DAV(PG) College, Karanpur, Dehradun (Uttarakhand)	**Swami Ram Himalayan University (SRHU), Jolly Grant, Dehradun (Uttarakhand)**	**Uttarakhand Council for Biotechnology (UCB), Biotech Bhawan, Haldi, Pantnagar (Uttarakhand)**

(Advertisement No.: DAV/2022/5/178 dated 26.5.2022)

Invitation of Applications

D.A.V. (P.G.) College, Dehradun and Swami Rama Himalayan University (SRHU), Dehradun are jointly organizing four days Training Workshop on 'Ganga Water in Eradication of Human Viruses through Bioinformatics Tools' in SRHU, Dehradun sponsored by **Uttarakhand Biotechnology Council, Haldi** during 13-16 June, 2022. Interested/ eligible students/ researchers/ faculty members can apply through details/ guidelines and "Application Format" provided at the websites (davpgcollege.in; srhu.edu.in and ucb.ac.in). The last date of receiving applications through email (hsbs@srhu.edu.in) is June 9, 2022 on first-cum first serve basis. There is no registration fee for participants. Also, TA & boarding/ lodging will be provided to selected outstation participants by organizers.

Principal

Background Note of the Training Workshop:

Since the discovery of computers, bioinformatics and computational biology have been instrumental in a wide range of discoveries in virology. These include early mathematical models of virus-host interaction, and more recently the analysis of viral nucleotide and protein sequences to track their function, epidemiology, and evolution. The genomics revolution has provided an unprecedented amount of sequence information from both viruses and their hosts. Through proposed training, it has been planned to provide training to youth/ students/ research scholars about how bioinformatics allows viral sequence data to be analyzed and interpreted.

The virosphere may contain the greatest diversity known to mankind. It has been estimated that there are 10^{31} viruses on Earth, and for billions of years their ongoing proliferation and mutation has contributed to an unparalleled genomic diversity globally. Viral mutation rates range from 10^{-8} to 10^{-6} substitutions per nucleotide per cell infection for DNA viruses and from 10^{-6} to 10^{-4} substitutions per nucleotide per cell infection for RNA viruses. The only way to efficiently analyses this biodiversity is by applying powerful computational tools to

(1) Identify viral sequences and their encoded functional elements,
(2) Predict, annotate, and compare their functions, and
(3) Structure the data to move from measuring to understanding.

Until recently, our full understanding of viruses was based on a few hundred viruses that were isolated and could be studied in detail. With recent bioinformatic developments, thousands of new viruses can be readily discovered in all natural and host-associated biomes. Including these naturally occurring viruses in comparative analyses opens up possibilities for *de novo* computational predictions, including about the structure and function of viral genes.

Bioinformatics analyses of omics and other biological datasets depend on specialized computational tools. The development of these tools begins with basic analyses that are then incrementally used to create more complex applications. Examples of basic applications include software to validate the data derived from next-generation sequencing machines, build alignments of gene or protein sequences, and perform statistical tests. Higher-level analyses may include pipelines for metagenomic analysis, genome annotation, or genotype-phenotype association. Taken together, bioinformatics is arguably one of the sub-disciplines in the life sciences with the broadest applicability. When calculated as the amount of computer time allotted to computational analyses, the largest consumer in virology is the analysis of omics datasets. Omics analyses are characterized as high-throughput, untargeted, and generally quantitative, and their application opens the door to systems level analysis of viruses and their effects on their hosts. For example, comparative genomics allows thousands of viruses to be analyzed, identifying important viral genes, their functions, and their evolution; metagenomics allows viruses to be discovered and identified with high throughput; and phylogenetic and phylo-genomics allow new viral taxonomic groups to be identified.

An outbreak of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was first reported in Wuhan City, China, in December2019.Since then, the outbreak has grown into a global pandemic. The slow translational progress in the field of research suggests that a large number of studies are urgently required. In this context, phage therapy came into the limelight and workers explores the impact of bacteriophages on SARS-CoV-2 and other viruses, especially concerning phage therapy (PT).

