

# Exploring Environmental Interactions Through Complex Networks: A Multilayer Analysis Of Ecological Relationships

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## Abstract

*This abstract presents a comprehensive study on environmental interactions utilizing complex network theory. The research focuses on employing a multilayer analysis framework to unravel the intricate web of ecological relationships. By leveraging the principles of network science, this study aims to elucidate the interconnectedness and dynamics within ecosystems. The methodology involves constructing multilayer networks that encapsulate various ecological dimensions, including species interactions, food webs, habitat networks, and environmental factors. By integrating these layers, the research endeavours to reveal emergent properties and synergies existing across these interconnected systems. Through the application of advanced analytical tools, the study aims to identify key nodes, central motifs, and structural patterns within the multilayered ecological networks. Additionally, the research seeks to investigate the resilience of these networks to perturbations, providing insights into the stability and robustness of ecological communities in response to environmental changes.*

**Keywords:** Ecological Networks, Multilayer Analysis, Environmental Interactions Complex Systems, Ecosystem Dynamic.

## 1. Introduction

Ecological systems are thermodynamically open, extremely ordered, and complicated systems. Different interactions between the biotic and abiotic components that make up the system lead to its organization[1]. These groups offer a <sup>1</sup>basic overview of the various laws and procedures that control the development, operation, and upkeep of ecosystems. When the biotic and abiotic components of various systems are combined in different ways, the interactions alter. Properties particular to each system, such as stability, maturity, and resilience, are defined by these interactions.

The intricacy of actual ecosystems is not sufficiently reflected by reductionist methodologies. To investigate such emergent aspects of any system, however, a holistic ecosystem approach that takes into account the system's food web, for example, in its totality, is far more scientifically adequate [2]. These models can also be used to investigate the effects of various exogenous stress factors on the resilience, organizations, and functions of a system.

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Models that are mass balanced or steady state can reflect the vast amounts of data needed to describe a whole food chain. As the name implies, these models operate under the assumption of a steady-state situation in which the system's inputs and outputs are equal[3]. This modelling approach necessitates measuring flows of materials or energy and how they interact with the various ecosystem components.

Ecosystems are changing quickly as a result of human pressures such as invasions by non-native species and climate change. In the face of increasing forces that are transforming the ecosystem, it is critical for the future health of society to preserve ecosystem services. Therefore, it is the responsibility of ecologists to comprehend the variables that govern the resilience and stability of ecosystem functioning[4]. Because these interactions affect ecosystem services both directly and indirectly, it is crucial that we comprehend how creatures interact in communities.

Because of the intricate relationships between so many different components, mechanistic investigations of the relationship between community organization and ecosystem performance are challenging. The shift in study focuses towards foundation species—species with significant ecosystem-wide effects—has been one significant advancement in the study of ecosystem dynamics[5]. Keystone species, dominating species, and ecosystem engineers are all included in the recently proposed foundation species idea.

It has been demonstrated that these species control ecosystem dynamics as a result. For instance, the mix of plant and ant communities has rapidly changed in Eastern North America due to the eradication of foundation species brought about by an alien pest resembling aphids. This implies that knowledge about a foundation species' expected response to environmental disturbances, including invasions by exotic species or changes in climate, will be crucial for comprehending the dynamics of the ecosystem as a whole[6].

The field of local area hereditary qualities, which is characterized as the investigation of the hereditary collaborations that happen among species and their abiotic climate in complex networks, has developed thanks by and large to the establishment species idea. Local area environment can be perceived as the examination and estimation of the interspecific wellsprings of normal determination according to a developmental perspective[7]. Other species that interact with a given species will probably undergo evolutionary changes in response to that species. Studies involving pairs and multiple species have confirmed this. Quantifying the evolutionary dynamics in communities, including intricate relationships across species, can be initiated by examining the community genetics of foundation species.

## **2. Literature Review**

### **2.1. "Studies on Ecological Networks and Biodiversity Dynamics"**

Dunne, Martinez, and Williams (2002) Their research demonstrated the favorable relationship between robustness and connectance, illuminating the crucial function that connectance plays in preserving biodiversity in ecosystems [8].

In their 2012 study, Poccock, Evans, and Memmott explored the resilience and rehabilitation of ecological networks [9]. Their research promoted network-centric ecosystem restoration solutions by highlighting the interconnection of diverse networks and the significance of network resilience in the face of disruptions.

Jordano and Bascompte (2014) the complex links that exist between species in mutualistic networks are thoroughly examined in their book, which also offers insights into the dynamics and stability of these ecological interactions[10].

## **2.2. "Ecological Network Dynamics: Modularity, Architecture, and Resilience"**

In their 2007 study, Olesen, Bascompte, Dupont, and Jordano uncovered the division of labour among pollination networks by focusing on their modularity[11]. By highlighting the importance of modular structures in pollination networks, their research shed light on the stability and resilience of these crucial ecological systems.

Thébault and Fontaine (2010) their research shed light on the complex relationship that exists between ecological stability and network architecture and advanced our knowledge of the mechanisms that underpin these networks' resilience[12].

Saavedra, Stouffer, Uzzi, and Bascompte (2011), strong contributors to network persistence are essential to the stability of ecosystems, but they also paradoxically confront increased vulnerability to extinction[13]. This seminal discovery highlighted the finely balanced relationship between the resilience of natural networks and the vulnerability of major actors, with significant ramifications for conservation tactics.

## **2.3. "Advancements in Ecological Network Science: Understanding, Conservation, and Complexity"**

The foundation for comprehending the complex interconnections within ecological systems was established by Newman's groundbreaking work on the formation and operation of complex networks in 2003[14]. His thorough analysis emphasized the importance of network structures in many settings, providing a theoretical framework for later research that employs network science to investigate environmental interactions.

