

Online Faculty Development Program on
“Computational Genomics and Proteomics”
(Under E & ICT Academy of IIITDM Jabalpur)

Jointly Organized by
IIITDM Jabalpur and JUIT Solan
28th Aug. 2022 to 10th Sept. 2022

1. About the FDP

The faculty development program (FDP) on Computational Genomics & Proteomics got successfully completed on 10.09.22. This event was sponsored by the Electronics & ICT Academy, an initiative of the Ministry of Electronics & Information Technology, Government of India. The event commenced on 28.08.22 and was jointly organized by ECE departments of Jaypee University of Information Technology (JUIT), Wagnaghat, Solan & IIITDM Jabalpur. During this two-week FDP eminent speakers delivered talks on the Fundamentals of Molecular Biology, Genome Sequencing, Signal Processing, Machine learning, Personalized Medicine, MATLAB Programming & Computer-aided drug design. Also, Numerous case studies were discussed to highlight the applicability of computational methods in facilitating molecular biology experimentations. The learned speakers who delivered the talks in this program include Prof. B.Jayaram (IIT Delhi), Prof. L. Shashidhara (IISER, Pune), Prof. Rajiv Saxena (JIIT Noida), Dr. Pushpendra Singh (Scientist, ICMR), Prof. S.N.Sharma (IIITDM, Jabalpur), Dr. D.K. Shakya (SATI, Vidisha), Dr. S.D. Sharma (JUIT, Wagnaghat) and Yashpal Yadav. Prof. Aparajita Ojha, Coordinator E&ICT Academy Jabalpur, emphasized the importance of such collaborative programs. In his concluding remarks Prof. R.K. Sharma, Vice Chancellor, JUIT Wagnaghat wished that this program will promote collaborative cross-disciplinary research and that participants will contribute towards nation-building by developing novel solutions for the existing molecular biology problems using computational tools. Prof. Rajiv Kumar (HOD, ECE) also briefed on the facilities and infrastructure of the department. Prof. S.N. Sharma, ECE Department, IIITDM Jabalpur & Dr. S.D. Sharma, ECE Department, and JUIT Wagnaghat were the coordinators of this program.

2. Coordinators

- Prof. Sanjeev Narayan Sharma (Prof. S.N.Sharma), ECE Department, PDPM IIITDM Jabalpur, M.P.
- Dr. Sunil Datt Sharma (Dr. S.D. Sharma), ECE Department, JUIT, Wagnaghat, Solan, H.P.

3. Number of Participants

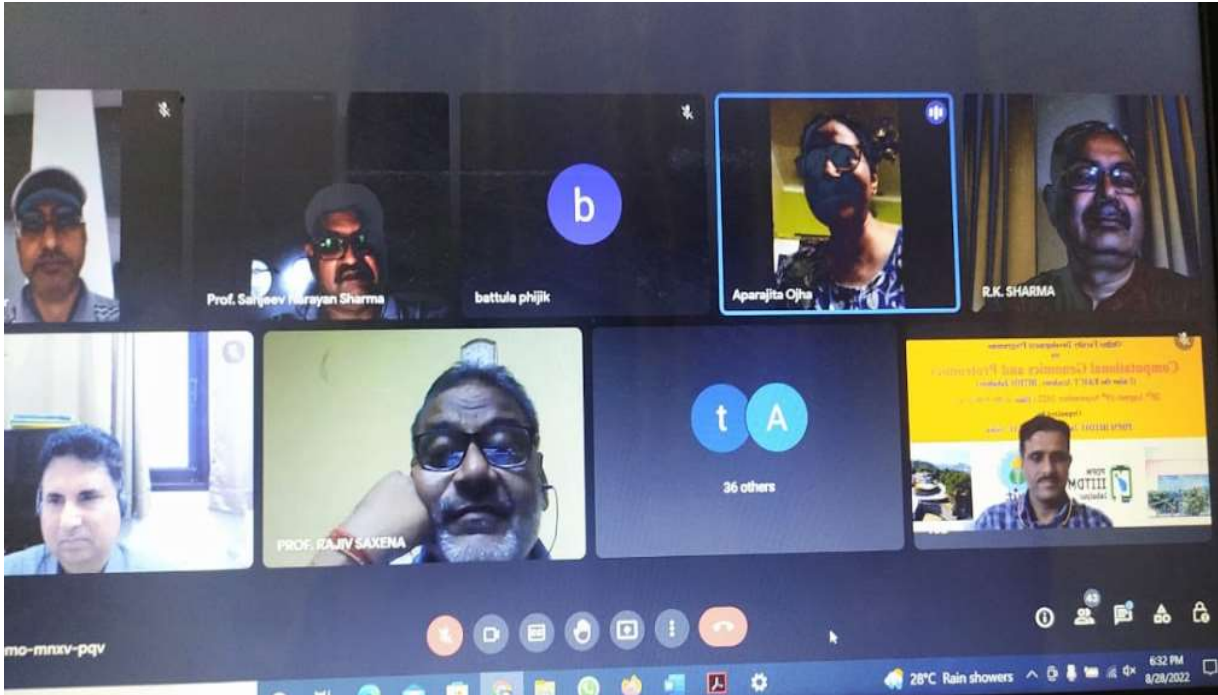
- External participants: 52
- Internal participants: 05

4. Highlights of the online FDP

Date: 28-08-22

Session-1: Inaugural Session on-28-08-22

During the inaugural ceremony, Prof. Aparajita Ojha (Head, E & ICT Academy, IIITDM Jabalpur), Prof. (Dr.) R.K. Sharma (Vice-Chancellor, JUIT), eminent academician Prof. Rajiv Saxena (Adjunct Professor, JIIT Noida), Prof. Sanjeev Narayan Sharma (ECE, PDPM IIITDM, Jabalpur), and Prof. Rajiv Kumar (HOD, ECE JUIT) were present. Total 57 participants from different parts of the country have been registered for the FDP. The session was coordinated by Prof. Sanjeev Narayan Sharma (PDPM IIITDM Jabalpur), and Dr. Sunil Datt Sharma (Jaypee University of Information Technology, Solan, H.P.) expressed the vote of thanks to distinguished dignitaries and participants for their kind presence at the end of the session.

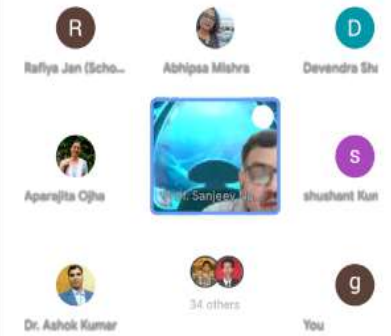
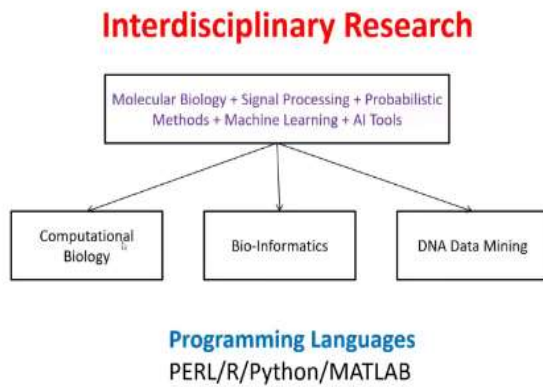


