



# Temporal Trends and Institutional Insights in Digital Sequence Information Practices: Perspectives from the Zoological Survey of India

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**Abstract:** This study investigates the management of Digital Sequence Information (DSI) by the Zoological Survey of India (ZSI) from 2018 to 2023, focusing on its impact on biodiversity conservation and taxonomic research. By analyzing temporal trends in DSI practices, this study examines the patterns and changes in how ZSI manages, utilizes, and preserves digital sequence data over time. The research combined quantitative analysis with qualitative insights from ZSI's reports on challenges, adaptations, and impacts on regulations., offering a comprehensive view of Zoological Survey of India Digital Sequence Information practices and guiding future biodiversity research strategies. The findings reveal significant growth in genetic sequencing efforts, with ZSI documenting a total of 6223 barcodes from 2017 species of faunal groups between the period of year 2018 and 2023, marking a notable increase from 2021 onwards. Insecta, including Lepidoptera, and Chordates, especially Mammalia, was prominently studied, underscoring ZSI's robust capacity in digitizing India's faunal diversity. Effective DSI management practices at ZSI include sample collection, storage, quality control, and DNA barcoding, bolstered by collaboration with taxonomic authorities (ENA, BOLD iBOL, EMBL, NCBI, etc) and adherence to international standards like the Nagoya Protocol. Challenges such as fluctuating barcode production and uneven taxonomic representation highlight operational hurdles, suggesting the need for standardized data collection methods and enhanced taxonomist capacity. Recommendations include fostering research collaborations, prioritizing biodiversity in research goals, and adopting advanced technologies for more efficient DSI initiatives. Institutions such as the Anthropological Survey of India (AnSI), Botanical Survey of India (BSI), Fishery Survey of India (FiSI), and Forest Survey of India (FSI), are integral to achieving these objectives, each contributing unique expertise crucial for comprehensive biodiversity conservation efforts. This research underscores ZSI's crucial role in biodiversity conservation through DSI, offering insights into optimizing future research for sustainable environmental stewardship and scientific progress.

**Keywords:** Temporal trends, Institutional Insights, Digital Sequence Information (DSI), DNA Barcoding, Zoological survey of India (ZSI)

## 1. INTRODUCTION:

The preservation of digital sequence information (DSI) has become crucial in modern biological research and biodiversity conservation. DSI includes a diverse range of genetic data, such as genomic and transcriptomic information, crucial for advancing our understanding of biological diversity and driving innovations in fields like medicine, agriculture, and environmental science. Advances in molecular biology and bioinformatics have revolutionized biodiversity studies, facilitating the collection, analysis, and storage of genetic information. Understanding the taxonomic diversity encompassed by DSI initiatives offers critical insights into the breadth of species covered, spanning from invertebrates to vertebrates, including endemic and endangered species. The methodologies employed, such as DNA barcoding and high-throughput sequencing, highlight ZSI's adaptive approach to effectively capturing and safeguarding genetic information.



As one of India's premier institutions dedicated to zoological research, the Zoological Survey of India plays a crucial role in documenting and conserving the nation's rich fauna through genetic data. The Zoological Survey of India (ZSI), established in 1916, is a premier organization dedicated to the exploration, documentation, and study of India's diverse fauna. Over the years, ZSI has recognized the growing importance of DSI and has embarked on various initiatives to generate, manage, and preserve this invaluable data. The efforts of ZSI in this domain are pivotal for ensuring that the rich genetic information of India's fauna is safeguarded for future research and conservation efforts. This study aims analyzing the temporal trends in data generation and preservation, to gain insights into the progression and impact of ZSI's initiatives. And examining the diversity of animal species covered under these initiatives will shed light on the breadth and depth of ZSI's efforts in capturing and conserving genetic information across different taxa.

## 2. LITERATURE REVIEW:

Liang (2023) examines the temporal trends of population structure, disease burden, healthcare resources, and expenditure in China from 2000 to 2019. Using data from the China Statistical Yearbook and the Global Burden of Diseases study, the research employs a comprehensive cross-sectional and longitudinal analysis. The findings highlight an urgent need for targeted health interventions to address the evolving healthcare landscape in China, emphasizing the increasing burden of non-communicable diseases and the demographic shift towards an aging population. Pordal et al.(2023) highlights the growing adoption of robotic surgery in general practice using the National Inpatient Database and studied national trends in robotic procedures across abdominal organ systems. They found significant increases, particularly in biliary and hernia surgeries, with varying trends by hospital size, teaching status, and geographic region in the US. Blowler et al. (2022) examined temporal trends in the spatial bias of species occurrence records within large-scale biodiversity databases in Germany. The study focused on how spatial bias, specifically in urban versus protected areas, has evolved. They found an increasing proportion of annual records from urban areas over time, contrasting with inconsistent changes in records from protected areas. Their findings underscore the need for biodiversity assessments to not only account for spatial bias but also consider how these biases change over time, particularly in relation to drivers of land-use change affecting species distributions.

