shows the center frequency based approximation of complex wavelets.

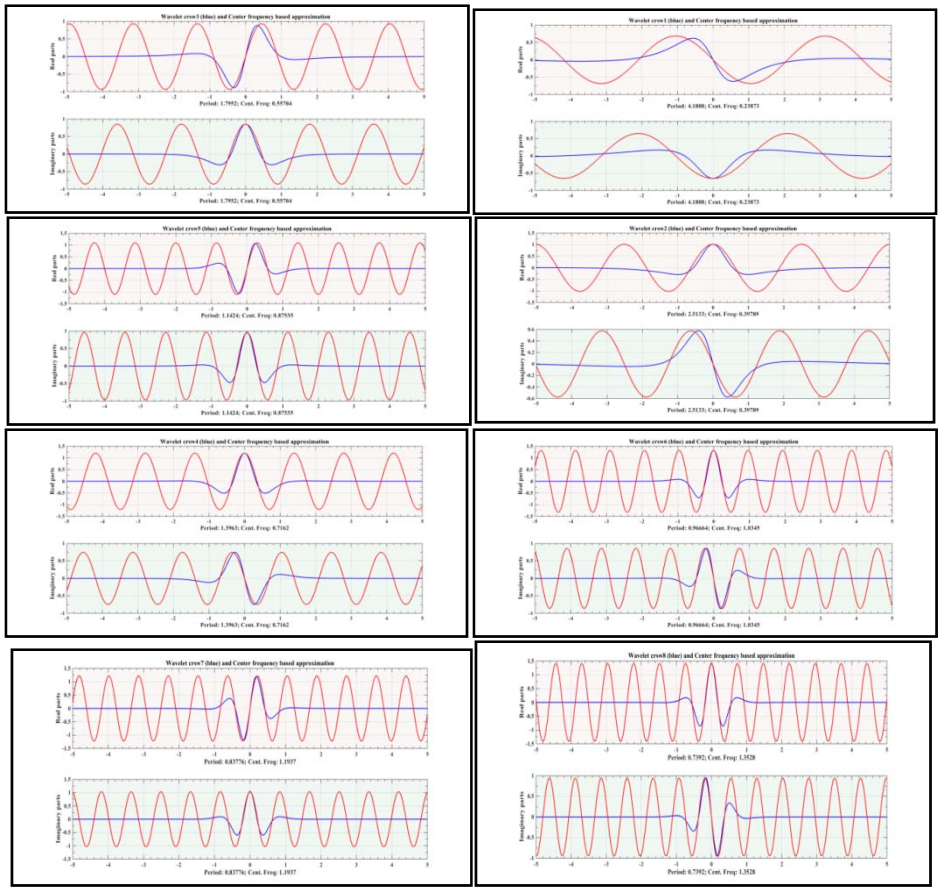

Figure 1: Central frequency based approximation of wavelets members

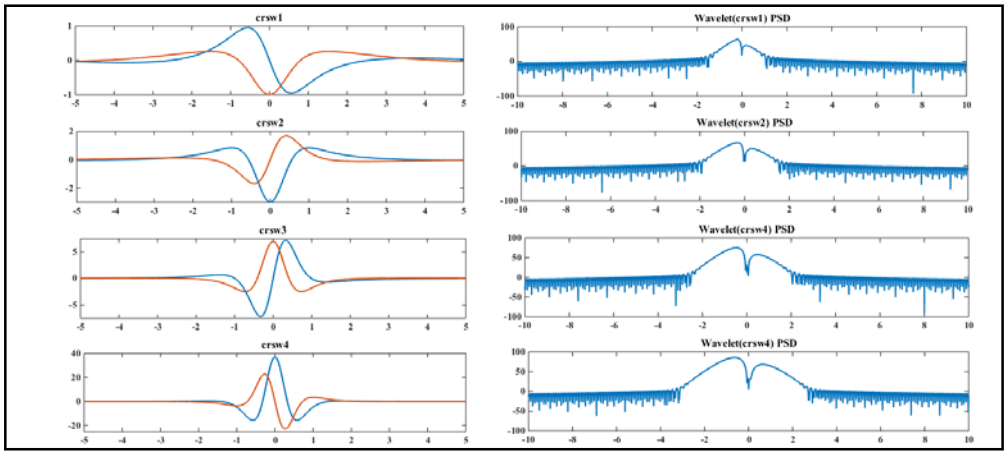

Figure 2: PSD of wavelets members 1-4

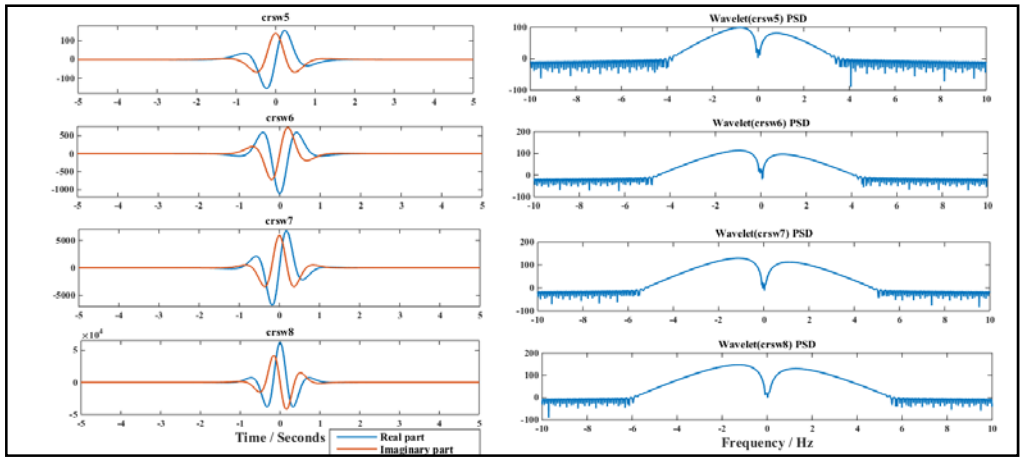

Figure 3: PSD of wavelets members 5-8

Conclusion.

The time width, frequency width and time-band width product for the new complex continuous wavelets are computed and observed that the time width and time-band width product have lesser values for some of the members of the new complex wavelets and are appropriate to use in those application which requires good localization in time. The plots of Power Spectral Density (PSD) for each members of the family are also computed. The scale to frequency relation using these new complex wavelets are also shown.

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Next Generation Sequencing: A New Platform for Disease Study

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Abstract: With the advent of high-throughput techniques, such as Next Generation Sequencing (NGS), it is possible to sequence the entire genome with massive parallel speed in less cost and time. The NGS as deep sequencing method has killed microarray techniques and opened several new avenues in biomedical research including deeper study of disease mechanism. However, computational analysis of NGS data is still challenging which requires complex computational methods and huge computation power. In this paper, we have reviewed brief background of NGS technologies, and an attempt has been made to present how it works as a new platform for disease studies.

