Professional Master's Degree

Precision Oncology: Genomics and Big Data

tech technological university

tech technological university

Professional Master's Degree

Precision Oncology: Genomics and Big Data

- Modality: **online**
- Duration: **12 months**
- Certificate: **TECH Technological University**
- Dedication: **16h/week**
- Schedule: **at your own pace**
- Exams: **online**

Website: **www.techtitute.com/us/medicine/professional-master-degree/master-precision-oncology-genomics-big-data**

Index

01 Introduction p. 4

02 Objectives p. 8

03 Skills p. 14

04 Course Management p. 18

05 Structure and Content p. 24

06 Methodology p. 36

07 Certificate p. 44

01

Introduction

The concept of genomic or precision oncology is not entirely new; physicians have been using blood type to tailor blood transfusions for over a century. What is different today is the rapid growth of genomic data that can be quickly and cheaply collected from the patient and the community at large, and the potential to gain insights from sharing this data. The measurements traditionally used in laboratory testing are dwarfed by the scale and complexity of genomic data.

Expand your knowledge of Precision Oncology: Genomics and Big Data through this program, where you will find the best teaching material with real practical cases. Learn here the latest advances in the specialty to be able to perform quality medical practice"

A fundamental objective of the program is to bring students closer to and disseminate computer knowledge, which is already applied in other fields of knowledge but has minimal implementation in the medical world, despite the fact that for genomic medicine to become a reality, it is necessary to accurately interpret the enormous volume of clinical information currently available and associate it with the biological data generated after a bioinformatic analysis.

While this is a difficult challenge, it will allow the effects of genetic variation and potential therapies to be explored quickly, inexpensively and with greater precision than is currently possible. Humans are not naturally equipped to perceive and interpret genomic sequences, to understand all the mechanisms, pathways and interactions that take place within a living cell, nor to make medical decisions with tens or hundreds of variables. To move forward, a system with superhuman analytical capabilities is required to simplify the work environment and show the relationships and proximities between variables.

In genomics and biology, it is now recognized that it is better to spend resources on new computational techniques than on pure data collection, something that is possibly the same in medicine and, of course, oncology.

We have millions ofpublications and enormous amounts of data, but when analyzed by physicians or biologists, the conclusions are totally subjective and relative to the available publications or data which are prioritized arbitrarily. This generates partial knowledge, which is increasingly distanced from the genetic and biological knowledge available and supported by computing, so a giant step in the implementation of precision medicine is to reduce this distance through the massive analysis of available medical and pharmacological information.

This **Professional Master's Degree in Precision Oncology: Genomics and Big Data** contains the most complete and up-to-date scientific program on the market. The most important features include:

- More than 75 practical cases presented by experts in Precision Oncology: Genomics and Big Data The graphic, schematic, and eminently practical contents with which they are created provide scientific and practical information on the disciplines that are essential for professional
- Novelties in precision oncology, genomics and big data
- Contains practical exercises where the self-evaluation process can be carried out to improve learning
- An algorithm-based interactive learning system for decision-making in the clinical situations presented throughout the course
- With special emphasis on evidence-based medicine and research methodologies in Precision Oncology: Genomics and Big Data
- All of this will be complemented by theoretical lessons, questions to the expert, debate forums on controversial topics, and individual reflection assignments
- Content that is accessible from any fixed or portable device with an Internet connection

Update your knowledge through the program in Precision Oncology: Genomics and Big Data"

This Professional Master's Degree may be the best investment you can make in the selection of a refresher program for two reasons: in addition to updating your knowledge of Precision Oncology: Genomics and Big Data, you will obtain a qualification from TECH"

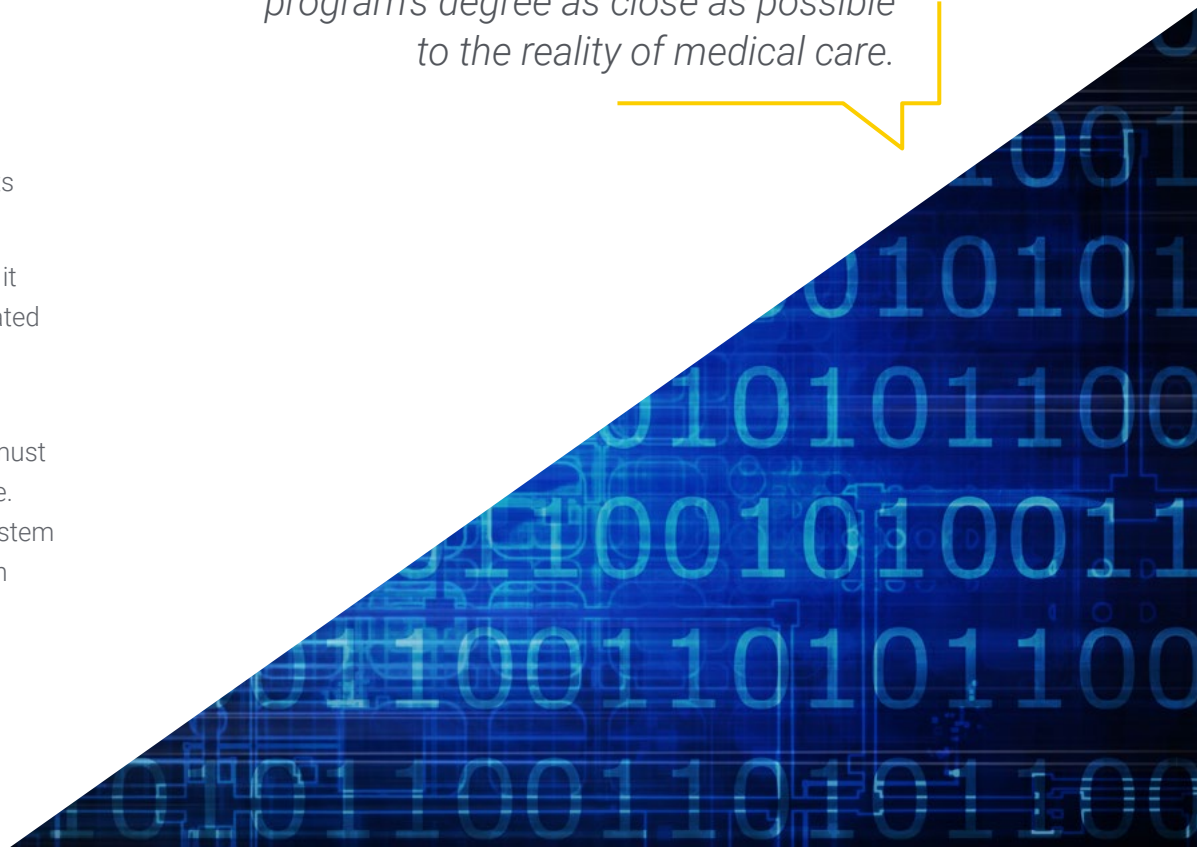
This Professional Master's Degree offers training in simulated environments, which provides an immersive learning experience designed to train for real-life situations.

It includes clinical cases to bring the program's degree as close as possible to the reality of medical care.

The teaching staff includes professionals from the field of precision oncology, who bring their experience to this specialization program, as well as renowned specialists from leading scientific societies.

Thanks to its multimedia content developed with the latest educational technology, it will allow the professional a situated and contextual learning, that is to say, a simulated environment that will provide an immersive learning programmed to train in real situations.

This program is designed around Problem Based Learning, whereby the physician must try to solve the different professional practice situations that arise during the course. For this purpose, the physician will be assisted by an innovative interactive video system created by renowned and experienced experts in the field of precision oncology with extensive teaching experience.



02

Objectives

This Professional Master's Degree in Precision Oncology: Genomics and Big Data is aimed at facilitating the performance of the physician dedicated to the treatment of oncological pathologies which require an accurate interpretation of the huge volume of clinical information currently available and to associate it with the biological data generated after a bioinformatic analysis.

This Professional Master's Degree is designed to help you update your knowledge of Precision Oncology: Genomics and Big Data with the use of the latest educational technology to contribute quality and confidence in decision-making, diagnosis, treatment, and patient support"

General Objective

- Be able to accurately interpret the volume of clinical information currently available and associated with the biological data generated after a bioinformatic analysis

Make the most of the opportunity and take the step to get up to date on the latest developments in Precision Oncology: Genomics and Big Data"

Specific Objectives

Module 1. Molecular Biology

- Update knowledge of the molecular biology of cancer, especially in relation to the concept of genetic heterogeneity, reprogramming of the microenvironment, the role of the immune response in cancer control and molecular mechanisms involved in the process of invasion and metastasis
- Provide and expand knowledge of immunotherapy as an example of a clear scientific advance in translational research and as one of the most promising lines of research in cancer treatment
- Learn a new approach to classifying the most common tumors based on genomic data available from The Cancer Genome Atlas (TCGA) Research Network, which not only renews traditional ideas about how malignancies are diagnosed and treated, but may also have a profound impact on the future landscape of drug development

Module 2. Genomic or precision oncology

- Discuss the change in the current landscape with the introduction of genomic data in the biological knowledge of tumors that has allowed a shift in the research and treatment of tumors from the classical view, which defines cancer as a disease according to the tissue in which it originated; and consider the genomic signature to identify tumor subtypes with independent prognostic and predictive value
- Explain how genomic classification, although correlated with tissue of origin, provides independent information to predict clinical outcomes, and will provide the biological basis for an era of personalized cancer treatment
- Learn the new genomic technologies currently used in DNA and RNA sequencing, based on the human genome sequence and made possible since the completion of the Human Genome Project, which has represented an unprecedented expansion of the capabilities of molecular genetics in genetic and clinical diagnostic research
- Comment on the bioinformatic process followed to interpret and apply biological data, which is fundamental since the advent of modern sequencing techniques, and which enable the organization, analysis and interpretation of biological information at the molecular, cellular and genomic levels, which is essential today, since the identification of nucleic acid sequences has become a ubiquitous and essential tool in all areas of biological science

Module 3. Changes in Current Clinical Practice and New Applications with Genomic Oncology

- Discuss and know how to interpret tumor mutational burden (TMB) as a genomic biomarker that has a significant impact on the landscape of cancer immunotherapy. This emerging marker measures the number of mutations within the tumor genome and has already shown to be associated with improved response to immune checkpoint inhibitors
- Learning how a liquid biopsy of circulating DNA allows us to understand specifically what kind of molecular changes are happening in the tumor in real time, which is a big step beyond current clinical tumor response and follow-up endpoints
- Describe the current paradigm of incorporating genomic data into current clinical practice, where treatment selection should be dictated by the specific molecular aberrations found in each patient's tumor. As a result, the classical clinical trial paradigm of patient eligibility based on clinicopathological parameters is being abandoned in favor of current clinical trials that recruit patients on the basis of specific molecular aberrations

Module 4. Use of Unix and Linux in Bioinformatics

- Learn about the Linux operating system, which is currently essential in the scientific world both for the interpretation of biological data from sequencing and it also should be for medical text mining when handling large-scale data. There are many reasons, but one that justifies this section is that Unix is the most popular system in the world and is widely used, especially in the scientific world. Moreover, being an open source system, it clearly corresponds to the scientific approach of sharing results and methods to ensure the reproducibility of the results
- Provide the basics of accessing a Linux server and how to find and install packages to install software locally
- Describe basic Linux commands for: creating, renaming, moving and deleting directories; listing, reading, creating, editing, copying and deleting files; how permissions work and how to decipher the most cryptic Linux permissions with ease; methods for searching files and directories; how to compare the contents of files; what pipes are, why they are useful and how to use them; how to zip files to save space and ease data transfer, etc.

