

Professional Master's Degree

Genomic and Precision Medicine in Hematology: Thrombosis



Professional Master's Degree Genomic and Precision Medicine in Hematology: Thrombosis

- » Modality: online
- » Duration: 6 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-genomic-precision-medicine-hematology-thrombosis

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01

Introduction

Venous Thromboembolism (VTE) occurs when blood clots inside the veins. Although it is a preventable and treatable disease, it still causes a high number of deaths. In fact, it is the third leading cause of cardiovascular death, after acute myocardial infarction and stroke. In this Professional Master's Degree, specialists will be trained in Genomic and Precision Medicine in Thrombosis to learn about the latest advances in the field and offer more effective treatments.





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This training program is the best option you can find to specialize in Genomic and Precision Medicine in Hematology: Thrombosis and establish more precise diagnoses”

Early detection of venous thrombosis is essential to treat the disease and reduce sequelae in patients. There are also preventive measures, such as physical or pharmacological ones.

During this Professional Master's Degree, students will focus on Genomic and Precision Medicine applied to the treatment of venous thrombosis. The program has been designed by specialists in the field, so students will receive a complete and specific training from experts in the matter.

Thus, the aim is to establish the bases of genomic and precision medicine in the field, starting from the knowledge of hemostasis and venous thromboembolism, and addressing the key aspects of diagnosis, treatment and prevention. Professionals will also learn about special situations they may encounter in their daily practice, such as thrombosis in oncology patients or in women.

After these more general aspects, the Professional Master's Degree will fully delve into the field of genomics as applied to venous thrombosis, where students will learn about the main studies in the field that will allow them to offer more effective and accurate treatments to their patients suffering from this pathology.

Therefore, after completing and passing the Professional Master's Degree, students will have acquired the theoretical knowledge necessary to carry out an effective treatment of venous thrombosis in the main areas of action of the professional.

This **Professional Master's Degree in Genomic and Precision Medicine in Hematology: Thrombosis** contains the most complete and up-to-date scientific program on the market. Its most notable features are:

- ♦ Case studies presented by experts in Genomic and Precision Medicine in Hematology
- ♦ The graphic, schematic, and practical contents with which they are created, provide scientific and practical information on the disciplines that are essential for professional development
- ♦ The latest news on Genomic and Precision Medicine in Hematology
- ♦ Practical exercises where self-assessment can be used to improve learning
- ♦ Special emphasis on innovative methodologies in Genomics and Precision Medicine in Hematology
- ♦ 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



Don't miss the opportunity to study this Professional Master's Degree in Genomic and Precision Medicine in Hematology: Thrombosis at TECH. It's the perfect opportunity to advance your career"

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This Professional Master's Degree may be the best investment you can make when selecting a refresher program for two reasons: in addition to updating your knowledge of Genomic and Precision Medicine in Hematology: Thrombosis, you will obtain a qualification from TECH Technological University”

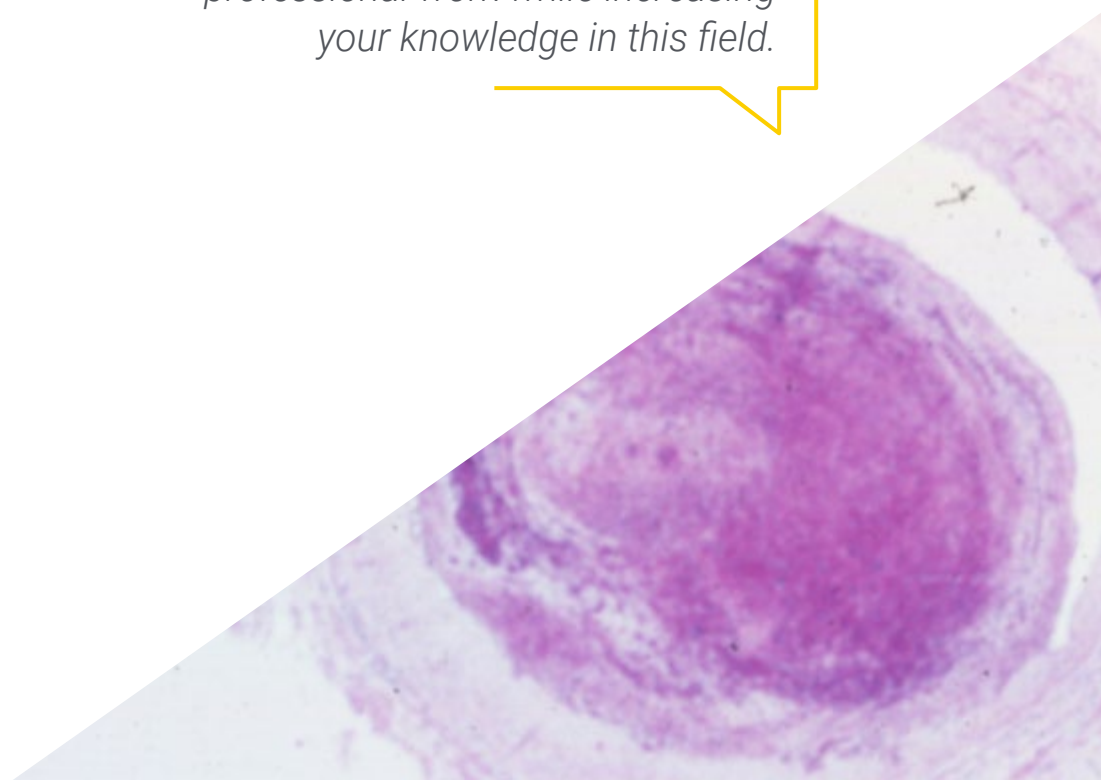
The teaching staff is made up of professionals who belong to the field of Genomic and Precision Medicine in Hematology: Thrombosis, who bring to this program the experience of their work, as well as recognized specialists from reference societies and prestigious universities.

The multimedia content, developed with the latest educational technology, will provide the professional with situated and contextual learning, i.e., a simulated environment that will provide immersive specialization programmed to learn in real situations.

This program is designed around Problem-Based Learning, whereby the specialist must try to solve the different professional practice situations that arise throughout the program. To do so, the professional will be assisted by an innovative, interactive video system created by renowned and extensively experienced experts in Genomic and Precision Medicine in Hematology: Thrombosis.

This program comes with the best educational material, providing you with a contextual approach that will facilitate your learning.

This 100% online Professional Master's Degree will allow you to combine your studies with your professional work while increasing your knowledge in this field.



02

Objectives

The Professional Master's Degree in Genomic and Precision Medicine in Hematology: Thrombosis is aimed at facilitating the professional performance in biomedicine with the latest advances and newest treatments in the area.



A close-up photograph of a hand wearing pink nitrile gloves, resting on a light-colored surface. The background is split into dark blue and white geometric shapes.

