CSIR-DBT NET LIFE SCIENCES

Merged
Complete Course
10000+ Pointer Book X4

Second Edition

TLS ONLINE ACADEMICS

Kanpur, India

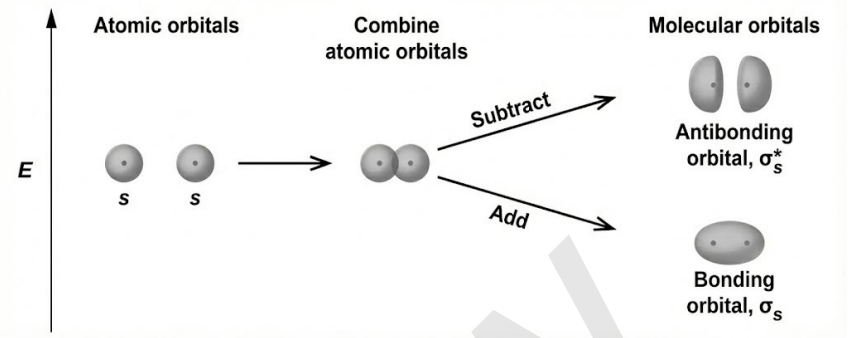
CSIR-NET LIFE SCIENCES
Complete Course 10000+ Pointer Book X4

Part I

Unit 1, Unit 2, Unit 3, Unit 4, Unit 5, Unit 6, Unit 7

- Atomic orbitals are regions in three-dimensional space around the nucleus where the probability of finding an electron is highest (about 90–95%).
- Atomic Orbitals (AOs) combine to form Molecular Orbitals (MOs), when two atoms approach each other, their atomic orbitals overlap. The overlapping orbitals add or subtract to form new orbitals called molecular orbitals.

- Constructive Combination of AO → Bonding Molecular Orbital (Ψ bonding) Occurs when wave functions add: $\psi_{bonding} = \psi_A + \psi_B$
- Electron density between nuclei increases
- Nuclei held together → lower energy
- Results in a bond
- Represented as σ (sigma) or π (pi)



- Destructive Combination → Antibonding Molecular Orbital (Ψ*) Occurs when wave functions subtract: $\psi_{antibonding} = \psi_A - \psi_B$
  - Electron density between nuclei decreases
  - Contains a node (region of zero electron density)
  - Higher energy → destabilizing
  - Represented as σ* or π*
- Different orbitals combine to yield molecular orbitals that generally fall into one of five different classes s orbitals combine to the binding s and the antibonding s* orbitals. Some p orbitals combine to the binding p and the anti-binding p*. Other p orbitals combine to form non-binding n orbitals.
- n = a non-bonding electron (typically a lone pair on atoms like O, N, S, or halogens). σ* = a sigma anti-bonding orbital (the higher energy counterpart of a sigma bond). So, n → σ* means:
- A lone pair electron is excited from a non-bonding orbital to a sigma anti-bonding orbital upon absorbing UV light.

Type of Transition	Orbital Involvement	Typical Wavelength Range (nm)	Example Systems
σ → σ*	Strong sigma bonds (e.g., C–C, H–H)	< 150 nm (far UV)	Saturated hydrocarbons (only UV)
n → σ*	Lone pairs → anti-bonding sigma	150–250 nm	Alcohols, ethers, amines
π → π*	π-bonding → π*-anti-bonding	200–400 nm	Alkenes, aromatic rings
n → π*	Lone pairs → π*-anti-bonding	250–600 nm	Carbonyls, azo groups

- Electrons in binding orbitals are usually paired with antiparallel spin orientation. The total spin S is calculated from the individual electron spins.
- The multiplicity M is obtained by M = 2 x S + 1

S = spin (electron 1) + spin (electron 2) = (+1/2) + (-1/2) = 0; The multiplicity is thus M = 2 × 0 + 1 = 1

- The wavelength L is the spatial distance between two consecutive peaks (one cycle) in the sinusoidal waveform and is measured in submultiples of metre, usually in nanometres (nm). The maximum length of the vector is called the amplitude.
- In case the spins of both electrons are oriented in a parallel fashion, the resulting state is characterized by a total spin of S=1, and a multiplicity of M= 3. Such a state is called a triplet state and usually exists only as one of the excited states of a molecule.