Bacteriophages have been used as an alternative to antibiotics against infectious diseases for over 90 years. Bacteriophages are viruses that infect and kill bacterial cells. Several studies have confirmed that in addition to their antibacterial abilities, bacteriophages also show antiviral and antifungal properties. The Ganges, river in India, which originates from the Himalayan range is known to harbor a large number of bacteriophages, which are released into the river gradually by the melting permafrost especially in the stream of Bhagirathi. Water from this river has traditionally been considered a therapeutic agent for several diseases.

Analysis of the fresh water sedimentary metagenome-viromes revealed that the holy river Ganges in Uttarakhand not only house novel viromes, but also include unexplored double stranded DNA viruses, The Indian Science Journal quotes. It is for the first time, scientists have come across new viruses, which were never reported earlier. These bacteriophages are active against certain clinical isolates, or viral strains and can be used against multi-drug resistant or MDR infections. These viruses were never reported earlier and are found to be active against certain clinical isolates. This makes them useful against multi-drug resistant infections, or MDR infections. Some of the MDR infections include, Typhoid (Salmonella), Cholera (Vibrio), Dysentery (Shigella), Meningitis, Pneumonia (Klebsiella and Acinetobacter).

Microbes of the Ganges Water: Various types of bacterial groups were found to be present in the samples of the waters of Ganga and the sediment. The sample of Ganges waters contained bacterial groups like Flavobacteria, β-proteobacteria and Oscillatoriphycudea. The sediment also contained some different strains like Actinobacteria, A-proteobacteria, Sphingobacteria and Deltaproteobacteria. The virus (bacteriophage) groups found in the waters include Siphoviridae, Podoviridae, Myoviridae etc.

Advances in phage therapy summarizes, though very crudely, the important steps in a possible mechanism of using Indian river phages and other viruses, especially those of the River Ganga, for treatment of the present COVID-19 pandemic and other exploiting them for other antibacterial, antifungal and antiviral properties. The findings on phages and their possible antiviral properties are preliminary and need to be validated by meticulous in vitro and in vivo studies.

Bioinformatics approaches allow PCR panels to be designed that capture an increasingly diverse array of viruses, but these assays will always remain limited to detecting viruses within a known range, and cannot extrapolate to identify completely novel ones. This may be resolved by untargeted (shotgun) sequencing of isolated viruses or complete sample DNA (metagenomics). Variants of known viruses may be detected by aligning the reads derived

from the sample to the reference sequence of the known virus that was originally used for designing the primers. If enough high-quality reads span the regions where the primer sequences should anneal with the target, specialized variant detection tools can call the variant with a high degree of confidence, and new PCR primers can be designed to capture them. For example, a recent PCR-based investigation of the widespread human gut-associated bacteriophage crAssphage designed globally applicable primers by screening an alignment of sequencing reads from a range of publicly available metagenomes and identifying highly variable regions of the appropriate size (1000–1400 nucleotides) that were flanked by conserved regions which could be targeted by primers, and were present in ≥90% of all metagenomic samples (<10% gaps).

Recently, a new source of viral genomic sequences has become increasingly important. Metagenomics samples genomic material directly from the environment, allowing for the reconstruction of complete viral sequences without cultivation. Early metagenomes did not allow for the assembly of large genome fragments, mostly because of a limited capacity in sequencing depth and assembly software available at the time. Hence, most analyses focused on individual marker genes or global comparison between datasets, i.e., "all-versus-all" similarity. While providing important information on the overall genetic diversity of viruses, these gene-level analyses suffered from major limitations. Specifically, gene-based approaches can only target specific groups of viruses since no universal viral marker gene exists and are thus limited in their ability to discover novel viral diversity and draw inference at the scale of whole viral communities.