Module 5. Data Analysis in Big Data Projects: R Programming Language

- Discuss how the adoption of next-generation sequencing (NGS) in a diagnostic context raises numerous questions regarding the identification and reporting of variants in secondary genes for patient pathology, making it critical to define those genes considered actionable due to their efficient curation process and published data collection
- Getting started with the R programming language, which has the advantages of being an open-source programming language, multiple statistical analysis packages, a community that strives to develop the various aspects of this tool, and provides an effective language for managing and manipulating data
- Learn basic R programming concepts such as data types, vector arithmetic and indexing
- Performing operations in R, including sorting, creating or importing data
- Learn how problem solving begins with a modular decomposition and then further decompositions of each module in a process called successive refinement
- Learn the basics of statistical inference to understand and calculate p-values and confidence intervals while analyzing data with R
- Provide examples of R programming in a way that will help make the connection between concepts and their implementation

Module 6. The Graphical Environment in R

- Using visualization techniques to explore new datasets and determine the most appropriate approach
- Learn how to visualize data to extract information, better understand data and make more effective decisions
- Teach how to take data that at first glance has little meaning and visually present that data in a form that makes sense for analysis
- Learn how to use the three main graph sources in R: base, lattice and ggplot2
- Know what each graphics package is based on in order to define which one to use and the advantages offered by one or the other

Module 7. Statistical analysis in R

- Describe the most appropriate statistical techniques as an alternative when data do not conform to the assumptions required by the standard approach
- Learn the basics of conducting reproducible research by using R scripts to analyze data

Module 8. Machine Learning for Analyzing Big Data

- Rapidly and automatically process and analyze enormous volumes of complex structured, semi-structured and unstructured data in big data
- Understand what machine learning is and to use some of the techniques for data classification (decision tree, k-NN, Support Vector Machines, neural networks, etc.)
- Learn how to divide data into a test set and a training set and discover the concepts of bias and variance

Module 9. Data Mining Applied to Genomics

- Learn how data mining facilitates finding patterns and regularities in databases, which will be very useful for making predictions and prognoses, and in general improving and expanding knowledge through interaction with data, which is being crucial for the enrichment of genetic variants and will be essential for clinical enrichment and implementation of precision oncology
- Learn to apply the principles of data mining to the analysis of large complex datasets (Big Data), including those in very large databases or on web pages
- Explore, analyze and leverage data and convert it into useful and valuable information for clinical practice

Module 10. Techniques Genomic Data Extraction

- Understand how most scientific data appear in documents such as web pages and PDF files that are difficult to process for further analysis. However, we can make them usable by means of scraping techniques
- Access many data sources through the web has made scraping techniques an essential part of the toolkit for the implementation of precision medicine, by allowing the massive extraction of information, its subsequent processing and conversion into useful data for interpretation

Module 11. New Techniques in the Genomic Era

- Put into practice the knowledge acquired for the interpretation of a genomic study in several cancer cases by extracting useful information that will help in decision making
- Using several algorithms performed with the R language for the extraction of knowledge from Pubmed, DGIdb and Clinical Trials databases based on the search for genetic information in certain tumors

Module 12. Application of bioinformatics in genomic oncology

- Understanding the function of genes with little clinical information based on ontological proximity
- Discover genes involved in a disease based on a massive Pubmed search and graphical representation of the level of scientific evidence

03

Skills

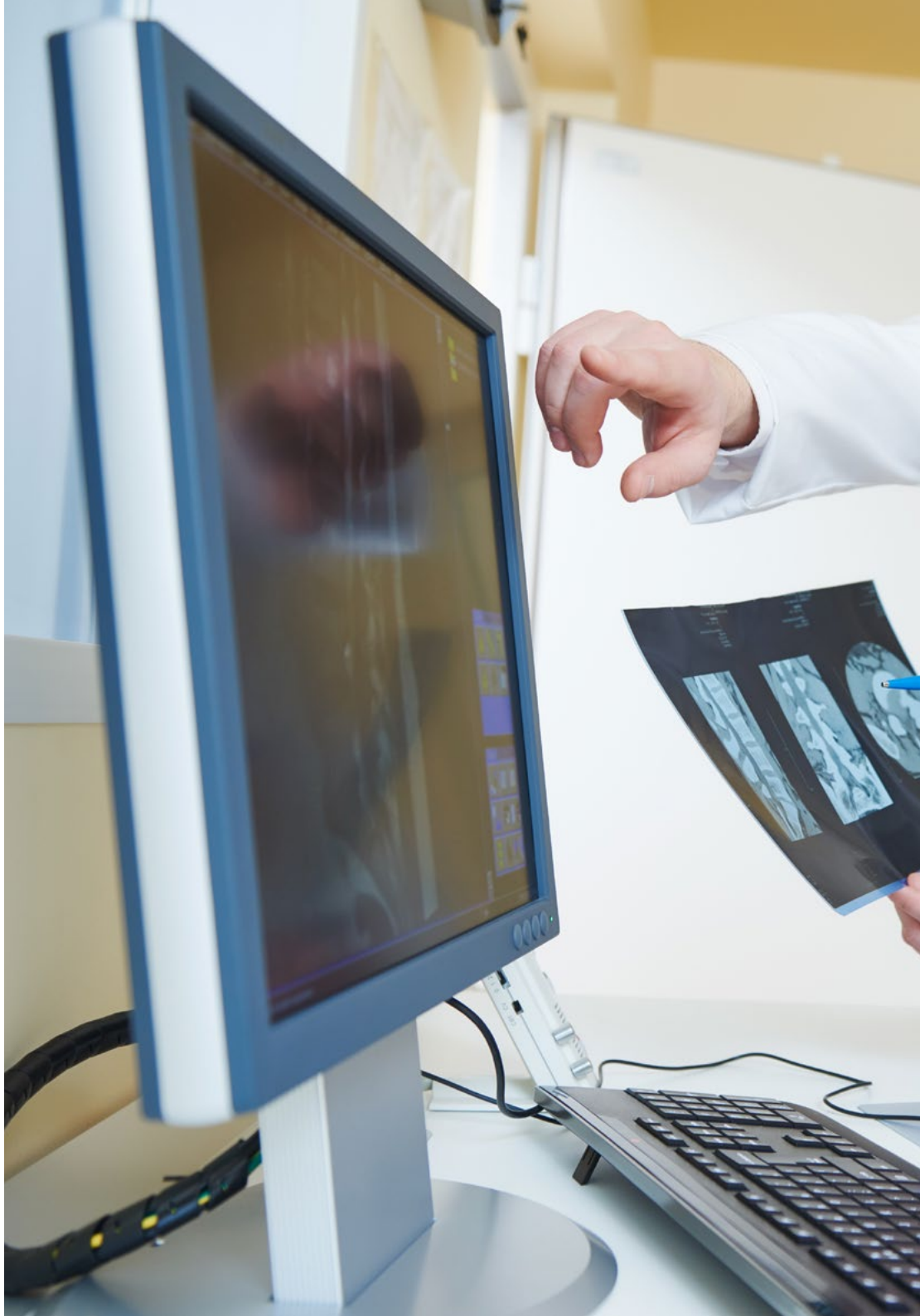
After passing the assessments on the Professional Master's Degree in Precision Oncology: Genomics and Big Data, the student will have acquired the professional skills required for quality, up-to-date practice based on the most recent scientific evidence.

With this program, you will master new diagnostic and therapeutic procedures in Precision Oncology: Genomics and Big Data"

General Skills

- Possess and understand knowledge that provides a basis or opportunity to be original in the development and/or application of ideas, often in a research context
- Apply acquired knowledge and problem-solving skills in new or unfamiliar environments within broader (or multidisciplinary) contexts related to their area of study
- Integrate knowledge and face the complexity of making judgments based on incomplete or limited information, including reflections on the social and ethical responsibilities linked to the application of their knowledge and judgments
- Know how to communicate their conclusions, the knowledge and ultimate reasons that support them, to specialized and non-specialized audiences in a clear and unambiguous manner
- Acquire the learning skills that will enable them to continue studying in a manner that will be largely self-directed or autonomous

This program will provide you with a sense of confidence in your medical practice, which will help you grow personally and professionally"



Specific Skills

- Create a global and updated vision of the exposed topics that will allow the student to acquire useful knowledge and at the same time, generate interest in expanding the information and discovering its application in their daily practice
- Understand the knowledge discovery process, including data selection, cleaning, coding, the use of different statistical and machine learning techniques and the visualization of the generated structuresa
- Understand how to evaluate the performance of supervised and unsupervised learning algorithms
- Learn how functions normally return only one value to the program unit, unlike procedures that can return zero, one or several values
- Learn the biological databases that have emerged in response to the enormous amount of data generated by DNA sequencing technologies. Data stored in biological databases are organized for optimal analysis and are characterized by being complex, heterogeneous, dynamic and yet inconsistent due to the lack of standards at the ontological level
- Learn how procedures and functions assist modular programming

04

Course Management

The program includes in its teaching staff leading experts in Precision Oncology: Genomics and Big Data and other related areas who pour their work experience to this training program. Additionally, other recognized specialists participate in its design and preparation, which means that the program is developed in an interdisciplinary manner.