Lecture-1: Fundamentals of Genomics & Proteomics by Prof. S.N.Sharma, IIITDM, Jabalpur

8/28/22, 7:24 PM

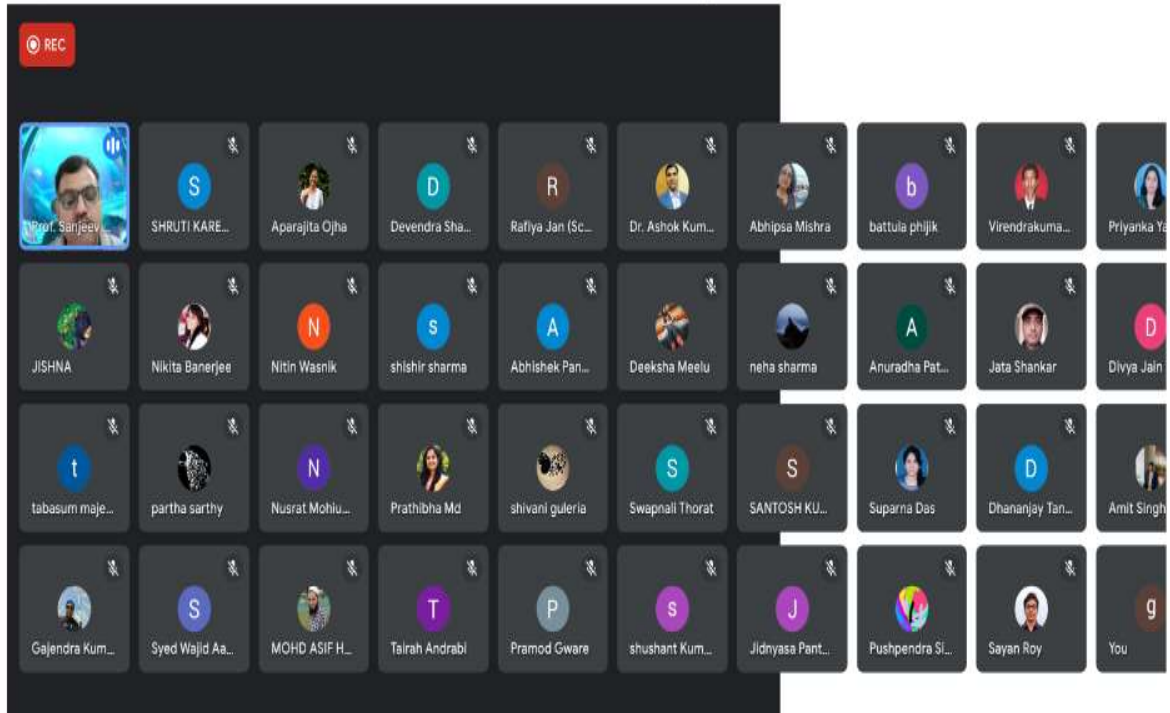
Meet - emo-mnxv-pqv

REC Prof. Sanjeev Narayan Sharma is presenting



8/28/22, 8:07 PM

Meet - emo-mnxv-pqv



Date: 29-08-22

Lecture-2: Fundamentals Signals & Systems by Prof. Rajiv Saxena (Former VC, Jaypee University, AnoopShahr, & Adjunct Professor, IIIT Noida)

RAJIV SAXENA is presenting

WHAT IS SIGNAL PROCESSING ?

- SIGNAL PROCESSING IS AN IMMENSE AND DIVERSE FIELD.
- IT IS ALSO A FIELD THAT REMAINS MYSTERIOUS OR QUITE UNKNOWN TO MOST PEOPLE.
- AT THE END OF THE 20TH CENTURY SIGNAL PROCESSING IS A VITAL TECHNOLOGY IN MANY AREAS –
 - COMMUNICATION AND INFO. PROCESS.
 - CONSUMER ELECTRONICS AND CONTROL SYSTEMS
 - MEDICAL DIAGNOSIS AND SCI. INSTRUMENTATION
 - PROTEIN MODELING & PERSONALISED MEDICINE.

August 29, 2022 Computational Geopros And Proteomics, PDFMISTOM • IIIT

Lecture-3: Accessing DNA, Protein and Cancer Databases, Numerical Mapping Schemes by Prof. S.N.Sharma

The screenshot shows a presentation slide with the following content:

How to Access Data – An Example

- The gene F56F11.4 is present on chromosome III of *C. Elegans* with and is having accession number NC003281.10. The gene length is 11,956 nucleotides extending from 2854558 to 2866513. The position of six exons and the amino acids coded by them are -
- Exon 1 – 2856229 to 2856790
- Exon 2 – 2858709 to 2858820
- Exon 3 – 2860309 to 2860638
- Exon 4 – 2861895 to 2862158
- Exon 5 – 2863246 to 2863425
- Exon 6 – 2865056 to 2865386

Date: 30-08-22

Lecture-4: Discrete Transforms by Prof. Rajiv Saxena (Former VC, Jaypee University, AnoopShahr, & Adjunct Professor, IIIT Noida)

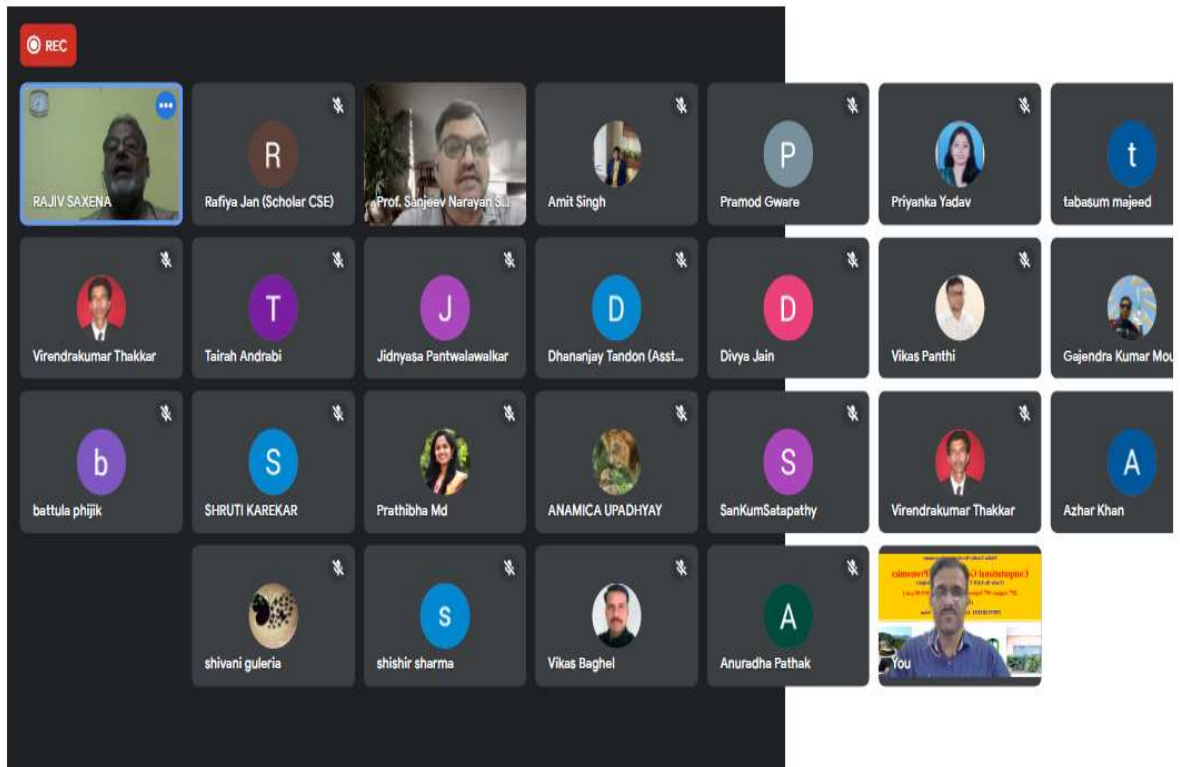
The screenshot shows a presentation slide with the following content:

Fast Fourier Transform (FFT)

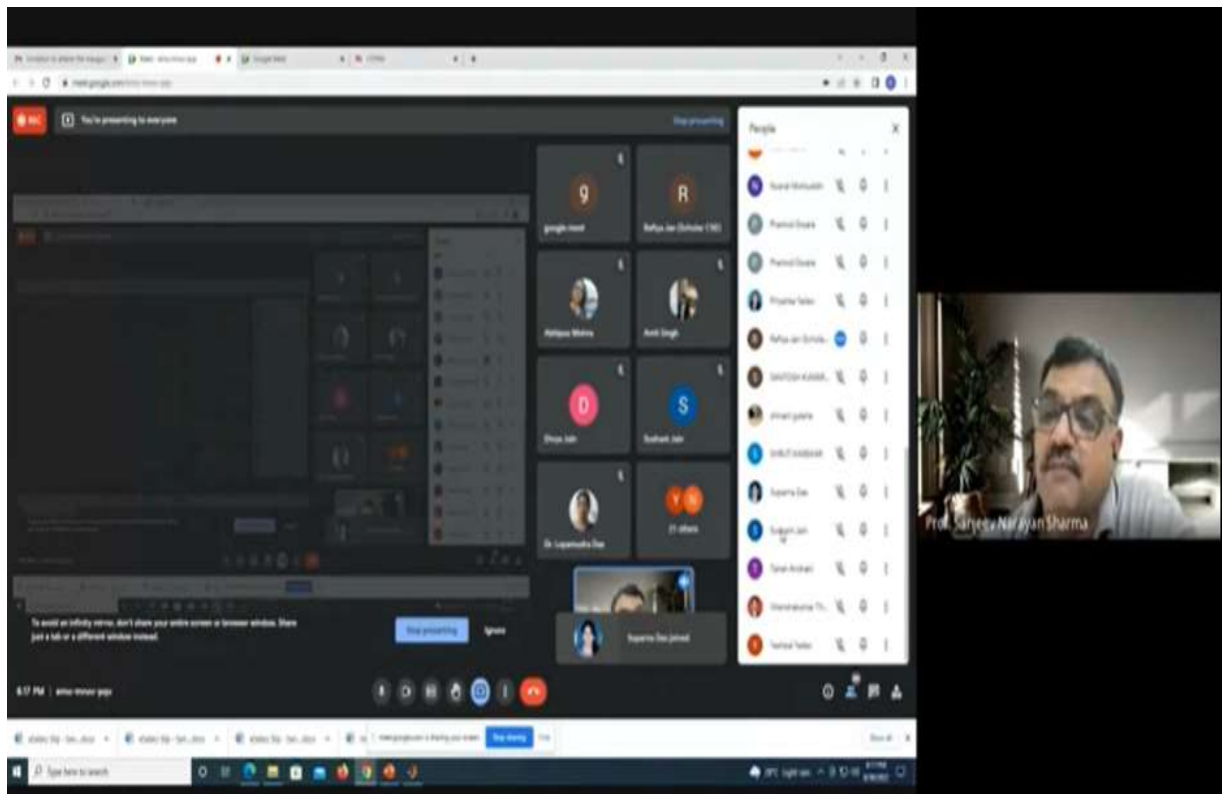
- Published in the year 1965 by Cooley & Tukey.
- **FFT CM = $(N/2) \log_2 N$**
- **FFT CA = $(N/2) \log_2 N$**

At the bottom of the slide, it says: August 30, 2022 WITOM - IIT (30-08-2022) 10

The slide is part of a Zoom meeting titled "Meet - emo-mnxv-pqv" with "RAJIV SAXENA is presenting". A grid of participant avatars is visible on the right side of the screen.



Lecture-5: Computation Using MATLAB-I by Prof. S.N. Sharma, IITDM Jabalpur



Date: 31-08-22.

Lecture-6: Digital Filters by Prof. Rajiv Saxena (Former VC, Jaypee University, AnoopShahr, & Adjunct Professor, IIIT Noida)

8/31/22, 6:17 PM

Meet - emo-mnxv-pqv

REC RAJIV SAXENA is presenting

Short Time Fourier Transform (STFT)

RAJIV SAXENA Prof. Sanjeev Na Amit Singh

battula phijik Pramod Gware Rafiya Jan (S)

ANAMICA UPAD... Prathibha Md Tairah Andrat

Jidnyasa Pantwa... 13 others You

Lecture-7: Computation Using MATLAB-II by Prof. S.N. Sharma, IITDM Jabalpur

8/31/22, 8:20 PM

Meet - emo-mnxv-pqv

REC Prof. Sanjeev Narayan Sharma is presenting

For Loops

50

- For loops allow a group of commands to be repeated for a fixed, predetermined number of times. The general form of a for Loop is

```
for x= Array
    (Commands)
end
```
- The commands between the for and end statements are executed once for every column in an array. At each iteration, x is assigned to the next column of array; during the nth time through the loop x= array (:, n)

Prof. Sanjeev Na Rafiya Jan (Scho...) Pramod Gware

tabasum majeed Divya Chauhan Virendrakumar

Virendrakumar T... Gajendra Kumar ... Azhar Khan

SHRUTI KAREKAR 13 others You

Date: 01-09-22

Lecture-8: Introduction to Bioinformatics MATLAB Toolbox by Dr. D.K. Shakya, SATI, Vidisha, M.P.

9/1/22, 6:21 PM

Meet - emo-mnxv-pqv

REC Devendra Shakya is presenting

1 Genomic, Proteomics and Bioinformatics Toolbox - Microsoft PowerPoint

Home Insert Design Animations Slide Show Review View Help

Clipboard Slides Font Paragraph Drawing Marking

Genomic Proteomic & Bioinformatics Toolbox : An Introduction

By
Dr. Devendra Kumar Shakya
Assistant Professor,
Department of Electronics Engineering,
Samrat Ashok Technological Institute, Vidisha(M.P.), India 464001
Email: dshakya.ec@satengg.in

Click to add notes

meet.google.com is sharing your screen. Stop sharing Hide

Type here to search

Devendra Shakya Amit Singh Rafiya Jan (S...
Prof. Sanjeev Na... Gajendra Kumar ... MOHD ASIF H...
Pramod Gware Priyanka Yadav Prathibha M...
Tairah Andrabi 9 others You