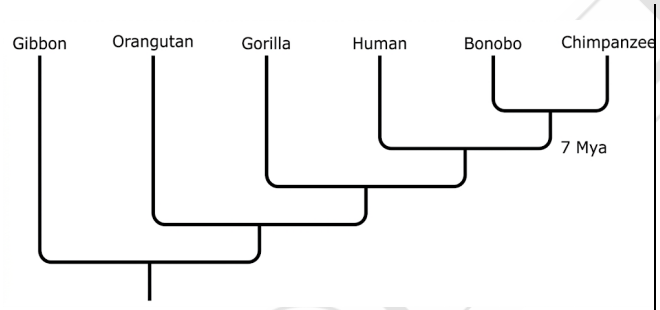
Human evolution

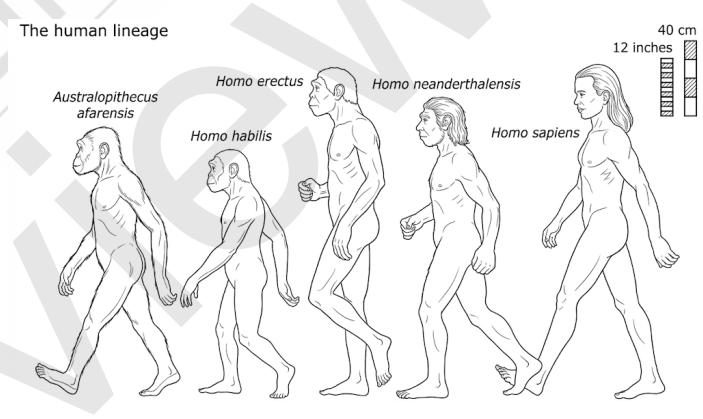
- Humans are descended from the last universal common ancestor (LUCA) of all living organisms on Earth. We share fundamental features with them: inheritance based on nucleic acids (DNA and RNA), the genetic code, proteins composed of L amino acids, and much more.

- Among the grand events in our earliest ancestry was the origin of the eukaryotes, a symbiosis between an archaean and a bacterium. That momentous event led to the evolution of diverse unicellular forms and several multicellular lineages, which then evolved tissues and organs. One lineage was the progenitor of animals.

- A descendant then gave rise, some 550 Mya, to the sea stars and other echinoderms on the one hand, and to the chordates on the other hand. Much later, from among diverse vertebrate chordates, arose the ancestor of tetrapods, with legs that evolved from fins. About 150 My after the first land dwelling tetrapod, some of its descendants stood on the brink of mammal hood. By about 70 Mya, some familiar groups of mammals had appeared, including the first primates.

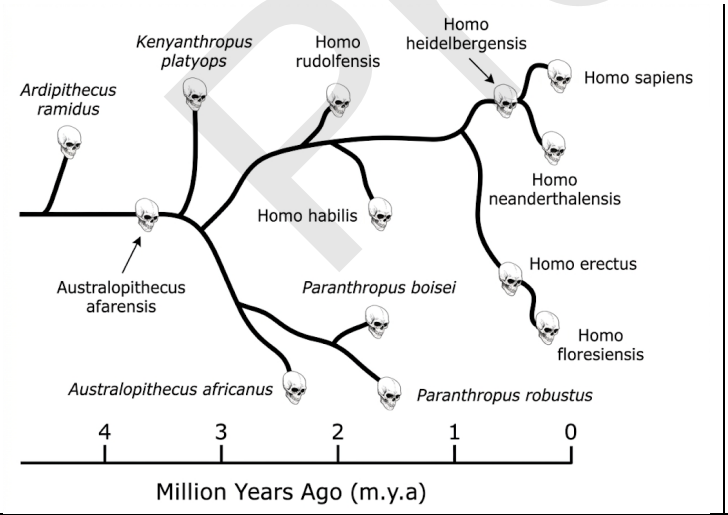
- Phylogeny of some of the living apes - The lineage that includes our own species is called the hominins, which diverged from the chimpanzee lineage about 7 Mya1. The hominin lineage gave rise to many more species, all of which went extinct save for one: Homo sapiens.

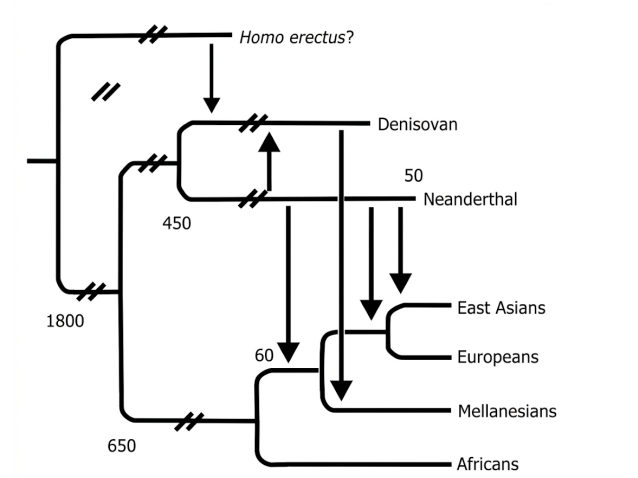




- Dryopithecus is considered as the common ancestor of the apes and man.

- Dryopithecus - Australopithecus afarensis- Homo habilis - Homo erectus - Homo heidelbergensis- Neanderthal and Homo sapiens.