“

It is the best option to learn about the latest advances in genomic medicine”



General Objectives

- Delve into the knowledge of venous thromboembolism as a complex disease
- Specialize in the field of omic data and bioinformatic methods applied to precision medicine
- Keep up with the latest updates on the disease





Specific Objectives

Module 1. Introduction to Hemostasis

- ◆ Understand and know the physiological processes involved in hemostasis and its importance
- ◆ Explain the concept of feedback in homeostatic equilibrium and its application
- ◆ Become acquainted with the technical scientific vocabulary in this area
- ◆ Correlate coagulation tests with the coagulation phases to help understand which fundamental physiologic process is failing in primary hemostasis or secondary hemostasis
- ◆ Relate and integrate all that has been learned
- ◆ Build values and criteria learned to relate to professional performance

Module 2. Pathophysiology and Epidemiology in Venous Thromboembolism

- ◆ Demonstrate the enormous biological and clinical complexity underlying venous thromboembolism
- ◆ Explain the pathological mechanisms by which a thrombus develops in the veins and the short- and long-term consequences it may have
- ◆ Analyze the relations of thrombus and recurrence with determinant variables such as age, sex or race
- ◆ Highlight the importance of the circumstances associated with thromboembolic events and how these circumstances largely determine the risk of recurrence
- ◆ Describe the environmental risk factors that are associated with the disease and the genetic basis known today
- ◆ Review the global impact on the worldwide burden of disease and the economic impact of thrombosis, its sequelae and the complications in treatment
- ◆ Delve into the concept of biomarkers or intermediate phenotypes with the risk of the disease, which can be studied in diagnosing the cause and estimating risk of recurrence, and that can be used as a starting point to discover the genes involved in phenotype variability and, therefore, in venous thromboembolisms
- ◆ Understand the concept of individual risk profile

Module 3. Diagnosis, Treatment and Prophylaxis in Venous Thromboembolism

- ♦ Learn how to diagnose venous thromboembolic disease
- ♦ Know the main treatments for this disease
- ♦ Learn about venous thrombosis prevention measures

Module 4. Special Situations I: Thrombosis in Oncology

- ♦ Know the specific characteristics of patients with thrombosis in the oncologic setting
- ♦ Recognize the preventive measures for oncology patients according to their characteristics, whether they are in-patients, surgical patients or patients undergoing systemic therapy in an outpatient setting
- ♦ Identify the preventive models in case of thrombosis risk
- ♦ Know the most effective treatments for cancer-associated thrombosis

Module 5. Special Situations II: Thrombosis in Women

- ♦ Know the pathophysiology of hemostasis in the different development stages in women
- ♦ Learn how to relate contraceptive and hormonal methods to venous thrombosis
- ♦ Learn about prevention strategies in non-pregnant women of childbearing age
- ♦ Know the relation of venous thrombosis and management with puerperium, cesarean section or assisted reproduction techniques
- ♦ Recognize the medication used during pregnancy, puerperium and lactation



Module 6. Omic Data: Introduction to the Programming Language R

- ♦ Learn about the Unix/Linux operating system and its importance
- ♦ Obtain notions of basic Unix/Linux administration
- ♦ Learn how to manage files and directories using the Unix/Linux command interpreter
- ♦ Learn the programming language R and how to manage its packages
- ♦ Recognize the different types of data in R and know which to use in each context
- ♦ Learn how to correctly manipulate each data type in R
- ♦ Know what control functions and loops are and how they are implemented in R
- ♦ Perform graphical representations of data and results in R
- ♦ Apply basic statistics in R depending on the characteristics of the data
- ♦ Learn how to implement proprietary functions in R to perform specific tasks

Module 7. Thrombosis in the Genomic Era I: Genome-Wide Association Studies (GWAS)

- ♦ Provide an overview of genetics, and in particular of genome-wide association studies
- ♦ Show the current status of the use of genetics in venous thromboembolism

Module 8. Thrombosis in the Genomic Era II: Massive Sequencing Studies

- ♦ Know the genetic basis and molecular study of thrombosis and hemostasis
- ♦ Identify DNA sequencing techniques
- ♦ Acquire knowledge of bioinformatic analysis of NGS data
- ♦ Learn how to interpret NGS results in thrombosis and hemostasis
- ♦ Learn about the future perspectives of NGS technologies

Module 9. Thrombosis in the Genomic Era III: Regulation of Gene Expression Studies (RNA and miRNA)

- ♦ Gain knowledge about RNA-seq
- ♦ Know the experimental designs and quality control for RNA-seq studies

Module 10. Predictive Models

- ♦ Identify the different types of statistical learning problems
- ♦ Understand and implement the steps involved in preprocessing a new dataset
- ♦ Understand the fundamentals of linear regression models and their scope of application
- ♦ Optimize linear regression models with the lowest possible number of variables
- ♦ List the different types of classification models and know when to use each of them
- ♦ Learn different ways to validate the performance of a predictive model
- ♦ Become familiar with decision trees and their extensions
- ♦ Adjust support vector machines to clinical data and assess their performance
- ♦ Learn different unsupervised learning methods for exploratory data analysis



Seize the opportunity and take the step to get up to date on the latest developments in Genomic and Precision Medicine in Hematology: Thrombosis”

03 Skills

After passing the assessments for this Professional Master's Degree in Genomic and Precision Medicine in Hematology: Thrombosis, students will have acquired the necessary professional skills for quality and up-to-date practice based on the most innovative teaching methodology.





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This program will help you acquire the skills you need to excel in providing quality patient care”



General Skills

- ♦ Recognize venous thromboembolism as a complex disease and carry out the most precise treatments
- ♦ Use omic data and bioinformatics methods applied to precision medicine in the diagnosis and treatment of venous thrombosis
- ♦ Apply the latest updates on this disease in daily practice with affected patients



Specific Skills

- ♦ Identify the blood coagulation phases and use blood regulatory mechanisms
- ♦ Perform blood draws and blood sampling
- ♦ Perform platelet studies
- ♦ Know the multiple causative factors associated with venous thrombosis, whether acquired or environmental, genetic or inherited
- ♦ Understand the high complexity and difficulty of quantifying individual risk of thrombosis, including the need to explore the genomics and epigenomics of at-risk patients, and to advance prophylaxis and treatment of the disease
- ♦ Effectively diagnose venous thromboembolic disease
- ♦ Apply the most effective treatments for venous thrombosis according to patient characteristics
- ♦ Apply the most appropriate venous thrombosis prevention measures for each patient
- ♦ Apply preventive measures for oncology patients according to their characteristics, whether in-patients, surgical patients or patients undergoing systemic therapy in an outpatient setting
- ♦ Recognize preventive models for thrombosis risk and offer them to patients
- ♦ Apply the most effective treatments for cancer-associated thrombosis
- ♦ Identify the pathophysiology of hemostasis in the different development stages of women
- ♦ Connect contraceptive and hormonal methods to venous thrombosis
- ♦ Apply prevention strategies in non-pregnant women of childbearing age
- ♦ Identify the relation of venous thrombosis and management with puerperium, cesarean section or assisted reproduction techniques
- ♦ Use the medication most suitable during pregnancy, puerperium and lactation
- ♦ Understand the importance of programming in the analysis of omic data