Learn from reference professionals, the latest advances in procedures in Precision Oncology: Genomics and Big Data"

Management

Dr. Oruezábal Moreno, Mauro Javier

- Head of the medical Oncology Service at La Paz University Hospital since 2017
- Research Fellow at University of Southampton (2016-present)
- Master's Degree in Bioinformatics and biostatistics UOC-UB (2016-ongoing)
- Master's Degree in bioinformatic analysis by the Pablo de Olavide University (2015-2016)
- Specialist (MIR) in Medical Oncology, University Hospital San Carlos of Madrid (2000)
- Degree in Medicine and Surgery, University of Navarra (1995)

Mr. Krallinger, Martin

- Head of the text mining unit at the Spanish National Cancer Research Center (CNIO)
- Expert in the field of biomedical and clinical text mining and linguistic technologies, and has been working on this and related research topics for more than ten years, resulting in more than 70 publications (more than 45 of them corresponding to JCR publications) and several domains
- Expert in specific text mining applications for drug safety, molecular systems biology and oncology
- Organizer of BioCreative community evaluation challenges for the evaluation of natural language processing tools and has participated in the organization of biomedical text mining tasks in various international community challenges, including IberEval and CLEF

Professors

Mr. Alberich Martí, Ricardo
- Full university professor of Mathematic Sciences and Computing (Director)
- Computer Science and Artificial Intelligence University of the Balearic Islands

Ms. Álvarez Cubero, María Jesús
- Professor of the Department of Biochemistry III and Immunology, University of Granada

Mr. Andrés León, Eduardo
- Head of the Bioinformatics Unit, Institute of Parasitology and Biomedicine, López-Neyra - CSIC
- Degree in Biology and Molecular Biology, Universidad Autónoma de Madrid

Ms. Astudillo González, Aurora
- Anatomic Pathology Service
- Full Professor at the University of Oviedo, linked to the Central University Hospital of Asturias Scientific Director of the Biobank of the Principality of Asturias

Ms. Burón Fernández, María del Rosario
- Internal Medicine Department, Infanta Cristina University Hospital

Mr. Carmona Bayonas, Alberto
- Medical Oncology Service, Morales Meseguer General University Hospital

Ms. Ciruelos, Eva M.
- MD, PhD Department of Medical Oncology 12 de Octubre University Hospital, Madrid
- HM CIOCC, Madrid

Mr. Galiana, Enrique de Andrés
- Mathematics Department, University of Oviedo

Mr. De la Haba Rodríguez, Juan
- Medical Oncology Service, University of Cordoba, Reina Sofía University Hospital

Mr. Fernández Martínez, Juan Luis
- Director of the Inverse Problems, Optimization and Machine Learning Group Department of Mathematics. University of Oviedo

Ms. Figueroa, Angelica
- Institute of Biomedical Research A Coruña (INIBIC).
- Research Group Leader, Epithelial Plasticity and Metástasis

Ms. García Casado, Zaida
- Laboratory of Molecular Biology Valencian Institute of Oncology Foundation

Mr. GarcíaFoncillas, Jesús
- Jiménez Diaz Foundation Medical Oncology Service

Mr. Gomila Salas, Juan Gabriel
- University Professor Mathematical Sciences and Computer Science and Artificial Intelligence University of the Balearic Islands

Mr. González Gomáriz, José
- IdiSNA (Institute for Health Research of Navarra) Researcher in Training

Mr. Hoyos Simón, Sergio
- Medical Oncology Department, Hospital Universitario Rey Juan Carlos, Madrid, Spain

Mr. Intxaurrondo, Ander
- Life Sciences-Text Mining
- Barcelona Supercomputing Center

Ms. Jiménez-Fonseca, Paula
- Coordinator of the Digestive and Endocrine Tumors Section Medical Oncology. Asturias Central University Hospital

Ms. Lage Alfranca, Yolanda
- Jiménez Diaz Foundation Medical Oncology Service

Mr. López Guerrero, José Antonio
- Medical Oncology Service, Valencian Institute of Oncology, Valencia, Spain

Mr. López López, Rafael
- Head of the Medical Oncology Department
- Santiago de Compostela University Hospital Complex
- Translational Medical Oncology Group Health Research Institute

Mr. Martínez González, Luis Javier
- PhD. Genomics Unit
- Pfizer center - University of Granada - Andalucía Government Center for Genomics and Oncology Research
- Pfizer - University of Granada - Andalucía Government Centre for Genomics and Oncological Research (GENYO)

Ms. Martínez Iglesias, Olaia
- Institute of Biomedical Research A Coruña (INIBIC)
- Research Group Leader, Epithelial Plasticity and Metástasis

Mr. Paramio Gonzalez, Jesús María
- CIEMAT Molecular Oncology Unit
- 12 de Octubre Research Institute of Madrid

Mr. Pascual Martínez, Tomás
- Barcelona Clinical Hospital
- Translational Genomics and Targeted Therapeutics in Solid Tumours Lab (IDIBAPS)

Ms. Pérez Gutiérrez, Ana María
- Student on the Master's Degree in the Clinical Bioinformatics Department of the Progress and Health Foundation, FPS, Virgen del Rocío Hospital, Seville
- PhD student in Biomedicine, UGR

Ms. Ribalta, Teresa
- MD, PhD Chief, Anatomic Pathology Service Hospital Sant Joan de Déu, Biobank
- Consultor, Anatomic Pathology Service, Hospital Clínic
- Professor of Pathology, Universitat de Barcelona

Mr. Sánchez Rubio, Javier
- Pharmacy Department, Getafe University Hospital

Mr. Olivas Varela, José Ángel
- Deputy Director, Department of Information Technologies and Systems, Higher School of Computer Science

Mr. Torres, Arnau Mir
- Full university Professor Mathematical Sciences and Computer Science and Artificial Intelligence University of the Balearic Islands

Mr. Soares, Felipe
- Research Engineer Text Mining
- Barcelona Supercomputing Center

Mr. Rueda Fernández, Daniel
- Research Unit of the 12 de Octubre University Hospital, Madrid

Mr. Segura Ruiz, Víctor
- CIMA University of Navarra (Bioinformatics Platform) Unit Director

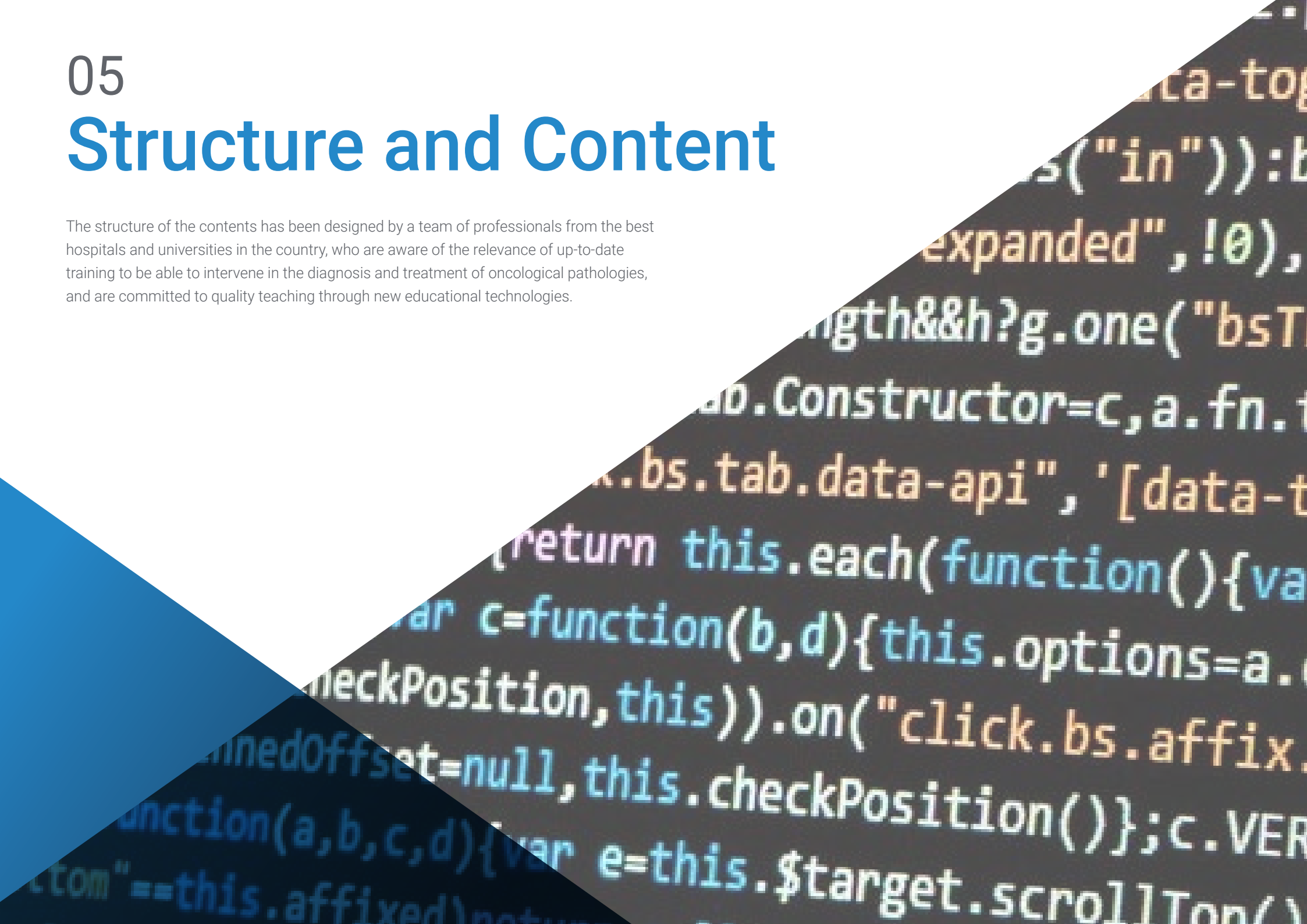
Mr. Vázquez García, Miguel
- Genome Informatics Group Leader
- Barcelona Supercomputing Center