In their 2010 study, Tylianakis, Laliberté, Nielsen, and Bascompte explored the topic of species interaction network conservation and emphasised the significance of protecting these complex ecological networks in order to preserve biodiversity[15]. The study highlighted the interdependence of ecosystems and species, promoting conservation policies that give priority to maintaining species interactions in order to protect the resilience of ecosystems.

The study by Blüthgen, Menzel, and Blüthgen (2006) their research shed light on the subtleties of species interactions and their contributions to the general stability and structure of ecological networks by developing useful approaches for assessing the degree of specialization within these networks[16].

James, Pitchford, and Plank (2012) made a substantial contribution by removing nestedness from ecological complexity models. Their research shed light on the complex patterns of interactions between species, explaining the elements that contribute to ecological networks' nested structure and its effects on the resilience and stability of ecosystems[17].

## **3. Methodology**

### **3.1. Ecological Network Analysis (ENA)**

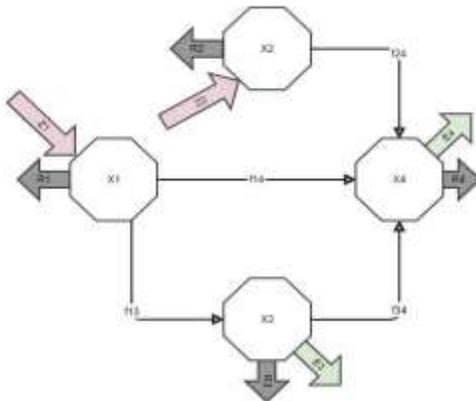
The Ecological Network Analysis (ENA) approach, a framework situated philosophy that reenacts and examinations framework collaborations to recognize all-encompassing properties (like health and stress resilience) that cannot be identified from direct observations, is the best way to study the aforementioned interrelationships[18]. The foundation of ENA includes the representation of flows via various system compartments (flow matrix), thermodynamics, input-output analysis, statistical mechanics, information theory, and taxonomic grouping.

The economic input-output analysis, first proposed by Leontief in 1951 and later modified by Hannon in 1973 to characterise the flow of materials or energy through specific ecosystem components, served as the foundation for the fundamentals of ENA. The term "flow analysis" was formerly used to describe this idea. The law of conservation of mass governs ecological network modelling; it expresses that the "mass of an arrangement of substances will stay consistent over the long run, no matter what the cycles acting inside the framework". All in all, the model catches the condition of the framework at a particular moment.

The primary benefit of this type of modelling approach is that it requires less time to assess the condition of the entire ecosystem, as well as the numerous individual components and the flows between them, utilising a small data set.

Network Construction: A network of nodes and edges serves as the system's representation in ENA. All of the system's biotic (producers, consumers, etc.) and abiotic (detritus, etc.) components are represented by nodes. Conversely, edges show the flow of materials and energy between each node. Nodes and edges, respectively, carry additional information such as the volume and direction of flow, as well as the standing stock of a certain component.

A simple network with four nodes or compartments ( $X_i=1$  to 4) connected by energy-matter flows ( $f_{ij} \rightarrow$  flow of matter or energy from node  $i$  to node  $j$ ) is shown in Figure 1.



**Figure 1: A diagrammatic representation of a hypothetical network comprising of four nodes (X1, X2, X3 and X4) and the different energy flows between them (f13, f14, f34 and f24); Z1 and Z2 represent imports into the system; E3 and E4 represent exports from the system and R1, R2, R3 and R4 represent respiration losses from the nodes**

Respiratory loss from biotic compartments, imports or flows that enter the system from outside, exports or flows that leave the system, and flows between each compartment or node are the four types of flows that make up ecological networks. These flows are denoted by vectors Z, E, R, and flow matrix F, respectively.

As previously mentioned, nodes and edges must have consistent units, which are usually expressed as amounts of energy or biomass per unit area or volume (e.g., calories m<sup>-2</sup> or tonnes km<sup>-2</sup>) for nodes and energy or biomass per unit area per unit time (e.g., tonnes km<sup>-2</sup> day<sup>-1</sup>) for flows[19]. These values correspond to the standing stock and magnitude of flux, respectively.

### 3.2. Development of Eco Path Model

A portion of the regularly involved programming projects for directing ENA are NETWRK, ECONET, WAND, EcoPath with EcoSim, NEA, and enaR. EcoPath with EcoSim (EwE) (revision 6.4.14040.0), which is openly accessible at <https://ecopath.org/>, is the program used in this review[20]. In various examinations, biological system properties have been evaluated, trophic relations and connections have been broken down, and the impacts of natural changes have been observed.

According to Kay et al., static models are reflective of the mass-balanced trophic network in an ecosystem; that is, they represent a snapshot that describes the resources and their numerous interactions in the system at a specific point in time. The following two governing equations for EwE models provide the fundamental premise of a mass balanced model:

- a) Production = Catch + Predation + Net Migration + Biomass Accumulation+ Other Mortality.
- b) Consumption= Production+ Respiration + Unassimilated Food.

It is possible to express a single equation by combining these two equations:

$$B_i \cdot \left(\frac{P}{B}\right)_i \cdot EE_i - \sum_{j=1}^i B_j \cdot \left(\frac{Q}{B}\right)_j \cdot DC_{ji} - EX_i = 0 \quad (1.1)$$

where I and j are the amounts of prey and tracker bundles in the structure, independently, and B<sub>i</sub> tends to the biomass of the social occasion I, (P/B)<sub>i</sub> is the creation to biomass extent for pack I (which is comparable to the total mortality coefficient Z at steady state), EE<sub>i</sub> is the ecotrophic viability of get-together I, B<sub>j</sub> is the biomass of the tracker, (Q/B)<sub>j</sub> is the extent of usage to biomass for tracker j, DC<sub>ji</sub> is the degree of j's eating routine gained from I, and EX<sub>j</sub> is the ware of social affair j.