- Become fluent in the Unix/Linux command interpreter as a complement to R for file and system management
- Acquire sufficient proficiency in the programming language R to self-analyze omic data sets and visualize results
- Perform the appropriate statistical analysis depending on the nature of the data and visualize the results in R
- Understand the theoretical concepts of genome-wide association analysis, genotyping, imputation, reference panels, linkage disequilibrium, and linkage disequilibrium
- Understand the different disease etiologies, and the relevance of the most appropriate genetic study methods for each (understand the pros and cons of the different methods)
- Know the main methods of genetic analysis and imputation, and the most used programs
- Know the genetic tools available to the public, and the most current reference panels
- Understand and discuss genetic results from a critical perspective and understand the contribution of GWAS studies in clinical genetics
- Know the current situation in the genetics of thromboembolisms, as well as the main studies and Consortia
- Establish the connection between the genetic basis and molecular study of thrombosis and hemostasis
- Know DNA sequencing techniques and use them in daily practice
- Use bioinformatics analysis of NGS data to treat practical cases
- Interpret NGS results in thrombosis and hemostasis
- Know RNA-seq and use it to treat patients
- Identify the experimental designs and quality control for RNA-seq studies to use them in daily practice
- Know and distinguish the characteristics, advantages and disadvantages of the different predictive models
- Understand the importance of pre-processing clinical data and perform exploratory data analyses
- Adjust and validate the appropriate predictive model according to the characteristics of the data and what is to be predicted
- Make use of critical thinking when interpreting and assessing models
- Self-sufficiently develop complete procedures in R for preprocessing, analyzing, training and validating predictive models from a clinical data set



Improve patient care by taking advantage of the knowledge offered in this Professional Master's Degree in Genomic and Precision Medicine in Hematology: Thrombosis"

04

Course Management

The program includes in its teaching staff experts in Venous Thromboembolism, who have contributed their years of work experience to this training program. Additionally, other recognized experts participate in its design and preparation, completing the program in an interdisciplinary manner.



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Leading professionals in the field have come together to teach you the latest advances in venous thromboembolism”

Management



Dr. Soria, José Manuel

- ♦ Genomics Group of Complex Diseases
- ♦ Sant Pau Hospital Research Institute (IIB Sant Pau)
- ♦ Santa Creu i Sant Pau Hospital Barcelona

Professors

Dr. López del Río, Ángela

- ♦ Bioinformatics and Biomedical Signals Laboratory (B2SLab) Polytechnic University of Catalonia Barcelona
- ♦ Biomedical Engineer, Polytechnical University of Madrid
- ♦ Master's Degree, Barcelona University and Polytechnic University of Catalonia
- ♦ Training at the European Bioinformatics Institute (EBI-EMBL), Cambridge, United Kingdom
- ♦ Center for Biomedical Research, Polytechnic University of Catalonia

Dr. Marzo, Cristina

- ♦ Degree in Medicine and Surgery, Faculty of Medicine University of Zaragoza
- ♦ Proprietary Master's Degree in Anticoagulant Treatment, obtaining the highest mark San Antonio Catholic University Murcia
- ♦ Master's Degree in Congenital and Acquired Coagulopathies University of Alcalá
- ♦ Assistant Physician in the Hematology and Hemotherapy Service Hemostasia Unit Arnau de Vilanova University Hospital, Lleida



Dr. Muñoz Martín, Andrés J.

- ◆ Degree in Medicine and Surgery from the Autonomous University of Madrid
- ◆ PhD in Medicine, Extraordinary Award, Complutense University of Madrid
- ◆ Diploma in Biostatistics in Health Sciences, Autonomous University of Barcelona
- ◆ Assistant Physician, Medical Oncology Department Unit of Digestive System Tumors Head of the Hepato-Bilio-Pancreatic Tumors and Cancer and Thrombosis Research Program Gregorio Marañón General University Hospital, Madrid
- ◆ Collaborating Professor in Practical Teaching, Department of Medicine, Faculty of Medicine, Complutense University of Madrid
- ◆ Vice-Chairman of the Ethics and Clinical Research Committee (CEIC), Gregorio Marañón General University Hospital, Madrid
- ◆ Coordinator of the Cancer and Thrombosis Section, Spanish Society of Medical Oncology (SEOM)

Dr. Llamas, Pilar

- ◆ PhD in Medicine and Surgery
- ◆ Degree in Medicine and Surgery, University of Córdoba 1989, Extraordinary Award
- ◆ Corporate Head of the Hematology and Hemotherapy Department, Quironsalud Madrid Public Hospitals; Jiménez Díaz Foundation, Rey Juan Carlos, Infanta Elena University Hospitals and Villalba General Hospital

Dr. Pina Pascual, Elena

- ◆ Degree in Medicine and Surgery, Autonomous University of Barcelona
- ◆ Specialist in Hematology and Hemotherapy, MIR program, Bellvitge University Hospital
- ◆ Since 2005, Assistant in the Thrombosis and Hemostasis Service, Bellvitge University Hospital
- ◆ Coordinator of the Functional Unit of Venous Thromboembolism, Bellvitge Hospital, since December 2007 Member of the Commission of Cancer-Associated Thrombosis, Institut Català d'Oncologia (ICO)

Ms. Ruperez Blanco, Ana Belen

- ◆ Degree in Medicine from the Complutense University of Madrid
- ◆ Specialist in Medical Oncology, Gregorio Marañón General University Hospital
- ◆ Assistant Physician, Medical Oncology Department Unit of Digestive Tumors, Sarcomas and Cutaneous Tumors Virgen de la Salud Hospital Toledo
- ◆ Specialist in VTE and Cancer, Católica San Antonio University, Murcia
- ◆ Members of the Cancer and Thrombosis Section, Spanish Society of Medical Oncology (SEOM)

Dr. Sabater Lleal, María

- ◆ Degree in Biology, University of Barcelona, 2000
- ◆ Specialized in Biomedicine
- ◆ PhD in Genetics, University of Barcelona, 2006
- ◆ Genomics Group of Complex Diseases Sant Pau Hospital Research Institute (IIB Sant Pau) Santa Creu i Sant Pau Hospital Barcelona
- ◆ Cardiovascular Genetics Research Associate, Cardiovascular Medicine Unit (KI)



**Dr. Souto, Juan Carlos**

- ◆ Degree in Medicine and Surgery, University Extension, UCB, Lleida 1987
- ◆ Specialist in Hematology and Hemotherapy
- ◆ PhD in Medicine and Surgery, UAB
- ◆ Member of the Hematology staff to date The current head of the Section of Diagnostic and Translational Research of Hemostasis Diseases
- ◆ Consultation work in antithrombotic treatment and thromboembolic and hemorrhagic diseases Elected member in 2017 of the Consell Directiu del Cos Facultatiu of the Hospital
- ◆ Author of 160 scientific articles in indexed journals, in 35 as primary author
- ◆ Author of 290 scientific talks at national and international congresses
- ◆ Member of the Research Team in 21 competitive Research Projects, in 7 of which as Lead Researcher
- ◆ Responsible for the scientific projects GAIT 1 and 2 (Genetic Analysis of Idiopathic Thrombophilia), 1995-present; ACOA (Alternative Control of Oral Anticoagulation), 2000-2005; RETROVE (Risk of Venous Thromboembolic Disease), since 2012; MIRTO (Modelling the Individual Risk of Thrombosis in Oncology), since 2015
- ◆ Senior Data Analyst (CNAG-CRG)

Dr. Vidal, Francisco

- ◆ Degree in Biology, Universitat of Barcelona
- ◆ Official Doctoral Program in Biochemistry, Molecular Biology and Genetics University of Barcelona
- ◆ Executive Master's Degree in Healthcare Organization ESADE Business School/ Ramon Llull University
- ◆ Specialist Physician, Blood and Tissue Bank (BST) Barcelona

05

Structure and Content

The contents have been structured and designed by the best professionals in the field of Genomic and Precision Medicine in Hematology: Thrombosis, who are extensively experienced and recognized prestige in the profession, backed by the volume of cases reviewed, studied and diagnosed, and with extensive knowledge of new technologies applied to genomic and precision medicine.