Lecture-9: Signal Processing Using MATLAB by Prof. S.N. Sharma, IIITDM Jabalpur

File Edit View Signal Processing Toolbox Help

Plotting Parameters

Response Type: Magnitude

Plot Style: Line

Plot Title: Magnitude Spectrum

Plot Range: 0 to 1000

Plot Resolution: 1000

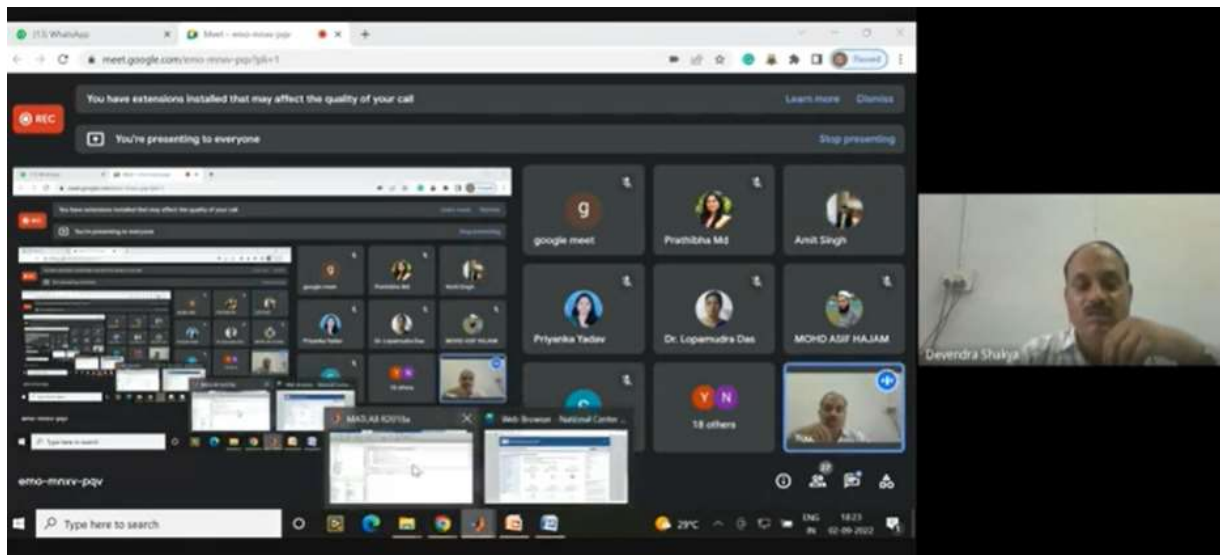
Plot Labels: X-axis: Frequency (Hz), Y-axis: Magnitude (dB)

Computing Response ... Done

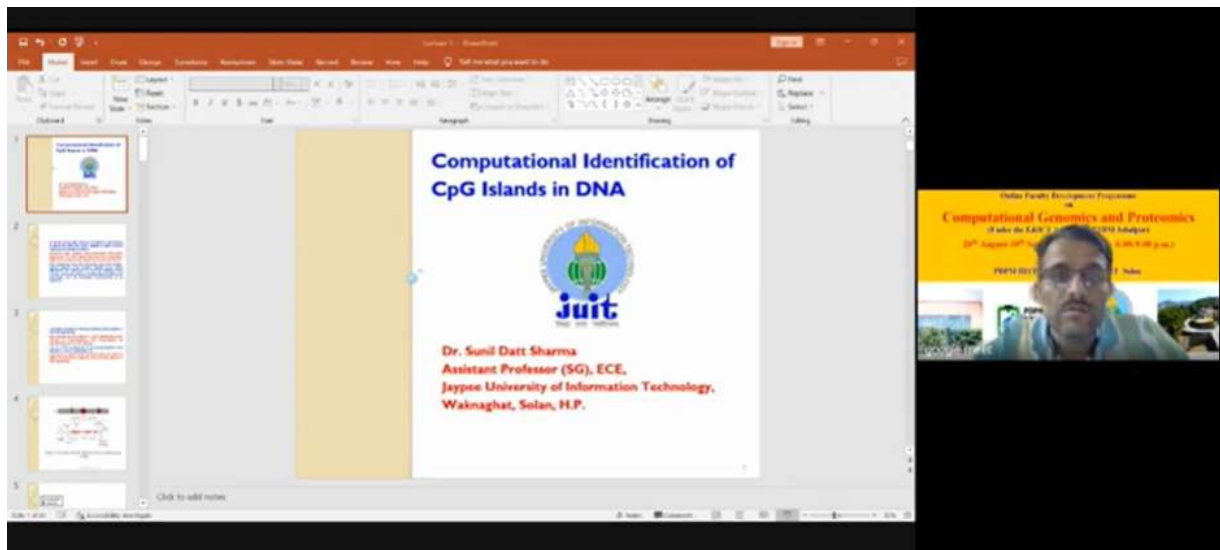
Prof. Sanjeev Narayan Sharma

Date: 02-09-22

Lecture-10: Hands on Bioinformatics MATLAB Toolbox by Dr. D.K. Shakya, SATI, Vidisha, M.P.

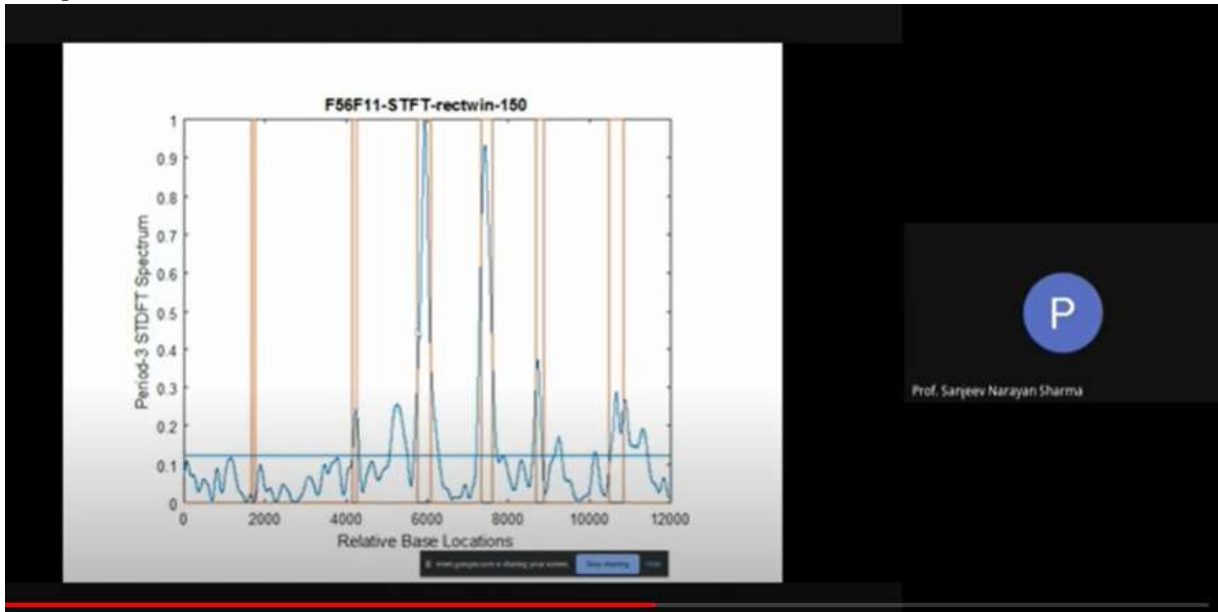


Lecture-11: Computational of Identification of CpG Islands in DNA by Dr. S.D.Sharma, JUIT, Solan



Date: 03-09-22

Lecture-12: Computational Identification of protein coding region in DNA by Prof. S.N. Sharma, IIITDM Jabalpur



Lecture-13: MATLAB Implementation of Computational Identification of protein coding region in DNA by Mr. Yashpal Yadav

9/3/22, 8:35 PM Meet - emo-mnxv-pqv

Date: 05-09-22

Lecture-14: Next generation sequencing by Dr. Pushendra Singh, ICMR (NIRTH), Jabalpur, M.P.