Ecotrophic effectiveness (EE), biomass (B), creation/biomass proportion (P/B), and utilization/biomass proportion (Q/B) are the fundamental information boundaries of an EcoPath model. For the model to be developed, information on each of the functional groups taken into account and the diet composition of at least three of the aforementioned factors must be provided[21]. Next, the fourth missing element is automatically estimated using the EcoPath parameterization technique.

### 3.3. Functional groups and their basic inputs:

Ataxonomic aggregation, which is the grouping of various creatures in the system according to their habitat or feeding habits rather than their taxonomic identities, is a fundamental concept in static modelling [22]. In order to avoid creating an overly complex and large model structure, treating each organism as a separate node is a crucial step in the development of a static model.

Based on their biological roles, such as habitats and feeding patterns, the majority of species in the Kakinada Bay model have been grouped. Certain taxa, including polychaetes, prawns, and crabs, on the other hand, have a taxonomic separation since the majority of their species in this system perform comparable ecological roles.

Twenty-four (24) functional categories make up the Kakinada Bay model, including detritus, phytoplankton, suspension feeding invertebrates (SFI), polychaetes, prawns, mullets, and catfish. The many functional groupings and specifics, like the species that belong to each group, are covered in more detail below and are also listed in Table [23]. All of the fundamental inputs and their sources for every node that were utilised to build the trophic structure model are included. The basic EwE package working environment is shown. The nodes and edges that make up this model are shown in the conceptual diagram.

**A. Principal Producers:** The principal producers in this system are benthic microphyto benthos (MPB) and pelagic phytoplankton (P). These have been treated as two distinct categories in order to better determine the impact of MPB on the overall health of the system. Microplastic Bacteria (MPB) are tiny, mobile photosynthetic algae that live in the uppermost layer of sediment, while phytoplankton are microscopic, motile plants that live in the water column. Although there are numerous species in common across both groups, environment is the primary difference between them[24]. Phytoplankton and MPB biomass were estimated using the following formula based on the chlorophyll values of water and sediment, respectively:

$$PC = -1 + 80*(\text{chlorophyll-a}) \quad (1.2)$$

Where PC addresses the carbon-containing biomass Furthermore, the P/B proportions for these two gatherings were registered. P/B proportions for those still up in the air by first working out the essential creation (PP) of P and MPB utilizing equation.

$$\ln PP = 1.254 + 0.728 \ln \text{Chl-a} \quad (1.3)$$

**B. Detritus:** Detritus, which is organic stuff that has decayed and is dead, is where the detrital food chain starts. This feeding chain transfers a large amount of matter and energy in shallow estuarine habitats. Consequently, debris is a crucial abiotic compartment in models of shallow estuary systems like Kakinada Bay.

Equation 1.4 was used to decide the biomass of debris in light of the essential not entirely set in stone in equation 1.3:

$$\log D = 0.954 \log PP + 0.863 \log E - 2.41 \quad (1.4)$$

Where D, PP, and E stand for the bay's euphotic depth, primary production, and detritus biomass, respectively

**C. Zooplankton and Bacteria:** While bacteria are a decomposer group that feeds on detritus, zooplankton is a primary consumer that feeds on phytoplankton, MPB, detritus, and bacteria. Field data gathered over a ten-month period from twelve distinct locations was used to determine the biomass of zooplankton. Due to a lack of field data, the biomass of bacteria and the fundamental inputs of each of these groups were gathered from literature.

**D. Benthic Invertebrates:** All benthic invertebrate species were grouped into seven groups, such as polychaetes, crabs, shrimps, omnivorous invertebrates, and suspension feeding invertebrates (groups 13–19 in Table 1), primarily based on their feeding habits, since the main goal of this study is to observe the effects of benthic components on overall system health. Suspension-feeding invertebrates, primarily bivalves like *Anadara granosa*, *Placuna placenta*, and *Tellina staurella*, link the benthic and pelagic food chains[25]. Later, this group was disturbed (scenario analysis) in order to investigate its impact on the integrity and general health of the system. Field data gathered from landing sites throughout the bay over the course of a full year has been used to estimate the biomass of these groupings.

**E. Fish groups:** The fish species present in this bay have been categorised into 12 distinct groups, which include reef-associated, omnivorous, carnivorous, croakers, mullets, and so on. Fish have been categorised according to their habitats and feeding patterns. Young fish from all fish groups make form the twelfth group of fish, known as fingerlings. Fingerlings have historically been regarded as a distinct group because of their distinct nutrition from that of adult fish. Although the fundamental inputs of each fish group have been gathered from earlier research, the biomass of every group has been approximated from field data gathered in a manner akin to the previously described technique.

→ **Diet matrix:** Various amounts of outflow from each prey group within the predator group in question make up each predator group's diet. The diet matrix, which is based on the idea of "who eats whom and by how much," shows the material flows from prey group I to predator group J. The nutrition matrix for the Kakinada Bay system is provided.

### 3.4. Model balancing & Uncertainties

The matrix was developed on the premise that there is no variation between the species based on published data about their diets in similar ecosystems. Testing the fundamental presumptions of the static model is required after the model inputs have been gathered. Before balancing a model, Link provided a set of pre-balance (PREBAL) diagnostics that should be examined. These diagnostics include the breadth of biomass ratios, critical rates, and total production at each trophic level. Following the PREBAL approach's testing of the static model's underlying assumptions, the model must be balanced in accordance with ecological and thermodynamic laws.