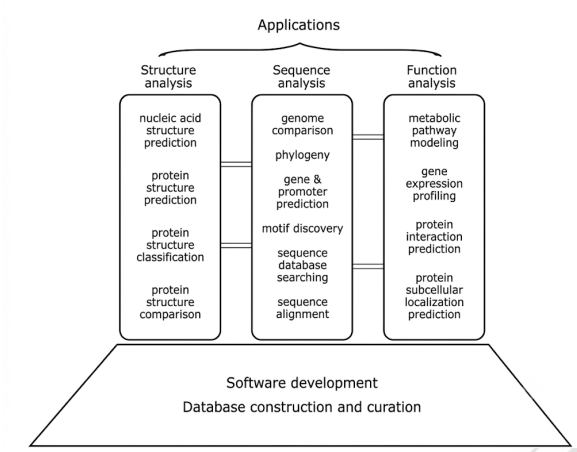
- Homo habilis – First tool maker and lived in caves. Homo erectus – Invent fire.

- Modern humans and Neanderthals show an average cranial capacity of around 1400–1500 cc.

- Comparison of DNA of living humans from different populations with DNA from Neanderthal and Denisovan fossils reveals there was hybridization among these

11A. Major Bioinformatic Resources

- Bioinformatics is an interdisciplinary field combining biology and computer science, focused on using computers for storing, retrieving, analyzing, and distributing information about biological macromolecules (DNA, RNA, proteins). It is essential for handling repetitive and complex genomic data analysis tasks.



- Bioinformatics primarily deals with sequence, structural, and functional analysis of genes and genomes.
- Computational biology is broader, covering all biological areas that use computation (e.g., ecosystem modeling, population dynamics, phylogenetics).
- Some define bioinformatics as tool development and application, while computational biology emphasizes theoretical algorithm development.
- The distinction between the two fields remains somewhat fluid due to their rapid evolution.

Biological Database

- Biological databases are organized repositories that store, manage, and provide access to biological information such as DNA sequences, protein sequences, gene expression data, protein structures, metabolic pathways, and functional annotations. These databases are indispensable in genomics, proteomics, structural biology, and bioinformatics.
- Based on content, databases are of three types:

Feature	Primary Database	Secondary Database
Definition	Stores raw experimental data directly submitted by researchers (e.g., DNA, RNA, protein sequences, structures).	Stores derived, curated, and interpreted data obtained by analyzing, annotating, or processing primary data.
Data Source	Direct submissions from scientists, sequencing projects, and labs.	Derived from primary databases through computational analysis or manual curation.
Content	Original biological sequences, structures, or experimental results.	Annotated information such as protein families, motifs, domains, pathways, or functional classification.
Nature of Data	Redundant (same sequence may appear multiple times with different accession numbers).	Non-redundant (organized and classified to remove duplication).
Examples	GenBank, EMBL, DDBJ (for nucleotide sequences), PDB (for protein 3D structures).	Pfam, PROSITE, SCOP, CATH, KEGG (for protein domains, families, and pathways).
Use	Acts as a repository/archive of experimental results.	Helps in interpretation, functional prediction, and classification of biological data.

1. Sequence Databases

- Sequence databases store nucleotide (DNA/RNA) and protein sequences along with annotations such as gene names, organism, coding regions, protein products, biological function, and literature references.
- They serve as the primary source of sequence information for genome analysis, comparative genomics, and molecular biology research.

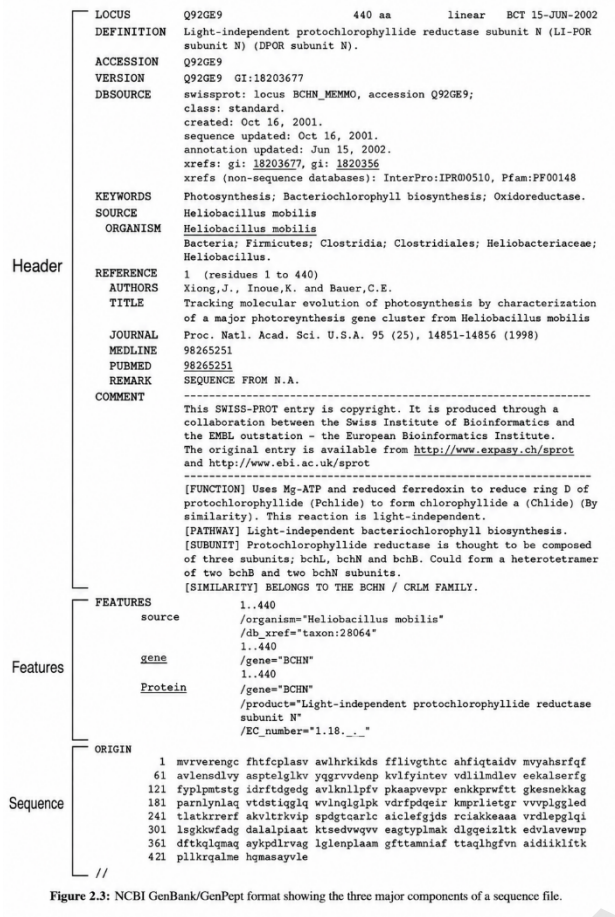


Figure 2.3: NCBI GenBank/GenPept format showing the three major components of a sequence file.

