### Registration

Register below for the Emerging Approaches for Tumor Analyses in Epidemiological Studies Workshop series

OMB No.: 0925-0740 Expiration Date: 09/30/2025

Public reporting burden for this collection of information is estimated to average 5 minutes per response, including the time for reviewing instructions, searching existing data sources, gathering and maintaining the data needed, and completing and reviewing the collection of information. An agency may not conduct or sponsor, and a person is not required to respond to, a collection of information unless it displays a currently valid OMB control number. Send comments regarding this burden estimate or any other aspect of this collection of information, including suggestions for reducing this burden to: NHI, Project Clearance Branch, 6705 Rockledge Drive, MSC 7974, Bethesda, MD 20892-7974, ATTN: PRA (0925-0740). Do not return the completed form to this address.

Last Name*	
NIH Email*	
Confirm email*	
Position*	
O Post-baccalaureate/Post-doctor	ral
Research Analyst/Contractor	
Research Fellow/Staff Scientist	

#### DCEG Branch/Program\*

- Biostatistics Branch
- Olinical Genetics Branch
- Infections and Immunoepidemiology Branch
- Integrative Tumor Epidemiology Branch
- Laboratory of Genetic Susceptibility
- Laboratory of Translational Genomics
- Metabolic Epidemiology Branch
- Occupational & Environmental Epidemiology Branch
- Radiation Epidemiology Branch
- Trans-Divisional Research Program
- Cancer Genomics Research Laboratory
- Ocenter for Cancer Research (CCR)
- Other...

## Of the 12 sections of the workshop, please select the lectures sections you are interested in The lectures are 9:30 - 10:30 If you participate in all the lectures and hands-on workshop, you will be provided with a certificate of completion from the Division of Cancer Epidemiology & Genetics. All lectures ☐ Session 1: Nov. 2, 2022: Introduction to Computing Clusters and Bioinformatics ☐ Session 2: Nov. 9, 2022: Public databases ☐ Session 3: Nov. 16, 2022: DNA sequencing strategies and quality control ☐ Session 4: Jan. 11, 2023: Mutation calling and analysis Session 5: Jan. 18, 2023: Mutational signatures Session 6: Jan. 25, 2023: Structural variant (SV) analysis ☐ Session 7: Mar. 8, 2023: Somatic copy number alterations (SCNAs) ☐ Session 8: Mar. 15, 2023: Identifying cancer drivers ☐ Session 9: Mar. 22, 2023: Clonal evolution ☐ Session 10: Apr. 26, 2023: Transcriptome-based study designs Session 11: May 3, 2023: RNA-seq data mining ☐ Session 12: May 10, 2023: Data visualization approaches

### Of the 12 sections of the workshop, please select the hands-on sections you are interested in

The hands-on workshop are 10:45-12:00

No previous experience on genomics analyses is required to attend the hands-on workshops; however, some basic knowledge on programming (e.g., R or Linux/Shell) and Next Generation Sequencing would be useful.

If you participate in all the lectures and hands-on workshop, you will be provided with a certificate of completion from the Division of Cancer Epidemiology & Genetics.
☐ All hands-on workshops
☐ Session 1: Nov. 2, 2022: Introduction to Computing Clusters and Bioinformatics
☐ Session 2: Nov. 9, 2022: Public databases
☐ Session 3: Nov. 16, 2022: DNA sequencing strategies and quality control
☐ Session 4: Jan. 11, 2023: Mutation calling and analysis
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□ Session 6: Jan. 25, 2023: Structural variant (SV) analysis
☐ Session 7: Mar. 8, 2023: Somatic copy number alterations (SCNAs)
☐ Session 8: Mar. 15, 2023: Identifying cancer drivers
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☐ Session 10: Apr. 26, 2023: Transcriptome-based study designs
☐ Session 11: May 3, 2023: RNA-seq data mining
☐ Session 12: May 10, 2023: Data visualization approaches

# Additional Questions for Those Attending the Hands-on Workshops **Computer Operating System** O Mac O PC Other... To get a sense of the participants' level of familiarity with Unix, please tell us how long have you been using Unix.\* O I do not use Unix O Less than 1 year of experience ○ 1 to 3 years of experience Over 3 years of experience To get a sense of the participants' level of familiarity with R programming, please tell us how long have you been programming in R. O I do not program in R O Less than 1 year of experience ○ 1 to 3 years of experience Over 3 years of experience To get a sense of the participants' level of familiarity with High-Performance Computing (HPC) cluster, please tell us how long have you been using an HPC cluster O I have not used an HPC cluster O Less than 1 year of experience ○ 1 to 3 years of experience Over 3 years of experience Please answer this question only if you are from DCEG. You will need to log into the NIH Biowulf account for the practical sessions. Do you have an NIH Biowulf account? If you already have an NIH Biowulf account, check the Yes box below. If you do not have an NIH Biowulf account, check the $\it No$ box below and we will create an NIH Biowulf account for you. For non-DCEG participants, please follow the instructions here to obtain an NIH Biowulf account if you do not have one: https://hpc.nih.gov/docs/accounts.htmld ☐ Yes □ No

### "Ask a Bioinformatician" Help Sessions

There will be four optional "Ask a Bioinformatician" help sessions that will run for 2 hours from 9:30am to 11:30am. No registration is required and access information will be communicated to all participants. The dates for the sessions will be:

- Nov. 23, 2022: "Ask a Bioinformatician" I
- Feb. 1, 2023: "Ask a Bioinformatician" II
- Mar. 29, 2023: "Ask a Bioinformatician" III
- May 17, 2023: "Ask a Bioinformatician" IV

Experience	in somatic gen	omic data a	nalysis			
O None						
○ 0-1 year	of experience					
○ 1-3 years	of experience					
O 3+ years	of experience					
-	experience with	_		analysis, ple	ease briefly o	lescrib
-		_		analysis, ple	ease briefly o	lescrib
-		_		analysis, ple	ease briefly c	lescrib
-		_		analysis, ple	ease briefly o	lescrib
-		_		analysis, ple	ease briefly c	lescrib