The following characteristics are necessary for an environmentally and thermodynamically balanced Eco Path model, as per the principles of static network models:

- Eco trophic Productivity (EE) values ought to be somewhere in the range of 0 and 1
- P/Q values ought to be inside 0.05 and 0.3
- non-negative breath values
- Naturally right rendezvous of trophic levels to each gathering
- The amount of all extents of commendation for every hunter should be equivalent to one in the eating routine framework.

After the foundation of the Kakinada Sound model, a few changes were made to the fundamental information sources utilizing environmental information and thinking, according to Christensen et al., to accomplish mass equilibrium. These changes included slight dietary changes as well as acclimations to the P/B and Q/B proportions of explicit gatherings. These adjustments complied with permitted limitations found in the literature and are a crucial part of any modelling process: calibration.

**Table 1: The basic inputs and sources of the Q/B and P/B ratios for each group are among the several groups that make up the Kakinada Bay Model and offer instances of particular species.**

	Group name	Species Included	Trophic level	Biomass t-1 km <sup>2</sup>	P/B year-1	Q/B year-1	EE	Source (of P/B & Q/B)
1	Pelagic Carnivorous fish	Pellonasp., Opisthopterus sp., Rastrelligersp.	3.574	0.313	5.94	29.83	0.625	Mohamed et al., 2005
2	Pelagic Omnivorous fish	Thryssasp., Hilsa ilisha	2.878	0.331	11	29.5	0.921	Mohamed et al., 2005 & Rakshit et al., 2017
3	Reef-associated fish	Hemiramphus sp., S. strongylurus, Epinephelus sp.	3.317	0.112	15	40	0.905	Das et al., 2018 & Fishbase
4	Hairtail fish	Trichiurus sp., Lepturacanthus sp.	3.815	0.180	2.17	6.72	0.009	Mohamed et al., 2005
5	Croakers	Johnius sp., Protonibeasp.	3.798	0.732	4.88	16.42	0.308	
6	Sardines	Oil sardines, Escualosasp.	2.581	0.833	6.74	52.23	0.397	
7	Mulletts	Liza sp., Mugil sp.	2.642	1.765	4.06	18.66	0.581	Mohamed et al., 2005

8	Catfish	A.arius	3.594	0.342	6.05	28.06	0.039	Mohamed et al., 2005
9	Large Demersal fish	Latessp.,C.chanos	3.164	0.065	4.47	15	0.940	Rakshit et al., 2017
10	Medium Demersal fish	Caranxsp.,Platycephalussp.	3.845	0.176	2.38	17.49	0.014	Mohamed et al., 2005
11	Small Demersal fish	Polynemussp., Cynoglossussp.	3.584	0.302	6.31	26.67	0.470	
12	Fingerlings	includes juveniles of all fish species	2.618	0.800	11.5	40	0.950	Calibrated
13	Suspension Feeding Invertebrates	Tellina staurella, Turritella duplicata, Vepricardium coronatum, Virgulariasp., Placuna placenta, Telligarca granosa	2.240	9.744	3	12.5	0.295	Mohamed et al., 2005
14	Carnivorous Invertebrates	Notocochlis tigrina, Pugilina cochlidium, Sinum sp., Unedogemmula indica, Pirenella cingulate	3.509	0.978	3.43	12.5	0.124	
15	Shrimps	Harpiosquilla harpax, Oratosquillasp., Penaeussp., Metapenaeussp.	2.624	2.286	6.68	19.2	0.612	
16	Omnivorous invertebrates	Babylonia spirata, Calliostoma tranquilbaricum, Dentaliumsp., Gyrinium natator	2.279	2.175	9	30	0.316	Tsehay et al., 2008
17	Crabs	Portunus pelagicus, Typhlocarcinussp., Charybdis sp., Scylla sp.	2.376	0.421	4.31	14.5	0.970	Mohamed et al., 2005

18	Scavenger Invertebrates	Nemerteans, Acaudina molpadioides	2.221	0.179	12	40	0.373	
19	Polychaetes	Amparetesp., Capitellasp., Glycerasp., Lumbrineriessp.	2.240	18.900	4.4	14.5	0.333	Ortiz and Wolff, 2002
20	Zooplankton		2.200	0.268	78	300	0.970	Anton y et al., 2010
21	Bacteria		2.000	50.000	1.5	2.71	0.889	Calibrated
22	Microphyto benthos		1.000	32.000	5.9		0.424	
23	Phytoplankton		1.000	46.270	8.22		0.480	
24	Detritus		1.000	0.857			0.639	

**Table 2: Nutritional chart for Kakinada Bay for each predator, the groups along the top row and second column stand in for the predator and the prey, respectively. The proportionate contribution of each prey group to each predator is shown by each matching box.**

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
1	<b>Pelagic Carnivorous fish</b>	0.3		0.3	0.3				0.5	0.2	0.5	0.2										
2	<b>Pelagic Omnivorous fish</b>	0.1		0.1	0.08	0.1			0.1	0.04	0.1											
3	<b>reef-associated fish</b>	0.3		0.3	0.06	0.05			0.1	0.05	0.04											

