

EVIDENCES OF UNIQUE MODES OF ASSESSMENTS ADOPTED DEPARTMENTS

Course coordinator – Dr Shaiesh Morajkar

Subject: Biotechnology

Semester: VI

Course Title: Industrial Biotechnology

Course Code: BIO-VI.C-8

An innovative method used in teaching learning and evaluation method–**Display Model Building**

Using model-making as a tool for learning and evaluation as this hands-on approach bridges the gap between theory and practical application, while enabling the following:

1. **Hands-On Learning:** Engage students actively, promoting kinesthetic learning, which helps reinforce theoretical concepts and aids retention.
2. **Enhances Creativity and Problem-Solving:** encourages to think critically and solve design challenges, fostering creativity and innovation.
3. **Visual and Spatial Understanding:** helps understand complex structures, spatial relationships, and proportions
4. **Improves Collaboration:** In group model-making promotes teamwork, communication, and collaborative problem-solving.
5. **Effective Evaluation Tool:** provides a tangible output for assessing students' comprehension, creativity, and ability to apply theoretical knowledge practically.

The following were the rubrics used:

1. Display Model –
 - a. Accuracy of representation
 - b. Materials used
 - c. Interpretability
2. Detailed report
3. Innovation from existing working models



DEPARTMENT OF BOTANY

Assignments as a Comprehensive Mode of Assessment

Assignments were conducted as a key mode of assessment, providing students with the opportunity to delve deeply into topics and apply their knowledge in practical contexts. These assignments were designed in various formats, including research papers, essays, and creative projects, allowing for flexibility and fostering creativity. This approach encouraged critical thinking and problem-solving skills, as students analyzed information, synthesized ideas, and presented their findings in a coherent manner.

To ensure a structured evaluation process, rubrics and assessment dates were communicated well in advance through classroom instructions and the Google Classroom platform. Marks were allocated based on specific criteria such as introduction, content, summary, references, and plagiarism.

Understanding the importance of academic integrity, anti-plagiarism tools and strategies were incorporated to reinforce originality and honesty. While plagiarism undermines the assessment process, analyzing instances of it provided educators with insights into student learning patterns, enabling tailored feedback and personalized learning approaches.

This comprehensive method of assessment promoted independent learning, time management, and deeper subject understanding, while equipping students with essential skills for academic and professional success.



PARVATIBAI CHOWGULE COLLEGE
OF ARTS AND SCIENCE

BIOINFORMATICS

BOT-V.E-9

CA1-ASSIGNMENT

**ALPHABET AND COMPLEXITY; PAIRWISE
DATABASE SEARCHING; BLAST**

SNEHAL PATIL

2102444

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INTRODUCTION

A Sequence alignment is a way of arranging primary sequences of DNA, RNA or Proteins to identify regions of similarity that may be consequences of functional, structural and evolutionary relationship between the sequences. It is the procedure of comparing two or more sequences by searching for a series of individual characters/patterns that are in the same order of the sequences. The sequence alignment is made between a known sequence and a unknown sequence or between two unknown sequences. The known sequence is called 'reference sequence' and the unknown sequence is called the 'query sequence'. Based on the number of comparing sequencing strand, sequence alignment is of two types: Pair-wise alignment and multiple sequence arrangement.

BLAST (Basic Local Alignment Search Tool), is a database search tool, developed and maintained primarily by the National Centre of Biotechnology Information (NCBI). The web-based tool is available at <http://www.ncbi.nlm.nih.gov>. BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance. BLAST can be used to infer functional and evolutionary relationships between sequences as well as help identify members of gene families.

•

PAIR-WISE SEQUENCE ALIGNMENT

Pair-wise sequence alignment is to arrange two sequences in such a fashion that pairs of matching characters between the two sequences are maximized. It is used to identify regions of similarity that may indicate functional, structural and/or evolutionary relationships between two biological sequences (protein or nucleic acid). To achieve this, one sequence needs to be shifted relative to the other to find the position where maximum matches are found.

There are two different pair-wise alignment strategies that are often used:

- a) Global alignment
- b) Local alignment

Global alignment

In Global alignment, two sequences to be aligned are assumed to be generally similar over their entire length. Alignment is carried out from the beginning to the end of both sequences to find the best possible alignment across the entire length between the two sequences. This method is more applicable for aligning two closely related sequences of roughly the same length. For divergent sequences and sequences of variable length, this method may not be able to generate optimal results because it fails to recognize highly similar local regions between the two sequences.

```
  L G P S S K Q T G K G S - S R I W D N
  |           | | | |           | |
  L N - I T K S A G K G A I M R L G D A
```

Global alignment

Local alignment

Local alignment, on the other hand, does not assume that the two sequences in question have similarity over their entire length. It only finds the local region with the highest level of similarity between the two sequences and aligns these regions without regard for the alignment of the rest of the sequence regions. This approach can be used for aligning more divergent sequences with the goal of searching for conserved patterns in DNA or protein sequences. The two sequences to be aligned can be of different length. This approach is more appropriate for aligning divergent biological sequences containing only modules that are similar.

```
  - - - - - T G K G - - - - -
           | | |
  - - - - - A G K G - - - - -
```

Local alignment

The biological sequences used for alignment, use many alphabets and involve many complexities.

ALPHABET AND COMPLEXITY

A sequence consists of letters selected from an alphabet. The complexity involved here is the number of different letters it uses. For example:

Complexity of English alphabet	26 (A to Z)
Complexity for DNA	4
Complexity for EST work	5
Complexity for protein	20
Additional characters are also used in an alphabet to indicate a degree of ambiguity in the identity of particular residue of base, Example: ⇒ Frequent additional characters in protein sequences ⇒ Either asparegene or aspirate (Asx) ⇒ Either glutamine or glutamate	 X B Z

Some alignment programs will deal with these characters as they stand, other will simply replace such ambiguities with dummy character.

PAIRWISE DATABASE SEARCHING

Performing a comparison of one sequence against a database of many thousands can be viewed as simply an extension of pair-wise alignment. Achieving a database search in an efficient manner is not trivial, as datasets gets larger, and more effort is being spent to try to improve efficiency. To perform a Needleman and Wunsch, or Smith-Waterman, which are the local alignment methods for the pair-wise sequence alignment, alignment is practicable for small numbers of sequences, but for large database searches the methods can become prohibitively time consuming.

Implementations of the Smith-Waterman algorithm have been developed for specialized computer hardware (for example, MPSrch running on the massively parallel MasPar supercomputer); however, these systems are expensive and rapidly become obsolete as hardware architectures develop and move on. Speed of execution is certainly an issue for database searching, and for both algorithms, described so far, speed depends critically on the length of the query sequence and on the size of the database searched. Hence different programs and tools are introduced that concentrate on finding short identical matches, which may contribute to a total match, using implementations that address issues of execution speed, without resorting the use of specialized computer hardware.

TOOLS AND DATABASES USED FOR PAIR-WISE DATABASE SEARCHING

1. ACANA

ACANA is an accurate and consistent alignment tool for DNA sequences. ACANA is specifically designed for aligning sequences that share only some moderately conserved regions and/or have a high frequency of long insertions or deletions. It attempts to combine the best of local and global alignments algorithms in searching for evolutionarily related regions of sequences in order to achieve the best alignment.

2. LALIGN

LALIGN finds internal duplications by calculating non-intersecting local alignments of protein or nucleotide sequences.

<https://www.ebi.ac.uk/Tools/psa/lalign/>

The screenshot displays the LALIGN web interface. At the top, there is a teal header with the 'LALIGN' logo and navigation links for 'Input form', 'Web services', 'Help & Documentation', 'Bioinformatics Tools FAQ', and 'Feedback'. Below the header, a breadcrumb trail reads 'Tools > Pairwise Sequence Alignment > LALIGN'. A light blue service announcement box contains text about a new Job Dispatcher Services beta website. The main heading is 'Pairwise Sequence Alignment', followed by a brief description: 'LALIGN finds internal duplications by calculating non-intersecting local alignments of protein or nucleotide sequences.' The interface is divided into two steps. 'STEP 1 - Enter your protein sequences' includes a dropdown menu for 'Enter a pair of' (currently set to 'PROTEIN') and a text area for 'sequences. Enter or paste your first protein sequence in any supported format:'. Below this is an option to 'upload a file' with a 'Choose File' button and 'No file chosen' text, along with links for 'example sequence', 'Clear sequence', and 'See more example inputs'. An 'AND' separator is followed by a second text area for 'sequences. Enter or paste your second protein sequence in any supported format:' and another 'upload a file' option.

LALIGN Website

3. EMBOSS Needle

EMBOSS Needle reads two input sequences and writes their optimal global sequence alignment to file. Needle is an alignment tool used by Bioinformaticians. It is a pairwise alignment tool; design to write the optimal global alignment. It's one of the sub-software/tool which is available in EMBOSS.

https://www.ebi.ac.uk/Tools/psa/emboss_needle/

The screenshot shows the EMBOSS Needle web interface. At the top, there is a teal header with the title "EMBOSS Needle" and navigation links for "Input form", "Web services", "Help & Documentation", "Bioinformatics Tools FAQ", and "Feedback". Below the header, a breadcrumb trail reads "Tools > Pairwise Sequence Alignment > EMBOSS Needle". A light blue box contains a "Service Announcement" about a new beta website. The main content area is titled "Pairwise Sequence Alignment" and includes a brief description: "EMBOSS Needle reads two input sequences and writes their optimal global sequence alignment to file." The interface is divided into two steps. "STEP 1 - Enter your protein sequences" is currently active. It features a dropdown menu labeled "Enter a pair of" with "PROTEIN" selected. Below this is a large text area for the first protein sequence, with a prompt: "sequences. Enter or paste your first protein sequence in any supported format:". Underneath the text area is a file upload option: "Or, upload a file: Choose File No file chosen". To the right of the upload option are links for "Use a example sequence", "Clear sequence", and "See more example inputs". The second step, "AND", is partially visible and prompts for a second protein sequence in a similar format.

EMBOSS Needle Website

4. SIM

SIM finds k best non-intersecting alignments between two sequences or within a sequence using dynamic programming techniques. The alignments are reported in order of decreasing similarity score and share no aligned pairs. SIM requires space proportional to the sum of the input sequence lengths and the output alignment lengths, so it accommodates 100,000-base sequences on a workstation.

<https://web.expasy.org/sim/>

SIM - Alignment Tool for Protein Sequences

SIM is a program which finds a user-defined number of best non-intersecting alignments between two protein sequences or within a sequence [more].

Once the alignment is computed, you can view it using LALNVIEW, a graphical viewer program for pairwise alignments [reference to LALNVIEW].

Note: You can use the PBIL server to align nucleic acid sequences with a similar tool.

Enter two sequences:

These sequences may either be specified by their UniProtKB accession number (AC), e.g. P05130, or by their entry name (ID), e.g. KPC1_DROME, or by pasting your own sequences into the boxes below.

SEQUENCE 1:

UniProtKB AC or ID:

OR

User-entered sequence

Sequence Name:

Paste your sequence below:

SEQUENCE 2:

UniProtKB AC or ID:

OR

User-entered sequence

Sequence Name:

Paste your sequence below:

Parameters:

Number of alignments to be computed:

Gap open penalty:

Gap extension penalty: [documentation]

Comparison Matrix: ▼

Activat
Go to Se

or

SIM Website

5. EMBOSS Stretcher

EMBOSS Stretcher calculates an optimal global alignment of two sequences using a modification of the classic dynamic programming algorithm which uses linear space.

https://www.ebi.ac.uk/Tools/psa/emboss_stretcher/

The screenshot shows the EMBOSS Stretcher web interface. At the top, there is a teal header with the title 'EMBOSS Stretcher' and navigation links for 'Input form', 'Web services', 'Help & Documentation', 'Bioinformatics Tools FAQ', and 'Feedback'. Below the header, a breadcrumb trail reads 'Tools > Pairwise Sequence Alignment > EMBOSS Stretcher'. A light blue box contains a 'Service Announcement' about a new Job Dispatcher Services beta website. The main section is titled 'Pairwise Sequence Alignment' and includes a brief description of the tool. The interface is divided into two steps: 'STEP 1 - Enter your protein sequences' and 'AND'. Each step has a dropdown menu for sequence type (currently set to 'PROTEIN'), a text area for pasting the sequence, and a file upload option with a 'Choose File' button. The first step also includes links for 'Use a example sequence', 'Clear sequence', and 'See more example inputs'.

EMBOSS Stretcher Website

6. EMBOSS Water

EMBOSS Water uses the Smith-Waterman algorithm (modified for speed enhancements) to calculate the local alignment of two sequences.

https://www.ebi.ac.uk/Tools/psa/emboss_water/

The screenshot shows the EMBOSS Water web interface. At the top, there is a teal header with the title "EMBOSS Water" and navigation links for "Input form", "Web services", "Help & Documentation", "Bioinformatics Tools FAQ", and "Feedback". Below the header, a breadcrumb trail reads "Tools > Pairwise Sequence Alignment > EMBOSS Water". A light blue service announcement box contains text about a new beta website. The main content area is titled "Pairwise Sequence Alignment" and includes a brief description of the tool. The interface is divided into two steps: "STEP 1 - Enter your protein sequences". The first step contains a dropdown menu labeled "Enter a pair of" with "PROTEIN" selected. Below this is a large text area for the first protein sequence, with a "Choose File" button and "No file chosen" text. A second step, labeled "AND", contains a similar text area and file upload options for the second protein sequence. At the bottom of the first text area, there are links for "Use a example sequence", "Clear sequence", and "See more example inputs".

EMBOSS Water Website

7. YASS (Yet Another Similarity Searcher)

YASS (Yet Another Similarity Searcher) is a free software, pair-wise sequence alignment software for nucleotide sequences, that is, it can search for similarities between DNA or RNA sequences. YASS accepts nucleotide sequences in either plain text or the FASTA format and the output format includes the BLAST tabular output. YASS uses several transition-constrained spaced seed k-mers, which allow considerably improved sensitivity. YASS can be used locally on a user's machine, or as SaaS on the YASS web server, which produces a browser based dot-plot.

<https://bioinfo.cristal.univ-lille.fr/yass/>

YASS :: genomic similarity search tool

YASS | **web server** | help | download | iedera | retrieve result with an ID

home > DNA > yass

Data [?]

(1/2) Select the *genomic (DNA/RNA) sequence(s)* to be compared with YASS (1 sequence selected = self-comparison)

Upload your sequence(s)
choose your file(s), then press *select*

Choose File No file chosen And/Or Choose File No file chosen

And/Or

Paste your sequence(s)
copy/paste your sequence(s), then press *select*

And/Or

And/Or

Use proposed sequence(s)
choose the species/database (hold down [] shift key + type first letters) and the sequence, then press *select*

-choose species/database- -choose sequence- (files)

(2/2) Please check the *selected DNA sequence(s)*, then run YASS

Selected DNA sequence(s)

(small fasta/multifasta file with few chunks)

(fasta/multifasta file)

If you use this program, please cite : L. Noe, G. Kucherov, YASS: enhancing the sensibility of DNA similarity search, 2005, NAR, 33(2)

YASS Website

8. AlignMe

AlignMe (for sequence Alignment of Membrane Proteins) is a very flexible sequence alignment program that allows the use of various different measures of similarity. AlignMe can be used to examine detailed similarity between homologous proteins if there is no notable sequence similarity. The predefined gap/weight sets have been optimized for membrane proteins, and so should be particularly useful for these difficult cases. This webserver is currently running version 1.2.

<https://www.bioinfo.mpg.de/AlignMe/AlignMePW.html>

NIH National Institute of
Neurological Disorders
and Stroke

AlignMe

Home Sequence to Sequence Alignment Align Two Multiple Sequence Alignments Manual / FAQ

Run AlignMe in pair-wise mode

Generate example input Reset form

1. Provide sequences ⓘ

Enter a sequence in fasta format: Enter another sequence in fasta format:

...or upload a fasta file: ...or upload another fasta file:

Choose File No file chosen Choose File No file chosen

2. Select optimized or user-defined parameters ⓘ

Parameters for α -helical membrane proteins

AlignMe P&T
Most accurate alignments for very distantly related proteins, <15% identity;
-9 mins for a 179 and 215-residue sequence pair

AlignMe P&S
Most accurate alignments for low-homology proteins, -15-45% identity;
-5 mins for a 179 and 215-residue sequence pair

AlignMe P
Most accurate alignments for very closely related proteins, >45% identity;
-5 mins for a 179 and 215-residue sequence pair

Fast, but less accurate alignments (~8 seconds)
based on a substitution matrix and a hydrophobicity scale

Or use your own alignment parameters

Define your own parameters

3. Anchors ⓘ

Residue 1	Residue 2	Weight
<input type="text"/>	<input type="text"/>	1000

...or upload an anchor file?

Choose File No file chosen

AlignMe Website

BLAST (Basic Local Alignment Search Tool)

BLAST (Basic Local Alignment Search Tool) is a heuristic approach for comparing nucleotide or protein sequences. As the name implies, BLAST performs local alignments. The BLAST algorithm and programs were designed by Stephen Altschul, Warren Gish, Webb Miller, Eugene Myers, and David J. Lipman, at the National Center for Biotechnology Information (NCBI) of National Institutes of Health (NIH). In BLAST, PAM (Point Accepted Mutation a.k.a. Percent Accepted Mutation) or BLOSUM (BLOcks SUBstitution Matrix) matrices are used to calculate the sequence similarity (a.k.a. positives).

