



IGA TRAINING 2018

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About us

The **Institute of Applied Genomics (IGA)** is an International Centre of Research dedicated to the study of **genetics** and **genomics** of living organisms.

Our scientific research relies on a number of disciplines ranging from genetics to **structural genomics, molecular biology** and **computational biology**. IGA was founded in 2006 by four scientists from the University of Udine.

Initially, IGA focused on **genome sequencing projects** of crop species. The genome of grapevine, citrus, peach, olive, coffee and Norway spruce were sequenced and assembled at IGA as part of international collaborative projects.

With the revolution of NextGen sequencing technology, IGA has expanded its research into the fields of **genetic diversity, genome biology**, and other **innovative solutions** for agriculture. The range of plant species investigated has widened to include maize, barley, wheat, melons, sweet cherries, and the poplar and conifer species.

Since 2009, its subsidiary IGA-Tech offers **customized services** for NextGen Sequencing and Data Analysis in **all living organisms** and **biological systems**. The latest investments in technology and the involvement in flagship national projects put IGA at the forefront of **metagenomics** and **epigenomics**.

Next Generation Sequencing (NGS) has revolutionized the approach to genomic studies enabling the sequencing of billions of bases in massively parallel reactions. These new sequencing technologies collectively referred to as "ultra-deep" sequencing or "massively parallel" sequencing are currently used for SNP discovery, detection of structural variants, genome-wide measurement of transcripts levels and many other applications, and are revolutionizing biological research.

Since 2008 IGA and our spin-off IGA Technology organize courses to train researchers and professional in providing high-level training.

DATA CRUNCHING: FROM HELL TO HEAVEN

25 > 27 JULY 2018

This course

This **practical** course is addressed to **researchers with a background in biology** willing to perform **basic analysis** on next generation sequencing data. Each topic will consist of frontal introduction and practical work to enable participants to **familiarize** with the tools and the Unix environment. Hands-on work will be performed by simulating a **real analysis** on data generated by an Illumina platform. The declared aim of this course is to **become self-sufficient in basic NGS data analysis**. Teachers and tutors will assist each participant to reach the objectives of the course.

Course overview

July 25th 9:00-18:00 Introduction to Unix and shell scripting. Quality control. Trimming and filtering. Alignment of short reads to a reference. Summary statistics.

July 26th 9:00-18:00 Approaches for variant discovery: detection of SNPs, indels and structural variants (Theoretical and practical).

July 27th 9:00-13:00 Analysis of RNAseq data (Theoretical and practical).

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Course Scientific Directors

Michele Morgante – Fabio Marroni.

Lecturers

Gabriele Magris - Fabio Marroni - Sara Pinosio.

Who should attend

The course is designed for biologists or data analysts with no or little experience in analysis of NGS data. No previous experience is required.

Venue

Università di Udine Polo Scientifico Rizzi, Via delle Scienze 208, Aula Beta3 – Udine.

Registration deadline

The registration is open from 25th May to 15th July 2018.

Fee

400 Euros within 30th June 2018

500 Euros from 1st July 2018

The fee includes 2 coffee break/day, lunches, course material.

How to register

To register fill in the [online form](#)

What makes our course different

- ✓ Maximum 20 participants
- ✓ More time to practice what you have learnt
- ✓ Qualified tutors to assist learners on the spot.

What people think about our course

A great overview on bioinformatics tools and applications - Good knowledge to set experiment design-

A complete overview of NGS tools.

Contact

Email misdariis@appliedgenomics.org - T.+39 0432-629782

“Life can only be understood backwards; but it must be lived forwards.”

Søren Kierkegaard

EPIGENETICS: ON THE TOP OF GENETICS

4 > 7 SEPTEMBER 2018

This course

This **practical** course is addressed to researchers with a background in biology willing to perform **basic analysis of epigenetic data**. We will focus on data produced by next generation sequencing. Topics will include, but will not be limited to: DNA methylation, histone modifications, small RNA, chromatin conformation. Analysis will be performed on study cases in humans and plants.

Each topic will consist of frontal introduction and practical work to enable participants to familiarize with the tools and the Unix environment. Hands-on work will be performed by **simulating real analyses** on data generated by an Illumina platform. The declared aim of this course is to **become self-sufficient in epigenetic data analysis**. Teachers and tutors will assist each participant to reach the objectives of the course.

Course overview

September 4th 9:00-18:00: Unix and shell scripting. Study of DNA methylation: analysis of BS-seq data (Part I).

September 5th 9:00-18:00: Study of DNA methylation: analysis of BS-seq data (Part II).

September 6th 9:00-18:00: Study of histone modifications: analysis of ChIP-seq data

September 7th 9:00-16:00: Analysis of small RNA. Analysis of chromatin conformation via Hi-C seq.

Course Scientific Directors

Michele Morgante – Fabio Marroni

Lecturers

Emanuele de Paoli - Mattia Forcato - Federico Zambelli.

Who should attend

The course is designed for biologists or data analysts with no or little experience in analysis of NGS data.

Familiarity with the main concepts and procedures of epigenetics is assumed. Some familiarity with Linux is beneficial but not required.

Venue

Università di Udine Polo Scientifico Rizzi, Via delle Scienze 208, Aula Beta3 – Udine

Registration deadline

1 June - 15 August 2018

Fee

400 Euros within 31st July 2018:

500 Euros from 1st August 2018:

The fee includes 2 coffee break/day, lunches, course material.

How to register

To apply please fill in the [online form](#)

Contact

misdariis@appliedgenomics.org - T. +39 0432-629782.

What makes our course different

- ✓ Maximum 20 participants
- ✓ More time to practice what you have learnt
- ✓ Qualified tutors to assist learners on the spot

“The world will not be inherited by the strongest, it will be inherited by those most able to change.”
Charles Darwin