- The image shows a GenBank/GenPept (Swiss-Prot) sequence database record, which is an example of a sequence retrieval (record-based) information retrieval system.

Summary of the image

Section	Information Included	Purpose
Header	LOCUS, DEFINITION, ACCESSION, VERSION, SOURCE, ORGANISM, REFERENCES, COMMENTS	Identifies and describes the sequence
Features	Source, gene, CDS/product, functional sites, domains	Biological annotation of sequence regions
Sequence	Amino acid or nucleotide sequence	Primary sequence used for analysis

3. Structure-Based Retrieval

- Structure-based retrieval searches databases using the three-dimensional structure of proteins or nucleic acids. Similar molecular folds or structural motifs are identified even when sequence similarity is low.

- This approach is valuable because protein structure is generally more conserved than amino acid sequence during evolution.

Major Databases and Tools

Database/Tool	Purpose
Protein Data Bank (PDB)	Retrieval of experimentally determined structures
MMDB	Structural comparison
DALI	Structural alignment
VAST	Comparison of protein structures

Applications

- Drug discovery
- Protein engineering
- Active-site prediction
- Functional analysis
- Structural classification

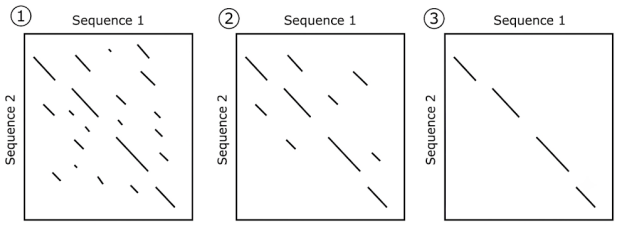
4. Functional Annotation Retrieval

- Functional annotation retrieval identifies biological functions associated with genes or proteins based on curated annotations and controlled vocabularies.

- Annotations may include molecular function, biological process, cellular localization, metabolic pathways, protein families, and conserved domains.

FASTA

- FASTA is another heuristic algorithm used for local sequence alignment and similarity searching in nucleotide and protein databases.
- It identifies short identical sequence segments (k-tuples) between the query and database sequences, joins nearby matching regions, and then refines the alignment to produce a final score.
- Although FASTA is generally slower than BLAST, it is often considered more sensitive for detecting distantly related homologous sequences, making it useful when sequence similarity is low.



- FASTA is widely applied in gene identification, protein family classification, evolutionary analysis, and functional annotation.

FASTA (FAST-ALL) was the first database similarity search tool, developed before BLAST and uses a "hashing" strategy to quickly find short identical segments (k-tuples).

- FASTA also performs local alignment using a heuristic approach but employs k-tuples instead of BLAST's word method. It is slower but slightly more sensitive than BLAST for detecting distant homologs.
- Three major steps of the FASTA algorithm for identifying the best local alignment between two sequences using the k-tuple (hashing) method. It shows how FASTA progressively filters many potential matching regions to obtain a single high-scoring alignment.
- FASTX: translates DNA → protein and searches protein databases.
- TFASTX: compares a protein query to a translated DNA database.

1. Given two amino acid sequences for comparision:

sequence 1 **AMPSDGL**
sequence 2 **GPSDNAT**

2. Construct a hashing table:

amino acid	sequence position		offset
	seq 1	seq 2	
A	1	6	-5
D	5	4	1
G	6	1	5
L	7	-	-
M	2	-	-
N	-	5	-
P	3	2	1
S	4	3	1
T	-	7	-

3. Identify residues with the same offset values (highlighted in grey).

4. Find the matching word of three residues in the order of 3, 4 and 5 in one sequence and 2, 3,and 4 in the other.

5. This allows establishment of alignment between the two sequences.

sequence 1 **AMPSDGL–**
sequence 2 **–GPSDNAT**

- This figure illustrates the FASTA algorithm, specifically the hashing (k-tuple) strategy used to rapidly identify similar regions between two protein sequences before performing detailed alignment.
- Unlike BLAST, which searches using words, FASTA first identifies identical short fragments (k-tuples) and then uses their relative positions (offsets) to locate candidate alignment regions.

K-tuples (ktups)

- Equivalent to "words" in BLAST but usually shorter.
- Protein sequences: ktup = 2 residues.
- DNA sequences: ktup = 6 residues.