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This Professional Master's Degree in Genomic and Precision Medicine in Hematology: Thrombosis contains the most complete and up-to-date scientific program on the market”


Module 1. Introduction to Hemostasis

- 1.1. Introduction: History and Evolution
 - 1.1.1. History
 - 1.1.2. Evolution
- 1.2. Endothelium and Platelets in the Physiology of Hemostasis
 - 1.2.1. The Role of Endothelium in Hemostasis
 - 1.2.2. Platelets: Platelet Membrane Receptors
 - 1.2.3. Platelet Plug Formation: Platelet Adhesion and Aggregation
 - 1.2.4. Microparticles
 - 1.2.5. Involvement of Other Cellular Elements in the Physiology of Hemostasis
- 1.3. Plasma Component of Coagulation: Fibrin Clots
 - 1.3.1. Coagulation Cascade
 - 1.3.2. Coagulation Factors
 - 1.3.3. Coagulation System
 - 1.3.4. Multicomponent Complexes
- 1.4. Coagulation Regulatory Mechanisms
 - 1.4.1. Inhibitors of Activated Factors
 - 1.4.2. Regulators of Cofactors
- 1.5. Fibrinolysis
 - 1.5.1. Fibrinolytic System
 - 1.5.2. Fibrinolysis Activation
 - 1.5.3. Fibrinolysis Regulation
 - 1.5.4. Cellular Receptors in Fibrinolysis
- 1.6. The Coagulation Laboratory: Pre-Analytical Phase
 - 1.6.1. Patients and Sample Extraction
 - 1.6.2. Sample Transportation and Processing
- 1.7. Platelet Study
 - 1.7.1. Methods to Measure Platelet Function
 - 1.7.2. Closure Time (PFA-100)
 - 1.7.3. Flow Cytometry

- 1.8. Exploring Coagulation Plasma Phase
 - 1.8.1. Classical Coagulation Techniques
 - 1.8.2. Coagulation Factor Quantification
 - 1.8.3. Study of Specific and Non-Specific Inhibitors
 - 1.8.4. Fibrinolysis Laboratory Tests
 - 1.8.5. Thrombophilia Study
 - 1.8.6. Laboratory Tests to Monitor Anticoagulant Medication
- 1.9. Techniques for the Global Analysis of Hemostasis
 - 1.9.1. Definition and Classification
 - 1.9.2. Thrombin Generation Test
 - 1.9.3. Viscoelastometric Techniques
- 1.10. Clinical Cases and Exercises
 - 1.10.1. Clinical Cases
 - 1.10.2. Exercises

Module 2. Pathophysiology and Epidemiology in Venous Thromboembolism

- 2.1. General Introduction to the Complexity and Clinical Impact of VTE
 - 2.1.1. General Introduction to Complexity
 - 2.1.2. Clinical Impact of VTE
- 2.2. Generation of a Pathological Thrombus
 - 2.2.1. Hemostasis Balance
 - 2.2.2. Break in Balance (Classic Virchow's Triad) and Consequences
 - 2.2.3. Normal and Pathological Venous Function
 - 2.2.4. The Role of Venous Valve in Pathological Thrombi
 - 2.2.5. The Role of the Vascular Endothelium
 - 2.2.6. The Role of Platelets and Polyphosphates
 - 2.2.7. The Role of Neutrophil Extracellular Traps (NETs)
 - 2.2.8. The Role of Circulating Microparticles
 - 2.2.9. Local inflammatory processes
 - 2.2.10. Paraneoplastic Thrombosis (see Module 4)
 - 2.2.11. Mechanism and Site in Thrombus Formation

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- A detailed 3D rendering of a blood vessel's interior, showing several red blood cells (erythrocytes) in various stages of flow. The cells are depicted with a textured, biconcave surface, and the surrounding plasma is a vibrant red color with fine, wavy lines suggesting fluid dynamics. The lighting is dramatic, highlighting the three-dimensional structure of the cells and the vessel wall.
- 2.3. Classification and Characteristics of VTE according to Anatomical Site
 - 2.3.1. Lower Limbs
 - 2.3.2. Upper Limbs
 - 2.3.3. Pulmonary Thromboembolism
 - 2.3.4. Atypical Sites
 - 2.3.4.1. Visceral
 - 2.3.4.2. Intracranial
 - 2.4. Classification of Thrombosis according to Associated Circumstances
 - 2.4.1. Spontaneous VTE vs. Secondary
 - 2.4.2. Environmental Risk Factors (Table a)
 - 2.4.3. The Role of Race, Age, and Sex
 - 2.4.4. The Role of Intravascular Devices (Intravenous Catheters)
 - 2.5. VTE Sequelae
 - 2.5.1. Post-Thrombotic Syndrome and Residual Thrombosis: Relation to Recurrence
 - 2.5.2. Chronic Pulmonary Hypertension
 - 2.5.3. Short- and Long-Term Mortality
 - 2.5.4. On Quality of Life
 - 2.6. Impact of VTE on the Global Burden of Disease
 - 2.6.1. Contribution to the Global Burden of Disease
 - 2.6.2. Impact on the Economy
 - 2.7. VTE Epidemiology
 - 2.7.1. Influencing Variables (Age, Race, Comorbidities, Medication, Seasonal Factors, etc)
 - 2.8. Risk and Epidemiology of Thrombotic Recurrence
 - 2.8.1. Differences between the Sexes
 - 2.8.2. Differences according to the Circumstances associated with the First Episode
 - 2.9. Thrombophilia
 - 2.9.1. Classical Conception
 - 2.9.2. Biological Biomarkers of Thrombophilia
 - 2.9.2.1. Genetic Biomarkers
 - 2.9.2.2. Plasmatic Biomarkers
 - 2.9.2.3. Cell Biomarkers