1. Introduction

History of sequencing techniques goes long back when Frederick Sanger announced the sequence of first protein (*bovine insulin*) in 1955. However, earlier methods of DNA sequencing were announced in 1977 by Frederick Sanger and his team (Sanger et al., 1977) which involved chain termination. This came to be known as 'Sanger Sequencing'. In the same year Allan Maxam and Walter Gilbert (Maxam and Gilbert, 1977) deployed fragmentation method for DNA sequencing. These two methods have been proven to be benchmark in the field of sequencing to study genes and genomes. Somehow due to use of more radioisotopes in later technique, gradually discouraged it and as a result Sanger sequencing became the prevailing DNA sequencing method for the next 30 years (Van Vliet, 2010).The Sanger sequencing method is popularly known as first generation of sequencing technique and is the most popular choice for sequencing genomes since last four decades (Voelkerding et al., 2009). In early 90's (1990) the production of DNA sequences was commonly done with semi-automated implementations of the Sanger biochemistry which is also a capillary based method (Sanger et al., 1977)

The various strategies for sequencing of DNA can be clustered into four categories (Shendure and Ji, 2008), as shown in Fig. 1. The NGS is the result of implementations of *cyclic-array sequencing*, which has been found to have extensive commercial applications.

Fig.1 Strategies for DNA sequencing

1.1. The conventional sequencing technology: Sanger sequencing

The key steps involved in genomic sequencing by Sanger sequencing method are (Shendure et al., 2005),

- Isolation of target DNA from samples.
- Amplification of interested region in DNA.
- "Cycle sequencing" reactions to generate sequencing product.
- Purifying reactions by removing fluorescent ddNTP, previously used in the sequencing procedure.
- Capillary electrophoresis of resultant products from sequencing after injecting into capillaries filled with polymer to determine sequence by high resolution electrophoretic separation.

Translation of raw data generated into electropherograms usesvarious software tools.

1.2. Advent of NGS Technology

According to International Human Genome Sequencing Consortium 2004 (IHGSC, 2004),the Sanger method has been the gold standard for DNA sequencing for the past 30 years.Sanger sequencing technique was later used in sequencing human genome in 2004.The contributors of Human Genome Project for first human genome sequencing had large sequencing facilities holding capillary sequencers and were supported by complex robotics and infrastructure. Despite this, it still was not well-suited to studying variations as it was merely the scaled-up version of simple Sanger sequencing (Sanger et al., 1977) which came into existence just 25 years beforehand (Kilpinen and Barrett, 2013).

The Human Genome Project (Lander et al., 2001) was time-consuming and required more set of advanced resources. This resulted in immediate need of faster, cheaper higher throughput technologies. Therefore, in same year (2004) the National Human Genome Research Institute (NHGRI) set funds for research aiming to reduce the time and cost of human genome sequencing to US$1000 in ten years (Schloss, 2008). The very first pyrosequencing platform that could perform massively parallel sequencing was launched in 2005 which initiated the dawn of new high throughput era of sequencing called next-generation sequencing (NGS) (Margulies et al., 2005; Shendure et al., 2005).

The next generation sequencing (NGS) is revolutionary technology which has a great positive impact on field of genomics which generates fast, economical, high resolution and accurate genome-scale sequence data with exquisite resolution and accuracy. It has accelerated the sequencing rate to several hundredsgbs of nucleotide sequence per instrument run, while reducing sequencing cost by over five orders of magnitude (Xuan et al., 2013).Since the starting in 2008, NGS platforms have reduced the cost of sequencing DNA by more than 50 000 folds of initial costing, thus making sequencing economical. (http://www.genome.gov/sequencingcosts/)

1.3. NGS advantage over Sanger sequencing technology

The First Generation Sequencing had some shortcomings which were later improvised end lead to development and commercialization of NGS technologies (Van Vliet, 2010).These improvements over Sanger sequencing method (First Generation sequencing methods) are:

- NGS library preparation unlike bacterial cloning of DNA fragments as in first generation.

- Millions of sequencing reactions can be produced parallel rather than few hundred as in Sanger technique.
- The result from NGS sequencing can be directly detected without the need for separate electrophoresis; base interrogation as is performed cyclically and in parallel (Van Vliet, 2010).
- Thus global advantages of second-generation (cyclic-array strategies) or NGS techniques over Sanger sequencing are (Shendure and Ji, 2008)-
- The *in vitro* construction of a sequencing library followed by *in vitro* clonal amplification for sequencing in NGS technology eradicates the disadvantage Sanger sequencing (ie.transformation of *E. coli* and colony picking).
- Array-based sequencing (NGS) has high degree of parallelism than conventional capillary-based sequencing (Sanger sequencing).
- Array features of NGS are immobilized to a planar surface which is advantageous because it can be enzymatically manipulated by a single reagent volume. This in turn lowers the costs for generation of DNA sequence.
- The resolution of NGS can be tuned according to the experimental needs.
- The natural competition among bases while synthesis minimizes incorporation bias leading to elimination of errors and missed calls related to homopolymers.

1.4. Limitations of microarray which paved path for NGS development:

- Hybridization techniques such as Microarray technology have short range for detecting transcript levels due to background noises, saturation and spot density (Van Vliet, 2010).
- Comparison of transcription levels in between microarray experiments is challenging and requires complex normalization methods (Hinton et al., 2004).
- Microarray technology merely measures the relative level of RNA expression so we can't distinguish between de novo synthesized transcripts and modified transcripts. Moreover, it cannot determine the promoter used for de novo transcription accurately (Van Vliet, 2010).

Majority of these issues can be overcome using high-throughput sequencing of cDNA libraries (AC't Hoenet al., 2008) and coupling microarrays and cDNA sequencing can efficiently generate data on full microbial transcriptomes synergistically (Van Vliet, 2010).The studies of gene expression have been switched from microarrays to NGS-based methods, enabling identification and quantification of transcripts regardless of any prior knowledge of genes. Also, provides information relating to sequence variation,alternative splicing and so on (Wang et al., 2009).

1.5. NGS Platforms

The 454 sequencing technology is used in the 454 Genome Sequencers and Roche Applied Science; Solexa technology is used in the Illumina Genome Analyzer; SOLiD platform is extensively used by Applied Biosystem and the HeliScope Single Molecule Sequencer technology is used in Helicos (Shendure and Ji, 2008).

1.6. Working Principle of NGS (Illumina)

Illumina NGS platform relies on sequencing by synthesis (SBS) technology which tracks down the attachment of fluorescent labeled nucleotides while copying DNA chain in parallel. **The Fig. 2**(Grada andWeinbrecht, 2013) represents the steps involved in NGS data generation. The raw input sample is cleaved into shorter fragments (read length of 100-150bp), sequencing machinery used. The longer fragments are firstly ligated to specific adaptors which enable them to anneal the slide later. Then the PCR is carried out to amplify each read separately, creating a spot with several copies of same read. Then separation of each strand to be sequenced is done. The slide is flooded with DNA polymerase, fluorescently labeled nucleotides with the colour corresponding to the specific base and a terminator ensuring addition of one base at a time. The output data from Illumina sequencing systems can range from 300 kilo-base up to 1 tb from a single sequencing run, depending on instrument type and its configuration. (http://www.illumina.com/technology/next-generation-sequencing.html)