<b>4</b>	<b>Hairt ail fish</b>																			
<b>5</b>	<b>Croa kers</b>	0 . 0 1		0 . 0 1	0 . 0 6	0 . 0 4				0 . 0 0	0 . 1 3	0 . 0 1								
<b>6</b>	<b>Sardi nes</b>	0 . 0 4	0 . 0 1	0 . 0 3	0 . 1 0	0 . 0 6				0 . 0 5	0 . 0 2	0 . 0 4	0 . 0 2							
<b>7</b>	<b>Mull ets</b>	0 . 0 4	0 . 0 1	0 . 0 2	0 . 1 0	0 . 0 6				0 . 2 0	0 . 0 4	0 . 1 4	0 . 0 5							
<b>8</b>	<b>Catfi shes</b>											0 . 0 3								
<b>9</b>	<b>Larg e deme rsal fish</b>	0 . 0 2		0 . 0 2	0 . 0 6	0 . 1 8						0 . 0 5	0 . 0 1							
<b>1 0</b>	<b>Medi um deme rsal fish</b>				0 . 0 1															
<b>1 1</b>	<b>Smal l deme rsal fish</b>	0 . 0 2		0 . 0 2	0 . 0 6	0 . 0 4						0 . 0 4	0 . 0 1							
<b>1 2</b>	<b>Fing erlin gs</b>	0 . 1 4	0 . 1 5	0 . 2 5	0 . 1 0	0 . 2 0	0 . 0 2			0 . 1 0	0 . 0 4	0 . 0 4	0 . 0 1					0 . 0 4		
<b>1 3</b>	<b>suspe nion feede r</b>	0 . 0 4	0 . 0 1	0 . 0 2	0 . 0 1		0 . 0 1	0 . 0 3	0 . 0 4	0 . 0 4		0 . 1 5			0 . 1 1	0 . 0 6	0 . 0 2	0 . 0 4		

14	carnivore	0 · 0 4	0 · 0 2	0 · 0 2	0 · 0 3	0 · 0 6	0 · 0 4	0 · 0 1	0 · 0 1	0 · 0 2	0 · 0 2	0 · 0 2	0 · 0 2						
15	shrimps	0 · 0 4	0 · 0 5	0 · 0 3	0 · 0 2	0 · 0 5	0 · 0 2	0 · 0 1	0 · 0 5	0 · 0 8	0 · 0 5	0 · 0 1	0 · 0 2						
16	omnivore	0 · 0 4	0 · 0 2	0 · 0 2	0 · 0 1	0 · 0 2	0 · 0 6	0 · 0 4	0 · 0 3	0 · 0 3	0 · 0 0	0 · 0 2	0 · 0 3						
17	crabs	0 · 0 2	0 · 0 5	0 · 0 4	0 · 0 3	0 · 0 9	0 · 0 8	0 · 0 3	0 · 0 5	0 · 0 8	0 · 0 3	0 · 0 1	0 · 0 0						
18	scavenger	0 · 0 2	0 · 0 1	0 · 0 1	0 · 0 0	0 · 0 2	0 · 0 4	0 · 0 3	0 · 0 8	0 · 0 1	0 · 0 2	0 · 0 1	0 · 0 2						
19	Polychaetes	0 · 0 8	0 · 0 8	0 · 0 0	0 · 0 8	0 · 0 4	0 · 0 0	0 · 0 1	0 · 0 3	0 · 0 5	0 · 0 0	0 · 0 6	0 · 0 2	0 · 0 4	0 · 0 1	0 · 0 2			
20	zooplankton	0 · 3 0	0 · 3 1	0 · 0 5	0 · 0 6	0 · 2 0	0 · 3 0	0 · 1 0	0 · 1 2	0 · 1 5	0 · 0 6	0 · 0 5	0 · 0 0	0 · 0 6	0 · 0 6	0 · 0 6	0 · 0 5		
21	bacteria					0 · 0 3						0 · 0 1	0 · 0 1		0 · 0 8	0 · 0 0			
22	MPB		0 · 1 2	0 · 0 7		0 · 1 8	0 · 1 0	0 · 1 3		0 · 2 0	0 · 1 0	0 · 0 9	0 · 0 8	0 · 0 4	0 · 0 7	0 · 0 5			
23	phytoplankton		0 · 1 5	0 · 0 9		0 · 3 1	0 · 3 0	0 · 0 7		0 · 1 5	0 · 3 0	0 · 1 0	0 · 1 3		0 · 3 0	0 · 2 5			
24	detritus		0 · ·	0 · ·		0 · ·	0 · ·	0 · ·		0 · ·	0 · ·	1 · ·							

			1 0	0 7			0 7	1 0		0 3			1 5	4 0		3 0	5 9	5 9	8 2	4 0	3 0	0 0
	<b>Sum of all prop ortio ns</b>	<b>1</b>																				

In accordance with Funtowicz and Ravetz, the Pedigree Analysis method of the EwE software was used to confirm the authenticity and dependability of

the supplied variables. Each data set is assigned a confidence interval by the routine, which depends on the data origin input. The accompanying recipe is utilized to decide the file:

$$P = \sum_{i=1}^n \sum_{j=1}^n \frac{l_{ij}}{n} \quad (1.5)$$

Where n is the all-out number of useful gatherings and  $l_{ij}$  signifies the family file for model gathering I and boundaries j.

### 3.5. Ecological network indices

It is not possible to determine every distinct qualitative and comprehensive characteristic of the structure and operation of a system using the mass balance model alone. The mass balanced model shows the range of various scenario analyses, including potential anthropogenic or natural disturbances that the system may experience, and is used to compute various network indices that aid in recognising such characteristics of the system. Some of the system-wide metrics that have been proposed and applied to various ecosystems, including freshwater ecosystems, marine ecosystems, and forests, are ascendancy, redundancy, and system throughput [26]. We go over the various network indices that were looked at for the Kakinada Bay system below.

**Productivity:** Complete essential efficiency to add up to biomass proportion (TPP/TB), all out essential efficiency to add up to breath proportion (TPP/TR), and net framework efficiency (NSP) are only a couple of the 24 biological system credits that Odum illustrated. These properties help in understanding the framework's degree of improvement and development.