## 3. OBJECTIVES:

- To analyze temporal trends in digital sequence information generation by Zoological Survey of India from 2018-2019 to 2022-2023.
- To examine utilization patterns of digital sequence information by ZSI, focusing on taxonomic queries and biodiversity research.
- To evaluate ZSI's data management practices for digital sequence information, including collection, storage and accessibility.
- To identify strengths and weaknesses in ZSI's digital sequence preservation practices and propose enhancements for efficiency.

## 4. METHODOLOGY:

This research employed a web-based descriptive approach to evaluate the Zoological Survey of India's (ZSI) methods for preserving digital sequence information. Annual reports sourced directly from the ZSI website served as the primary data, covering five distinct annual periods from 2018-2019 to 2022-2023. To portray the species data sequences, the data were sourced from the European Nucleotide Archive website used the BOLD/NCSI ID search feature. Species data were systematically collected and processed using with Google Sheets utilized for visual representations and analytical tools to facilitate thorough data exploration. Quantitative analysis assessed trends in Digital Sequence Information practices at the Zoological Survey of India focusing on changes in DSI generation and shifts in taxonomic focus. Qualitative insights from ZSI's annual reports complemented this by providing context on challenges faced, strategic adaptations made, and the impact of policy changes. This dual approach offered a comprehensive understanding of the development of DSI practices at ZSI, guiding effective strategies for future biodiversity research.

## 5. TEMPORAL TREND ANALYSIS:

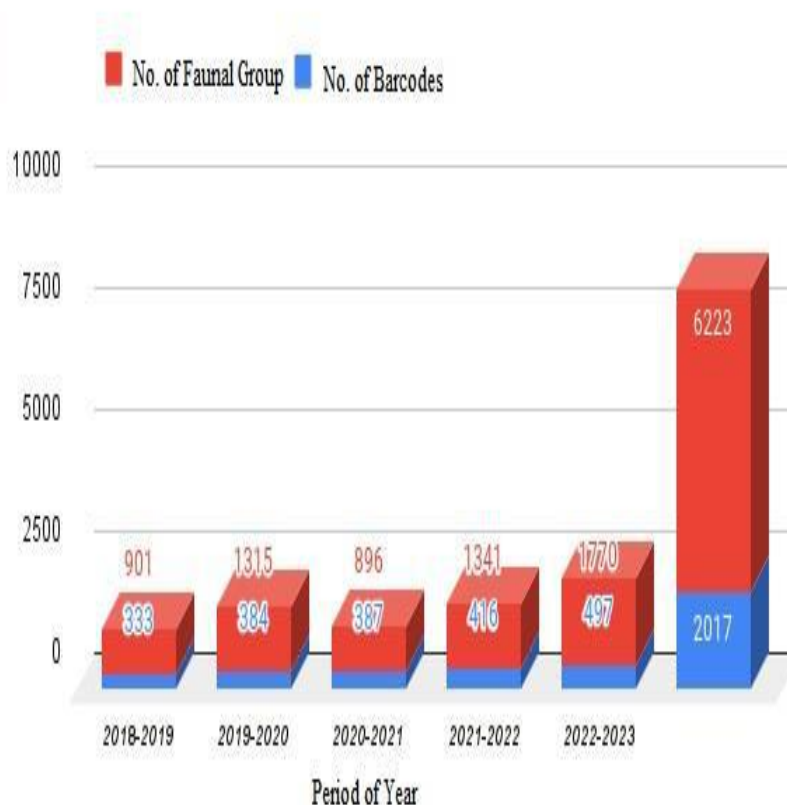
**Growth Pattern of Digital Sequence Information:** The year-wise distribution of Digital Sequence Information (DSI) for faunal groups reveals notable fluctuations in research output and data accumulation over recent years. A total of 2017 faunal groups were documented and 6223 DSI barcodes were collected across the examined period. An examination of DSI for faunal groups reveals a pattern of fluctuation in research output across recent years. The most recent period (2022-2023) witnessed the documentation of 497 faunal groups and 1770 DSI barcodes, reflecting a



sustained effort in genetic research. This trend is consistent with previous years (2020-2021 and 2021-2022). Interestingly, a peak was observed in 2022-2023, with 497 faunal groups and 1770 DSI barcodes documented, suggesting a period of intensified research activity. These findings provide valuable insights into the temporal dynamics of DSI documentation at the Zoological Survey of India (ZSI), essential for advancing biodiversity research and informing effective conservation strategies tailored to faunal genetics. The activities at ZSI play a pivotal role in these efforts, contributing to broader scientific endeavours and conservation initiatives focused on faunal genetic diversity.