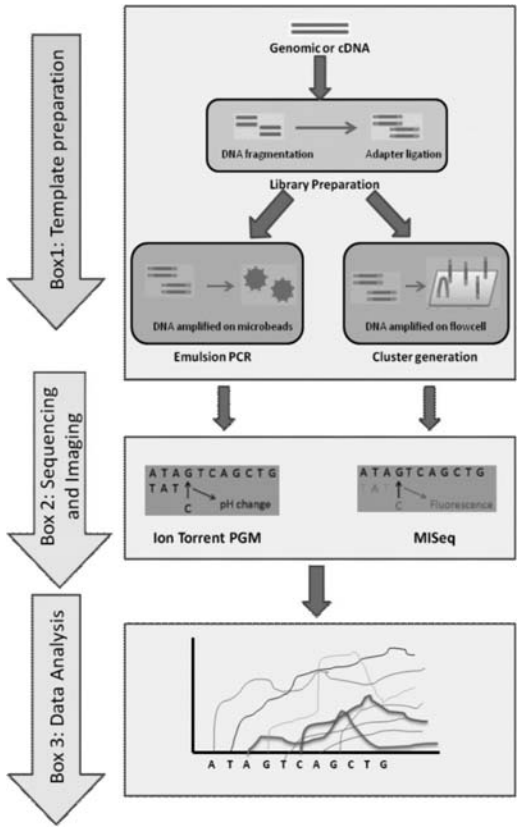

Fig.2 Steps involved in NGS data generation. BOX 1) Template preparation in which genomic or cDNA is used to generate library by fragmenting, ligating to specific adapters and at last amplifying it. Box 2) Next step is sequencing the fragments and imaging. Box 3)Data analysis and interpretation

1.7. NGS as Sub-field for Bioinformatics

There are different types of NGS approaches currently in practice, some of which can be enumerated as (Raza and Ahmad, 2016; Voelkerding et al., 2009; http://www.illumina.com/technology/next-generation-sequencing.html):

- Targeted sequencing.
- RNA sequencing
- Metagenomic sequencing
- Transcriptome sequencing
- Paired-end sequencing
- Whole-exome sequencing
- bisulfite-treated DNA sequencing
- ChIP-Seq

- Nuclease fragmentation and sequencing
- Molecular barcoding

The NGS technology is new in trend and development in this field is being done gradually. Several software tools are under development and NGS data analysis tools are available as open source. Functions of these tools are concerned majorly in subfields as shown in **Fig. 3** (Zhang et al., 2011).

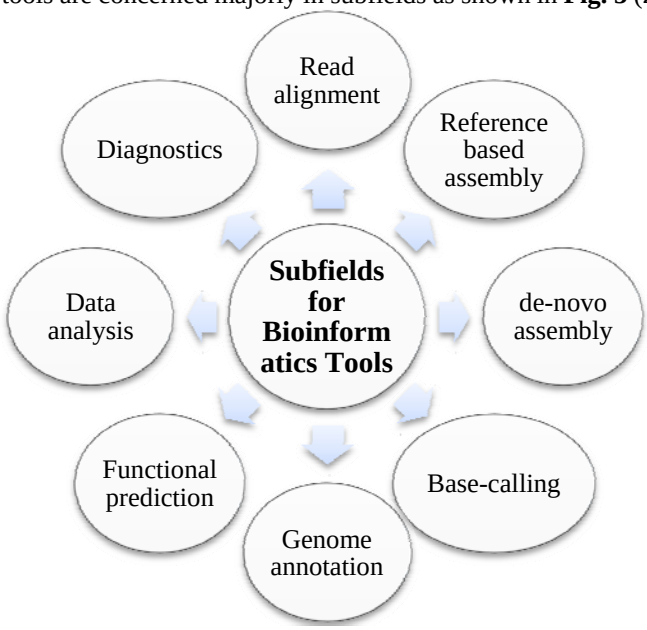

Fig. 3 Various NGS subfields concerned for development of bioinformatics tools

2. Promises in Disease Studies

The NGS has proven to be easy and inexpensive high throughput technique for profiling gene expression and genome annotation. It is found to be useful in area of genomic, transcriptomic, regulomic, metagenomic, epigenomic and diagnostic research (Mutz et al., 2013). It also supports the research in field of agrigenomics, and forensic science (Van Vliet, 2010). It is also advantageous in clinical diagnostics and other aspects of diseases, medicines and drugs like disease risk assessment, therapeutic identification, and prenatal testing (Koboldt et al., 2013).

NGS has already been used in field of diagnostics and forensic studies which resulted in generation of high-throughput data. They successfully answered some questions which were overlooked by Sanger sequencing (Weber-Lehmann et al., 2014).

Several science projects have been benefited from the low cost and high throughput of NGS. Two of the most popular examples regarding this are stated as following.

- **HapMap Project:** The international collaborative project called HapMap Project (International HapMap Consortium, 2005). Wasintroduced Genome Wide Association Studies (GWAS)era by studying common SNPs inthe human genome in detail. This informationenabled researchers to design arrays of several SNPs that were able to successfully capture nearly all the commonvariationin European populations (Barrett et al., 2006).

- **1000 Genomes Project:** The data from 1000Genomes pilot project (1000 Genomes Project Consortium, 2010) from 179 samples have been exclusively utilized in the study of complex diseases. This is done either by improving imputationreference sets or by designing of next-generation genotypingarrays. The 1000 genome project reduced the cost of sequencing an individual genome upto ~$1,000 per person (von Bubnoff, 2008) which showed the way towards personalized medicine (Mardis, 2006; Lunshof et al., 2010).
- **Study of Mendelian diseases:** NGS has been utilized in studying mendelian disease in an affected family by searching for the causes of mutation. For this linkage analysis was done, followed by fine-mapping and then Sanger sequencing of positional candidate genes. Exome sequencing is successful to such diseases most of the causal alleles disrupt protein-coding (exonic) sequences (Stenson et al., 2009).
- **ENCODE project**: NGS enabled us to get genome-wide annotation of functional sites in mouse and human which gave us information regarding regulatory sequences of their genomes. (ENCODE Project Consortium, 2004).
- **Human Microbiome Project:** NGS characterized diversity and types of bacteria and viruses dwelling within human body of several healthy individuals. Thus it defined the baseline for microbial health of human and any changes in their population signifies the marker of disease, etc (Peterson et al., 2009).

The RNA-Seq data obtained from NGS platforms could help researchers interpreting the "personalized transcriptome" that would help in understanding the changes occurring in human transcriptome. This detection could enable identifying key genes for a disease. But this approach is sensitive to time and money (Mardis, 2006; Lunshof et al., 2010).

The completion of human genome sequencing and thus availability of dataset, the use of NGS in studying diseases and variations discoveries has become easy and almost intellectually effortless (Kilpinen and Barrett, 2013).

The NGS provides coverage of large genomic regions of interest which can be successfully laid to develop a precise and strong therapeutic workflow for both germline and somatic cancers (Grada andWeinbrecht, 2013).

Areas to be looked for disease research can be categorized into following (Xuan et al., 2013), as shown in **Fig. 4.**

- Regulatory Networks
- Biomarker discovery
- Diagnostics
- Personalized medicine
- Phylogenetic traits
- Cancer Genomics
- Microbial Genomics
- Agriculture and Animal research

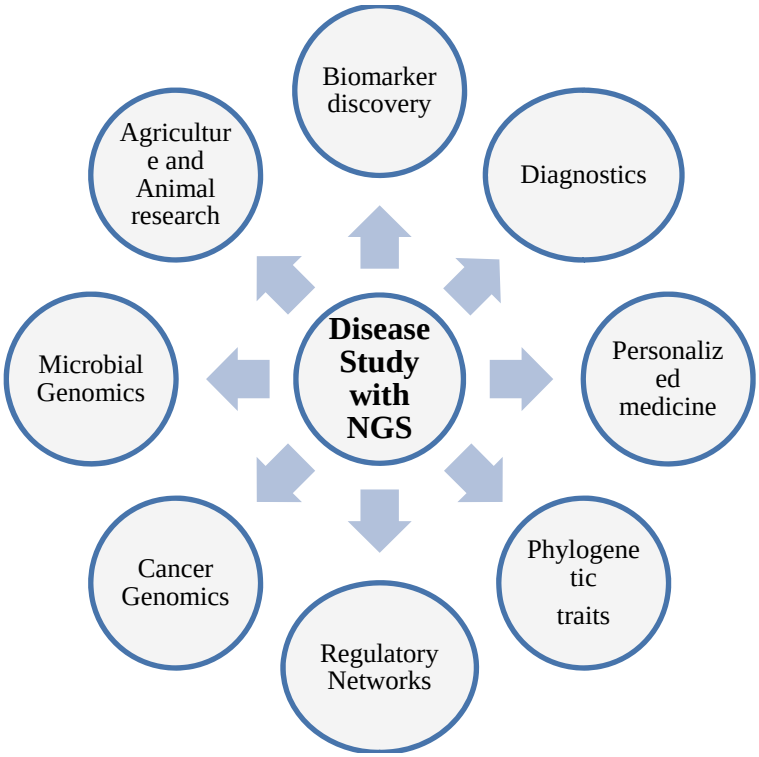

Fig.4 Applications of NGS in disease study.