The direct sampling of viruses without host information complicates the interpretation of the ecological roles of viruses, including fulfillment of Koch's postulates in the case of samples from diseased organisms. Thus, host prediction is an important current challenge in understanding the role of viruses identified from metagenomics. Metagenomics may reveal sequences that are distinct from those of known viruses; thus, their hosts cannot be predicted based on similarity to viruses that have been experimentally characterized. Recent advances in machine learning hold promise for predicting virus-host interactions, including several approaches that are based on the genome sequences alone. These approaches exploit genomic signals including, for example-

(1). The nucleotide usage profile of the genome sequence that is adapted in viruses as a result of co-evolution with their hosts;

(2) Regions of sequence similarity between virus and host genomes, which could reflect integrated proviruses, horizontally transferred genes, or other mechanisms;

(3) CRISPR spacers in the bacterial genome matching the genomes of bacteriophages that infected that host lineage in the past; and several other signals.

Nevertheless, most virus genomes assembled from metagenomes remain without any predicted host at this point, and designing new approaches to establish these linkages remains a major computational challenge in the field.

Bioinformatics opens up a vast range of possibilities for new analyses and interpretations of viruses. While computational predictions always need to be validated by relevant in vitro experimental follow-up, the unprecedented availability of big omics datasets in the public domain already allow bioinformaticians to perform many initial validations *in silico*. These best practices can be used to estimate the accuracy of diverse bioinformatics tools, providing an important focus for wet laboratory experiments and saving valuable time and resources. Thus, bioinformatics has already become an integral and transformative component of virus research, much like techniques such as culturing, microscopy, and molecular biology have done in the past.

Tentative Programme Schedule

Four days Training Workshop on
'Ganga Water in Eradication of Human Viruses Through Bioinformatics Tools'

Organized Jointly by:

D.A.V. (P.G.) College, Dehradun and

Swami Rama Himalayan University (SRHU), Dehradun

Financially and Technically Supported by:

Uttarakhand Council for Biotechnology, Haldi, Pantnagar

Dated: 13-16 June, 2022

Venue: Himalayan School of Biosciences, Swami Rama Himalayan University (SRHU), Dehradun

Phase I: Theory of Training Workshop (13 June- 14 June 2022)

Time	Session title	Lead
13/06/2022	**FIRST DAY**	**Monday**
08:00 am - 9.00 am	Registration	Dr. Geeta Bhandari
9:00 am - 09:30 am	Introduction to the course and Workshop overview	Dr. Prashant Singh and Prof. Sanjay Gupta
09:30 am -10:30 am	Inaugural Function with Plenary Lecture	Invited VIP's, Guests and Experts
10:30 am -11.00 am	High Tea	
11.00 am -12.30 pm	Theory – Basics of Molecular biology of Viruses	Dr. Akhilesh Kumar/ Dr. Vijay Kumar/ Dr. Vivek Kumar
12.30 pm - 1.30 pm	**LUNCH**	
1:30 pm - 2:30 pm	Introduction of Bioinformatics	Dr. Geeta Bhandari
2:30 pm - 3.30 pm	Phage Therapy: Role of Ganges water in Therapeutics	Dr. Sanjay Gupta
3.30 pm - 4:15 pm	Role of Bioinformatics in Eradication of Viruses	Dr. Geeta Bhandari
4.15 pm – 4.30 pm	Tea	
14/06/2022	**SECOND DAY**	**Tuesday**
9.00 am - 10:00 am	Theory – PCR, Gel casting and loading of PCR products	Dr. Akhilesh Kumar/Dr. Vijay Kumar/ Dr. Geeta Bhandari
10.00 am - 10:45 am	Major human viruses in Ganga water	Dr. Vivek Kumar

10:30 am - 11:30 am	Isolation strategies for viruses from Ganges water: A metagenomics approach	Dr. Vijay Kumar
11.30 am - 12:30 pm	Ganges water in controlling of SARS-COVID-19: An immunological mechanism	Dr Sanjay Gupta
12.30 pm - 1.30 pm	**LUNCH**	
1:30 pm - 3:00 pm	Theory - Overview of Bioinformatics Tools Used in Virology	Guest speaker
3.00 pm - 3.30 pm	High Tea	
3:30 pm - 4:15 pm	Distribution of certificates to first 50 candidates	Dr. Akhilesh Kumar/ Dr. Geeta Bhandari/ Dr. Vijay Kumar
4.15 pm – 4.30 pm	Tea	