Table 1 Growth Trends of Digital Sequence Information

| Sl No.       | Period of Year | No. of Species | No. of Barcodes |
|--------------|----------------|----------------|-----------------|
| 1            | 2018-2019      | 333            | 901             |
| 2            | 2019-2020      | 384            | 1315            |
| 3            | 2020-2021      | 387            | 896             |
| 4            | 2021-2022      | 416            | 1341            |
| 5            | 2022-2023      | 497            | 1770            |
| <b>Total</b> |                | <b>2017</b>    | <b>6223</b>     |



### Distribution Patterns of Digital Sequence Information analysis:

Distribution Patterns of Digital Sequence Information analysis in 2022-2023 showed that the Zoological Survey of India extensively conducted DNA barcoding across a diverse range of faunal groups, documenting 276 species. Insecta particularly stood out with 674 barcoded species, indicating significant research attention to this class. Pisces was also prominently featured with 154 species barcoded, underscoring substantial efforts in documenting insect biodiversity. The phylum Arthropoda encompasses a wide variety of organisms, including arachnids, crustaceans, insects, and even tardigrades, totaling 296 documented species barcoded with 712. Various vertebrate taxa such as Pisces, Amphibians, Reptilians, Aves, and Mammalian's contribute significantly to ongoing studies. This reflects a robust scientific effort aimed at understanding the biodiversity and evolutionary relationships across these diverse groups.

During 2021-2022, the Zoological Survey of India continued its DNA barcoding activities across various faunal groups, documenting a total of 416 species with 1341 barcodes. Arthropoda, particularly Insecta, prominently featured with 161 species barcoded, contributing to a total of 519 barcodes. Chordates, groups also made significant contributions with 223 and 761 barcodes, reflecting comprehensive efforts in documenting Pisces and mammal species.





Table 2 Year wise distribution Patterns of Digital Sequence Information (2021-2022:2022-23)

| 2022-2023 |              |                |                 | 2021-2022    |               |                |                 |
|-----------|--------------|----------------|-----------------|--------------|---------------|----------------|-----------------|
| SI No.    | Faunal Group | No. of Species | No. of Barcodes | SI No.       | Faunal Group  | No. of Species | No. of Barcodes |
| 1         | Protozoa     | 3              | 11              | 1            | Bacteria      | 1              | 2               |
| 2         | Cnidaria     | 3              | 7               | 2            | Protozoa      | 8              | 13              |
| 3         | Arachnida    | 8              | 9               | 3            | Proffera      | 1              | 1               |
| 4         | Insecta      | 276            | 674             | 4            | Cnidaria      | 3              | 7               |
| 5         | Crustecea    | 11             | 26              | 5            | Arachnida     | 1              | 2               |
|           | Tardigrada   | 1              | 3               | 6            | Insecta       | 161            | 519             |
| 6         | Mollusca     | 5              | 7               | 7            | Crustecea     | 13             | 31              |
| 7         | Pisces       | 109            | 154             | 8            | Mollusca      | 1              | 1               |
| 8         | Amphibia     | 12             | 66              | 9            | Echinodermata | 4              | 4               |
| 9         | Reptilia     | 26             | 87              | 10           | Pisces        | 125            | 287             |
| 10        | Aves         | 2              | 9               | 11           | Amphibia      | 22             | 124             |
| 11        | Mammalia     | 41             | 717             | 12           | Reptilia      | 25             | 63              |
|           | <b>Total</b> | <b>497</b>     | <b>1770</b>     | 13           | Aves          | 5              | 18              |
| 14        |              |                |                 | Mammalia     | 46            | 269            |                 |
|           |              |                |                 | <b>Total</b> | <b>416</b>    | <b>1341</b>    |                 |

In the period spanning 2020-2021, a total of 896 barcodes were assigned to 387 species across various faunal groups. Significant focus was placed on Arthropoda, particularly Insecta, which accounted for 161 species barcoded, totaling 444 barcodes. Chordates, including Pisces and Mammalia, also received substantial attention, contributing 227 and 76 barcodes, respectively. Other groups within Arthropoda (Crustacea) and Chordates (Aves and Amphibians) showed comparatively lower levels of barcoding activity, while Protozoa and Mollusca had minimal representation.

Table 2.1 Year wise distribution Patterns of Digital Sequence Information (2020-2021:2019-2020)