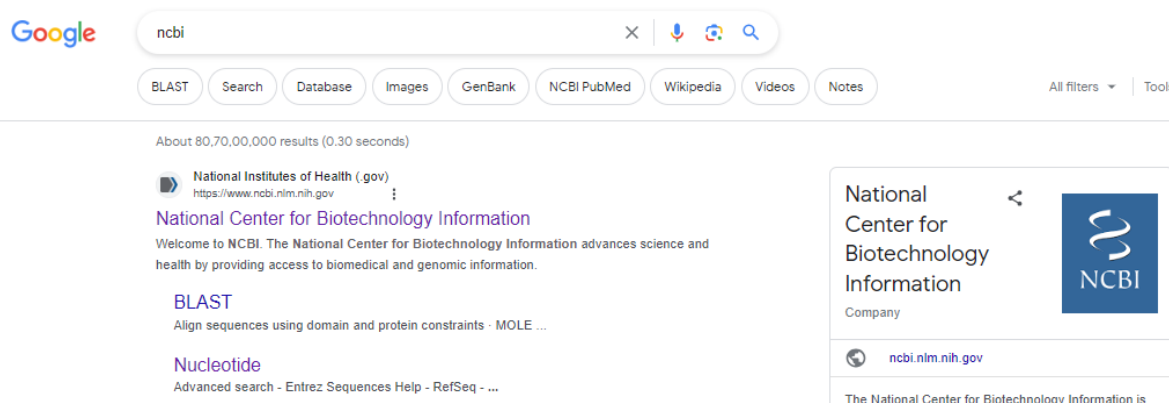
BLAST Programs

There are many different flavors of online/offline/API/cloud BLAST programs as listed below:

- BLASTN program compares the nucleotide query sequence with the nucleotide sequences in the database.
- BLASTP program compares the protein query sequence with the protein sequences in the database.
- BLASTX program translates the nucleotide query sequence and compares with the protein sequences in the database.
- TBLASTN program compares the protein query sequence with the nucleotide sequences in the database, by instantly translating the nucleotide sequences in the database before comparison.
- TBLASTX program compares the translated six reading frames of nucleotide query sequence with the translated six reading frames of nucleotide sequences in the database. The query is translated on the fly before searching sequences in the database.
- MEGA-BLAST program compares the nucleotide query sequence with the nucleotide sequences in the database by optimizing very similar sequences (in the same or in closely related species), first looks for an exact match of 28 bases, and then attempts to extend that initial match into a full alignment.

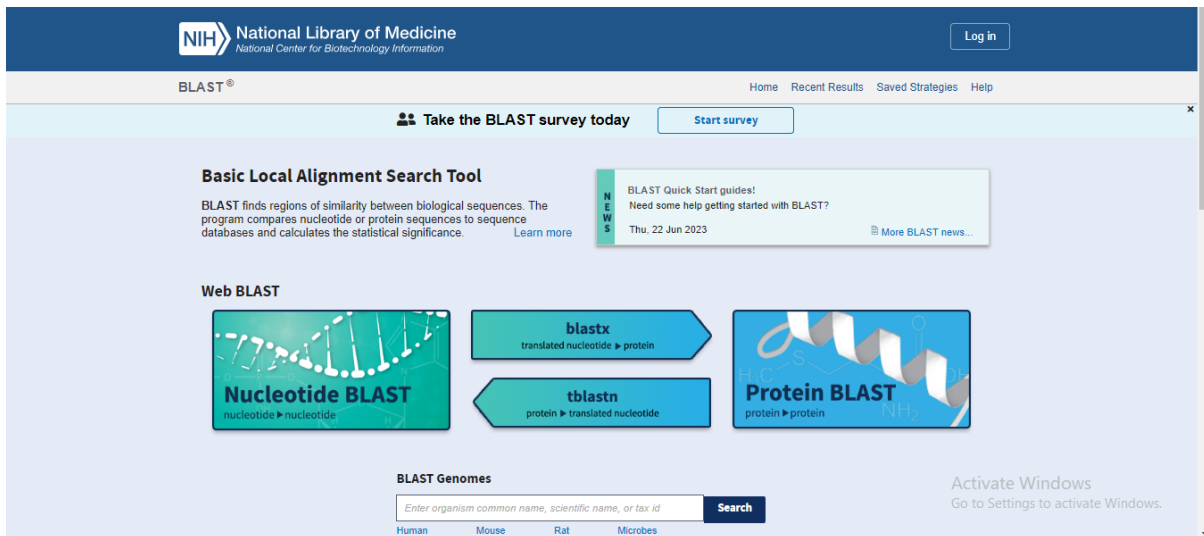
Steps to perform BLAST search

1. In google search box search for NCBI.

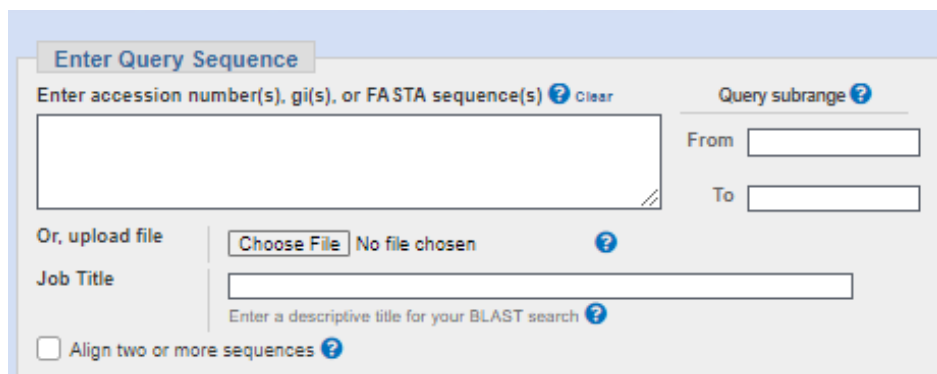


The screenshot shows a Google search for 'ncbi'. The search bar contains 'ncbi' and the search button is highlighted. Below the search bar, there are several filters: BLAST, Search, Database, Images, GenBank, NCBI PubMed, Wikipedia, Videos, and Notes. The search results show 'About 80,70,00,000 results (0.30 seconds)'. The first result is from the National Institutes of Health (NIH) website, titled 'National Center for Biotechnology Information'. The description says 'Welcome to NCBI. The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information.' Below this, there are two links: 'BLAST' with the description 'Align sequences using domain and protein constraints - MOLE ...' and 'Nucleotide' with the description 'Advanced search - Entrez Sequences Help - RefSeq - ...'. On the right side of the search results, there is a card for the National Center for Biotechnology Information (NCBI) with the NCBI logo and the website address 'ncbi.nlm.nih.gov'.

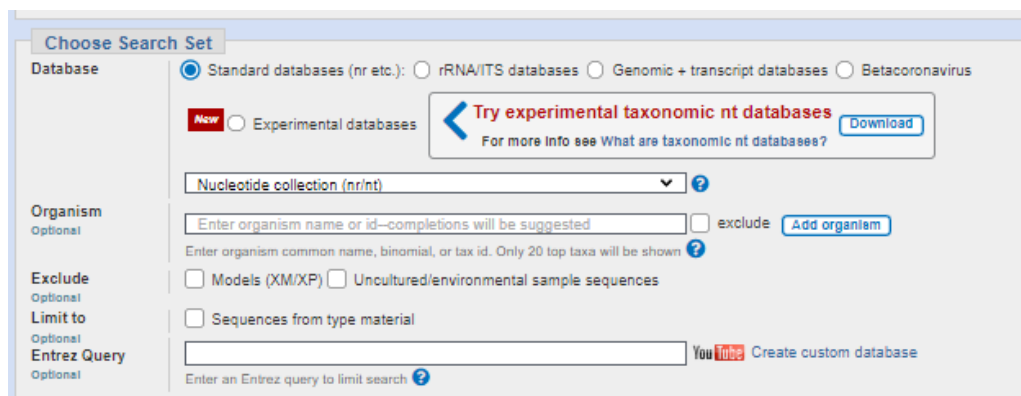
2. Click on BLAST.



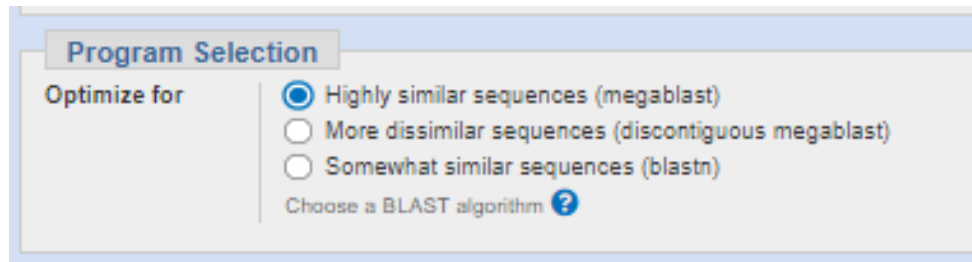
3. Click on the “Nucleotide BLAST” box.
4. In the “Enter Query Sequence” selection box, click “Choose File”.
5. Navigate to a query file on your desktop and click “Choose”. The query file name should appear next to “Choose File”.
6. In the “Job Title” field, enter a unique name for the Blast query.



7. In the “Choose Search Set” selection box, click “Standard databases”.
8. In the drop-down list choose “Nucleotide collection (nr/nt)”. Leave all other fields in their default state.

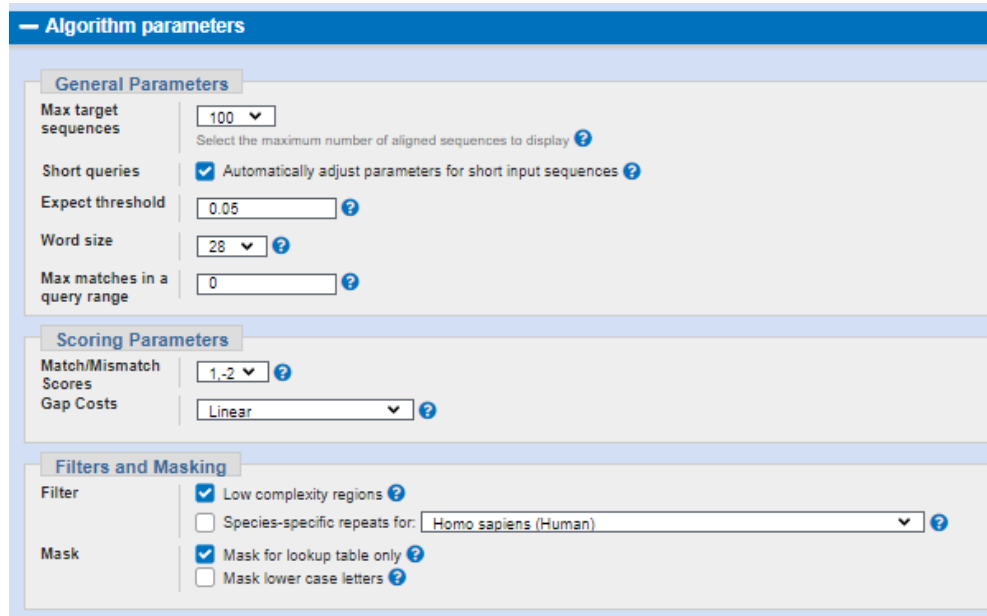


9. In the “Program Selection” selection box, choose “Highly similar sequences (megablast)”.



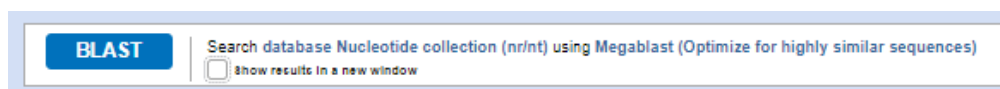
10. Click the plus (“+”) sign by “Algorithm parameters” to expand the parameters list.

11. Ensure that all of the default settings are configured correctly.



12. Click the minus (“-”) sign by “Algorithm parameters” to close the parameters list.

13. Click the “BLAST” button to initiate a Blast search.



Applications of BLAST

BLAST can be used for several purposes. These include identifying species, locating domains, establishing phylogeny, DNA mapping, and comparison.

Identifying species - With the use of BLAST, we can possibly correctly identify a species or find homologous species. This can be useful, for example, when we are working with a DNA sequence from an unknown species.

- Locating domains - When working with a protein sequence we can input it into BLAST, to locate known domains within the sequence of interest.
- Establishing phylogeny - Using the results received through BLAST we can create a phylogenetic tree using the BLAST webpage. Phylogenies based on BLAST alone are

less reliable than other purpose-built computational phylogenetic methods, so should only be relied upon for “first pass” phylogenetic analyses.

- DNA mapping - When working with a known species, and looking to sequence a gene at an unknown location, BLAST can compare the chromosomal position of the sequence of interest, to relevant sequences in the database(s). NCBI has a “Magic-BLAST” tool built around BLAST for this purpose.
- Comparison - When working with genes, BLAST can locate common genes in two related species, and can be used to map annotations from one organism to another.

SUMMARY

The sequence alignment is the process by which sequences are compared by searching for common character patterns and establishing residue-residue correspondence among related sequences. We usually compare sequences in order to check the evolutionary relationship and prediction of protein structure and function. It is an important first step toward structural and functional analysis of newly determined sequences. Sequence alignment is broadly classified into two types: pair-wise sequence alignment and multiple sequence alignment. Pair-wise sequence alignment is further classified as local sequence alignment and global sequence alignment. It is used to find the best-matching local or global alignment of two sequences.

The biological sequences used for alignment, uses many alphabets and involves many complexities. Different databases and tools are now used to examine the sequences to identify region of similarity that may indicate functional, structural and/or evolutionary relationship between them. Some of them are ACARA, AlignMe, YASS, EMBOSS Needle, EMBOSS Water, EMBOSS Stretcher, LALIGN, SIM etc.

Today, one of the most commonly used tools to examine DNA and protein sequences is the Basic Local Alignment Search Tool (BLAST). It is a computer algorithm that is available for use online at the National Centre for Biotechnology Information (NCBI) website and many other websites. It breaks the query and database sequences into fragments and seeks matches between them. It is fast, accurate and web-accessible. BLAST can be used for several purposes. These include identifying species, locating domains, establishing phylogeny, DNA mapping, and comparison.

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PLAGIARISM SCAN REPORT

	12% Plagiarised		88% Unique	Date	2023-07-30
				Words	997
				Characters	8383

Content Checked For Plagiarism

BIOINFORMATICS
BOT-V.E-9
CA1-ASSIGNMENT

ALPHABET AND COMPLEXITY; PAIRWISE DATABASE SEARCHING; BLAST

SNEHAL PATIL
2102444
TYBSc BOTONY

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INTRODUCTION

A Sequence alignment is a way of arranging primary sequences of DNA, RNA or Proteins to identify regions of similarity that may be consequences of functional, structural and evolutionary relationship between the sequences.

It is the procedure of comparing two or more sequences by searching for a series of individual characters/patterns that are in the same order of the sequences.

The sequence alignment is made between a known sequence and a unknown sequence or between two unknown sequences.

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BLAST finds regions of similarity between biological sequences.

The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance.

BLAST can be used to infer functional and evolutionary relationships between sequences as well as help identify members of gene families.

Pair-wise sequence alignment is to arrange two sequences in such a fashion that pairs of matching characters between the two sequences are maximized.

It is used to identify regions of similarity that may indicate functional, structural and/or evolutionary relationships between two biological sequences (protein or nucleic acid).

To achieve this, one sequence needs to be shifted relative to the other to find the position where maximum matches are found.

There are two different pair-wise alignment strategies that are often used:

- a) Global alignment
- b) Local alignment

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In Global alignment, two sequences to be aligned are assumed to be generally similar over their entire length. Alignment is carried out from the beginning to the the end of both sequences to find the best possible alignment across the entire length between the two sequences. This method is more applicable for aligning two closely related sequences of roughly the same length. For divergent sequences and sequences of variable length, this method may not be able to generate optimal results because it fails to recognize highly similar local regions between the two sequences.

Local alignment

Local alignment, on the other hand, does not assume that the two sequences in question have similarity over their entire length. It only find s the local region eith the highest level of similarity between the two sequences and align these regions without regard for the alignment of the rest of the sequence regions.

This approach can be used for aligning more divergent sequences with the goal of searching for conserved patterns in DNA or protein sequences.

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Complexity of English alphabet 26 (A to Z)

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Additional characters are also used in an alphabet to indicate a degree of ambiguity in the identity of particular residue of base, Example:

- Frequent additional characters in protein sequences
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- Either glutamine or glutamate

X

B

Z

Some alignment programs will deal with these characters as they stand, other will simply replace such ambiguities with dummy character.

PAIRWISE DATABASE SEARCHING

Performing a comparison of one sequence against a database of many thousands can be viewed as simply an extension of pair-wise alignment. Achieving a database search in an efficient manner is not trivial, as datasets get larger, and more effort is being spent to try to improve efficiency. To perform a Needleman and Wunsch, or Smith-Waterman, which are the local alignment methods for the pair-wise sequence alignment, alignment is practicable for small numbers of sequences, but for large database searches the methods can become prohibitively time consuming.