9/5/22, 6:18 PM Meet - emo-mnxv-pqv

REC Pushendra Singh is presenting

1 Primer elongation and chain termination

2 Capillary gel electrophoresis separation of DNA fragments

3 Laser detection of fluorochromes and computational sequence analysis

Participants: Pushendra Singh, neha kumari, Nitin Wasnik, Nivedita Thakur, shivani guleria, Divya Chauhan, Shriram Waman, Sunita Singh, Devendra Sharma, Prof. Sanjeev Na..., 13 others, You

Lecture-15: From Genetics to Cancer Genome by Prof L. Shashidhara, IISER, Pune

9/5/22, 7:52 PM Meet - emo-mnxv-pqv

REC Ls Shashidhara is presenting

Basic features of all forms of life: Central Dogma of Life!

Transcription

Translation

Reverse Transcription

Protein

Cell

DNA

mRNA

Replication

Participants: L.S. Shashidhara, Ls Shashidhara, Gajendra Kur..., Prof. Sanjeev Na..., shivani guleria, Prathibha M..., SHIRUTI KAREKAR, rajeswari naraya..., Nitin Wasnik, Divya Jain, 10 others, You

Date: 06-09-22

Lecture-16: Computational Identification of Hot Spot in Protein by Prof. S.N. Sharma, IITDM Jabalpur

• The characteristic frequency can be determined from

$$S(e^{j\omega}) = |X_1(e^{j\omega})| |X_2(e^{j\omega})| |X_3(e^{j\omega})| \dots |X_M(e^{j\omega})|$$

• $S(e^{j\omega})$ is known as the consensus spectrum.

Hot-spot locations correspond to the regions in the numerical sequence where the characteristic freq. is dominant.

Consensus spectrum of Cytochrome -C functional group.

Peak at the characteristic frequency

Squared Magnitude

Frequency

Characteristic frequency

Prof. S.N. Sharma

Lecture-17: MATLAB Implementation of Computational Identification of Hot Spot in Protein by Mr. Yashpal Yadav

```
127 % Load data from MAT-file into workspace
128
129 mat_cn = diag(cnf_c_tcnat); % diagonal of a matrix
130
131 F_mat = (abs(mat_cn*hot_stfc_mat)).^2;
132
133 % Multiplication of characteristic Eigen
134
135 figure; mesh(stfc_t*103/max(stfc_t1,stfc_t*0.5)/max(stfc_t1,F_mat));
136 xlabel('Amino Acid Domain');
137 ylabel('Frequency');
138 zlabel('Amplitude');
139 title('Hotspot for Type Cytochrome C');
140 axis tight % axis TIGHT - sets the axis limits to the range of
141 view(3) % view(3) - sets the default 3-D view
```

See also periodogram, pwelch, goestzel.

Reference page for spectrum

Mr. Yashpal Yadav

Date:07-09-22

Lecture-18: Molecular Dynamics Based Genome Annotation by Prof. B. Jayaram, IIT Delhi

Supercomputing Facility for Bioinformatics & Computational Biology, IIT Delhi
www.scfbio-iitd.res.in
A Centre of Excellence of the Department of Biotechnology, Govt. of India

atggccctgtggatgpcgccctctgccctctgctggcctgctggccctctggggacctgac.....
MALWMRLPLALLALWGPD.....

Docking at a Supercomputer

Best Docked Structures

Send the best molecule to top pharmacologists for synthesis, clinical trials, assembly and manufacturing or directly to a panel of doctors, all online

11 AM: Disease reported on a smart phone along with genome card and other reports/ symptoms.
5 PM: Drug delivered at door stop what ever the disease!
Turns her into a healthy person.

A Dream Plan

Tools: Genomics + Proteomics + Information Technology + Chemistry

Date: 08-09-22

Lecture-19: Basics of machine learning-I by Dr. S.D. Sharma, JUIT Solan, H.P.

Basics of Machine Learning: I

Dr. Sunil Datt Sharma
Assistant Professor (SG), ECE,
Jaypee University of Information Technology,
Wanknaghat, Solan, H.P.

Lecture-20: Basics of machine learning-II by Dr. S.D. Sharma, JUIT Solan, H.P.

Support Vector Machine Algorithm

- Support Vector Machine or SVM is one of the most popular Supervised Learning algorithms, which is used for Classification as well as Regression problems.
- However, primarily, it is used for Classification problems in Machine Learning.
- The goal of the SVM algorithm is to create the best line or decision boundary that can segregate n-dimensional space into classes so that we can easily put the new data point in the correct category in the future.
- This best decision boundary is called a hyperplane.
- SVM chooses the extreme points/vectors that help in creating the hyperplane.
- These extreme cases are called as support vectors, and hence algorithm is termed as Support Vector Machine.

The screenshot shows a presentation slide with a red header and a list of bullet points. A video inset on the right shows a man in a blue shirt speaking. The background of the slide is white with a light blue border.

Date: 09-09-22

Lecture-21: Machine learning Application in Genomics & Proteomics-I by Dr. S.D. Sharma, JUIT Solan, H.P.

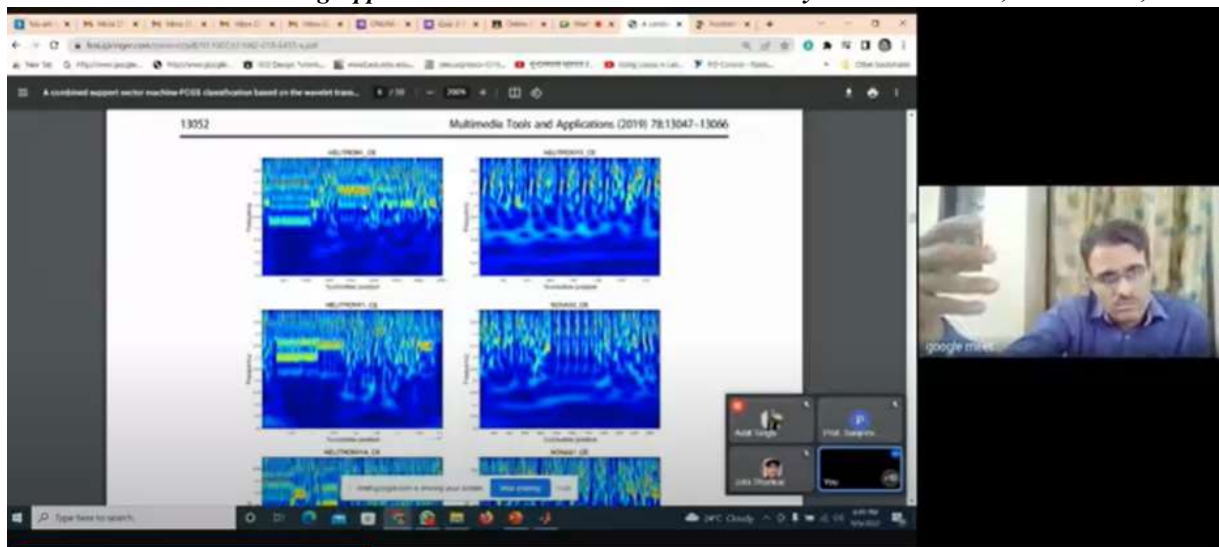
Machine Learning Application in Genomics: I



Dr. Sunil Datt Sharma
Assistant Professor (SG), ECE,
Jaypee University of Information Technology,
Waknaghat, Solan, H.P.