Some of the applications of NGS in disease study are (Mutz et al., 2013; Mardis, 2008; Grada and Weinbrecht, 2013):

- Detecting the genetic mutations and role of gene involved in diseases such as cancer and other pathological conditions.
- Discovery of noncoding RNA (ncRNA) and miRNAs responsible for the development of drug resistance.
- Detecting and quantifying the low frequency variants like rare drug-resistant viral mutations as in case of HIV, hepatitis B virus, or microbial pathogens that are involved in phenotypic traits and diseases.
- Identifying key genes responsible for skin diseases.
- RNA identification of drug-related genes and genes for fusion proteins in Cancer.
- Quantifying RNA expression levels.
- It can be used in examining epigenetic modifications on a genomic scale which plays important role in cellular processes (gene regulation, disease mechanisms, and oncogenetic development, etc.).
- Identifying undiscovered, novel virulence factors through sequencing the bacterial and viral genomes.

Some of the other area of applications of NGS (Mutz et al., 2013; Zainab et al., 2015) are:

- de novo sequencing (specially eukaryotic genomes)

- Identification of Single Nucleotide Polymorphisms (SNPs), small insertions/deletions (indels), copy number variations (CNVs) and other structural variations.
- Analyzes gene regulation events (DNA–protein interactions, transcription factor bindings, nucleosome positioning, etc.)
- Gene expression profiling (e.g. differentially expressed genes identification)
- Discovery of novel small RNAs, sPiwi-interacting RNAs (piRNAs) by ncRNA and small RNA profiling studies.
- Study microbial diversity in humans or in the environment.
- Analysis of genome-wide methylation.
- Protein-nucleic acid interaction analysis by ChIP-Seq.
- Moreover, in last few years NGS-based methods were widely used for genome analysis to discover new mutations and fusion transcripts in cancer.
- The perception regarding several genes by medical profession and researches are continually changed along with evolving gene sequencing on account of variations in human genome. Likewise, the development in NGS also increases the versatility of genomics field (Mardis, 2008).

3. Challenges

It is quiet cheaper than first generation sequencing approaches in terms of time and money but still it is too expensive for many labs having startup cost of ~$100,000 and individual sequencing reactions of ~$1,000 per genome (Zhang et al., 2011; Xuan et al., 2013).

- Large dataset from NGS can implicate storage problem (Van Vliet, 2010).
- Data analysis of vast high throughput data can be time-consuming.
- Data analysis (analysis, interpretation and visualization) for result from NGS may require special and accurate bioinformatics analytical skill (Zhang et al., 2011).
- Moreover, the Microarrays measure a response in terms of a position on a spectrum, whereas cDNA sequencing in terms of scores (number of hits) for each transcript thus is census-based method (Van Vliet, 2010). This census-based method used in sequencing raises complex statistical issues in data analysis (Jiang and Wong, 2009; Oshlack and Wakefield, 2009).
- Difference in data formats, read lengths, etc. among different NGS platforms results in need of development of bioinformatics tools for management and interpretation of NGS data.
- Guidelines for minimal requirements for online publication of NGS datasets (genomics and proteomics) is needed to be setup, similar to MIAME guidelines (Brazma et al., 2001) for microarray datasets (Van Vliet, 2010).
- Read-lengths are much shorter for all currently available NGS platforms (Van Vliet, 2010).
- The base-calls generated by new platforms are ten-times less accurate than those by Sanger sequencing.
- cDNA sequence should be accurately predetermined and poor quality sequence should be removed, enabling correct mapping onto Genome (Van Vliet, 2010).
- Sequence errors due to inaccurately sequencing of homopolymeric regions (repeating nucleotides) occur on certain NGS platforms (Ion Torrent PGM) and short read length data are generated (Grada andWeinbrecht, 2013).

- The cDNA library construction requires amplification of cDNA, therefore, risk of over-representation of shorter transcripts can lead to unstable result.

These limitations create important algorithmic challenges for the future research perspective and paves path of these technologies to upgrade its specifications and versatility. It is really appreciable that the technical performance of sequencing technologies has progressed to this current level gradually over last three decades.

The NGS technology is new in trend and development in this field is being done gradually. Several software tools are under development and many are available online for NGS data analysis. Functions of these tools are concerned majorly in subfields like (Fig. 5) (Zhang et al., 2011):

- read alignment to a reference sequence;
- de novo assembly;
- reference-based assembly;
- base-calling or genetic variation detection (such as SNV, Indel);
- genome annotation, & functional prediction (Functional variant prediction, Variant detection(Structural/genomic variant& Single nucleotide variant), Differences between genomes)
- data analysis utilities
- diagnostics/utilities

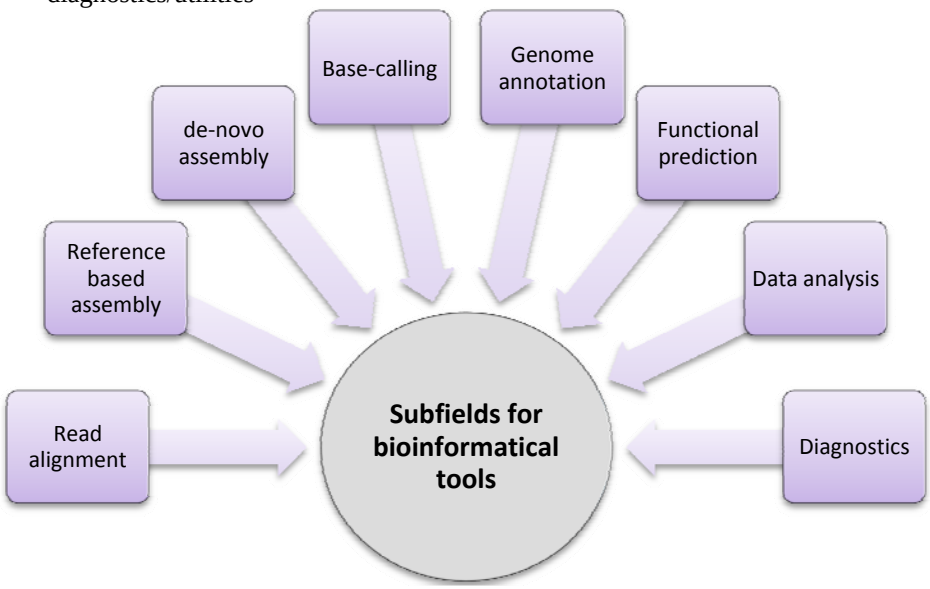

Fig. 5 Various NGS subfields concerned for development of bioinformatical tools.