Implementations of the Smith-Waterman algorithm have been developed for specialized computer hardware (for example, MPSrch running on the massively parallel MasPar supercomputer); however, these systems are expensive and rapidly become obsolete as hardware architectures develop and move on. Speed of execution is certainly an issue for database searching, and for both algorithms, described so far, speed depends critically on the length of the query sequence and on the size of the database searched. Hence different programs and tools are introduced that concentrate on finding short identical matches, which may contribute to a total match, using implementations that address issues of execution speed, without resorting to the use of specialized computer hardware.

TOOLS AND DATABASES USED FOR PAIR-WISE DATABASE SEARCHING

1. ACANA

ACANA is an accurate and consistent alignment tool for DNA sequences.

ACANA is specifically designed for aligning sequences that share only some moderately conserved regions and/or have a high frequency of long insertions or deletions.

It attempts to combine the best of local and global alignments algorithms in searching for evolutionarily related regions of sequences in order to achieve the best alignment.

2. LALIGN

LALIGN finds internal duplications by calculating non-intersecting local alignments of protein or nucleotide sequences.

<https://www.ebi.ac.uk/Tools/psa/lalign/>

LALIGN Website

3. EMBOSS Needle

EMBOSS Needle reads two input sequences and writes their optimal global sequence alignment to file.

Needle is an alignment tool used by Bioinformaticians. It is a pairwise alignment tool; design to write the optimal global alignment. It's one of the sub-software/tool which is available in EMBOSS.

https://www.ebi.ac.uk/Tools/psa/emboss_needle/

EMBOSS Needle Website

Matched Source

Similarity 34%

Title: [Sequence Alignment - an overview | ScienceDirect Topics](#)

Sequence alignment is a way of arranging protein (or DNA) sequences to identify regions of similarity that may be a consequence of evolutionary ...

<https://www.sciencedirect.com/topics/agricultural-and-biological-sciences/sequence-alignment>

Similarity 34%

Title: [Sequence Alignment](#)

➤The procedure of comparing two (pair-wise alignment) or more multiple sequences is to search for a series of individual characters or patterns that are in ...

<https://opencourses.emu.edu.tr/mod/resource/view.php?id=17143>

Similarity 6%

Title:blast.ncbi.nlm.nih.gov › [BlastBasic Local Alignment Search Tool - BLAST](#)

Jun 22, 2023 · The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance of matches. BLAST can be used to infer functional and evolutionary relationships between sequences as well as help identify members of gene families.

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

Similarity 12%

Title:[BLAST: Basic Local Alignment Search ToolOverview — ElasticBLAST 1.1.0 documentation](#)

BLAST can be used to infer functional and evolutionary relationships between sequences as well as help identify members of gene families. BLAST can be used to infer functional and evolutionary relationships between sequences as well as help identify members of gene families.

<https://blast.ncbi.nlm.nih.gov/>

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1. SIM

SIM finds k best non-intersecting alignments between two sequences or within a sequence using dynamic programming techniques.

The alignments are reported in order of decreasing similarity score and share no aligned pairs.

SIM requires space proportional to the sum of the input sequence lengths and the output alignment lengths, so it accommodates 100,000-base sequences on a workstation.

<https://web.expasy.org/sim/>

SIM Website

2. EMBOSS Stretcher

EMBOSS Stretcher calculates an optimal global alignment of two sequences using a modification of the classic dynamic programming algorithm which uses linear space.

https://www.ebi.ac.uk/Tools/psa/emboss_stretcher/

EMBOSS Stretcher Website

3. EMBOSS Water

EMBOSS Water uses the Smith-Waterman algorithm (modified for speed enhancements) to calculate the local alignment of two sequences.

https://www.ebi.ac.uk/Tools/psa/emboss_water/

EMBOSS Water Website

4. YASS (Yet Another Similarity Searcher)

YASS (Yet Another Similarity Searcher) is a free software, pair-wise sequence alignment software for nucleotide sequences, that is, it can search for similarities between DNA or RNA sequences.

YASS accepts nucleotide sequences in either plain text or the FASTA format and the output format includes the BLAST tabular output.

YASS uses several transition-constrained spaced seed k-mers, which allow considerably improved sensitivity.

YASS can be used locally on a user's machine, or as SaaS on the YASS web server, which produces a browser based dot-plot.

<https://bioinfo.cristal.univ-lille.fr/yass/>

YASS Website

5. AlignMe

AlignMe (for sequence Alignment of Membrane Proteins) is a very flexible sequence alignment program that allows the use of various different measures of similarity.

AlignMe can be used to examine detailed similarity between homologous proteins if there is no notable sequence similarity.

The predefined gap/weight sets have been optimized for membrane proteins, and so should be particularly useful for these difficult cases.

This webserver is currently running version 1.2.

<https://www.bioinfo.mpg.de/AlignMe/AlignMePW.html>

AlignMe Website

BLAST (Basic Local Alignment Search Tool)

BLAST (Basic Local Alignment Search Tool) is a heuristic approach for comparing nucleotide or protein sequences.

As the name implies, BLAST performs local alignments.

The BLAST algorithm and programs were designed by Stephen Altschul, Warren Gish, Webb Miller, Eugene Myers, and David J.

Lipman, at the National Center for Biotechnology Information (NCBI) of National Institutes of Health (NIH). In BLAST, PAM (Point Accepted Mutation a.k.a. Percent Accepted Mutation) or BLOSUM (BLOCKS SUBstitution Matrix) matrices are used to calculate the sequence similarity (a.k.a. positives).

BLAST Programs

There are many different flavors of online/offline/API/cloud BLAST programs as listed below:

- BLASTN program compares the nucleotide query sequence with the nucleotide sequences in the database.
- BLASTP program compares the protein query sequence with the protein sequences in the database.
- BLASTX program translates the nucleotide query sequence and compares with the protein sequences in the database.
- TBLASTN program compares the protein query sequence with the nucleotide sequences in the database, by instantly translating the nucleotide sequences in the database before comparison.
- TBLASTX program compares the translated six reading frames of nucleotide query sequence with the translated six reading frames of nucleotide sequences in the database.

The query is translated on the fly before searching sequences in the database.

- MEGA-BLAST program compares the nucleotide query sequence with the nucleotide sequences in the database by optimizing very similar sequences (in the same or in closely related species), first looks for an exact match of 28 bases, and then attempts to extend that initial match into a full alignment.

Steps to perform BLAST search

1. In google search box search for NCBI.
2. Click on BLAST.
3. Click on the "Nucleotide BLAST" box.
4. In the "Enter Query Sequence" selection box, click "Choose File".
5. Navigate to a query file on your desktop and click "Choose". The query file name should appear next to "Choose File".
6. In the "Job Title" field, enter a unique name for the Blast query.

7. In the "Choose Search Set" selection box, click "Standard databases".
8. In the drop-down list choose "Nucleotide collection (nr/nt)". Leave all other fields in their default state.
9. In the "Program Selection" selection box, choose "Highly similar sequences (megablast)".
10. Click the plus "+" sign by "Algorithm parameters" to expand the parameters list.
11. Ensure that all of the default settings are configured correctly.
12. Click the minus "-" sign by "Algorithm parameters" to close the parameters list.
13. Click the "BLAST" button to initiate a Blast search.

Applications of BLAST

BLAST can be used for several purposes.

These include identifying species, locating domains, establishing phylogeny, DNA mapping, and comparison.

Identifying species - With the use of BLAST, we can possibly correctly identify a species or find homologous species.

This can be useful, for example, when we are working with a DNA sequence from an unknown species.

- Locating domains - When working with a protein sequence we can input it into BLAST, to locate known domains within the sequence of interest.
- Establishing phylogeny - Using the results received through BLAST we can create a phylogenetic tree using the BLAST webpage.

Phylogenies based on BLAST alone are less reliable than other purpose-built computational phylogenetic methods, so should only be relied upon for "first pass" phylogenetic analyses.

- DNA mapping - When working with a known species, and looking to sequence a gene at an unknown location, BLAST can compare the chromosomal position of the sequence of interest, to relevant sequences in the database(s). NCBI has a "Magic-BLAST" tool built around BLAST for this purpose.
- Comparison - When working with genes, BLAST can locate common genes in two related species, and can be used to map annotations from one organism to another.

Matched Source

Similarity 50%

Title: [web.expasy.org > sim > sim_notes](http://web.expasy.org/sim/sim_notes) SIM - Local similarity program - Expasy

SIM finds k best non-intersecting alignments between two sequences or within a sequence using dynamic programming techniques. The alignments are reported in order of decreasing similarity score and share no aligned pairs.

https://web.expasy.org/sim/sim_notes.html/

Similarity 25%

Title: [EMBOSS Stretcher - Pairwise Sequence Alignment](http://www.ebi.ac.uk/Tools/psa/emboss_stretcher/) EMBOSS Stretcher (Nucleotide Alignment)

EMBOSS Stretcher calculates an optimal global alignment of two sequences using a modification of the classic dynamic programming algorithm which uses linear ... EMBOSS Stretcher calculates an optimal global alignment of two sequences using a modification of the classic dynamic programming algorithm which uses linear ...

https://www.ebi.ac.uk/Tools/psa/emboss_stretcher/

Similarity 13%

Title: [www.ebi.ac.uk > Tools > services](http://www.ebi.ac.uk/Tools/services/web_emboss_water/toolform.ebi/) EMBOSS Water < Pairwise Sequence Alignment < EMBL-EBI

EMBOSS Water uses the Smith-Waterman algorithm (modified for speed enhancements) to calculate the local alignment of two sequences. sequences. Enter or paste your first protein sequence in any supported format: Or, upload a file: Use a example sequence | Clear sequence | See more example inputs.

https://www.ebi.ac.uk/Tools/services/web_emboss_water/toolform.ebi/

Similarity 10%

Title: [en.wikipedia.org > wiki > Yass_\(software\)](https://en.wikipedia.org/wiki/Yass_(software)) Yass (software) - Wikipedia

YASS (Yet Another Similarity Searcher) [1] [2] is a free software, [3] pairwise sequence alignment software for nucleotide sequences, that is, it can search for similarities between DNA or RNA sequences. YASS accepts nucleotide sequences in either plain text or the FASTA format and the output format includes the BLAST tabular output.

[https://en.wikipedia.org/wiki/Yass_\(software\)](https://en.wikipedia.org/wiki/Yass_(software))

Similarity 7%

Title: [www.bioinfo.mpg.de > AlignMe](#)AlignMe - Alignment of membrane proteins based on ...

AlignMe (for sequence Alignment of Membrane Proteins) is a very flexible sequence alignment program that allows the use of various different measures of similarity. These similarity measures include: substitution matrices, hydrophobicity scales and any kind of profiles (i.e. secondary structure predictions or transmembrane predictions).

<http://www.bioinfo.mpg.de/AlignMe/>

Similarity 4%

Title: [Peatix: Basic local alignment search tool pdf](#)

... blast (basic local alignment search tool) is a heuristic approach for comparing nucleotide or protein sequences. biochemistry 324. as the name implies, ...

<https://basic-local-alignment-search-tool-pdf-153.peatix.com/>

Similarity 4%

Title: [BLAST \(biotechnology\) - Wikipedia](#)Basic Local Alignment Search Tool - BioGem.Org

<https://www.biogem.org/downloads/notes/kau/Basic%20Local%20Alignment%20Search%20Tool.pdf>

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SUMMARY

The sequence alignment is the process by which sequences are compared by searching for common character patterns and establishing residue-residue correspondence among related sequences. We usually compare sequences in order to check the evolutionary relationship and prediction of protein structure and function. It is an important first step toward structural and functional analysis of newly determined sequences. Sequence

alignment is broadly classified into two types: pair-wise sequence alignment and multiple sequence alignment. Pair-wise sequence alignment is further classified as local sequence alignment and global sequence alignment.

It is used to find the best-matching local or global alignment of two sequences.

The biological sequences used for alignment, uses many alphabets and involves many complexities. Different databases and tools are now used to examine the sequences to identify region of similarity that may indicate functional, structural and/or evolutionary relationship between them. Some of them are ACARA, AlignMe, YASS, EMBOSS Needle, EMBOSS Water, EMBOSS Stretcher, LALIGN, SIM etc.

Today, one of the most commonly used tools to examine DNA and protein sequences is the Basic Local Alignment Search Tool (BLAST). It is a computer algorithm that is available for use online at the National Centre for Biotechnology Information (NCBI) website and many other websites.

It breaks the query and database sequences into fragments and seeks matches between them. It is fast, accurate and web-accessible. BLAST can be used for several purposes.

These include identifying species, locating domains, establishing phylogeny, DNA mapping, and comparison.

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Embl-Ebi. (n.d.-c). LALIGN < Pairwise Sequence Alignment < EMBL-EBI. Retrieved July 29, 2023, <https://www.ebi.ac.uk/Tools/psa/lalign/>

Matched Source

Similarity 34%

Title: [Bioinformatics Test](#)

b) It is an important first step toward structural and functional analysis of newly determined sequences c) This is the process by which sequences are ...

<https://www.sanfoundry.com/bioinformatics-questions-answers-test/>

Similarity 15%

Title: [Chapter 13. MULTIPLE SEQUENCE ALIGNMENT Flashcards](#)

Pairwise sequence alignment methods are used to find the best-matching piecewise (local) or global alignments of two query sequences.

<https://quizlet.com/nl/227786524/chapter-13-multiple-sequence-alignment-flash-cards/>

Similarity 10%

Title: [Computational phenotyping of potential plant growth](#)

It breaks the query and database sequences into fragments and seeks matches between them. Advantages i. Character string comparison against all the.

<https://vdocument.in/computational-phenotyping-of-potential-plant-growth-impact-on-human-health-diverse.html>

Similarity 8%

Title: [omicstutorials.com > basic-local-alignment-search](#) Basic Local Alignment Search Tool (BLAST) for bioinformatics

BLAST can be used for several purpose. These include identifying species, locating domains, establishing phylogeny, DNA mapping and comparison. In addition, for identifying species with the use of BLAST we can correctly identify or find homologous species. For instance, when we are working with a DNA sequence from an unknown species it can be ...

<https://omicstutorials.com/basic-local-alignment-search-tool-blast-for-bioinformatics/>

Unique Mode of Assessment

Botany department

Botany Department of Parvatibai Chowgule College of Arts and Science (Autonomous) Margao Goa organized Plant Drive Programme on 11th August 2023, from 1:30 pm onwards at Botanical Garden. The main objective of the Plant Drive was to launch a community seed bank and to raise awareness towards the importance of planting and saving trees. Plant Drive consisted of 3 main activities –

1. Plant Walk curated by Botany Department
2. Exchange of seeds and saplings (also as a part of *Meri Maati, Mera Desh*).
3. Medicinal sapling plantation in Botanical Garden

For Plant walk in the campus the topics were assigned for Continuous assessment from Courses Plant Drug Technology and Pharmacognosy for TY students and Systematics of Taxonomy for SY students. They were assessed for on campus presentation of Systematic positions, diagnostic characteristics and economic uses of the plants present in the campus for 15 marks. Activity was open for all for which about 30 students and faculty members participated from college.



DEPARTMENT OF BOTANY

Unique Mode of Assessment: Power Point Presentation

A PowerPoint presentation was conducted as an innovative mode of assessment (CA-II) for the T.Y.B.Sc. students in the paper titled *Applied Mycology (BOT-VI.E-16)*. Topics were assigned from Module II of the syllabus, allowing students to explore subject matter in depth and demonstrate their understanding.

The rubrics and date of assessment were communicated well in advance through detailed classroom instructions and the Google Classroom platform to ensure smooth execution. Students presented their topics to the class, showcasing their comprehension and communication skills.

The evaluation was based on specific criteria, including introduction, content, presentation skills (expression, vocabulary, tone, and explanation), summary, and references utilized in preparing the PowerPoint presentation. The assessment carried a total of 15 marks, providing a structured and transparent framework for grading.

This approach effectively combined subject knowledge with essential skills such as public speaking, organization, and research, contributing to the students' holistic development.