The screenshot shows a presentation slide with a white background and a red header. The title is in bold black text. Below the title is the JUIT logo, which features a stylized 'J' and 'U' with a green and yellow emblem. Below the logo is the presenter's name and title in red and black text. A video inset on the right shows a man in a blue shirt speaking. The background of the slide is white with a light blue border.

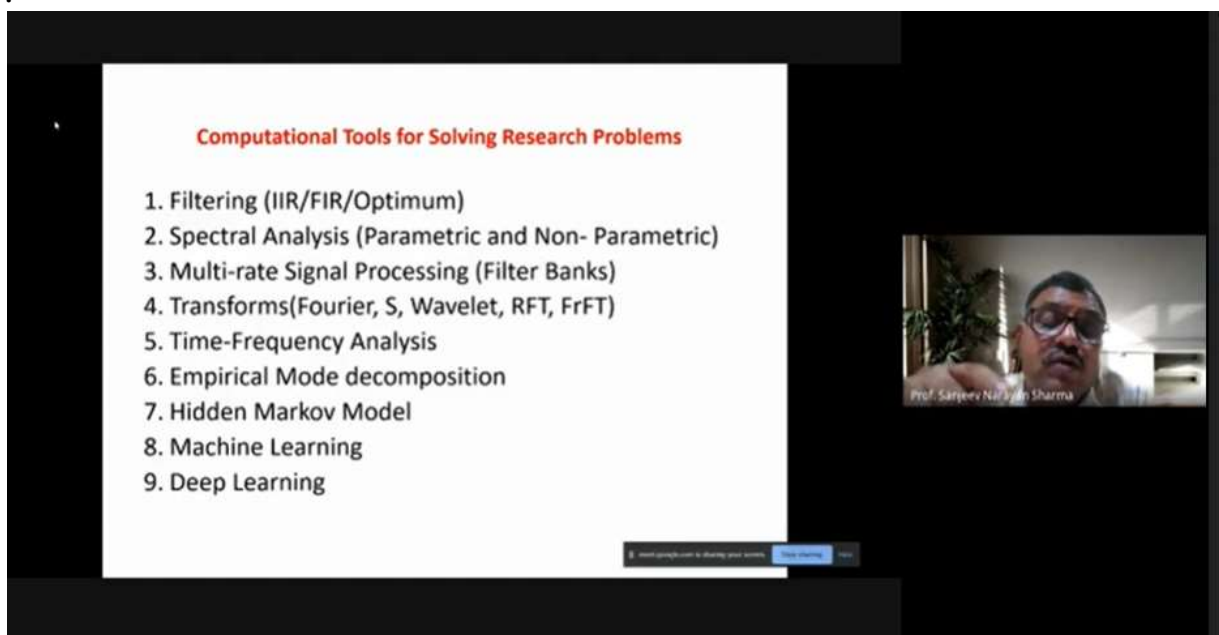
Lecture-22: Machine learning Application in Genomics & Proteomics-II by Dr. S.D. Sharma, JUIT Solan, H.P.



The screenshot displays a video lecture interface. The main content is a slide titled "Multimedia Tools and Applications (2019) 78:13047-13066" with the number "13052" in the top left. The slide features six heatmaps arranged in a 3x2 grid, each showing a different visualization of data. The heatmaps have a color scale from blue to yellow. The video feed on the right shows a man in a blue shirt, identified as Dr. S.D. Sharma, speaking. The interface includes a search bar at the top, a taskbar at the bottom, and a video control panel on the right side of the slide.

Date:10-09-22

Lecture-23: Some open research problems in computational Genomics and Proteomics & Useful referencing by Prof. S.N. Sharma, IITDM Jabalpur



The screenshot shows a video lecture interface. The main content is a slide titled "Computational Tools for Solving Research Problems" in red text. Below the title is a numbered list of nine items: 1. Filtering (IIR/FIR/Optimum), 2. Spectral Analysis (Parametric and Non- Parametric), 3. Multi-rate Signal Processing (Filter Banks), 4. Transforms(Fourier, S, Wavelet, RFT, FrFT), 5. Time-Frequency Analysis, 6. Empirical Mode decomposition, 7. Hidden Markov Model, 8. Machine Learning, and 9. Deep Learning. The video feed on the right shows a man in a white shirt, identified as Prof. Sarjendra Nath Sharma, speaking. The interface includes a search bar at the top, a taskbar at the bottom, and a video control panel on the right side of the slide.

**Some Potential Research Problems
in
Computational Genomics & Proteomics**

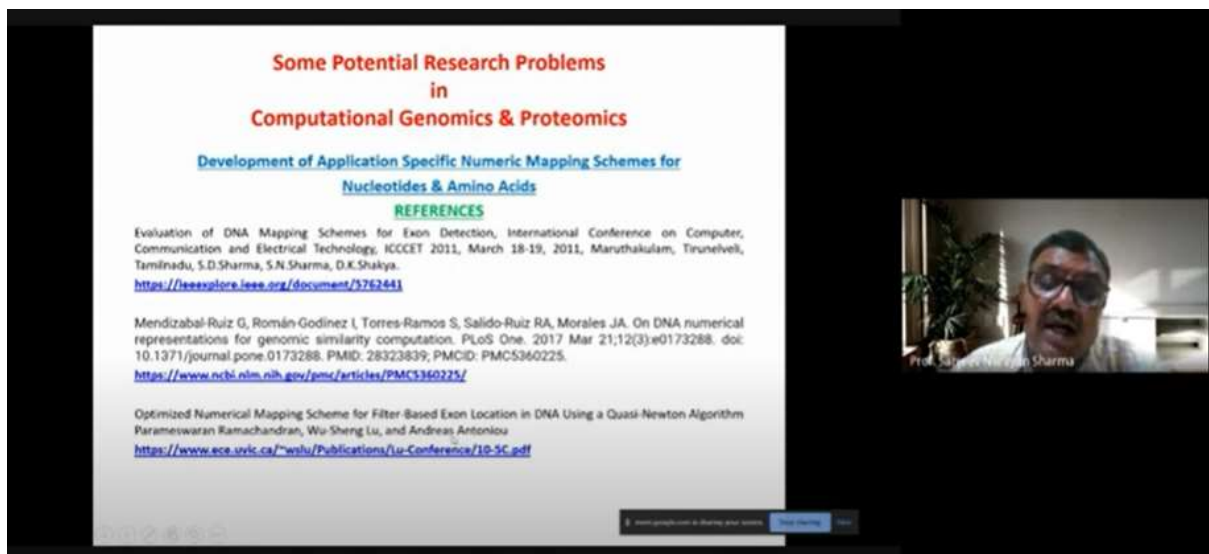
**Development of Application Specific Numeric Mapping Schemes for
Nucleotides & Amino Acids**