Phase II: Hands on Training Workshop (15-16 June 2022)

15/06/2022	**THIRD DAY**	**Wednesday**
9:00 am - 11:30 am	Practical–Preparation of DNA/RNA of Viruses from Ganges Water	Dr. Akhilesh Kumar/ Dr. Vijay Kumar
11:30 am - 12:00 noon	**High Tea**	
12.00 noon - 1.00 pm	Quantification of Nucleic Acids	Dr. Geeta Bhandari/ Dr. Akhilesh Kumar
12.30 pm - 1.30 pm	**Lunch**	
1:30 pm - 4:15 pm	Practical–Detection of viruses from Ganges Water using PCR	Dr. Akhilesh Kumar/ Dr. Vijay Kumar
4.15 pm – 4.30 pm	Tea	
16/06/2022	**FOURTH DAY**	**Thursday**
9:30 pm - 11:00 pm	Practical Based on Primer Designing	Dr. Akhilesh Kumar
10:30 pm - 11.00 pm	**High Tea**	
11.00 pm - 12.00 pm	Practical – Basic Tools of Bioinformatics	Dr. Geeta Bhandari
1.00 pm - 2.00 pm	**Lunch**	
2:00 pm - 3.30 pm	Validatory Function	Invited Guests
3:30 pm - 4.00 pm	Distribution of Certificates and Tea	

Guidelines for Selection of Participants and Training Workshop

1. The total number of seats for the training workshop is limited to 100 only.
2. There is no registration fee for the Workshop
3. The interested/ eligible candidates have to submit the "Application Form" given/ provided for expressing their willingness to join. If found as per qualification/merit/experience by the organizing committee, he/ she will be selected for the training workshop of four days from 13-16 June at SRHU, Dehradun.
4. The candidate must have eligible qualification from any educational institution/ university located in the state of Uttarakhand.
5. The participants should possess minimum Ist Division/ 60% aggregate/ CGPA 6.0 in graduate/ postgraduate degree/ Ph.D. Degree in concerned field with relevant experience.
6. Graduate Students, Post Graduate Students, Research Scholars, Faculty Members and Scientists of Applied Sciences including, but not limited to, Biotechnology, Microbiology, Biochemistry, Bioinformatics, Biochemistry, Food Science & Technology are eligible to apply. In case of non-availability of such suitable candidates, the applicants from Basic Sciences subjects namely Chemistry, Botany, Zoology and Environmental Sciences will be selected from Self-financed UG/PG colleges/ institutes, grant-in-aid UG/PG colleges, government UG/PG colleges, Self-financed state universities, State Universities and Central University under the geographical area of the Uttarakhand state and currently enrolled/ studying/ doing research/ in service with relevant background/ experience.
7. Priority will be given to the candidates, who have studied Bioinformatics and its applications as one of the courses of their program/ course/ degree.
8. Weightage in selection will also be given to the candidates, who have past experience in the concerned field/ domain area of the training workshop.
9. Selection of the candidates will be done on the basis of qualifying marks in the last exam. It is mandatory to attach the mark sheet (from the educational institution of Uttarakhand) of the last/ latest qualifying exam (B.Sc./M.Sc./Ph.D.) in the concerned subject along with **"Application Form"** (provided/ attached below).
10. Students studying in B.Sc./ M.Sc. will be given preference only when the seats are vacant. Students selected against the vacant seats shall be considered on the basis of marks obtained/CGPA till VIIth and IIIrd semester examination of qualifying exam for B.Sc. and M.Sc., respectively
11. An advertisement for inviting application has been published in national daily newspapers namely (i) Dainik Jagran, (ii) Dainik Amar Ujala and (iii) Dainik Hindustan in Uttarakhand edition on 1st June 2022. The last date of submission of application using **"Application Form"** provided hereunder along with/ attaching required documents (as mentioned) by interested/ eligible candidates through given email **(hsbs@srhu.edu.in**) only is **09 June 2022 up to 11.59 pm. No other way of submitting "Application Form" will be accepted and applications submitted by other means/ mode will be summarily rejected.**
12. The list of the selected candidates of THE TRAINING WORKSHOP will be displayed at the websites of the all the 3 organizing Institutes namely DAV(PG) College (davpgcollege.in, Dehradun), SRHU, Dehradun (srhu.edu.in) and UCB, Dehradun (ucb.ac.in/) on **11 June 2022 afternoon**. Also, email will be sent to all the selected candidates.
13. The decision of the organization committee for the same will be final.
14. The overall training workshop is divided in to two phases.
15. First phase comprises of two days i.e. **13th and 14th of June 2022,** where selected participants will be exposed to theory/ classroom teaching/ tutorials on different aspects of Virology/ Molecular Biology/Bioinformatics, followed by a **written test in the evening of 14th June.**

