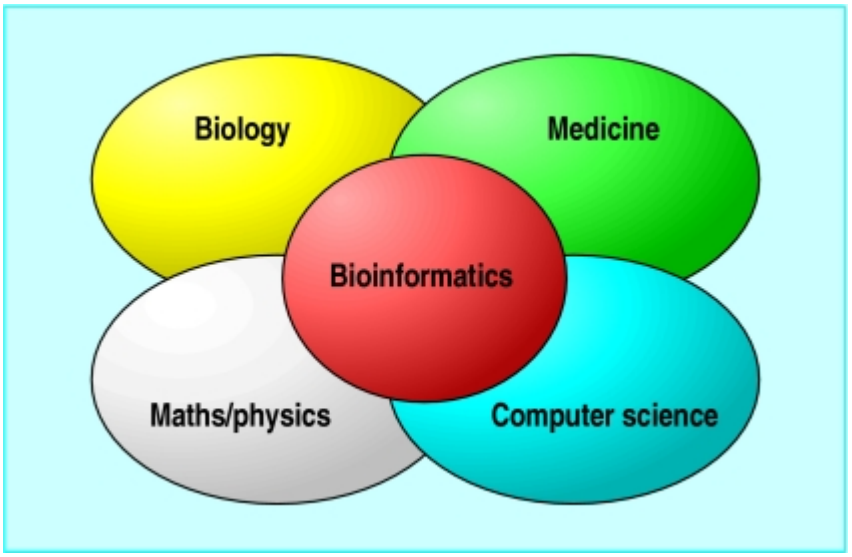
Bioinformatics, an interdisciplinary field combining computer science, mathematics, physics, and biology, helps analyze and interpret this data. It plays a crucial role in managing biological and medical information.



- Bioinformatics applies computational tools to interpret biological data.
- It is essential for modern biology and medicine.
- Tools like **BLAST** and Ensembl rely on internet access for data analysis.
- A major achievement is genome sequence analysis, especially of the human genome.
- Future developments could improve understanding of the genome, aiding drug discovery and personalized treatments.

With the massive influx of genome data, computer databases are crucial for organizing and analyzing biological information. Public and private databases store genetic data, some available for free while others require subscriptions. Bioinformatics is a rapidly growing field, essential for modern biology, medicine, and drug discovery.

Bioinformatics and Genomics

The sequencing of the entire human genome, along with many other organisms, is a major achievement in bioinformatics. The first complete genome of a free-living organism, *Haemophilus influenzae*, was sequenced in 1995 using the "shotgun" technique. Since then, genomes of bacteria (*Mycoplasma genitalium, Mycobacterium tuberculosis*) and eukaryotic species (*yeast, worms, fruit flies, mustard weed*) have been sequenced. Ongoing projects include zebrafish, pufferfish, mice, rats, and primates. This growing database of genetic information will greatly enhance our understanding of biology, disease, and medicine.

Useful Bioinformatics Websites

- **NCBI (www.ncbi.nlm.nih.gov)** – Provides bioinformatics tools and databases

- **GenBank (www.ncbi.nlm.nih.gov/Genbank)** – Stores DNA sequences
- **Ensembl (www.ensembl.org)** – Genome annotation database
- **SWISS-PROT (www.expasy.org/sprot/)** – **Protein** sequence database
- **EBI (www.ebi.ac.uk)** – Research center for bioinformatics
- **Unigene (www.ncbi.nlm.nih.gov/UniGene)** – Collects gene sequence data
- **ISCB (www.iscb.org/)** – Advances computational biology

Bioinformatics Tools

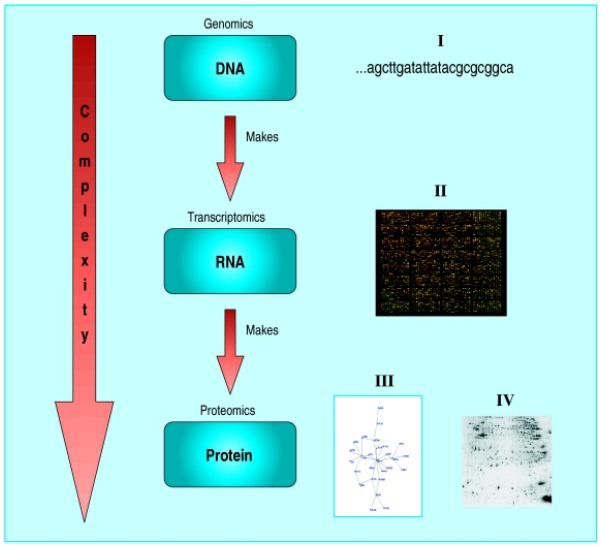
Bioinformaticians use specialized software and the internet to analyze DNA and protein sequences. Tools like **BLAST** allow scientists to compare genetic sequences and identify similar genes in different species. Pharmaceutical companies and biomedical labs increasingly rely on bioinformatics for large-scale data analysis. Tools like **BLAST** help researchers compare unknown sequences with existing data to predict functions and relationships between genes.

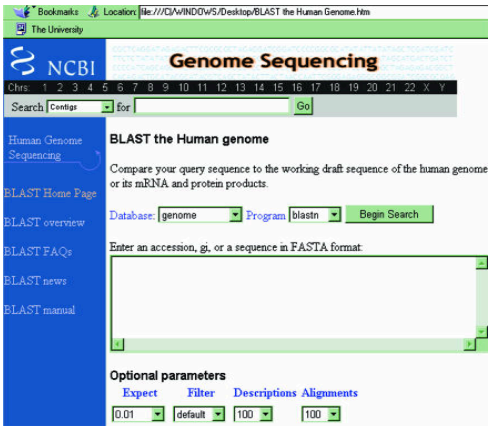
Simplified Explanation of Functional Genomics

Since the human genome was first mapped, the focus has shifted from studying genes to understanding their functions. Functional genomics explores how genes work, how they produce proteins, and what roles those proteins play in the body.