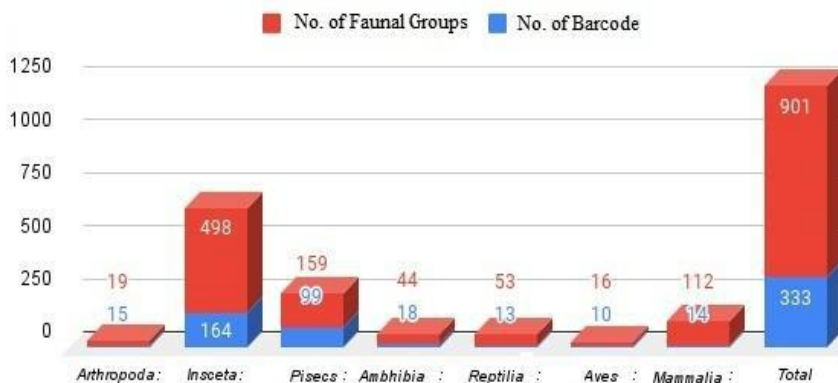
| 2020-2021 |                 |                |                 | 2019-2020    |                       |                |                 |
|-----------|-----------------|----------------|-----------------|--------------|-----------------------|----------------|-----------------|
| SI No     | Faunal Group    | No. of Species | No. of Barcodes | SI No        | Faunal Group          | No. of Species | No. of Barcodes |
| 1         | Protozoa        | 8              | 10              | 1            | Bacteria (Associates) | 1              | 1               |
| 2         | Porifera        | 1              | 1               | 2            | Protozoa(ciliates)    | 5              | 5               |
| 3         | Cnidaria        | 17             | 17              | 3            | Dianoflagellata       | 1              | 1               |
| 4         | Platyhelminthes | 5              | 10              | 4            | Bryozoa               | 1              | 1               |
| 5         | Nemetoda        | 8              | 17              | 5            | Cnidaria              | 3              | 7               |
|           | Arachnida       | 5              | 3               | 6            | platyhelminthes       | 1              | 1               |
| 6         | Mayriapoda      | 1              | 7               |              | Arachnida             | 62             | 289             |
| 7         | Insecta         | 161            | 444             | 7            | Insecta               | 113            | 314             |
| 8         | Crustecea       | 17             | 26              | 8            | Crustecea             | 25             | 34              |
| 9         | Mollusca        | 1              | 1               | 9            | Mollusca              | 3              | 4               |
| 10        | Amphibia        | 10             | 27              | 10           | Amphibia              | 5              | 7               |
| 11        | Pisces          | 110            | 227             | 11           | Pisces                | 102            | 183             |
| 12        | Reptilia        | 19             | 29              | 12           | Reptilia              | 25             | 81              |
| 13        | Aves            | 1              | 1               | 13           | Aves                  | 3              | 3               |
| 14        | Mammalia        | 23             | 76              | 14           | Mammalia              | 34             | 384             |
|           | <b>Total</b>    | <b>387</b>     | <b>896</b>      | <b>Total</b> | <b>Total</b>          | <b>384</b>     | <b>1315</b>     |



In its 2019-2020 DNA barcoding efforts, the Zoological Survey of India documented a total of 384 species with 1315 barcodes across various faunal groups. Among arthropods, Insecta, Arachnida, and Crustacea accounted for 200 species and 637 barcodes. Within Chordates, Pisces were prominently studied, contributing 102 species and 183 barcodes. The Insecta group of arthropods also showed significant representation with 113 species and 314 barcodes. Minor contributions came from other groups such as Amphibians, Reptiles, Aves, and other faunal groups.

Table 2.2 Year wise distribution Patterns of Digital Sequence Information (2018-2019)

| 2018-2019    |              |            |            |
|--------------|--------------|------------|------------|
| Sl No.       | Faunal Group | No. of     | No. of     |
| 1            | Arthropoda   | 15         | 19         |
| 2            | Insecta      | 164        | 498        |
| 3            | Pisces       | 99         | 159        |
| 4            | Amphibia     | 18         | 44         |
| 5            | Reptilia     | 13         | 53         |
| 6            | Aves         | 10         | 16         |
| 7            | Mammalia     | 14         | 112        |
| <b>Total</b> |              | <b>333</b> | <b>901</b> |

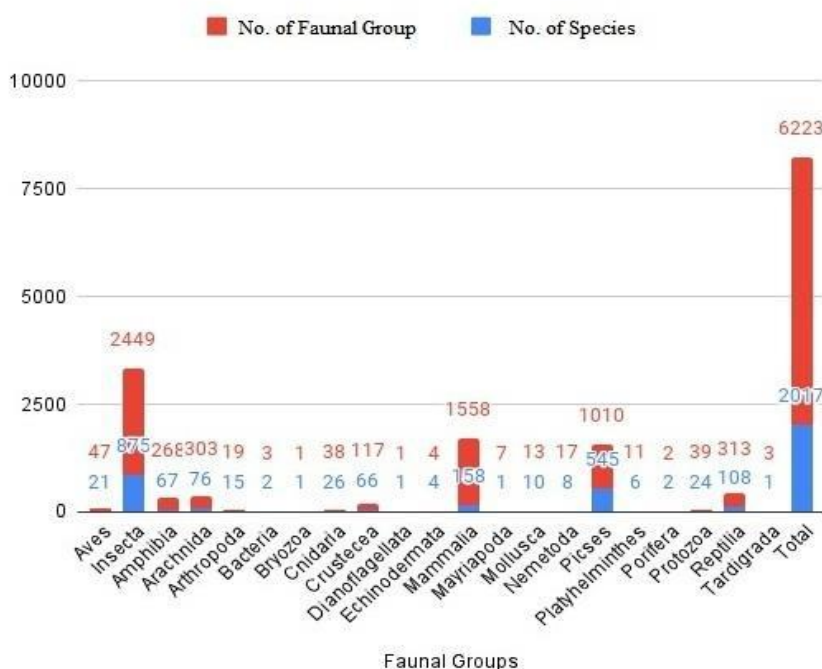


In its 2018-2019 DNA barcoding efforts, the Zoological Survey of India documented 333 species from diverse animal groups and barcoded 901 of them. The Insecta group was prominently studied, contributing significantly with 164 species and 498 barcodes. Among Chordates, Pisces and Amphibia were well-represented with 159 and 112 barcodes, respectively. Other faunal groups within Arthropoda also made notable contributions, highlighting ongoing efforts in biodiversity documentation and conservation crucial for ecological management and scientific research.