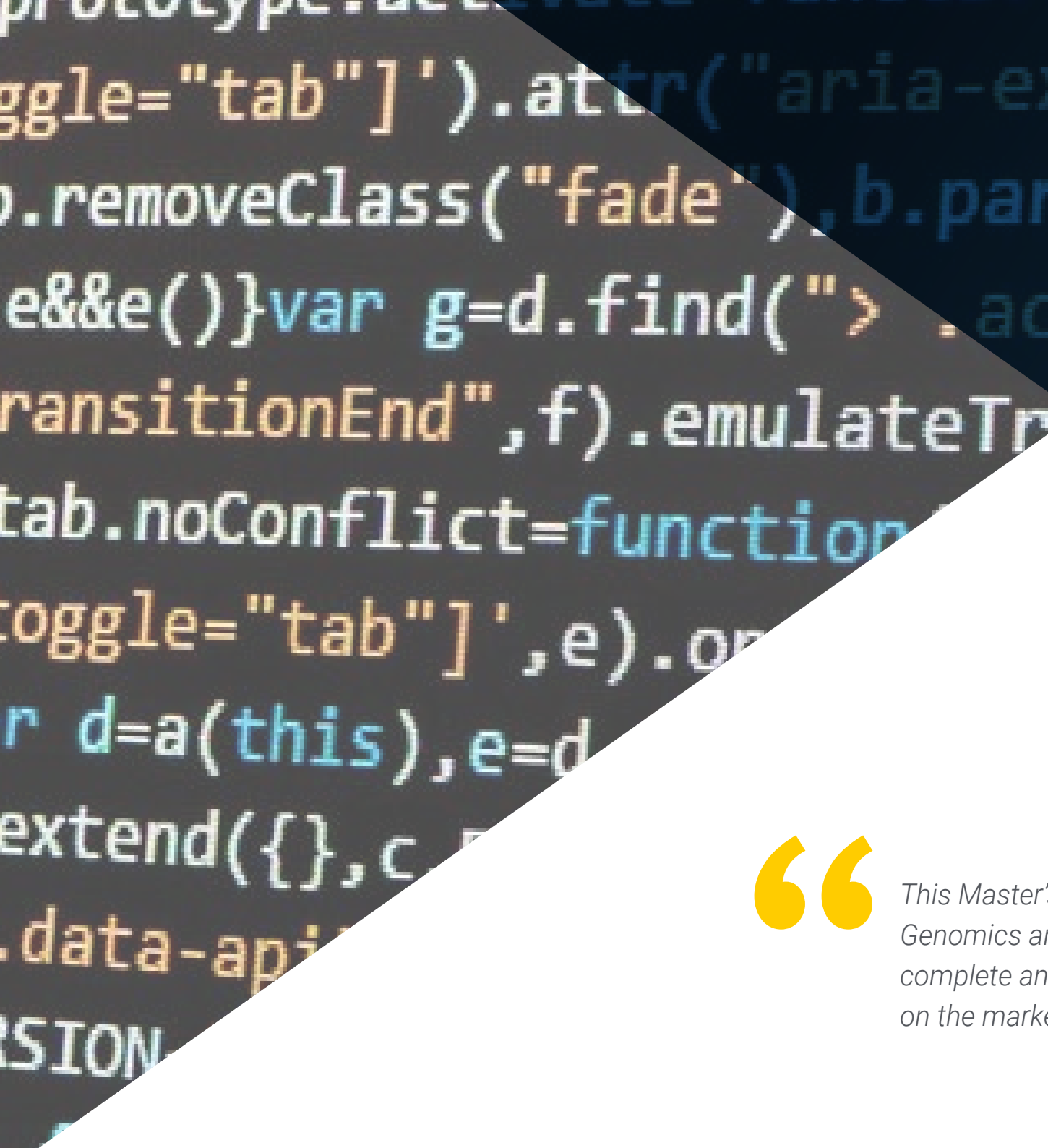
Mr. Velastegui Ordoñez, Alejandro
- Medical Oncology Department, Hospital Universitario Rey Juan Carlos, Madrid, Spain

05

Structure and Content

The structure of the contents has been designed by a team of professionals from the best hospitals and universities in the country, who are aware of the relevance of up-to-date training to be able to intervene in the diagnosis and treatment of oncological pathologies, and are committed to quality teaching through new educational technologies.





This Master's Degree in Precision Oncology: Genomics and Big Data contains the most complete and up-to-date scientific program on the market"

Module 1. Molecular Biology

1.1. Molecular Mechanisms of Cancer
- 1.1.1. Cellular Cycle
- 1.1.2. Detachment of Tumor Cells

1.2. Reprogramming of the Tumor Microenvironment
- 1.2.1. Tumor Microenvironments: An Overview
- 1.2.2. TME as a Prognostic Factor in Lung Cancer
- 1.2.3. TME in the Progression and Metastasis of Lung Cancer
  - 1.2.3.1. Cancer-Associated Fibroblasts (CAF)
  - 1.2.3.2. Endothelial Cells
  - 1.2.3.3. Hypoxia in Lung Cancer
  - 1.2.3.4. Inflammation
  - 1.2.3.5. Immune Cells
- 1.2.4. Contribution of TME to Therapeutic Resistance
  - 1.2.4.1. Contribution of TME to Radiotherapy Resistance
- 1.2.5. TME as a Target Treatment in Lung Cancer
  - 1.2.5.1. Future Directions

1.3. Tumor Immunology: Basis of Cancer Immunotherapy
- 1.3.1. Introduction to the Immune System
- 1.3.2. Tumor Immunology
  - 1.3.2.1. Tumor-Associated Antigens
  - 1.3.2.2. Identification of Tumor-Associated Antigens
  - 1.3.2.3. Types of Tumor-Associated Antigens
- 1.3.3. The Bases of Immunotherapy in Cancer
  - 1.3.3.1. Introduction to the Immunotherapeutic Approaches
  - 1.3.3.2. Monoclonal Antibodies in Cancer Therapy
    - 1.3.3.2.1. Production of Monoclonal Antibodies
    - 1.3.3.2.2. Types of Therapeutic Antibodies
    - 1.3.3.2.3. Mechanisms of Action of Antibodies
    - 1.3.3.2.4. Modified Antibodies
- 1.3.4. Non-Specific Immune Modulators
  - 1.3.4.1. Bacillus Calmette-Guérin
  - 1.3.4.2. Interferon-α
  - 1.3.4.3. Interleucina-2
  - 1.3.4.4. Imiquimod
- 1.3.5. Other Approaches for Immunotherapy
  - 1.3.5.1. Dendritic Cell Vaccines
  - 1.3.5.2. Sipuleucel-T
  - 1.3.5.3. CTLA-4 Blocking
  - 1.3.5.4. Adoptive T-cell Therapy
    - 1.3.5.4.1. Adoptive Cell Therapy With T-cell Clones
    - 1.3.5.4.2. Adoptive Cell Therapy with Tumor-Infiltrating Lymphocytes

1.4. Molecular Mechanisms Involved in the Invasion and Metastasis Process

Module 2. Genomic or precision oncology

2.1. Use of Gene Expression Profiling in Cancer

2.2. Molecular Subtypes of Breast Cancer

2.3. Prognostic-Predictive Genomic Platforms in Breast Cancer

2.4. Therapeutic Targets in Non-Small Cell Lung Cancer
- 2.4.1. Introduction
- 2.4.2. Molecular Detection Techniques
- 2.4.3. EGFR Mutation
- 2.4.4. ALK Translocation
- 2.4.5. ROS Translocation
- 2.4.6. BRAF Mutation
- 2.4.7. NRTK Rearrangements
- 2.4.8. HER2 Mutation
- 2.4.9. MET Mutation/Amplification
- 2.4.10. RET Rearrangements
- 2.4.11. Other Molecular Targets

2.5. Molecular Classification of Colon Cancer
2.6. Molecular Studies in Gastric Cancer
  2.6.1. Treatment of Advanced Gastric Cancer
  2.6.2. HER2 Overexpression in Advanced Gastric Cancer
  2.6.3. Identification and Interpretation of HER2 Overexpression in Advanced Gastric Cancer
  2.6.4. Drugs With Activity Against HER2
  2.6.5. Trastuzumab in the First Line of Advanced Gastric Cancer
    2.6.5.1. Treatment of HER2+ Advanced Gastric Cancer After Progression to Trastuzumab-Based Regimens
  2.6.6. Activity of Other Anti-HER2 Drugs in Advanced Gastric Cancer
2.7. GIST as a Model of Translational Research: 15 Years of Experience
  2.7.1. Introduction
  2.7.2. Mutations of KIT and PDGFRA as Major Promoters in GIST
  2.7.3. Genotype in GIST: Prognostic and Predictive Value
  2.7.4. Genotype in GIST and Resistance to imatinib
  2.7.5. Conclusions
2.8. Molecular and Genomic Biomarkers in Melanoma
2.9. Molecular Classification of Brain Tumors
2.10. Molecular and Genomic Biomarkers in Melanoma
2.11. Immunotherapy and Biomarkers
  2.11.1. Landscape of Immunological Therapies in Cancer Treatment and the Need to Define the Mutational Profile of a Tumor
  2.11.2. Checkpoint Inhibitor Biomarkers: PD-L1 and Beyond
    2.11.2.1. The Role of PD-L1 in Immune Regulation
    2.11.2.2. Clinical Trial Data and PD-L1 Biomarker
    2.11.2.3. Thresholds and Assays for PD-L1 Expression: a Complex Picture
    2.11.2.4. Budding Biomarkers
      2.11.2.4.1. Tumor Mutational Burden (TMB)
        2.11.2.4.1.1. Quantification of the Tumor Mutational Burden
        2.11.2.4.1.2. Evidence of the Tumor Mutational Burden
        2.11.2.4.1.3. Tumor Burden as a Predictive Biomarker
        2.11.2.4.1.4. Tumor Burden as a Prognostic Biomarker
        2.11.2.4.1.5. The Future of the Mutational Burden
      2.11.2.4.2. Microsatellite Instability
      2.11.2.4.3. Immune Infiltrate Analysis
      2.11.2.4.4. Toxicity Markers
  2.11.3. Immune Checkpoint Drug Development in Cancer
  2.11.4. Available Drugs