Key areas include:

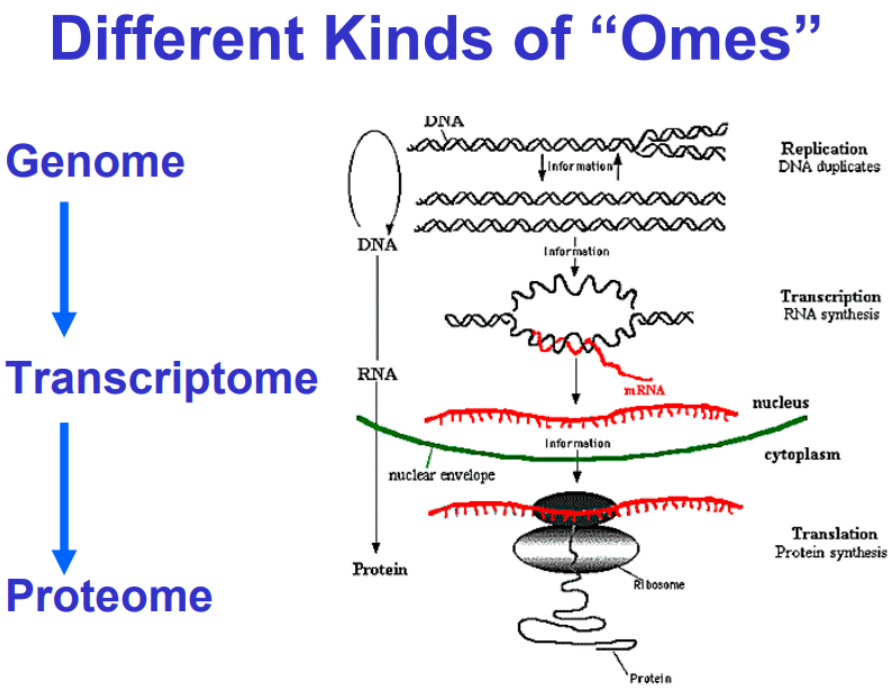
- Proteomics: Studying all proteins (proteome) a cell produces.
- Transcriptomics: Analyzing messenger RNA (transcriptome), which helps create proteins.
- DNA Microarrays: Technology that tracks gene activity and classifies diseases like cancer for better treatments.





Bioinformatics helps analyze vast amounts of genetic data. It aids in:

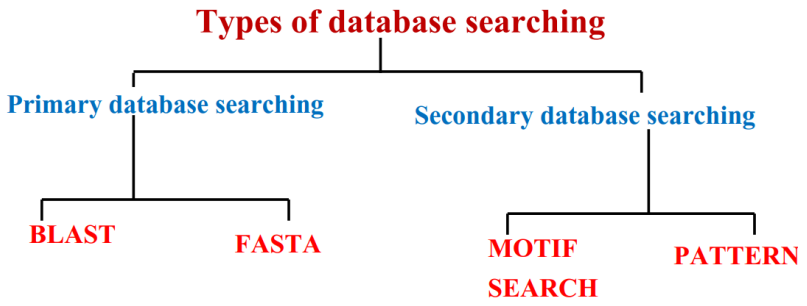
- Predicting gene and protein functions.
- Understanding gene-disease links.
- Designing drugs based on genetic markers (e.g., targeted cancer therapies like Imatinib).
- Personalizing medicine through pharmacogenomics, where treatments are tailored based on a person's genetic profile.



Types of Biological Databases

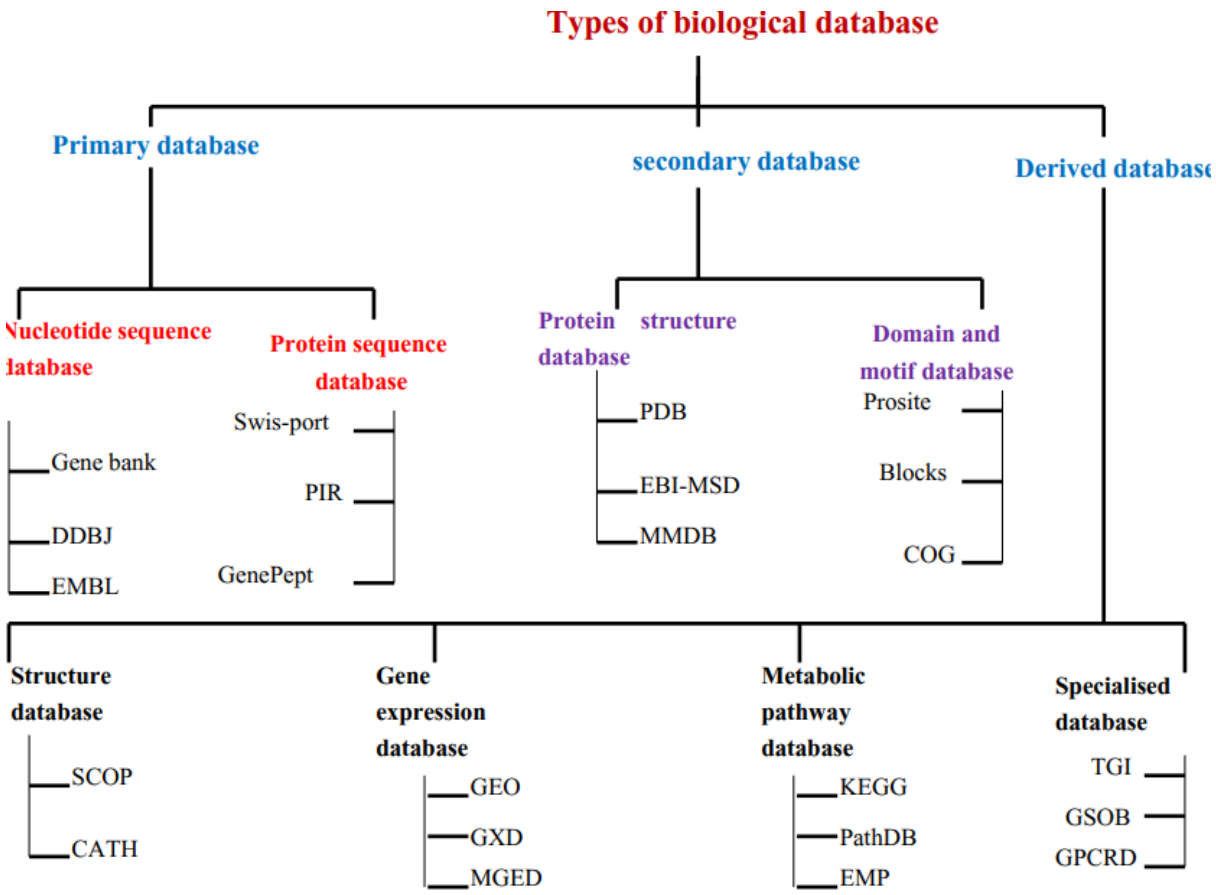
Biological databases are categorized into three types based on their content:

1. **Primary Databases** – Store raw biological data like DNA sequences or protein structures. Examples: GenBank, PDB, DDBJ.
2. **Secondary Databases** – Contain curated or processed information derived from primary databases. Examples: PIR, SWISS-PROT, Pfam.
3. **Specialized Databases** – Focus on specific organisms or data types. Examples: Flybase, HIV Sequence Database, Ribosomal Database Project.