**Distribution of Faunal Groups and DNA Barcoding Efforts (2018-2023):**

Table 3 Distribution of Faunal Groups and DNA Barcoding Efforts

| Faunal Groups   | No. of Species | No. of Barcodes |
|-----------------|----------------|-----------------|
| Aves            | 21             | 47              |
| Insecta         | 875            | 2449            |
| Amphibia        | 67             | 268             |
| Arachnida       | 76             | 303             |
| Arthropoda      | 15             | 19              |
| Bacteria        | 2              | 3               |
| Bryozoa         | 1              | 1               |
| Cnidaria        | 26             | 38              |
| Crustacea       | 66             | 117             |
| Dianoflagellata | 1              | 1               |
| Echinodermata   | 4              | 4               |
| Mammalia        | 158            | 1558            |
| Mayriapoda      | 1              | 7               |
| Mollusca        | 10             | 13              |
| Nemotoda        | 8              | 17              |
| Pisces          | 545            | 1010            |
| Platyhelminthes | 6              | 11              |
| Porifera        | 2              | 2               |
| Protozoa        | 24             | 39              |
| Reptilia        | 108            | 313             |
| Tardigrada      | 1              | 3               |
| <b>Total</b>    | <b>2017</b>    | <b>6223</b>     |



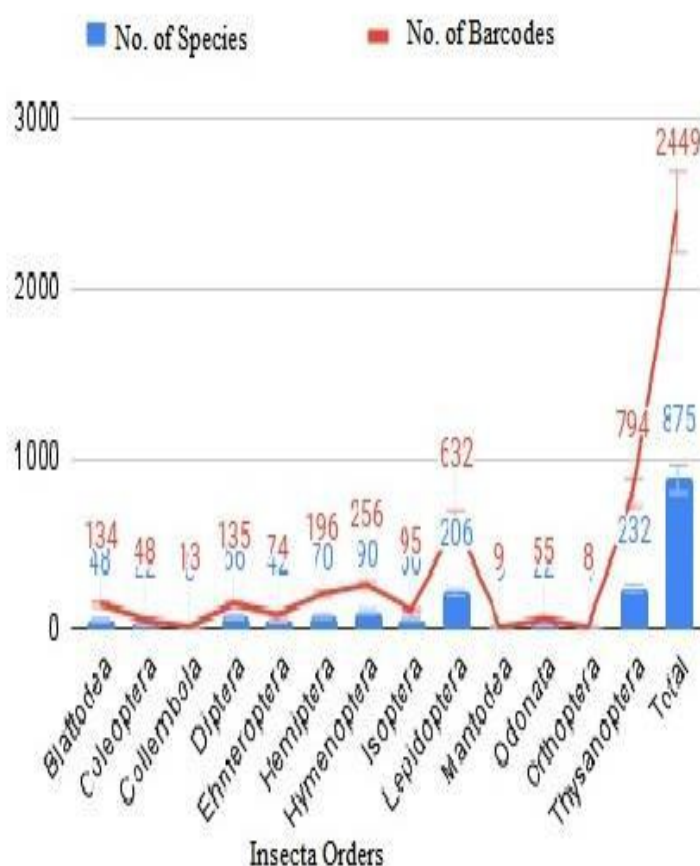


**Order-wise distribution of Faunal group Insecta (2018-2023):**

The table 4 presents a detailed distribution of species and DNA barcodes across various orders within the Insecta class. Among the orders listed, notable observations include the high species richness and barcode coverage in orders such as Thysanoptera, Lepidoptera, Hymenoptera, and Hemiptera. Thysanoptera stands out with the highest species count of 232 and the highest barcode count of 794, indicating a comprehensive genetic data repository for these species. Conversely, orders like Orthoptera and Mantodea exhibit lower diversity with only 4 and 9 species respectively, accompanied by minimal barcode representation. Overall, the cumulative data of 875 species and 2449 barcodes reflects significant strides in genetic documentation, emphasizing priorities in biodiversity research and conservation. This effort particularly targets orders characterized by greater species richness and genetic diversity, reinforcing their importance in ecological studies and conservation strategies.

Table 4 Order-wise distribution of faunal group Insecta

| Insecta: Order | No. of Species | No. of Barcodes |
|----------------|----------------|-----------------|
| Blattodea      | 48             | 134             |
| Coleoptera     | 22             | 48              |
| Collembola     | 8              | 13              |
| Diptera        | 66             | 135             |
| Ehmeroptera    | 42             | 74              |
| Hemiptera      | 70             | 196             |
| Hymenoptera    | 90             | 256             |
| Isoptera       | 56             | 95              |
| Lepidoptera    | 206            | 632             |
| Mantodea       | 9              | 9               |
| Odonata        | 22             | 55              |
| Orthoptera     | 4              | 8               |
| Thysanoptera   | 232            | 794             |
| <b>Total</b>   | <b>875</b>     | <b>2449</b>     |