**Total System Through flow (TST):** characterized by Ulanowicz and Kay, TST is "the amount of all compartmental through streams in an environment" and is a proportion of the "size of the whole framework regarding streams". TST is subject to the biological system's construction.

But it's crucial to distinguish TST from another comparable metric called Total System Throughput (T..), which Allesina and Ulanowicz characterize as "the amount of the connection extents in the framework."

Individual flows across a node are formulated using related equations, where  $T_{iout}$  and  $T_{iin}$  denote the compartment's inflow and outflow, respectively.

$$T_i^{out} = \sum_{j=1}^n f_{ij} + y_i \quad (1.6)$$

$$T_i^{in} = \sum_{j=1}^n f_{ji} + z_i \quad (1.7)$$

The flows entering compartment I from the outside are represented by  $Z_i$  in the foregoing equations, while the fluxes out of compartment I are represented by  $y_i$ . Since the current model is a steady state mass-balanced model, TST is represented by Equation 1.8 and  $T_{iin}$  is equal to  $T_{iout}$ . Finn and Faith and Patten.

$$TST = \sum_{i=1}^n T_i \quad (1.8)$$

Other indices like Ascendancy and Developmental Capacity are also computed using TST.

**Ascendancy (A):** According to Bodini et al., ascendancy is a metric that may gauge a system's expansion as well as its development. It gauges the amount of material or energy that is efficiently dispersed [27]. Higher values of A are obtained when a few number of channels carry the majority of the material. It is the result of multiplying Average Mutual Information (AMI) by Total System Throughput (T).

To estimate flow specialisation in ecological networks, the idea of AMI was modified from information theory. AMI was characterized by Ulanowicz as the distinction between the restrictive likelihood and the probability of a stream occasion happening. Prohibitive probability is the likelihood of known inflow and overflowing from the source compartment happening one time step earlier, however probability is the opportunity of a known inflow into a compartment occurring. Higher AMI values suggest a rigid and efficient network organisation where flows occur via more specialised paths. System ascendancy is estimated using given equation.

$$A = \sum_{ij} T_{ij} \log \left( \frac{T_{ij} T_{..}}{T_i T_j} \right) \quad (1.9)$$

Command moves toward its hypothetically conceivable most noteworthy worth when all parts have particular sources of info and results.

**Developmental Capacity (C):** The provided Equation is used to calculate the theoretical maximum value of A, which is referred to as developmental capacity. It is derived from the product of flow diversity and total system throughput. -

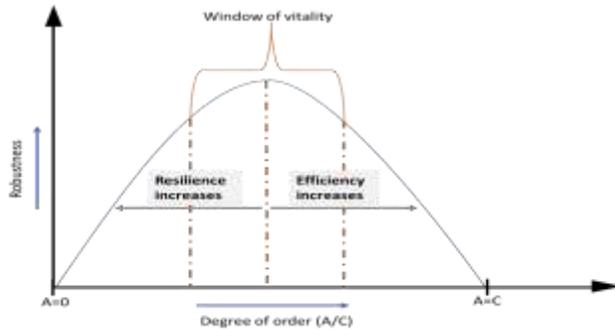
$$C = - \sum_{ij} T_{ij} \log \left( \frac{T_{ij}}{T_{..}} \right) \quad (1.10)$$

**Overhead (O):** In a nutshell, overhead is determined by the following formula and is the difference between developmental capacity and ascendancy:

$$\phi = - \sum_{i,j} T_{ij} \log \left\{ \frac{T_{ij}^2}{T_i * T_j} \right\} \quad (1.11)$$

Higher overhead values suggest a more resilient system since high ascendancy systems, which are highly structured systems, are sensitive to stress. As a result, Heymans et al. suggested using this index to gauge system resilience.

**Degree of organization and Robustness:** The degree of organization in a system can be determined by measuring the ascendancy to developmental capacity ratio ( $a=A/C$ ).



**Figure 2: Robustness against degree of order graph, displaying zones of increasing resilience and efficiency as well as windows of liveliness.**

The following formula can be used to determine the robustness of the system using this ratio:

$$\text{Robustness} = -a \log a$$

Another way to state the equation is as follows:

$$R = \sum_{i=1}^n \sum_{j=1}^n (T_{ij}) \log \left\{ \frac{T_{ij}^2}{\sum_{j=1}^n T_{ij} \sum_{i=1}^n T_{ij}} \right\} \quad (1.12)$$

A/C values can theoretically range from 0 to 1. Both when A approaches zero and when A approaches C, A/C approaches zero. In any case, for both A's most extreme and least qualities (A=C and A=0, separately), the power esteem drops to nothing. Various examinations have exhibited that in normal environments, there is a harmony among command and improvement capacity (inside windows of essentialness), which prompts maximal strength and ideal framework working. The "windows of vitality" contain these maximum robustness values, which show the ideal ratio between the system's resilience and degree of order.

**Finn's Cycling Index (FCI):** FCI is determined utilizing the accompanying recipe to decide the level of TST that is cycled inside the framework, implying that the stream gets back to a similar compartment from which it began:

$$FCI = \frac{TST_c}{TST} \quad (1.13)$$

Where TSTc addresses the amount of TST that is burned through the framework. As indicated by Monaco and Ulanowicz, FCI is a pivotal indication of the flexibility, trustworthiness, and construction of a biological system. Subsequently, it fills in as a pressure and framework development marker.