- 2.9.3. Thrombophilia Laboratory Study
 - 2.9.3.1. Debate on its Utility
 - 2.9.3.2. Classical Abnormalities
 - 2.9.3.3. Other Biomarkers or Intermediary Phenotypes (Table b)
- 2.10. Thrombophilia as a Complex and Chronic Pathology Concept
 - 2.10.1. High Complexity (see 2.1)
 - 2.10.2. Importance of the Genetic basis: Concept of Heritability
 - 2.10.3. Known Genetic Risk Factors (Table c): Connection to Modules 7 and 8
 - 2.10.4. Heritability to Be Discovered
- 2.11. Individual Risk Profile
 - 2.11.1. Concept
 - 2.11.2. Permanent Components (Genetic)
 - 2.11.3. Changing Circumstances
 - 2.11.4. New and Powerful Mathematical Models to Jointly Assess All Risk Variables (see Module 9)

Module 3. Diagnosis, Treatment and Prophylaxis in Venous Thromboembolism

- 3.1. VTE Diagnosis:
 - 3.1.1. Clinical Presentation and Diagnostic Probability Scales
 - 3.1.2. Complementary Tests (D-Dimer, Imaging)
 - 3.1.3. Prognostic Risk Stratification of Patients with Parkinson's Disease
- 3.2. VTE Treatment
 - 3.2.1. Antithrombotic Medication
 - 3.2.2. Treating the Initial Phase (Acute Phase and up to 3-6 Months)
 - 3.2.3. Length of Treatment and Long-Term Treatment (> 6 Months)
 - 3.2.4. Complications in Antithrombotic Treatment
- 3.3. VTE Prophylaxis:
 - 3.3.1. Medical Patient Prophylaxis
 - 3.3.2. Surgical Patient Prophylaxis
 - 3.3.3. Clinical Cases

Module 4. Special Situations I: Thrombosis in Oncology

- 4.1. Epidemiology and Risk Factors
 - 4.1.1. Epidemiology
 - 4.1.2. Patient-Related Risk Factors
 - 4.1.3. Tumor-Related Risk Factors
 - 4.1.4. Treatment-Related Risk Factors
- 4.2. Thromboprophylaxis in Admitted Medical Oncology Patients
 - 4.2.1. Introduction
 - 4.2.2. Thromboprophylaxis in Admitted Medical Oncology Patients
- 4.3. Surgical Patient Prophylaxis
 - 4.3.1. Introduction
 - 4.3.2. Surgical Patient Prophylaxis
- 4.4. Thromboprophylaxis in Oncology Patients Receiving Systemic Therapy in an Outpatient Setting
 - 4.4.1. Introduction
 - 4.4.2. Thromboprophylaxis in Oncology Patients Receiving Systemic Therapy in an Outpatient Setting
- 4.5. Predictive Risk Models for Thrombosis
 - 4.5.1. Khorana Score
 - 4.5.2. Others Predictive Risk Models
 - 4.5.3. Other Potential Applications of Predictive Risk Models
- 4.6. Initial Treatment of Cancer-Related Thrombosis
 - 4.6.1. Introduction
 - 4.6.2. Initial Treatment of Cancer-Related Thrombosis
- 4.7. Long-Term Treatment of Cancer-Related Thrombosis
 - 4.7.1. Introduction
 - 4.7.2. Long Term Treatment of Cancer-Related Thrombosis
- 4.8. Predictive Models for Bleeding and Recurrence: Interactions of Direct Acting Oral Anticoagulants
 - 4.8.1. Predictive Models for Bleeding and Recurrence
 - 4.8.2. Interactions of Direct Acting Oral Anticoagulants

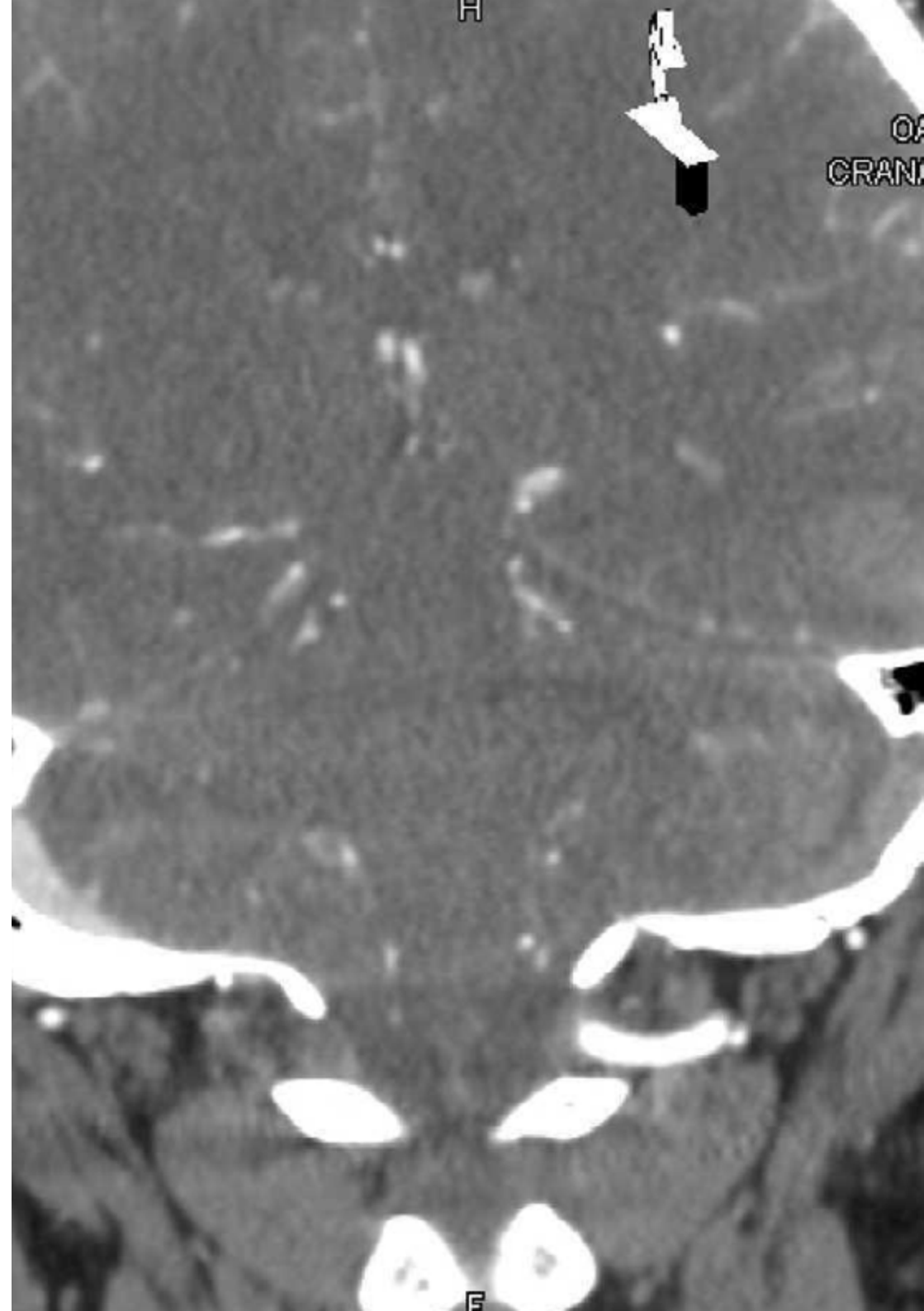
- 4.9. Antitumor Therapy and Risk of Thrombosis
 - 4.9.1. Chemotherapy
 - 4.9.2. Hormone Therapy
 - 4.9.3. Biological Medication
 - 4.9.4. Immunotherapy
 - 4.9.5. Supportive therapy