Application of fungi in food industry Enzyme (Cellulases)

Name: Joshvel Fernandes

Class: TY B.Sc. Botany

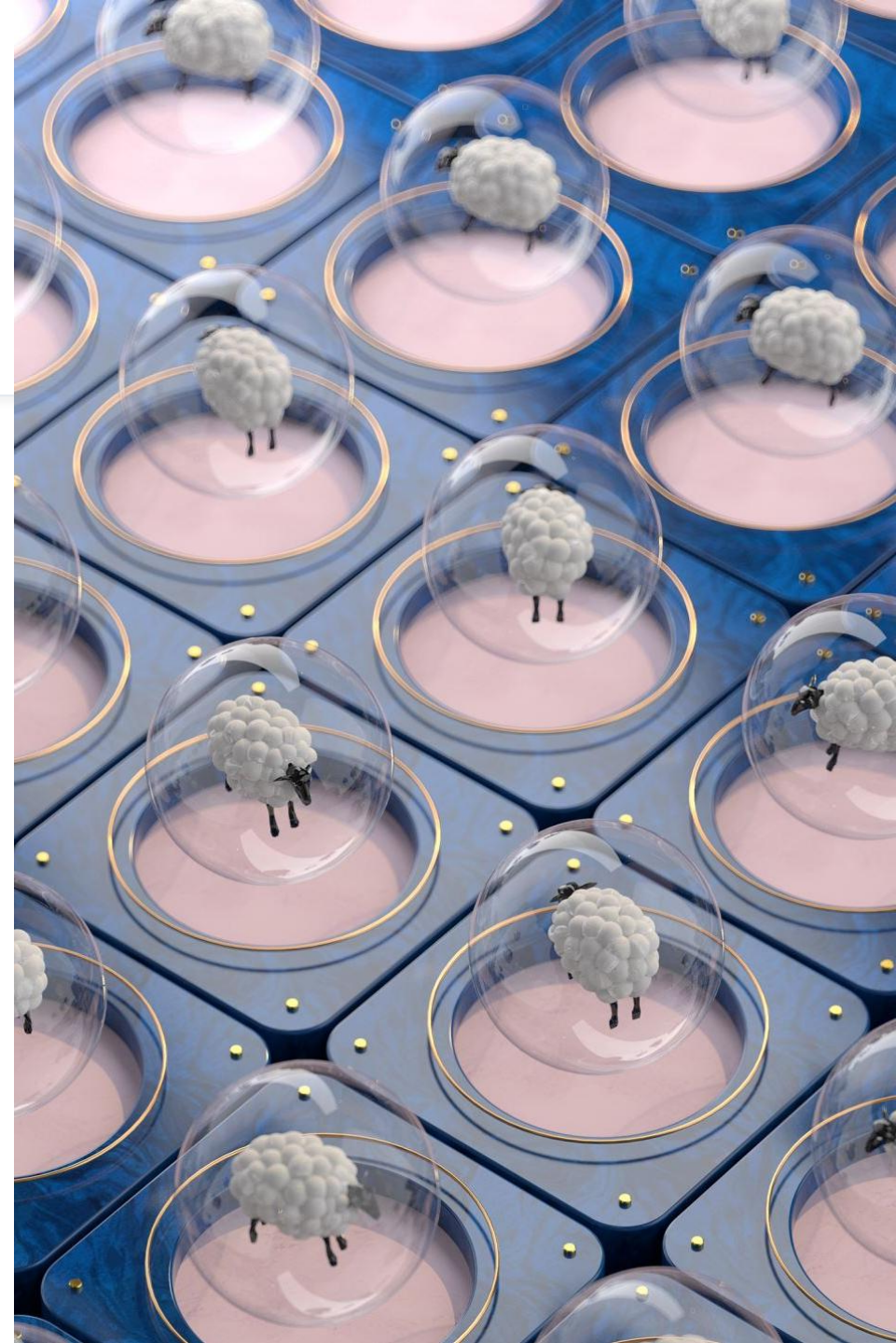
Roll. No.: 2102404

Assessment: CA 2

Course: BOT-IVE-16: Applied Mycology

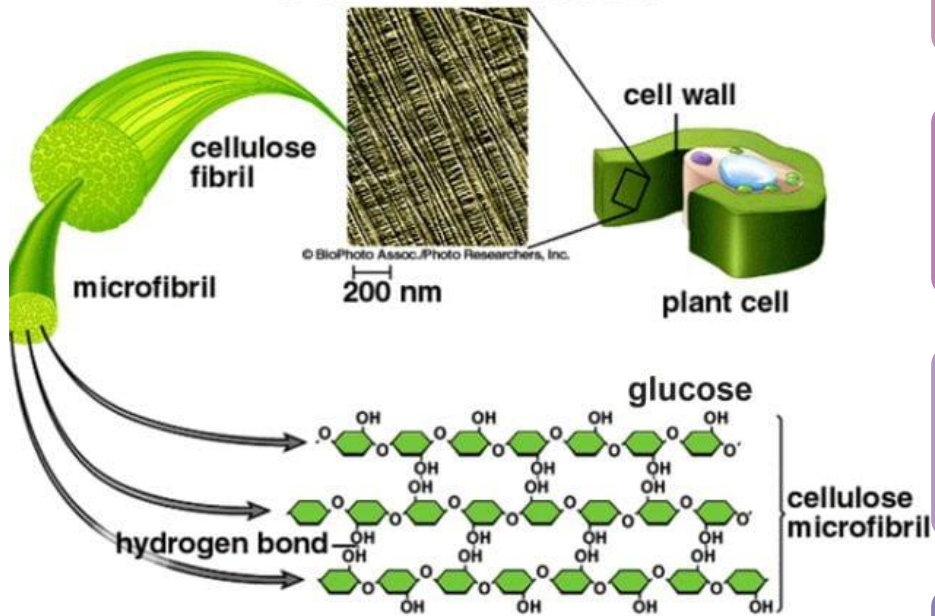
Contents

1. Introduction
2. Cellulases
3. Cellulase producing fungi
4. Production of fungal cellulases
5. Applications of fungal cellulases
6. Summary
7. References



Introduction

Cellulose fibrils



Cellulose: Most abundant biomaterial derived from the living organisms on the earth derived from plants.



β -D-glucopyranoside units that are linked together via β -D-glucosyl bonds (Ahmed et al. 2017b)



For the cellulose to be utilized in various industrial applications it needs first to be converted into its building blocks (Glucose) by the hydrolysis of β -D-(1,4) glucosidic linkages.

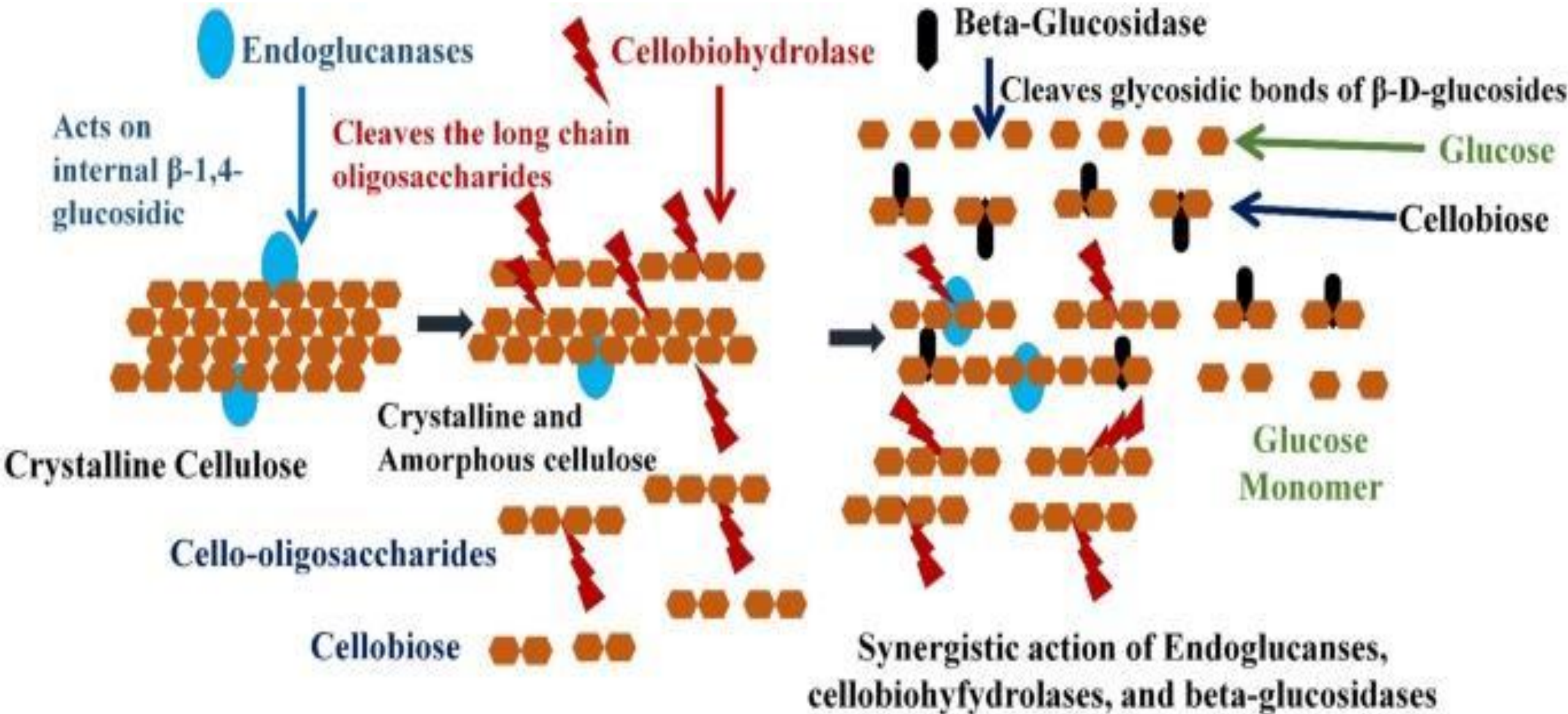


Cellulose degradation is mediated by an enzymatic system referred to as cellulases.



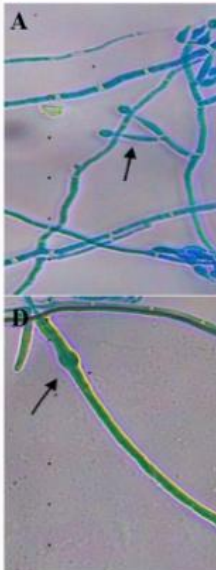
Synthesized by bacteria, fungi, plants and some animals.

Cellulases

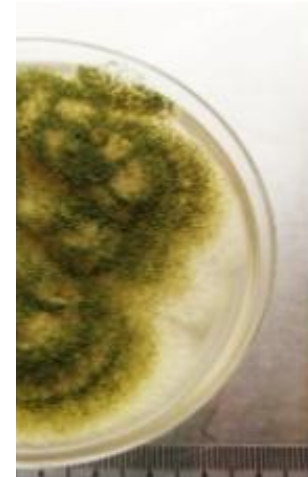


Cellulase producing fungi

Figure 2.
Trichoderma
pattern (arrows)
conidia (arrows)
(E) hyphal
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under a light
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eaves. (A):
s, (B): Full

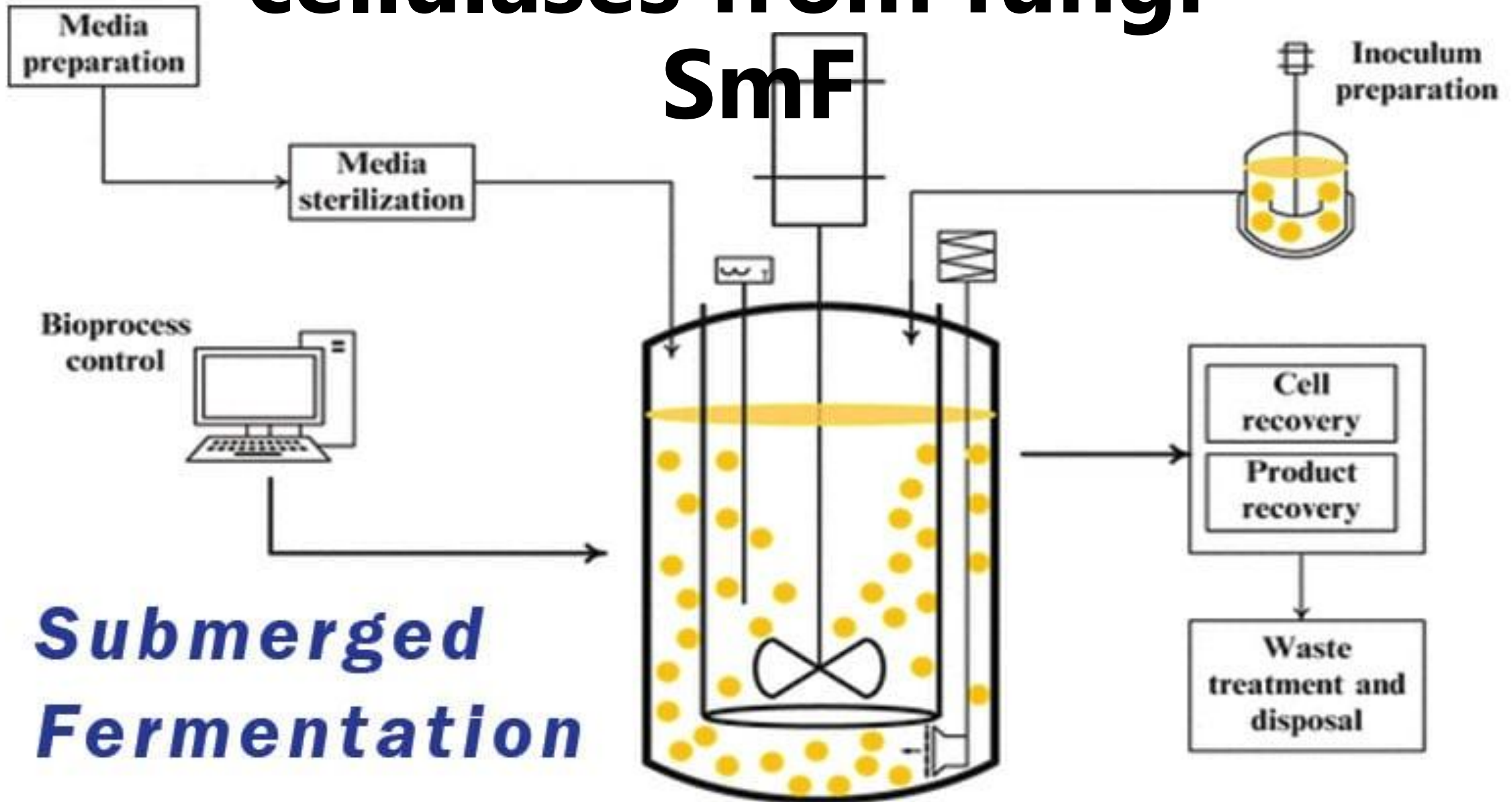


Production of cellulases from fungi - SSF

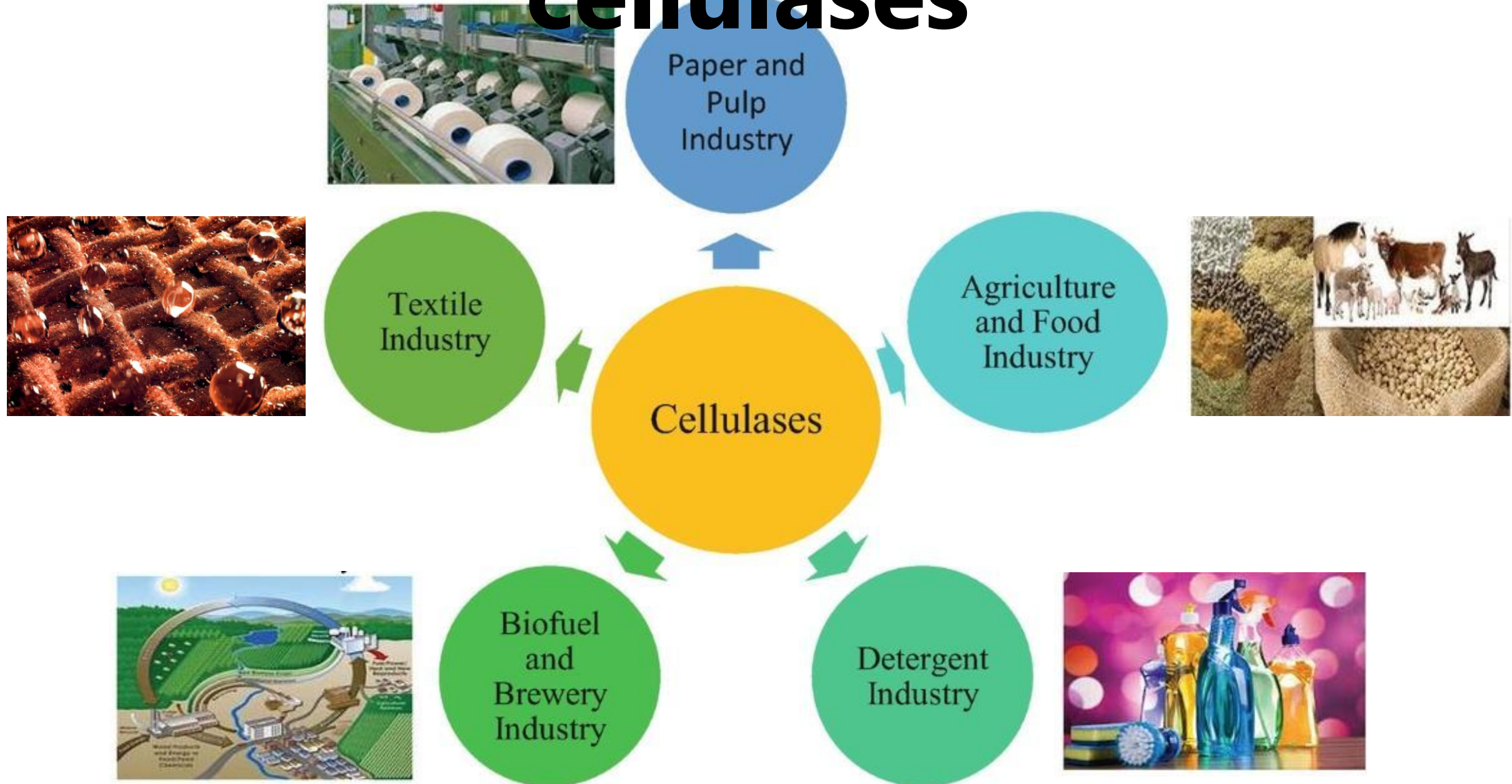


Fig. 1 Steps of Solid State Fermentation process to obtain enzyme from the fungus *Aspergillus niger*

cellulases from fungi - SmF



General applications of fungal cellulases

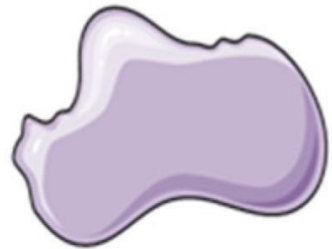


Applications of fungal cellulases in food industry

Bacteria and fungi



Fermentations



Cellulases



- Tenderization of fruits
- Clarification of fruit juices,
- Extraction of flavoring materials and essential oils
- Improvement in filterability of vanilla extracts
- Reduction of roughage in dough
- Hydrolysis of roasted coffee
- Extraction of tea polyphenols
- Extraction of oil from olives
- Increase aroma and taste