Advent of Third Generation Sequencing "Nanopore Sequencing": Since NGS enabled completion of whole genome sequencing and revealed the depth of genomes but on the other side it also laid wide range of new questions and some questions were made more difficult to answer.

- We are able to identify correlated variants associated to disease successfully through NGS but how can we further identify its causal alleles and their effect in depth?
- How can we find association between rare alleles with moderate effect, when their confirm association needs impossibly large sample sizes with statistical significance?

- Integration of genomic function, including sequence, epigenetic state, chromatin structure, and conformation in the nucleus to understand phenotypic effects is still challenging?

These unexplored issues might be looked by 'third-generation' technologies, such as 'Nanopore-based technologies' (Manrao et al., 2012), which can sequence least amount of DNA (even single molecules). In this method a small DNA molecule passes by a small pore and resulting into electric current or optical signal as a read sequence (Clarke et al., 2009). Nanopore technology is considered as third-generation technology because it enables the sequencing of few molecules even a single molecules in real time (Van Vliet, 2010).

4. Conclusion

NGS is a sequencing technology that performs high throughput parallel sequencing simultaneously. In this high-throughput technology several DNA fragments gets sequenced simultaneously. Thus entire genome gets sequenced in less than a day. The NGS has been a boon for researchers who keep keen interest in studying biological systems and disease.The advent of NGS has fueled a revolution in biological research. Its promises are accessibility for whole genome sequencing in less duration of time ,limitless dynamic range of expression profiling, allows to tune the level of data resolution to meet specific experimental needs, thus is highly scalable, gives large extent of information as possible about the 'transcriptome' representing complete collection of transcribed sequences in a cell, separates different classes of RNA species into de novo synthesized RNA (primary transcripts) and post-transcriptionally modified (secondary) transcripts, used in sequencing of the human genome and, the Hap-Map project that have helped in studying human disease and resequences many 'normal' human genomes to efficiently capture the spectrum of variability to establish an important baseline for complex disease studies.

In effect, the sequencing of a human genome can now be completed within 2 weeks and the cost of data generation will be ~$5,000 (Ku et al., 2013).The conventional sequencing (Sanger sequencing) is still the most choice for small-scale projects in future because of its'sequencing granularity' but still large projects will depend on NGS.NGS successfully leads to accesswhole genome sequencing in less duration of time and has limitless dynamic range of expression profiling. Moreover, it is highly scalable.NGS has proven to be easy and inexpensive technique for gene expression profiling and genome annotation. High throughput sequencing is found to be useful in the area of genomic, transcriptomic, metagenomic, epigenomic and diagnostic research. But it still face some challenges, like problems for data storage, data analysis requires highly skilled professionals, requires platform specific bioinformaticstools,etc. Moreover, sequencing errors occur for homopolymeric regions. These limitations of NGS create important algorithmic challenges for the future research provides foundation for improvements and removing the causatives which hinders its technical parameters.Taken together, the continuing trends in data-generation facility and cost reduction in NGS platforms will probably contribute, over the long term, to increasing our genome-wide knowledge of organisms,organism systems, and overall provide deeper insight of disease mechanism.

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On Intuitionistic Fuzzy Projective And Injective Modules

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Abstract: In this paper, we will introduce the notion of intuitionistic fuzzy free, projective and injective submodule of a module and discuss some of their properties.
Keywords: Intuitionistic fuzzy submodule (IFSM), intuitionistic fuzzy projective (IF projective), intuitionistic fuzzy injective (IF injective), intuitionistic fuzzy free (IF free) submodule, homomorphism.
Mathematics Subject Classification: 03F55, 08A72, 13C10, 13C11, 16D40, 16D50.

1. Introduction

The concept of intuitionistic fuzzy sets was introduced by K.T. Atanassov [1, 2] as a generalization of the notion of fuzzy sets in [13] and it is a very effective tool to study the case of vagueness. Further many researches applied this notion in various branches of mathematics especially in algebra and defined intuitionistic fuzzy subgroups, intuitionistic fuzzy subrings, and intuitionistic fuzzy sublattices, intuitionistic fuzzy submodules and so forth, for example see ([3], [5-6], [9-12]). Lambek [7] described the notion of free module, projective and injective module and presented some interesting results. The idea of fuzzy free module and their basis was given by Muganda [8]. Zedehi and Amari [14] introduced the notion of fuzzy projectivity and fuzzy injectivity and discussed many results.

In this paper we will define the notion of intuitionistic fuzzy free, projective and injective submodule of a module and discuss some of their properties.

2. Preliminaries

In this section we recall some definitions and results which will be used later

Definition 2.1.[1] Let X be a fixed non-empty set. An intuitionistic fuzzy set (IFS) A of X is an object of the following form $A = \{ \langle x , \mu_A(x) , \nu_A(x) \rangle : x \in X\}$, where $\mu_A : X \to I$ and $\nu_A : X \to I$ define the degree of membership and degree of non-membership of the element $x \in X$ respectively and for any $x \in X$, we have $0 \leq \mu_A(x) + \nu_A(x) \leq 1$, where I = [0,1].

Remark 2.2. [2,10](i): When $\mu_A(x) + \nu_A(x) = 1$, i.e., when $\nu_A(x) = 1 - \mu_A(x) = \mu^c{}_A(x)$. Then A is called a fuzzy set**.**

(ii) We write $A = (\mu_A , \nu_A)$ to denote the IFS $A = \{ \langle x, \mu_A(x), \nu_A(x) \rangle : x \in X\}$.

(iii) An IFS $A = (\mu_A , \nu_A)$ can also be represented by a mapping $(\mu_A , \nu_A) : X \to I \times I$.

Definition 2.3. [6 , 8] Let M be a modules over a ring R. An IFS $A = (\mu_A , \nu_A)$ of M is called intuitionistic fuzzy (left) submodule (IFSM) if

(i) $\mu_A(0) = 1$, $\nu_A(0) = 0$;

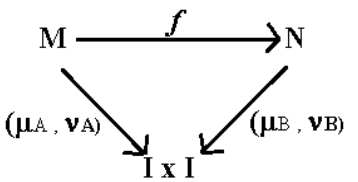
(ii) $\mu_A(x + y) \geq \min\{ \mu_A(x) , \mu_A(y)\}$ and $\nu_A(x + y) \leq \max \{\nu_A(x) , \nu_A(y)\}$, $\forall x, y \in M$;

(iii) $\mu_A(rx) \geq \mu_A(x)$ and $\nu_A(rx) \leq \nu_A(x)$, $\forall x \in M, r \in R$.

If we replace the condition (iii) with $\mu_A(xr) \geq \mu_A(x)$ and $\nu_A(xr) \leq \nu_A(x)$, $\forall x \in M$, $r \in R$, it is called intuitionistic fuzzy (right) module. When R is a commutative ring, then these two modules coincides. From this onward, R will be a commutative ring with unity.

Definition 2.4. [10] Let A = (μ_A , ν_A)be an IFS of a set X and if Y $\subseteq$ X, then the restriction of the IFS A to the set Y is denoted by $A|_Y = (\mu_{A|_Y}, \nu_{A|_Y})$ and is defined as $\mu_{A|_Y}(x) = \mu_A(x)$ and $\nu_{A|_Y}(x) = \nu_A(x)\ \forall\ x \in Y$.