Module 3. Changes in Current Clinical Practice and New Applications with Genomic Oncology

3.1. Liquid Biopsies: Fashion or Future?
  3.1.1. Introduction
  3.1.2. Circulating Tumor Cells
  3.1.3. ctDNA
  3.1.4. Clinical Applications
  3.1.5. ctDNA Limitations
  3.1.6. Conclusions and Future
3.2. Role of the Biobank in Clinical Research
  3.2.1. Introduction
  3.2.2. Is it Worth the Effort to Create a Biobank?
  3.2.3. How to Begin Establishing a Biobank?
  3.2.4. Informed Consent for the Biobank
  3.2.5. Collecting Samples for the Biobank
  3.2.6. Quality Control
  3.2.7. Access to Samples

3.3. Clinical trials: New Concepts Based on Precision Medicine
  3.3.1. What Are Clinical Trials? What Sets Them Apart from Other Types of Research?
    3.3.1.1. Types of Clinical Trials
      3.3.1.1.1. According to the Objectives
      3.3.1.1.2. According to The Number of Participating Centers
      3.3.1.1.3. According to the Methodology
      3.3.1.1.4. According to the Level of Masking
  3.3.2. Results of Clinical Trials in Thoracic Oncology
    3.3.2.1. Related to Survival Time
    3.3.2.2. Results Related to the Tumor
    3.3.2.3. Results Notified by the Patient
  3.3.3. Clinical Trials in the New Age of Precision Medicine
    3.3.3.1. Precision Medicine
    3.3.3.2. Terminology Relate to the Design of Trials in the Era of Precision Medicine
3.4. Incorporation of Actionable Markers in Clinical Practice
3.5. Application of Genomics in Clinical Practice by Type of Tumor
3.6. Decision support Systems in Oncology Based on Artificial Intelligence

Module 4. Use of Unix and Linux in Bioinformatics

4.1. Introduction to the Linux Operating System
  4.1.1. What is an Operating System?
  4.1.2. The Benefits of Using Linux
4.2. Linux Environment and Installation
  4.2.1. Linux Distributions
  4.2.2. Linux Installation Using a USB Memory
  4.2.3. Linux Installation Using a CD-ROM
  4.2.4. Linux Installation Using a Virtual Machine
4.3. The Command Line
  4.3.1. Introduction
  4.3.2. What is a Command Line?
  4.3.3. Working on the Terminal
  4.3.4. Shell and Bash
4.4. Basic Browsing
  4.4.1. Introduction
  4.4.2. How to Learn the Current Location?
  4.4.3. Absolute and Relative Routes
  4.4.4. How to Navigate in the System?
4.5. File Manipulation
  4.5.1. Introduction
  4.5.2. How to Build a Directory?
  4.5.3. How to Move to a Directory?
  4.5.4. How to Create an Empty File?
  4.5.5. Copying a File and Directory
  4.5.6. Deleting a File and Directory
4.6. VI Text Editor
  4.6.1. Introduction
  4.6.2. How to Save and Exit?
  4.6.3. How to Browse a File in the VI Text Editor?
  4.6.4. Deleting Contents
  4.6.5. The Undo Command
4.7. Wildcards
  4.7.1. Introduction
  4.7.2. What are Wildcards?
  4.7.3. Examples of Wildcards
4.8. Licenses
  4.8.1. Introduction
  4.8.2. How to See the License of a File?
  4.8.3. How to Change the Licenses?
  4.8.4. License Configuration
  4.8.5. Licenses for Directories
  4.8.6. The “Root” User

4.9. Filters
- 4.9.1. Introduction
- 4.9.2. Head
- 4.9.3. Tail
- 4.9.4. Sort
- 4.9.5. nl
- 4.9.6. wc
- 4.9.7. cut
- 4.9.8. sed
- 4.9.9. uniq
- 4.9.10. tac
- 4.9.11. Other Filters

4.10. Grep and Common Expressions
- 4.10.1. Introduction
- 4.10.2. eGrep
- 4.10.3. Common Expressions
- 4.10.4. Some Examples

4.11. Pipelines and Redirection
- 4.11.1. Introduction
- 4.11.2. Redirect to a File
- 4.11.3. Save a File
- 4.11.4. Redirect From a File
- 4.11.5. STDERR Redirection
- 4.11.6. Pipelines

4.12. Managing Processes
- 4.12.1. Introduction
- 4.12.2. Active Processes
- 4.12.3. Closing a Corrupt Program
- 4.12.4. Foreground and Background Work

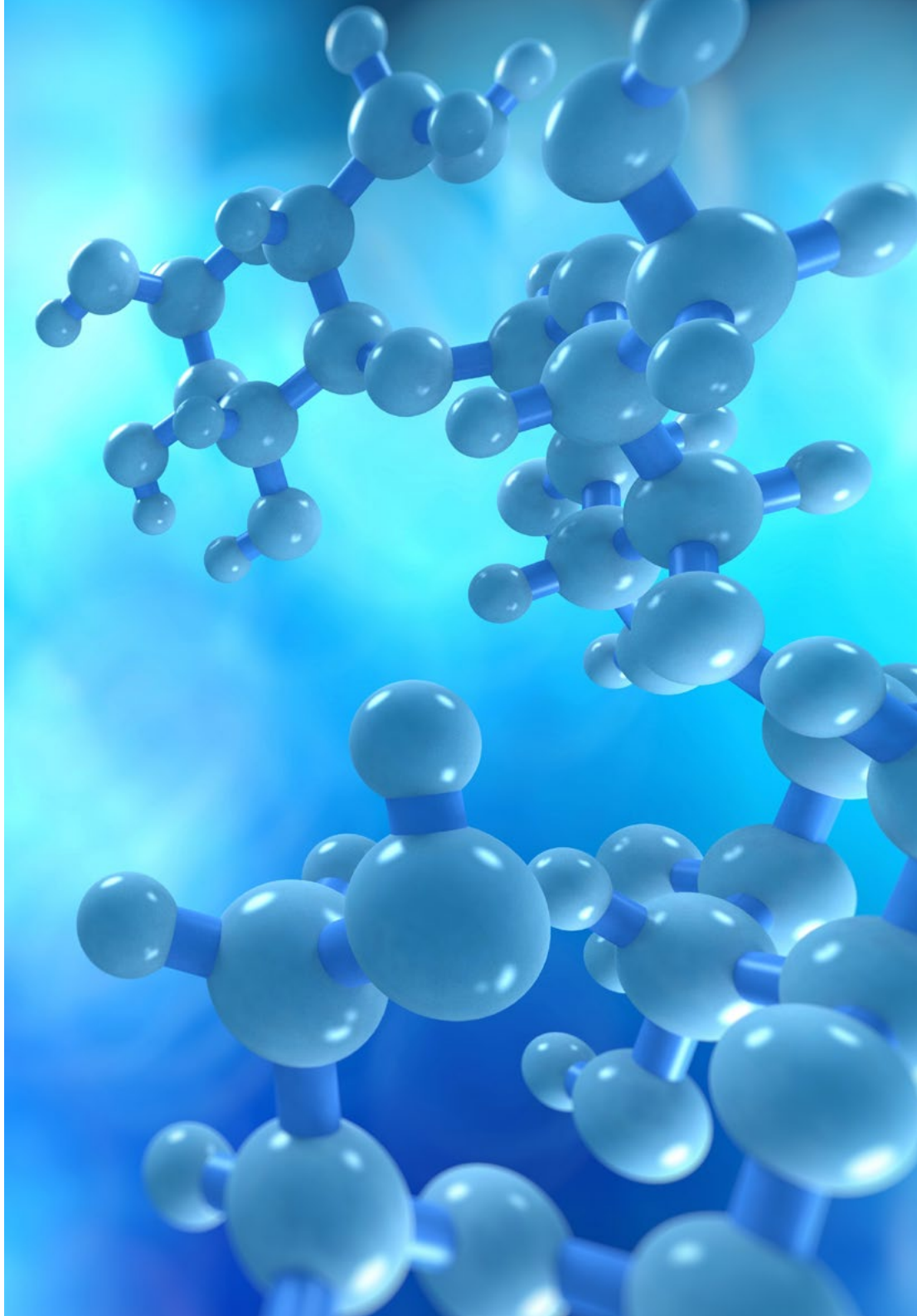
4.13. Bash
- 4.13.1. Introduction
- 4.13.2. Important Points
- 4.13.3. Why "./ "?
- 4.13.4. Variables
- 4.13.5. Declarations

Module 5. Data Analysis in Big Data Projects: R Programming Language

5.1. Introduction to R Programming Language
- 5.1.1. What is R?
- 5.1.2. R Installation and the Graphic Interface of R
- 5.1.3. Packages
  - 5.1.3.1. Standard Packages
  - 5.1.3.2. Contributed Packages and CRAN

5.2. Basic Features of R
- 5.2.1. The Environment of R
- 5.2.2. Software and Related Documentation
- 5.2.3. R and Statistics
- 5.2.4. R and the Window System
- 5.2.5. Using R Interactively
- 5.2.6. An Introductory Session
- 5.2.7. Obtaining Help with Functions and Features
- 5.2.8. R Commands, Cap Sensitivity, etc.
- 5.2.9. Recovery and Correction of Previous Commands
- 5.2.10. Execute Commands or Diverting the Output to a File
- 5.2.11. Data Storage and Object Deletion

5.3. Types of Objects in R
- 5.3.1. Simple Manipulations; Numbers and Vectors
  - 5.3.1.1. Vectors and Their Assignment
  - 5.3.1.2. Vector Arithmetic
  - 5.3.1.3. Generating Regular Sequences
  - 5.3.1.4. Logical Vectors
  - 5.3.1.5. Lost Values
  - 5.3.1.6. Character Vectors
  - 5.3.1.7. Index Vectors
    - 5.3.1.7.1. Selecting and Modifying Subsets of a Dataset
  - 5.3.1.8. Other Types of Objects



