A GIAN course on

A hands-on introduction to Next Generation Sequencing and Metagenomics Analysis

Brochure link:

Course overview

The advent of Next Generation Sequencing (NGS) technologies have transformed how biological research is being performed. Today, a human genome can be sequenced in a very short time, giving unprecedented possibilities for investigating human traits, evolution, and diseases. Similarly, whole bacterial communities and their interplay with the environment can be studied, unravelling novel enzymes and organisms. Although less than 1% of most microorganisms can be grown and studied in the lab, with the advent of low-cost high-throughput DNA sequencing technologies, it has become possible to explore the genetic material from entire microbial communities directly without the need of culturing the organisms under study. This emerging field, known as Metagenomics, utilizes a huge genetic reservoir of non-cultivable organisms as a resource for biotechnological and medical products and processes.

As these genomic and metagenomics experiments produce massive amounts of data, bioinformatics skills and supercomputing are crucial for the analysis. The aim of the special course is to give the participant knowledge of the NGS technology with the focus on data analysis. It will qualify the student to understand genomic and metagenomics shotgun sequencing data and enable them to analyze these in a UNIX/Linux working environment.

Course objectives

A student who has met the objectives of the course will be able to:

- Explain the applications of the different NGS technologies, including the weakness and strengths of the approaches.
- Explain the concept of metagenomics and its applications opposed to single genomics.
- Apply programs in Unix for analysis of NGS data.
- Execute a proper Quality Assurance of NGS data.
- Understand and explain the steps involved in a general NGS data analysis.
- Explain key theoretical concepts of alignment and *de novo* assembly.
- Execute gene calling and annotation of a metagenomics sample.

Dates	December 2 – 6, 2019 Number of participants for this course will be limited to 40.
You should attend if	• You are an executive or an engineer or a researcher from a manufacturing, service industry or a government organization/Institution including R&D laboratories. • You are a faculty from an academic institution interested in learning about genomics and metagenomics. • You are student at all levels (BTech/MSc/MTech/PhD) aspiring to learn about genomics and metagenomics. • You are keen on upgrading your bioinformatics skills.
Fees	The participation fee (including taxes) for taking the course for different categories is as follows **Industry: INR 30,000** **Government organizations and NGOs: INR 15000** **Students: INR 6000** **Participants from outside of India: INR 90000** The above fee includes all instructional materials, computer use for tutorials and assignments, 24 hr free internet facility, lunch and tea during session breaks. **Accommodation**: The participants will be provided with accommodation on payment basis subject to availability

The faculty

Dr. Thomas Sicheritz-Pontén (TSP) is a Professor of Computational Biodiscovery, at the highly reputed Natural History Museum of Denmark at the University of Copenhagen, Copenhagen Denmark. He also holds a position at the Centre of Excellence for Omics-Driven Computational Biodiscovery (COMBio), Faculty of Applied Sciences, AIMST University, Kedah, Malaysia. Previously, **Prof. Sicheritz-Pontén** has served as one of the 6 Institute Professors at the Center for Biological Sequence Analysis at the Technical University of Denmark. He was also the first bioinformatics PhD to be examined from Uppsala University. TSP is collecting different samples from all-over the world and develops new tools that will address many of the unique challenges of metagenomics data sets. The majority of his projects are based on at least one of following three simple question: *Who is in there? What are they doing? How are they doing it?*

TSP works in collaborations with scientific groups with widely different interests and experience in bioinformatics from all over the world and his group is constantly exploring new areas within the world utilising NGS, Omics, Big Data and AI. He collects samples from all branches of the tree of life from all over the world and engages in expeditions across the globe including India, the Amazon rainforest, Australian bush, Arabian desert, Greenland wilderness, Polar seas and the Southeast Asian rainforests.

TSP has co-authored over 100 peer-reviewed papers, of which 15 are published in Nature and Science (5 as cover stories). He has currently an H-factor of 42 with 25,000 citations with an average of 162 citations per publication and is involved in several national and international research projects.

Dr. Bent Petersen (BP) is an Associate Professor at the Natural History Museum of Denmark, Copenhagen University, Copenhagen Denmark. He has a thorough experience in machine learning and has further specialized within the field of genomics and metagenomics where he is working extensively with Next Generation Sequencing data. The metagenomics research group actively collects samples from all over the world and develops new tools that address the unique challenges of microbial and antique systems biology often by using machine learning. Currently, BP is working extensively on genome and metagenome projects from various branches of the tree of life where he is using supercomputers to analyse the data. BP has the necessary skills to run large scale big data projects that were acquired by analysing data from numerous projects for the past 6 years. Currently, he is contributing as data governance officer on the Big Data project b10k, which aims to sequence and analyse all ~10.500 bird species in the world. Hands-on work on environmental data projects provided BP with the knowledge of how to plan and execute scientific expeditions. BP has co-authored 30 peer reviewed papers, of which 3 has been highlighted with cover pages in Science and PNAS. BP has currently a H-index of 13 and over with a total of 2400 citations with an average of more than 80 citations per publication. BP is currently actively involved in international genome projects in Chile, Brazil, Malaysia, New Zealand, USA and China.

