

7 Days Online **Workshop on**Advanced Genomic Analysis and Annotation

Workshop Highlights

- √ Introduction to Genomic Assembly and Annotation
- ✓ Gene Calling and Functional Annotation
- ✓ Pathway Annotations and Gene-Based Alignments
- ✓ Pan-Genome Analysis and Core Genome Analysis
- √ Phylogenomic Analysis and Circular Plots
- √ Synteny Plots and Manuscript Preparation

For Registration

Email: contact@negenome.com

Whatsapp:+918812881948

October 9-15, 2023 Time: 6:30 pm – 8:00 pm



Workshop Features

- Approximately 11 hours of comprehensive learning in just seven days.
- . E-certificate for all participants.
- **Session recordings**
- Last date of Registration: October 7, 2023.

Fee Plan

Student (INR: 2000/-)

Ph.D. Scholar / Researcher (INR:

2500/-)

Academician / Faculty (INR: 3000/-)

Industry Professional (INR: 3500/-)

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Workshop Title: Workshop on Advanced Genomic Analysis and **Annotation**

The Next-Generation Sequencing (NGS) Data Analysis workshop is designed to provide hands-on training on WGS data analysis tools and techniques for analyzing large-scale genomic data generated by next-generation sequencing technologies.

Aim: The workshop has been structured to incorporate a combination of online tools (predominantly) and offline tools (with comprehensive installation guidance). During the practical session, participants will have the opportunity to analyze their individual datasets. Subsequently, they can engage in discussions about their findings during the following workshop session. This progression aims to assist participants in preparing their final manuscripts.

Duration: 7 Days

Location: Online

Target Participants

This workshop is aimed at faculty, post-doctoral fellows, researchers and technicians who wish to employ Whole Genome Sequencing NGS methods in their work. Ph.D. students/ Post-Doctoral Fellows/JRFs/SRFs/faculty involved in relevant research are eligible to apply.

Important Dates & Time	
Workshop Date: October 9-15, 2023	Time: 6:30 pm – 8:00 pm
Registration Ends: October 7, 2023 At Indian Standard Time 6:00pm	Duration: 1 hour 30 minutes/day, with the possibility of a slight extension if required

Registration:

Interested participants may visit www.negenome.com or click on this registration link: https://forms.gle/QdUVetN1RfGdMvTD7

F	EE PLAN
Student (INR: 2000/-)	Ph.D. Scholar / Researcher (INR: 2500/-)
Academician / Faculty (INR: 3000/-)	Industry Professional (INR: 3500/-)



Workshop Outline:

Day 1: Introduction to Genomic Assembly and Annotation

- Overview of workshop objectives and agenda
- Basics of genomic assembly: principles and challenges
- Introduction to various DE novo assemblers and their applications
- Hands-on session: Running a simple de novo assembly using a sample dataset
- Q&A and discussion

Day 2: Gene Calling and Functional Annotation

- Understanding gene calling and its importance
- Introduction to RAST (Rapid Annotation using Subsystem Technology) for functional annotation
- Hands-on session: Running RAST for gene calling and functional annotation
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 Assembly the session of the ses
- Interpreting RAST results and identifying key gene functions
- Q&A and discussion

Day 3: Pathway Annotations and Gene-Based Alignments

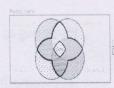
- Exploring metabolic pathways and their significance
- Overview of pathway annotation tools and databases
- Hands-on session: Pathway annotation using a real dataset
- Gene-based alignments: importance and applications
- Practical exercises: Performing gene-based alignments on selected genes
- Q&A and discussion

Day 4: Pan-Genome Analysis and Core Genome Analysis

- Understanding pan-genomes and their implications
- Introduction to pan-genome analysis methods
- Hands-on session: Building and analyzing a pan-genome
- Introduction to core genome analysis and its role in comparative genomics
- Practical exercises: Core genome analysis using bioinformatics tools
- Q&A and discussion

Day 5: Phylogenomic Analysis and Circular Plots

- Phylogenomic analysis: combining genomics and phylogenetics
- Introduction to phylogenetic tree construction methods
- Hands-on session: Building a phylogenetic tree using genomic data
- Circular plots: visualizing genomic information
- Practical exercises: Creating circular plots for selected genomes
- Q&A and discussion







Day 6: Synteny Plots and Manuscript Preparation

- Understanding synteny and its significance in genomics
- Introduction to synteny plot tools and visualization
- Hands-on session: Generating synteny plots for comparative analysis
- Manuscript writing: structuring and presenting your genomic analysis findings
- Tips for effective data presentation and manuscript organization
- Q&A and discussion

Day 7: Finalizing Analyses and Workshop Conclusion

- Review of the entire workshop content
- Final hands-on exercises: Integrating various analyses for a comprehensive study
- Participants present their findings from practical sessions
- Group discussion: Challenges faced, lessons learned, and future directions

Note: This workshop is designed for prokaryotic genome data analysis, if anyone is interested in eukaryotic WGS data analysis training on their own data sets you can join our custom online courses. For additional details call or WhatsApp us at 8812881948

Prerequisites:

- ✓ Participant must have laptop or computer with genuine windows 10 or 11 with 8 gb RAM and i5/i7 processor
- ✓ A stable internet connection is necessary.
- ✓ No prior programming experience or specialized prerequisites are necessary to attend this workshop. However, participants should possess a fundamental understanding of certain concepts, namely fastq files and whole-genome sequencing (WGS).
- ✓ Participants should have a basic grasp of fastq files, which are commonly used in genomics to store raw sequencing data.

It is important to note that while no programming background is required, these fundamental concepts will serve as a foundation for the workshop's content. Participants with knowledge of fastq files and WGS will be better positioned to engage with the hands-on activities and discussions throughout the workshop.



Software's/online database or tools to be used

Denovo Assembly	AbySS/Spades
Gene Calling and Functional Annotation	RAST (Rapid Annotation using Subsystem
Pathway Annotations Gene-Based Alignments Pan-Genome Analysis and Core Genome Analysis	Technology)
	KEGG, KAAS, MINPATH
	MaffT/ClustalW
	Agent-Spine (online)
	Get-homologus (offline)
Phylogenomic Analysis	
Circular Plots	Pyani-Master/Phylophalan
	BRIG
Synteny Plots ools may be changed as per need of worksh	Simple Synteny/Synima/MultiSyn

If you have any questions or need further information, please don't hesitate to contact us at contact@negenome.com/negenome@gmail.com.

We look forward to having you at the Advanced Genomic Analysis and Annotation Workshop. Let's dive into the fascinating world of NGS data analysis together!

Team NEGenome

www.negenome.com