5.3.2. Objects, Their Modes and Attributes
5.3.2.1. Intrinsic Attributes: Mode and Length
5.3.2.2. Changing the Length of an Object
5.3.2.3. Obtaining and Configuring Attributes
5.3.2.4. The Class of an Object
5.3.3. Sorted and Unsorted Factors
5.3.3.1. A Specific Example
5.3.3.2. The Tapply () Function and Unequal Matrices
5.3.3.3. Sorted Factors
5.3.4. Matrices
5.3.4.1. Matrices
5.3.4.2. Matrix Indexation. The Subsections of a Matrix
5.3.4.3. Index Matrices
5.3.4.4. The Array () Function
5.3.4.5. Mixed Arithmetic of Vectors and Matrices. The Recycling Rule
5.3.4.6. The Outer Product of Two Matrices
5.3.4.7. The General Transposition of a Matrix
5.3.4.8. Matrix Multiplication
5.3.4.9. Eigenvalues and Eigenvectors
5.3.4.10. Decomposition of Singular Values and Determinants
5.3.4.11. Forming Partitioned Matrices, Cbind () and Rbind ()
5.3.4.12. The Concatenation Function, c (), With Matrices
5.3.5. Factor Frequency Tables
5.3.6. Lists
5.3.6.1. Creating and Modifying Lists
5.3.6.2. Concatenation Lists
5.3.7. DataFrames
5.3.7.1. How to Create DataFrames?
5.3.7.2. Attach () and Separate ()
5.3.7.3. Working With DataFrames

5.4. Reading and Writing Data
5.4.1. The Read.Table () Function
5.4.2. The Scan () Function
5.4.3. Access to the Sets of Incorporated Data
5.4.4. Loading Data from Other R Packages
5.4.5. Editing Data
5.5. Grouping, Loops and Conditional Execution
5.5.1. Grouped Expressions
5.5.2. Control Statements
5.5.2.1. Conditional Execution: IF Sentences
5.5.2.2. Repetitive Execution: For Loops, Repetition and Time
5.6. Writing Your Own Functions
5.6.1. Simple Examples
5.6.2. Defining New Binary Operators
5.6.3. Arguments with Name and Default Value
5.6.4. Argument "..."
5.6.5. Assignments within Functions

Module 6. The Graphical Environment in R

6.1. Graphical Procedures
6.1.1. High-Level Plotting Commands
6.1.1.1. The Plot () Function
6.1.1.2. Multivariate Data Visualization
6.1.1.3. Screen Graphics
6.1.1.4. High-Level Plotting Arguments
6.1.2. Low-Level Plotting Commands
6.1.2.1. Mathematical Annotation
6.1.2.2. Hershey Vectorial Sources
6.1.3. Interacting With Graphics
6.1.4. The Use of Graphic Parameters
6.1.4.1. Permanent Changes: The Par () Function
6.1.4.2. Temporary Changes: Arguments to Graphic Functions

6.1.5. List of Graphic Parameters
6.1.5.1. Graphical Elements
6.1.5.2. Axles and Markings
6.1.5.3. Figure Margins
6.1.5.4. Multi-Figure Environment
6.1.6. Descriptive Statistics: Graphical Representations

Module 7. Statistical analysis in R

7.1. Discrete Probability Distributions
7.2. Continuous Probability Distributions
7.3. Introduction to Inference and Sampling (Point Estimate)
7.4. Confidence Intervals
7.5. Hypothesis Testing
7.6. ANOVA of a Factor
7.7. Adjustment kindness (Chi-- Square Test)
7.8. QFitdist Package
7.9. Introduction to Multivariant Statistics

Module 8. Machine Learning for Analyzing Big Data

8.1. Introduction to Machine Learning
8.2. Presentation of the Problem, Loading Data and Libraries
8.3. Data Cleaning (NAs, Categories, Dummy Variables)
8.4. Exploratory Data Analysis (ggplot) + Crossed Validation
8.5. Prediction Algorithms: Multiple Linear Regression, Support Vector Machine, Regression Trees, Random Forest...
8.6. Classification Algorithms: Logistic Regression, Support Vector Regression, Classification Trees, Random Forest...
8.7. Adjustment of the Hyper Parameters of the Algorithm
8.8. Predicting Data with Different Models
8.9. ROC Curves and Confusion Matrices for Assessing Model Quality

Module 9. Data Mining Applied to Genomics

9.1. Introduction
9.2. Initiation to Variables
9.3. Text Cleaning and Conditioning
9.4. Generating the Word Matrix
9.4.1. Creating the TDM Word Matrix
9.4.2. Visualizations on the TDM Word Matrix
9.5. Description of the Word Matrix
9.5.1. Graphic Representation of the Frequencies
9.5.2. Creating a Word Cloud
9.6. Creating a Data Frame for K-NN
9.7. Creating a Classification Model
9.8. Validating a Classification Model
9.9. Guided Practical Exercise on Data Mining in Cancer Genomics

Module 10. Techniques Genomic Data Extraction

10.1. Introduction to "Scraping Data"
10.2. Importing Spreadsheet Data Files Stored Online
10.3. Scraping HTML Text
10.4. Scraping Data from an HTML Table
10.5. Using APIs for Data Scraping
10.6. Extracting Relevant Information
10.7. Using the Rvest Package of R
10.8. Obtaining Data Distributed Over Multiple Pages
10.9. Extracting Genomic Data from the "My Cancer Genome" Platform
10.10. Extracting Information on Genes from the "HGNC HUGO Gene Nomenclature Committee" Database
10.11. Extracting Pharmacological Data from the "OncoKG" (Precision Oncology Knowledge Base) Database

Module 11. New Techniques in the Genomic Era

11.1. Understanding the New Technology: Next Generation Sequence (NGS) in Clinical Practice
- 11.1.1. Introduction
- 11.1.2. Background
- 11.1.3. Problems in the Application of Sanger Sequencing in Oncology
- 11.1.4. New Sequencing Techniques
- 11.1.5. Advantages of Using NGS in Clinical Practice
- 11.1.6. Limitations of Using NGS in Clinical Practice
- 11.1.7. Terms and Definitions of Interest
- 11.1.8. Types of Studies Depending on Their Size and Depth
  - 11.1.8.1. Genome
  - 11.1.8.2. Exomes
  - 11.1.8.3. Multigenic Panels
- 11.1.9. Stages of NGS Sequencing
  - 11.1.9.1. Preparing Samples and Libraries
  - 11.1.9.2. Preparing Templates and Sequencing
  - 11.1.9.3. Bioinformatic Processing
- 11.1.10. Annotation and Classification of Variants
  - 11.1.10.1. Population Databases
  - 11.1.10.2. Locus-Specific Databases
  - 11.1.10.3. Bioinformatic Predictors of Functionality

11.2. DNA Sequencing and Bioinformatic Analysis
- 11.2.1. Introduction
- 11.2.2. Software
- 11.2.3. Procedure
  - 11.2.3.1. Extracting Raw Sequences
  - 11.2.3.2. Aligning Sequences
  - 11.2.3.3. Alignment Refinement
  - 11.2.3.4. Variant Call
  - 11.2.3.5. Variant Filtering

11.3. RNA Sequencing and Bioinformatic Analysis
- 11.3.1. Introduction
- 11.3.2. Software
- 11.3.3. Procedure
  - 11.3.3.1. QC Evaluation of Raw Data
  - 11.3.3.2. rRNA Filtering
  - 11.3.3.3. Filtered Quality Control Data
  - 11.3.3.4. Quality Trimming and Adapter Removal
  - 11.3.3.5. Alignment of Reads to a Reference
  - 11.3.3.6. Variant Call
  - 11.3.3.7. Differential Gene Expression Analysis

11.4. ChIP-seq Technology
- 11.4.1. Introduction
- 11.4.2. Software
- 11.4.3. Procedure
  - 11.4.3.1. CHIP-seq Data Set Description
  - 11.4.3.2. Obtaining Information About the Experiment Using the GEO and SRA Websites
  - 11.4.3.3. Quality Control of the Sequencing Data
  - 11.4.3.4. Trimming and Filtering Reads
  - 11.4.3.5. Visualizing Results with the Integrated Genome Browser (IGV)

11.5. Big Data Applied to Oncology Genomics
- 11.5.1. The Process of Analysis Data

11.6. Genomic Servers and Databases of Genetic Variants
- 11.6.1. Introduction
- 11.6.2. Online Genomic Servers
- 11.6.3 Genomic Server Architecture
- 11.6.4 Data Recovery and Analysis
- 11.6.5. Personalization

11.7. Annotation of Genetic Variants
- 11.7.1. Introduction
- 11.7.2. What is Variant Calling?
- 11.7.3. Understanding the VCF Format
- 11.7.4. Variant Identification
- 11.7.5. Variant Analysis
- 11.7.6. Predicting the Effect of the Variation of a Protein's Structure and Function

Module 12. Application of bioinformatics in genomic oncology

12.1. Clinical and Pharmacological Enrichment of Gene Variants
12.2. Mass Search in PubMed for Genomic Information
12.3. Mass Search in DGIdb for Genomic Information
12.4. Mass Search in Clinical Trials for Clinical Trials on Genomic Data
12.5. Gene Similarity Search for the Interpretation of a Gene Panel or Exome
12.6. Mass Search for Genes Connected to a Disease
12.7. Enrich-Gen: Platform for the Clinical and Pharmacological Enrichment of Genes
12.8. Procedure to Produce a Genomic Report in the Age of Precision Oncology

A unique, key, and decisive training experience to boost your professional development"

06

Methodology

This academic program offers students a different way of learning. Our methodology uses a cyclical learning approach: **Relearning.**