Popular Biological Databases:

- **GenBank** – A comprehensive DNA sequence database by NCBI.
- **EMBL** – A nucleotide sequence database managed by EBI.
- **DDBJ** – Japan's nucleotide sequence repository, collaborating with GenBank and EMBL.
- **PDB** – Stores 3D structures of proteins, DNA, and RNA.
- **PIR** – A protein information database with multiple related resources.
- **PROSITE** – A database of protein patterns and functional sites.
- **Pfam** – Stores protein family and domain information.
- **KEGG** – Contains data on genomes, pathways, and diseases.
- **OMIM** – A database of human genes and genetic disorders.



Importance of Biological Databases:

- Organize vast biological data.
- Aid researchers in analysis and discovery.
- Enable the development of bioinformatics tools.
- Support collaboration and data sharing.

Bioinformatics Tools

Bioinformatics tools are essential for analyzing biological data, focusing on sequence, structure, and function analysis.

Types of Bioinformatics Tools:

1. Sequence Analysis Tools

These tools compare and analyze DNA/protein sequences to identify relationships and similarities.

- **BLAST**: Identifies similar sequences and determines evolutionary relationships.
- **ClustalW**, **T-Coffee**: Multiple sequence alignment tools for comparing DNA/protein sequences.
- **MEME**: Discovers sequence motifs and performs motif analysis.
- **MEGA**, **PHYLIP**: Tools for phylogenetic analysis to study evolutionary relationships.

2. Structure Analysis Tools

These tools help visualize and analyze the 3D structures of biomolecules like proteins and nucleic acids.

- **CN3D**, **PyMOL**, **RasMol**: Molecular visualization tools for viewing and manipulating 3D macromolecule structures.
- **MODELLER**: A tool to predict protein structures based on known homologous structures.

3. Function Analysis Tools

These tools help understand gene/protein functions, interactions, and biological pathways.

- **GEO**: A public repository for gene expression data, including tools to analyze gene expression datasets.
- **InterProScan**: Scans protein sequences against databases to identify functional domains and families.
- **COBRA Toolbox**, **Pathway Tools**: Analyze and simulate metabolic pathways.

4. Other Tools

- **R**: A statistics program and programming language widely used in bioinformatics for data analysis and visualization.

These tools are indispensable for studying biological data, assisting in tasks ranging from sequence analysis to functional predictions and pathway simulations.

Applications of Bioinformatics Tools:

- Study genetic and evolutionary relationships.
- Identify and classify genes, proteins, and metabolic pathways.
- Predict protein structures and functions.
- Assist in drug discovery and disease research.

BLAST

https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Web&PAGETYPE=BLASTHome

BLAST QuickStart: Simplified Guide

What is BLAST?

BLAST (**Basic Local Alignment Search Tool**) finds similar regions between nucleotide or protein sequences. It compares a query sequence to a database and calculates the significance of matches. This chapter introduces BLAST and explains how to use different BLAST programs with step-by-step tutorials.

---

1. Introduction to BLAST

BLAST aligns a **query** sequence (your input) with **subject** sequences (in a database). It **originally worked for proteins but later expanded to nucleotides and even cross-comparisons between them.**

- **Web & Standalone Versions**: Available at NCBI.
- **Genome Searches**: BLAST can scan entire genomes, including human, mouse, rat, and plants like *Arabidopsis thaliana*.

1.1 Query and Database Formats

- Sequences use **FASTA format** (starts with > followed by an identifier).
- BLAST databases are built from FASTA sequences using **formatdb**.

1.2 Scoring Alignments

- Alignments pair letters (nucleotides or amino acids) between sequences.
- **Scoring:**
    - **Protein matches** use **substitution matrices** (e.g., *BLOSUM62*, *PAM*).
    - **Nucleotide matches**:
        - Identical letters: +2 points
        - Mismatches: -3 points
    - **Gaps**: Have penalties, with new gaps costing more than extensions.

1.3 How BLAST Works

- **Indexing:** BLAST breaks the query sequence into small words (default: **3 for proteins, 11 for nucleotides**).
- **Search:** It scans the database for exact (nucleotides) or high-scoring (proteins) matches.
- **Extension:** Matches are extended until scores stop increasing or drop too much (*dropoff* value).

1.4 Statistical Significance

- BLAST assigns an **Expect Value (E-value)** to matches:
    - **Higher E-value**: More matches, but lower accuracy.
    - **Lower E-value** (0.001 to 0.0000001): More reliable alignments.
    - **Default = 10** (ensures no important match is missed).

BLAST (**Basic Local Alignment Search Tool**) is a widely used bioinformatics tool for **comparing biological sequences.** Since its release in 1990, it has been continuously updated to improve speed and accuracy. It plays a crucial role in research and has inspired other sequence comparison tools.

Types of BLAST

BLAST has five main types, depending on whether the query and database sequences are DNA or protein:

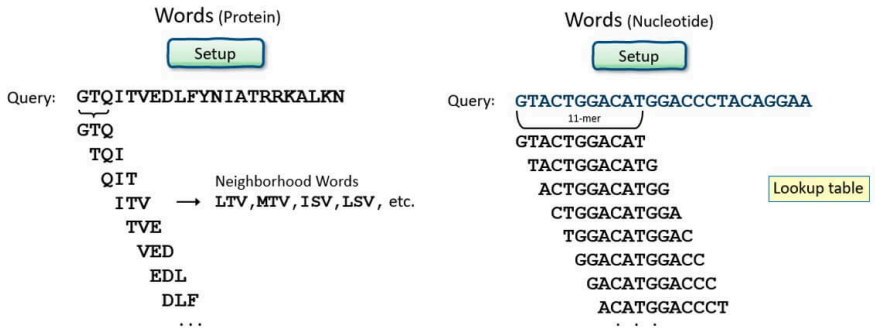
1. **BLASTN** – Compares a **nucleotide** query to a **nucleotide** database.
2. **BLASTP** – Compares a **protein** query to a **protein** database.
3. **BLASTX** – Translates a **nucleotide** query into six protein reading frames and compares it to a **protein** database.
4. **TBLASTN** – Translates a **nucleotide** database into six protein reading frames and compares it to a **protein** query.
5. **TBLASTX** – Translates both the **nucleotide** query and **nucleotide** database into six protein reading frames and compares them.

BLAST compares a query sequence to a database to find similarities using a fast, heuristic approach.

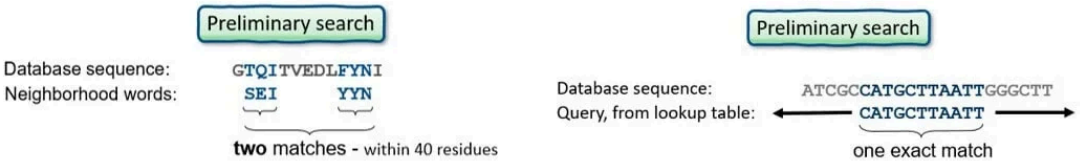
Steps in BLAST Alignment

1. **Seeding** – The query sequence is broken into short segments (**words**) for searching:

    - **Protein:** 3 amino acids per word
    - **DNA:** 11 nucleotides per word



2. **Searching** – The database is scanned for sequences containing matching words.