Module 5. Special Situations II: Thrombosis in Women

- 5.1. Hemostasis Pathophysiology in the Different Development Stages of Women
 - 5.1.1. Introduction
 - 5.1.2. Physiological Risk Factors
 - 5.1.3. Acquired Risk Factors
- 5.2. Thrombophilia and Women
 - 5.2.1. Hereditary Thrombophilia
 - 5.2.2. Acquired Thrombophilia
 - 5.2.3. Study Indications
- 5.3. Contraception and Hormone Therapy and Venous Thromboembolism
 - 5.3.1. Introduction
 - 5.3.2. Contraception in Women with Thrombotic Risk Factors
 - 5.3.3. Contraception in Women after a Thrombotic Event
- 5.4. Prevention Strategies for Venous Thromboembolism in Non-Pregnant Women in Childbearing Age
 - 5.4.1. Non-Pregnant Women without a History of Thrombosis
 - 5.4.2. Non-Pregnant Woman with a History of Thrombosis
- 5.5. Venous Thromboembolism during Gestation and Puerperium
 - 5.5.1. Incidence and Epidemiology
 - 5.5.2. Risk Factors: Risk Assessment Scales
 - 5.5.3. Clinical Presentation
 - 5.5.4. Diagnostic Strategy
 - 5.5.5. Treatment
 - 5.5.6. Prophylaxis
 - 5.5.7. Managing Patients with Heart Valves
- 5.6. Venous Thromboembolism and Cesarean Section
 - 5.6.1. Incidence and Epidemiology
 - 5.6.2. Risk Factors: Risk Assessment Scales
 - 5.6.3. Treatment and Prophylaxis
- 5.7. Assisted Reproductive Techniques and Venous Thromboembolism
 - 5.7.1. Incidence and Risk Factors
 - 5.7.2. Clinical Presentation
 - 5.7.3. Treatment
 - 5.7.4. Prophylaxis
- 5.8. Anticoagulant Medication used during Pregnancy, Postpartum and Lactation
 - 5.8.1. Unfractionated Heparin
 - 5.8.2. Low Molecular Weight Heparin
 - 5.8.3. Vitamin K Antagonists
 - 5.8.4. Peripartum Anticoagulant Therapy Management
 - 5.8.5. Complications Arising from Anticoagulant Therapy
- 5.9. Obstetric Antiphospholipid Syndrome
 - 5.9.1. Incidence and Epidemiology
 - 5.9.2. Laboratory Diagnosis of Obstetric APS
 - 5.9.3. Treatment of Obstetric APS
 - 5.9.4. Approach to Women in Childbearing Age with Isolated Antiphospholipid Antibodies
- 5.10. Climacteric Age, Menopause and Thrombosis
 - 5.10.1. Incidence and Epidemiology
 - 5.10.2. Cardiovascular Risk
 - 5.10.3. Hormone Replacement Therapy

Module 6. Omic Data: Introduction to the Programming Language R

- 6.1. Basic Introduction to the UNIX/ Linux Operating System
 - 6.1.1. History and Philosophy
 - 6.1.2. Command Interpreter (Shell)
 - 6.1.3. Basic Linux Commands
 - 6.1.4. Word Processors
- 6.2. File Management in UNIX/Linux
 - 6.2.1. File System
 - 6.2.2. Users and Groups
 - 6.2.3. Licences
- 6.3. System Management in UNIX/Linux
 - 6.3.1. Tasks (*Jobs*)
 - 6.3.2. Register (*Logs*)
 - 6.3.3. Monitoring Tools
 - 6.3.4. Networks
- 6.4. Introduction and Basic Features of R
 - 6.4.1. What is R?
 - 6.4.2. First Steps
 - 6.4.2.1. Installation and Graphic Interface
 - 6.4.2.2. *Workspace*
 - 6.4.3. Extension in R
 - 6.4.3.1. Standard Packages
 - 6.4.3.2. Contributed Packages, CRAN and Bioconductor
- 6.5. Types of Data in R
 - 6.5.1. Vectors
 - 6.5.2. Lists
 - 6.5.3. *Arrays* and Matrices
 - 6.5.4. Factors
 - 6.5.5. *Data Frames*
 - 6.5.6. *Text Strings*
 - 6.5.7. Other Types of Data



- 6.6. Data Management in R
 - 6.6.1. Import and Export Data
 - 6.6.2. Data Manipulation
 - 6.6.2.1. Vectors
 - 6.6.2.2. Matrices
 - 6.6.2.3. Text *Strings*
 - 6.6.2.4. Data Sheets
- 6.7. Control Functions and Loops in R
 - 6.7.1. Conditional Execution: *if*
 - 6.7.2. Cycles: *For, Repeat, While*
 - 6.7.3. *Apply* Functions
- 6.8. Statistical Models in R
 - 6.8.1. Univariate Data
 - 6.8.2. Multivariate Data
 - 6.8.3. Hypothesis Test
- 6.9. Graphic Representation in R
 - 6.9.1. Basic Representations
 - 6.9.2. Graphical Parameters and Elements
 - 6.9.3. The *ggplot2* Package
- 6.10. Defining Functions in R
 - 6.10.1. Simple Examples
 - 6.10.2. Default Arguments and Values
 - 6.10.3. Assignments within Functions

Module 7. Thrombosis in the Genomic Era I: Genome-Wide Association Studies (GWAS)

- 7.1. Introduction to Genetics
 - 7.1.1. Introduction and Basic Concepts
 - 7.1.1.1. Genes
 - 7.1.1.2. Polymorphisms, Alleles and *Loci*
 - 7.1.1.3. Haplotypes
 - 7.1.1.4. Concept of Linkage Disequilibrium
 - 7.1.1.5. Genotype
 - 7.1.1.6. Phenotype
 - 7.1.2. Genetics to Study Complex Diseases
 - 7.1.2.1. Complex and Rare Diseases
 - 7.1.2.2. Study of Candidate Genes vs. Global Genome Studies
 - 7.1.3. Types of Polymorphism, Nomenclature and Genome Versions
 - 7.1.4. Genotyping Chips
- 7.2. Introduction to Global Genome-Wide Analysis Studies (GWAS)
 - 7.2.1. What Is a GWAS?
 - 7.2.2. GWAS Study Design
 - 7.2.2.1. Heritability
 - 7.2.2.2. Case-Control vs. Quantitative Trait Analysis
 - 7.2.2.3. Sample Size and Statistical Power
 - 7.2.2.4. Biases by Population Substructure
 - 7.2.2.5. Phenotypes: Standardization and *Outliers*
 - 7.2.3. The Genetic Association Test
 - 7.2.4. Useful *Software* for GWAS
- 7.3. Genetic Imputation
 - 7.3.1. Concept of Imputation
 - 7.3.2. Reference Panels
 - 7.3.1.1. *Hap Map* Project
 - 7.3.1.2. *1000 Genomes* Project
 - 7.3.1.3. *Haplotype Reference Consortium* Project
 - 7.3.1.4. Other Population-Specific Projects