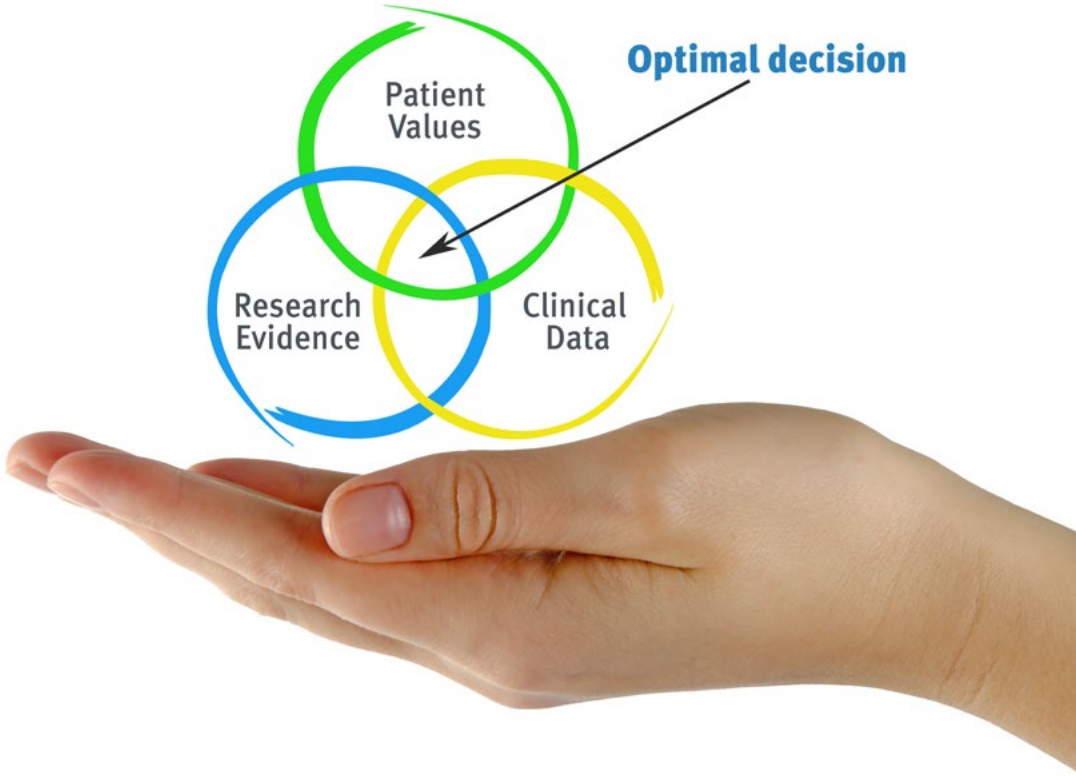
This teaching system is used, for example, in the most prestigious medical schools in the world, and major publications such as the **New England Journal of Medicine** have considered it to be one of the most effective.

Discover Relearning, a system that abandons conventional linear learning, to take you through cyclical teaching systems: a way of learning that has proven to be extremely effective, especially in subjects that require memorization"

At TECH we use the Case Method

What should a professional do in a given situation? Throughout the program, students will face multiple simulated clinical cases, based on real patients, in which they will have to do research, establish hypotheses, and ultimately resolve the situation. There is an abundance of scientific evidence on the effectiveness of the method. Specialists learn better, faster, and more sustainably over time.

With TECH you will experience a way of learning that is shaking the foundations of traditional universities around the world.



According to Dr. Gérvas, the clinical case is the annotated presentation of a patient, or group of patients, which becomes a "case", an example or model that illustrates some peculiar clinical component, either because of its teaching power or because of its uniqueness or rarity. It is essential that the case is based on current professional life, trying to recreate the real conditions in the physician's professional practice.

Did you know that this method was developed in 1912, at Harvard, for law students? The case method consisted of presenting students with real-life, complex situations for them to make decisions and justify their decisions on how to solve them. In 1924, Harvard adopted it as a standard teaching method"

The effectiveness of the method is justified by four fundamental achievements:

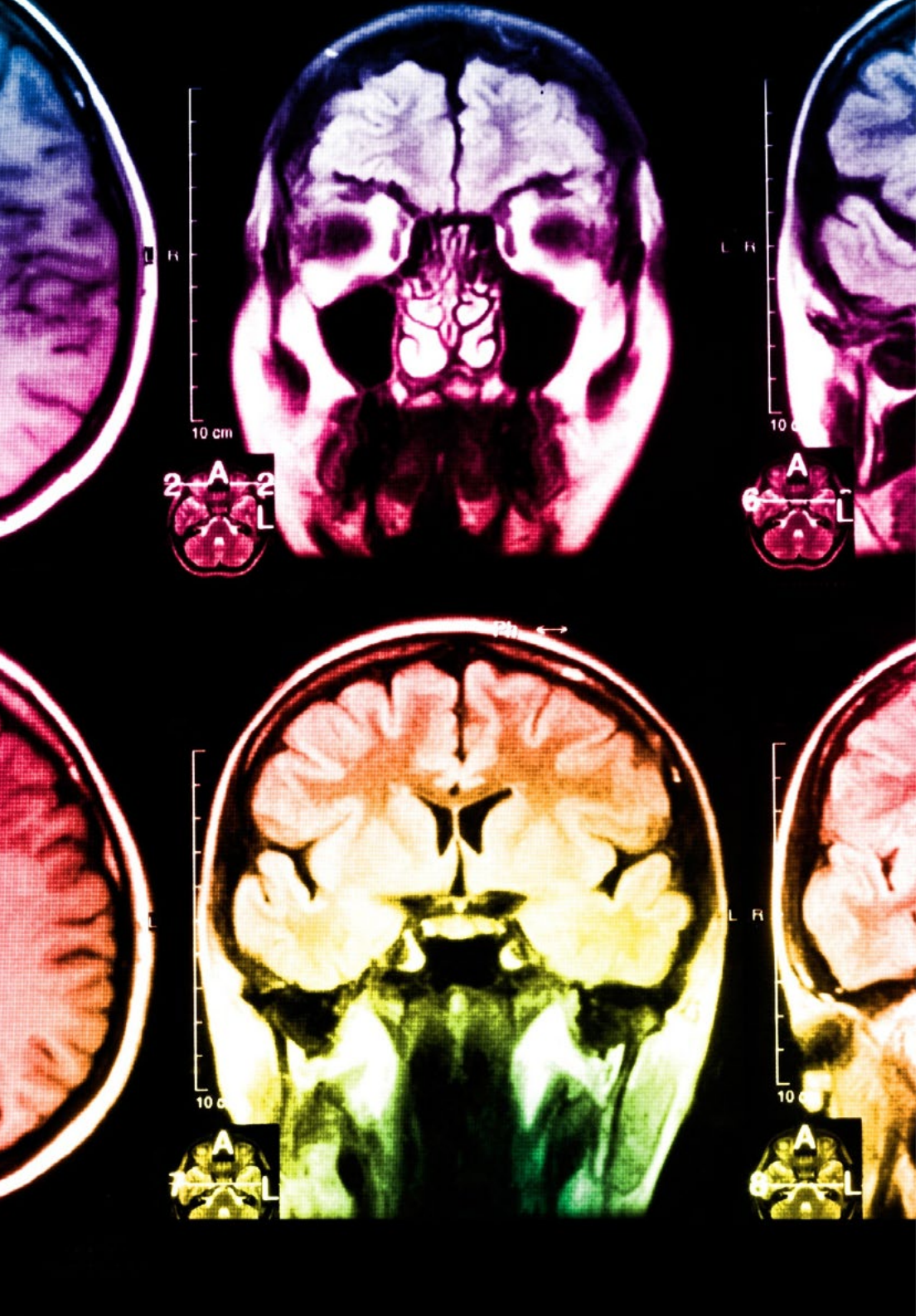
1. Students who follow this method not only achieve the assimilation of concepts, but also a development of their mental capacity, through exercises that evaluate real situations and the application of knowledge.
2. Learning is solidly translated into practical skills that allow the student to better integrate into the real world.
3. Ideas and concepts are understood more efficiently, given that the example situations are based on real-life.
4. Students like to feel that the effort they put into their studies is worthwhile. This then translates into a greater interest in learning and more time dedicated to working on the course.

Relearning Methodology

At TECH we enhance the case method with the best 100% online teaching methodology available: Relearning.

This university is the first in the world to combine the study of clinical cases with a 100% online learning system based on repetition, combining a minimum of 8 different elements in each lesson, a real revolution with respect to the mere study and analysis of cases.

Professionals will learn through real cases and by resolving complex situations in simulated learning environments. These simulations are developed using state-of-the-art software to facilitate immersive learning.



At the forefront of world teaching, the Relearning method has managed to improve the overall satisfaction levels of professionals who complete their studies, with respect to the quality indicators of the best online university (Columbia University).

With this methodology, more than 250,000 physicians have been trained with unprecedented success in all clinical specialties regardless of surgical load. Our pedagogical methodology is developed in a highly competitive environment, with a university student body with a strong socioeconomic profile and an average age of 43.5 years old.

Relearning will allow you to learn with less effort and better performance, involving you more in your specialization, developing a critical mindset, defending arguments, and contrasting opinions: a direct equation to success.

In our program, learning is not a linear process, but rather a spiral (learn, unlearn, forget, and re-learn). Therefore, we combine each of these elements concentrically.

The overall score obtained by TECH's learning system is 8.01, according to the highest international standards.

This program offers the best educational material, prepared with professionals in mind:

Study Material

All teaching material is produced by the specialists who teach the course, specifically for the course, so that the teaching content is highly specific and precise.

These contents are then applied to the audiovisual format, to create the TECH online working method. All this, with the latest techniques that offer high quality pieces in each and every one of the materials that are made available to the student.

Surgical Techniques and Procedures on Video

TECH introduces students to the latest techniques, the latest educational advances and to the forefront of current medical techniques. All of this in direct contact with students and explained in detail so as to aid their assimilation and understanding. And best of all, you can watch the videos as many times as you like.