Food industry



Food service



Food supply



Food preservation

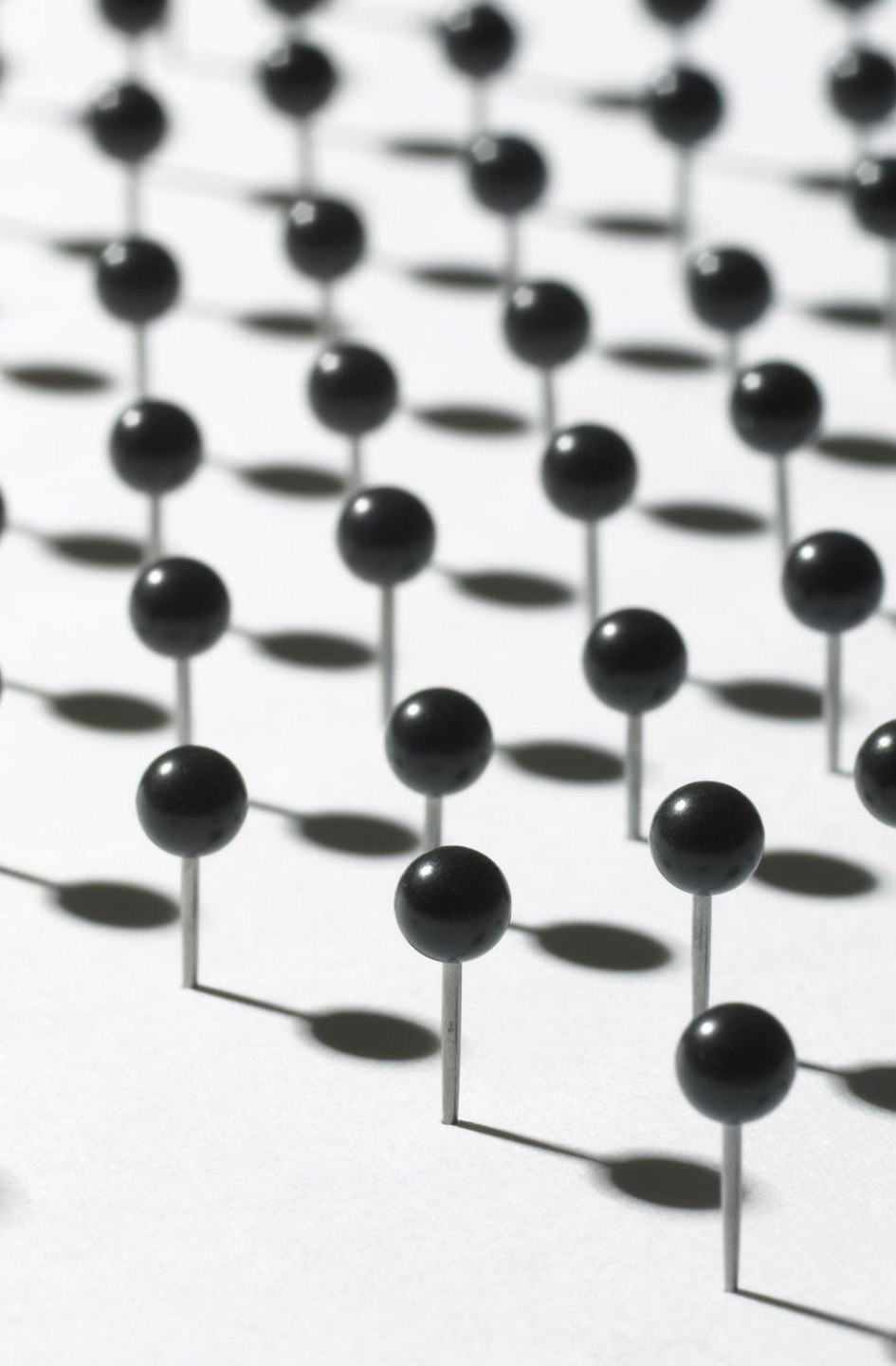


Summary



Cellulose is the most abundant biomaterial derived from the living organisms on the earth; plant is the major contributor to the cellulose pool present in the biosphere. Cellulase is the enzymatic system, which degrades cellulose chains to glucose monomers. Cellulase is a group of three enzymes endoglucanase, cellobiohydrolase and β -glucosidases which act together to hydrolyze cellulose to glucose units. Fungi are the preferred source of cellulase for industrial applications since they secrete large quantities of cellulase to culture medium. Cellulases have been produced and characterized from different aerobic fungi such as *Aspergillus* (Bansal et al. 2012), *Trichoderma* (Ellilä et al. 2017), *Penicillium* (Prasanna et al. 2016), among others. Fungal cellulases have been produced through solid state fermentation (SSF) and submerged fermentation (SmF). In SSF, the fungal species is grown on one or more solid substrate such as straw while in SmF, free flowing liquid like molasses/broths supplemented with different nutrients is used to cultivate of microorganisms and the enzymes including cellulase and metabolic byproducts are secreted into fermentation medium. Cellulase enzymes have got tremendous applications in different industries including biofuel production, paper and pulp industry, detergent industries, food and food processing industries, animal feeds among others.

Cellulase Enzyme Powder



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**Thank
you**



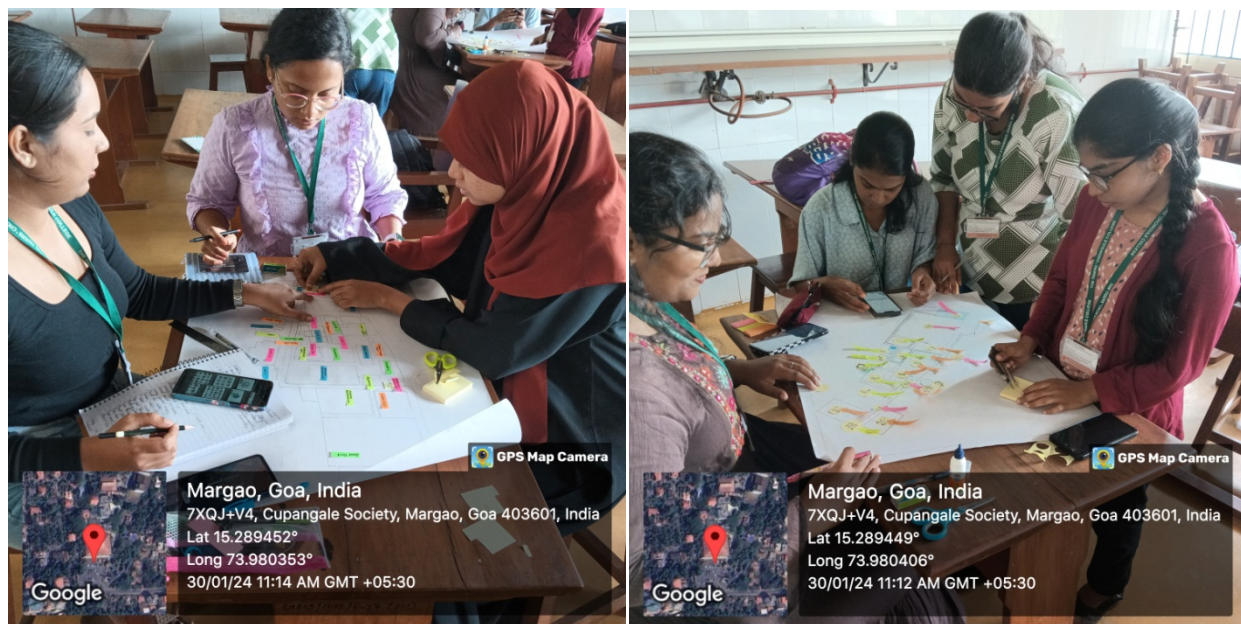
**Any
question
?**

Course Title: Field Techniques and Village Survey

Course Code: PGMP-GEG-DSC-408

Mode of Assessment Title: Collective Critical Mapping Tool (Classroom Activity)

Collective Critical Mapping was utilized as one of the mode of assessment for the Field Techniques and Village Survey course. The purpose of classroom-activity for collective mapping was used in order to assess students' understanding of spatial concepts, critical thinking, and collaboration skills that are required for field surveys. The maps prepared by students through collective critical mapping provide clear visualizations of spatial data, making it easier to identify patterns, relationships, and areas of concern that may not be evident in text-based reports. Overall, this assessment helped students highlight and understand the patterns and resource distribution, making complex data more accessible and understandable.

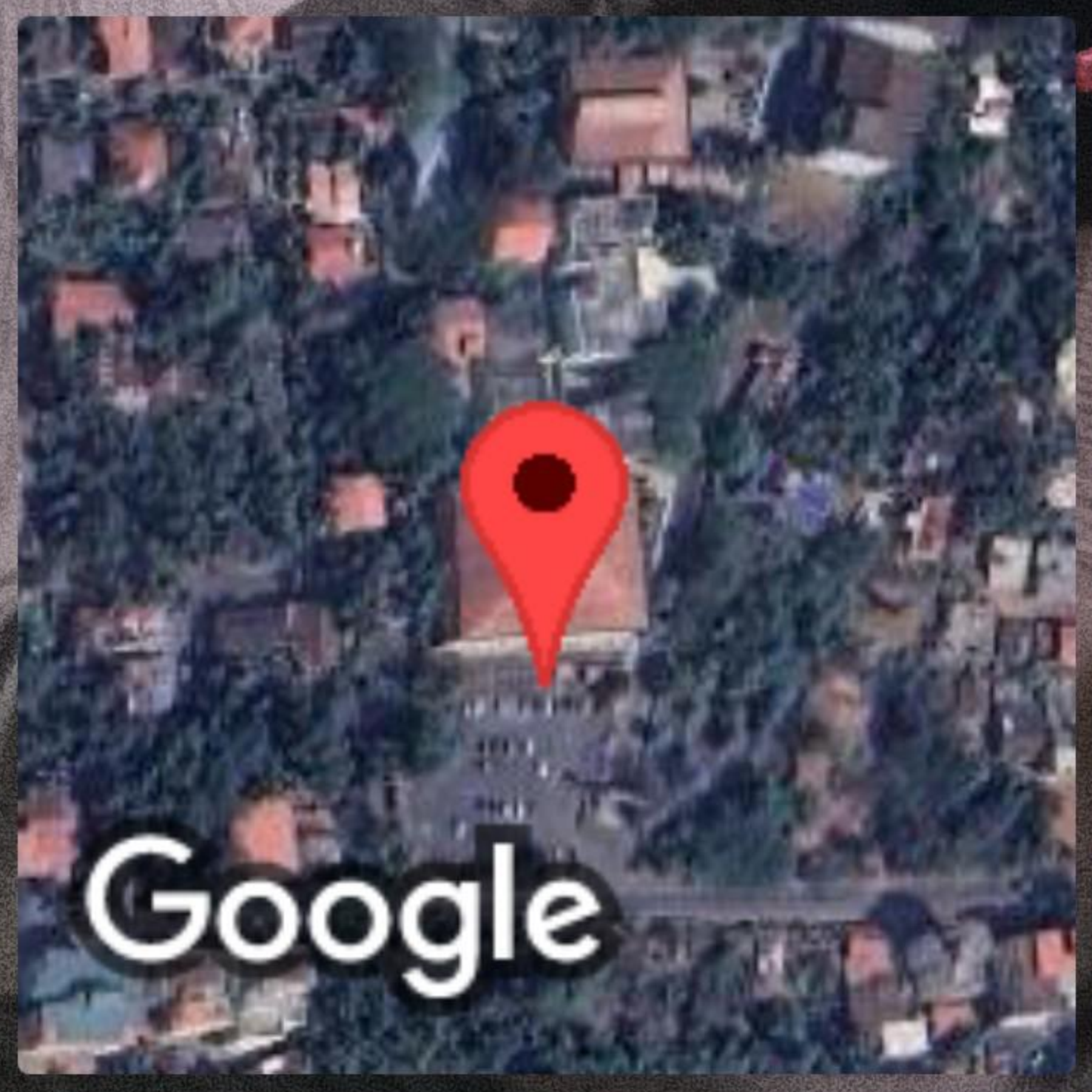


Students carrying out the Collective Mapping Classroom-Activity as a mode of assessment




 **GPS Map Camera**

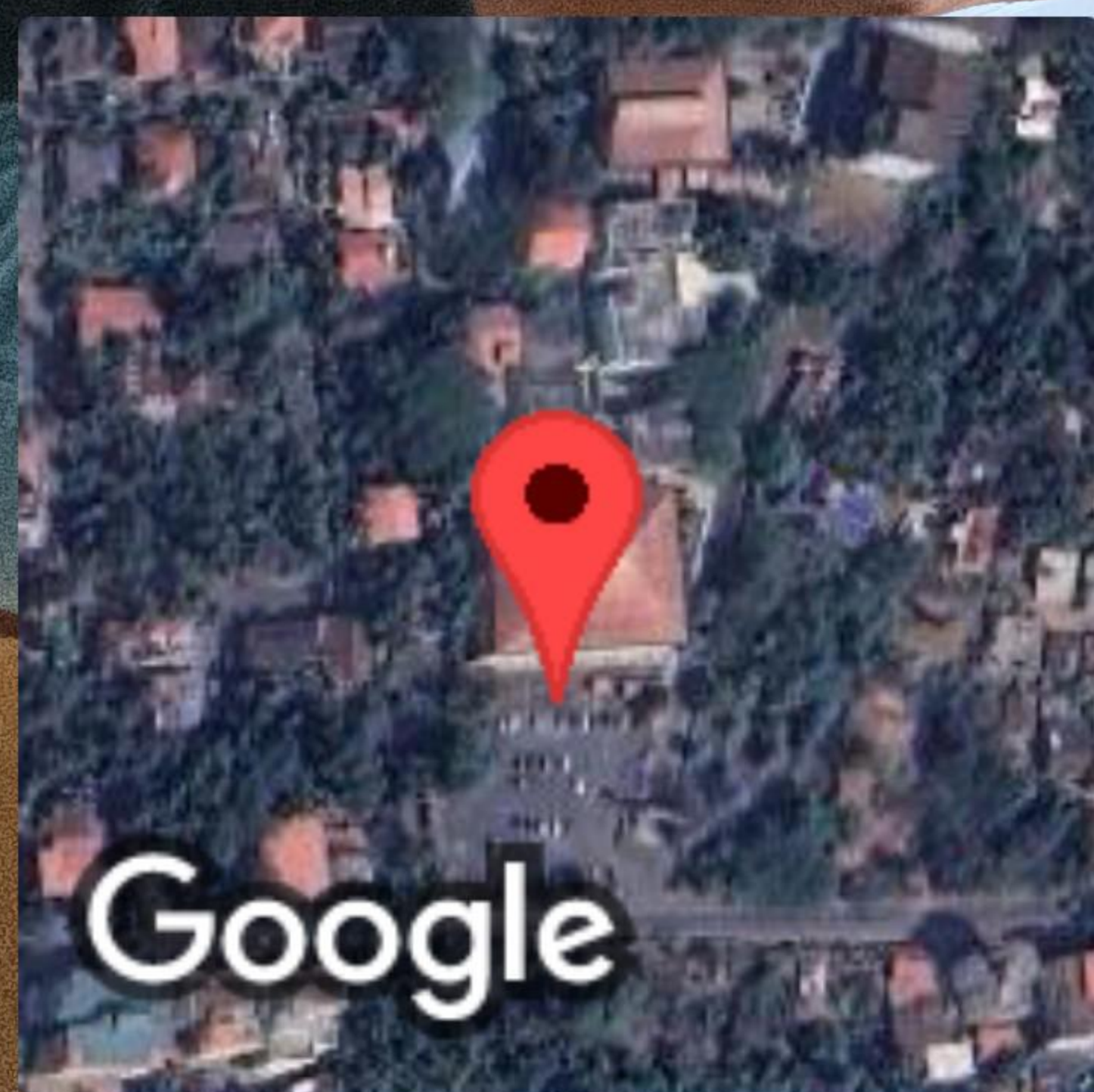
Margao, Goa, India
7XQJ+V4, Cupangale Society, Margao, Goa 403601, India
Lat 15.289449°
Long 73.980406°
30/01/24 11:12 AM GMT +05:30





 **GPS Map Camera**

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CONTINUOUS ASSESSMENT

Course Code: CHE-GE-502

Course Title: Environmental Chemistry

Department: Post Graduate in Analytical Chemistry

Semester: III

The Generic elective course was incepted in the AY 2023-24 for PG students not belonging to Chemistry specialization and was taken by Dr. Luann Romaine D'souza, Assistant Professor in Chemistry. The course was floated for M.Sc. Part 2 students from Geoinformatics (08 students) and Information Technology (09 students).