3. **Scoring** – Matches are scored using **substitution matrices**:

    - **Protein:** Uses **PAM or BLOSUM matrices.**
    - **Nucleotide:** Uses match-mismatch scoring.
    - Matches above a certain threshold are considered significant.
4. **Alignment Extension** – Matching words are extended in both directions while tracking alignment scores.

    - If the score drops below a threshold, extension stops.
    - The highest-scoring segment pair (HSP) is recorded.
5. **Statistical Significance (E-value)** – BLAST calculates the **Expect Value (E-value)**, which represents the probability of a random match:

    - **Lower E-value** = More significant match.
    - **Higher E-value** = More likely a random match.

Key Features of BLAST

- **Fast & Efficient** – Handles large databases quickly.
- **Versatile** – Works with both nucleotide and protein sequences.
- **Highly Sensitive** – Detects even small sequence similarities.
- **Local Alignment** – Focuses on similar regions rather than full-sequence alignment.
- **User-Friendly** – Easy to input sequences and interpret results.

Applications of BLAST

- **Identifying Unknown Sequences** – Compares sequences to known databases to predict gene or protein function.
- **Phylogenetic Analysis** – Helps determine evolutionary relationships between species.
- **Detecting Conserved Protein Domains** – Finds functional regions within proteins.

BLAST is an essential tool for genetic research, evolution studies, and functional genomics.

ATGCGCCTCCATCCTCGCCTGCCTTCTCTCGGTCCCTCGTGATTGATTCCACCCTTGCTTCCCCTTTC

TCCGCGCCGCCTGTTCCGTGCTCGTTTTCCCCTCTTCCTCCTTAAGTCTGGTCCTTCCACCCCCTCCTCT

TCAAGCTGTGCGTGTCCCCTGATTCTAATGCTTTCTGTGTAACTCATTGAAACTGCGTTCTGGTTCCCCT

CCCGCGTCCATTCTCCATTCATGCGCGACCGCCCTTCCCGCGCCCCAGTTCCCTCTCGCCGCCCCTCCCC

CTGCTTGCTGGTCACGTCCGCTCCCCCGCATCCCCTTCCTCGCCTGGCGTGTCCGCTCCCTCCCTCCCTC

TCTGCTCTGGTCGCGCCCGCCCACTTGCTCCGGTCTCCGAGCGCGGTCCCACCCCCCTTTTCCATCACCG

CCTCCCAGCTCCCAGCAGGCTCGGGCGGTGCTGAGGCCCCGTGTCCGGGGCGGGCGGGCGGAGGGCTGGG

CTGGGTGCCCCGCGCGGCGGGCGGGATGCGGCGGCCCGGGGGCAGCTGGAGACTTACGTAACGTTGGCCT

GCCCCGCTGCCGGGAGGCAGGGCGGTTGCCCCTGCGGCGCGGTGCCGTCCCCTGTGGCCGGGATTAGATG

GGCGGCCTGCGAGGGCCTGGGAATGGCTCGGGGCCCGAGAGCTCGACCGGCCCTTGCCGGGTGGCCGCCA

GGGACCACGCTCCATCTCGCCGCGGCCGGGCTGCACGTAGCGGCCGCGCCCAGGGCCCACCCCGCTTCAC

CGGGCGATGGCCTTGGGCCTCGTAACGGGCGGGATAAACCTCTGCAGGCTTTGCTGGGGCCTCCTGGCCC

TCGCCCGTTCCGCGCCTCTCCGGCACGTTTCTTTCTTTTCCTTTCTTTTTTCTTTCTTTTTTTTTTTTTT

AATTATCCGGCACATTTTTTAACAAATGCGTCCTGATTGTGGAACGCGGAGGCCGCGGGGTGGGGTGGGG

ATCTGGTTACGGAGGGGGCAGGAAATCTGTCGCGTTCACTGAACGCAAACGGTGTGGGTCAAGGGCTGTT

TGGGGGTCAGAGTTAGAGACCAGGATGACTAGACGAGTCATAGCCCACCGAGCTCACAATCTTAAAATGT

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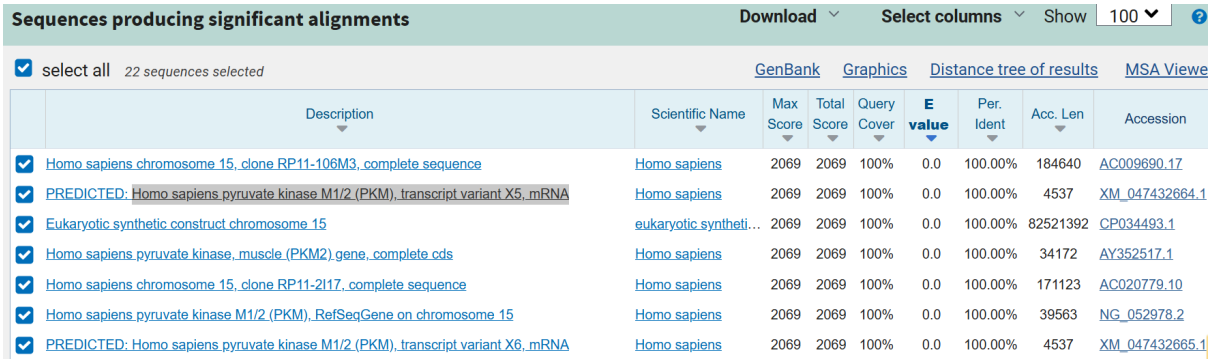


Sequences producing significant alignments Download Select columns Show 100

select all *22 sequences selected* GenBank Graphics Distance tree of results MSA Viewe

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
Homo sapiens chromosome 15, clone RP11-106M3, complete sequence	Homo sapiens	2069	2069	100%	0.0	100.00%	184640	AC009690.17
PREDICTED: Homo sapiens pyruvate kinase M1/2 (PKM), transcript variant X5, mRNA	Homo sapiens	2069	2069	100%	0.0	100.00%	4537	XM_047432664.1
Eukaryotic synthetic construct chromosome 15	eukaryotic syntheti…	2069	2069	100%	0.0	100.00%	82521392	CP034493.1
Homo sapiens pyruvate kinase, muscle (PKM2) gene, complete cds	Homo sapiens	2069	2069	100%	0.0	100.00%	34172	AY352517.1
Homo sapiens chromosome 15, clone RP11-2I17, complete sequence	Homo sapiens	2069	2069	100%	0.0	100.00%	171123	AC020779.10
Homo sapiens pyruvate kinase M1/2 (PKM), RefSeqGene on chromosome 15	Homo sapiens	2069	2069	100%	0.0	100.00%	39563	NG_052978.2
PREDICTED: Homo sapiens pyruvate kinase M1/2 (PKM), transcript variant X6, mRNA	Homo sapiens	2069	2069	100%	0.0	100.00%	4537	XM_047432665.1

In Homo sapiens, pyruvate kinase M1/2 (PKM) is encoded by the PKM gene, and transcript variant X5, which encodes the M2 isoform, is a key enzyme in glycolysis, catalyzing the conversion of phosphoenolpyruvate to pyruvate.