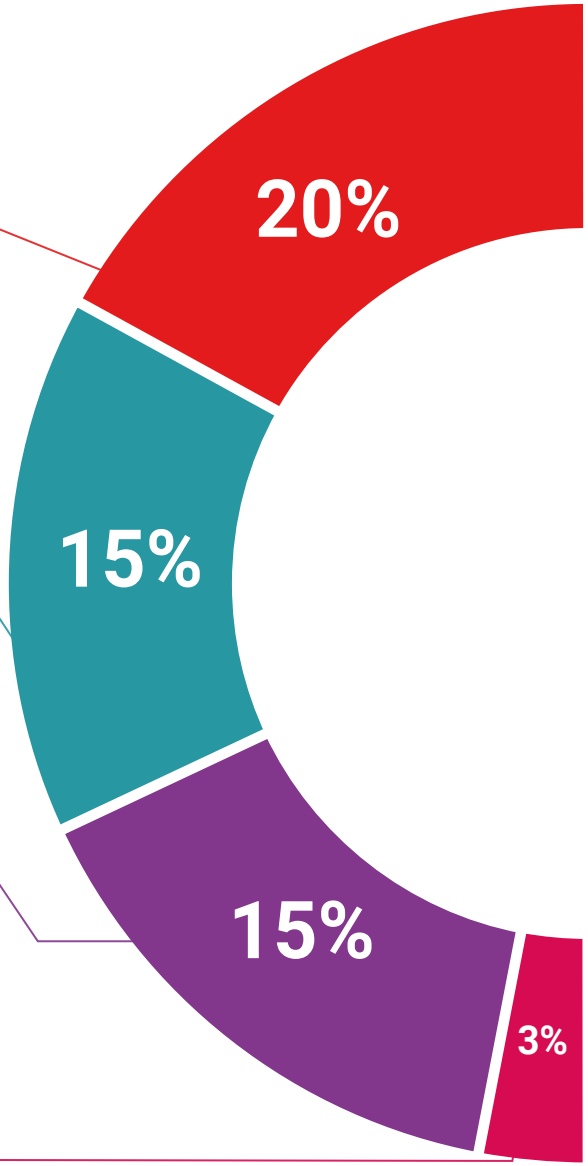
Interactive Summaries

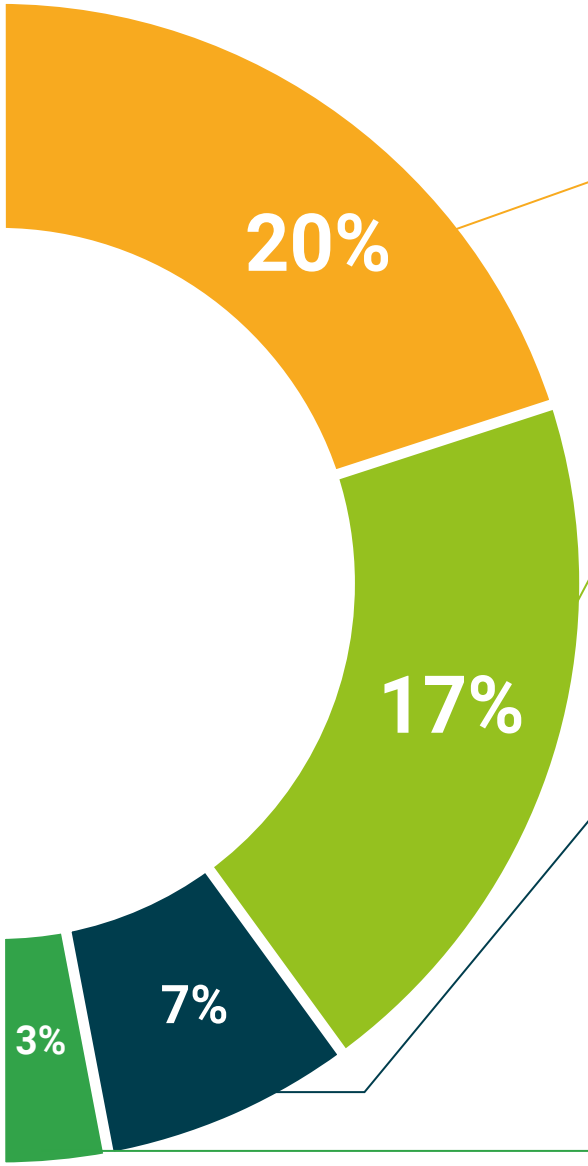
The TECH team presents the contents attractively and dynamically in multimedia lessons that include audio, videos, images, diagrams, and concept maps in order to reinforce knowledge.

This exclusive educational system for presenting multimedia content was awarded by Microsoft as a "European Success Story".

Additional Reading

Recent articles, consensus documents and international guidelines, among others. In TECH's virtual library, students will have access to everything they need to complete their course.





Expert-Led Case Studies and Case Analysis

Effective learning ought to be contextual. Therefore, TECH presents real cases in which the expert will guide students, focusing on and solving the different situations: a clear and direct way to achieve the highest degree of understanding.

Testing & Retesting

We periodically evaluate and re-evaluate students' knowledge throughout the program, through assessment and self-assessment activities and exercises, so that they can see how they are achieving their goals.

Classes

There is scientific evidence on the usefulness of learning by observing experts. The system known as Learning from an Expert strengthens knowledge and memory, and generates confidence in future difficult decisions.

Quick Action Guides

TECH offers the most relevant contents of the course in the form of worksheets or quick action guides. A synthetic, practical, and effective way to help students progress in their learning.

07

Certificate

This Professional Master's Degree in Precision Oncology: Genomics and Big Data guarantees, in addition to the most rigorous and updated education, access to a Professional Master's Degree issued by TECH Technological University.

Successfully complete this program and receive your university degree without travel or laborious paperwork"

This **Master's Degree in Precision Oncology: Genomics and Big Data** contains the most complete and up-to-date scientific program on the market.

After the student has passed the assessments, they will receive their corresponding **Professional Master's Degree** issued by **TECH Technological University** via tracked delivery*.

The diploma issued by **TECH Technological University** will express the qualification obtained in the Professional Master's Degree, and meets the requirements commonly demanded by job exchanges, competitive examinations, and professional career evaluation committees.

Title: **Professional Master's Degree in Precision Oncology: Genomics and Big Data**

Official Nº of hours: **1,500 h.**

tech technological university

Awards the following

DIPLOMA

to

Mr./Ms. _____, with identification number _____.

For having successfully passed and accredited the following program

PROFESSIONAL MASTER'S DEGREE

in

Precision Oncology: Genomics and Big Data

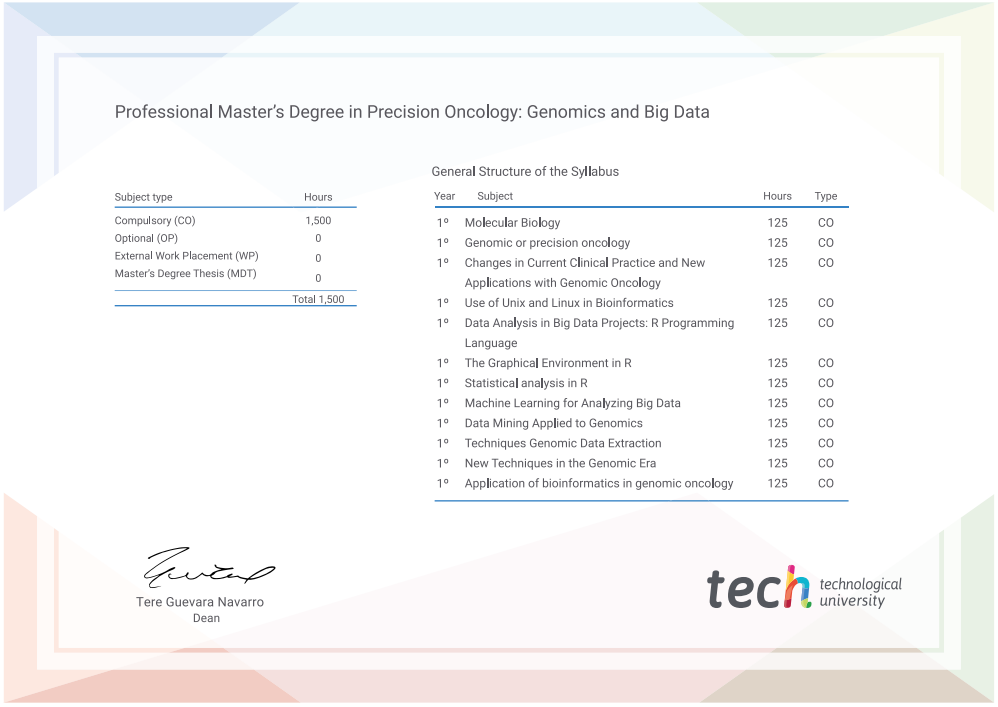
This is a qualification awarded by this University, equivalent to 1,500 hours, with a start date of dd/mm/yyyy and an end date of dd/mm/yyyy.

TECH is a Private Institution of Higher Education recognized by the Ministry of Public Education as of June 28, 2018.

June 17, 2020

Tere Guevara Navarro
Dean

This qualification must always be accompanied by the university degree issued by the competent authority to practice professionally in each country. Unique TECH Code: AFWORD23S techtitute.com/certificates



Professional Master's Degree in Precision Oncology: Genomics and Big Data

Subject type	Hours
Compulsory (CO)	1,500
Optional (OP)	0
External Work Placement (WP)	0
Master's Degree Thesis (MDT)	0
	Total 1,500

General Structure of the Syllabus

Year	Subject	Hours	Type
1º	Molecular Biology	125	CO
1º	Genomic or precision oncology	125	CO
1º	Changes in Current Clinical Practice and New Applications with Genomic Oncology	125	CO
1º	Use of Unix and Linux in Bioinformatics	125	CO
1º	Data Analysis in Big Data Projects: R Programming Language	125	CO
1º	The Graphical Environment in R	125	CO
1º	Statistical analysis in R	125	CO
1º	Machine Learning for Analyzing Big Data	125	CO
1º	Data Mining Applied to Genomics	125	CO
1º	Techniques Genomic Data Extraction	125	CO
1º	New Techniques in the Genomic Era	125	CO
1º	Application of bioinformatics in genomic oncology	125	CO

Tere Guevara Navarro
Dean

tech technological university

*Apostille Convention. In the event that the student wishes to have their paper diploma issued with an apostille, TECH EDUCATION will make the necessary arrangements to obtain it, at an additional cost.

tech technological university

Professional Master's Degree

Precision Oncology: Genomics and Big Data

- Modality: **online**
- Duration: **12 months**
- Certificate: **TECH Technological University**
- Dedication: **16h/week**
- Schedule: **at your own pace**
- Exams: **online**

Professional Master's Degree

Precision Oncology: Genomics and Big Data

tech technological university