The course syllabus included the types of environmental pollution, sources, effects and measures for mitigation. After a brief teaching period, the 1st CA was conducted on 03/08/2024 on Module 1 covering air pollution by creating a "Newspaper" in the proforma given below,

STEPS TO MAKE YOUR OWN NEWSPAPER

- 1** An Indian state/city is provided to you. Browse through the air pollution level of the target place.
- 2** Check out newspaper articles & other sources from 2022 to 2024 for the target places
- 3** Find out the pollutants responsible for air pollution in the target place & report the AQIs.
- 4** Compile (screenshots of articles, tabulated data, pictures, captions) so as to fit on A3 in any format using word/powerpoint/Canva.
- 5** Give your newspaper a strong & captivating title.
- 6** Email your creative concern for the environment in PDF to lr000@chowgules.ac.in

Marks distribution (15 marks):

- 1) Creativity & content relevance of the newspaper = **08 marks**
- 2) Presenting the newspaper to the audience = **02 marks**
- 3) Viva based on the concepts covered = **05 marks**

Through this mode of CA, the students covered CLO 1 and 2 on Air pollution: Sources, causes and related technical aspects with a visual representation of creativity. It created an excitement and awareness on browsing through different Indian states/cities afflicted by air pollution. Thus, enhancing their knowledge and fostering concern for the environment.

The recounts of the assessment is enclosed as a PDF entitled "Evidence_Newspaper CA_PG Chemistry" for your perusal.



Glimpse of the "Newspaper" assessment for the Generic elective course.

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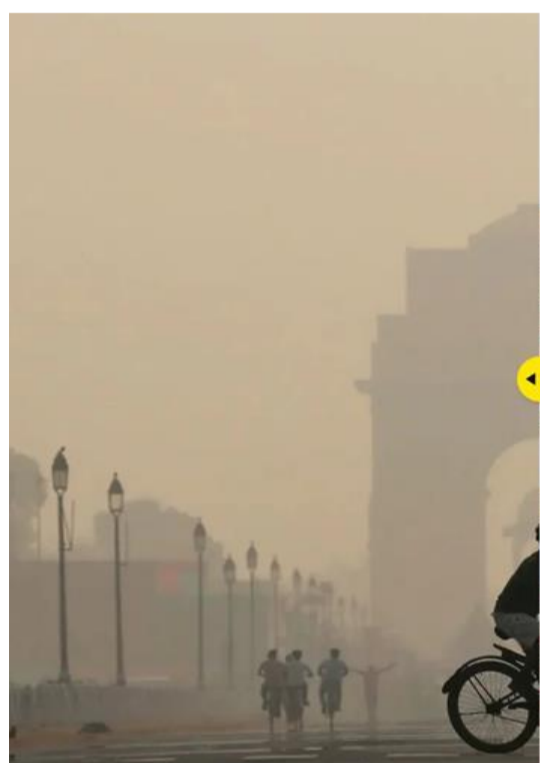
14TH MOST POLLUTED IN INDIA | 'Delhi February air cleanest in 8 years'

NT Correspondent
 NEW DELHI: Delhi, which was the most polluted city in the country in January, recorded significant improvement in air quality in February, logging its lowest monthly average PM2.5 concentration in eight years, an analysis carried out by the Centre for Research on Energy and Clean Air (CREA) released on Thursday has revealed.
 According to the analysis, the Capital in February was the 14th most polluted city in the country with an average PM2.5 concentration of 103 µg/m³ – far better than the 200 µg/m³ in January.
 "Delhi, which was the most polluted city in India in January showed some improvement and was the 14th most polluted in February recording the lowest PM2.5 level for February since 2016. But it was still severely polluted, recording PM2.5 concentration of 103 µg/m³ – which was nearly two times the prescribed daily national ambient air quality standards (NAAQS) and seven times the World Health Organisation (WHO) prescribed safe levels," said CREA in its analysis.
 The analysis looked at 253 cities across the country, finding Bhopal as the most polluted across the country – recording an average PM2.5 concentration of 200 µg/m³, followed by Aarata in Bihar (133), Hapur in Uttar Pradesh (125), Hanamangah in Rajasthan (120), and Nalbari in Assam (117).
 The national daily safe standards for PM 2.5 are 60 µg/m³, and WHO standards are 15 µg/m³.
 Sunil Dahiya, analyst at CREA said 160 out of the 253 cities surveyed had data for more than 80% of days in the month. Out of these, only one city – Samsi in Madhya Pradesh – met the WHO standard.
 "Delhi in February has shown a significant improvement from January, but this also shows what an important role meteorological conditions play. The average PM 2.5 levels have almost halved from January, mainly due to rain and good wind speed, but even then, this is two times the national standard and well away from WHO guidelines," he said.



Delhi's Air Quality Reaches Alarmingly Hazardous Levels, death by breath Can Delhi Breathe Clean????

- Action from stages II to IV to be imposed (three days in advance)**
 - Restrictive action under previous stages to continue in the next stage if AQI worsens
 - Regular review of GRAP implementation by a group of experts
 - Cars (LMVs) running on BS-IV diesel to be restricted under 'severe+' category projections
 - IITM developed an 'Air Quality Early Warning System' for air quality forecast for Delhi-NCR



Sunil Dahiya, analyst at the Centre for Research on Energy and Clean Air, said:
 "The heightened pollution levels in Delhi this Jan underscore two crucial realities. First, stubble burning isn't the primary cause of year-round hazardous air quality in Delhi-NCR, except for a brief period from Oct to mid-Nov. Second, insufficient effort or virtually none has been made to curtail emission load from various sectors in the broader airshed surrounding Delhi."

Parts of city in deep red as AQI nears 400 mark

North India's skies turn grey
 Delhi's air quality has deteriorated significantly in parts of the city, with AQI nears 400 mark. The pollution rise puts kids at greater risk of anaemia, respiratory disease.

BAD AIR TOP HEALTH RISK

ACCORDING TO CSE REPORT
 Delhi is among the worst polluted cities in the country. It had the second worst winter PM2.5 of 188 µg/m³ in 2023; worst was Begusarai in Bihar at 213.5 µg/m³

ENTERIC DISEASES | Caused by contaminated water and food
 3,085 Deaths in 2021
 82.4% Due to diarrhoeal diseases
 17.1% Due to typhoid and paratyphoid
 0.5% Due to other intestinal infectious diseases

Air pollution is #1 health risk in Delhi
 Other risks: High blood pressure, dietary risks, tobacco, high fasting plasma glucose, high LDL cholesterol and kidney dysfunction

Diseases that cause most deaths
 In 2021, cardiovascular diseases were the top reason of deaths.

Cardiovascular disease	Respiratory infections & TB	Neoplasms
Chronic respiratory disease	Diabetes & chronic kidney disease	Other Covid outcomes

SLOW WIND SPEED SPIKES WINTER CONCENTRATION

MAJOR FINDINGS
 PM2.5 level 2% higher in 2023 compared with 2022; 6% higher compared

- Delhi has been witnessing a gradual yet consistent decline in its annual PM2.5 level since 2015-17, but PM2.5 saw an increase in 2023
- Winter undid the gains of summer and monsoon months – summer months of 2023 significantly less polluted (14-36%) than those of 2022; winter months more polluted (12-34%)
- Slow wind speed spiked winter concentration; in November, average surface wind speed in Delhi was 9.8 m/s, the lowest in last six years
- 2023 still had the highest number of days (151) meeting the national ambient air quality standard for 24 hours
- In the last six years, highest number of smog episodes (three) seen in the winter of 2023

Average of 2018-22 winters higher than that of 2023



Delhi breathes easier: April 2024 sees air quality spike.

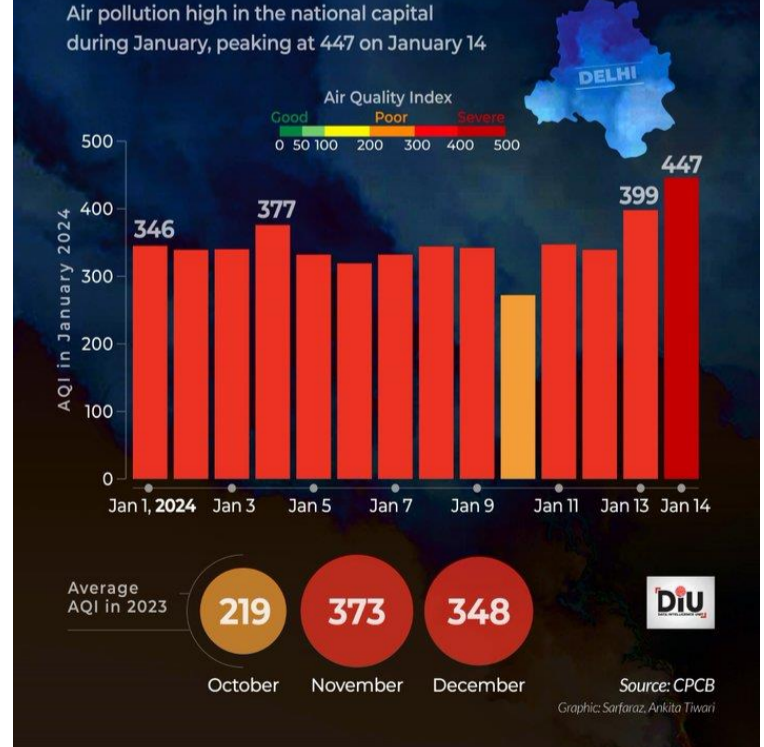
New Delhi: Delhi's air quality showed marked improvement in April 2024, recording 23 "Good to Moderate" air quality days, the highest for April since 2018, excluding 2020 due to the COVID-19 lockdown. In comparison, April 2023 saw 17 such days, zero in 2022, 18 in 2021, 30 in 2020, 12 in 2019, and 8 in 2018, according to the Commission for the Air Quality Management in NCR and Adjoining Areas (CAOM). April 2024 also saw a reduction in the "Poor to Severe" air quality days (AQI > 200) with only 7 such days, down from 13 in 2023, 30 in 2022, 12 in 2021, 18 in 2019, and the 22 in 2018.

MOST POLLUTED AIR QUALITY STATION

Station	AQI
1 Pooth Khurd, Bawana	898
2 Aya Nagar, New Delhi - IMD	169
3 NSIT Dwarka, New Delhi - CPCB	102
4 Anand Vihar, Delhi - DPCC	94
5 Anand Vihar	90
6 Vivek Vihar	66
7 DTU, New Delhi - CPCB	62
8 Dwarka, Sec-8	60
9 Dwarka-Sector 8, Delhi - DPCC	60
10 Burari Crossing, New Delhi - IMD	54

Swachh Vayu Survekshan is an initiative by the MoEF & CC to rank cities on the basis of the implementation of the activities approved under the city and air quality action plans in the 131 NCAP cities.

Delhi's Air Quality Plummet to 'Severe' Levels



Health Advice For New Delhi

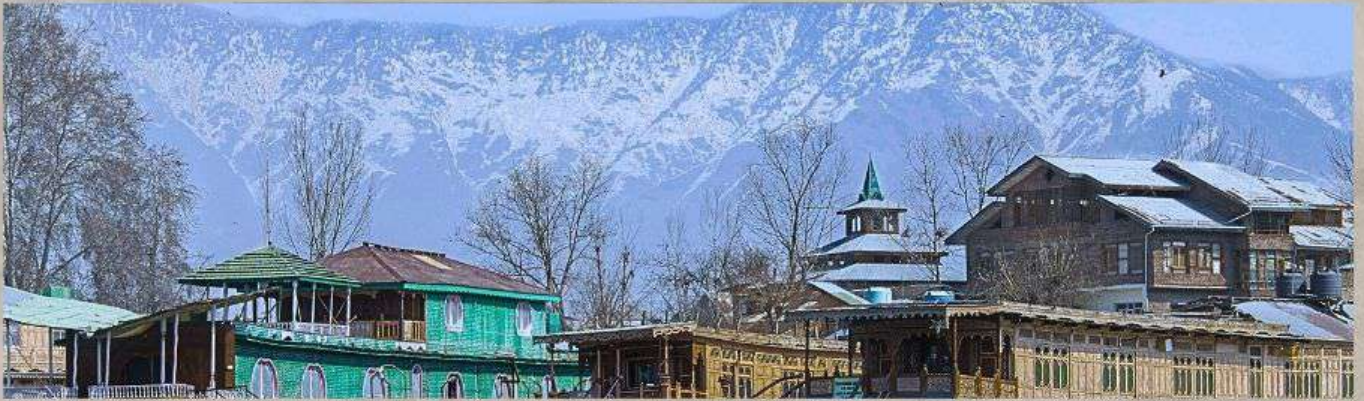
How to protect yourself from air pollution around New Delhi, India?

- Wear Mask Required
- Stay Indoor Not Required
- Windows Keep Close
- Use Purifier Required
- Family Allow Outdoor

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- <https://www.aqi.in/in/dashboard/india/delhi/new-delhi>

The Haze Herald



Jammu and Kashmir, celebrated for its breathtaking natural beauty and tranquil landscapes, is now facing an urgent and insidious threat: air pollution. The region, known for its pristine air and picturesque vistas, is increasingly experiencing deteriorating air quality that threatens both its environment and public health. Air quality varies, especially in cities like Srinagar, Jammu and Bandipura. Pollution levels can become quite high, particularly during the winter months.

Air quality in Srinagar

US AQI
89
LIVE AQI INDEX
Moderate

Air quality in Jammu

US AQI
87*
LIVE AQI INDEX
Moderate

Air quality in Bandipura

US AQI
78*
LIVE AQI INDEX
Moderate

The Air Quality Index (AQI) in key cities often ranges from moderate to poor, with particulate matter (PM2.5 and PM10) are the main culprits. These tiny particles are dangerous because they can get deep into our lungs and even enter our bloodstream, leading to serious health issues. Other pollutants like nitrogen dioxide (NO₂) and sulfur dioxide (SO₂) are also making things worse. They contribute to worsening air quality, which can trigger or worsen respiratory and heart problems for many people. Improving air quality is key to protecting our health and enhancing our lives.

Srinagar



Srinagar has been facing significant air pollution, especially during the winter months. This is primarily due to temperature inversions, which trap pollutants close to the ground. The city's AQI often ranges from moderate to poor, with PM_{2.5} and PM₁₀ levels frequently exceeding safe limits.

Pollution Levels in Jammu also experiences fluctuating air quality, with AQI levels sometimes reaching hazardous levels during peak pollution periods. The city struggles with pollutants such as PM_{2.5} and PM₁₀, largely from industrial activities and vehicular emissions. Seasonal Factors Similar to Srinagar, Jammu sees a deterioration in air quality during winter due to increased heating demand and agricultural residue burning in surrounding areas



Jammu



Bandipura generally maintains better air quality compared to the major urban centers. However, it is not immune to pollution spikes, particularly during certain weather conditions that trap pollutants in the valley

Bandipura

BY-MANSI M NAIK

MASTER OF SCIENCE IN INFORMATION TECHNOLOGY

POLLUTION WATCHDOG

PUNJAB | FRIDAY | 02 / 08 / 2024

PUNJAB AQI LEVELS TODAY

↑↓	Status	↑↓	AQI-US	↑↓	PM2.5	↑↓	PM10	↑↓
Abohar	GOOD		16		4		6	
Amritsar	MODERATE		75		24		53	
Haripur	MODERATE		70		21		41	
Jalandhar	MODERATE		87		29		57	
Khem Karan	GOOD		38		8		18	
Ludhiana	POOR		133		49		88	
Malaut	GOOD		24		6		15	

<https://www.aqi.in/in/dashboard/india/punjab>

SEMINAR PUTS FOCUS ON AIR QUALITY IN AMRITSAR, ITS HARMFUL HEALTH EFFECTS



Amritsar 9th May

To push for monitoring air quality and implementation of effective air pollution checks in Amritsar, several organisations including Breathe Free, FLO Amritsar and Rotary Club jointly hosted a seminar to create awareness regarding importance of air quality and its impact on health.

The seminar focused on harmful effects of air pollution, respiratory illnesses and steps to ensure better air quality

Experts highlighted the importance of collaboration among organisations to address respiratory allergies being caused due to rising air pollution

<https://www.tribuneindia.com/news/amritsar/seminar-puts-focus-on-air-quality-in-amritsar-its-harmful-health-effects-619745>

STUBBLE BURNING: PUNJAB RECORDS OVER 1000 FARM FIRES IN A SINGLE DAY; HIGHEST IN THE SEASON



Punjab, 30 Oct 2023

Despite the rising number of farm fire cases in the state this season, a look at previous year's data will reflect on the reduction in stubble burning in Punjab.