Interpretation of FASTA Statistical Parameters

Parameter	Good Result	Meaning

- The Arithmetic mean $\bar{x}$ of n observations (x1, x2, x3, ..., xn) is given by

$$\bar{x} = \frac{\text{Sum of Observations}}{\text{Total Number of Observations}}$$

- In case of frequency distribution, The Arithmetic mean is obtained by

$$\bar{x} = \frac{f_1x_1 + f_2x_2 + f_3x_3 + \cdots + f_nx_n}{f_1 + f_2 + f_3 + \cdots + f_n}$$

- Equivalently

$$\bar{x} = \frac{1}{N}\sum_{i=1}^{n} f_i\, x_i$$

where

$$N = \sum_{i=1}^{n} f_i$$

Where fi is the frequency of the variable xi.

- Combined mean - If the numbers of observations of two or more related groups are known, we can calculate the combined arithmetic mean of these groups.

The formula shown is the Combined Mean (Pooled Mean) of two groups:

$$\bar{X}_{12} = \frac{\bar{X}_1N_1 + \bar{X}_2N_2}{N_1 + N_2}$$

- N1 = Number of observations in first group N2 = Number of observations in second group $\bar{x}1$ = Mean of the first group $\bar{x}2$ = Mean of second group. $\bar{x}12$ = Combined mean of two group.

- **Median "**The median is that value of the variable which divides the group into two equal parts, one part comprising all values greater and other all values less than the median."

- In case of ungrouped data Determination of median using following procedure.

- Data are arranged in ascending or descending order

- Median is the value of $\left(\frac{N+1}{2}\right)^{th}$ term

where N is the number of terms in the series.

- Locate median by the value of items are even, the median would be the mean of two mid-terms.

- Determination of Median in discrete frequency distribution in case of discrete frequency distribution the procedure determining median is

(i) Data are arranged in ascending or descending order

(ii) Obtain the cumulative frequency

(iii) Find the $\left(\frac{N+1}{2}\right)^{th}$ term

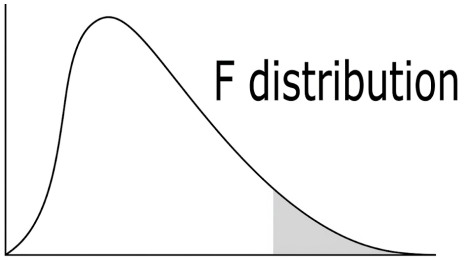
(iv) The corresponding value of x is Median.

- Determination of Median in continuous frequency distribution: In case of continues frequency distribution, the procedure determining median is (Compute cumulative frequencies. (c.f.), Find the size of N/2th term. Corresponding Class is Median Class, Obtain the median value by applying the formula:

- The formula in the image is the Median Formula for a Continuous Frequency Distribution:

- NOVA differs from T tests in that ANOVA can compare three or more groups while T tests are only useful for comparing two groups at one time.
- There are two main types of ANOVA: one-way (or unidirectional) and two-way. There also variations of ANOVA.

- For example, MANOVA (multivariate ANOVA) differs from ANOVA as the former tests for multiple dependent variables simultaneously while the latter assesses only one dependent variable at a time.
- One-way or two-way refers to the number of independent variables in your analysis of variance test.
- A one-way ANOVA evaluates the impact of a sole factor on a sole response variable. It determines whether all the samples are the same.



- The one-way ANOVA is used to determine whether there are any statistically significant differences between the means of three or more independent (unrelated) groups.
- A two-way ANOVA is an extension of the one-way ANOVA. With a one-way, you have one independent variable affecting a dependent variable. With a two-way ANOVA, there are two independents. For example, a two-way ANOVA allows a company to compare worker productivity based on two independent variables, such as salary and skill set. It is utilized to observe the interaction between the two factors and tests the effect of two factors at the same time.
- Test statistics for ANOVA is F-test - Assumption for ANOVA. Samples follow normal distribution. Samples have been selected randomly and independently. Each group should have common variance. Data are independent.
- **Chi square test -** chi square test is an important test amongst the several tests of significance. It was developed by karl pearson in 1900. The chi-square test is a non-parametric test not based on any assumption or distribution of any variable. This statistical test follows a specific distribution known as chi square distribution. The chi-square test we use to measure the differences between what is observed and what is expected according to an assumed hypothesis is called the chi-square test.
- Important characteristics of a chi square test - the chi-square test (as a non-parametric test) is based on frequencies and not on the parameters like mean and standard deviation. The chi-square test can also be applied to a complex contingency table with several classes.
- The chi-square test is an important non-parametric test as no rigid assumptions are necessary in regard to the type of population, no need of parameter values and relatively less mathematical details are involved.
- Degree of freedom:(d.f.) - it denotes the extent of independence (freedom) enjoyed by a given set of observed frequencies suppose we are given a set of n observed frequencies which are subjected to k independent constraints(restrictions) then, d.f. = (number of frequencies) – (number of independent constraints on them)
- Contingency table: when the table is prepared by enumeration of qualitative data by entering the actual frequencies, and if that table represents occurrence of two sets of events, that table is called the contingency table. It is also called the association table.
- Conditions for the application of chi SQUARE TEST - The following conditions should be satisfied before chi square $\chi 2$ test can be applied:
  - The data must be in the form of frequencies
  - The frequency data must have a precise numerical value and must be organised into categories or groups.
  - Observations recorded and used are collected on a random basis.
  - All the items in the sample must be independent.