REFERENCES

Evaluation of DNA Mapping Schemes for Exon Detection, International Conference on Computer, Communication and Electrical Technology, ICCCT 2011, March 18-19, 2011, Maruthakulam, Trunelveli, Tamilnadu, S.D.Sharma, S.N.Sharma, D.K.Shakya.
<https://ieeexplore.ieee.org/document/5762441>

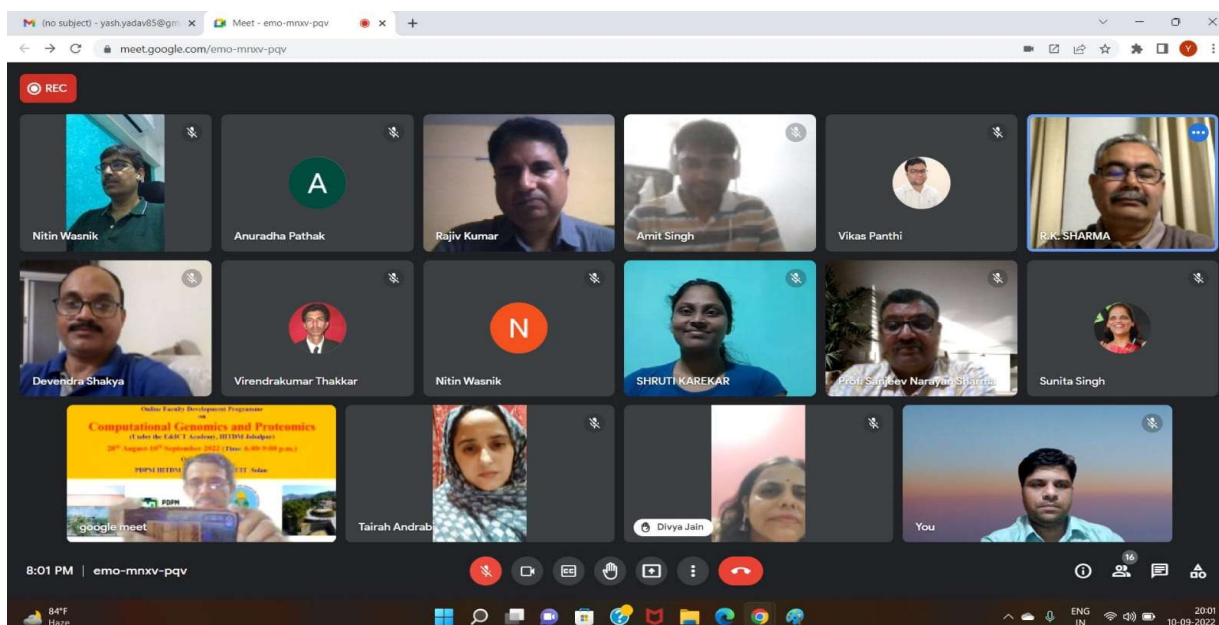
Mendizabal-Ruiz G, Román-Godínez I, Torres-Ramos S, Salido-Ruiz RA, Morales JA. On DNA numerical representations for genomic similarity computation. PLoS One. 2017 Mar 21;12(3):e0173288. doi: 10.1371/journal.pone.0173288. PMID: 28323839; PMCID: PMC5360225.
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5360225/>

Optimized Numerical Mapping Scheme for Filter-Based Exon Location in DNA Using a Quasi-Newton Algorithm Parameswaran Ramachandran, Wu Sheng Lu, and Andreas Antoniou
<https://www.ece.uvic.ca/~wslu/Publications/Lu-Conference/10-5C.pdf>



Closing ceremony

During the closing ceremony of this program, **Prof. R.K. Sharma (Hon'ble VC, JUIT), Prof. S.N. Sharma (ECE, IITDM, Jabalpur), and Prof. Rajiv Kumar (HOD, ECE JUIT)** were present. The FDP was coordinated by Prof. S.N. Sharma, IITDM Jabalpur & Dr. S.D. Sharma JUIT Waknaghat.



The screenshot shows a Google Meet session with the following participants visible in the grid:

- Nitin Wasnik
- Anuradha Pathak
- Rajiv Kumar
- Amit Singh
- Vikas Panthi
- R.K. SHARMA
- Devendra Shakya
- Virendrakumar Thakkar
- Nitin Wasnik
- SHRUTI KAREKAR
- Prof. Sangeev Narayan Sharma
- Sunita Singh
- Tairah Andrab
- Divya Jain
- You

A presentation slide is visible in the bottom-left corner of the grid, titled "Online Faculty Development Programme Computational Genomics and Proteomics (Under the ECE T. Academic, IITDM Jabalpur) 09th September-10th September 2022, Time: 6:00-9:00 pm".

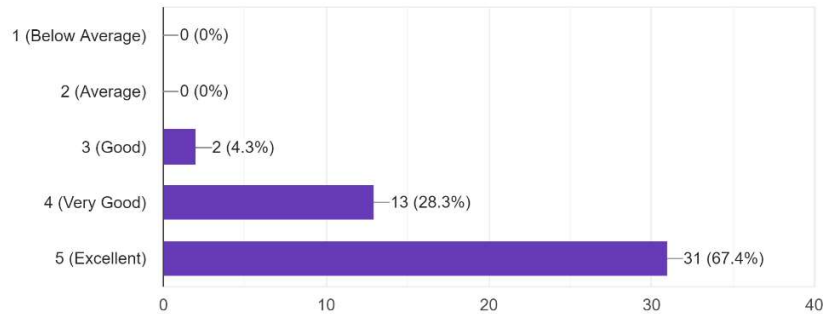
5. Evaluation

- Quiz-1-Online-FDP-E & ICT-Computational Genomics and Proteomics-02-09-2022 (9:00pm- 9:30 pm)
- Quiz-2-Online-FDP-E & ICT-Computational Genomics and Proteomics-09-09-2022 (9:00pm- 9:30 pm)

6. Feedback from the participants

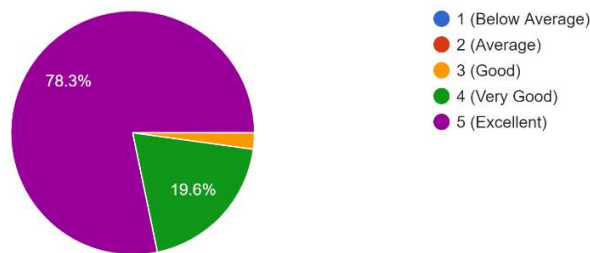
How will you evaluate FDP in overall on the scale of 1 to 5 (with 1 being lowest and 5 being highest)?

46 responses



How will you evaluate Experts on the scale of 1 to 5 (with 1 being lowest and 5 being highest)?

