**Genomac Institute Inc. Hands-on Training Program in Cancer Genomics and Bioinformatics**

**Duration: 4 Weeks | Time: 4:00 PM WAT | Mode: Virtual & Hands-On**

**YOUR LEARNING JOURNEY IN THIS PROGRAM**

As a participant, this intensive 4-week program will introduce you to the principles and practices of cancer genomics through a combination of virtual lectures and hands-on sessions. Designed for beginners and intermediate learners, the program will walk participants through real-world workflows involving data preprocessing, genome assembly, genome annotation, variant analysis, and data visualization, all anchored by a mini project using real cancer data.

Participants will gain practical experience using Usegalaxy, Geneious, Excel, R, and Tableau, while learning essential bioinformatics methods and ethical considerations in the field of cancer genomics.

**✅ 1. Program Overview (Executive Summary)**

This 4-week virtual training program in Cancer Genomics and Bioinformatics offers participants a practical introduction to cancer genome analysis using real data. Through guided mini projects, participants will explore genome annotation, sequence alignment, variant detection, and functional insights using different bioinformatics tools.

✅ **2. Target Audience**

This program is designed for:

* Undergraduate and postgraduate students in life sciences
* Early-career researchers and public health professionals
* Laboratory scientists and molecular biologists interested in genomic tools
* Anyone seeking hands-on skills in cancer data analysis

**✅ 3. Learning Outcomes**

By the end of the program, participants will be able to:

* Retrieve and curate cancer genome data from public repositories
* Perform quality assessment and preprocessing of cancer sequences
* Annotate and align cancer sequences using Geneious
* Map sequences to a reference genome and identify variants
* Predict functional impacts of mutations
* Create visual summaries of genomic data
* Understand ethical considerations in cancer genomic studies

**✅ 4. Tools and Platforms Used**

Participants will gain hands-on experience using:

* Biological databases (NCBI for data retrieval)
* Geneious software (sequence annotation, alignment, variant calling)
* Usegalaxy (quality control)
* Excel/Tableau/ R/ClustVis (metadata analysis and visualization)

**✅ 5. Mini Project**

Participants will select a cancer of interest and carry out a mini project that includes genome retrieval, quality assessment and preprocessing, annotation, alignment, variant calling, and visualization.

**✅ 6. Certification**

A certificate of participation will be awarded upon completion of all hands-on sessions and submission/presentation of the mini project.

**✅ 7. Mentorship and Support**

Participants will receive mentorship from experienced facilitators throughout the program. Interactive Q&A sessions, and one-on-one support will be available during key hands-on modules.

**✅ 8. Program Requirements (Prerequisites)**

Participants are expected to:

* Have a background or interest in biological sciences or bioinformatics
* Have a computer for hands-on sessions

**Program Structure, Timeline, and Objectives**

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| **Week** | **Session** | **Topics** | **Objectives/Hands-on Activities** |
| 1 | 1 | Introduction to cancer Genomics | Introduction to the foundational concepts of cancer genomics, including cancer genome structures, types, and the significance of genome analysis in the study of cancer. |
|  | 2 | Biological Databases and Data Collection | Explore biological databases, identify appropriate subjects and reference cancer genomes, and retrieve data in standard formats. |
|  | 3 | Mini Project – Define Study Design | Define the goals of mini projects, select and retrieve genomes of target cancer for analysis  |
| 2 | 4 | Quality Check & Preprocessing | Overview of usegalaxy. Perform quality check and trimming using fastqc and trimmomatic  |
|  | 5 | Genome assembly  | Perform genome assembly on usegalaxy  |
|  | 6 | Sequence Exploration and Annotation | Mapping cancer genomes to a reference sequence and generate consensus sequences to support mutation analysis. |
| 3 | 7 | Variant Calling & Mutation Analysis | Call variants (VCF), identify SNPs and indels using Geneious or Galaxy |
|  | 8 | Variant Effect Prediction | Annotate variant effects on genes/coding regions using Geneious to understand biological impact. |
|  | 9 | Data Cleaning & Integration | Clean and organize mutation/sample metadata using spreadsheet tools (Excel) and visualization platforms (Tableau). |
| 4 | 10 | Data Visualization  | Create effective visualizations, such as heatmaps and summary charts, to communicate patterns in variant and genomic data using tools like ClustVis, R, or Tableau. |
|  | 11 | Project wrap-up | Project wrap-up, Q&A |
|  | 12 | Bioethics and Biosafety in Cancer Genomics | Importance of ethical considerations and biosafety in cancer genomics research, including responsible data use, sharing, and biosecurity awareness. |