Definition 2.5. Let A = (μ_A ,ν_A) and B = (μ_B , ν_B) be two IFSMs of the module M and N over R respectively. A function f: M → N is said to be a function from A to B



if μ_B o f= μ_A and ν_B o f = ν_A.

Further if f is a module homomorphism, then f is said to be a homomorphism from A to B. In this case, we say that A is homomorphic to B. Similarly, if $f$is a module epimorphi-sm, monomorphism or isomorphism satisfying the above conditions, then we say that f is an epimorphism, monomorphism or isomorphism respectively from A to B.

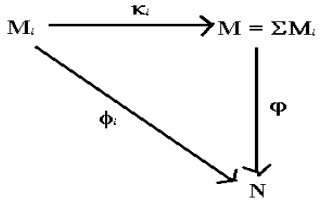
Definition 2.6. [7] The direct product $M = \prod_{i \in J} M_i$ of a family of modules { M_i | i∈ J } over a ring R, is the Cartesian product with operations defined component wise. Thus if $m \in M$, then $m : J \to \bigcup_{i \in J} M_i$ with $m(i) \in M_i$ for all $i \in J$. The external direct sum $M = \sum_{i \in J} M_i$ of a family of modules { M_i | i∈ J } over a ring R consist of $m = \sum_{i \in J} m(i)$, where $m(i)$ = 0 for all but finite many $i \in J$.

Definition 2.7. [7] If $M = \prod_{i \in J} M_i$, then the canonical epimorphism p_i : M →M_i, and the canonical monomorphism k_i : M_i→ M are defined as $p_i(m) = m(i)$ and

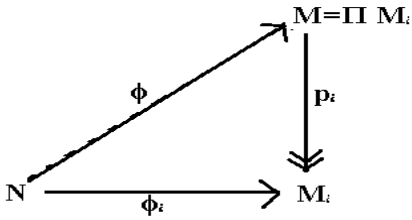
$$k_i(m(j)) = \begin{cases} m & ; if\ j = i \\ 0 & ; if\ j \neq i \end{cases}.$$

Clearly, p_i o k_i = I (identity map)

Proposition 2.8. [7] If M is a direct sum of a family of modules { M_i | i∈ J } with canonical monomorphism k_i : M_i→ M, then for every module N and for every family of homomorphism {ϕ_i : M_i→ N | i∈ J} there exists a unique homomorphism φ : M → N such that φ o k_i = ϕ_i, for all i∈ J.



Proposition 2.9. [7] If M is a direct product of a family of modules { M_i | i∈ J }. If for each i∈ J, $p_i : M \to M_i$, be the canonical epimorphism, then for every module N and for every family of homomorphism $\{\phi_i : N \to M_i \mid i \in J\}$ there exists a unique homomorphism $\varphi : M \to N$ such that $p_i \circ \varphi = \phi_i$, for all $i \in J$.



Definition 2.10. Let M be a module over R which is a direct product of a family of modules $\{M_i \mid i \in J\}$over R.Let $A_i = (\mu_{Ai}, \nu_{Ai})$be IFSMs of M_i. We define an IFS $A = (\mu_A, \nu_A)$ of M by $\mu_A(m) = Inf\{\mu_{A_i}(m(i)) \mid i \in J\}$ and $\nu_A(m) = Sup\{\nu_{A_i}(m(i)) \mid i \in J\}, \forall\ m = \prod_{i \in J} m(i) \in M$.

Then A is an IFSM of M. We say this IFSM A as the direct product of the IFSMs A_i and in this case we write $A = \prod_{i \in J} A_i$.

Next, let M be the direct sum of the family $\{M_i \mid i \in J\}$. If we define
$\mu_A(m) = \min\{\mu_{A_i}(m(i)) \mid i \in J\}$ and $\nu_A(m) = \max\{\nu_{A_i}(m(i)) \mid i \in J\}, \forall\ m = \sum_{i \in J} m(i) \in M$.

[Note that $m(i) = 0$ for all but infinite many i]. Then A is an IFSM of M. We say this IFSM A as the direct sum of the IFSMs A_i and in this case we write $A = \sum_{i \in J} A_i$.

Definition 2.11. Let $A = \prod_{i \in J} A_i$ or $A = \sum_{i \in J} A_i$, where $A = (\mu_A, \nu_A)$ and $A_i = (\mu_{Ai}, \nu_{Ai})$ are IFSMs on M and M_i respectively. Then we say the canonical epimorphism p_i from M to M_i as the canonical epimorphism from A to A_i if $\mu_{A_i} o\ p_i = \mu_A$ and $\nu_{A_i} o\ p_i = \nu_A$. Similarly, we say the canonical monomorphism k_i from M_i to M as the canonical monomorphism from A_i to A if $\mu_{A_i} o\ k_i = \mu_A$ and $\nu_{A_i} o\ k_i = \nu_A$.

3. Intuitionistic fuzzy projective submodules

Definition 3.1. Let S be a subset of a module M over a ring R and let $A = (\mu_A, \nu_A)$ be an IFSM of M. Let B be an IFS of S such that $B \subseteq A|_S$. Then B is said to be linearly independent (L.I.) in A if
(i) S is L.I subset of M;

(ii) For any $x \in$ M, if $x = \sum_{i=1}^{k} r_i s_i$, where $r_i \in R$, $s_i \in S$ (i = 1,2,...., k) is an irredundant representation of x, then

$\mu_A(x) = \min\{\mu_B(s_i) \mid i = 1, 2, ..., k\}$ and $\nu_A(x) = \max\{\nu_B(s_i) \mid i = 1, 2, ..., k\}$.

Note 3.2. If B is L.I in A, then B = A on S.

Example 3.3. Let M = R^2 be a vector space over R. Let A = (μ_A ,ν_A) be an IFSM of M defined by

$$\mu_A(x) = \begin{cases} 1 & if\ x = 0 \\ 0.5 & if\ x \neq 0 \end{cases} \quad \text{and} \quad \nu_A(x) = \begin{cases} 0 & if\ x = 0 \\ 0.2 & if\ x \neq 0 \end{cases}, \ \forall x \in M.$$

Let S = { β_1 , β_2 } be a subset of M, where β_1 , β_2 are L.I. elements of M. Let B be an IFS on S, defined by

$$\mu_B(x) = \begin{cases} 1 & if\ x \in S \\ 0.5 & if\ x \notin S \end{cases} \quad \text{and} \quad \nu_{\chi_S}(x) = \begin{cases} 0 & if\ x \in S \\ 0.2 & if\ x \notin S \end{cases}, \ \forall\ x \in M$$

Clearly, B$\subseteq$ $A|_S$. Let $0 \neq x = r_1\beta_1 + r_2\beta_2$, be an irredundant representation, then

$\mu_A(x) = \min\{\mu_B(\beta_1),\ \mu_B(\beta_2)\} = 0.5 \wedge 0.5 = 0.5$ and $\nu_A(x) = \max\{\nu_B(\beta_1),\ \nu_B(\beta_2)\} = 1 \vee 1 = 1.$

Therefore, B is an linearly independent in A.