Gene Expression Tools and Databases for Gene Expression:

https://www.ncbi.nlm.nih.gov/geo/

https://www.ncbi.nlm.nih.gov/sra

https://www.ebi.ac.uk/biostudies/arrayexpress

https://www.ebi.ac.uk/gxa/home

CLUSTAL-W

The sensitivity of the commonly used progressive multiple sequence alignment method has been significantly improved for aligning divergent protein sequences. Several key improvements have been made:

1. **Sequence Weighting**: Each sequence in a partial alignment is given a weight to reduce the influence of nearly identical sequences and increase the focus on more divergent sequences.

2. **Dynamic Amino Acid Matrices**: The amino acid substitution matrices are adjusted throughout the alignment process based on the divergence of the sequences.

3. **Gap Penalties**: Specific gap penalties are applied depending on the residue's location, with reduced penalties in hydrophilic regions and early alignments where gaps are already introduced. This encourages the opening of new gaps in potential loop regions.

4. **Reduced Gap Penalties in Early Alignments**: Gaps opened early in the alignment receive reduced penalties to allow new gaps to form in those positions.

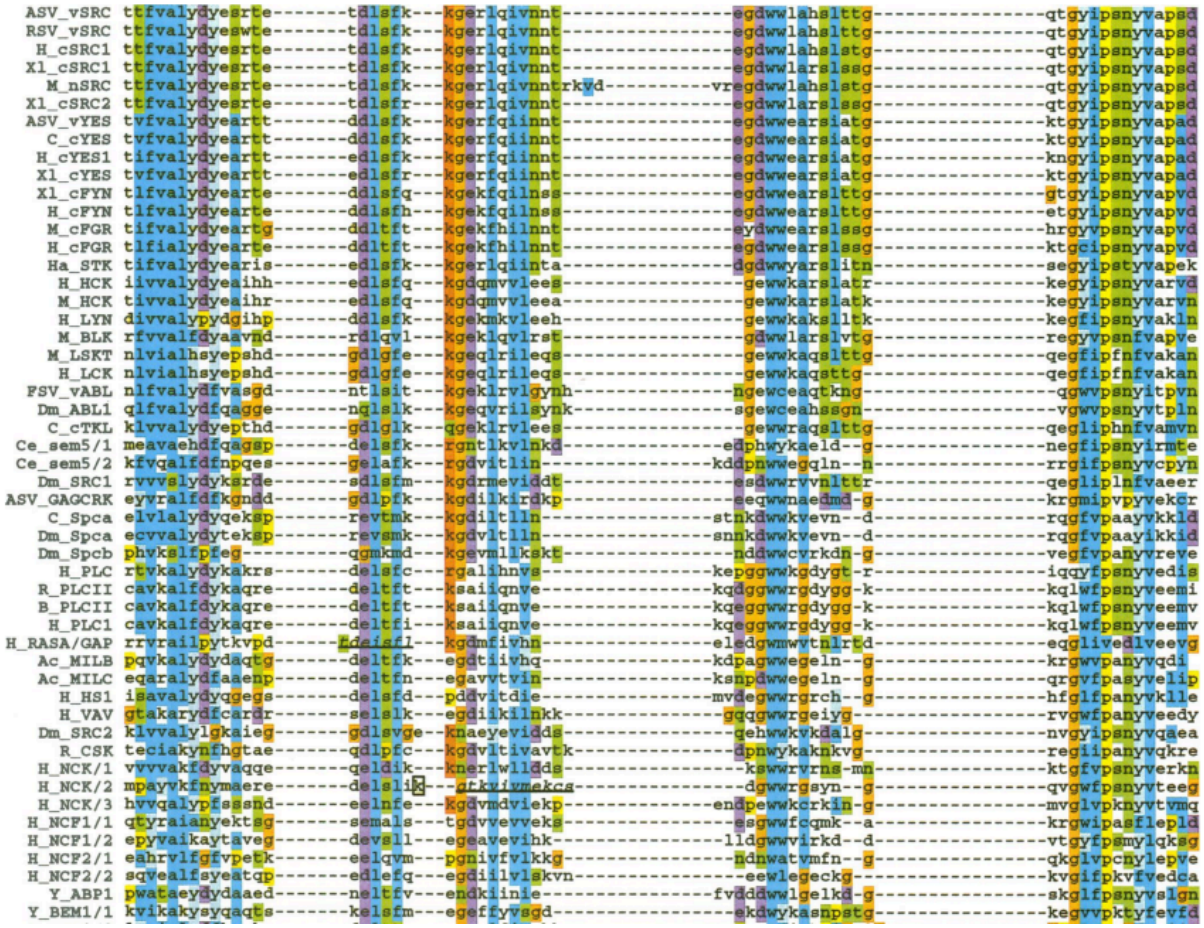
These changes have been integrated into the CLUSTAL W program, which is freely available.

Introduction

Multiple sequence alignment is essential in molecular biology, helping to find diagnostic patterns, detect sequence homology, predict protein structures, and support evolutionary analysis. With the increase in new sequence data, the need for efficient, accurate alignment methods has grown. The majority of automatic multiple alignments are now done using the "progressive" approach, which is fast and practical.

In contrast to aligning just two sequences using dynamic programming, which guarantees an optimal alignment, multiple alignments are more complex. For more than eight sequences, current computer power makes direct solutions impractical. Instead, heuristic methods are used, where sequences are aligned progressively based on their evolutionary relationships.

The progressive approach first aligns the most similar sequences and gradually adds more distant ones. This method is fast, works well for data sets with varying degrees of sequence divergence, and gives accurate results for closely related sequences. For more divergent sequences, the initial alignments provide a good starting point for further refinement.



https://www.ebi.ac.uk/jdispatcher/msa/clustalo

https://www.genome.jp/tools-bin/clustalw

The progressive multiple sequence alignment method works well for closely related sequences but becomes less reliable for distantly related ones, especially when sequences share less than 25-30% identity. The method faces two main issues:

1. **Local Minimum Problem**: The greedy approach used in the alignment process can lead to early misalignments that carry through the process and can't be corrected as more sequences are added. This happens due to errors in initial alignments and the incorrect branching order of the guide tree.