Stubble burning in Punjab is considered as one of the main reasons behind the severe air pollution that chokes north Indian states during the winter season in October and November. Most of the farmers opt for burning crop residue to prepare their fields for the next crop in a shorter time.

<https://www.livemint.com/news/india/stubble-burning-punjab-records-over-1000-farm-fires-in-a-single-day-highest-in-the-season-11698655708395.html>

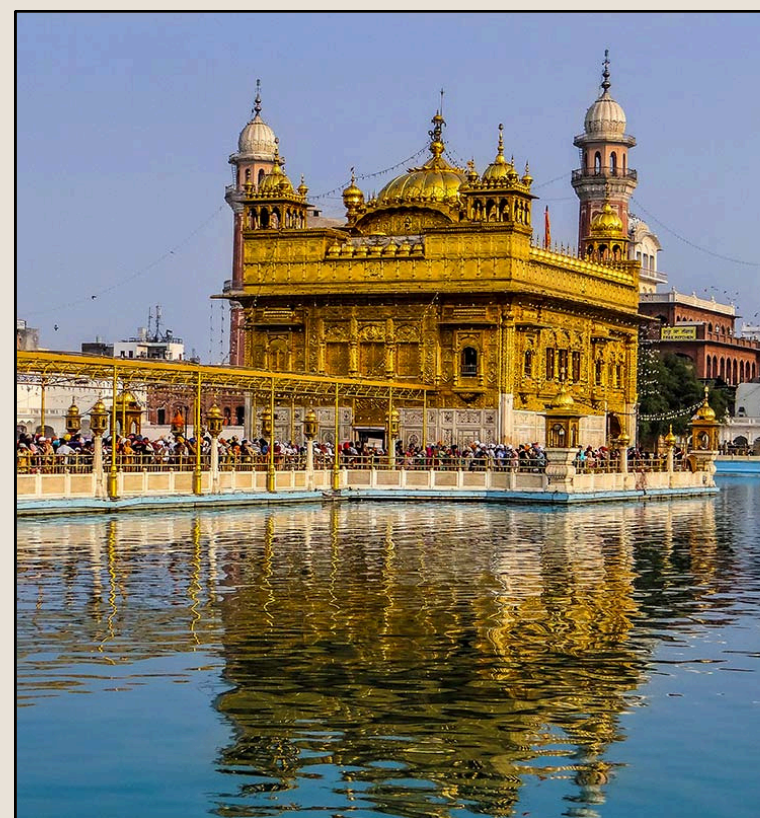
LUDHIANA AMONG TOP 100 MOST POLLUTED CITIES IN COUNTRY

Ludhiana, Jul 29, 2024

Despite having witnessed the cleanest air of the ongoing year on July 6, Ludhiana has not made long-term progress in terms of air quality with AQI 40, yet Ludhiana is among the top 100 most polluted cities of the country in the first half of 2024 by a study conducted by the Centre for Research on Energy and Clean Air (CREA).

<https://timesofindia.indiatimes.com/city/ludhiana/ludhiana-ranked-among-top-100-most-polluted-cities-in-india/articleshow/112092461.cms>

AMRITSAR: RISING POLLUTION TAKING THE SHINE OFF GOLDEN TEMPLE



Amritsar Apr 03, 2022

The gold plating and marble surface of the holiest Sikh shrine, Golden Temple are losing their sheen, thanks to the rising pollution in the holy city. This has made the Shiromani Gurdwara Parbandhak Committee (SGPC) getting it cleaned frequently. To monitor the ambient air quality within and around the Golden Temple, an air quality monitoring station was set up on its premises in 2016. As per data assessed by the Punjab Pollution Control Board (PPCB), the quantity of air pollutants that affect the gold plating and marble surface is increasing.

<https://www.hindustantimes.com/cities/chandigarh-news/amritsar-rising-pollution-taking-the-shine-off-golden-temple-101648930040667.html>

DEPARTMENT OF PSYCHOLOGY
REPORT ON INNOVATIVE MODE OF ASSESSMENT

2023-24

1. Dr. Sobita Kirtani had a Pecha Kucha style of presentation followed for CA presentation for two courses, namely Basic Course in Psychology I (UG-PSY-101) of Semester I and Child Psychology (PSY-III.E-2) for Semester III. In this style of presentation, students must present the topic in the form of 20 slides containing images, and each image is presented for not more than 20 seconds.
2. Dr. Sobita Kirtani conducted a CA for Child Psychology course (PSY-III.E-2) of Semester III in which students were given 03 questions for group work that they could answer using online resources and books followed with a group discussion. The last question was a higher order based on the first three and had to be answered individually. This was designed such that students could gain from team work while also be assessed individually.
3. For an elective course titled Gerontology (PSY-VI.E-13) of Semester VI taught by Dr. Sobita Kirtani, students were required to design and demonstrate activities (both physical and mental) for older persons, which had to be rooted into Goan culture. Students had to present research related information using power point presentation and demonstrate the activities in the class room. The instructions had to be delivered in any one of the following regional languages – Konkani, Marathi, or Hindi.
4. For an elective course titled Gerontology (PSY-VI.E-13) of Semester VI taught by Dr. Sobita Kirtani, students had to submit a proposal of an idea (hypothetically to the Govt of Goa) based on the knowledge acquired through the course as well as through research-based identification of needs of older persons. Students were given a detailed format following which they had to prepare the proposal.

Evidence:

CA 3- PROBLEM SOLVING

Physical and Mental Activities

Mareshah Pereira 2101222

Alyssa Colaco 2101264



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- RESEARCH EVIDENCE ON PHYSICAL ACTIVITY
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PHYSICAL ACTIVITY

NALACHO ZUMVO

MATERIALS USED


- A bat made of coconut branch
- Small coconut used as a ball
- Obstacles made of clay pots
- Stepping stones made of coconut shells
- Goal post made of bottles and rope
- Bowling pins made of cans
- Mini goals made of bottles and rope



Why Nalacho Zumvo?

- The game is designed to provide gentle exercise to older persons to keep them active
- Health benefits
- The game can be played with multiple people and a time limit can be added to make it more competitive
- “Island stepping stones” helps in bending limitations
- Can drive an elderly to be determined to complete the whole course because of the fun and interesting segments involved
- Celebrates Goan heritage by incorporating facilities available in goa

RESEARCH EVIDENCE FOR HOCKEY DRILLS


- Benefits of hockey or hockey drills include agility, coordination, improved muscular system and flexibility (Top 10 Health Benefits of Hockey, 2015).
 - Research by Castana et al.(2020) showed that hockey as a recreational activity improved cardiovascular system and blood profile across both sexes.
 - Another research showed that coordination improved especially hand eye coordination as a result of a ball and stick game like hockey(Dunsky, 2019)
 - A research survey in England displayed evidences of muscular strengthing due to hockey drills like dodging the cones(Foster & Skelton, 2018)(Daw, 2016).
- 

RESEARCH EVIDENCE FOR HOCKEY DRILLS

- Numerous studies proven that dribbling sports like hockey help in preventing diseases and mental health illness that are caused by problems faced by elderly(Thomas et al., 2019).
- In studies where interviews are conducted on older persons part of masters sports leagues like hockey say that they have healthy muscle mass and maximum oxygen uptake capacity compared what they had in their 30's(Deneau et al., 2020)



RESEARCH EVIDENCE FOR STEPPING STONES AND GOAL SCORING

- A research was conducted on group of people older 60 and it was found that there was improvement in balance and walking after walking on cobblestone mats or paths(Stowe, n.d.).
 - Another research provided evidences that stepping stones also decreases chances of high blood pressure (Stowe, n.d.).
 - Responses of Chinese doctors and people who practice stepping stones report reduction in backpain and flexibility(Patchareeya & Wongphon, 2020).
 - While there are not many physical benefits, researches show that hitting through a target or goal scoring has improved functions like flexibility or control of speed, power and direction and further have many cognitive benefits(Tomaselli, 2022) (Oliveira et al., n.d.)
- 



MENTAL ACTIVITY

PICTURE BINGO

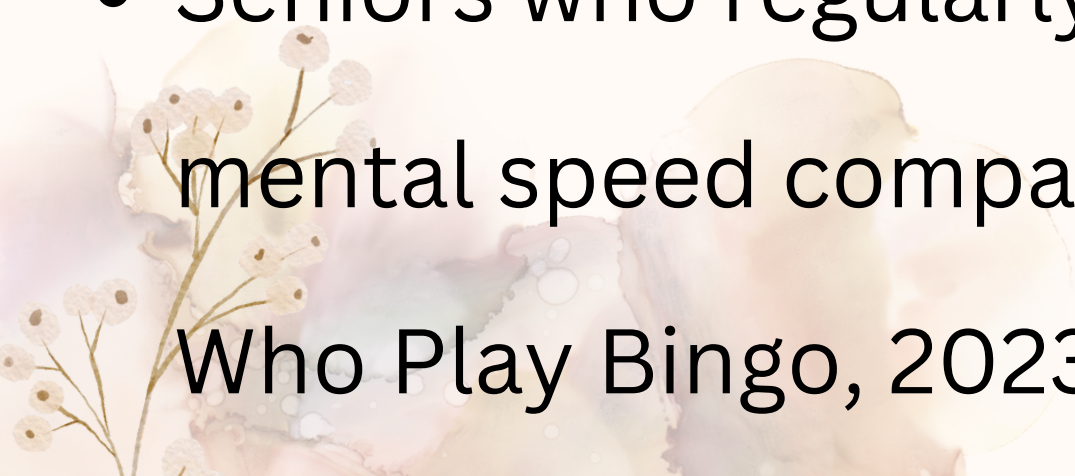


WHY BINGO ?

- BINGO IS A FUN AS WELL AS A COGNITIVELY ENRICHING GAME
- IT FOSTERS COMMUNITY ENGAGEMENT AND IMPROVES EMOTIONAL WELLNESS MAKING THEM ACTIVE AND ENERGETIC (CARETECT, 2022).
- PICTURE BINGO FOCUSES ON VISUAL ASPECTS, LITERARY ABILITIES AND ATTENTION CAPACITY OF THE ELDERLY (CRONIN, 2011).
- CAN BE PLAYED WHEN OUT DOOR FACILITIES ARE NOT AVAILABLE (EFFECTIVENESS OF A PHYSICAL ACTIVITY ENHANCING PROGRAM FOR USE DURING INDOOR RECESS, 2009)
- IT HELPS WITH MEMORY AND THE USE OF GOAN ITEMS REFRESHES THEIR OWN EXPERIENCES AND LONG TERM MEMORY

MEMORY AND ATTENTION

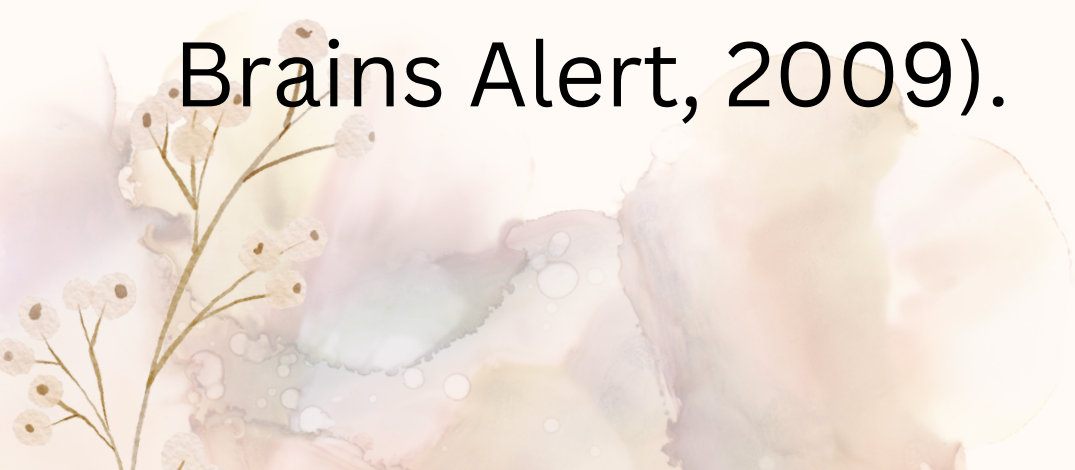
RESEARCH SUGGESTS

- As we age there is a noticeable decline in our memory (National Institute of Health, 2023) and age related reduction in attention and focus (Guarnera, 2008).
 - Results shows that continuous playing of bingo for seven consecutive week improves the memory (Robles, 2019).
 - Bingo stimulates many areas within the cognitive apparatus including attention, focus, concentration, and immediate memory (Sobel, 2023).
 - Seniors who regularly played bingo scored higher on tests evaluating memory and mental speed compared to people who did not play (6 Major Advantages for Seniors Who Play Bingo, 2023).
- 

MEMORY AND ATTENTION


RESEARCH SUGGESTS

- Bingo has positive impact to the brain where the brain is able to train the person to think faster and the brain to work quicker (Robles, 2019).
- Julie Winstone, of Southampton University, said players were faster and more accurate than non-bingo players on tests measuring mental speed, the ability to scan for information, and memory (Bingo Calculations Help Elderly People Keep Their Brains Alert, 2009).



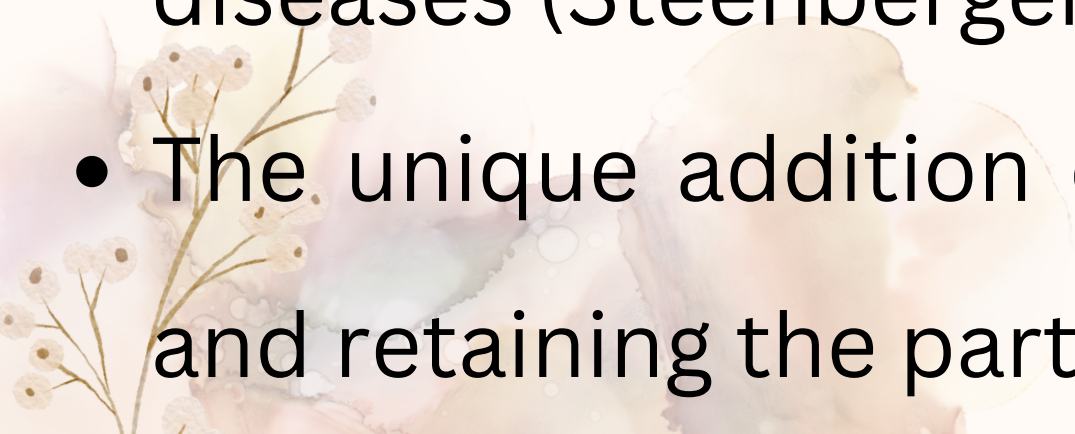
MOTOR MOVEMENTS

RESEARCH SUGGESTS

- Older aged adults showing a relationship between reduced strength and reduced hand steadiness (Martin, 2015).
 - Bingo helps hand eye coordination (CareFect, 2022) .
 - The arranging of cards helps with fine motor skills.
 - Playing bingo helps with pain and stiffness associated with arthritis (6 Major Advantages for Seniors Who Play Bingo, 2023).
- 

SOCIAL ENGAGEMENT

RESEARCH SUGGESTS

- Research suggests that as age increases social circles reduce (Martin, 2015). However more socially active elderly people experience less cognitive decline (James, 2011).
 - Bingo is excellent for bringing people together and fostering healthy friendships (CareFect, 2022).
 - Participation in just bingo alone has been found to increase socialization and some aspects of cognitive performance in older adults with Parkinson's and Alzheimer's diseases (Steenbergen, 2015).
 - The unique addition of bingo as a program enhancer was successful at attracting and retaining the participants of one study (Crandall, 2009).
- 

Conclusion

- To conclude, staying active in both body and mind is essential for older persons.
- Physical activities like Nalacho Zumvo promote mobility and independence from illness.
- Mental activities like picture bingo fosters cognitive functions like attention and memory.
- They also allow the older person to engage with others, fostering healthy relationships.