Example 3.4. Let M ={ $(a, a) \mid a \in R$} be a vector subspace of R^2 over R. Let A = (μ_A ,ν_A) be an IFSM of M defined by

$$\mu_A(x) = \begin{cases} 1 & if\ x = 0 \\ 0.5 & if\ x \neq 0 \end{cases} \quad \text{and} \quad \nu_A(x) = \begin{cases} 0 & if\ x = 0 \\ 0.2 & if\ x \neq 0 \end{cases}, \ \forall x \in M.$$

Let S = { β_1} be a subset of M, where β_1 is a non-zero element of M. Let B be the intuitionistic fuzzy characteristic function on S, i.e.,

$$\mu_B(x) = \begin{cases} 1 & if\ x \in S \\ 0 & if\ x \notin S \end{cases} \quad \text{and} \quad \nu_{\chi_S}(x) = \begin{cases} 0 & if\ x \in S \\ 1 & if\ x \notin S \end{cases}, \ \forall\ x \in M$$

Clearly, B$\subseteq$ $A|_S$. Let (1,1) = $r_1\beta_1$ be an irredundant representation of (1,1), then

$\mu_A(1,1) = \mu_B(\beta_1) = 0 \neq 0.5$ and $\nu_A(1,1) = \nu_B(\beta_1) = 1 \neq 0.2.$

Therefore, B is not linearly independent in A.

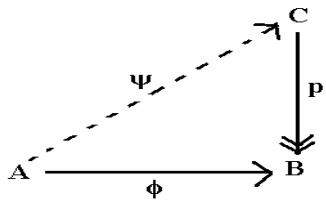
Definition 3.5. Let A be an IFSM of a module M over a ring R, S be a subset of M and B an IFS on S such that B $\subseteq$ $A|_S$. Then B is said to be a basis for A if S is a basis of M, B is linearly independent in A and < B > = A, i.e., A is the smallest IFSM of M such thatB $\subseteq$ $A|_S$.

Definition 3.6. Let A be an IFSM of a module M over a ring R. Then A is said to be free if A has a basis, i.e., there exists a basis S of M and an IFS B of S such that B $\subseteq$ $A|_S$ and B is linearly independent such that < B > = A.

Remark 3.7. An IFSM A of a module M over a ring R may or may not be free

For example: An IFSM A as in example (3.3) is free as B is L.I. in A and A = < B >, where as an IFSM A asin example (3.4) is not free, for < B >$\neq$ A.

Definition 3.8. Let N and P be any two modules over a ring R andlet A be an IFSM of M over R. Then A is said to be intuitionistic fuzzy projective (IF projective) submodule if for any IFSMs B of N, C of P, any epimorphism p from C to B and homomorphism ϕ from A to B, there exists a homomorphism ψ from A to C such that p o ψ = ϕ.



In short the above diagram is commutative.

Theorem 3.9. *Every intuitionistic fuzzy free submodule of a module is IF projective.*

Proof. Let A=(μ_A, ν_A) be an intuitionistic fuzzy free submodule of a module M over a ring R. Let { m_i | i∈ I} be a basis of M. Let N and P be any two modules over R. Let B = (μ_B ,ν_B) , C = (μ_C , ν_C) be two IFSM of N and P respectively. Let p be an epimorphism from C to B and ϕ be a homomorphism from A to B. Now for any i∈ J, there exists b_i∈ P such that ϕ (m_i) = p(b_i). Thus, for any $m = \sum_{i\in J} r_i m_i \in M$, we define ψ : M → P by ψ(m) =ψ($\sum_{i\in J} r_i m_i$) = $\sum_{i\in J} r_i b_i$. Then it is easy to check that ψ is a homomorphism.

$$\textit{Also,}\quad (po\psi)(m) = p(\psi(m)) = p\left(\sum_{i\in J} r_i b_i\right) = \sum_{i\in J} r_i p(b_i) = \sum_{i\in J} r_i \phi(m_i) = \sum_{i\in J} \phi(r_i m_i) = \phi\left(\sum_{i\in J} r_i m_i\right) = \phi(m).$$

Hence poψ = ϕ.Finally, we show that ψ is a homomorphism from A to C, for this we have $\mu_C o\psi = (\mu_B op)o\psi = \mu_B o(\,po\psi\,) = \mu_B o\phi = \mu_A$. Similarly, we get $\nu_C o\psi = \nu_A$.

Therefore ψ is a homomorphism from A to C such that p o ψ= ϕ. Hence A is IF projective.

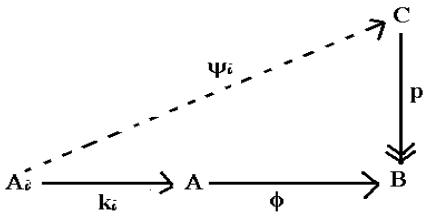
Theorem 3.10. *Let M be the direct sum of the modules {M_i| i ∈ J} over a ring R. Let A be an IFSM of M and A_i be that of M_i for all i ∈ J. Let* $A = \sum_{i\in J} A_i$ *. Then A is IF projective if and only if each A_i is IF projective.*

Proof. Let A = (μ_A ,ν_A) and A_i = (μ_{Ai} , ν_{Ai}) be IFSMs on M and M_i respectively for all i∈ J. and letk_i : A_i→ A be the canonical monomorphism. First we assume that each $A_i$is IF projective. Let N and P be two modules over R and let B = (μ_B ,ν_B) , C = (μ_C , ν_C) be IFSMs of N and P respectively. Let p : C → B be an epimormorhism, k_i : M_i→ M be canonical injection and ϕ : A → B be a homomorphism. Then

$$\left(\left(\mu_B o\phi\right)ok_i\right)(m_i) = \left(\mu_A ok_i\right)(m_i) = \mu_{A_i}(m_i),\quad \forall\ m_i \in \mathrm{M}_i.$$

Therefore, $\left(\mu_B o\phi\right)ok_i = \mu_{A_i}$ i.e., $\mu_B o(\phi ok_i) = \mu_{A_i}$. Similarly, we can get $\nu_B o\left(\phi ok_i\right) = \nu_{A_i}$.

Thus, ϕ o k_i is a homomorphism from A_i to B. Since A_i is IF projective, so there exists a homomorphism ψ_i : A_i→ C such that poψ$_i$ = ϕ o k_i.

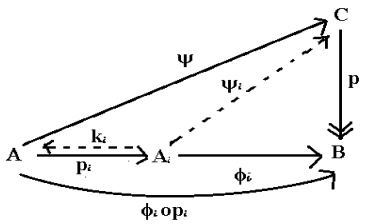


By proposition (2.8), there exists a unique homomorphism $\psi : M \rightarrow P$ such that ψ o $k_i = \psi_i$, for all $i \in J$.Since p o ψok_i = p o ψ_i= ϕ o k_i , so by uniqueness of k_i, we get p o $\psi = \phi$.Finally, we have to show that ψ is a homomorphism from A to C. For this we have $\mu_C o\psi = (\mu_B op)o\psi = \mu_B o(\, po\psi\,) = \mu_B o\phi = \mu_A$. Similarly, we can get $\mu_C o\psi = \nu_A$.

Thus ψ is a homomorphism fromA to C such that p o $\psi = \phi$. Hence A is IF projective.

Conversely, let A be IF projective. Let $\phi_i : A_i \rightarrow B$ be a homomorphism and $p : C \rightarrow B$ be an epimorphism. Let p_i: C $\rightarrow$ A_i be the canonical epimorphism. Now, $\mu_B o(\phi_i op_i) = (\mu_B o\phi_i)op_i = \mu_{A_i}$ o $p_i = \mu_A$. Similarly, we can get $\nu_B o(\phi_i op_i) = \nu_A$.