2. **Alignment Parameter Choice**: Selecting the right alignment parameters is crucial. Traditional approaches use one weight matrix and gap penalties for all sequences, which works for closely related sequences but not for divergent ones. For highly divergent sequences, different weight matrices and gap penalties are required, as the correct alignment depends on these parameters.

Improvements have been made to dynamically adjust gap penalties based on residue type and position, making the alignment process more accurate, especially for more divergent sequences. Additionally, the use of the Neighbour-Joining method for building guide trees provides more reliable branch lengths, improving alignment sensitivity. These updates make the alignment process more robust and flexible for diverse datasets.

Improvements to the progressive alignment method focus on refining gap penalties and sequence weighting during the final alignment stage:

1. **Sequence Weighting**: Weights are assigned based on the guide tree, with closely related sequences given lower weights and more divergent ones given higher weights. This helps in scoring positions accurately.

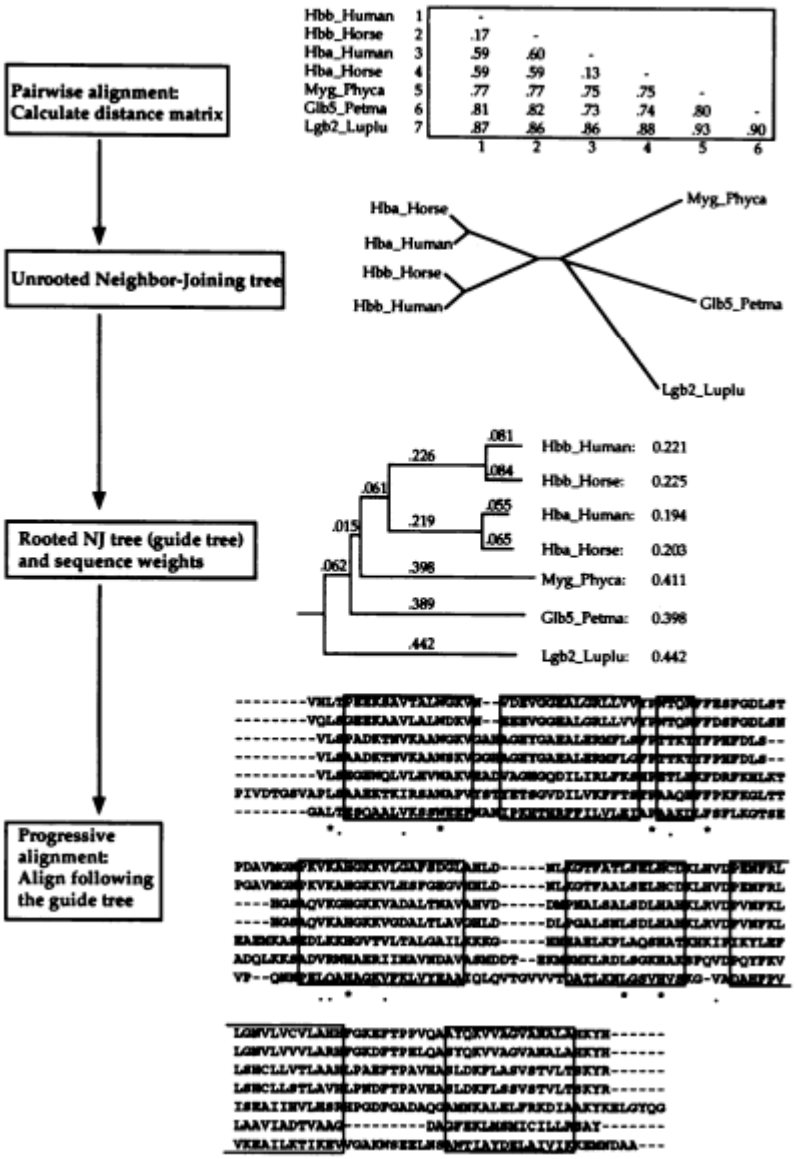
2. **Gap Penalties**: Gap penalties are adjusted depending on factors like sequence similarity, length, and hydrophilic regions. For example, gap penalties are reduced near existing gaps, increased near other gaps, and lowered in hydrophilic stretches that indicate loop regions in proteins.

3. **Weight Matrices**: Different weight matrices (e.g., BLOSUM or PAM) are used as the alignment progresses, depending on the evolutionary distance between sequences.

4. **Divergent Sequences**: Very divergent sequences (with less than 40% identity) are added later in the alignment process to avoid misalignments in the early stages.

5. **Dynamic Programming**: The alignment uses a memory-efficient dynamic programming algorithm that can handle long sequences with less memory, though it sacrifices some processing speed. This allows large datasets to be aligned more efficiently.

These adjustments enhance the accuracy and efficiency of aligning both closely and distantly related sequences.



Key Bioinformatics Tools & Databases for Immunology

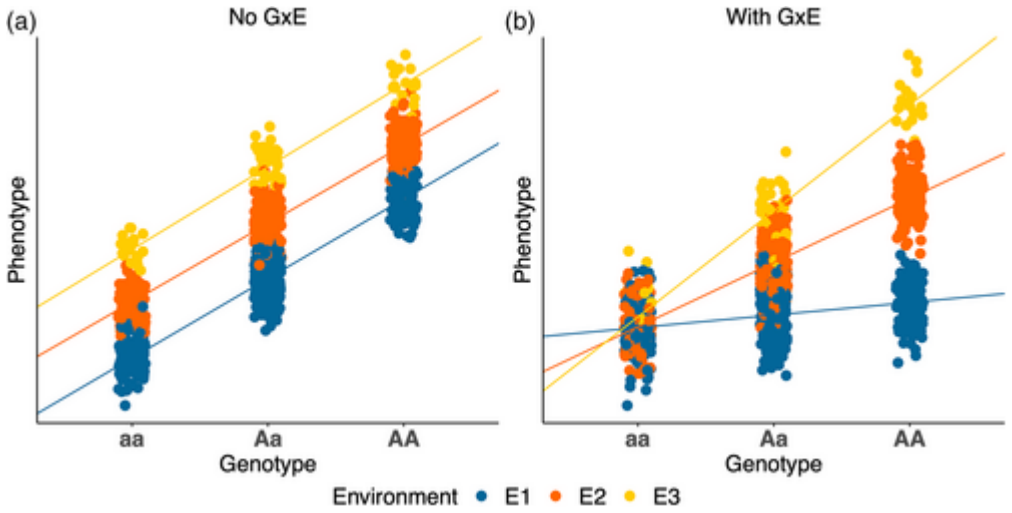
- **Microbiome Analysis:** Tools like **Greengenes, SILVA, and Human Oral Microbiome Database (HOMD)** help identify bacteria in the body.
- **Pathogen Detection:** Tools like **MG-RAST, PathSeq, and ezVIR** analyze sequencing data to find known and unknown viruses, bacteria, and fungi in patient samples.
- **Drug Resistance Studies:** Databases like **CARD, ARDB, and ResFinder** help identify genes that make bacteria resistant to antibiotics.
- https://ardb.cbcb.umd.edu/
- https://card.mcmaster.ca/
- https://www.cancer.gov/ccg/research/genome-sequencing/tcga
- **Pathogenicity & Virulence:** Tools like **PathogenFinder and PATRIC** help predict whether a newly discovered bacterium is harmful.
- https://cge.food.dtu.dk/services/PathogenFinder/