Dr. Santosh Noronha (SN) is a Professor in the Department of Chemical Engineering of IIT Bombay. SN is at IIT Bombay since 2005. His primary interests are in large scale production and purification of recombinant proteins, protein structural analysis, statistical tools and bioinformatics. Of particular interest to SN is development and application of geometric mathematical techniques for comparison of protein structures. SN has published more than 70 papers in peer-reviewed Journals. In addition, SN is spearheading multitude of start-ups to address immediate Indian societal needs. Among many courses, SN teaches Biostatistics, Artificial intelligence in Process Engineering, Analysis of Biological and Bioprocess systems

Dr. Kiran Kondabagil ` is an Associate professor in the Department of Biosciences and Bioengineering of IIT Bombay with biochemistry, bioinformatics, and structural biology background. He has published more than 40 papers including in journals like Cell, PNAS, Molecular Cell, Journal of Molecular Biology, Journal of Biological Chemistry, Journal of Virology, etc. His research has helped in understanding the first detailed atomic level structure of the most powerful molecular motor that used by bacteriophages for genome encapsidation during the later stages of assembly. KK's group at IIT Bombay has isolated and sequenced several large DNA viruses for the first from India. KK's group has made significant contributions to our understanding of the evolutionary origins of large DNA viruses. His research interests include, genome encapsidation in viruses, evolution of large DNA viruses and their ecology. KK teaches Microbiology and Genetic Engineering Lab courses, Biology 101, Genetic

Engineering, Topics in Evolution, and Topics in Biotechnology courses.

Dr. Anirvan Chatterjee (AC) is the CEO and founder of HaystackAnalytics Pvt Ltd. (HAPL) a startup (at SINE IIT Bombay) that specializes in disease genomics. He is also working as a "Tata IGPEDU Fellow" in the Department of Biosciences and Bioengineering, IIT Bombay. AC obtained his PhD from University of Mumbai for his work on Tuberculosis Epidemiology carried out at the "Foundation for Medical Research", Mumbai, followed by a post-doctoral stint at Oxford University and another one at IIT Bombay on viral genomics. He has coauthored more than 20 papers including in journals like Nature Genetics, Tuberculosis, etc. AC's startup *HAPL* focuses on making genomic diagnostics accessible to every stratum of the population. Currently *HAPL* is offering genomics-based diagnostic solution for drug resistant forms of TB. *Haystack* was recently adjudged the winner in the Healthcare category in the Maharashtra Start-up Week, which had more than 2500 applicants.

Course outline

Day	9:30-11:00	11:30 -1:00	14:00-15:30	16:00-17:30
1	Introduction to Bioinformatics and supercomputing **(TSP)**	History of Sequencing **(BP/KK)**	Introduction to UNIX and the shell **(BP/AC)**	Hands-on training UNIX and Supercomputing **(TSP)**
2	Sequencing technologies **(BP)**	Sequencing projects **(TSP)**	Hands-on training, QC, filtering and trimming (with a break of 20 minutes in-between) **(BP/AC)**	
3	Introduction to Metagenomics **(TSP)**	Human and environmental microbiomes **(KK)**	Hands-on training, mapping and de-novo assembly **(BP & TSP)**	
4	Gene prediction, genome annotation **(TSP)**	Guidelines to Statistical Analysis of Microbial Composition Data Inferred from Metagenomic Sequencing **(SN)**	Hands-on training, gene calling and annotation **(BP & TSP)**	
5	Restructuring metagenomics data **(TSP)**	Abundance binning **(TSP)**	Hands-on training, metagenomic species identification **(BP & TSP)** Summary of the course **(TSP/KK)**	

All communications including the completed registration form (please see next page) may kindly be mailed to:

Prof. Kiran Kondabagil,
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IIT Bombay, Powai, Mumbai 400076. Tel: +91-22-25767758.
E-mail: kirankondabagil@iitb.ac.in

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on
A hands-on introduction to Next Generation Sequencing and Metagenomics Analysis
Dec 2-6, 2019

Registration Form

Name (in block Letters): _______________ _____________________

Qualification: _______________________

Designation: ________________________

Organization: __________________________

Mailing address: ____

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Mobile: _________________

Fax: ____________________

Email: ___________________

Payment: Rs. _______________

IIT Guest House/Hostel stay needed (will be arranged as per the availability on a payment basis): YES/NO

(Please contact the course coordinator for the availability details)

Signature of the applicant: _______________

Date:

COURSE FEE:

Industry: INR 30,000
Government organizations and NGOs: INR 15000
Students: INR 6000
Participants from outside of India: INR 90000

The above fees include all instructional materials, computer use for tutorials and assignments, laboratory usage charges, free internet facility. Subject to availability, the participants will be provided with accommodation on payment basis. This payment will be made separately by the participant at the accommodation venue.

The course fees are being paid by (Please tick appropriate option on the next page)

(i) Logging in at https://portal.iitb.ac.in/ceqipapp.

You will have to create a login ID, look up this course and fill up a registration form. After approval of the faculty co-ordinator, you can pay the fees. Please include the transaction details here:

Date:

Transaction number:

Transaction amount:

OR

(ii) Demand draft drawn in favour of "The Registrar, IIT Bombay - CEP Account".

If payment is by DD, please furnish the following details:

DD No.:____________________ Date: ________

All completed registration forms **with bank transaction details** may be mailed to:
Prof. Kiran Kondabagil,
Department of Bioengineering & Bioengineering,
IIT Bombay, Powai, Mumbai 400076.