THANK YOU



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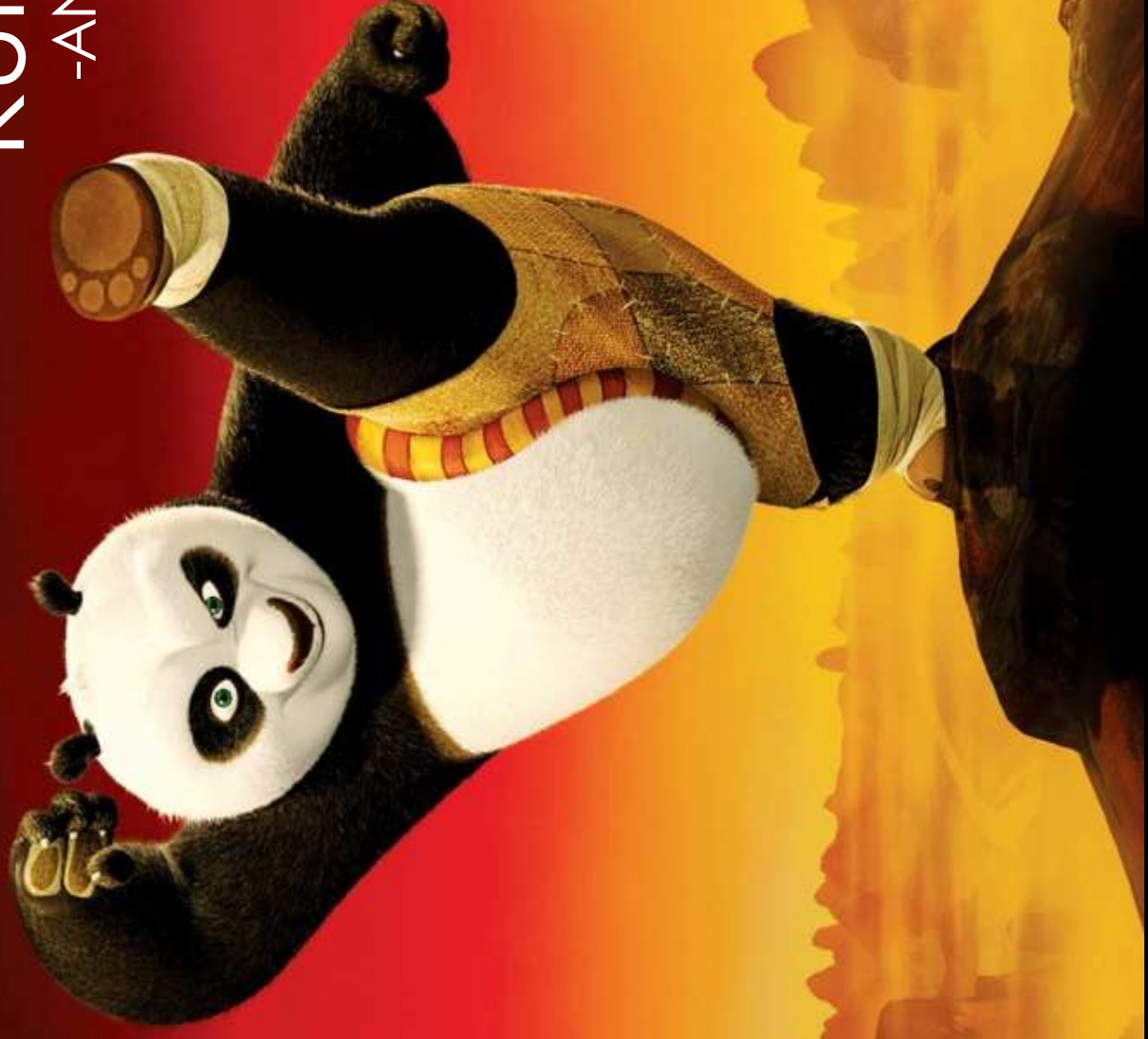
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KUNG FU PANDA -AN EMOTIONAL ANALYSIS

PRATISHTHA SHENOY

2301043

UG-PSY-101



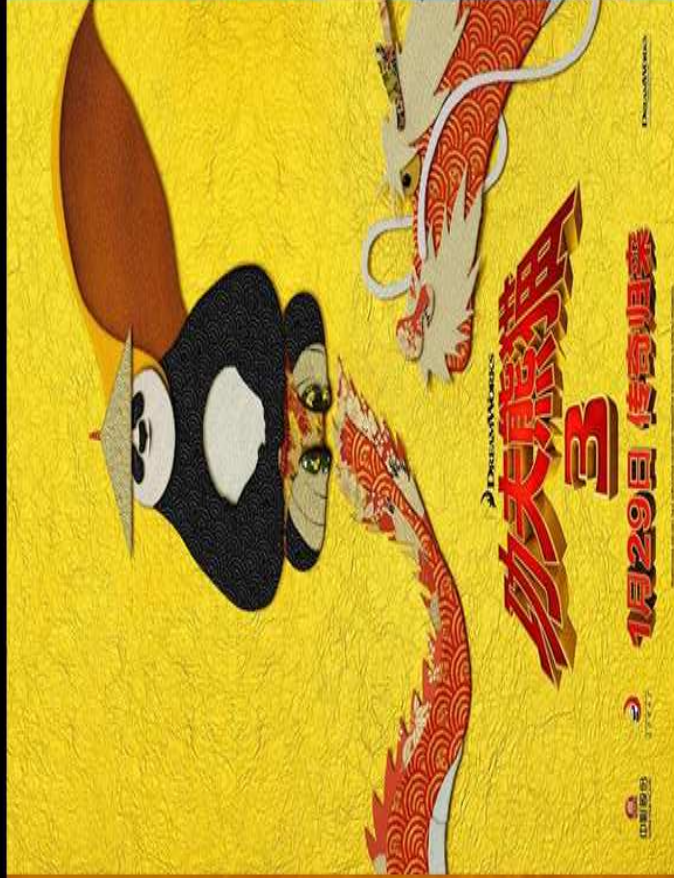
A C K B L A C K

POOSH



MAY 2011
COMING TO THEATRES IN 3D
ALSO PLAYING IN 2D

KungFuPanda.com



功夫熊猫 3

1月29日 传奇归来



무적의 5인방

타이그리스
안젤리나 톰리

功夫熊猫 3

1월 28일 대개봉



THE WEIGHT IS OVER

KUNG FU PANDA

JANUARY 2016



J A C K B L A C K

KUNG FU PANDA

PREPARE FOR AWESOMENESS
SUMMER 2008



MAY 2

COMING TO THEATRES
ALSO PLAYING IN 3D

KungFuPanda.com



A central dark blue circle contains the text "Emotional Intelligence". Surrounding it are five light blue circles, each containing a component of emotional intelligence: "Self Awareness", "Empathy", "Motivation", "Self Regulation", and "Social Skills".

Social Skills

Self Regulation

Emotional Intelligence

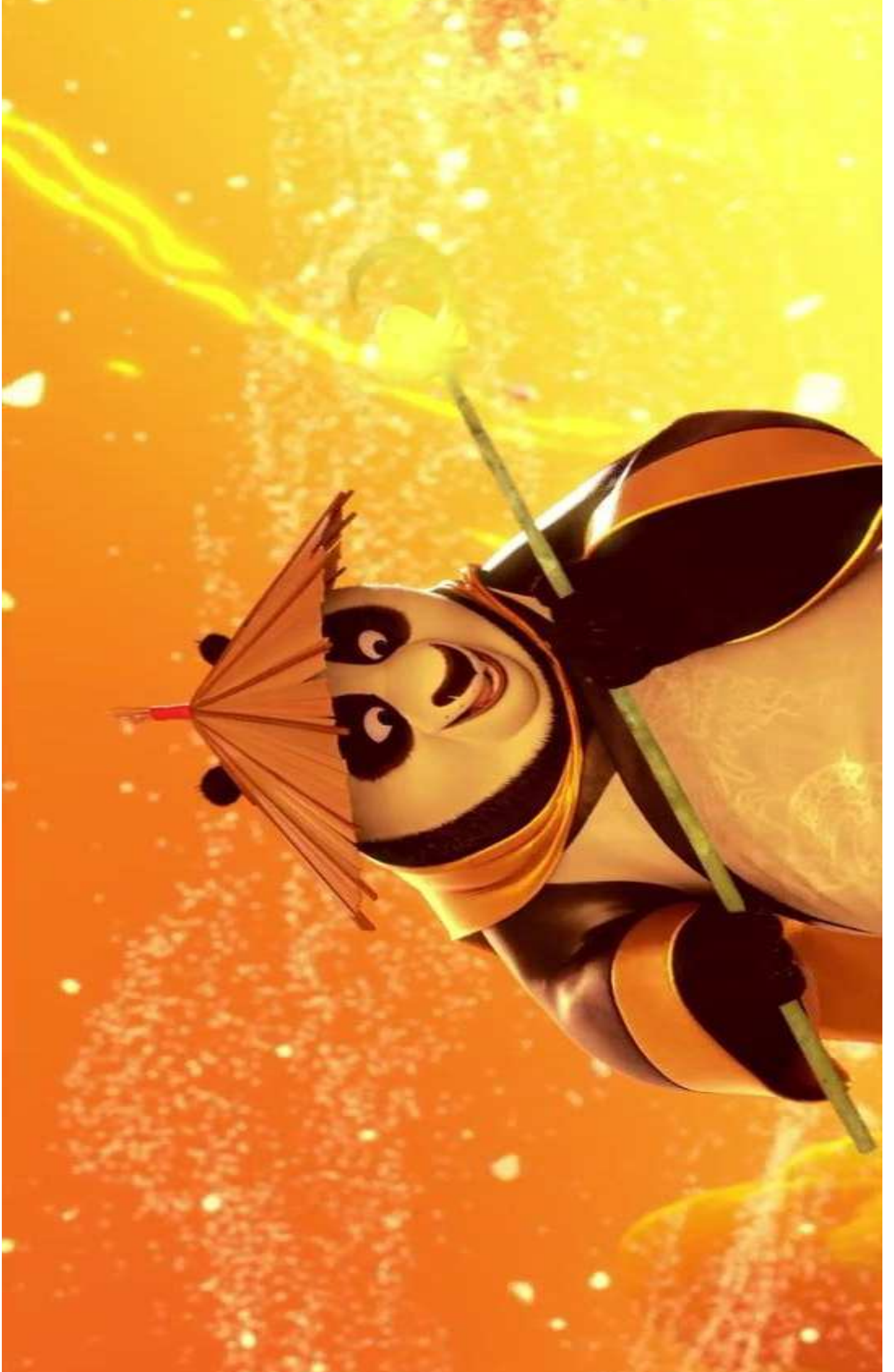
Motivation

Self Awareness

Empathy







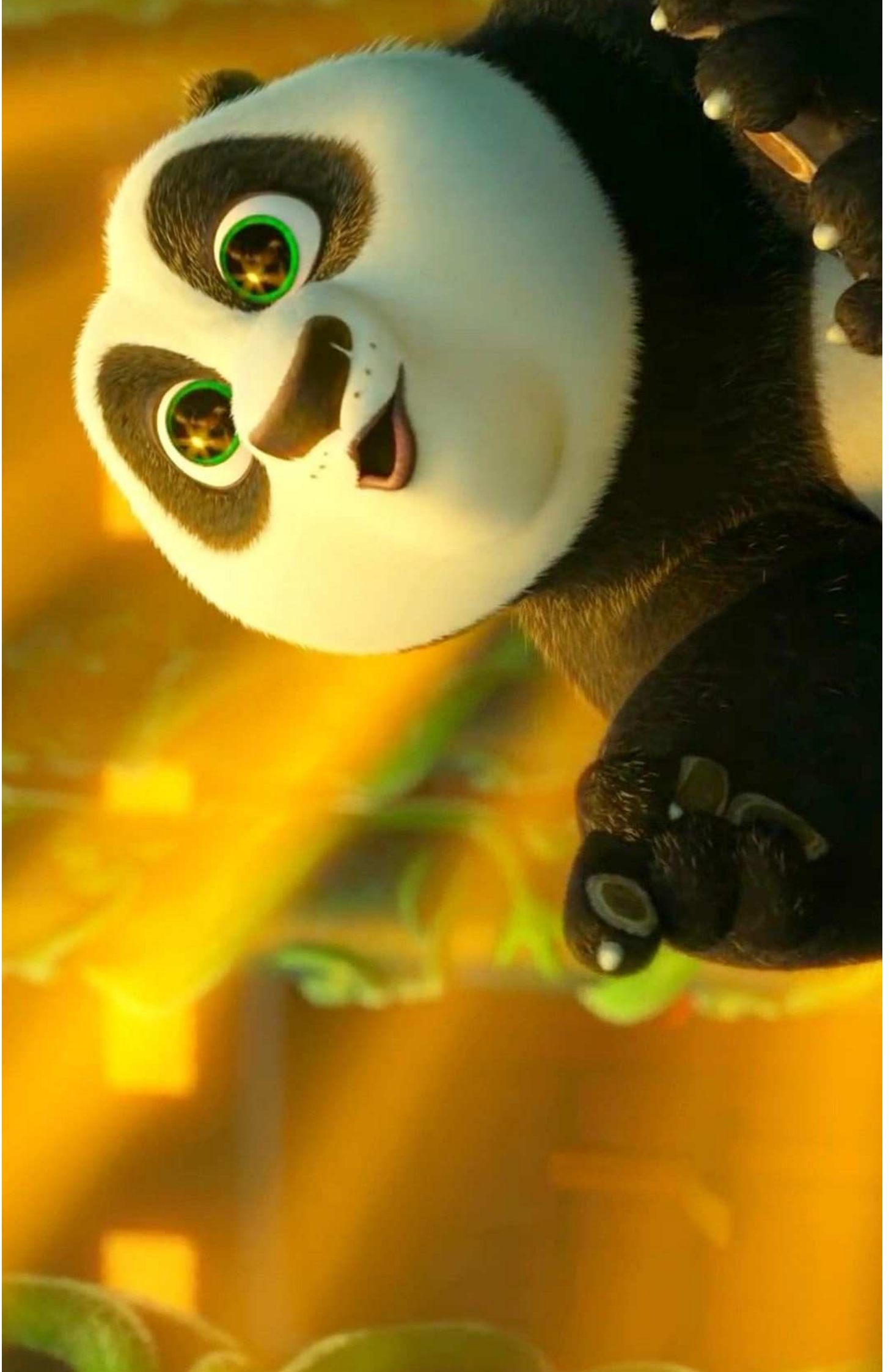


















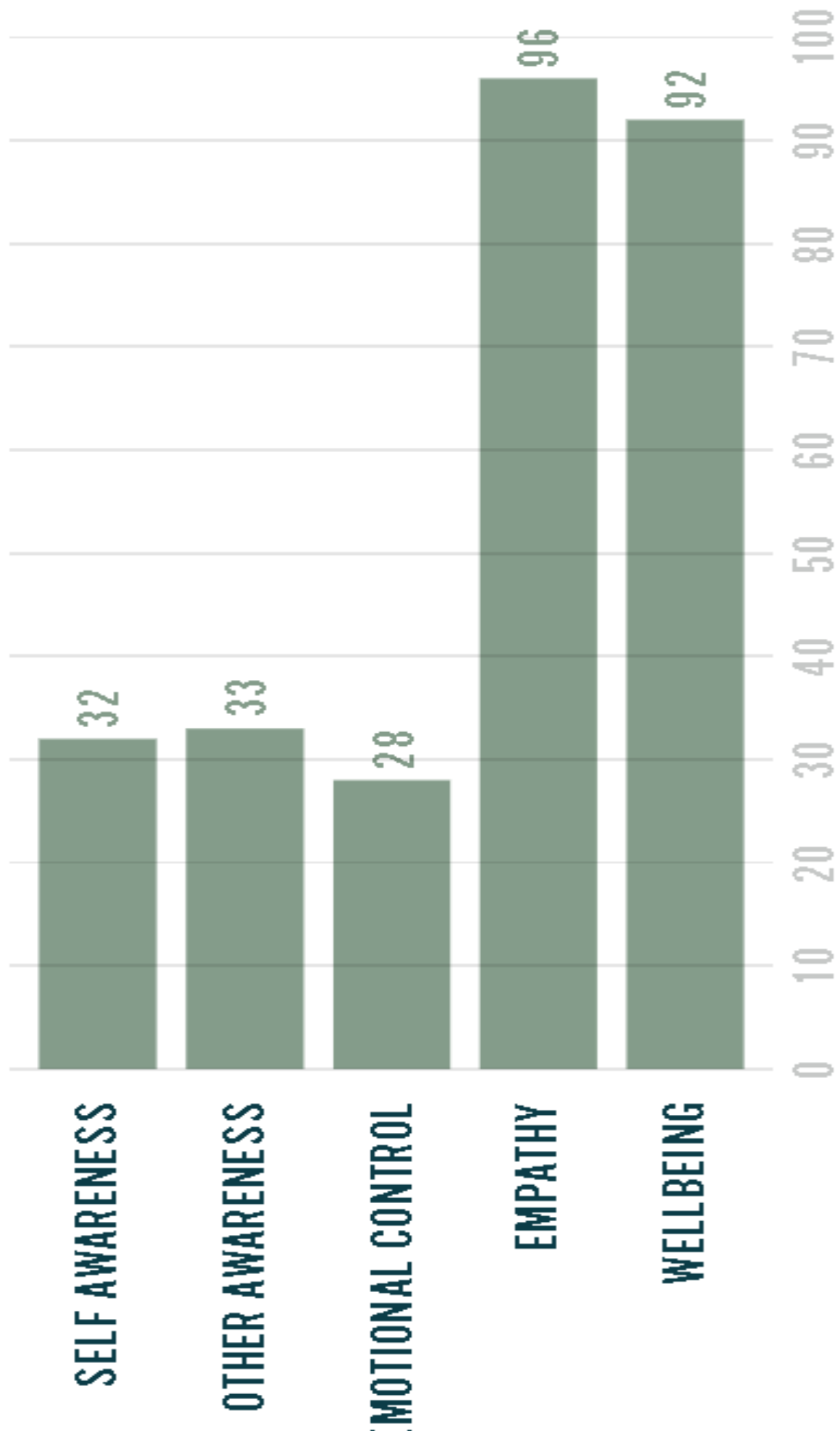








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HOME ENTERTAINMENT
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THANK YOU!