Type of IP	Protects	Duration (India)	Example
Patent	New inventions, products, processes	20 years from filing date	Recombinant insulin production process
Copyright	Literary, artistic, musical, dramatic works, software	Life of author + 60 years	Books, research articles, computer software
Trademark	Brand names, logos, symbols, slogans	10 years (renewable indefinitely)	Company logos, brand names
Industrial Design	Shape, configuration, pattern, ornamentation of products	10 years + 5-year extension	Unique product packaging
Geographical Indication (GI)	Products linked to a specific geographical origin	10 years (renewable)	Darjeeling Tea, Banarasi Saree
Trade Secret	Confidential business information	As long as secrecy is maintained	Coca-Cola formula, proprietary processes
Plant Variety Protection (PVP)	New plant varieties	15–18 years depending on crop	Improved crop varieties
Layout Design of Integrated Circuits	Semiconductor chip layouts	10 years	Microprocessor circuit design

Indian Patent Databases

Indian patent databases are online repositories that provide access to patent applications, granted patents, patent specifications, legal status, and patent-related information. These databases are important for conducting prior-art searches, assessing novelty, monitoring competitors, and verifying patent status.

Database	Purpose	Features
InPASS (Indian Patent Advanced Search System)	Official Indian patent search database	Search patent applications, granted patents, inventors, applicants, legal status, abstracts, and complete specifications
Patent Office Journal	Weekly publication by Indian Patent Office	Lists patent applications, grants, amendments, and patent-related notices
e-Register of Patents	Legal status verification	Provides information on granted patents, renewal status, ownership, and patent history
IPAIRS (Indian Patent Information Retrieval System)	Earlier patent search system	Access to published patent applications and patent documents (largely replaced by InPASS)
Patent Facilitation Centre (PFC-DBT/TIFAC)	Patent information and assistance	Supports patent searches, filing guidance, and IPR awareness

Biosafety

- Biosafety refers to the principles, practices, and containment measures designed to prevent accidental exposure to or release of potentially harmful biological agents, genetically modified organisms (GMOs), and recombinant DNA products.
- Biosafety ensures the protection of laboratory personnel, the environment, and public health during biological research and biotechnology applications. In India, biosafety regulations are governed under the Environment (Protection) Act, 1986 and implemented through regulatory committees such as IBSC, RCGM, GEAC, SBCC, and DLC.
- Biological safety measures are the practices, containment procedures, and regulatory guidelines used to protect laboratory personnel, the environment, and the public from exposure to potentially hazardous biological agents, pathogens, recombinant DNA molecules, genetically modified organisms (GMOs), and biological toxins. Biosafety aims to minimize accidental infection, contamination, environmental release, and misuse of biological materials.
- The choice of biosafety measures depends on the risk group of the organism, the nature of the experiment, the route of transmission, and the potential hazard to humans, animals, and the environment.
- Effective biosafety relies on a combination of laboratory practices, safety equipment, facility design, waste management, and personnel training.

Part A General Aptitude

Simplification

1. Simplify the expression: $25 \times 24 + 28 \times 10 - 45 \div 15$

Solution:
Perform division first: $45 \div 15 = 3$
Perform multiplications: $25 \times 24 = 600$ and $28 \times 10 = 280$
Combine the results: $600 + 280 - 3 = 877$
Answer: 877

2. Find the exact value of: $\frac{3}{5}$ of $\frac{4}{7}$ of $\frac{5}{9}$ of 2100

Solution:
Convert 'of' to multiplication: $\frac{3}{5} \times \frac{4}{7} \times \frac{5}{9} \times 2100$
Simplify terms: $\left(\frac{3 \times 4 \times 5}{5 \times 7 \times 9}\right) \times 2100 = \frac{4}{21} \times 2100$
Calculate final value: $4 \times 100 = 400$
Answer: 400

3. Evaluate using BODMAS: $108 \div 36$ of $\frac{1}{4} + \frac{2}{5} \times 3\frac{1}{4}$

Solution:
Evaluate 'of': 36 of $\frac{1}{4} = 36 \times \frac{1}{4} = 9$
Division: $108 \div 9 = 12$
Convert mixed fraction and multiply: $\frac{2}{5} \times \frac{13}{4} = \frac{13}{10} = 1.3$
Addition: $12 + 1.3 = 13.3$ (or $13\frac{3}{10}$)
Answer: 13.3 or $13\frac{3}{10}$