- 7.4. Quality Control and Filters
 - 7.4.1. Pre-Imputation Filters
 - 7.4.1.1. Minor Allele Frequency
 - 7.4.1.2. Hardy-Weinberg Equilibrium
 - 7.4.1.3. Genotyping Errors (*Call Rate*)
 - 7.4.1.4. Excess Heterozygosity
 - 7.4.1.5. Mendelian Errors
 - 7.4.1.6. Sex Errors
 - 7.4.1.7. Chain Direction
 - 7.4.1.8. Family Relationships
 - 7.4.2. Post-Imputation Filters
 - 7.4.2.1. Monomorphic Variants, Frequencies
 - 7.4.2.2. Imputation Quality
 - 7.4.3. Post GWAS Filters
 - 7.4.4. Quality Control *Software*
- 7.5. Analyzing and Interpreting GWAS Results
 - 7.5.1. Manhattan Plot
 - 7.5.2. *Multiple Testing* Correction and *Genome-Wide* Significant Results
 - 7.5.3. Concept of Genetic Locus
- 7.6. Meta-Analysis and Replication
 - 7.6.1. Common *Workflow* in GWAS Studies
 - 7.6.2. Meta-Analysis
 - 7.6.2.1. Meta-Analysis Methods
 - 7.6.2.2. Required Information for Meta-Analyses
 - 7.6.2.3. Meta-Analysis Result
 - 7.6.2.4. Meta-Analysis *Software* Examples
 - 7.6.3. The Most Relevant Consortia
- 7.7. Post GWAS Analysis
 - 7.7.1. *Fine-Mapping* and Regional Graphic
 - 7.7.2. Conditional Analysis
 - 7.7.3. Selecting the Best Gene Candidate (from Locus to Gene)
 - 7.7.3.1. Exploiting Information on Expression
 - 7.7.3.2. *Gene Set Enrichment Analyses*
 - 7.7.3.3. Study of the Potential Functional Effect of Polymorphism

- 7.8. The Era of GWAS
 - 7.8.1. GWAS Data Repositories
 - 7.8.2. Taking Stock of the GWAS Era Results
- 7.9. Use of GWAS Results
 - 7.9.1. Risk Estimation Models
 - 7.9.2. Mendelian Randomization Studies
- 7.10. Genetic Analysis of Venous Thromboembolism (VTE)
 - 7.10.1. Some History
 - 7.10.2. The Most Relevant GWAS Studies on VTE
 - 7.10.3. Latest Studies Results
 - 7.10.4. Clinical Implications of Genetic Results: The Importance of Coagulation Cascades and New Metabolic Pathways
 - 7.10.5. Future Strategies

Module 8. Thrombosis in the Genomic Era II: Massive Sequencing Studies

- 8.1. Genetic Basis and Molecular Study in Thrombosis and Hemostasis
 - 8.1.1. Molecular Epidemiology in Thrombosis and Hemostasis
 - 8.1.2. Genetic Study of Congenital Diseases
 - 8.1.3. Classical Approach to Molecular Diagnostics
 - 8.1.4. Indirect Diagnosis or Genetic Linkage Techniques
 - 8.1.5. Direct Diagnostic Techniques
 - 8.1.5.1. Mutation Screening
 - 8.1.5.2. Direct Mutation Identification
- 8.2. DNA Sequencing Techniques
 - 8.2.1. Sanger's Traditional Sequencing
 - 8.2.1.1. Characteristics of the Technique, Limitations and Application in Thrombosis and Hemostasis
 - 8.2.2. Next-Generation Sequencing (NGS)
 - 8.2.2.1. NGS Platforms in Molecular Diagnostics
 - 8.2.2.2. General Information on the Technology, Possibilities and Limitations of NGS vs. Traditional Sequencing
 - 8.2.3. Third-Generation Sequencing (TGS)

- 8.3. Different Approaches to Genetic Studies Using NGS
 - 8.3.1. Gene Panel Sequencing
 - 8.3.2. Whole Exome Sequencing and Whole Genome Sequencing
 - 8.3.3. Transcriptomics by RNA-Seq
 - 8.3.4. MicroRNA Sequencing
 - 8.3.5. Mapping Protein-DNA Interactions with CHIP-Seq
 - 8.3.6. Epigenomics Analysis and DNA Methylation Using NGS
- 8.4. Bioinformatics Analysis of NGS Data
 - 8.4.1. The Challenge of Bioinformatics Analysis of Massive NGS Generated Data
 - 8.4.2. IT Requirements for NGS Data Management and Analysis
 - 8.4.2.1. NGS Data Storage, Transfer and Sharing
 - 8.4.2.2. Computing Power Required for NGS Data Analysis
 - 8.4.2.3. Software Requirements for NGS Data Analysis
 - 8.4.2.4. Bioinformatics Skills Required for NGS Data Analysis
 - 8.4.3. Base Calling, FASTQ File Format and Base Quality Scoring
 - 8.4.4. NGS Data Quality Control and Pre-processing
 - 8.4.5. Read Mapping Bioinformatics Required for NGS Data Analysis
 - 8.4.6. Variant Calls
 - 8.4.7. Tertiary Analysis
 - 8.4.8. Structural Variation Analysis by NGS
 - 8.4.9. Methods to Estimate Copy Number Variation from NGS Data
- 8.5. Concept and Types of Mutation Detectable by NGS
 - 8.5.1. Molecular Etiology of Thrombotic and Hemorrhagic Disorders
 - 8.5.2. Mutation Nomenclature
 - 8.5.3. Functional Implication of Identified Variants/Mutations
 - 8.5.4. Difference between Mutation and Polymorphism
- 8.6. Fundamental Molecular Databases in NGS
 - 8.6.1. Locus Specific Databases (LSDB)
 - 8.6.2. Previous Mutation Descriptions in Databases
 - 8.6.3. Databases of Variants Detected in Healthy Population by NGS
 - 8.6.4. Molecular Databases with Clinical Annotations
- 8.7. Analysis and Interpretation of NGS Results on Thrombosis and Hemostasis
 - 8.7.1. Mutation Validation
 - 8.7.2. Concept of Mutation Pathogenicity
 - 8.7.3. Genotype-Phenotype Correlation
 - 8.7.3.1. *In Silico* Studies
 - 8.7.3.2. Expression Studies
 - 8.7.3.3. *In Vitro* Functional Studies
- 8.8. Role of NGS in Genetic Counseling and Prenatal Diagnosis
 - 8.8.1. Genetic Counseling in the NGS Era
 - 8.8.2. Ethical Issues Specific to NGS and Whole Genome Sequencing for Genetic Counseling and Clinical Diagnostics
 - 8.8.3. Conventional Prenatal Diagnosis and Methods
 - 8.8.4. Pre-implant Genetic Diagnostic
 - 8.8.5. Non-invasive Prenatal Diagnosis
 - 8.8.5.1. Use of Fetal DNA in Maternal Circulation for Prenatal Diagnosis
 - 8.8.5.2. Sequencing of SNPs from Circulating Fetal DNA
 - 8.8.5.3. Limitations and Challenges of NGS-Based Non-invasive Prenatal Testing
 - 8.8.5.4. Clinical Implementation of Non-Invasive Prenatal Testing for Aneuploidies
- 8.9. Future Perspectives in NGS Technologies and Data Analysis
 - 8.9.1. Technological Development of Sequencing in the Mid-Term
 - 8.9.2. Evolution of Bioinformatics Tools for High-Throughput Sequencing Data Analysis
 - 8.9.3. Standardization and Rationalization of NGS Analytical Processes
 - 8.9.4. Parallel Computation
 - 8.9.5. Cloud Computing