Eco-exergy: "how much put away useful energy in the framework" is the way Jørgensen portrayed it. It is determined utilizing the equation beneath:

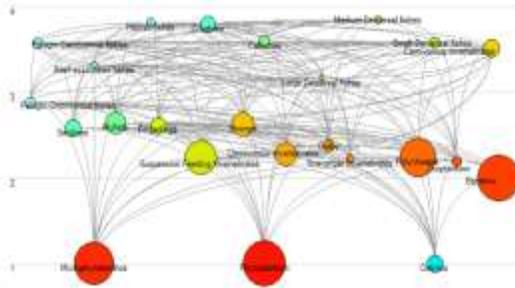
$$Eco - exergy\ or\ Ex = \sum_{i=1}^n \beta_i C_i \tag{1.14}$$

In this case,  $C_i$  is the  $i$ th component concentration expressed in gm m<sup>-2</sup>, and  $\beta_i$  is the organism complexity and weighting factor for the  $i$ th component. Since rubbish has minimal measure of intricacy and put away energy ( $\beta_i = 1$ ), gm waste identical m<sup>-2</sup> is the unit of eco-exergy. [28] Earlier exploration has given the transformation variables to the different biological system parts.

**4. Results**

To appreciate how the framework capabilities and the associations between its different parts, some examinations have used natural organization investigation to food web models. The thoughts put out by Odum, Odum and Barrett, and Ulanowicz portray the particular standards that manage the estimation of assorted ENA pointers.

The produced Kakinada Narrows environment model has a family record of 0.409 and a proportion of spasm of 2.054, proposing that it is an adequate estimate of the genuine framework. Also, all useful gatherings in the model have EE values of short of what one (1.0). Most of gatherings' P/Q values range from 0.05 to 0.3 too. An even model is demonstrated by both of these qualities.



**Figure 3: Conceptual model for Kakinada Bay illustrating the relationships between all the various groups.**

Given Figure shows the applied outline of the model that addresses the sound framework's food web. The trophic level inside the food web is addressed by the numbers on the left-hand side, and the singular hubs are addressed by the circles, the size of which demonstrates the biomass of that particular gathering.

**4.1. Ecosystem Health Indicators**

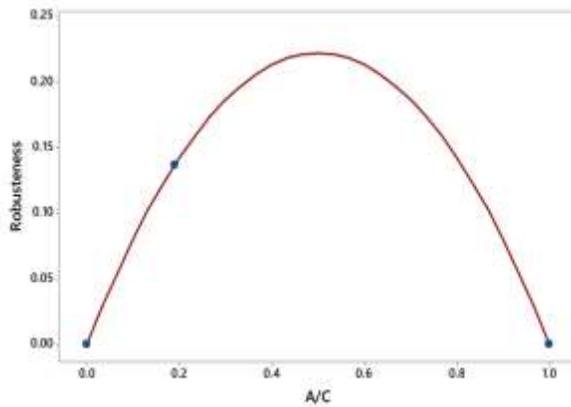
The different ecological elements for the narrows biological system are recorded in Table. Utilization, products, and breath represent 41.73%, 10.09%, and 20.21% of the all-out TST, separately; the excess 27.97% is lost as debris. The framework's Typical Common Data (AMI) is shown by the upsides of power (18.98%) and above (81.02%).

**Table 3: According to Sinha et al., the Kakinada Bay ecosystem's ecological attributes were determined using the EwE programme.**

Parameters	Kakinada Bay Model	Unit
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Sum of all consumption	913.19	tkm-2year-1
Sum of all exports	220.93	t km-2 year-1
Sum of all respiratory flows	442.32	t km-2 year-1
Sum of all flows into detritus	612.23	t km-2 year-1
Total system throughflow	2188.35	t km-2 year-1
Sum of all production	857.41	t km-2 year-1
Calculated total net primary production	569.25	t km-2 year-1
Total primary production/total respiration	1.31	
Net system production	126.14	t km-2 year-1
Total primary production/total biomass	3.47	
Total biomass/total throughput	0.19	year-1
Total biomass (excluding detritus)	169.28	t km-2
Connectance Index	0.53	
System Omnivory Index	0.39	
Shannon diversity index	1.92	
Ascendancy	18.19	

Overhead	81.13	
F.C.I	11.24%	
APL	3.43	
D/H	1.19	



**Figure 4: Vigor versus A/C proportion**

This plots vigor versus A/C proportion (level of request), shows how powerful the organization is. The power an incentive for the Kakinada Narrows framework is to one side and beyond the "windows of imperativeness." This proposes that the framework isn't especially versatile and that its proficiency is second rate compared to its flexibility.

**4.2. Trophic level analysis & Transfer Efficiency:**

Any framework has two particular ways for the progression of materials and energy: the touching pecking order (GFC) and the waste pecking order (DFC). The Lindeman spine examination demonstrates that roughly 59.8% of the energy stream (391.3 t km long term 1 of issue) in the Kakinada Cove environment happens through DFC. This is a quality of estuaries and has likewise been seen in the Hooghly-Matla estuarine framework. GFC moves the leftover 40.2% of energy (262.6 t km long term 1 of issue). The different parts are all remembered for the 10 particular trophic levels (TL-I to TL-X) of the framework. As per Sinha et al., hairtail fishes in this framework have the most elevated fragmentary trophic degree of 3.8, while the least jungle level for waste and makers is 1. The exchange efficiencies for GFC and DFC are displayed in Given Table.

**Table 4: Transfer efficiencies in Kakinada Bay**

Source \ Trophic level	II	III	IV	V	VI	VII	VIII	IX	X	%values
Producer	23.71	15.44	14.54	10.95	9.519	9.407	8.742			13.19
Detritus	29.97	23.52	15.47	14.2	10.81	9.517	9.307			16.11
All flows	27.37	20.77	15.23	13.42	10.56	9.497	9.214	7.783	2.597	12.94

## 5. Discussion & Conclusion

With a typical environment trophic degree of 2.67, Kakinada Narrows is to some degree more like the Hooghly-Matla estuary framework in India (2.72; Rakshit et al.,) than it is to Kuosheng Sound, Taiwan (2.35; Lin et al.,). The dissimilarity in trophic levels between Kakinada Sound and the Kuosheng Cove framework might actually be ascribed to the more prominent wealth of predatory fish species in the previous.