4. Find the value of x in the equation: $x^2 + 126 = 24^2 - 15^2$

Solution:
Calculate RHS using $a^2 - b^2 = (a - b)(a + b)$: $24^2 - 15^2 = (24 - 15)(24 + 15) = 9 \times 39 = 351$
Set up equation: $x^2 + 126 = 351 \Rightarrow x^2 = 351 - 126 = 225$
Solve for x: $x = \sqrt{225} = 15$
Answer: 15

5. Simplify using algebraic identities: $(4.5 \times 4.5) - (2.5 \times 2.5)$

Solution:
Apply identity $a^2 - b^2 = (a - b)(a + b)$ where $a = 4.5$ and $b = 2.5$:
$$(4.5 - 2.5)(4.5 + 2.5) = 2 \times 7 = 14$$
Answer: 14

6. Evaluate the decimal expression: $\frac{0.87 \times 0.87 \times 0.87 + 0.13 \times 0.13 \times 0.13}{0.87 \times 0.87 - 0.87 \times 0.13 + 0.13 \times 0.13}$

Solution:
Apply identity $\frac{a^3 + b^3}{a^2 - ab + b^2} = a + b$ where $a = 0.87$ and $b = 0.13$:
$$a + b = 0.87 + 0.13 = 1$$
Answer: 1

7. Find the value of x: $\sqrt{x} + 14 = \sqrt{2601}$

- **Solution:**

Simplify square root: $\sqrt{2601} = 51$
Solve for $\sqrt{x}$: $\sqrt{x} + 14 = 51 \Rightarrow \sqrt{x} = 37$
Square both sides: $x = 37^2 = 1369$

$$252 = 2^2 \times 3^2 \times 7$$
$$308 = 2^2 \times 7 \times 11$$
$$198 = 2 \times 3^2 \times 11$$
$$\text{LCM} = 2^2 \times 3^2 \times 7 \times 11 = 2772 \text{ seconds}$$

Convert to minutes and seconds: $2772 \div 60 = 46$ **minutes** 12 **seconds**
Answer: 2772 **seconds (or** 46 **minutes** 12 **seconds)**

10. The sum of two numbers is 216 and their HCF is 27. How many such pairs of numbers exist?

Solution:
Let the numbers be $27a$ and $27b$, where a and b are co-prime integers (HCF$(a, b) = 1$).
$$27a + 27b = 216 \Rightarrow 27(a + b) = 216 \Rightarrow a + b = 8$$
Identify co-prime pairs (a, b) that add up to 8:
$(1, 7) \Rightarrow$ HCF$(1, 7) = 1$ (Valid)
$(2, 6) \Rightarrow$ HCF$(2, 6) = 2$ (Invalid)
$(3, 5) \Rightarrow$ HCF$(3, 5) = 1$ (Valid)
$(4, 4) \Rightarrow$ HCF$(4, 4) = 4$ (Invalid)
Valid co-prime pairs are $(1, 7)$ and $(3, 5)$.
Answer: 2 pairs

Number Systems

Part 1: Questions

1. Find the unit digit of the expression 7^{105}.

Solution:
The cyclicity of the unit digits of 7 is 4 ($7^1 = 7$, $7^2 = 9$, $7^3 = 3$, $7^4 = 1$).
Divide the exponent by 4: $105 \div 4 = 26$ with a remainder of 1.
The unit digit corresponds to $7^1 = 7$.
Answer: 7

2. What is the remainder when 17^{200} is divided by 18?

Solution:
Express 17 in terms of modulus 18: $17 \equiv -1 \pmod{18}$.
Raise to the power of 200: $17^{200} \equiv (-1)^{200} \equiv 1 \pmod{18}$.
Answer: 1

3. Determine the number of trailing zeros at the end of $100!$ (100 factorial).

Solution:
Use Legendre's formula to count factors of 5:
$$\lfloor 100/5 \rfloor = 20$$
$$\lfloor 100/25 \rfloor = 4$$
Total trailing zeros $= 20 + 4 = 24$.
Answer: 24

4. Find the largest 4-digit number which is exactly divisible by 12, 15, and 18.

Solution:
Find the LCM$(12, 15, 18)$:
$12 = 2^2 \times 3$, $15 = 3 \times 5$, $18 = 2 \times 3^2$
$$\text{LCM} = 2^2 \times 3^2 \times 5 = 180$$
Divide the largest 4-digit number (9999) by 180: $9999 \div 180 = 55$ with a remainder of 99.
Subtract remainder: $9999 - 99 = 9900$.
Answer: 9900

5. A number when divided by 899 gives a remainder of 63. What will be the remainder when the same number is divided by 29?

Solution:

Answer: ₹38,000

7. Charity/Donation Percentage

A and B invest in a business in the ratio $3:2$. If 5% of the total profit goes to charity and A's share of the profit is ₹855, what is the total profit?