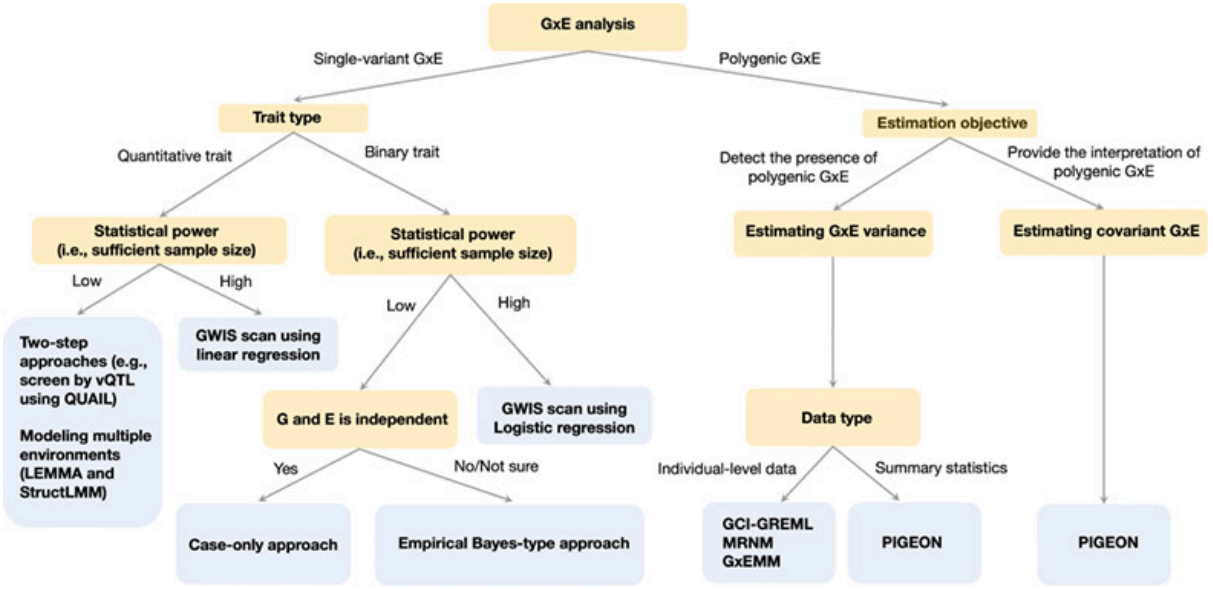
- https://www.mg-rast.org/

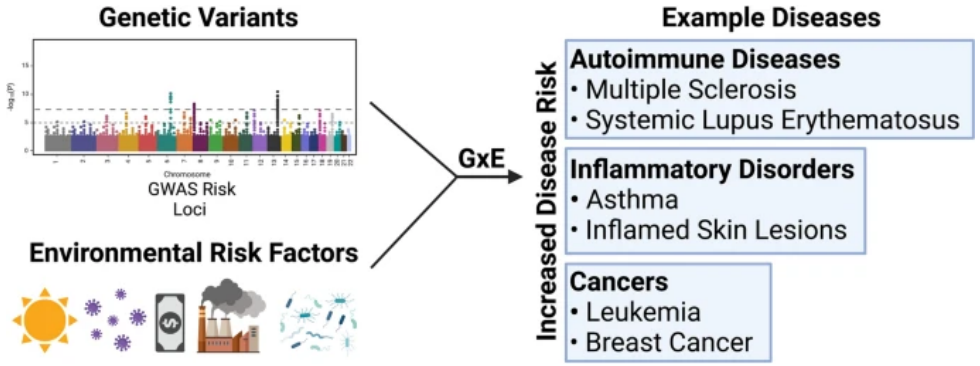
Important Tools and Links:

https://www.genscript.com/conversion.html#p2

https://en.wikipedia.org/wiki/List_of_bioinformatics_software







Location	Latitude (°N)	Longitude (°E)	Altitude (m)	Soil texture	Min and max daily Temp (°C)	Average annual rainfall (mm)
Abakaliki	6° 19′ 30N	8° 6′ 49E	116	Sandy loam	26.2 – 29.0 °C	1800.3
NRCRI Iresi	7°30′0″N	4°30′0″ E	246	Sandy loam	24.7 – 27.8 °C	2024.1

Umudike: Agro-meteorological Unit, National Root Crops Research Institute, Umudike, Abia State.

Sources of variation	Mean squares								
	Degrees of freedom	Number of marketable roots	Number of unmarketable roots	Total root number	Wt. of marketable roots	Wt. of unmarketable roots	Total root weight	Root yield	Cylas severity
Rep	2	16.0733	4.6426	11.4314	2.6747	0.0328	3.2441	109.1065	1.9259
Year	1	34.7041^{ns}	741.3983***	1071.2141**	1.7998ns	0.1894*	3.4475ns	52.1796ns	2.5556*
Genotype	40	75.1750***	109.0174***	280.1644***	4.7343***	0.0562*	5.0521***	83.1419***	0.4375ns
Gen. × Year	40	41.8796**	72.6024**	169.7607**	3.2940**	0.0387ns	3.6141**	43.1045ns	0.5001ns
Error	120	23.5595	40.3275	91.2070	1.3839	0.0328	1.5771	30.6534	0.4303

**means significant at P = 5%; **means Highly significant at P = 1%; ***means Very highly significant at P = 0.1%.*
Wt., weight; ns, not significant.

Field Layout and Experimental Design:

The trial used a randomized complete block design (RCBD) with three replications. Each plot consisted of three rows, each 3 meters long, with 1 meter between rows and 0.3 meters between plants, totaling 30 plants per plot. The sweet potato was planted in June and harvested in October in 2018 and 2019 at two locations: Abakaliki (rainforest) and Iresi (savannah). Fertilizer (NPK 15:15:15) was applied at 400 kg/ha, and weeding was done as needed.