46 responses



7. News in social media:

Facebook:

<https://www.facebook.com/JUITWSolan/photos/pcb.2637864179683412/2637864119683418/>

[https://www.facebook.com/JUITWSolan/photos/a.608184322651418/2634832023319961/?_cft__\[0\]=AZXV77ix0ER8veZpRDztjNccLXIMJFNw5Z4CoscsGzXkUT9TBRgfM4KwszSvzRRMFfCgd8oNDd6510jelVFraVx8M_MljWpMGjj_2mmRaT1Xtk3ZN2xTg6W9Qw3deeE9z3uMS6c9Y6kK26tYIMUqwDyg6nWtrTf1y-oLvpMV0fAmRipt4djhYY95eEodGKerCemYDWyiBpzpofPmfnoG-&_tn=EH-R](https://www.facebook.com/JUITWSolan/photos/a.608184322651418/2634832023319961/?_cft__[0]=AZXV77ix0ER8veZpRDztjNccLXIMJFNw5Z4CoscsGzXkUT9TBRgfM4KwszSvzRRMFfCgd8oNDd6510jelVFraVx8M_MljWpMGjj_2mmRaT1Xtk3ZN2xTg6W9Qw3deeE9z3uMS6c9Y6kK26tYIMUqwDyg6nWtrTf1y-oLvpMV0fAmRipt4djhYY95eEodGKerCemYDWyiBpzpofPmfnoG-&_tn=EH-R)

[https://www.facebook.com/JUITWSolan/photos/pcb.2623673207769176/2623671477769349/?_cft__\[0\]=AZU3Y6rKuR94u48IhLNeVqefv6jbiT6PEYEsPnpbpdZywxEmz2rsCTyoO7PzA-Yn--BMdHm3xkFWpnKeWbjaag1YvyjR9mYRVFopVzHSOQOfbS6Y9GggmJwT_9j-I6oNYVLtKgCW7ojaSwUOP5otCNMWCCs43WcoUjIJT8ydgApRk6BdTt2ocrkvDvK9bMj23nFyjpN0_KeDS8cAZjMZi&_tn=*bH-R](https://www.facebook.com/JUITWSolan/photos/pcb.2623673207769176/2623671477769349/?_cft__[0]=AZU3Y6rKuR94u48IhLNeVqefv6jbiT6PEYEsPnpbpdZywxEmz2rsCTyoO7PzA-Yn--BMdHm3xkFWpnKeWbjaag1YvyjR9mYRVFopVzHSOQOfbS6Y9GggmJwT_9j-I6oNYVLtKgCW7ojaSwUOP5otCNMWCCs43WcoUjIJT8ydgApRk6BdTt2ocrkvDvK9bMj23nFyjpN0_KeDS8cAZjMZi&_tn=*bH-R)

LinkedIn

<https://www.linkedin.com/feed/update/urn:li:activity:6970074681236180993>

8. News in Print Media:

जे.यू.आई.टी. ने कंप्यूटेशनल जीनोमिक्स और प्रोटीओमिक्स पर करवाया संकाय विकास कार्यक्रम

● मेटलैब प्रोग्रामिंग और कंप्यूटर एडेड ड्रग डिजाइन के बुनियादी सिद्धांतों पर चर्चा की

सवेरा न्यूज

नई दिल्ली, 12 सितंबर : जे.यू.आई.टी. सोलन में आई.आई.आई.टी.डी.एम. जबलपुर के सहयोग से कंप्यूटेशनल जीनोमिक्स और प्रोटीओमिक्स पर संकाय विकास कार्यक्रम (एफ.डी.पी.) आयोजित किया गया। कंप्यूटेशनल जीनोमिक्स और प्रोटीओमिक्स पर संकाय विकास कार्यक्रम (एफ.डी.पी.) को सफलतापूर्वक पूरा हुआ। ये कार्यक्रम इलेक्ट्रॉनिक्स और सूचना प्रौद्योगिकी मंत्रालय भारत सरकार की एक पहल, इलेक्ट्रॉनिक्स और आई.सी.टी. अकादमी द्वारा प्रायोजित किया गया था। ये कार्यक्रम 28.08.22 को शुरू हुआ और जे.पी. यूनिवर्सिटी ऑफ इंफॉर्मेशन टेक्नोलॉजी (जे.यू.आई.टी.) वाकनाघाट, सोलन और आई.आई.आई.टी.डी.एम. जबलपुर के ई.सी.ई. विभागों द्वारा संयुक्त रूप से आयोजित किया गया था। इस दो सप्ताह के संकाय विकास कार्यक्रम

के दौरान प्रख्यात वक्ताओं ने आणविक जीवविज्ञान, जीनोम अनुक्रमण, सिग्नल प्रोसेसिंग, मशीन लर्निंग, पर्सनलाइज्ड मैडिसिन, मेटलैब प्रोग्रामिंग और कंप्यूटर एडेड ड्रग डिजाइन के बुनियादी सिद्धांतों पर चर्चा की। इसके अलावा आणविक जीव विज्ञान प्रयोगों को सुविधाजनक बनाने में कम्प्यूटेशनल विधियों की प्रयोज्यता को उजागर करने के लिए कई केस स्टडीज पर चर्चा की गई। इस कार्यक्रम में विद्वान वक्ताओं में प्रो. बी. जयराम (आई.आई.टी. दिल्ली), प्रो. एल. शशिधर (आई.आई.एम.ई. आर., पुणे), प्रो. राजीव सक्सेना (जे.आई.आई.टी. नोएडा), डा. पुष्पेंद्र सिंह (वैज्ञानिक, आई.सी.एम.आर.), प्रो. एस.एन. शर्मा (आई.आई.आई.टी.डी.एम., जबलपुर), डा. डी.के. शाक्व, डा. एस.डी. शर्मा और यशपाल वादव शामिल थे। प्रो. अपराजिता ओझा, समन्वयक ई एंड आई.सी.टी. अकादमी जबलपुर ने ऐसे सहयोगी कार्यक्रमों के महत्व पर जोर दिया। कार्यक्रम के दौरान डा. राजीव कुमार भी समापन समारोह में उपस्थित थे।

FDP on Computational Genomics & Proteomics at JUIT Solan in Collaboration with IIITDM Jabalpur

The faculty development program (FDP) on Computational Genomics & Proteomics got successfully completed on 10.09.22. This event was sponsored by Electronics & ICT Academy, an initiative of Ministry of Electronics & Information Technology, Government of India. The event commenced on 28.08.22 and was jointly organized by ECE departments of Jaypee University of Information Technology (JUIT), Wagnaghat, Solan & IIITDM Jabalpur. During this two-week FDP eminent speakers delivered talks on Fundamentals of Molecular Biology, Genome Sequencing, Signal Processing, Machine learning, Personalized Medicine, MATLAB Programming & Computer aided drug design. Also, Numerous case studies were discussed to highlight the applicability of computational methods in facilitating molecular biology experimentations. The learned speakers who delivered the talks in this program include Prof. B.Jayaram (IIT Delhi), Prof. L. Shashidhara (IISER, Pune), Prof. Rajiv Saxena (JIIT Noida), Dr. Pushpendra Singh (Scientist, ICMR), Prof. S.N.Sharma (IIITDM, Jabalpur), Dr. D.K. Shakya (SATI, Vidisha), Dr. S.D. Sharma (JUIT, Wagnaghat) and Yashpal Yadav. Prof. Aparajita Ojha, Coordinator E&ICT Academy Jabalpur, emphasized the importance of such collaborative programs. In his concluding remarks Prof. R.K. Sharma, Vice Chancellor, JUIT Wagnaghat wished that this program will promote collaborative cross-disciplinary research and participants will contribute towards the nation building by developing novel solutions for the existing molecular biology problems using computational tools. During the program Dr. Rajiv Kumar (Professor & Head, ECE, JUIT Solan) was also present in the closing ceremony. The program concluded with vote of thanks delivered by Prof. S.N. Sharma, IIITDM Jabalpur & Dr. S.D. Sharma JUIT Wagnaghat, Coordinators of this events.

The Hindu (14-09-2022),