Solution:
Let total profit be P.
Remaining profit = 95% of $P = 0.95P$
A's share = $\frac{3}{5} \times 0.95P = 0.57P$

$$0.57P = 855 \Rightarrow P = \frac{855}{0.57} = 1500$$

Answer: ₹1,500

8. Equivalent Rent (Pasture Problem)

A, B, and C rent a pasture. A puts 10 oxen for 7 months, B puts 12 oxen for 5 months, and C puts 15 oxen for 3 months for grazing. If the total rent of the pasture is ₹1,750, how much must C pay as his share of the rent?

Solution:
Usage ratio $A:B:C = (10 \times 7):(12 \times 5):(15 \times 3) = 70:60:45 = 14:12:9$
Total parts = $14 + 12 + 9 = 35$
C's share = $\frac{9}{35} \times ₹1,750 = ₹450$
Answer: ₹450

9. Finding Ratio of Time Periods

The investments made by A and B are in the ratio $4:5$. If their profits at the end of the year are in the ratio $2:3$, find the ratio of the time periods for which their capitals were invested.

Solution:

$$\frac{I_1 \times T_1}{I_2 \times T_2} = \frac{P_1}{P_2} \Rightarrow \frac{4}{5} \times \frac{T_1}{T_2} = \frac{2}{3}$$
$$\frac{T_1}{T_2} = \frac{2}{3} \times \frac{5}{4} = \frac{10}{12} = \frac{5}{6}$$

Answer: $5:6$

10. Total Capital Given, Individual Deduced

A, B, and C enter into a partnership by investing a total of ₹50,000. A invests ₹4,000 more than B, and B invests ₹5,000 more than C. Find A's share in a total profit of ₹35,000.

Solution:
Let $C = x \Rightarrow B = x + 5000 \Rightarrow A = x + 9000$
Total = $3x + 14000 = 50000 \Rightarrow 3x = 36000 \Rightarrow x = 12000$
Investments: $C = 12000$, $B = 17000$, $A = 21000$
Ratio $A:B:C = 21:17:12$ (Total = 50 parts)
A's share = $\frac{21}{50} \times ₹35,000 = ₹14,700$
Answer: ₹14,700

Mixture & Alligation

1. Basic Alligation (Price Variation)

In what ratio must a grocer mix two varieties of pulses costing ₹40 per kg and ₹60 per kg so that the resulting mixture is worth ₹55 per kg?

Solution:
Apply the rule of alligation:

$$\text{Ratio} = (\text{CP}_2 - \text{Mean}):(\text{Mean} - \text{CP}_1)$$
$$\text{Ratio} = (60 - 55):(55 - 40) = 5:15 = 1:3$$

Calculate each term individually:
$(-2)^5 = -32$ (odd power of negative is negative)
$(-3)^3 = -27$ (odd power of negative is negative)
$(-1)^{100} = 1$ (even power of negative is positive)
Combine the values:

$$-32 + (-27) - 1 = -32 - 27 - 1 = -60$$

Answer: -60

10. Finding Unknown n: If $\left(\frac{3}{5}\right)^3 \times \left(\frac{3}{5}\right)^{-6} = \left(\frac{3}{5}\right)^{2n-1}$, find n.

Solution:
Combine the exponents on the left-hand side:

$$\left(\frac{3}{5}\right)^{3+(-6)} = \left(\frac{3}{5}\right)^{-3}$$

Equate exponents since the bases are equal:

$$-3 = 2n - 1 \Rightarrow 2n = -2 \Rightarrow n = -1$$

Answer: -1

Number & Letter Series

1. Simple Arithmetic: $5,11,17,23,29,\underline{?}$

Solution:
Common difference $d = +6$
Next term $= 29 + 6 = 35$
Answer: 35

2. Square Sequence: $1,4,9,16,25,\underline{?}$

Solution:
Pattern: $1^2, 2^2, 3^2, 4^2, 5^2$
Next term $= 6^2 = 36$
Answer: 36

3. Cube Sequence: $1,8,27,64,125,\underline{?}$

Solution:
Pattern: $1^3, 2^3, 3^3, 4^3, 5^3$
Next term $= 6^3 = 216$
Answer: 216

4. Prime Number Series: $2,3,5,7,11,13,\underline{?}$

Solution:
Consecutive prime numbers sequence.
Next prime number after 13 is 17.
Answer: 17

5. Alternating Series: $10,20,15,25,20,30,\underline{?}$

Solution:
Alternating operations: $+10, -5, +10, -5, +10, -5$
Next term $= 30 - 5 = 25$
Answer: 25

6. Multiplicative Growth: $2,6,18,54,162,\underline{?}$

Solution:
Common ratio $= \times 3$
Next term $= 162 \times 3 = 486$
Answer: 486

7. Square ± 1 Pattern: $0,3,8,15,24,35,\underline{?}$