Quality Traits Analysis:

Sweet potato genotypes were tested for chemical traits in Abakaliki. Dry matter, protein, fiber, and ash content were measured using standard methods, while fat content was determined by Soxhlet extraction. Carbohydrate content was assessed using the Gravimetric Copper Reduction Method, and total carotenoid content was measured by a specific procedure.

Data Collection and Analysis:

Agronomic data like the number and weight of marketable and unmarketable roots and root Cylas severity were recorded. The data were analyzed using ANOVA with SAS 9.2, treating genotype as a fixed factor and replication as random. Marketable roots were those weighing ≥100g or ≥25mm in diameter. Root yield was calculated in tons per hectare. Cylas severity was rated on a 1-5 scale based on the level of damage to plants.

The data were analyzed by location due to variance differences, then combined for genotype × environment interaction analysis. The ANOVA model considered genotype, year, and block effects, with random error included.

The ANOVA model used for the single-site analysis is as stated below:

$$Y_{ij} = \mu + \alpha_i + \gamma_j + \beta_k + e_{ij}$$

where

y_{ij} = observation on experimental unit in block *k* assigned treatments *i and j*;
μ = overall mean averaged over all treatments and all blocks;
α_i = effect of genotype *i;* considered as fixed variable;
γ_j = effect of year *j* considered as random variable;
β_k = effect of block *k* considered as random variable;
e_{ijk} = random error associated with experimental units assigned to treatments *i and j* in block *k*.

Traits	Vg	Vgy	Ve	Vp	H_B
Number of marketable roots	8.87	−3.74	23.56	12.89	0.69
Number of unmarketable roots	0.18	1.62	40.33	11.07	0.02
Total root number	12.34	4.69	91.21	37.49	0.33
Wt. of marketable roots	1.10	0.07	1.38	1.48	0.74
Wt. of unmarketable roots	0.00	0.00	0.03	0.01	0.00
Total root wt	1.11	0.13	1.58	1.57	0.71
Root yield	16.47	−7.44	30.65	20.42	0.81
Cylas severity	0.01	−0.01	0.43	0.11	0.08

Variance components and broad-sense heritability estimates of agronomic traits of sweet potato genotypes evaluated at Abakaliki, Ebonyi State across 2 years.

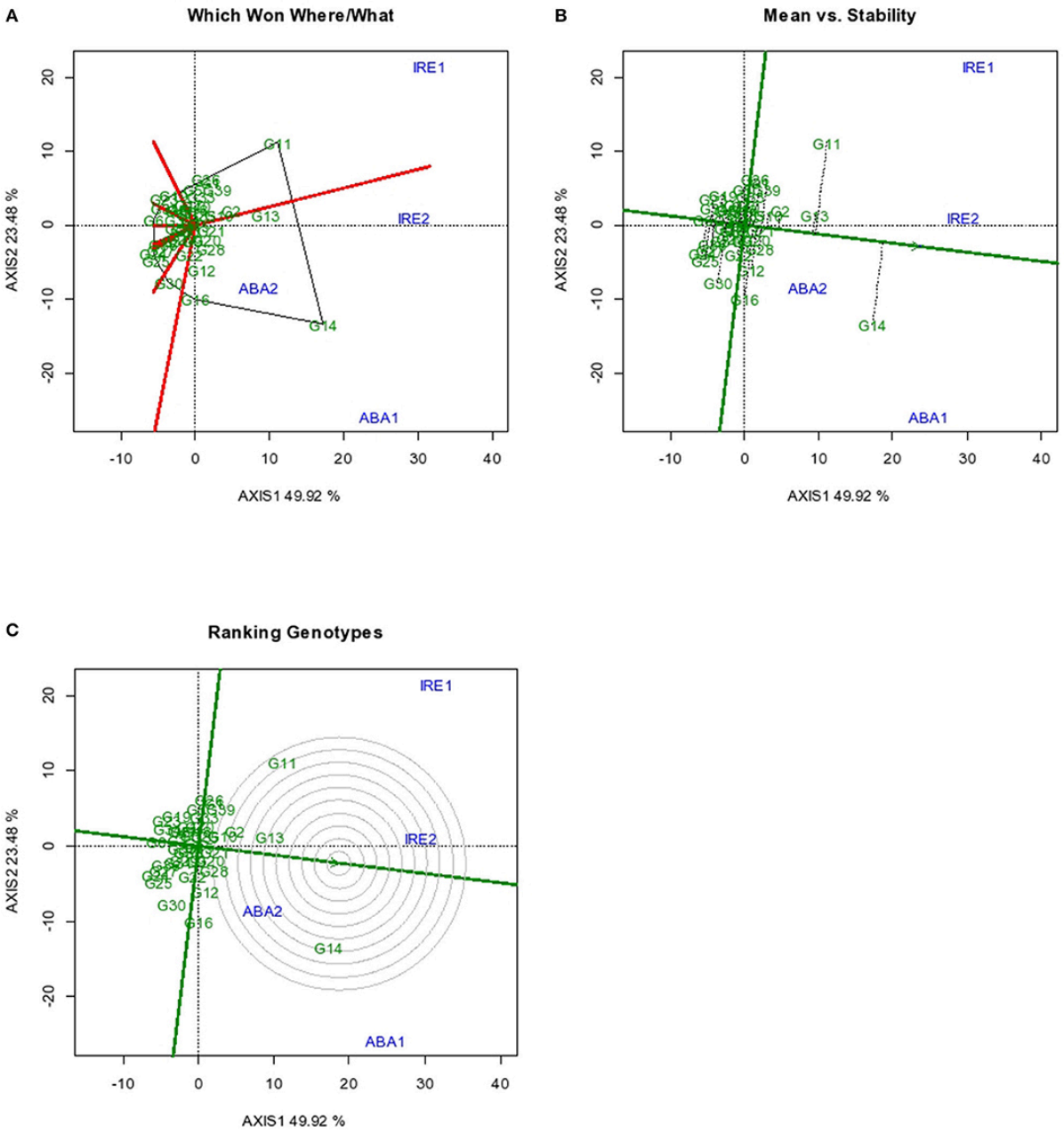


Figure 1: GGE Biplot for Root Yield

- **(A)** Identifies the superior genotype for each environment.
- **(B)** "Mean vs. Stability" shows that G14 had the highest mean root yield, followed by G11 and G13. G13 was the most stable, while G11 and G14 showed more variability. Stable genotypes with high yield are preferred.
- **(C)** Ranking of genotypes indicates that G13, with high yield and stability, is closest to the ideal genotype, though G14 had the highest yield.

https://www.youtube.com/watch?v=BFDyqtLvt7A