**Year wise Distribution of Faunal group Insecta (2018-2023):**

The year-wise distribution of faunal group Insecta order from 2018-2019 to 2022-2023 reveals significant trends in insect species identification and genetic barcoding. In 2022-2023, researchers identified 276 species with 674 barcodes, led by Lepidoptera (99 species), Hymenoptera, and Diptera. Ehmeroptera also contributed notably with 18 species and 39 barcodes, indicating detailed genetic analysis. Thysanoptera stood out in 2021-2022 with 72 species and 277 barcodes, reflecting extensive genetic profiling. In 2020-2021, Ephemeroptera was represented by 22 species with 23 barcodes, Blattodea by 26 species with 48 barcodes, and Thysanoptera by 72 species with 277 barcodes. Hemiptera (43 species, 145 barcodes) and Thysanoptera (41 species, 72 barcodes) showed diversity in 2019-2020. Tyschoptera in 2018-2019 featured prominently with 84 species and 277 barcodes, emphasizing detailed genetic characterization. These findings underscore advances in biodiversity research, highlighting genetic barcodings crucial role in understanding and conserving insect diversity.





### Publically available Digital Sequence data:

The publically available digital sequence data was retrieved from the European Nucleotide Archive using the BOLD/NCBI ID for the Assam macaque. This DNA sequence represents a sample of mitochondrial genomic DNA, comprising 307 nucleotide bases and classified under the Mammalia taxonomic division. Identified by the accession number OQ689744, the sequence is categorized as standard sequence data (STD). The sample, designated as 'ZSI/SRC RH405\_BTR-WB,' originates from the mitochondrion, emphasizing its relevance for studying mitochondrial genetics and functions. Its Md5 checksum (dc716731b714428a78291da38669645e) ensures data integrity, confirming the sequence's authenticity and integrity against any alterations or corruption. This dataset offers essential information for researchers studying the genetic material and biological functions of the Assam macaque.

**Sequence: OQ689744.1**  
 Macaca assamensis isolate ZSI/SRC RH405 BTR-WB D-loop, partial sequence; mitochondrial

|                      |                                   |
|----------------------|-----------------------------------|
| <b>Organism:</b>     | Macaca assamensis (Assam macaque) |
| <b>Mol Type:</b>     | genomic DNA                       |
| <b>Topology:</b>     | linear                            |
| <b>Base Count:</b>   | 307                               |
| <b>Dataclass:</b>    | STD                               |
| <b>Tax Division:</b> | MAM                               |
| <b>Accession:</b>    | OQ689744                          |
| <b>Isolate:</b>      | ZSI/SRC RH405_BTR-WB              |
| <b>Organelle:</b>    | mitochondrion                     |
| <b>Md5 Checksum:</b> | dc716731b714428a78291da38669645e  |

**FASTA:** >ENA|OQ689744|OQ689744.1 Macaca assamensis isolate ZSI/SRC RH405\_BTR-WB D-loop, partial sequence; mitochondrial  
 CTTAAATAAGACATCTCGATGGATCACGGGTCTATCACCTATTAACCAGTCACGGGAGC  
 TTCCCATGCATTGGTATCTTTATCTCTGGTCTGCACGCAACCCCATTCAGAAATGCTG  
 ACTCCACCCCATCCCGTCTGTATGGACCTGTCTTTGATTCCCTAGTTCATGTAGTTATT  
 AACCGCACCTACGTTCAATATCCTAGCTCCACGCAAGCTTTAGCAAGGGTGTATTTAATT  
 CATGCTTGAAGGACATACCAATAATTACTCTAGCCAACGCCACCCCTCTACACCAACCC  
 GCAACAA

Figure 2 Publicly available Digital sequence data of Assam macaque

### FATSA Format:

The FASTA format is a standard, straightforward way to represent and exchange genetic sequence data, ensuring compatibility with various bioinformatics tools and databases. The provided FASTA format sequence starts with a header line that provides essential information. The header begins with >, indicating the start of the header, followed by ENA|OQ689744|OQ689744.1. This unique identifier in the European Nucleotide Archive (ENA) database specifies the database name (ENA), the primary accession number (OQ689744), and the sequence version (OQ689744.1). The scientific name of the organism, *Macaca assamensis* (Assam macaque) is given next. The header includes isolate information, "isolate ZSI/SRC RH405\_BTR-WB", where ZSI/SRC stands for the Zoological Survey of India, Southern Regional Centre, and RH405\_BTR-WB is a unique sample identifier. The sequence region and type are described as "D-loop Control region of the mitochondrial DNA, partial sequence indicates that this is not the full D-loop region; mitochondrial Specifies that the sequence is from the mitochondrion specifies its origin. The sequence itself consists of 307 bases, represented as a series of letters (A, T, C, G) corresponding to the four nucleotide bases of DNA: adenine (A), thymine (T), cytosine (C), and guanine (G). This metadata ensures the sequence is well-documented and identifiable for research and analysis.