This shows that $\phi_i op_i$ is a homomorphism from A to B. Since A is IF projective, so there exists a homomorphism $\psi : A \rightarrow C$ such that p o ψ = $\phi_i op_i$. But p_i o k_i = I (identitymapping) and so p o ψok_i = $\phi_i op_i ok_i = \phi_i$. Let ψ o $k_i = \psi_i$, then $\psi_i : M_i \rightarrow P$ is a homomorphism. Also,



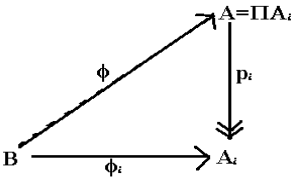
$\mu_C o\psi_i = \mu_C o(\psi ok_i) = (\mu_C o\psi)\,o\,k_i = \mu_A ok_i = \mu_{A_i}$. Similarly, we can get $\nu_C o\psi_i = \nu_{A_i}$.

Therefore, ψ_i is a homomorphism from A to C. Also, p o $\psi ok_i = \phi_i$i mplies p o $\psi_i = \phi_i$, hence A_i is IF projective.

Lemma 3.11. Let A module M over a ring R is the direct product of a family of modules $\{M_i \mid i \in J\}$ over R, A be an IFSM of M and A_i be that of M_i. Let $A = \prod_{i \in J} A_i$ and $p_i : A \rightarrow A_i$ be the canonical epimorphism. Then for every IFSM B of any module N over R and for every family of homomorphism $\phi_i : B \rightarrow A_i$, there exists a unique homomorphism $\phi : B \rightarrow A$ such that p_i o $\phi = \phi_i$.

Proof. Let $A = (\mu_A, \nu_A)$ and $A_i = (\mu_{Ai}, \nu_{Ai})$ be IFSMs on M and M_i respectively for all $i \in J$. We recall that for any $m \in M$, $p_i(m) = m(i) \in M_i$. Define $\phi : N \rightarrow M$ such that for each $i \in J$, we have$\phi(n)(i) = \phi_i(n)$, $\forall n \in N$. Then it is easy to check that ϕ is a homomorphism. Also $(p_i$ o $\phi)(n) = p_i(\phi(n)) = \phi(n)(i) = \phi_i(n)$ and thus p_i o $\phi = \phi_i$. Finally,

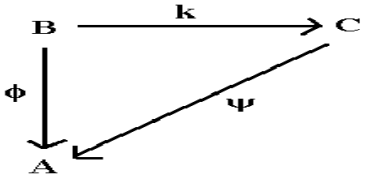
$\mu_A o\phi = (\mu_{A_i} op_i)\,o\,\phi = \mu_{A_i}$ o$(p_i o\,\phi) = \mu_B$. Similarly, we can get $\nu_A o\phi = \nu_B$.



Therefore,ϕ:B $\rightarrow$ A such that p_i o $\phi = \phi_i$. Again, if $\psi : B \rightarrow A$ is another homomorphism such that p_i o $\psi = \phi_i$, then $(\psi(n))(i) = p_i(\psi(n)) = (p_i$ o $\psi)(n) = \phi_i(n) = (\phi(n))(i)$ and so$\psi = \phi$. Hence ϕ is

unique.

Definition 3.12. Let N and P be any two modules over a ring R and A be an IFSM of a module M over R. Then A is said to be an intuitionistic fuzzy injective (IF injective) submodule if for any IFSM B of N, C of P, and momorphism k from B to C and homomorphism ϕ from B to A, there exists a homomorphism ψ from C to A such that ψ o k = ϕ.



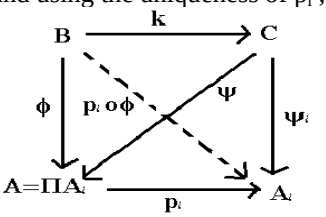
Theorem 3.13. Let M be the direct product of the modules $\{M_i \mid i \in J\}$ over a ring R. Let A be an IFSM of M and A_i be that of M_i for all $i \in J$. Let $A = \prod_{i \in J} A_i$. Then A is IF injective if and only if each A_i is IF injective.

Proof. Let $A = (\mu_A, \nu_A)$ and $A_i = (\mu_{Ai}, \nu_{Ai})$ be IFSMs on M and M_i respectively for all $i \in J$. Let $p_i : A \rightarrow A_i$ be the canonical epimorphism.

First let each A_i be IF injective. SupposeN and P be any two modules over R and B and C be IFSM of N and P respectively. Letk: B → C be amonomorphism and ϕ : B →A be a homomorphism. Now $p_i o \phi$: N →M_i is a homomorphism such that

$\mu_{A_i} o(p_i \, o \phi) = (\mu_{A_i} \, op_i) \, o \phi = \mu_A \, o \phi = \mu_B$. Similarly, we can get $\nu_{A_i} o(p_i \, o \phi) = \nu_B$.

Therefore, p_i o ϕ is a homomorphism from B to A_i. Since A_i is IF injective , there exists a homomorphism $\psi_i : C \rightarrow A_i$ such that ψ_i o k = p_i o ϕ. Also, by proposition (2.8), there exists a unique homomorphism $\psi : C \rightarrow A$ such that p_i o $\psi = \psi_i$. Now, ψ_i o k = p_i o $\phi \Rightarrow$ (p_io ψ) o k = p_i o $\phi \Rightarrow$ p_i o(ψ o k) = p_i o ϕ and using the uniqueness of p_i , we get ψ o k =ϕ.



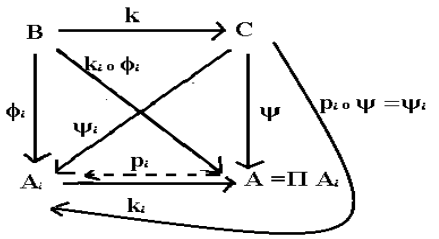
Finally, we have

$\mu_A \, o \psi = (\mu_{A_i} \, op_i) \, o \psi = \mu_{A_i} \, o(p_i o \psi) = \mu_{A_i} \, o \psi_i = \mu_C$. Similarly, we can get $\nu_A \, o \psi = \nu_C$.

Therefore, ψ : C → A is a homomorphism such that ψ o k = ϕ. Hence A is IF injective. Conversely, let A be IF injective. Let k : B → C be a monomorphism, ϕ_i : B → A_i a homomorphism, p_i : M →M_i the canonical epimorphism and k_i : M_i→ M the canonical monomorphism. Then k_i o ϕ_i : N → M is a homomorphism. Also,

$\mu_A \, o(k_i \, o \phi_i) = (\mu_A \, o \, k_i) \, o \phi_i = \mu_{A_i} \, o \phi_i = \mu_B$. Similarly, we can get $\nu_A \, o(k_i \, o \phi_i) = \nu_B$.

Therefore, k_i o $\phi_i$is a homomorphism from B to A. Since A is IF injective so there exists a homomorphism ψ : C → A such that ψ o k = k_i o ϕ_i.



Let p_i o ψ = ψ_i, then ψ_i: P $\rightarrow M_i$ is a homomorphism. Also, $\mu_{A_i} o\psi_i = \mu_{A_i} o(p_i o\psi) = (\mu_{A_i} op_i) o\psi = \mu_A o\psi = \mu_C$. Similarly, we can get $\nu_{A_i} o\psi_i = \nu_C$. Therefore, ψ_i is a homomorphism from C to A_i. Also, ψ_i o k = (p_i o ψ) o k = p_i o (ψ o k) = p_i o (k_i o ϕ_i) = (p_i o k_i) o ϕ_i= I o ϕ_i = ϕ_i. Hence A_i is IF injective.

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