16. Candidates securing **first 50 positions will undergo laboratory exposure for the next two days.** The remaining candidates will be given certificates of participation for two days i.e. First phase of the Workshop.
17. The stay/ accommodation will be managed by the organizer at Swami Rama Himalayan University, Jolly Grant, Dehradun.
18. TA/DA of the outstation participants will be borne through financial support received from Uttarakhand Council for Biotechnology, Govt. of Uttarakhand, Haldi. The participants selected from district Dehradun will not be provided with accommodation/TA.
19. The candidate, who will undergo overall training of both Phases-I & II, will be given certificate of four days training workshop.

अमर उजाला

: 12+4 | मूल्य : सात रुपये

देहरादून
बुधवार, 1 जून 2022
ज्येष्ठ शुक्ल-द्वितीया
विक्रम संवत-2079

DAV(PG) College
Karanpur, Dehradun
(Uttarakhand)

UTTARAKHAND COUNCIL FOR BIOTECHNOLOGY
Biotech Bhavan, Haldi, Pantnagar
Phone Fax: 05844-236567 Email: statebiotech@rediffmail.com

(Advertisement No.: DAV/2022/5/178 dated 26.5.2022)

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Principal

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DAV(PG) College
Karanpur, Dehradun
(Uttarakhand)

UTTARAKHAND COUNCIL FOR BIOTECHNOLOGY
Biotech Bhavan, Haldi, Pantnagar
Phone/Fax: 05944-230587 Email: statebiotech@rediffmail.com

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Application Form

Four days Training Workshop on
'Ganga Water in Eradication of Human Viruses
Through Bioinformatics Tools'
Organized Jointly by:
D.A.V. (P.G.) College, Dehradun and
Swami Rama Himalayan University (SRHU), Dehradun
Financially and Technically Supported by:
Uttarakhand Council for Biotechnology, Haldi, Pantnagar
Dated: 13-16 June, 2022
Venue: Himalayan School of Biosciences, Swami Rama Himalayan University (SRHU), Dehradun

PART I: GENERAL INFORMATION

1. Name of the District of Uttarakhand, where presently employed/ working/ studying:
2. Name of Faculty/ Scientist/ Researcher/ Student:
3. Current Designation/ Position/ Class with UG/PG Level and subject(s) with semester:
4. Department/ Division/ Subject(s):
5. Name and Address of the Institute/College/University/Organisation:
6. Have you studied Bioinformatics and its applications as one of the courses of program/ course/ degree at any level:
7. Date of Birth:
8. Past Experience in the concerned field/ domain area of the training Workshop, if any:
9. Marks obtained/ CGPA till VIIth and IIIrd semester examination of B.Sc. and M.Sc. Students only:
10. Scientific Training Programmes conducted/ attended in the related field:
11. Number of years of research/ teaching experience in the relevant field (as the case be):
12. Specific achievement in the field (if any):
13. Write only 2 lines, how you plan to utilize the acquired training/ knowledge in future:

Date: **Sign. of candidate/ Applicant**

Place: **Name, Designation with full Address and Seal (if any)**

Mobile No.: ……., Email:……..

Forwarded and Recommended

Sign. with Seal of Executive / Competent Authority/ Principal/ Registrar/ Vice-Chancellor of your Institute/ /Organization/ University, where you are working/ studying

Date:
Place:
Note: Please attach all the documents mentioning enclosure no., which strengthen your case for selection.