## 6. INSTITUTIONAL INSIGHTS ANALYSIS:

### Practices for Effective Digital Sequence Information (DSI) Management:

Zoological Survey of India employs a comprehensive approach to managing Digital Sequence Information (DSI) through its 16 strategically located regional centers across India. Digital Sequence Information (DSI), the genetic data obtained from animal samples, is a critical tool for ZSI's research efforts. However, managing DSI effectively is crucial for maximizing its impact. Potential practices for DSI management, including collection & Storage and Quality control & analysis aspects.



In the collection and storage phase, ZSI employs standardized protocols to ensure proper sample collection and preservation. Each sample is meticulously documented with essential details, including collection location, date, species identification, and a unique identifier code. Samples are then stored in bio repositories at regional centers under controlled conditions to maintain their integrity and prevent contamination. In the quality control and analysis phase, DNA extraction is conducted using standardized protocols to ensure the purity and quantity of genetic material. ZSI uses DNA barcoding for species identification, which involves the amplification and sequencing of a specific gene region. For new or taxonomically uncertain species, ZSI collaborates with taxonomic authorities (European Molecular Biology Laboratory Nucleotide Archives, Barcode of Life Data System, International Barcode of Life (iBOL) National Center for Biotechnology Information etc) to assign unique registration numbers. Finally, the confirmed DSI sequences are submitted to the NCBI GenBank or genetic sequence database, generating unique accession numbers for global access and reference.

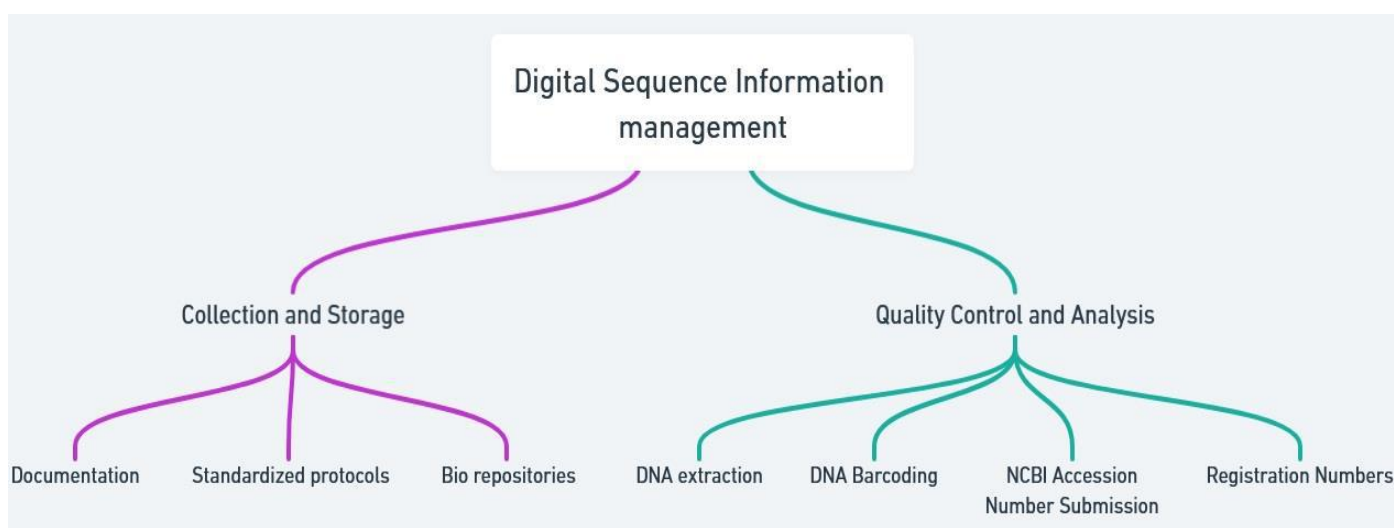


Fig. 3 Practices of Digital Sequence Information Management

#### Protocol for Digital Sequence Information:

The Nagoya Protocol, an international agreement, complements these efforts by aiming to ensure fair and equitable sharing of benefits derived from the use of genetic resources. It provides a framework for accessing these resources while respecting the sovereignty and rights of countries where they originate. Emphasizing informed consent, benefit-sharing agreements, and compliance with regulations, the protocol promotes biodiversity conservation and sustainable resource use. Compliance with the Nagoya Protocol is therefore integral to DSI protocols, reinforcing ethical practices in genetic resource utilization. Protocols for digital sequence information (DSI) encompass standardized procedures and guidelines for managing, sharing, and utilizing genetic sequence data. DSI is typically formatted according to international standards (e.g., FASTA format) to facilitate seamless data exchange and analysis among researchers. Crucial to these protocols are NCBI accession numbers and species registration numbers, which ensure accurate identification and traceability of genetic data.