With 10 unmistakable trophic levels, the sound model's mean exchange effectiveness of 12.94% is like that of Tongoy Narrows, Chile (14%; Wolff,) and Chiku Tidal Pond, Taiwan Interestingly, Kuosheng Sound's exchange proficiency is generally low (6.5%; Lin et al.,), which is brought about by Kakinada Narrows' lower D/H proportion. This proposes that Kuosheng Sound has a higher release of flotsam and jetsam than Kakinada Narrows. The relationship that is considered in different frameworks to be well between the D/H proportion and trophic exchange effectiveness is displayed in Table. As indicated by Odum and Barrett move efficiencies frequently fall somewhere in the range of 10% and 20%, which is the very case for most of this framework's exchange efficiencies.

TPP/TR values draw nearer to solidarity and the TPP/TB proportion diminishes as the framework draws nearer to development. The framework isn't yet developed, as shown by its TPP/TR (1.29) and TPP/TB (3.36) appraisals.[29]

Notwithstanding having practically identical complete biomasses, Kakinada Narrows has a low all out framework through stream (169.17 t km long term 1) when contrasted with the TST of other comparative frameworks. Kakinada Straight's lower TPP/TB proportion is the reason for the low TST. The low A/C proportion of the narrows is brought about by a low TST esteem.

### **Table 5: Comparative Analysis of Biomass and Productivity in Different Coastal Regions**

Study Site	Climate	Total biomass (excluding detritus) (t/km <sup>2</sup> /year)	TST (t km <sup>-2</sup> year <sup>-1</sup> )	NP P (t km <sup>-2</sup> year <sup>-1</sup> )	TPP /TR	TP P/T B	D / H	F.C. I (%)	A P L	Mean Tropic Transfer efficiency (%)
Kakinada Bay	Tropical	169.17	2188.24	569.14	1.29	3.36	1.1	11.13	3.3	12.94
Kuosheng Bay (Lin et al., 2004)	Subtropical	278	31713	7821	1.17	51	2.5	43	4.5	6.6
Tongoy Bay (Wolff, 1994)	Tropical	374	31946	8236	1.88	41	0.9	10.2	4.1	25
Chiku Lagoon (Lin et al., 1999)	Tropical	3117	157653	50600	1.1	24	1.4	10.8	2.9	12
Hooghly-Matla Estuarine system (Rakshit et al., 2017)	Tropical	257.46	12615.7	10381.7	4.65	41.57	0.9	8.4	2.84	14.74
Chesapeake Bay (M. E. Monaco and Ulanowicz, 1997)	Temperate	10.99	4542.5	333.07	0.5	30.30	6.9	24.1	3.2	17.4
Daya Bay (Chen et al., 2015)	Subtropical	55.6	11409.3	4582.6	3.64	82.6	0.13	2.28	2.32	10.1
Gulf of Cadiz (Torres et al., 2013)	Temperate	80.13	7734.1	3187.7	3.4	39.9	0.93	4	2.54	14.1

The framework's strength esteem is situated outside the "window of essentialness" on the left. This recommends that the framework is pressure open minded and has a low A/C proportion. However, it doesn't take full advantage of its true capacity. The framework contains more elective ways between its numerous compartments, which adds to its better strength to stretch. On the off chance that there is a recognizable addition in framework productivity, heartiness values could likewise rise.

**Table 6: Organism Groups and Exergy Distribution in an Ecosystem**

<b>Groups</b>	<b>β</b>	<b>Biomass t km<sup>-2</sup></b>	<b>Exergy</b>
Pelagic Carnivorous fish	500	0.424	156.21
Pelagic Omnivorous fish	500	0.442	165.28
reef-associated fish	500	0.223	55.91
Hairtail fish	500	0.291	89.93
Croakers	500	0.843	365.38
Sardines	500	0.944	415.78
Mulletts	500	1.876	880.85
Catfish	500	1.453	170.77
Large Demersal fish	500	0.176	32.55
Medium Demersal fish	500	0.287	87.93
Small Demersal fish	500	0.413	261.81
Fingerlings	500	0.911	399.31
Suspension feeding Invertebrates	318	9.855	2893.18
Carnivores	423	0.189	305.34
Shrimps	343	2.397	530.46
Omnivores	422	2.286	674.36
Crabs	343	0.532	97.72
Scavengers	421	0.281	55.51
Polychaetes	244	18.1	2513.81
Zooplankton	274	0.379	43.79
Bacteria	9.6	60	425.11
MPB	77	43	2112.11
Phytoplankton	31	46.38	925.51
Detritus	2	0.968	0.97
<b>TOTAL EXERGY</b>		<b>13547.09</b>	

A more elevated level of framework development and association is shown by a blend of high relative power (A/C) and high FCI. Contrasted with Kuosheng Narrows and Tongoy

Cove, Kakinada Sound has a lower cycling file and a higher one. Kakinada Narrows' low A/C proportion and moderate FCI esteem propose that the framework isn't yet experienced.

A focused-on framework is shown by high normal way length (APL) and FCI values as well as a high recurrence of cycles with more limited way lengths. In the Kakinada Cove framework, extended ways (containing in excess of eight hubs) represent more than 96% of cycling[30]. This recommends that there is no heap on the framework, along with the gentle FCI and APL levels.

As indicated by Table 6, the eco-exergy worth of 13547.09 g debris identical km<sup>-2</sup> approves the past observing that the cove framework is youthful.

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