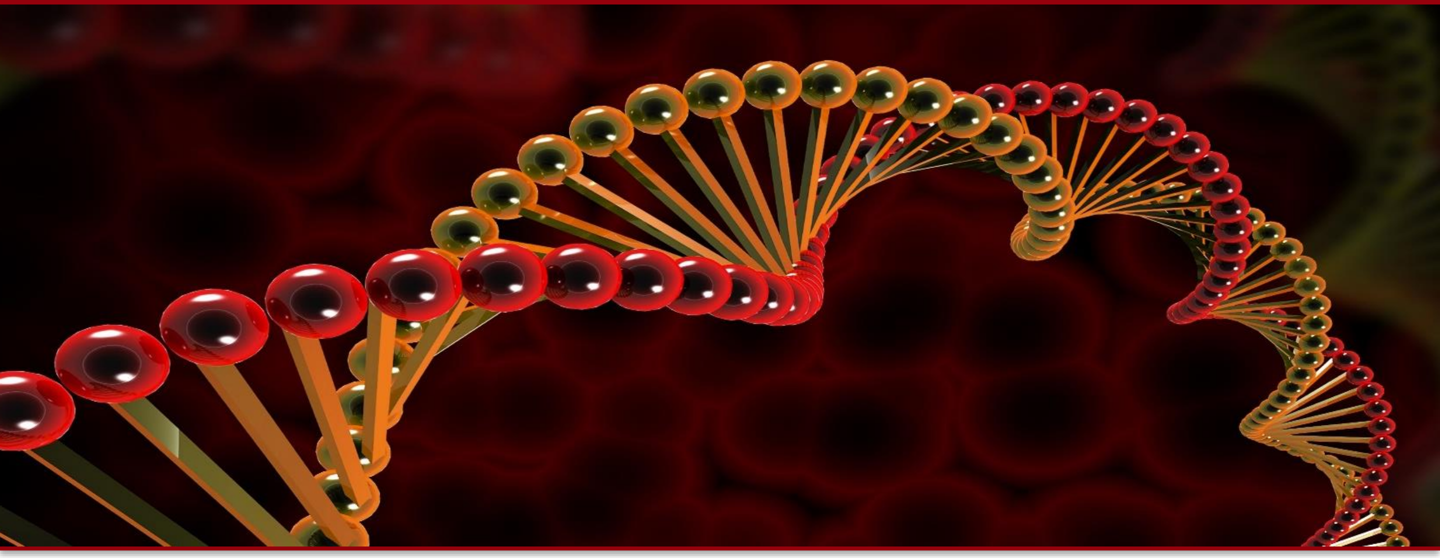
1222·2022 800 ANNI

Università degli Studi di Padova

DiSCOG

University of Padova
Department of Surgery, Oncology and Gastroenterology

PhD Course in Clinical and experimental Oncology and Immunology



Genetic evolution of cancer and access to "Big Data": an introductory course

Zoom meeting: ore 15:00
https://unipd.zoom.us/j/89283271332

OTTOBRE 2021

01/10/2021, 15:00 - Lecture 1. DARWINIAN EVOLUTION

Andrea Sottoriva, *Centre for Evolution and Cancer of The Institute of Cancer Research, London (UK)*

We will introduce the fundamental concepts behind Darwin's theory of evolution and how these ideas have developed in the last 150 years into the so-called 'modern evolutionary synthesis' where evolutionary biology and genetics meet to form molecular evolution and explain the evolution of species, from bacteria to humans.

15/10/2021, 15:00 - Lecture 2. CLONAL EVOLUTION IN CANCER

Andrea Sottoriva, *Centre for Evolution and Cancer of The Institute of Cancer Research, London (UK)*

We will present how tumours emerge through a process of somatic evolution and how they transform from benign, to malignant, to metastatic. We will also study how this process leads to inter-patient and intra-tumour heterogeneity.

29/10/2021, 15:00 - Lecture 3. TREATMENT RESISTANCE

Andrea Sottoriva, *Centre for Evolution and Cancer of The Institute of Cancer Research, London (UK)*

Arguably the biggest problem in cancer therapy today is the emergence of resistance to treatments. We will show how evolution is the central conceptual framework to understand therapy failure, when driven by genetic, non-genetic and even non-Darwinian mechanisms.

NOVEMBRE 2021

12/11/2021, 15:00 - Lecture 4. WHAT IS A CANCER DRIVER GENE?

Andrea Sottoriva, *Centre for Evolution and Cancer of The Institute of Cancer Research, London (UK)*

We will introduce the concept of cancer driver, how driver genes are identified and functionally validated. We will focus on DNA changes in cancer driver genes discovered by large-scale genomic studies and use cBioPortal (cbioportal.org) and IntoGen (intogen.org) to actively explore the huge amount of available data.

26/11/2021, 15:00 - Lecture 5. WHAT IS A CANCER VULNERABILITY?

Francesco Iorio, *Wellcome Sanger Institute, Hinxton - Cambridgeshire (UK)*

How do we identify novel drug targets in cancer by exploiting vulnerabilities of cancer cells in terms of their functional dependencies on certain genes, or their oncogene addictions. We will introduce the fundamental concepts of essentiality, dependency, and actively explore the DepMap portal (depmap.org) to learn how to extract useful information from these large-scale CRISPR and RNAi screenings.

DICEMBRE 2021

10/12/2021, 15:00 - Lecture 6. IS THE RIGHT TIME FOR A NEXT GENERATION HISTOPATHOLOGICAL DIAGNOSTICS?

Matteo Fassan, *Dipartimento di Medicina – Università degli Studi di Padova*

How has evolved the histopathological report in the last decade with particular focus on the integration of next generation sequencing data in the clinic and the implementation of digital pathology. The evolution of the clinical impact of the pathology report in the personalized medicine era.

GENNAIO 2022

14/01/2022 , 15:00 - Lecture 7. DIGITAL PATHOLOGY WITH ARTIFICIAL INTELLIGENCE

NICHOLAS TRAHEARN, ***Centre for Evolution and Cancer of The Institute of Cancer Research, London (UK)***

We will introduce the concept of Deep Learning for image analysis. We will provide an overview of how a neural network is constructed and trained. We will demonstrate application of Deep Learning to histopathological images to automatically classify millions of single cells and construct geographical tumour maps.

28/01/2022, 15:00 - Lecture 8. USING R FOR DATA ANALYSIS

ANGELA GRASSI, ***Istituto Oncologico Veneto***

Review of some key aspects of R programming in view of the next lecture.

FEBBRAIO 2022

11/02/2022, 15:00 - Lecture 9 (ADVANCED).

MACHINE LEARNING AND POPULATION GENETICS METHODS FOR GENOMIC DATA ANALYSIS

GIULIO CARAVAGNA, ***Centre for Evolution and Cancer of The Institute of Cancer Research, London (UK)***

Whole-genome sequencing is being enrolled as an instrument for precision medicine in many countries. In this advanced course, we will deep dive into the tools used to analyse genomic data in cancer, specifically whole-genome sequencing, to extract functional and clinical information in a way that can inform precision medicine. Specifically, we will use data-driven machine learning approaches combined with model-based population genetics theory (requires solid background in R and statistics).