Module 9. Thrombosis in the Genomic Era III: Regulation of Gene Expression Studies (RNA and miRNA)

- 9.1. Introduction to RNA-seq
 - 9.1.1. Technique Description
 - 9.1.2. Advantages over Expression Arrays
 - 9.1.3. Limitations
- 9.2. Experimental Design for RNA-seq Studies
 - 9.2.1. Concept of *Randomization* and *Blocking*
 - 9.2.2. Biological Replicas vs. Technical Replicas
 - 9.2.3. Number of Replicas
 - 9.2.4. Sequencing Depth
 - 9.2.5. Type of Library
- 9.3. Quality Control for RNA-seq
 - 9.3.1. Quality Metrics for RNA-seq
 - 9.3.2. Programs Designed for RNA-seq Quality Control
- 9.4. RNA Alignment and Quantification
 - 9.4.1. Reference Genome (*Genome-based*)
 - 9.4.2. Reference Genome (*Transcriptomics-Based*)
- 9.5. De Novo Assembly and RNA Annotation
 - 9.5.1. *Pipeline* without Reference Transcriptome
 - 9.5.2. Annotation of Coding and Non-Coding Transcripts
- 9.6. Differential Expression with RNA-seq
 - 9.6.1. Standardization
 - 9.6.2. Latent Variable Elimination
 - 9.6.3. Programs and Statistics Methods
 - 9.6.4. Functional Enrichment
- 9.7. Other Applications of RNA-seq Technology
 - 9.7.1. *Alternative Splicing* Detection
 - 9.7.2. Chimera Transcript Detection
 - 9.7.3. Mutation Detection
 - 9.7.4. *Allele-specific Expression* Detection

- 9.8. *Small* RNA-seq
 - 9.8.1. *Small* RNA-seq Library Building
 - 9.9.8.1. Quality Control for *Small* RNA-seq
 - 9.8.2. Alignment and Quantification for *Small* RNA-seq
 - 9.8.3. miRNA Annotation
 - 9.8.4. miRNA targets
- 9.9. Gene *Co-expression Networks*
 - 9.9.1. Concept of Gene *Co-expression Networks*
 - 9.9.2. Differential Co-expression vs. Differential Expression
 - 9.9.3. *Weighted* Gene *Co-expression Networks Analysis* (WGCNA)
 - 9.9.4. Gene *Co-expression Networks* Visualisation
- 9.10. Gene Expression Regulation Analysis in Venous Thromboembolism (VTE)
 - 9.10.1. A Bit of History
 - 9.10.2. Relevant Studies on VTE
 - 9.10.3. Latest Studies Results
 - 9.10.4. Clinical Implications in the Results
 - 9.10.5. Practical Examples and Exercises

Module 10. Predictive Models

- 10.1. Statistical Learning
 - 10.1.1. Estimating f
 - 10.1.2. Supervised and Unsupervised Learning
 - 10.1.3. Regression and Classification Problems
 - 10.1.4. Linear and Non-Linear Models
- 10.2. Data Pre-Processing
 - 10.2.1. Standardization
 - 10.2.2. Imputability
 - 10.2.3. Atypical Values (*Outliers*)
- 10.3. Linear Regression
 - 10.3.1. Linear Models
 - 10.3.2. Variance Analysis (ANOVA)
 - 10.3.3. Mixed Effects Models

- 10.4. Classification
 - 10.4.1. Logistic Regression
 - 10.4.2. Linear Discriminant Analysis
 - 10.4.3. K Nearest Neighbors (KNN)
- 10.5. Resampling Methods
 - 10.5.1. Cross Validation
 - 10.5.1.1. Validation Set or Test
 - 10.5.1.2. *Leave One Out* Cross Validation
 - 10.5.1.3. Cross Validation of k Iterations (*k-Fold*)
 - 10.5.2. *Bootstrap*
- 10.6. Linear Model Selection
 - 10.6.1. Nested Model Comparison
 - 10.6.2. *Stepwise* Algorithms
 - 10.6.3. Linear Model Diagnosis
- 10.7. Regularization
 - 10.7.1. The Curse of Dimensions
 - 10.7.2. Principal Component Regression
 - 10.7.3. Partial Least Squares Regression
 - 10.7.4. *Shrinkage* Methods
 - 10.7.4.1. *Ridge* Regression
 - 10.7.4.2. Lasso
- 10.8. Methods Based on Decision Trees
 - 10.8.1. Introduction to Decision Trees
 - 10.8.2. Types of Decision Trees
 - 10.8.2.1. *Bagging*
 - 10.8.2.2. *Random Forests*
 - 10.8.2.3. *Boosting*
- 10.9. Support Vector Machines
 - 10.9.1. Maximum Margin Classifiers
 - 10.9.2. Support Vector Machines
 - 10.9.3. Hyperparameter Tuning

- 10.10. Unsupervised Learning
 - 10.10.1. Main Component Analysis
 - 10.10.2. *Clustering* Methods
 - 10.10.2.1. *K-Means* Clustering
 - 10.10.2.2. Hierarchical Clustering



A unique, key, and decisive 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.

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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

The Professional Master's Degree in Clinical, Medical and Health Care Management guarantees students, in addition to the most rigorous and up-to-date education, access to a Professional Master's Degree issued by TECH Technological University.



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Successfully complete this program and receive your university qualification without having to travel or fill out laborious paperwork”

This **Professional Master's Degree in Genomic and Precision Medicine in Hematology: Thrombosis** 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** diploma issued by **TECH Technological University** via tracked delivery*.

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

Title: **Professional Master's Degree in Genomic and Precision Medicine in Hematology: Thrombosis**

Official Number of Hours: **1,500 h.**



*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.

future

health confidence people

education information tutors

guarantee accreditation teaching

institutions technology learning

community commitment

personalized service innovation

knowledge present online training

development language

virtual classroom

tech technological
university

Professional Master's Degree

Genomic and Precision
Medicine in Hematology:
Thrombosis

- » Modality: online
- » Duration: 6 months
- » Certificate: TECH Technological University
- » Dedication: 16h/week
- » Schedule: at your own pace
- » Exams: online

Professional Master's Degree

Genomic and Precision Medicine in Hematology: Thrombosis