#### Digital Sequence Information Practices Strengthen and Weakness:

The Zoological Survey of India (ZSI) demonstrates commendable strengths in managing Digital Sequence Information (DSI). Their systematic data handling, advanced analytical tools, and focus on taxonomic research solidify them as a valuable resource for biodiversity studies. Transparency through annual reporting further bolsters their credibility. Notably, ZSI has generated a significant number of DSI barcodes (4,781 species documented between 2019 and 2023) showcasing their dedication to digitizing biodiversity data. However, opportunities for improvement exist. Fluctuations in barcode production and uneven representation across faunal groups suggest a need for operational streamlining and prioritization strategies. Effectively managing the vast volume of DSI data while balancing scientific openness with legal and ethical obligations, such as those outlined in the Nagoya Protocol, presents another challenge. Securing adequate funding and resources for research, infrastructure, and capacity building remains a persistent hurdle. Additionally, integrating advanced data processing technologies is crucial for further optimization. By addressing these areas, ZSI can solidify its position as a leader in DSI practices and ensure a more comprehensive and equitable representation of India's remarkable biodiversity.





## 7. FINDINGS:

The Zoological Survey of India (ZSI) exhibited a consistent increase in DNA barcoding efforts from 2018 to 2023, culminating in a peak of 497 species and 1770 barcodes in 2022-2023. Over this five-year period, a total of 6223 barcodes were generated for 2017 species of faunal groups, highlighting ZSI's sustained commitment to research and technological progress. ZSI systematically increased species documentation: 333 species in 2018-2019, 1315 in 2019-2020, 896 in 2020-2021, 416 in 2021-2022, and 1770 in 2022-2023, with a focus on Insecta within Arthropoda and diverse Chordates taxa crucial for biodiversity conservation. Among faunal groups, Arthropoda, notably Insecta, stood out with 875 species and 2449 barcodes. Notable trends emerged in species identification and genetic barcoding: Lepidoptera recorded 206 species with 632 barcodes, while Thysanoptera accounted for 232 species and 794 barcodes. Ehmeroptera also highlighted significant genetic profiling efforts. In the chordates group, Pisces had 446 species with 581 barcodes, Mammalia had 144 species with 1446 barcodes, and Reptilians had 108 species with 313 barcodes, underscoring significant species representation. The substantial representation of Lepidoptera, Thysanoptera, Ehmeroptera, Pisces, Mammalia, and Reptilians underscores the importance of genetic barcoding in understanding and preserving the intricate web of India's biodiversity. The evolution in DSI at ZSI, exemplified by the mitochondrial genomic data of the Assam macaque, consisting of 307 nucleotide bases, illustrated its pivotal role in genetic studies. Effective DSI management practices included standardized protocols, collaboration with taxonomic experts, and integration with global databases like NCBI, GenBank, BOLD, ENA ensuring data accuracy and transparency. Despite strengths in systematic data collection and analytical capabilities, ZSI faced challenges such as fluctuating barcode production and uneven taxonomic representation, necessitating enhanced protocols and capacity-building initiatives for taxonomists.

## 8. RECOMMENDATIONS AND SUGGESTIONS:

Based on this research, future studies should conduct comparative analyses across multiple research institutions in India, encompassing both fauna and flora studies to comprehensively understand DSI practices. It is essential to involve a diverse array of organizations beyond ZSI to achieve a holistic national perspective on biodiversity conservation efforts, such as Anthropological Survey of India (AnSI), Botanical Survey of India, Fishery Survey of India (FiSI) and Forest Survey of India (FIS). These institutions play crucial roles in mapping and preserving India's rich biodiversity and geological resources. Encouraging collaboration among institutions will facilitate enhanced data sharing, methodological improvements, and the development of robust infrastructure for integrating DSI effectively. Challenges include a disproportionate distribution of DSI barcodes among faunal groups and fluctuations in yearly production, suggesting operational hurdles. To enhance efficiency, ZSI should standardize data collection protocols across all taxa, prioritize biodiversity importance in barcode production, and invest in taxonomist capacity building. Improved coordination and advanced technology integration can optimize DSI preservation efforts for comprehensive representation of India's biodiversity. Researchers should also consider adopting advanced technologies such as high-throughput sequencing and bioinformatics tools to expand the efficiency and scope of DSI initiatives. These steps will contribute significantly to optimizing biodiversity research and conservation strategies in India.

## 9. LIMITATIONS:

Acknowledging the existence of DSI initiatives across various domains the presence of DSI initiatives in various domains of fauna research beyond ZSI, this study does not directly compare or incorporate their practices. This limitation potentially restricts the broader applicability of findings to other research institutions engaged in similar endeavours across India. Future research could address these limitations by conducting comparative analyses across multiple institutions, encompassing fauna studies, and exploring collaborative frameworks to enhance DSI integration and conservation efforts on a broader scale.

## 10. CONCLUSION:

This study examines DSI temporal trends and institutional practices at the Zoological Survey of India (ZSI) from 2018 to 2023, highlighting significant biodiversity research milestones. ZSI's documentation of 6,223 barcoded species underscores its commitment, especially in Insecta and Chordata. Despite variability in barcode production, ZSI's standardized protocols and global collaborations have enhanced data reliability. Moving forward, fostering partnerships and adopting advanced technologies will be crucial for sustaining and expanding biodiversity conservation efforts nationwide. Future research should conduct comparative analyses across institutions to optimize DSI integration and conservation strategies in India, addressing broader applicability and collaborative frameworks.

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